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Detection of tissue-specific genes and computational analysis of testis-specific gene expression regulatory regions

（組織特異的遺伝子の検出と精巣特異的遺伝子の発現制御領域のコンピュータを使った解析）

by

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Contents

LIST of ABBREVIATIONS

bp	base pair(s)
cAMP	cyclic adenosine 3′, 5′-monophosphate
cDNA	DNA complementary to RNA
CRE	cAMP response element
CSS	cardiac specific sequence
GNF	Genomics Institute of the Novartis Research Foundation
S.D.	standard deviation
TPA	12-*O*-tetradecanoylphorbol-13-acetate
TRE	TPA-responsive element
TSS	transcription start site
UCSC	University of California, Santa Cruz, USA
A	Adenine
T	Thymine
G	Guanine
C	Cytosine
R	Guanine or Adenine (puRine)
Y	Thymine or Cytosine (pYrimidine)
H	Adenine or Thymine or Cytosine (not Guanine, H follows G)
V	Guanine or Cytosine or Adenine (not Thymine (Uracil), V follows U)
B	Guanine or Cytosine or Thymine (not Adenine, B follows A)
N	Any nucleotide (aNy)

ABSTRACT

Accumulation of microarray data has enabled the computational analysis of gene expressions in various tissues. We have collected genes showing tissue, organ or cell specific genes using GNF mouse gene expression database. Thereafter, we searched for features of regulatory regions of testis-specific genes, because the genes showing testis-specific expression are the most abundant among the genes exhibiting tissue-specific expression, and no systematic study has been conducted for over-represented motifs within their regulatory regions. We have identified 117 over-represented 8 nucleotide sequences (8-mers) that appeared 2,648 times within the regulatory regions of 634 testis-specific genes. Of these, 64 over-represented 8-mers were significantly more frequent in the regulatory regions of testis-specific genes than in those of non-testis-specific genes. In this group of 8-mers, 4 8-mers differed from the canonical cAMP response element (CRE) 8-mer by 1 nucleotide, but appearance frequency of the canonical CRE in the regulatory regions of testis-specific genes is not significantly differ from those of non-testis-specific genes. We consider that these CRE-like 8-mers participate in the regulatory expression of testis-specific genes to a greater extent than the canonical CRE 8-mer.

1. INTRODUCTION

The difference of cell types in a multicellular organism comes from the difference of gene expression. Gene expression can be regulated at many of the steps in the pathway from DNA to protein, such as transcriptional control, RNA processing control, RNA transport and localization control, translational control, mRNA degradation control, and protein activity control. For most genes, the major cause of the regulation is the transcriptional control. The transcriptional control of each gene is, whether complex or simple, done by the interactions between gene regulatory proteins and short stretches of DNA of defined sequence in a regulatory region relatively near the site where transcription begins (Molecular biology of The Cell, fourth edition chapter 7).

Now, we are able to search for such DNA sequences from the regulatory regions based on statistical methods, because of the determination of genomic sequences of more than 48 eukaryotes (http://www.ensembl.org/ on 2008' Nov. 21) and transcription start sites (TSSs) of genes. FitzGerald et al. (2004) used the database of the TSSs (dbTSS, Suzuki et al., 2004) to collect human promoter sequence and investigated the distribution of 8 nucleotide sequences (8-mers). They found that 156 8-mers which cluster very significantly near the TSS could be placed into 9 groups of related sequences and 7 of them are found to be known transcription factor binding sites.

Further, microarray technology enabled us to know the expression level of many genes in many different tissues. This technology can be used to find genes with unique expression pattern, such as tissue-specific genes. For example, Bono et al.

(2003) identified 7,206 separate mRNA clones that satisfied stringent criteria for tissue-specific expression based on the expression profile of 57,931 clones on 20 mouse tissues using cDNA microarrays.

In this way, we are able to collect tissue-specific genes and their regulatory regions. We started our research detecting tissue-specific genes. Thereafter, we used testis-specific genes to investigate the mechanism of regulation of tissue-specific gene expression, because spermatogenesis is an excellent model for studying the regulation of gene expression during differentiation (Wolgemuth and Wartrin, 1991), and because no systematic study has been conducted for frequently appearing sequences within these regulatory regions to search for the candidates of transcription factor binding sites.

To find these motifs, we initiated the systematic isolation of testis-specific genes based on the method of Bono et al. (2003) with more stringent parameters, using the latest gene expression database of the Genomics Institute of the Novartis Research Foundation (GNF), which provides gene expression data of 36,182 mouse genes obtained from 2 independent experiments with 61 tissues, organs, and cells (Su et al., 2004). Functions of these testis-specific genes were checked, and then the regulatory sequences were extracted based on the positional information of the TSS (Suzuki et al., 2004). Then we attempted to identify the regulatory motifs participating in the testis-specific gene expression on the basis of the following working hypotheses: (i) Most of the regulatory motifs are localized within the 5′-regulatory regions between –300 bp and +50 bp ([–300 to +50]) relative to the TSSs (FitzGerald et al., 2004), (ii) a length of 8 nucleotides (8-mer) is adequate for searching the regulatory motifs (FitzGerald et al., 2004), and (iii) most of the significantly over-represented motifs are regulatory motifs.

To find significantly over-represented motifs within these regulatory regions, we conducted the following two-step analysis. First, to find these significantly over-representing 8-mers, we estimated the expected appearance of each 8-mers from the nucleic content of these regions. If appearance of an 8-mer is significantly more frequent than the expected one, the 8-mer is regarded as over-represented 8-mer. After collecting 8-mers showing the greatest significance in each regulatory region, we proceeded to the next step: we compared the appearance frequency of these 8-mer per regulatory region among testis-specific genes with those among non-testis-specific genes. If an 8-mer appears significantly more frequent in the regulatory region of testis-specific genes than in those of non-testis-specific genes, the 8-mer seems to be related to the expression of testis-specific genes.

2. METHODS

2.1. Detection of tissue-specific genes

Tissue-specific genes were selected from the Mouse GNF1M (MAS5-condensed) expression database, which was downloaded from the GNF website (http://wombat.gnf.org/index.html). This database contains the gene expression data of 36,182 mouse genes obtained from 2 independent experiments with 61 tissues, organs, and cells (hereafter, they will be referred to simply as tissues). The gene expression intensities of the 2 experiments were averaged, and thereafter log-transformed. Since each gene has expression data from 61tissues, these data for each gene were normalized. Bono et al. (2003) denoted the gene as tissue specific if the normalized value exceeded mean + 3 standard deviation (S.D.) for their cDNA microarray data and mean + 2 S.D. for Affy chips. However, we denoted the gene as "tissue-specific" if the normalized value in the testis exceeded mean + 4 S.D., for more stringent evaluation. We will refer to this value as the tissue specificity of the gene.

2.2. Annotation of tissue-specific genes

We downloaded the Chip Annotation Mouse GNF1M from the abovementioned GNF site and searched for either the FANTOM cDNA clone ID (Carninci et al., 2005) or reference mRNA sequence (RefSeq) ID corresponding to each of the selected tissue-specific genes. Subsequently, the gene annotations were checked in the GNF annotation data and in the FANTOM 3 and RefSeq databases.

Specially, for testis-specific genes with no available functional annotations, we performed a BLAST search against the National Center for Biotechnology Information

(NCBI) non-redundant (nr) and/or RefSeq database and attempted to identify homologous genes having functional annotations (Altschul et al., 1997). We classified the genes with no functional annotations into 2 groups: the “hypothetical protein” group, which comprised genes encoding unidentified proteins with more than 100 amino acid residues, and the “unclassifiable gene” group, which comprised genes encoding unidentified proteins either with fewer than 100 amino acid residues or those without any reading frames.

2.3. Extracting the 5′-regulatory regions

Next, we checked whether the selected cDNA clones have experimental evidence to cover the intact 5′-ends either in the RIKEN FANTOM3 database (Carninci et al., 2005) or in the database of transcriptional start sites (dbTSS; http://dbtss.hgc.jp/; Suzuki et al., 2004). FitzGerald et al. (2004) searched for regulatory motifs within the [–2500 to +500] region and showed in the figure of FitzGerald et al. (2004) that they mainly appear within the genomic [–300 to +50] regions relative to the TSS; therefore, we referred to these regions as the regulatory regions in our study. These regulatory regions were extracted from the genomic sequence of mouse mm5 provided by the University of California, Santa Cruz, USA (UCSC) (Karolchik et al., 2003). When the regulatory regions of 2 testis-specific genes were found to overlap on the same strand, the region with the higher testis specificity was selected as the representative region. All regulatory regions without a complete sequence were excluded from further analysis.

2.4. Selection of over-represented 8-mers

Over-represented 8-mers within the extracted regulatory regions were selected as follows: (i) The appearances of each possible 8-mer (4^8 = 65,536 8-mers) within the extracted regulatory regions of testis-specific genes were counted; (ii) a set of the shuffled sequences corresponding to each extracted regulatory region was generated from the original regulatory regions by random sampling with replacement (Matsumoto and Nishimura, 1998); (iii) the number of appearances of all possible 8-mers in the shuffled sequence set were counted; (iv) after repeating steps (ii) and (iii) 10,000 times, the average appearance and variance were calculated for each possible 8-mer; and (v) to estimate the statistical significance with regard to the over-representation of each 8-mer, the Z value was calculated using the following formula:

$$\mathrm{Z}_i = (x_{io} - \bar{x}_i)/\sqrt{v_i},$$

$\bar{x}_i$ and v_i were calculated as follows:

$$\bar{x}_i = \frac{1}{n}\sum_{j=1}^{n} x_{ij} \text{ and}$$

$$v_i = \frac{n\sum_{j=1}^{n} x_{ij}^2 - \left(\sum_{j=1}^{n} x_{ij}\right)^2}{n(n-1)}$$

In this equation, Z_i is the Z value of the 8-mer i, x_{io} is the observed number of appearances of the 8-mer *i* in the extracted regulatory regions, $\bar{x}_i$ $\bar{x}_i$ is the average number of appearances of the 8-mer *i* in the shuffled sequences, v_i is its variance, *n* is the number of trials (*n* = 10,000 in this study), and x_{ij} is the number of appearances of the 8-mer *i* at trial *j*. Finally, for each selected testis-specific regulatory region, the 8-mer showing the highest Z value was considered as the representative of the gene and these representative 8-mers were collected for each of the regulatory regions of the testis-specific genes.

2.5. Comparison of the 8-mer frequency within regulatory regions of testis-specific genes with those of non-testis-specific genes.

To confirm if the 8-mers were over-represented particularly within the regulatory regions of testis-specific genes, we examined the frequency of 8-mers within regulatory regions of other mouse genes with testis specificities ranging from mean –1.0 S.D. to +1.0 S.D. (non-testis-specific genes). Since we can expect the appearance frequency of each 8-mer to be low, we presumed that their appearance is under Poisson distribution and used the following formulae to determine whether they were significantly more frequent within the regulatory regions of testis-specific genes than within those of non-testis-specific genes:

$\mathrm{Z}_i = (\mathrm{O}_i - \lambda_i)/\sqrt{\lambda_i}$ and

$\lambda_i = n\mathrm{P}_i$

where n is the number of testis-specific genes, P_i is the appearance ratio of the 8-mer i within regulatory regions of the non-testis-specific genes, and O_i is the number of occurrences of 8-mer i within regulatory regions of testis-specific genes. Z_i represents the significance of the 8-mer. A positive value means that the 8-mer appears more frequently within the regulatory regions of testis-specific genes than within those of non-testis-specific genes. We refer to this value as the testis association level of the 8-mer.

3. RESULTS

3.1. Detection of tissue-specific genes

Starting from the GNF gene expression data of 36,182 mouse genes obtained from 61 tissues, we obtained list of tissue-specific genes (**Appendix Table 1**). Among these tissues examined, top 5 tissues most abundantly exhibit their specific genes are testis (1,012 genes), pancreas (431), oocyte (371), fertilized egg (326), and liver (233) (**Fig. 1**, **Table 1**). Number of testis-specific genes is more than twice of that of the pancreas specific genes, while number of pancreas-specific genes is only about 1.2 times more abundant than that of oocyte-specific genes (**Table 1**).

3.2. Selection of testis-specific genes which can be used for the following analysis

Among the 1,012 testis-specific genes, 118 have neither FANTOM cDNA clone nor RefSeq IDs, and the IDs of 18 cDNAs are found to be duplicated. We obtained 876 cDNA clones of testis-specific genes, of which 719 have experimental evidence to cover the intact 5′-ends. Finally, we isolated 634 regulatory regions [–300 to +50] from the UCSC mm5 mouse genomic sequences that are completely sequenced and do not overlap with other testis-specific regulatory regions (**Fig. 2**, **Appendix Table 2**). In the same way, we obtained regulatory regions of 8,466 non-testis-specific genes.

We annotated these 634 testis-specific genes and categorized them into 5 groups. The first group contains 193 genes (30.4%) encoding previously known proteins; the second, 91 genes (14.4%) encoding proteins similar to previously known proteins; the third, 160 genes (25.2%) encoding proteins containing previously known domains, structures, profiles, or motifs; the fourth, 142 genes (22.4%) encoding hypothetical proteins; and the fifth, 48 genes (7.6%) encoding proteins either with less than 100 amino acid residues or with no coding regions (**Fig. 3**, **Appendix Table 2**).

3.3. Classification of the over-represented 8-mers

We identified 117 over-represented 8-mers as representatives for testis-specific genes (**Table 2**). Each of these 8-mers appears in at least 1 of the 634 regulatory regions and appears a total of 2,648 times (**Table 2**, **Appendix Table 2a**). Many 8-mers that relate to regulatory expression are known to cluster within the [–100 to –1] region (FitzGerald et al., 2004). Indeed, we determined that 1,163 of the 2,648 8-mers (43.9%) appear within this region (**Table 2**). The 117 8-mers are tentatively classified into 3 groups—A, B, and C—according to the testis association level of the 8-mers.

Group A contains 8-mers that are significantly more frequent within the regulatory regions of 634 testis-specific genes than within those of 8,466 non-testis-specific genes (testis association level > 2). This group contains 64 members including 10 reverse complement pairs, i.e., more than half of the representative 8-mers belong to this group. The incidence of 8-mers within the [–100 to –1] region relative to that within other regions increases with the testis association level of the 8-mer (**Table 2**). The most testis associated 8-mer is A1. This 8-mer differs from the canonical cAMP response element (CRE) by 1 nucleotide (Mayr and Montminy, 2001). There are 3 other 8-mers, in this group A, that are different from the canonical CRE by one nucleotide (A1*, A16, and A16*). However, the canonical CRE itself does not belong to group A, but belongs to group B (**Table 2 B7**). The 2nd most testis associated 8-mer is A2. We found that A2*, which is the reverse complement sequence of A2, covers a part of cardiac specific sequence (CSS)-A defined as

5′-CCATTGTGAAGGAC-3′, which is one of the three protected region of DNase-I footprinting assay of CSS domain (Dhar et al., 1997). Hereafter, we will tentatively call A2 and A2* as partial CSS-A. We also found that CCTAGCAA (A17) and CCATGGCA (A24) cover parts of X-box sequence defined as 5'-GTNRCC(0-3N)RGYAAC-3' (where N is any nucleotide, R is a purine, and Y is a pyrimidine) (vanWert et al., 2008). We will tentatively call A17 and A24 as partial X-box. Group A also contains TCACAGAG (A13*). This 8-mer covers the ZII domain of TRE derived from the BZLF1 promoter of the Epstein-Barr virus. Its sequence is 5′-AAACCATGACATCACAGAG-3′ (Flemington and Speck, 1990). We will tentatively call A13* and its reverse complement 8-mer A13 as partial ZII.

Group B contains 8-mers whose appearance ratios in testis-specific regulatory regions do not significantly differ from those in non-testis-specific genes (-2 ≤ testis association level ≤ 2). This group contains 46 members including 5 reverse complement pairs. The canonical CRE 8-mer belongs to this group (**Table 2 B7**).

Group C contains 8-mers that are significantly less frequent in the regulatory regions of testis-specific genes than in those of non-testis-specific genes (testis association level < –2). This group contains 7 members including 3 reverse complement pairs (**Table 2**). All the 8-mers in this group cover parts of Sp1 binding sites (Letovsky and Dynan, 1989).

3.4. Conservation of the flanking region of highlighted 8-mers

Among these representative 8-mers, we searched for 8-mer groups in which an 8-mer overlaps with the other 8-mer by 4 or more nucleotides within the regulatory regions of testis-specific genes. We found that there are 35 such groups appearing within equal to or more than 4 testis-specific regulatory regions. Among these groups, 9 groups contain CRE-like 8-mers, 6 groups contain partial ZII, and 2 groups contain partial CSS-A (**Table 3**), but canonical CRE does not form such groups. We also investigated frequencies of bases surrounding CRE-like, partial CSS-A, partial X-box, and partial ZII 8-mers within the regulatory regions of testis-specific genes and those of non-testis-specific genes. We found that canonical CRE and CRE-like sequences except for A1 within testis-specific regulatory regions conserve tgTGAxxTCAca (xx = CA, CC, GG, and CG) while those within non-testis-specific regulatory regions do not (**Fig. 4B-E**). Instead, A1 within testis-specific regulatory regions conserves ngTGATGTCAca, while within non-testis-specific regulatory regions, it conserves only gTGATGTCAc (**Fig. 4A**). The partial ZIIs conserve vtgangTCACAGAGgng and bntCTCTGTGAcntnagc, which are similar to CRE-like 8-mer (underlined region) (**Fig. 4F, G**), where V represents Guanine or Cytosine or Adenine (not Thymine); and B represents Guanine or Cytosine or Thymine (not Adenine). The partial CSS-As within testis-specific regulatory regions conserve gnhgacnTCACAATGvvha and vnngcCATTGTGAcgt, where H represents Adenine or Thymine or Cytosine (not Guanine). These sequences do not match the sequence of CSS-A (5′-CCATTGTGAAGGAC-3′) (**Fig. 4H, I**). We found that the partial X-boxes within testis-specific regulatory regions conserve sequences that are similar to the X-box consensus sequences (5'-GTNRCCNRGYAAC-3' in **Fig. 4J**, and 5'-GTNRCCNNrGYAAC-3' where r is substituted to T in **Fig. 4K**).

4. DISCUSSION

The number of testis-specific genes is significantly larger than any other tissue-specific genes investigated (**Table 1**). This result clearly shows that testis is a special tissue. Large number of testis-specific genes suggests the requirement of additional genes to perform continuous meiosis and morphogenesis to generate sperms in testis.

Hong et al. (2005) isolated 467 testis-specific genes from the mouse round spermatid UniGene library and annotated the functions of 149 genes (31.9%). Bono et al. (2003) selected 1,749 testis-specific genes using RIKEN cDNA microarrays and profiled their molecular functions by Gene Ontology, and they found that functions could not be assigned to 1,001 of the 1,749 genes (57.2%). In the present study, we selected 634 testis-specific genes, of which 193 (30.4%) encoded known proteins and 91 (14.4%) encoded proteins similar to known proteins. Nevertheless, the functions of 190 genes (30.0%) have not yet been elucidated (**Fig. 3**). These results indicate that although the knowledge regarding testis-specific genes has been accumulated, many genes are yet to be identified.

We identified 117 over-represented 8-mers from the regulatory regions of the 634 testis-specific genes. These 8-mers appear a total of 2,648 times within these regions (**Table 2**, **Appendix Table 2a**). Since all these 8-mers are significantly over-represented within the regulatory regions of testis-specific genes, there must be some reasons for their frequent occurrence.

Group A members in **Table 2** are highly testis associated 8-mers. In this group, 8-mers with high testis association level must be regulatory motifs for testis specific gene expression, because appearance of the 8-mers within [–100 to –1] region tend to increase with their increase in testis association level, and many 8-mers related to regulatory expression are known to cluster within this region (FitzGerald et al., 2004). We found that the most testis associated 8-mer is CRE-like TGATGTCA (A1). We also found 3 other CRE-like 8-mers and their flanking sequences in this group, but the canonical CRE sequence (TGACGTCA) itself is categorized in group B (B7). This result suggests that the non-canonical CREs such as TGATGTCA (A1), TGACCTCA (A16), and these reverse complement sequences participate in the regulatory expression of the testis-specific genes to a greater extent than the canonical CRE. This idea is consistent with the result of the previous study in which CpG-containing sequences are enriched in promoters of housekeeping genes (Rozenberg et al., 2008). Since TGATGTCA is not affected by methylation (Zhang et al., 2005; Smith et al., 2007), the substitution of the central dinucleotide of CRE from CpG to TpG may help in escaping the methylation-induced silencing. It is conceivable that this substitution may also change the pattern of gene expressions by altering the affinity of the sequences to the CRE-binding proteins. We also found that canonical CRE and CRE-like 8-mer conserve partial palindromic 12-mer tgTGAxxTCAca (xx= CA, CC, GG, and CG) only within testis-specific regulatory regions (**Fig. 4B-E**). CRE-like A1 conserves ngTCATGTCAca only within testis-specific regulatory regions (**Fig. 4A**). This result suggests that CRE-binding proteins for non-testis-specific genes recognize only the 8 nucleotide sequence of CRE (TGAxxTCA; mainly xx=CG), while testis-specific CRE-binding proteins (probably, the protein will be CREM, because CREM is known as a master gene that govern post-meiotic gene expression; Sassone-Corsi, 1998) recognize this partial palindromic 12 bp nucleotide sequence (tgTGAxxTCAca; xx=TG, CA, CC or GG), or CRE-like 8-mer TGATGTCA.

The reverse complement 8-mer of the 2nd most testis associated 8-mer (A2*: CATTGTGA) is also highly testis associated 8-mer. This 8-mer covers a part of CSS-A defined as 14bp sequence: 5′-CCATTGTGAAGGAC-3′, which is one of the three protected region of DNase-I footprinting assay of CSS domain (Dhar et al., 1997). But, flanking sequence of partial CSS-As do not cover the whole 14 bp sequence (**Fig. 4H, I**). Instead, A2 appear together with CRE-like TGATGTCA (A1) 4 times (**Table 3-2**) and A2* appear together with A1-like sequence (TTGTGATG) 4 times (**Table 3-15**). These results suggest that A2 and A2* are not the parts of CSS-A sequence, but relate to CRE-like sequences.

A17 (CCTAGCAA) and A24 (CCATGGCA) cover parts of consensus sequence of relatively abundant gene promoter regulatory motif: X-box defined as 5'-GTNRCC(0-3N)RGYAAC-3' (vanWert, et al., 2008). Conservation of the flanking regions of these 8-mers suggests that A17 corresponds to the consensus sequence of X-box: 5'-GTNRCCNRGYAAC-3' (**Fig. 4J**) and A24 corresponds to that of X-box: 5'-GTNRCCNNRGYAAC-3' (**Fig. 4K**). vanWert et al. (2008 and 1998) showed that mutation of X-box 1 and X-box 2 in the rat testis-specific linker histone H1t promoter abolished expression of the transgene. This report supports the idea that A17 and A24 are parts of X-box and these 8-mers are taking parts in the regulation of testis-specific gene expression.

A13* covers part of the reverse complement sequence of the ZII domain of TRE derived from the BZLF1 promoter of the Epstein-Barr virus (5′-AAACCATGACATCACAGAG-3′, Flemington and Speck, 1990). Although A13 and A13* do not conserve whole sequence of this ZII domain sequence, they conserved sequences which are similar to CRE-like sequence (**Fig. 4F, G**), and A13* appeared together with CRE-like TGAGGTCA within the regulatory regions of 5 testis-specific genes (**Table 3-8**). These results suggest that A13 and A13* are parts of CRE-like sequence, or they are related to CRE-like sequence.

The appearance frequencies of group B members within testis-specific regulatory regions do not significantly differ from those within non-testis-specific regulatory regions. This property shows that, these group members are not associated with the process of tissue-specific expression; rather, they probably participate in general mechanisms of gene expression.

All member of group C cover parts of binding site of Sp1, which expresses ubiquitously (Saffer et al., 1991). Group C is composed of 8-mers that are significantly more frequent within the regulatory regions of non-testis-specific genes than within those of testis-specific genes. This property shows that although 8-mers of this group are over-represented within the regulatory regions of testis-specific genes, they are more related to the expression of non-testis-specific genes than that of testis-specific genes. This result suggests that, although these Sp1 binding sites appear very frequently within the regulatory regions of testis-specific genes, they do not seem to be involved in the specific regulatory expression of testis-specific genes.

We have identified 117 over-represented 8-mers from the regulatory regions of 634 testis-specific genes as candidates of regulatory motifs of testis-specific genes. We compared the appearance frequency of these over-represented 8-mers within the regulatory regions of 634 testis-specific genes with those of 8,466 non-testis-specific genes and found that more than half of these over-represented 8-mers appear significantly more frequent within the regulatory regions of testis-specific genes than within those of non-testis-specific genes. It should be noteworthy that CRE-like 8-mers appear significantly more frequent within the regulatory regions of testis-specific genes than within those of non-testis-specific genes, while canonical CRE does not. This suggests that CRE-like 8-mers participate in the regulatory expression of testis-specific genes to a greater extent than the canonical CRE 8-mer.

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Tables

Table 1. Number of tissue-specific genes

#	Tissue	number	#	Tissue	number	#	Tissue	number
1	testis	1,012	21	B220+ B-cells	56	41	epidermis	12
2	pancreas	431	22	large intestine	55	42	preoptic	10
3	oocyte	371	23	stomach	48	43	embryo day 7.5	9
4	fertilized egg	326	24	prostate	45	44	adipose tissue	9
5	liver	233	25	vomeralnasal organ	42	45	trigeminal	8
6	thyroid	146	26	heart	38	46	uterus	8
7	small intestine	131	27	umbilical cord	36	47	CD8+T-cells	8
8	kidney	111	28	adrenal gland	35	48	lymph node	7
9	salivary gland	95	29	digits	32	49	hypothalamus	7
10	eye	93	30	bone	31	50	hippocampus	7
11	medial olfactory epithelium	87	31	lung	31	51	ovary	7
12	blastocysts	85	32	cerebellum	30	52	embryo day 10.5	7
13	placenta	80	33	embryo day 6.5	28	53	dorsal striatum	5
14	skeletal muscle	80	34	pituitary	26	54	embryo day 9.5	4
15	thymus	74	35	brown fat	23	55	embryo day 8.5	4
16	snout epidermis	68	36	bladder	21	56	spinal cord lower	3
17	mammary gland (lact)	62	37	olfactory bulb	20	57	substantia nigra	3
18	bone marrow	61	38	dorsal root ganglia	20	58	amygdala	2
19	spleen	60	39	trachea	15	59	spinal cord upper	1
20	tongue	57	40	CD4+T-cells	14	60	frontal cortex	1
						61	cerebral cortex	1

List of tissue-specific genes are shown in **Appendix Table 1.**

Table 2. Classification of 117 representative 8-mers on the basis of their testis association level

ID	Sequence	#1	#2		#3		#4		#5	
A1	TGATGTCA	18.0	52	(8.2%)	43	(82.7%)	86	(1.0%)	44	(51.2%)
A2	TCACAATG	17.6	26	(4.1%)	23	(88.5%)	25	(0.3%)	11	(44.0%)
A3	ATGTCACA	16.1	30	(4.7%)	26	(86.7%)	38	(0.4%)	11	(28.9%)
A4	GATGTCAC	12.9	31	(4.9%)	28	(90.3%)	57	(0.7%)	22	(38.6%)
A3*	TGTGACAT	12.7	26	(4.1%)	22	(84.6%)	43	(0.5%)	14	(32.6%)
A5	ATGTCATA	12.5	19	(3.0%)	16	(84.2%)	25	(0.3%)	7	(28.0%)
A6	TTGTGATG	11.4	20	(3.2%)	15	(75.0%)	32	(0.4%)	16	(50.0%)
A7	GTGATGTC	11.0	27	(4.3%)	20	(74.1%)	57	(0.7%)	31	(54.4%)
A2*	CATTGTGA	10.8	22	(3.5%)	19	(86.4%)	41	(0.5%)	22	(53.7%)
A1*	TGACATCA	9.8	34	(5.4%)	27	(79.4%)	98	(1.2%)	38	(38.8%)
A8	TCTGTGAC	9.4	26	(4.1%)	18	(69.2%)	67	(0.8%)	24	(35.8%)
A9	TCACAAAG	9.3	22	(3.5%)	22	(100.0%)	51	(0.6%)	11	(21.6%)
A4*	GTGACATC	9.1	22	(3.5%)	19	(86.4%)	53	(0.6%)	18	(34.0%)
A10	ACATCACA	8.9	21	(3.3%)	18	(85.7%)	50	(0.6%)	18	(36.0%)
A11	TGTGAGGT	8.8	21	(3.3%)	12	(57.1%)	51	(0.6%)	17	(33.3%)
A12	CTGTGACA	8.6	23	(3.6%)	15	(65.2%)	61	(0.7%)	14	(23.0%)
A13	CTCTGTGA	8.0	27	(4.3%)	17	(63.0%)	88	(1.0%)	26	(29.5%)
A9*	CTTTGTGA	7.8	22	(3.5%)	14	(63.6%)	65	(0.8%)	20	(30.8%)
A14	TTGTGAGG	7.7	18	(2.8%)	8	(44.4%)	47	(0.6%)	12	(25.5%)
A15	GGTTGCTA	7.3	17	(2.7%)	11	(64.7%)	46	(0.5%)	20	(43.5%)
A16	TGACCTCA	6.8	21	(3.3%)	19	(90.5%)	71	(0.8%)	29	(40.8%)
A17	CCTAGCAA	6.5	17	(2.7%)	13	(76.5%)	53	(0.6%)	16	(30.2%)
A16*	TGAGGTCA	6.1	21	(3.3%)	16	(76.2%)	80	(0.9%)	31	(38.8%)
A13*	TCACAGAG	6.1	24	(3.8%)	15	(62.5%)	99	(1.2%)	28	(28.3%)
A18	TCTGTGAG	5.9	20	(3.2%)	8	(40.0%)	78	(0.9%)	19	(24.4%)
A12*	TGTCACAG	5.7	17	(2.7%)	14	(82.4%)	63	(0.7%)	17	(27.0%)
A19	CCTTAGCT	5.6	16	(2.5%)	1	(6.3%)	58	(0.7%)	12	(20.7%)
A20	AGGTCACA	5.4	17	(2.7%)	14	(82.4%)	66	(0.8%)	16	(24.2%)
A21	CAAAGCCC	5.1	19	(3.0%)	5	(26.3%)	84	(1.0%)	28	(33.3%)
A22	TCTGAGGC	4.7	18	(2.8%)	5	(27.8%)	84	(1.0%)	20	(23.8%)
A23	TGCTTTCC	4.6	18	(2.8%)	4	(22.2%)	86	(1.0%)	22	(25.6%)
A24	CCATGGCA	4.4	17	(2.7%)	11	(64.7%)	82	(1.0%)	28	(34.1%)
A25	TGAGAAGG	4.3	18	(2.8%)	6	(33.3%)	90	(1.1%)	23	(25.6%)
A26	GAGCTCTG	4.2	23	(3.6%)	7	(30.4%)	131	(1.5%)	43	(32.8%)
A27	AGGTTCTG	4.1	17	(2.7%)	8	(47.1%)	87	(1.0%)	22	(25.3%)
A28	GGTCCTCT	4.0	16	(2.5%)	6	(37.5%)	82	(1.0%)	14	(17.1%)
A8*	GTCACAGA	3.9	16	(2.5%)	14	(87.5%)	83	(1.0%)	25	(30.1%)
A29	CCTCACAG	3.8	17	(2.7%)	8	(47.1%)	93	(1.1%)	24	(25.8%)
A30	CTGTTGCT	3.8	16	(2.5%)	7	(43.8%)	86	(1.0%)	23	(26.7%)
A31	CCTGAGCA	3.8	17	(2.7%)	5	(29.4%)	94	(1.1%)	22	(23.4%)
A32	TCTCTGTG	3.6	23	(3.6%)	8	(34.8%)	146	(1.7%)	30	(20.5%)
A33	TTTCTCCA	3.6	17	(2.7%)	5	(29.4%)	98	(1.2%)	19	(19.4%)
A34	TGCCCAGG	3.4	21	(3.3%)	6	(28.6%)	136	(1.6%)	33	(24.3%)
A35	TCCAGGAG	3.4	19	(3.0%)	7	(36.8%)	119	(1.4%)	33	(27.7%)
A36	TTCTGGAA	3.2	16	(2.5%)	3	(18.8%)	97	(1.1%)	16	(16.5%)
A37	CAGAGAGA	3.2	25	(3.9%)	3	(12.0%)	177	(2.1%)	42	(23.7%)
A38	CTTCCAGA	3.2	16	(2.5%)	4	(25.0%)	99	(1.2%)	25	(25.3%)
A39	TTTAAAAA	2.8	26	(4.1%)	3	(11.5%)	200	(2.4%)	37	(18.5%)
A32*	CACAGAGA	2.8	18	(2.8%)	4	(22.2%)	125	(1.5%)	32	(25.6%)
A40	CTGAGGCT	2.7	21	(3.3%)	5	(23.8%)	156	(1.8%)	31	(19.9%)
A41	GAGGCCAG	2.7	23	(3.6%)	8	(34.8%)	177	(2.1%)	50	(28.2%)
A42	GGCCAGCC	2.6	24	(3.8%)	7	(29.2%)	189	(2.2%)	55	(29.1%)
A43	GGCTGTGG	2.6	23	(3.6%)	8	(34.8%)	180	(2.1%)	65	(36.1%)
A44	CTCTGTCT	2.6	20	(3.2%)	1	(5.0%)	151	(1.8%)	31	(20.5%)
A45	CTCCTCTT	2.5	18	(2.8%)	9	(50.0%)	133	(1.6%)	38	(28.6%)
A46	AGGAGCAG	2.5	24	(3.8%)	7	(29.2%)	195	(2.3%)	48	(24.6%)
A47	AGAGAGAC	2.4	16	(2.5%)	8	(50.0%)	117	(1.4%)	24	(20.5%)
A48	CTCCCAGA	2.4	20	(3.2%)	4	(20.0%)	157	(1.9%)	48	(30.6%)
A49	TCTCAGCC	2.4	19	(3.0%)	1	(5.3%)	148	(1.7%)	25	(16.9%)
A50	CCTGGCTG	2.2	25	(3.9%)	4	(16.0%)	215	(2.5%)	56	(26.0%)
A51	CAGAGATG	2.2	13	(2.1%)	1	(7.7%)	95	(1.1%)	20	(21.1%)
A52	AGGCTGTG	2.2	17	(2.7%)	7	(41.2%)	135	(1.6%)	45	(33.3%)
A53	CCAGGGAG	2.2	21	(3.3%)	2	(9.5%)	176	(2.1%)	53	(30.1%)
A54	CTCCAGAG	2.1	17	(2.7%)	3	(17.6%)	136	(1.6%)	27	(19.9%)

B1	TGCCTCTG	1.8	19	(3.0%)	3	(15.8%)	167	(2.0%)	39	(23.4%)
B2	AGGAAGAA	1.8	20	(3.2%)	2	(10.0%)	178	(2.1%)	41	(23.0%)
B3	CTCTTCCT	1.7	21	(3.3%)	5	(23.8%)	192	(2.3%)	57	(29.7%)
B4	AGGGAGGC	1.7	20	(3.2%)	7	(35.0%)	183	(2.2%)	66	(36.1%)
B5	TGGGAGGA	1.7	21	(3.3%)	6	(28.6%)	194	(2.3%)	75	(38.7%)
B6	CAGCCAAT	1.7	20	(3.2%)	8	(40.0%)	184	(2.2%)	83	(45.1%)
B7	TGACGTCA	1.5	24	(3.8%)	17	(70.8%)	235	(2.8%)	139	(59.1%)
B8	TTTATTTT	1.4	17	(2.7%)	1	(5.9%)	160	(1.9%)	28	(17.5%)
B9	CTGAGCCA	1.4	17	(2.7%)	2	(11.8%)	161	(1.9%)	40	(24.8%)
B10	GGCAGCTG	1.4	20	(3.2%)	3	(15.0%)	195	(2.3%)	56	(28.7%)
B11	AGCAGCTG	1.4	21	(3.3%)	4	(19.0%)	209	(2.5%)	62	(29.7%)
B12	GCCTCCTG	1.3	20	(3.2%)	5	(25.0%)	200	(2.4%)	69	(34.5%)
B13	GCTCTGGG	1.2	19	(3.0%)	6	(31.6%)	192	(2.3%)	66	(34.4%)
B14	AGAGAAAG	1.2	20	(3.2%)	4	(20.0%)	204	(2.4%)	43	(21.1%)
B15	AAAAAAAA	1.1	33	(5.2%)	4	(12.1%)	364	(4.3%)	68	(18.7%)
B16	CAGGCTGG	1.1	22	(3.5%)	4	(18.2%)	233	(2.8%)	61	(26.2%)
B17	CAGAGCAG	1.0	18	(2.8%)	5	(27.8%)	192	(2.3%)	47	(24.5%)
B18	TCTCTTCC	0.9	18	(2.8%)	3	(16.7%)	194	(2.3%)	59	(30.4%)
B19	GCCAATCA	0.9	17	(2.7%)	11	(64.7%)	183	(2.2%)	94	(51.4%)
B20	CCTGGGCT	0.9	20	(3.2%)	5	(25.0%)	220	(2.6%)	63	(28.6%)
B21	CAGCCTCC	0.8	20	(3.2%)	3	(15.0%)	221	(2.6%)	60	(27.1%)
B22	CAGGAAGT	0.8	15	(2.4%)	9	(60.0%)	163	(1.9%)	75	(46.0%)
B23	AGAGGCAG	0.8	20	(3.2%)	4	(20.0%)	224	(2.6%)	60	(26.8%)
B24	CTCTGCCT	0.8	19	(3.0%)	4	(21.1%)	213	(2.5%)	44	(20.7%)
B24*	AGGCAGAG	0.7	21	(3.3%)	4	(19.0%)	239	(2.8%)	60	(25.1%)
B25	CCTTCCTC	0.7	21	(3.3%)	3	(14.3%)	240	(2.8%)	80	(33.3%)
B26	AAAACAAA	0.7	21	(3.3%)	4	(19.0%)	242	(2.9%)	33	(13.6%)
B27	CCTCTCTC	0.6	20	(3.2%)	3	(15.0%)	231	(2.7%)	77	(33.3%)
B28	GCAGCTGC	0.6	22	(3.5%)	6	(27.3%)	256	(3.0%)	73	(28.5%)
B29	TGCTGGGA	0.6	17	(2.7%)	4	(23.5%)	195	(2.3%)	50	(25.6%)
B30	GAAAAAAA	0.5	22	(3.5%)	3	(13.6%)	263	(3.1%)	52	(19.8%)
B31	AGAGGAAG	0.5	21	(3.3%)	4	(19.0%)	253	(3.0%)	81	(32.0%)
B32	AAACAAAA	0.5	21	(3.3%)	1	(4.8%)	254	(3.0%)	45	(17.7%)
B33	CACACACA	0.5	18	(2.8%)	3	(16.7%)	216	(2.6%)	44	(20.4%)
B34	GGCAGAGG	0.2	21	(3.3%)	6	(28.6%)	270	(3.2%)	79	(29.3%)
B33*	TGTGTGTG	0.0	17	(2.7%)	4	(23.5%)	225	(2.7%)	42	(18.7%)
B35	CTCTCTCT	-0.1	18	(2.8%)	1	(5.6%)	245	(2.9%)	76	(31.0%)
B36	CTTCCTGG	-0.1	16	(2.5%)	5	(31.3%)	220	(2.6%)	65	(29.5%)
B37	TGGGCGGG	-0.2	30	(4.7%)	22	(73.3%)	415	(4.9%)	226	(54.5%)
B38	CCCACCCC	-0.7	33	(5.2%)	11	(33.3%)	501	(5.9%)	194	(38.7%)
B39	CCCCACCC	-0.8	36	(5.7%)	19	(52.8%)	548	(6.5%)	203	(37.0%)
B40	CCCTCCTC	-1.0	22	(3.5%)	10	(45.5%)	365	(4.3%)	139	(38.1%)
B41	CCTCCCTC	-1.3	24	(3.8%)	7	(29.2%)	415	(4.9%)	169	(40.7%)
B38*	GGGGTGGG	-1.5	29	(4.6%)	12	(41.4%)	514	(6.1%)	188	(36.6%)
B15*	TTTTTTTT	-1.7	22	(3.5%)	6	(27.3%)	424	(5.0%)	115	(27.1%)
B39*	GGGTGGGG	-1.8	30	(4.7%)	10	(33.3%)	556	(6.6%)	230	(41.4%)
C1	GGGAGGGG	-2.2	33	(5.2%)	17	(51.5%)	650	(7.7%)	285	(43.8%)
C1*	CCCCTCCC	-2.7	33	(5.2%)	20	(60.6%)	700	(8.3%)	316	(45.1%)
C2	GGCGGGGC	-2.8	50	(7.9%)	34	(68.0%)	987	(11.7%)	635	(64.3%)
C2*	GCCCCGCC	-3.0	44	(6.9%)	27	(61.4%)	923	(10.9%)	515	(55.8%)
C3	GGGCGGGG	-3.2	59	(9.3%)	38	(64.4%)	1193	(14.1%)	741	(62.1%)
C4	GGGGCGGG	-4.2	48	(7.6%)	29	(60.4%)	1167	(13.8%)	742	(63.6%)
C3*	CCCCGCCC	-4.3	45	(7.1%)	28	(62.2%)	1121	(13.2%)	631	(56.3%)
	Total		2648		1163	(43.9%)	24977		9422	(37.7%)

The IDs with asterisks represent the reverse complements of the corresponding 8-mers represented by the same IDs without asterisks.

#1: Testis association level of the 8-mer.

#2: Appearance of the 8-mers within the regulatory regions of 634 testis-specific genes. Percentages to these regulatory regions are shown in parentheses.

#3: Appearance of the 8-mers within the [–100 to –1] regions of testis-specific genes. Percentages to the whole 8-mer appearance are shown in parentheses. Gray boxes indicate appearance frequencies greater than half within the [–100 to –1] regions.

#4: Appearance of the 8-mers within the regulatory regions of 8,466 non-testis-specific genes. Percentages to these regulatory regions are shown in parentheses.

#5: Appearance of the 8-mers within the [–100 to –1] regions of non-testis-specific genes. Percentages to the whole 8-mer appearance are shown in parentheses. Gray boxes indicate appearance frequencies greater than half within the [–100 to –1] regions.

Data of the other 8-mers are shown in **Supplementary Table 1** which can be downloaded from:

http://www.gen-info.osaka-u.ac.jp/~uhmin/study/others/tissue_specific/Supplementary_Table1.xlsx

Table 3. 8-mers which appeared nearby other representative 8-mers

CRE-like
1. 5 genes.
GTGATGTC (A7)
TGATGTCA (A1)
GATGTCAC (A4)
ATGTCACA (A3)
TGTCACAG (A12*)

2. 4 genes.
TGATGTCA (A1)
GATGTCAC (A4)
ATGTCACA (A3)
TCACAATG (A2)

3. 4 genes.
CTTTGTGA (A9*)
TTGTGATG (A6)
GTGATGTC (A7)
TGATGTCA (A1)

4. 12 genes.
TGATGTCA (A1)
ATGTCATA (A5)

5. 5 genes.
CTGTGACA (A12)
TGTGACAT (A3*)
GTGACATC (A4*)
TGACATCA (A1*)
ACATCACA (A10)

6. 6 genes.
TCTGTGAC (A8)
CTGTGACA (A12)
TGTGACAT (A3*)
GTGACATC (A4*)
TGACATCA (A1*)

7. 4 genes.
TGACCTCA (A16)
CCTCACAG (A29)

8. 5 genes.
TGAGGTCA (A16*)
AGGTCACA (A20)
GTCACAGA (A8*)
TCACAGAG (A13*)

9. 10 genes.
TGTGAGGT (A11)
TGAGGTCA (A16*)

Partial ZII
10. 6 genes.
TCTCTGTG (A32)
CTCTGTGA (A13)
TCTGTGAC (A8)

11. 4 genes.
TCTCTGTG (A32)
CTCTGTGA (A13)
TCTGTGAG (A18)

12. 4 genes.
CTCTGTGA (A13)
TCTGTGAC (A8)
CTGTGACA (A12)

13. 5 genes.
CCTCACAG (A29)
TCACAGAG (A13*)

14. 4 genes.
TCACAGAG (A13*)
CACAGAGA (A32*)

Partial CSS A
15. 4 genes.
CATTGTGA (A2*)
TTGTGATG (A6)

Sp1 binding site (group C)
16. 4 genes.
GGGCGGGG (C3)
GGCGGGGC (C2)
GGGGCGGG (C4)
GGGCGGGG (C3)
GGCGGGGC (C2)

17. 6 genes.
GGGGCGGG (C4)
GGGCGGGG (C3)
GGCGGGGC (C2)
GGGGCGGG (C4)
GGGCGGGG (C3)

18. 19 genes.
TGGGCGGG (B37)
GGGCGGGG (C3)
GGCGGGGC (C2)

Others
19. 4 genes.
ATGTCACA (A3)
TGTCACAG (A12*)
GTCACAGA (A8*)

20. 5 genes.
CTTTGTGA (A9*)
TTGTGAGG (A14)
TGTGAGGT (A11)

21. 6 genes.
GAGCTCTG (A26)
GCTCTGGG (B13)

22. 4 genes.
CCCTCCTC (B40)
CTCCTCTT (A45)

23. 6 genes.
AGCAGCTG (B11)
GCAGCTGC (B28)

24. 6 genes.
CAGCCAAT (B6)
GCCAATCA (B19)

25. 8 genes.
AGGCTGTG (A52)
GGCTGTGG (A43)

26. 5 genes.
GAGGCCAG (A41)
GGCCAGCC (A42)

27. 5 genes.
TCTGTGAG (A18)
TGTGAGGT (A11)

28. 11 genes.
TCTCTTCC (B18)
CTCTTCCT (B3)

29. 5 genes.
TCTGAGGC (A22)
CTGAGGCT (A40)

30. 4 genes.
TGCCTCTG (B1)
CTCTGCCT (B24)

31. 9 genes.
GGCAGCTG (B10)
GCAGCTGC (B28)

32. 6 genes.
CAGAGAGA (A37)
AGAGAGAC (A47)

33. 7 genes.
AGGCAGAG (B24*)
GGCAGAGG (B34)

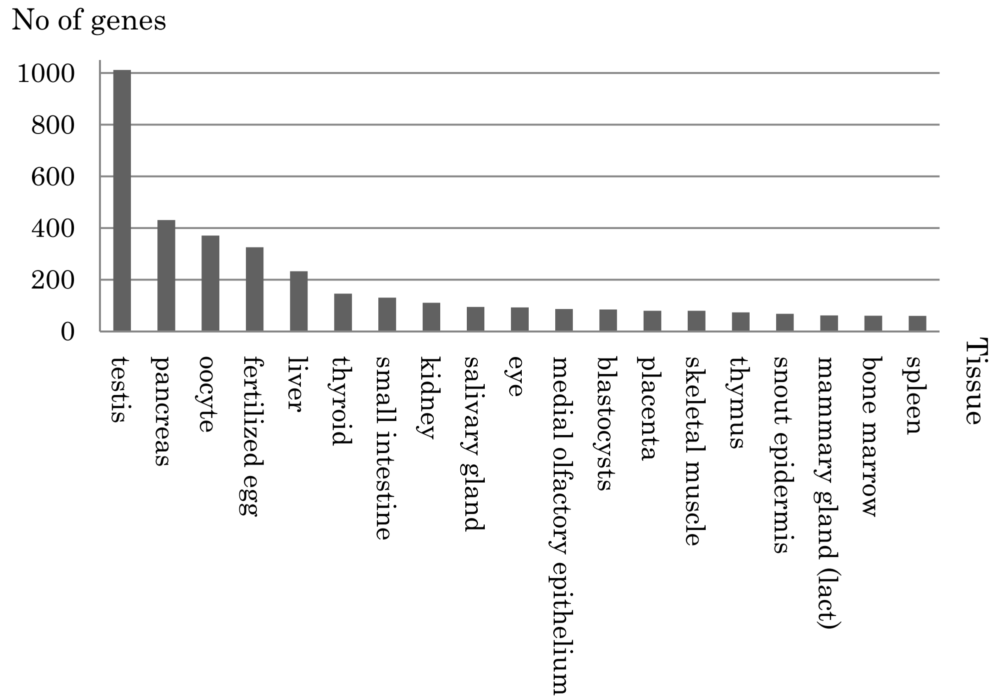
34. 20 genes.
GGGGTGGG (B38*)
GGGTGGGG (B39*)

35. 21 genes.
CCCCACCC (B39)
CCCACCCC (B38)

Blue colored 8-mers represent CRE-like 8-mers, red colored 8-mers represent partial ZII element 8-mers, and orange colored 8-mers represent partial CSS-A 8-mers.

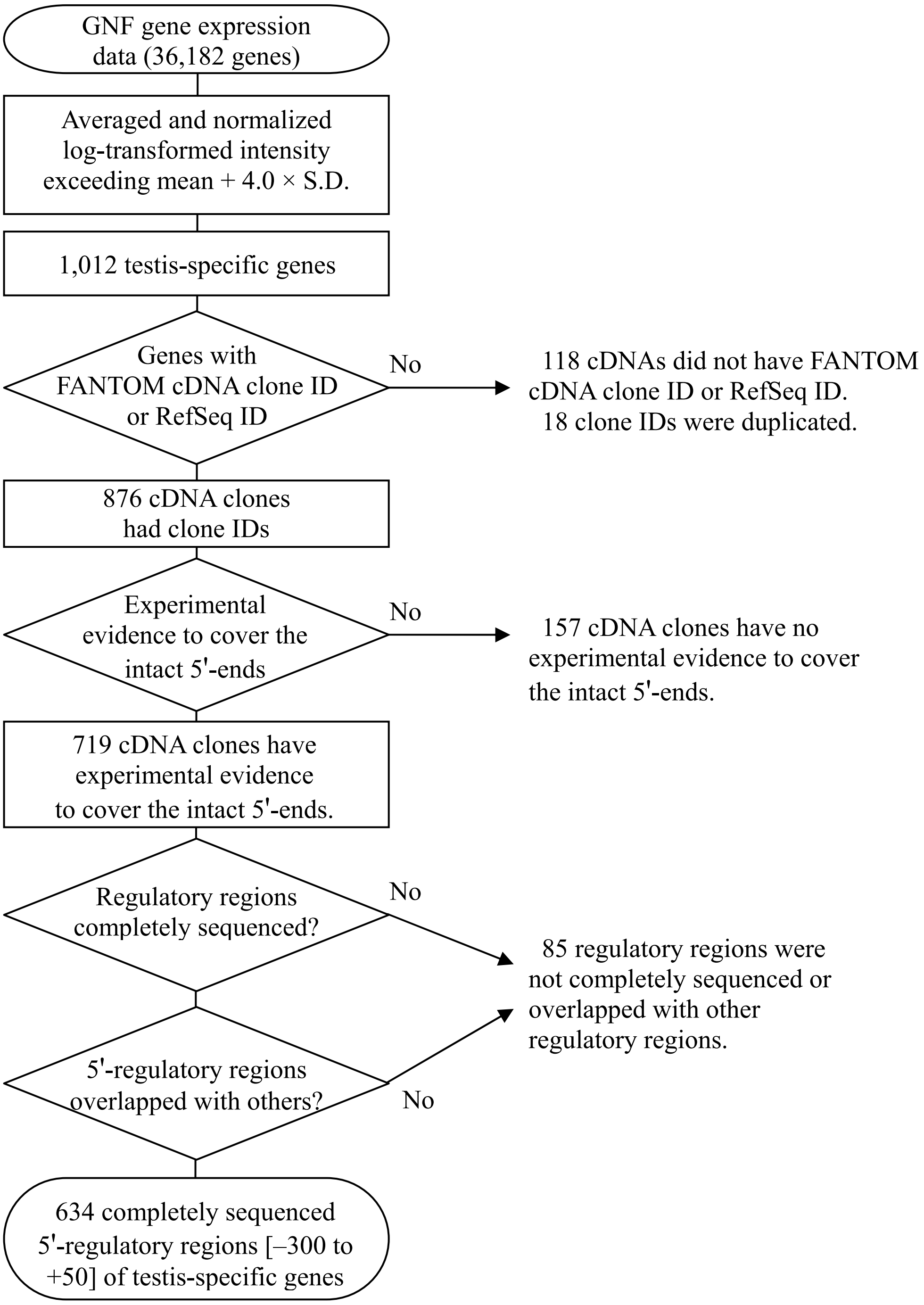
Figures

Fig. 1. Number of tissue-specific genes



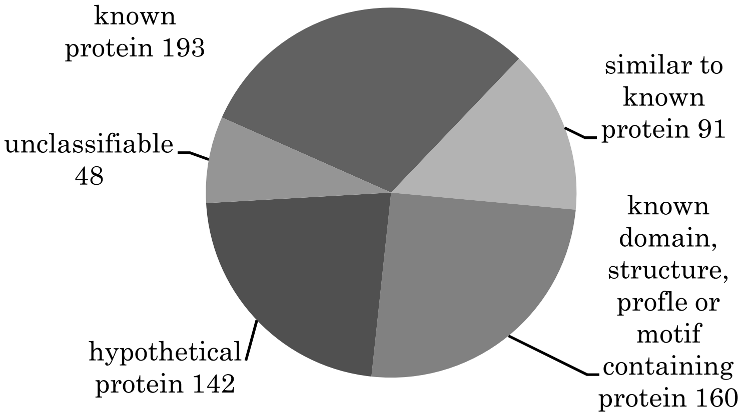
Number of tissue-specific genes for top 20 tissues that most abundantly exhibit their specific genes is shown. Horizontal axis represents the name of tissues, and vertical axis represents the number of tissue-specific gene.

Fig. 2. Identification of testis-specific genes and their 5′-regulatory regions



Starting from the GNF gene expression data of 36,182 genes, we obtained 1,012 testis-specific cDNAs. Of these, we excluded 118 cDNAs because they were not linked to either the FANTOM cDNA clone ID or RefSeq ID. Further, 18 clone IDs were found to be duplicated. Thus, of the 1,012 testis-specific cDNAs, 876 had clone IDs. Of these, 719 had experimental evidence to cover the intact 5′-ends. The regulatory regions of genes that were not completely sequenced or those that overlapped with testis-specific genes were not used. Finally, we obtained 634 completely sequenced 5′-regulatory regions [–300 to +50] of testis-specific genes. Annotations and testis specificities of these genes are shown in **Appendix Table 2**.

Fig. 3. Profiling of 634 testis-specific genes

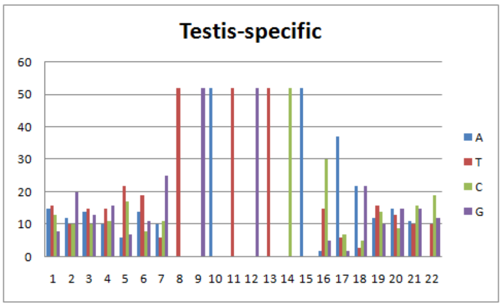


The selected 634 testis-specific genes were annotated and categorized into the following 5 groups on the basis of our knowledge about their functions: known proteins; similar to known proteins; known domain-, structure-, profile-, or motif-containing proteins; hypothetical proteins; and unclassifiable genes. Hypothetical proteins were defined as proteins with more than 100 amino acids and having no known homologous genes. Genes without known homologous genes coding for proteins with fewer than 100 amino acids were assigned to the unclassifiable gene group.

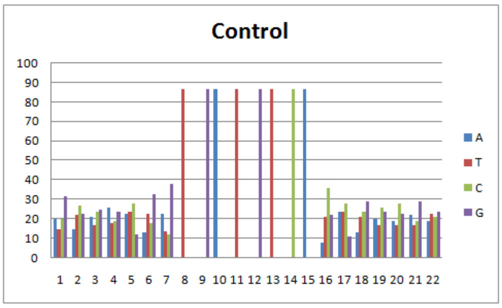
Fig. 4. Conservations of flanking region of the highlighted 8-mers in testis-specific and non-testis-specific regulatory regions

CRE-like

A. TGATGTCA (A1)

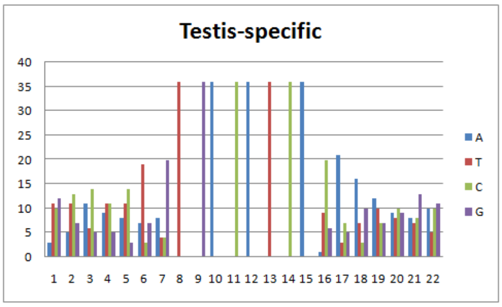


tngTGATGTCAcar

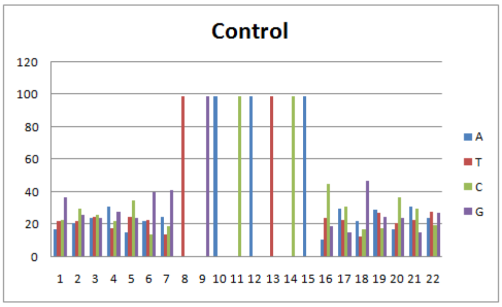


gTGATGTCAc

B. TGACATCA (A1*)

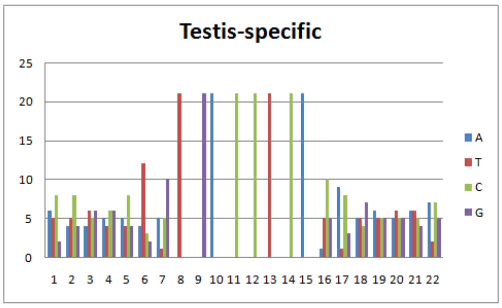


bnnndtgTGACATCAcad

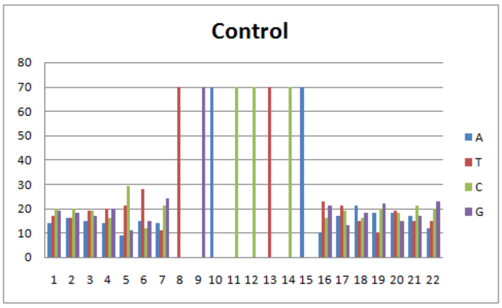


ggTGACATCAcng

C. TGACCTCA (A16)

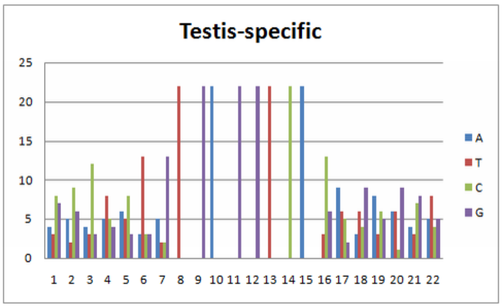


hnnnntgTGACCTCAcannnnv

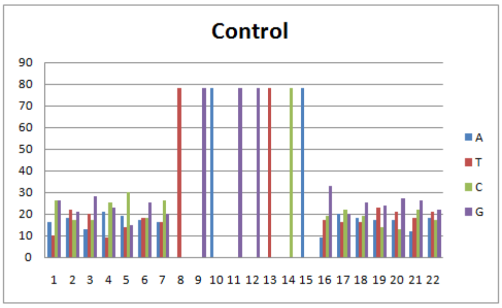


ctnTGACCTCA

D. TGAGGTCA (A16*)

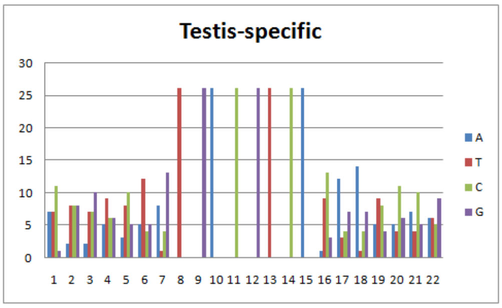


ccnntgTGAGGTCAcagng

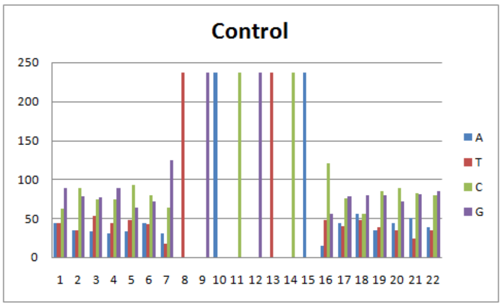


vnnnTGAGGTCAg

E. TGACGTCA (B7)



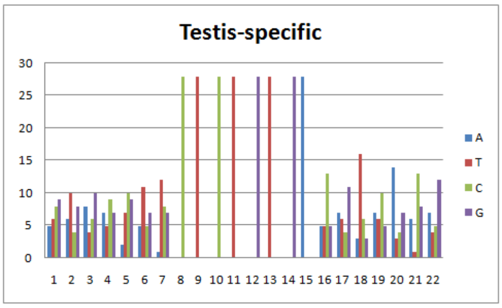
cbbnbtgTGACGTCAcaa



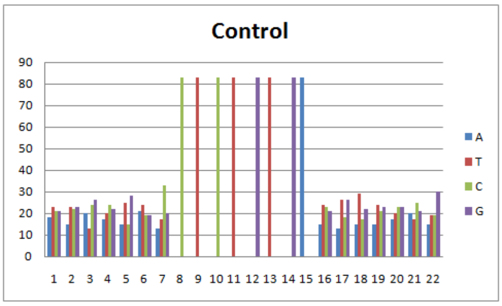
gTGACGTCAcnnnnv

Partial ZII

F. CTCTGTGA (A13)

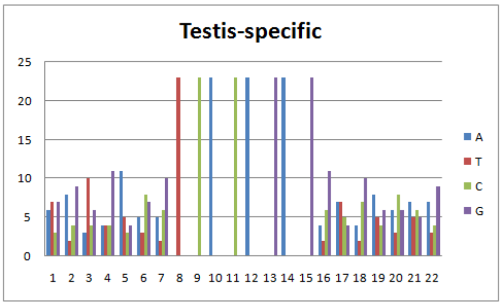


bntCTCTGTGAcntnacg

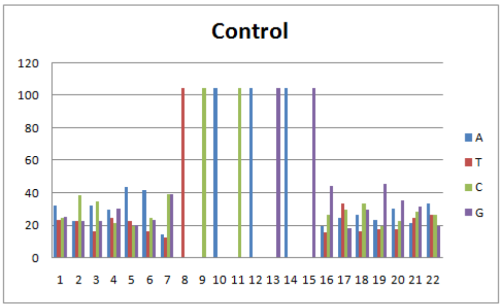


CTCTGTGA

G. TCACAGAG (A13*)



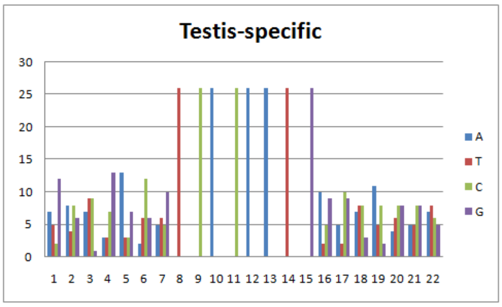
vtgangTCACAGAGgng



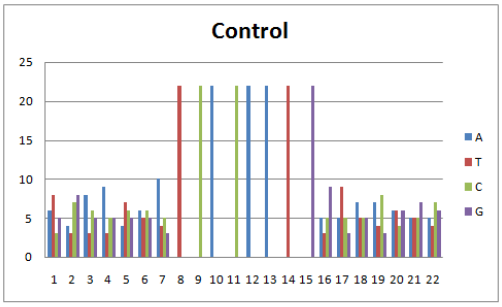
anvTCACAGAGgnng

Partial CSS-A

H. TCACAATG (A2)

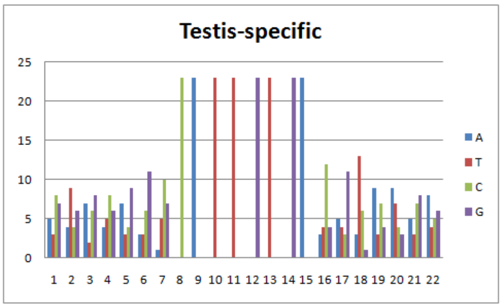


gnhgacnTCACAATGvvha

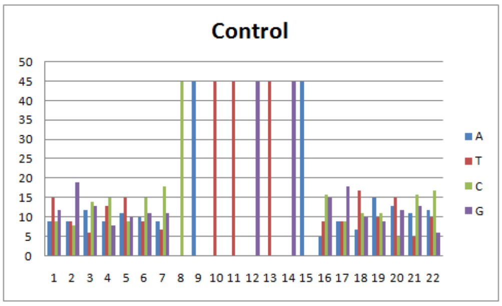


annaTCACAATGgt

I. CATTGTGA (A2*)



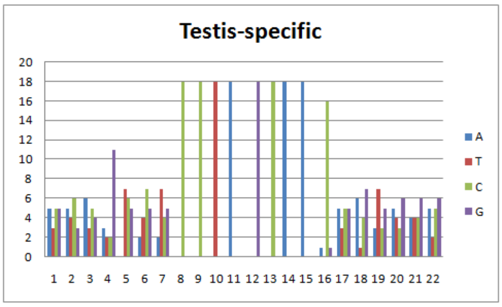
vnngcCATTGTGAcgt



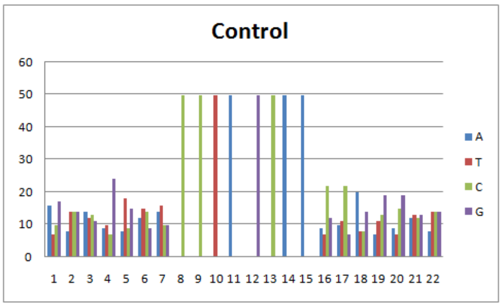
gnnnncCATTGTGAbgnndv

Partial X-box

J. CCTAGCAA (A17)

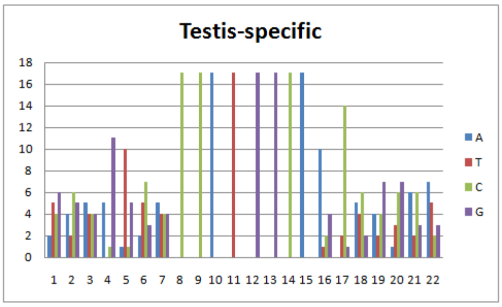


gbbbCCTAGCAAcnvnnnv

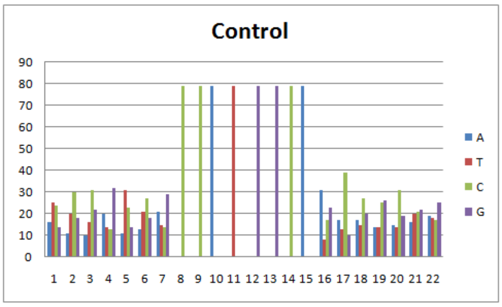


gnnnCCTAGCAAcca

K. CCATGGCA (A24)



bvngtcnCCATGGCAachggva



gnnnCCATGGCAvc

The graphs show conservations of flanking region (from 7 bp upstream to 7 bp downstream) of the highlighted 8-mers in testis-specific and non-testis-specific regulatory regions. “Testis-specific” graphs show conservation of flanking region of the 8-mers within the testis-specific regulatory regions. “Control” graph shows those within the non-testis-specific regulatory regions. The horizontal axis represents the position of the nucleotide site from the 7 bp upstream of the 8-mer start site. Vertical axis represents the occurrence of the nucleotides: blue bar represents adenine, red bar represents thymine, green bar represents cytosine, and purple bar represents guanine. Conservation of the flanking nucleotides are assigned as follows: if one nucleotide occurs most frequently and occupy > 40% on a site, the nucleotide is arbitrarily regarded as conserved in the site; if one nucleotide occupy <12.5%, the nucleotide is arbitrarily regarded as negatively conserved (for example if adenine is negatively conserved, the site is assigned as ‘b’; if thymine and cytosine is negatively conserved, the site is assigned as ‘r’, see LIST of ABBREVIATIONS for abbreviations of nucleotide names). Nucleotides of flanking regions are written in lower-case, while nucleotides of the 8-mers are written in uppercase.

Appendix Table 1. List of tissue specific genes

This list is also available at http://www.gen-info.osaka-u.ac.jp/~uhmin/study/others/tissue_specific/

#1 Tissue specificity level ranking.
#2 Tissue specificity level.
#3 Microarray probe ID.
#4 RefSeq ID.
#5 FANTOM Clone ID.
#6 Annotation.

No. 1, testis specific genes

#1	#2	#3	#4	#5	#6
1	7.3	gnf1m21655_at	NM_199034	4922502D21	weakly similar to predicted CD69 antigen (p60, early T-cell activation antigen)
2	7.3	gnf1m18736_a_at	XM_918780	1700015G11	unclassifiable
3	7.2	gnf1m01980_a_at	NM_009619		a disintegrin and metallopeptidase domain 3 (cyritestin)
4	7.2	gnf1m07925_a_at	NM_172515	4931432L23	hypothetical Zn-finger, B-box/Zinc finger B-box type profile containing protein Mus musculus
5	7.1	gnf1m11104_a_at	NM_013580	4930544H24	lactate dehydrogenase C (Ldhc)
6	7.1	gnf1m04918_a_at	NM_026317	4930551D19	hypothetical Serine proteases, trypsin family containing protein
7	7.1	gnf1m03878_a_at	NM_019981	1700008H15	testis expressed gene 101
8	7.1	gnf1m16565_a_at	NM_029324	1700018C11	hypothetical protein
9	7.1	gnf1m01166_at	NM_008085		glyceraldehyde-3-phosphate dehydrogenase, spermatogenic
10	7.1	gnf1m04973_a_at	NM_026457	1700086N05	testis-specific leucine zipper protein nurit
11	7.0	gnf1m18408_at	NM_183284	1700007F22	serine peptidase inhibitor, Kazal type 2
12	7.0	gnf1m07353_a_at	NM_153519		thioredoxin domain containing 2 (spermatozoa)
13	7.0	gnf1m31778_at	NM_001033267	2410022A04	glutamine rich 2 (Qrich2)
14	7.0	gnf1m02827_a_at	NM_011483	1700010L20	zinc and ring finger 4
15	7.0	gnf1m01622_a_at	NM_008933	1700007K08	protamine 2
16	7.0	gnf1m04562_a_at	NM_025496	1700025H18	hypothetical protein
17	7.0	gnf1m31206_a_at	XM_914003	1700019B01	weakly similar to predicted coiled-coil domain containing 89 (Ccdc89)
18	7.0	gnf1m09241_a_at	NM_144827		spermatogenesis associated 20
19	7.0	gnf1m05640_a_at	NM_031190	4933431I08	phosphoglycerate kinase 2
20	7.0	gnf1m14004_a_at	NM_183282	1700029I08	hypothetical Actin-like ATPase domain structure containing protein
21	7.0	gnf1m05106_a_at	NM_027028	1700008P20	Tescalcin (TSC)
22	6.9	gnf1m01533_a_at	NM_008757		outer dense fiber of sperm tails 1
23	6.9	gnf1m29756_a_at	XM_913802	1700021F07	similar to low in lung cancer 1
24	6.9	gnf1m02291_a_at	NM_010293	4922501K24	glycerol kinase-like 1
25	6.9	gnf1m08571_a_at	NM_175390	1700049L16	hematological and neurological expressed 1-like Mus musculus
26	6.9	gnf1m05233_a_at	NM_027960	1700018F16	dipeptidase 3
27	6.9	gnf1m29029_a_at	XM_908448	4930553D05	unclassifiable
28	6.9	gnf1m16054_a_at	XM_912277	1700009N14	weakly similar to RAN protein
29	6.9	gnf1m01872_a_at	NM_009407	1700029H23	hypothetical transition protein 1
30	6.9	gnf1m14508_a_at	XM_908969	1700095G12	C-5 cytosine-specific DNA methylase containing protein
31	6.9	gnf1m18742_a_at	XM_909947	1700022P22	hypothetical protein
32	6.9	gnf1m12377_a_at	NM_009056	A930013E12	coiled-coil domain containing 60 (Ccdc60)
33	6.9	gnf1m04031_a_at	NM_021318	1700027G07	hypothetical activator of CREM in testis
34	6.9	gnf1m28688_at	XM_920937		expressed sequence AI507611
35	6.9	gnf1m08595_a_at	NM_177901	4933402J07	hypothetical protein
36	6.9	gnf1m23057_a_at		1700112D12	unclassifiable
37	6.9	gnf1m21680_a_at	NM_199023	4930526D03	PUTATIVE NOVEL PROTEIN (FRAGMENT) [Homo sapiens]
38	6.9	gnf1m01973_a_at	NM_009581		zona pellucida 3 receptor
39	6.9	gnf1m04179_a_at	NM_021898		testis specific gene A8
40	6.8	gnf1m18731_a_at	XM_905113	1700007H20	predicted heat shock protein, alpha-crystallin-related, B9
41	6.8	gnf1m02317_a_at	NM_010352	1700025C22	germ cell-specific gene 1
42	6.8	gnf1m03620_a_at	NM_018792	1700007I14	histone H1-like protein in spermatids 1
43	6.8	gnf1m31560_x_at			inferred: ref|NP_001331.1| (NM_001340) cylicin 2 [Homo sapiens] mCG7553
44	6.8	gnf1m29482_a_at	XM_622835	4933409I12	gametogenetin binding protein 1
45	6.8	gnf1m02157_a_at	NM_009979	1700027J17	cystatin 9
46	6.8	gnf1m16813_a_at	XM_919931	1700003F12	Bcl-2-like protein
47	6.8	gnf1m16162_a_at		1700001F04	cysteine-rich perinuclear theca 12
48	6.8	gnf1m13969_a_at		4933433O19	unclassifiable
49	6.8	gnf1m18818_a_at	NM_001039593	1700015E13	unclassifiable
50	6.8	gnf1m07713_at		4930583E11	TATA-binding protein-like factor-interacting protein isoform 1
51	6.8	gnf1m05107_a_at	NM_027031	4930403C08	EF-hand containing protein
52	6.8	gnf1m21688_a_at	XM_923531	4930571K11	hypothetical protein LOC629141
53	6.8	gnf1m29198_at			A kinase (PRKA) anchor protein 4
54	6.8	gnf1m07749_a_at	NM_030052	4930503O21	cytochrome c oxidase subunit VIIb2
55	6.8	gnf1m01424_a_at	NM_008574	4933417G15	sperm mitochondria-associated cysteine-rich protein
56	6.8	gnf1m14498_a_at	NM_028825	1700011F03	hypothetical protein
57	6.8	gnf1m17312_a_at	XM_919557	4933405J11	hypothetical protein
58	6.7	gnf1m10448_a_at	NM_133711	1700001N01	spermatogenesis associated 4
59	6.7	gnf1m30572_a_at		4933413C15	weakly similar to coiled-coil domain containing 67 (Ccdc67)
60	6.7	gnf1m05112_s_at	XM_925615	1700018F24	hypothetical Ras GEF structure containing protein
61	6.7	gnf1m02000_a_at	NM_009650		A kinase (PRKA) anchor protein 3
62	6.7	gnf1m05189_a_at	NM_027597	4921509E07	hypothetical protein
63	6.7	gnf1m04371_a_at		1700012M14	hypothetical Yeast DNA-binding domain containing protein
64	6.7	gnf1m32513_at	XM_906877		similar to leucine rich repeat containing 45
65	6.7	gnf1m03516_a_at	NM_016901	4930567P17	ornithine decarboxylase antizyme 3 (Oaz3)
66	6.7	gnf1m05703_a_at	NM_032004	4930402K08	testis-specific serine kinase 6
67	6.7	gnf1m05614_a_at	NM_030744	1700008N21	ropporin, rhophilin associated protein 1 (Ropn1)
68	6.7	gnf1m02899_a_at	NM_011651		serine/threonine kinase 22 substrate 1
69	6.7	gnf1m30318_a_at	NM_026094	1700122B10	ATPase, Class I, type 8B, member 3
70	6.7	gnf1m05024_a_at	NM_026627	4930470K20	weakly similar to LATE HISTONE H2A.1 [Psammechinus miliaris]
71	6.6	gnf1m04821_a_at	NM_026084	3110070M22	hypothetical protein
72	6.6	gnf1m31337_at			cDNA sequence BC061194
73	6.6	gnf1m15067_a_at	XM_913562	4930571C24	hypothetical Proline-rich region profile containing protein
74	6.6	gnf1m31231_s_at	XM_916339		hypothetical gene supported by BC052145
75	6.6	gnf1m01847_a_at	NM_009355		testicular serine protease 1
76	6.6	gnf1m05319_at	NM_028539	1700052K11	tousled-like kinase 2 (Arabidopsis)
77	6.6	gnf1m17380_at	NM_183103	1700112C13	similar to testis-specific serine protease-6 (Tessp6)
78	6.6	gnf1m13831_a_at	XM_619618	4921511C04	Peptidase, eukaryotic cysteine peptidase active site containing protein
79	6.6	gnf1m04906_a_at	NM_026290	1700006G11	hypothetical ARM repeat structure containing protein
80	6.6	gnf1m31877_at	NM_001033255	4933439L02	hypothetical protein
81	6.5	gnf1m05831_a_at	NM_053216	1700102P08	hypothetical protein
82	6.5	gnf1m28824_a_at	XM_924743	1700021P22	hypothetical protein
83	6.5	gnf1m05103_at	NM_027022	4922505K21	CKLF-like MARVEL transmembrane domain containing 2A
84	6.5	gnf1m31282_a_at	NM_001033547	4922505E12	beta tubulin containing protein (Fragment) Mus musculus
85	6.5	gnf1m08577_a_at	NM_177791	4922504H04	potassium channel tetramerisation domain containing 19
86	6.5	gnf1m28686_a_at	XM_917702	1700095K08	TBC1 domain family, member 21
87	6.5	gnf1m29239_s_at	NM_028560	1700051A02	weakly similar to Phosphatidylethanolamine binding protein [Homo sapiens]
88	6.5	gnf1m31096_a_at		1700003O08	unclassifiable
89	6.5	gnf1m22667_a_at	XM_920441	4930550F01	immunity-related GTPase family, cinema 1
90	6.5	gnf1m29365_a_at		1700001P01	hypothetical protein
91	6.5	gnf1m03322_a_at	NM_013859	E030006L06	Janus kinase 3
92	6.5	gnf1m17232_a_at		1700019A02	Glutamic acid-rich region containing protein
93	6.5	gnf1m16484_a_at	XM_910139	1700015M15	PLAC8-like 1
94	6.5	gnf1m18668_a_at	NM_028942	4921521J18	hypothetical solute carrier organic anion transporter family, member 6c1
95	6.5	gnf1m30974_a_at	NM_001039049	1700007F21	predicted cytochrome c oxidase, subunit VIIIc
96	6.5	gnf1m19018_a_at	NM_183405	1700067P11	cytochrome c oxidase subunit VIb polypeptide 2
97	6.5	gnf1m16159_a_at	XM_913064	1700025M08	sperm acrosome associated 3
98	6.5	gnf1m05191_a_at	NM_027617	4921536I21	spermatogenesis associated 1 (Spata1)
99	6.5	gnf1m18375_a_at	XM_920814	1700016G14	unclassifiable
100	6.5	gnf1m05036_a_at	NM_026645	4933406G04	IQ motif containing F3
101	6.5	gnf1m16969_a_at	XM_914392	1700011H22	hypothetical protein
102	6.5	gnf1m02714_a_at	NM_011253	4930569O14	RNA binding motif protein, Y chromosome, family 1, member A1
103	6.5	gnf1m18161_at		1700036B12	unclassifiable
104	6.5	gnf1m32279_at	XM_909667		similar to Glycosyl-phosphatidylinositol-anchored molecule-like protein precursor
105	6.5	gnf1m04422_a_at	NM_024279	1700094C09	hypothetical protein
106	6.5	gnf1m01267_a_at	NM_008299	1700007A15	DnaJ (Hsp40) homolog, subfamily B, member 3
107	6.4	gnf1m18660_at		1700108N11	ovo-like 2 (Drosophila)
108	6.4	gnf1m11095_a_at	NM_023781	1700020D05	weakly similar to predicted mage-g2 protein
109	6.4	gnf1m17095_a_at	XM_915516	4930579F01	similar to predicted stromal protein associated with thymii and lymph nodes isoform 2

110	6.4	gnf1m23194_a_at	NM_013637	1700123E07	protamine 1
111	6.4	gnf1m16837_a_at	NM_009618	4932435D11	a disintegrin and metallopeptidase domain 2
112	6.4	gnf1m18722_a_at		4930597B14	leucine rich repeat containing 56
113	6.4	gnf1m05482_at	NM_029587	1700012A03	hypothetical protein
114	6.4	gnf1m30466_a_at	NM_001033159	4933407K12	zinc finger protein 597
115	6.4	gnf1m23185_a_at	XM_484951	1700056E22	hypothetical protein
116	6.4	gnf1m03233_a_at	NM_013687	1700025P05	weakly similar to t-complex protein 11
117	6.4	gnf1m01645_a_at	NM_008978	4921505B14	protein tyrosine phosphatase, non-receptor type 20 (Ptpn20)
118	6.4	gnf1m04833_a_at	NM_026105	1700093K21	hypothetical protein
119	6.4	gnf1m06613_at	NM_145746		outer dense fiber of sperm tails 4
120	6.4	gnf1m14421_at		1700056P15	thioredoxin domain containing 3 (spermatozoa)
121	6.4	gnf1m15372_a_at	XM_918155	1700006F03	predicted cystatin 12
122	6.4	gnf1m00200_a_at	NM_178388	4930425N13	similar to hexosaminidase A
123	6.3	gnf1m16785_at		1700012F11	weakly similar to predicted late cornified envelope-like proline-rich 1-like [Macaca mulatta]
124	6.3	gnf1m30605_a_at		4930467B22	ATP-binding cassette, sub-family C (CFTR/MRP), member 12
125	6.3	gnf1m13528_a_at		4930553D19	MAS20 protein import receptor signature containing protein
126	6.3	gnf1m11098_a_at	NM_030237	1700027M20	spermatogenic Zip 1
127	6.3	gnf1m31104_at			ENSMUST00000065798 transcript (in rel.37.34e)
128	6.3	gnf1m17234_a_at	NM_028525	1700049K14	weakly similar to predicted Plasma kallikrein precursor (Plasma prekallikrein) (Kininogenin) (Fletcher factor)
129	6.3	gnf1m13649_a_at	XM_921926	4933424C13	weakly similar to SH2 domain containing 6, transcript variant 3
130	6.3	gnf1m16782_a_at	XM_916123	1700030E15	PMP22 claudin domain-containing protein (Pmp22cd)
131	6.3	gnf1m03152_a_at	NM_013558	1700029P08	heat shock protein 1-like (Hspa1l)
132	6.3	gnf1m17328_a_at		4933432N21	homologue testis specific 10 (Tsga10)
133	6.3	gnf1m03870_a_at	NM_019964	1700016F14	DnaJ (Hsp40) homolog, subfamily B, member 8
134	6.3	gnf1m23680_a_at	NM_001024910	4921515A04	septin 10
135	6.3	gnf1m22992_a_at	NM_029160	4933402H05	hypothetical G-protein beta WD-40 repeats containing protein
136	6.3	gnf1m05228_s_at	NM_198677	1700001F09	hypothetical Cytochrome c family heme-binding site containing protein
137	6.3	gnf1m30747_at			Transcribed locus, weakly similar to XP_059954.2 PREDICTED: hypothetical protein XP_059954 [Homo sapiens]
138	6.2	gnf1m13976_a_at		4930570O04	unclassifiable
139	6.2	gnf1m29757_a_at	XM_905853	1810013N20	testis specific 10 interacting protein (Tsga10ip)
140	6.2	gnf1m17352_a_at	XM_913680	4921530D09	hypothetical protein
141	6.2	gnf1m05022_a_at	NM_026624	4931415M17	hypothetical protein
142	6.2	gnf1m07572_a_at	NM_026916	4930579G22	predicted Nuclear protein 1 (Protein p8) (Candidate of metastasis 1) Canis familiaris
143	6.2	gnf1m23028_a_at		1700025B10	unclassifiable
144	6.2	gnf1m11087_a_at	NM_013694	1700007A05	transition protein 2
145	6.2	gnf1m18372_a_at		1700006H02	cysteine-rich perinuclear theca 3 (Cypt3)
146	6.2	gnf1m03522_a_at	NM_016910	1700003P16	protein phosphatase 1D magnesium-dependent, delta isoform
147	6.2	gnf1m30439_a_at	NM_030107	1700047N01	nucleoporin 50-like, homologue [Rattus norvegicus]
148	6.2	gnf1m21699_a_at	NM_198623	4933400K24	ubiquilin 3
149	6.2	gnf1m04674_a_at	NM_025743	4933400A11	weakly similar to F-actin capping protein subunit alpha 1
150	6.2	gnf1m09684_a_at	NM_029606	1700029K01	weakly similar to coiled-coil domain containing 46
151	6.2	gnf1m09290_s_at	NM_198677	1700001F09	hypothetical Cytochrome c family heme-binding site containing protein
152	6.2	gnf1m16418_a_at		1700047I16	aldehyde dehydrogenase family 5, subfamily A1
153	6.2	gnf1m13790_a_at	XM_908032	1700056A17	melanoma antigen, family B, 5
154	6.2	gnf1m32681_at	XM_907853		gene model 77, (NCBI)
155	6.2	gnf1m21711_at	XM_900549	4933433K01	hypothetical Phospholipase D/nuclease structure containing protein
156	6.2	gnf1m01883_a_at	NM_009420		cysteine-rich secretory protein 2
157	6.2	gnf1m11535_a_at	NM_021317	1700021F12	DnaJ (Hsp40) homolog, subfamily B, member 7
158	6.2	gnf1m31557_at	NM_001033821	4933416C03	TATA box binding protein-associated factor, RNA polymerase II, Q
159	6.2	gnf1m04827_a_at	NM_026092	1700038F02	lysozyme-like 1
160	6.2	gnf1m13309_a_at	XM_917701	4933411K16	unclassifiable
161	6.2	gnf1m28993_at		4932432C05	similar to hypothetical P-loop containing nucleotide triphosphate hydrolases structure containing protein Mus musculus
162	6.1	gnf1m04975_a_at	NM_026461	1700129C05	hypothetical protein
163	6.1	gnf1m13089_a_at	NM_008807	4933432H20	tubby-like protein 2
164	6.1	gnf1m05414_a_at	NM_029131	4930503E14	weakly similar to alpha12-takusan
165	6.1	gnf1m30191_s_at	XM_913604	I920062J18	Proline-rich region profile containing protein
166	6.1	gnf1m04681_a_at		1700027I20	aldolase 1, A isoform, pseudogene 1
167	6.1	gnf1m29783_a_at	XM_910496	1700125D06	basic proline-rich protein [Sus scrofa]
168	6.1	gnf1m06267_a_at	NM_138657	M5C1099J02	suppressor of cytokine signaling 7 (Socs7)
169	6.1	gnf1m05339_a_at	NM_028671	4930432H15	hypothetical protein
170	6.1	gnf1m23650_at		4833401A03	polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like
171	6.1	gnf1m29197_a_at	NM_001033147	4921523C20	hypothetical protein
172	6.1	gnf1m01836_a_at	NM_009341	4921503O11	t-complex protein 10a
173	6.1	gnf1m18379_a_at	XM_907328	1700028F16	transmembrane and coiled-coil domains 2
174	6.1	gnf1m04828_a_at		1700065E01	ATPase, Class I, type 8B, member 3
175	6.1	gnf1m03186_a_at	NM_013615	I920013F22	outer dense fiber of sperm tails 2
176	6.1	gnf1m29413_a_at	NM_001033162	4922505A09	unnamed protein product putative GE36-like
177	6.1	gnf1m16899_a_at	XM_925370	4921508H09	IQ motif containing H
178	6.1	gnf1m16285_at		4930571K23	unclassifiable
179	6.1	gnf1m17304_a_at		1700029M20	unclassifiable
180	6.1	gnf1m02292_a_at	NM_010294	1700037H23	glycerol kinase 2
181	6.1	gnf1m08368_a_at	NM_178722	D330025M16	zinc finger, HIT domain containing 2
182	6.1	gnf1m05467_a_at	NM_029472	4930583C14	glutathione S-transferase, theta 4 (Gstt4)
183	6.1	gnf1m28744_a_at	NM_001008547	1700001J03	Ras GEF structure containing protein
184	6.1	gnf1m10484_a_at	NM_029019	4833424I06	hypothetical StAR-related lipid transfer (START) domain containing 6
185	6.1	gnf1m04449_a_at	NM_025271	1700051E21	weakly similar to hypothetical actin-like 7b
186	6.1	gnf1m17100_a_at		4921517L17	Cyclic nucleotide-binding domain/cAMP/cGMP binding motif profile containing protein, [Mus musculus]
187	6.0	gnf1m35021_at	XM_905573		similar to Protein tyrosine phosphatase type IVA protein 2 (Protein-tyrosine phosphatase 4a2) (Protein-tyrosine phosphatase of regenerating liver-2) (PRL-2)
188	6.0	gnf1m13320_a_at		1700058G18	hypothetical protein
189	6.0	gnf1m18464_x_at	XM_900744	4933402N22	spermatogenesis associated glutamate (E)-rich protein 1, pseudogene 1
190	6.0	gnf1m03507_a_at	NM_016875	4930590O05	Y box protein 2
191	6.0	gnf1m04122_a_at	NM_021497		poliovirus receptor-related 3
192	6.0	gnf1m13535_a_at	XM_905691	1700006E09	hypothetical protein
193	6.0	gnf1m23176_x_at	NM_001025241	1700029H17	similar to predicted Ssty2 protein isoform 1
194	6.0	gnf1m31219_at	XM_916339		similar to ribosomal protein L10
195	6.0	gnf1m29281_a_at	NM_001033371	4930560D22	leucine rich repeat containing 36
196	6.0	gnf1m00010_at	NM_011571	G630012H19	testis specific protein kinase 1
197	6.0	gnf1m18469_a_at	NM_027631	4922502J23	putative unnamed protein product
198	6.0	gnf1m16052_a_at	NM_028560	1700081D17	similar to PEBP family protein precursor
199	6.0	gnf1m13311_a_at		4933436O18	similar to ankyrin repeat and SOCS box-containing protein 17
200	6.0	gnf1m25487_at		A230094D06	G protein-coupled receptor 106
201	6.0	gnf1m05152_a_at	NM_027304	1700026P10	H1 histone family, member N, testis-specific (H1fnt)
202	6.0	gnf1m14468_at		4930405A07	unclassifiable
203	6.0	gnf1m21682_at		4930551J12	unclassifiable
204	6.0	gnf1m15984_a_at	NM_177593		hypothetical protein MGC48079
205	6.0	gnf1m31099_a_at		1700027A15	hypothetical protein
206	6.0	gnf1m05413_a_at		4930500C14	ATPase, H+ transporting, lysosomal V1 subunit E2
207	6.0	gnf1m15286_a_at	XM_906366	1700054J20	hypothetical protein
208	6.0	gnf1m17051_a_at	NM_029671	1700034O15	hypothetical protein
209	6.0	gnf1m17239_a_at	XM_909411	1700016M24	ARM repeat structure containing protein
210	6.0	gnf1m04675_a_at	XR_000398	4933415F23	protein phosphatase 1, regulatory (inhibitor) subunit 14B (Ppp1r14b) Mus musculus
211	6.0	gnf1m30192_a_at	XM_913604	I920062J18	Proline-rich region profile containing protein
212	6.0	gnf1m02858_a_at	NM_011569	4930512O07	tektin 1
213	6.0	gnf1m04830_a_at	NM_026099	1700124G06	hypothetical protein
214	6.0	gnf1m33287_at			gene model 555, (NCBI)
215	5.9	gnf1m13343_at		1700007N18	coiled-coil domain containing 54
216	5.9	gnf1m13524_at	NM_013811		dynein, axonemal, heavy chain 8
217	5.9	gnf1m14497_at	XM_921014	1700016H13	hypothetical protein
218	5.9	gnf1m09323_a_at	NM_144953	1700030B07	hypothetical protein
219	5.9	gnf1m16460_a_at	NM_198000	4930558A17	unclassifiable
220	5.9	gnf1m04659_a_at	NM_025719	4921504I05	hypothetical Lysine-rich region profile containing protein
221	5.9	gnf1m01977_a_at	NM_009611	1700038F08	actin-like 7a
222	5.9	gnf1m10564_at		3830408C23	ankyrin repeat and SOCS box-containing protein 17
223	5.9	gnf1m16879_a_at	XM_925391	1700028D05	coiled-coil domain containing 19
224	5.9	gnf1m35156_at	XM_912668		similar to KIAA1683
225	5.9	gnf1m11727_a_at	NM_019586	1700120K02	ubiquitin-conjugating enzyme E2, J1
226	5.9	gnf1m00890_a_at	NM_007593	4930590H21	centrin 1
227	5.9	gnf1m32036_at	NM_001039242	4922503O18	hypothetical Proline-rich region profile containing protein
228	5.9	gnf1m11092_a_at	NM_023508	4922504H01	phosducin-like 2
229	5.9	gnf1m05047_a_at	NM_026668	4930400A03	weakly similar to Suppressor Of Clr family member (soc-2) [Macaca mulatta]
230	5.9	gnf1m29416_a_at	NM_027283	F630225G14	testis specific protein kinase 1
231	5.9	gnf1m16355_a_at		1700110M21	gamma-aminobutyric acid (GABA-B) receptor binding protein
232	5.9	gnf1m00498_a_at	NM_026314	4930439O17	dyslexia susceptibility 1 candidate 1 homolog (human)
233	5.9	gnf1m30571_a_at	XM_908332	3300001K11	tektin 5 (Tekt5)

234	5.9	gnf1m23054_a_at	NM_183272	1700119N03	unclassifiable
235	5.9	gnf1m14530_a_at	XM_904411	4933422M21	ADP-ribosylation factor-like 13
236	5.9	gnf1m30644_at	NM_199312		cDNA sequence BC051628
237	5.9	gnf1m03857_at	NM_019943		poly (A) polymerase beta (testis specific)
238	5.8	gnf1m16867_a_at	NM_027074	1700025F22	hypothetical protein
239	5.8	gnf1m13851_a_at	NM_027970	1700023E05	similar to testicular haploid expressed gene product isoform 2 Rattus norvegicus
240	5.8	gnf1m16809_a_at	XM_913316	1700029J11	hypothetical protein
241	5.8	gnf1m22995_a_at		4933425D22	unclassifiable
242	5.8	gnf1m07900_a_at	NM_177765	4921538O11	tubulin tyrosine ligase-like family, member 13 (Ttll13)
243	5.8	gnf1m17150_a_at	XM_915196	1700017N19	zinc finger CCCH type containing 11A (MGC134438) Bos taurus
244	5.8	gnf1m15272_a_at	XM_914729	1700106J16	hypothetical protein
245	5.8	gnf1m17672_at		1700080P15	protocadherin 8
246	5.8	gnf1m04678_a_at	NM_025750	4933411N24	hypothetical protein
247	5.8	gnf1m04672_a_at	NM_025738	4931420D14	Cysteine-rich region containing protein
248	5.8	gnf1m09776_a_at	NM_175368	4933402P03	hypothetical protein
249	5.8	gnf1m11493_a_at	NM_007605	4930594D03	capping protein (actin filament) muscle Z-line, alpha 3
250	5.8	gnf1m10353_at	NM_178254		transcription factor-like 5 (basic helix-loop-helix)
251	5.8	gnf1m02095_a_at	NM_009839	4922503G10	chaperonin subunit 6b (zeta)
252	5.8	gnf1m30330_at	XM_908720		gene model 1276, (NCBI)
253	5.8	gnf1m08603_a_at	NM_177867	4933414G08	spermatogenesis associated 21 (GO:0005509 InterPro|IPR002048)
254	5.8	gnf1m34593_at	NM_001033338	4932412L17	SH3/Fibronectin, type III/Src homology 3 (SH3) domain profile/Fibronectin, type III-like fold containing protein
255	5.8	gnf1m15591_a_at	NM_009978	6030447N09	hypothetical cystatin 8 (cystatin-related epididymal spermatogenic)
256	5.8	gnf1m34052_at	NM_027041		RIKEN cDNA 1700003M02 gene
257	5.8	gnf1m31382_at			inferred: gb|AAB21180.2|(S79195) alpha-tubulin [Schistosoma mansoni] mCG1132
258	5.8	gnf1m21654_a_at	XM_910194	4922501K12	hypothetical protein
259	5.8	gnf1m18367_a_at		1700001K23	hypothetical protein
260	5.8	gnf1m04557_a_at	NM_025487	1700093C11	keratin type II (fragment) [Ovis sp.]
261	5.8	gnf1m13765_a_at		1700023B23	TSC22-related inducible leucine zipper protein 2 homolog [Mus musculus]
262	5.8	gnf1m05914_a_at	NM_080510	4921519C19	similar to ring finger protein 36
263	5.8	gnf1m16440_at		4930442P07	unclassifiable
264	5.8	gnf1m08509_a_at	NM_177576	4930517I12	Sad1 and UNC84 domain containing 1
265	5.8	gnf1m09369_a_at	XM_911762	1700129L13	host cell factor C2
266	5.8	gnf1m05019_a_at	NM_026619	1700111D04	glutathione S-transferase omega 2
267	5.8	gnf1m29993_a_at	XM_916773	1700057K13	hypothetical protein
268	5.8	gnf1m09975_a_at	NM_027699	1700108M19	hypothetical protein
269	5.8	gnf1m16805_a_at	NM_199419	1700017D11	zona pellucida binding protein 2
270	5.7	gnf1m07901_a_at	NM_177076	4921539K22	F-box and leucine-rich repeat protein 13
271	5.7	gnf1m30626_at	NM_001024841	G630078G02	maelstrom homolog (Drosophila)
272	5.7	gnf1m16137_a_at	XM_924059	1190002A17	hypothetical Adenylate kinase containing protein
273	5.7	gnf1m16786_at	NM_030097	1700034E13	hypothetical Zinc finger, C2H2 type containing protein
274	5.7	gnf1m32047_at			ATPase, Na+/K+ transporting, alpha 4 polypeptide
275	5.7	gnf1m14460_a_at	XM_908910	4930415F15	hypothetical protein
276	5.7	gnf1m14533_a_at	XM_619327	4933426G20	P-loop containing nucleotide triphosphate hydrolases structure containing protein
277	5.7	gnf1m18623_a_at	XM_915135	4933413L02	kinesin family member 2B
278	5.7	gnf1m05111_a_at	NM_027063	1700013G24	hypothetical protein
279	5.7	gnf1m05805_a_at	NM_053156	1700012B22	allantoicase
280	5.7	gnf1m30457_a_at		1700019G24	unclassifiable
281	5.7	gnf1m16775_a_at	NM_011516	4930447O18	atonal homolog 8 (Drosophila)
282	5.7	gnf1m14505_at	NM_028852	1700084J23	spermatogenesis and centriole associated 1
283	5.7	gnf1m23842_s_at	XM_916109	4932442C03	hypothetical KIAA1211 protein
284	5.7	gnf1m18943_a_at	XM_917572	1700026H02	similar to AMP-dependent synthetase and ligase containing protein
285	5.7	gnf1m16848_at		1700010B08	hypothetical protein
286	5.7	gnf1m07557_at	NM_178776	A930027N24	cDNA sequence BC049715
287	5.7	gnf1m23721_a_at	XM_909931	1700026A08	potassium channel tetramerisation domain containing 16
288	5.7	gnf1m09162_s_at	XM_891342	1700023A18	phosphatidylethanolamine binding protein 2
289	5.7	gnf1m07836_s_at	XM_356072	4932703D08	a disintegrin and metallopeptidase domain 25 (testase 2)
290	5.7	gnf1m17137_a_at	NM_025499	4922505M08	EP300 interacting inhibitor of differentiation 3 (Eid3) Mus musculus
291	5.7	gnf1m05102_a_at	NM_027019	1700011O04	outer dense fiber of sperm tails 3
292	5.7	gnf1m00905_a_at	NM_007628	4933406P14	cyclin A1
293	5.7	gnf1m01946_x_at	NM_009529		Xlr-related, meiosis regulated
294	5.7	gnf1m04090_a_at	NM_021440	4921507E16	testis specific protein, Ddc8
295	5.7	gnf1m29211_at	NM_198673	D330014A03	outer dense fiber of sperm tails 3-like 1
296	5.7	gnf1m14454_a_at	XM_915983	4930404H21	hypothetical protein
297	5.7	gnf1m22221_a_at	NM_001033550	C920025L08	sperm mitochondria-associated cysteine-rich protein
298	5.7	gnf1m04909_a_at	NM_026294	1700025O14	RHO GTPASE (FRAGMENT) homolog [Platichthys flesus]
299	5.7	gnf1m01894_a_at	NM_009436		testis-specific serine kinase 2
300	5.7	gnf1m11503_a_at	NM_028513	4931440G22	actin-related protein T2
301	5.7	gnf1m04667_a_at	NM_025731	4921526K24	HRAS-like suppressor family, member 5
302	5.6	gnf1m19286_s_at	NM_181816	4933401K09	coiled-coil domain containing 67 (Ccdc67)
303	5.6	gnf1m16079_a_at	XM_924997	6330543E12	IQ motif and WD repeats 1
304	5.6	gnf1m11500_a_at	NM_177785	4931430D02	hypothetical Serine-rich region profile containing protein Mus musculus
305	5.6	gnf1m29836_a_at	XM_910312	1700013F07	hypothetical protein
306	5.6	gnf1m31171_a_at		3526402J02	ataxia telangiectasia and rad3 related
307	5.6	gnf1m29816_a_at	XM_920535	1700092M07	unclassifiable
308	5.6	gnf1m19128_at	NM_198251	1700042K15	ring finger protein 133
309	5.6	gnf1m18415_a_at	XM_913826	1700030G11	weakly similar to novel protein containing an anlyrin domain
310	5.6	gnf1m06632_a_at	NM_145852	1700000A07	ropporin 1-like
311	5.6	gnf1m23688_at	NM_029467	4921523E13	testicular cell adhesion molecule 1
312	5.6	gnf1m04680_s_at	NM_025753	1700021A04	hypothetical protein
313	5.6	gnf1m00717_a_at	NM_177313	1700006J14	hypothetical protein
314	5.6	gnf1m04829_a_at	NM_026096	1700054O13	HUNTINGTIN INTERACTING PROTEIN HYPM (FRAGMENT) [Homo sapiens]
315	5.6	gnf1m29329_a_at	XM_914291	1700013E09	weakly similar to arrestin domain containing 5
316	5.6	gnf1m16354_at		1700110M21	gamma-aminobutyric acid (GABA-B) receptor binding protein
317	5.6	gnf1m16828_a_at	NM_029627	2410015A16	ring finger protein 148
318	5.6	gnf1m05108_a_at	NM_027036	1700001F22	high-mobility group box 4
319	5.6	gnf1m05415_a_at	NM_029141	4930511M11	glutamate receptor Gr1 [Bombyx mori]
320	5.6	gnf1m18640_a_at		4930414N22	hypothetical protein
321	5.6	gnf1m04194_a_at	NM_022033	4933401C12	3-oxoacid CoA transferase 2A
322	5.6	gnf1m31519_at	XM_908009		coiled-coil domain containing 27
323	5.6	gnf1m09496_a_at	NM_029597	1700084O22	hypothetical protein
324	5.6	gnf1m31638_at	NM_001004193		reproductive homeobox 8
325	5.6	gnf1m27335_a_at		D030060E19	hypothetical S-adenosyl-L-methionine-dependent methyltransferases structure containing protein
326	5.6	gnf1m16801_a_at		1700034G24	unclassifiable
327	5.6	gnf1m04835_a_at	NM_026108	4921518O14	haloacid dehalogenase-like hydrolase domain
328	5.6	gnf1m08596_at	NM_175349	4933402O15	lactate dehydrogenase A-like 6B
329	5.6	gnf1m04609_a_at	NM_025601	4933405L11	hypothetical protein
330	5.6	gnf1m04774_a_at		1700095P10	hypothetical protein
331	5.6	gnf1m21667_at		4930427O07	hypothetical protein
332	5.6	gnf1m16762_at	XM_913921	1700024P04	HISTONE H2B
333	5.6	gnf1m13456_at	NM_029779	4930432J16	coiled-coil domain containing 116
334	5.5	gnf1m33591_at	XM_910994		similar to regulator of G-protein signalling 22
335	5.5	gnf1m31460_at	XM_909445		zinc finger protein 711
336	5.5	gnf1m17287_a_at	XM_911180	4930509B16	motile sperm domain containing 4
337	5.5	gnf1m02604_a_at	NM_011033	4933413O15	poly A binding protein, cytoplasmic 2
338	5.5	gnf1m02518_a_at	NM_010787	2700096H08	male enhanced antigen 1
339	5.5	gnf1m19258_at		4931412E05	zinc finger protein 148, pseudogene 1
340	5.5	gnf1m03383_a_at	NM_015773		sperm associated antigen 6
341	5.5	gnf1m13500_a_at		1700113H08	hypothetical protein
342	5.5	gnf1m32251_at	NM_001037749		solute carrier family 22 (organic cation transporter), member 14
343	5.5	gnf1m00135_a_at	NM_029772	4921522D01	cation channel, sperm associated 3
344	5.5	gnf1m28600_a_at		4930414P16	proacrosin binding protein
345	5.5	gnf1m15462_at		1700031F10	hypothetical DnaJ (Hsp40) homolog, subfamily B, member 8
346	5.5	gnf1m11486_s_at	NM_177203	4930554N06	hypothetical protein
347	5.5	gnf1m15497_a_at		1700021J15	hypothetical adenylate kinase 3
348	5.5	gnf1m29059_a_at		1700109H08	EF-hand containing protein
349	5.5	gnf1m16931_a_at	XM_920040	1700034K16	hypothetical Leucine-rich repeat/Leucine-rich repeat, typical subtype containing protein
350	5.5	gnf1m05913_a_at	NM_080470		SMC (structural maintenace of chromosomes 1)-like 2 (S. cerevisiae)
351	5.5	gnf1m14420_at	NM_199455	1700055M20	similar to testis/prostate/placenta-expressed protein (Tepp), Rattus norvegicus
352	5.5	gnf1m34195_at	XM_904650		RIKEN cDNA 4930455B06 gene
353	5.5	gnf1m30329_at	NM_183190		membrane-spanning 4-domains, subfamily A, member 5
354	5.5	gnf1m22181_at	NM_198421	C330046L10	ubiquitin specific peptidase 49
355	5.5	gnf1m17690_at		A630039F22	spermatogenesis associated 21
356	5.5	gnf1m30109_a_at		4930403E08	hypothetical protein
357	5.5	gnf1m04912_a_at	NM_026300	4930549C01	hypothetical Arginine-rich region containing protein
358	5.5	gnf1m17628_s_at	XM_909667		hematopoietic cell transcript 1
359	5.5	gnf1m17481_a_at	NM_029202	4933402A08	weakly similar to ANKYRIN MOTIF [Homo sapiens]
360	5.5	gnf1m07933_a_at	NM_172879	4932412H11	Leucine-rich repeat/Leucine-rich repeat, typical subtype containing protein
361	5.5	gnf1m05432_a_at	NM_029299	1700001L23	spermatogenesis associated 19
362	5.5	gnf1m17365_a_at		1700104L12	unclassifiable
363	5.5	gnf1m18797_at		1700096P12	hypothetical protein
364	5.5	gnf1m03390_s_at	NM_015785	4921520L14	zona pellucida binding protein
365	5.5	gnf1m02854_s_at	NM_011560	1700026A18	t-complex-associated testis expressed 3
366	5.5	gnf1m30831_a_at	XM_905557	1700012C08	unclassifiable
367	5.4	gnf1m18455_at	XM_914292	3830402K23	synaptonemal complex protein 2 (Sycp2)
368	5.4	gnf1m04665_a_at	NM_025727	4933430B12	kelch-like 10 (Drosophila)
369	5.4	gnf1m23022_a_at		1700108A15	unclassifiable
370	5.4	gnf1m07331_a_at	NM_153397	1700008E04	a disintegrin and metallopeptidase domain 32
371	5.4	gnf1m04911_a_at	NM_026298	1700016A07	intraflagellar transport 172

					homolog (Chlamydomonas)
372	5.4	gnf1m08607_a_at	NM_177738	4933421C08	hypothetical protein
373	5.4	gnf1m04668_a_at	NM_025732	4933434E03	Ankyrin repeat profile/Ankyrin-repeat/Ankyrin repeat region circular profile/Yeast DNA-binding domain containing protein
374	5.4	gnf1m05232_at	XM_895197	1700017G21	weakly similar to GERM CELL-LESS 1 PROTEIN [Mus musculus]
375	5.4	gnf1m02371_a_at	NM_010445		H6 homeo box 1
376	5.4	gnf1m04565_a_at	NM_025503	1700121E04	NEURONAL PROTEIN 15.6 [Mus musculus]
377	5.4	gnf1m12700_at	NM_029992	C530035A16	similar to trichoplein, keratin filament binding
378	5.4	gnf1m28807_a_at		1700016K02	hypothetical protein
379	5.4	gnf1m29282_a_at	NM_028888	4931428F04	hypothetical protein
380	5.4	gnf1m04663_a_at	NM_025724	4921510H08	Glutamic acid-rich region containing protein
381	5.4	gnf1m23777_at		4930555L03	IBR domain containing 3
382	5.4	gnf1m08585_a_at	NM_177719	4932411A10	hypothetical microrchidia 2B
383	5.4	gnf1m13287_a_at	NM_017397	F630042F15	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20 (Ddx20)
384	5.4	gnf1m34642_at	XM_916095		RIKEN cDNA 1700001J11 gene
385	5.4	gnf1m29752_a_at	NM_001033043		ring finger protein 17
386	5.4	gnf1m05313_a_at	NM_028494	4931430J05	weakly similar to unnamed protein product putative DC44 [Homo sapiens]
387	5.4	gnf1m17372_a_at	XM_922004	4921510J17	hypothetical EF-hand containing protein
388	5.4	gnf1m23355_a_at	NM_008265	2810017G21	homeo box A4
389	5.4	gnf1m35671_at	XM_909608		similar to IQ motif containing F4
390	5.4	gnf1m05104_a_at	NM_027026	1700006D24	leucine rich repeat containing 46
391	5.4	gnf1m21705_at	NM_175033	4933406N18	selenoprotein W
392	5.4	gnf1m01900_s_at	NM_009449	4922505K03	tubulin, alpha 3
393	5.4	gnf1m29143_at	NM_001039114		acyl-CoA synthetase bubblegum family member 2
394	5.4	gnf1m04115_a_at	NM_021482	1700016O14	weakly similar to synaptogyrin 4
395	5.4	gnf1m16886_a_at	XM_917213	1700011E24	hypothetical protein
396	5.4	gnf1m16866_a_at	XM_621008	4930527E24	weakly similar to Xlr-like
397	5.4	gnf1m13830_a_at	XM_132958	1700023A16	hypothetical protein
398	5.4	gnf1m14298_a_at	XM_913910	4930535E05	weakly similar to predicted T-cell activation Rho GTPase-activating protein isoform b
399	5.4	gnf1m12062_a_at	NM_178914	4922505M13	predicted spermatogenesis associated 7
400	5.3	gnf1m22798_a_at		4930544D05	cholinergic receptor, nicotinic, epsilon polypeptide
401	5.3	gnf1m11136_s_at	NM_026370	I920045M18	MYST histone acetyltransferase 1
402	5.3	gnf1m21707_a_at	NM_199019	4933407P14	intramembrane protease 5 Rattus norvegicus
403	5.3	gnf1m13520_at		4930452G13	unclassifiable
404	5.3	gnf1m16055_a_at	NM_027660	4933407G07	tektin 3
405	5.3	gnf1m02761_a_at	NM_011353	1700008J04	small EDRK-rich factor 1
406	5.3	gnf1m08962_s_at	NM_177759	C130098D09	ATP/GTP binding protein-like 5 (Agbl5), transcript variant 3
407	5.3	gnf1m09361_a_at	NM_023431	8030492M19	melanoma associated antigen (mutated) 1
408	5.3	gnf1m00690_a_at	NM_028848	4930513F16	hypothetical IQ calmodulin-binding motif containing protein
409	5.3	gnf1m18944_a_at		1700085A12	similar to partial Cypt15 gene for putative cysteine-rich perinuclear theca protein Mus musculus
410	5.3	gnf1m17104_at		4933438K21	unclassifiable
411	5.3	gnf1m16949_a_at		1700020N01	weakly similar to ZINC FINGER PROTEIN (FRAGMENT) [Homo sapiens]
412	5.3	gnf1m31215_s_at	XM_917051	4933439H17	hypothetical Peptidase, eukaryotic cysteine peptidase active site containing protein
413	5.3	gnf1m17145_a_at		1700058C13	weakly similar to Short palate, lung and nasal epithelium carcinoma-associated protein 3 homolog precursor Rattus norvegicus
414	5.3	gnf1m13380_a_at	XM_910715	4933427K18	PROTEIN PHOSPHATASE INHIBITOR 2 (IPP-2) [Rattus norvegicus]
415	5.3	gnf1m18853_a_at	NM_029939	5930422B18	unclassifiable
416	5.3	gnf1m04972_a_at	NM_026449	4930599B21	hypothetical Glycosyl transferase, family 2/Microbodies C-terminal targeting signal containing protein
417	5.3	gnf1m14433_s_at		4930551J12	unclassifiable
418	5.3	gnf1m28768_a_at	XM_917740	A530057A03	similar to predicted similar to mitochondrial glycerol 3-phosphate acyltransferase
419	5.3	gnf1m18365_a_at	XM_131958	4930584F24	hypothetical protein
420	5.3	gnf1m31738_at	XM_910141		hypothetical LOC433757
421	5.3	gnf1m14127_a_at	XM_915378	4921539E11	hypothetical protein
422	5.3	gnf1m18795_at		1700099I09	unclassifiable
423	5.3	gnf1m10020_a_at	NM_178387	1700067I02	spermatogenesis associated 18 (Spata18)
424	5.3	gnf1m17067_a_at		1700008A04	hypothetical protein
425	5.3	gnf1m04901_a_at	NM_026283	1700021J16	similar to sterile alpha motif domain containing 8
426	5.3	gnf1m02318_a_at	NM_010353		germ cell-specific gene 2
427	5.3	gnf1m16472_a_at	XM_910123	4930578N16	SH2 domain containing 4B Macaca mulatta
428	5.3	gnf1m04878_a_at	NM_026208	1700027I10	hypothetical protein
429	5.3	gnf1m09173_s_at	XM_922236	4930506L13	tetratricopeptide repeat domain 30A1 (Ttc30a1) homologue [Mus musculus]
430	5.3	gnf1m09049_at	NM_174885		a disintegrin and metallopeptidase domain 6
431	5.3	gnf1m18414_at		1700030L20	developmentally regulated repeat element-containing transcript 1a
432	5.3	gnf1m00344_s_at	NM_011973		renal tumor antigen
433	5.3	gnf1m15214_at	NM_030150		DNA segment, Chr 11, Lothar Hennighausen 2, expressed
434	5.3	gnf1m13810_a_at		4932700H03	a disintegrin and metalloprotease domain 5
435	5.3	gnf1m30921_s_at		4921509O09	weakly similar to predicted Sycp3 like Y-linked
436	5.3	gnf1m23031_a_at		4930558C23	unclassifiable
437	5.3	gnf1m01899_x_at	NM_009446		tubulin, alpha 3
438	5.3	gnf1m00213_at	NM_178936	4930577M16	transmembrane protein 56
439	5.3	gnf1m23872_at		4933434I20	hypothetical Prokaryotic membrane lipoprotein lipid attachment site containing protein
440	5.2	gnf1m18610_a_at	XM_923498	1700031M16	unclassifiable
441	5.2	gnf1m21700_a_at	NM_001001177	4933401F02	weakly similar to hypothetical Cysteine-rich region profile/Lysine-rich region profile containing protein
442	5.2	gnf1m32619_at			RIKEN cDNA 1700023F06 gene
443	5.2	gnf1m18956_a_at		8030402F09	Retroviral matrix proteins structure containing protein
444	5.2	gnf1m05322_a_at	NM_028557	1700095H13	methyl-CpG binding domain protein 3-like 1
445	5.2	gnf1m02161_a_at	NM_009989	1700048D19	hypothetical cytochrome c, testis
446	5.2	gnf1m14679_a_at	XM_919213	4930505A04	hypothetical protein
447	5.2	gnf1m08609_at	NM_172808	4933430J11	anthrax toxin receptor-like (Antxrl) Mus musculus
448	5.2	gnf1m04025_a_at	NM_021308	B830005G15	piwi-like homolog 2 (Drosophila)
449	5.2	gnf1m11101_a_at		6030488D03	hypothetical protein
450	5.2	gnf1m14102_a_at	XM_910370	4921511I05	solute carrier organic anion transporter family, member 6d1
451	5.2	gnf1m01563_a_at	NM_008811	4930458G11	pyruvate dehydrogenase E1 alpha 2
452	5.2	gnf1m13386_a_at		4932411E05	similar to predicted restin-like 2
453	5.2	gnf1m30782_a_at	XM_924920	1700006H03	hypothetical protein
454	5.2	gnf1m05324_a_at	NM_028562	1700080E11	Nucleoside diphosphate-linked moiety X motif 16 (Nudix motif 16) like [Rattus norvegicu]
455	5.2	gnf1m07926_a_at	NM_172864	4931433A13	hypothetical TESTIS DEVELOPMENT PROTEIN NYD-SP29 [Homo sapiens]
456	5.2	gnf1m05446_s_at	NM_029373	1700025E21	hypothetical protein
457	5.2	gnf1m13832_a_at	XM_924281	4921509B22	hypothetical Leucine-rich repeat/bZIP (Basic-leucine zipper) transcription factor family/Leucine-rich repeat, typical subtype containing protein
458	5.2	gnf1m04669_a_at	NM_025733	4921530L21	ATP/GTP-binding site motif A (P-loop) containing protein Mus musculus
459	5.2	gnf1m05221_s_at	NM_027891	I1C0027N22	leucine-rich repeats and WD repeat domain containing 1 (Lrwd1)
460	5.2	gnf1m22978_a_at	NM_183254	1700027K06	hypothetical protein
461	5.2	gnf1m05023_a_at	NM_026625	1700067P10	hypothetical protein
462	5.2	gnf1m33789_x_at	XM_920110		similar to spermatogenesis associated glutamate (E)-rich protein 2
463	5.2	gnf1m30265_a_at	XM_912989	I920019O09	ribonuclease H2, large subunit
464	5.2	gnf1m23745_s_at		4930469D11	cAMP responsive element modulator
465	5.2	gnf1m16802_a_at	XM_916850	4933406J07	synaptonemal complex central element protein 1
466	5.2	gnf1m01842_a_at	NM_009350	4930551A18	adenosine deaminase domain containing 1 (testis specific) (Adad1)
467	5.2	gnf1m04883_a_at	NM_026226	4932702K14	POLY A BINDING PROTEIN, CYTOPLASMIC 1 homolog [Mus musculus]
468	5.2	gnf1m04978_s_at	NM_026470	1700062C23	zinc finger protein 217
469	5.2	gnf1m11470_s_at	NM_009435	4930487F03	testis-specific serine kinase 1
470	5.2	gnf1m23825_at	NM_001004025	4932413P05	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type II)
471	5.2	gnf1m16041_a_at		1700020N15	hypothetical protein
472	5.2	gnf1m07614_at	NM_027616	4921517C16	similar to predicted Myosin heavy chain A (MHC A) Rattus norvegicus
473	5.2	gnf1m28992_s_at	NM_029714	4932441M08	P-loop containing nucleotide triphosphate hydrolases structure containing protein Mus musculus
474	5.2	gnf1m28680_a_at	XM_917134	1810037J08	phosphoglycerate kinase 2
475	5.2	gnf1m08576_at	NM_177677	4922503E23	DnaJ (Hsp40) homolog, subfamily C, member 5 gamma
476	5.2	gnf1m11501_at		4931433M19	Leucine-rich repeat containing protein
477	5.2	gnf1m13833_at		4930449C09	unclassifiable
478	5.2	gnf1m34257_at	XM_908619		similar to testis derived transcript isoform 1
479	5.2	gnf1m15086_a_at	NM_030089	4930471G03	unclassifiable
480	5.2	gnf1m04283_s_at	NM_023197	D130020I06	weakly similar to unnamed protein product TSG118.1 [Mus musculus]
481	5.2	gnf1m23167_a_at		1700018G05	unclassifiable
482	5.2	gnf1m10438_a_at	NM_026097	1700112P14	ring finger and FYVE like domain containing protein
483	5.2	gnf1m05239_a_at	NM_027985	G530145B18	MAD2 mitotic arrest deficient-like 2 (yeast) (Mad2l2)
484	5.2	gnf1m23188_a_at	NM_183271	1700085B22	hypothetical ELAFIN-LIKE PROTEIN I [Mus musculus]
485	5.2	gnf1m07706_at	NM_029294	4933430D15	phosphoribosyl pyrophosphate synthetase 1-like 1 (Prps1l1)
486	5.2	gnf1m05113_a_at	NM_027076	1700019M22	weakly similar to Lysine-rich region containing protein
487	5.2	gnf1m14022_a_at	XM_924671	1700028J19	RNA-binding region RNP-1 (RNA recognition motif) containing protein

488	5.2	gnf1m21712_a_at	NM_001007591	4933440E22	similar to Salivary glue protein Sgs-4 precursor
489	5.1	gnf1m04602_a_at	NM_025585	1700016J15	hypothetical protein
490	5.1	gnf1m18790_a_at	XM_485737	1700023L04	hypothetical protein
491	5.1	gnf1m18537_s_at	XM_916095	1700001J11	RING FINGER PROTEIN 19 (XY BODY PROTEIN) (XYBP) (GAMETOGENESIS EXPRESSED PROTEIN GEG-154) (UBCM4-INTERACTING PROTEIN 117) (UIP117) [Mus musculus]
492	5.1	gnf1m18868_a_at	XM_912521	4933440C21	DC-STAMP domain containing 1
493	5.1	gnf1m08593_at	NM_177801	4933400C05	hypothetical protein
494	5.1	gnf1m13575_a_at	XM_909321	1700055J15	IQ motif containing F1
495	5.1	gnf1m04869_a_at	NM_026188	4921527B01	hypothetical protein
496	5.1	gnf1m14147_at		4932703K07	heat shock protein 1, alpha
497	5.1	gnf1m33886_at			RIKEN cDNA D030041N04 gene
498	5.1	gnf1m16237_at		4930555P18	ring finger protein 139
499	5.1	gnf1m17677_a_at	NM_001039557	4921509H06	ribophorin II
500	5.1	gnf1m16806_a_at	NM_027025	1700001D09	adenosine A3 receptor (Adora3), transcript variant 2
501	5.1	gnf1m07287_a_at	NM_153109	4930524L02	TGIF homeobox 1
502	5.1	gnf1m30771_a_at		4930578E11	unclassifiable
503	5.1	gnf1m13328_a_at	XM_916685	4933422B16	hypothetical Tetratricopeptide repeat (TPR) structure containing protein
504	5.1	gnf1m29009_s_at	XM_917509	1700001J11	RING FINGER PROTEIN 19 (XY BODY PROTEIN) (XYBP) (GAMETOGENESIS EXPRESSED PROTEIN GEG-154) (UBCM4-INTERACTING PROTEIN 117) (UIP117) [Mus musculus]
505	5.1	gnf1m18620_a_at		1700048O14	unclassifiable
506	5.1	gnf1m13049_s_at	NM_016845	4930414P16	proacrosin binding protein
507	5.1	gnf1m23019_a_at	XM_925014	1700096M17	unclassifiable
508	5.1	gnf1m05230_a_at	NM_027949	1700010P14	PHD finger protein 7
509	5.1	gnf1m05869_a_at	NM_054066	1700041H07	phospholipase C, zeta 1
510	5.1	gnf1m16843_s_at	XM_910844	4921511M17	hypothetical protein
511	5.1	gnf1m29533_a_at	NM_008588	1700026M06	mesoderm posterior 1
512	5.1	gnf1m14871_a_at	NM_194065	1700111I05	Williams-Beuren syndrome chromosome region 28 Mus musculus
513	5.1	gnf1m16116_a_at	XM_924436	3110013H01	proline-rich polypeptide 6
514	5.1	gnf1m01008_a_at	NM_007827		decay accelerating factor 2
515	5.1	gnf1m04825_at		1700042N06	IQ motif containing F4
516	5.1	gnf1m14121_a_at	NM_027603	4930412D12	hypothetical protein
517	5.1	gnf1m18655_at		4931438A05	weakly similar to predicted vitamin A-deficient testicular protein 11-like
518	5.1	gnf1m17085_a_at		4930435E18	unclassifiable
519	5.1	gnf1m00466_a_at	NM_170777	E430037N03	WD repeat domain 62
520	5.1	gnf1m13998_a_at	XM_908598	1700017D01	hypothetical protein
521	5.1	gnf1m08583_a_at	NM_177616	4931408E15	hypothetical Glutamine-rich region profile containing protein Mus musculus
522	5.1	gnf1m09512_a_at	NM_144528	A630082B21	regulatory factor X, 2 (influences HLA class II expression)
523	5.1	gnf1m04671_a_at	NM_025737	4931417E11	JNK1-associated membrane protein, transcript variant 2 Pan troglodytes
524	5.1	gnf1m06454_a_at	NM_145157	4930563B01	similar to predicted defensin beta 19
525	5.1	gnf1m28673_a_at	XM_917268	4930469G21	hypothetical protein
526	5.1	gnf1m17273_a_at		1700063H04	hypothetical protein
527	5.0	gnf1m00611_a_at		4930563A13	XAP-5-LIKE PROTEIN homolog [Mus musculus]
528	5.0	gnf1m31643_at	XM_909045		similar to solute carrier organic anion transporter family, member 6c1
529	5.0	gnf1m03287_a_at	NM_013783	F630024E10	mel transforming oncogene-like 1
530	5.0	gnf1m30047_a_at	NM_029663	1700026P12	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
531	5.0	gnf1m31572_at			ENSMUST00000017126 transcript (in rel.37.34e)
532	5.0	gnf1m11449_at	NM_033077	4921521M13	DNA segment, Chr 1, Pasteur Institute 1
533	5.0	gnf1m04905_at		4930465K10	asteroid homolog 1 (Drosophila)
534	5.0	gnf1m08258_a_at	NM_175477	F630036J15	weakly similar to zinc finger protein 574
535	5.0	gnf1m05026_a_at	NM_026630	1700067M22	DJ1028D15.4 (NOVEL PROTEIN) [Homo sapiens]
536	5.0	gnf1m09678_a_at	NM_026293	4930540L03	similar to sperm acrosome membrane protein
537	5.0	gnf1m08579_a_at	NM_177567	4930503F14	hypothetical protein
538	5.0	gnf1m10425_a_at	NM_027300	1700029H01	spermatogenesis associated 3
539	5.0	gnf1m00518_a_at	NM_026359	1700008K17	calcium homeostasis endoplasmic reticulum protein like
540	5.0	gnf1m29254_a_at		1700010G02	weakly similar to predicted 5-oxoprolinase (ATP-hydrolysing)
541	5.0	gnf1m04677_a_at	NM_025749	4933409D10	zinc finger protein 474
542	5.0	gnf1m09987_s_at	NM_173019	F630205N16	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 (Pfkfb4)
543	5.0	gnf1m10164_a_at	NM_029602	4933417P13	ring finger protein 39
544	5.0	gnf1m11605_a_at	NM_025651	5430408G21	WW domain binding protein 11
545	5.0	gnf1m30510_at	NM_207232	4922505P07	hypothetical tyrosine specific protein phosphatase and dual specificity protein phosphatase family containing protein (Fragment) homolog [Mus musculus]
546	5.0	gnf1m32037_at	XM_907217		similar to Angiotensin-converting enzyme, testis-specific isoform precursor (ACE-T) (Dipeptidyl carboxypeptidase I) (Kininase II)
547	5.0	gnf1m03538_a_at	NM_016964	I530012K17	stromal antigen 3 (Stag3)
548	5.0	gnf1m17780_a_at		4921530L18	unclassifiable
549	5.0	gnf1m08599_a_at	NM_177570	4933406A14	schlafen like 1
550	5.0	gnf1m11446_a_at	NM_027588	4921514H13	5'-nucleotidase, cytosolic IB
551	5.0	gnf1m21698_a_at	NM_182785	4933400F01	Ly6/Plaur domain containing 4
552	5.0	gnf1m13868_a_at		4933409F16	hypothetical protein
553	5.0	gnf1m18614_at		1700036D21	SERINE PROTEASE-LIKE 1 homolog [Mus musculus]
554	5.0	gnf1m33866_at	XM_911493		phosphatidylglycerophosphate synthase 1
555	5.0	gnf1m07703_at	NM_029252	4930429C23	hypothetical protein
556	5.0	gnf1m17299_a_at	NM_183113	4932414N04	hypothetical protein
557	5.0	gnf1m10318_a_at	NM_013455	1700116D15	preproacrosin
558	5.0	gnf1m29406_a_at	NM_028957	4933406A08	hyaluronoglucosaminidase 5
559	5.0	gnf1m19292_a_at	NM_001002787	4933417A14	calicin
560	5.0	gnf1m07602_a_at	NM_153777	5730427C23	melanoma associated antigen (mutated) 1
561	5.0	gnf1m01239_a_at	NM_008232	4932442B12	hepatoma derived growth factor-like 1
562	5.0	gnf1m13975_a_at		4930432J01	unclassifiable
563	5.0	gnf1m05200_a_at	XM_917400	4933432K11	fibrous sheath-interacting protein 1
564	5.0	gnf1m16773_a_at	XM_921987	1110017D15	diablo homolog (Drosophila)
565	5.0	gnf1m09001_a_at	NM_172789	4932415D10	hypothetical protein
566	4.9	gnf1m07673_a_at	NM_175200	4921537E06	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 11 (human)
567	4.9	gnf1m05904_a_at	NM_080442	4930594I21	testis-specific serine kinase 3
568	4.9	gnf1m26405_a_at	NM_008468	1700093L14	karyopherin (importin) alpha 6
569	4.9	gnf1m15241_at	XM_889674	1700024G10	hypothetical Cytochrome c family heme-binding site containing protein
570	4.9	gnf1m29797_a_at	NM_028434	2900092C05	hypothetical protein
571	4.9	gnf1m30625_at	NM_198628		gene model 711, (NCBI)
572	4.9	gnf1m13484_a_at		1700021C14	SSTK-INTERACTING PROTEIN VARIANT (SIMILAR TO RIKEN CDNA 1700021C14 GENE) [Homo sapiens]
573	4.9	gnf1m31344_at			PREDICTED: Mus musculus similar to hypothetical protein LOC84070 (LOC545136)
574	4.9	gnf1m23957_a_at	XM_921833	5330437G15	serine/threonine kinase 33
575	4.9	gnf1m30296_at	XM_899628	3632444A02	tetratricopeptide repeat domain 21B
576	4.9	gnf1m07910_at	NM_176965	4930563A03	EF-hand calcium binding domain 5 (Efcab5)
577	4.9	gnf1m34001_at	XM_910563		tudor domain containing 6
578	4.9	gnf1m13582_a_at	XM_914306	1700013H16	hypothetical protein
579	4.9	gnf1m01668_a_at	NM_009028	1700025K02	RAS-like, family 2, locus 9
580	4.9	gnf1m15387_a_at	NM_028672		RIKEN cDNA 4930430E16 gene
581	4.9	gnf1m05337_a_at	NM_028634	1110014P06	solute carrier family 22 (organic cation transporter), member 21
582	4.9	gnf1m18132_a_at		1700003H21	EF hand calcium binding protein 1
583	4.9	gnf1m13378_a_at		4930488L21	unclassifiable
584	4.9	gnf1m03933_a_at	NM_020487	1700023E12	protease, serine, 21
585	4.9	gnf1m08598_a_at	NM_175296	G630083P15	maelstrom homolog (Drosophila)
586	4.9	gnf1m03696_a_at	NM_019457	4933408D12	leucine rich repeat containing 6 (testis)
587	4.9	gnf1m30255_at	NM_199309	4933411H15	zinc finger, DHHC domain containing 19
588	4.9	gnf1m04832_a_at	NM_026104	1700095F04	transmembrane and coiled-coil domains 5
589	4.9	gnf1m11445_a_at	NM_020330	4921506L22	a disintegrin and metallopeptidase domain 21 (Adam21)
590	4.9	gnf1m05105_a_at	NM_027027	1700011M07	ankyrin repeat and SOCS box-containing protein 9
591	4.9	gnf1m19031_at	XM_147508	4933404M19	weakly similar to predicted proline-rich cyclin A1-interacting protein isoform 1
592	4.9	gnf1m05196_a_at	XM_911175	4933411G06	weakly similar to SMT3 suppressor of mif two 3 homolog 1 isoform b precursor
593	4.9	gnf1m16749_a_at		1700025C14	unclassifiable
594	4.9	gnf1m32998_at			uncharacterized Celera prediction mCG131172
595	4.9	gnf1m29721_a_at	XM_916831	4930403N07	Centromeric protein E (CENP-E protein) like Rattus norvegicus
596	4.9	gnf1m14178_a_at		4933422A05	unclassifiable
597	4.9	gnf1m23783_a_at		4930568O20	hypothetical leucine rich repeat containing 9 (Lrrc9)
598	4.9	gnf1m04559_at	NM_025490	1700010M22	hypothetical SCP-2 sterol transfer domain containing protein
599	4.9	gnf1m21616_a_at	NM_175020	1700020H15	hypothetical Serine proteases, trypsin family containing protein
600	4.9	gnf1m18718_s_at	XM_925327	4921517J08	weakly similar to predicted speedy homolog 1 (Drosophila)
601	4.9	gnf1m29853_a_at	NM_029381	1700028O09	testis expressed gene 22
602	4.9	gnf1m09828_a_at	NM_134126	F830031M20	intraflagellar transport 140 homolog (Chlamydomonas)
603	4.9	gnf1m31891_at			inferred: ref|NP_035319.1| (NM_011189) proteasome (prosome, macropain) 28 subunit, alpha; protease (prosome, macropain) 28 subunit, alpha [Mus musculus] mCG50047
604	4.9	gnf1m33005_at	XM_906387		RIKEN cDNA 6430706D22 gene
605	4.9	gnf1m00618_a_at	NM_026225	4933405E16	component of oligomeric golgi complex 6
606	4.9	gnf1m30687_a_at	NM_001037941	1700006L23	DnaJ (Hsp40) homolog, subfamily B, member 6
607	4.9	gnf1m01426_a_at		1700122H24	meiosis expressed gene 1
608	4.9	gnf1m08682_a_at	NM_177759	C130098D09	ATP/GTP binding protein-like 5 (Agbl5), transcript variant 3

609	4.9	gnf1m17184_a_at		4921517J08	weakly similar to predicted speedy homolog 1 (Drosophila)
610	4.8	gnf1m02204_a_at	NM_010086	4932412H23	a disintegrin and metallopeptidase domain 24 (testase 1)
611	4.8	gnf1m05434_a_at	NM_029303	1700012P12	profilin 3
612	4.8	gnf1m16015_at		4933429H19	hypothetical TonB-dependent receptor protein containing protein
613	4.8	gnf1m03853_a_at	NM_019938	1700065B04	sperm tail associated protein
614	4.8	gnf1m04341_a_at	NM_023630	1700011N16	general transcription factor II A, 1-like factor
615	4.8	gnf1m30845_a_at	XM_908035	4930408G06	unclassifiable
616	4.8	gnf1m16811_a_at	NM_027024	1700006C19	similar to predicted cystatin 13
617	4.8	gnf1m00515_a_at	NM_029599	1700021O15	sperm associated antigen 4-like
618	4.8	gnf1m04153_a_at	NM_021611	1700027I08	myosin light chain 2, precursor lymphocyte-specific (Mylc2pl)
619	4.8	gnf1m31390_at	XM_904650		RIKEN cDNA 4930455B06 gene
620	4.8	gnf1m34576_at			PREDICTED: Mus musculus similar to hypothetical protein MGC44505 (LOC544830)
621	4.8	gnf1m17688_at		4931436F15	hypothetical protein
622	4.8	gnf1m04624_a_at	NM_025636	1700027L03	hypothetical AAA ATPase superfamily containing protein
623	4.8	gnf1m21663_at	NM_001024730	4930415L07	similar to hypothetical protein LOC546166
624	4.8	gnf1m14866_at		1700003F17	hypothetical protein
625	4.8	gnf1m05419_a_at	NM_029199	4930542N07	hypothetical protein
626	4.8	gnf1m29447_a_at	NM_029309	1700010A17	MORN motif containing protein
627	4.8	gnf1m34600_at	NM_183174		homeodomain leucine zipper-encoding gene
628	4.8	gnf1m03440_a_at	NM_181329	I730062F04	coilin
629	4.8	gnf1m13937_a_at	NM_001039244	C920013G19	hypothetical protein
630	4.8	gnf1m30004_a_at		7120447D04	thioredoxin reductase 3
631	4.8	gnf1m30753_at	NM_001033246	4922504L10	similar to Salivary glue protein Sgs-4 precursor
632	4.8	gnf1m05185_a_at	NM_027564	4921507P07	hypothetical Bacterial extracellular solute-binding protein, family 1 containing protein
633	4.8	gnf1m31291_a_at		2010109A12	fibrous sheath-interacting protein 1
634	4.8	gnf1m16980_a_at	NM_027745	4933434G05	coiled-coil domain containing 57 (Ccdc57)
635	4.8	gnf1m29201_at	XM_914515	I0C0026C19	hypothetical protein
636	4.8	gnf1m00465_a_at	NM_175105	1700023J02	aquaporin 11
637	4.8	gnf1m08260_a_at	NM_172755	A630079E18	splicing factor, arginine/serine-rich 14
638	4.8	gnf1m13863_a_at	NM_027661	4933413G11	heat shock transcription factor, Y linked 2
639	4.8	gnf1m31889_at	XM_913655		similar to fibrous sheath interacting protein 2
640	4.8	gnf1m13323_a_at	XM_909141	4930433I05	cylicin, basic protein of sperm head cytoskeleton 1
641	4.8	gnf1m17727_a_at		4930421J07	hypothetical protein
642	4.8	gnf1m16168_at		1700029F09	Esterase/lipase/thioesterase family active site containing protein
643	4.8	gnf1m04664_a_at	NM_025726	4921522P10	hypothetical protein
644	4.8	gnf1m02430_a_at	NM_010589	E430014A10	AN1, ubiquitin-like, homolog (Xenopus laevis)
645	4.8	gnf1m13957_at		4930518C04	unclassifiable
646	4.8	gnf1m32587_at	NM_177655	4930408K01	cystatin-like 1
647	4.8	gnf1m17050_at	XM_909493	1700007L12	IQ motif containing F5
648	4.8	gnf1m03386_a_at	NM_015777	1700021G14	immunoglobulin (CD79A) binding protein 1b
649	4.8	gnf1m29246_s_at	NM_178872	9230104I23	tripartite motif-containing 36
650	4.8	gnf1m03716_a_at	NM_019497	4921526M11	G protein-coupled receptor kinase 2, groucho gene related (Drosophila)
651	4.8	gnf1m16360_a_at	XM_908211	1700030H21	vitelliform macular dystrophy 2 homolog (human)
652	4.7	gnf1m05464_a_at	NM_029453	4930511H01	Trp-Asp (WD) repeats profile/Trp-Asp (WD) repeats circular profile/G-protein beta WD-40 repeats containing protein
653	4.7	gnf1m05443_a_at	NM_029343	1700030K01	hypothetical spermatogenesis associated 9 (Spata9)
654	4.7	gnf1m23751_s_at		1700065F16	IQ calmodulin-binding motif containing protein
655	4.7	gnf1m33184_at		1700014P15	solute carrier family 9, member 10 (Slc9a10)
656	4.7	gnf1m15242_at	NM_009832	I920045P05	cyclin K
657	4.7	gnf1m15253_a_at	XM_922616	1700003E16	short-chain dehydrogenase/reductase Homo sapiens
658	4.7	gnf1m16929_at		1700024J04	hypothetical TNFR/CD27/30/40/95 cysteine-rich region/von Willebrand factor, type C repeat containing protein
659	4.7	gnf1m03674_s_at	NM_175667	4930570K13	weakly similar to predicted DNA binding protein with his-thr domain
660	4.7	gnf1m11488_a_at	NM_027226	4930557G02	forty-two-three domain containing 1
661	4.7	gnf1m07481_a_at	NM_181731	4922505I06	calcium-binding tyrosine-(Y)-phosphorylation regulated (fibrousheathin 2)
662	4.7	gnf1m12672_a_at	NM_023232	4933428M04	diablo homolog (Drosophila)
663	4.7	gnf1m23708_at		4930408P03	HISTONE H2B (FRAGMENT) homolog [Mus musculus]
664	4.7	gnf1m11483_a_at	NM_026296	4933406G10	hypothetical protein
665	4.7	gnf1m16842_a_at	XM_910844	4921511M17	hypothetical protein
666	4.7	gnf1m09582_s_at	NM_025744	1700026G17	unclassifiable
667	4.7	gnf1m05317_a_at	NM_028524	1700013O04	CKLF-like MARVEL transmembrane domain containing 2B
668	4.7	gnf1m29612_a_at	XM_911841	1700020H17	molybdenum cofactor synthesis 3
669	4.7	gnf1m21689_at	NM_001004158	4930580A02	hypothetical protein
670	4.7	gnf1m31664_at	XM_905323	F630047G17	X-ray radiation resistance associated 1 protein
671	4.7	gnf1m00673_a_at	XM_924684	4921511E02	hypothetical FAD/NAD(P)-binding domain structure containing protein
672	4.7	gnf1m11491_a_at	NM_175488	4930570A05	coiled-coil domain containing 38
673	4.7	gnf1m16043_at		4930518J20	unclassifiable
674	4.7	gnf1m23757_a_at		4930523O13	unclassifiable
675	4.7	gnf1m04696_a_at	NM_025789	4930588C21	radial spokehead-like 2
676	4.7	gnf1m23030_a_at		4930517G24	unclassifiable
677	4.7	gnf1m15504_at		1700085L02	antizyme inhibitor 1
678	4.7	gnf1m32897_at	NM_001033176	4930569G22	hypothetical Sodium:neurotransmitter symporter/Sodium:neurotransmitter symporter family profile containing protein, full insert sequence
679	4.7	gnf1m33206_at	XM_916318		TATA element modulatory factor 1
680	4.7	gnf1m02810_a_at	NM_011449	1700000E13	sperm autoantigenic protein 17
681	4.7	gnf1m30953_a_at	XM_907160	4933437F05	NAD(P)-binding Rossmann-fold domains structure containing protein
682	4.7	gnf1m28689_a_at	XM_908853	4921511K06	hypothetical sarcolemma associated protein isoform 5
683	4.7	gnf1m30975_at	NM_177698	4933412E13	hypothetical SEC7-like domain/SEC7 domain profile containing protein
684	4.7	gnf1m07701_a_at	NM_029200	1700049P18	unclassifiable
685	4.7	gnf1m31156_a_at	XM_922719	C330017P09	hypothetical protein
686	4.7	gnf1m18101_at		9930109I05	kinesin family member 2B
687	4.7	gnf1m14489_at		4933412L11	unclassifiable
688	4.7	gnf1m08597_a_at	NM_177742	4933403D14	Domain in various gamma-carboxylases and other proteins containing protein
689	4.7	gnf1m05872_at	NM_054073	1700023D02	hypothetical testis specific gene A13
690	4.7	gnf1m14537_a_at	XM_923591	4933427G17	hypothetical protein
691	4.7	gnf1m07302_a_at	NM_153144		gametogenetin binding protein 2
692	4.6	gnf1m09247_a_at	NM_029163	4930511O11	ubiquitin specific peptidase 50
693	4.6	gnf1m14693_a_at	XM_919429	4930527J03	hypothetical Alanine-rich region containing protein
694	4.6	gnf1m17163_a_at	XM_911673	1700061J05	hypothetical protein
695	4.6	gnf1m17712_a_at	XM_905792	1700120B22	hypothetical protein LOC621121
696	4.6	gnf1m04730_a_at	NM_025851	1700010I14	hypothetical protein
697	4.6	gnf1m09400_a_at	NM_027089	4933408H04	weakly similar to predicted Acr formation associated factor Pan troglodytes
698	4.6	gnf1m30390_a_at	XM_917051	4930453N24	hypothetical Peptidase, eukaryotic cysteine peptidase active site containing protein
699	4.6	gnf1m14422_at		1700064D17	hypothetical protein
700	4.6	gnf1m04070_a_at	NM_021397	4930524C15	zinc finger and BTB domain containing 32
701	4.6	gnf1m17313_at	NM_028648	4930432K09	hypothetical protein
702	4.6	gnf1m11086_a_at	NM_013754	1700003B04	hypothetical insulin-like 6
703	4.6	gnf1m29012_a_at	XM_910825	4921528H16	RNI-like structure containing protein
704	4.6	gnf1m23738_s_at	NM_001033043	4930476G21	ring finger protein 17
705	4.6	gnf1m32280_a_at	XM_909681	M5C1026A22	glycosyltransferase 8 domain containing 3
706	4.6	gnf1m14207_at		4933435G04	hypothetical protein
707	4.6	gnf1m08625_a_at	NM_145825	1700129C13	centrin 4
708	4.6	gnf1m00997_a_at	NM_007809	6030448H16	hypothetical cytochrome P450, family 17, subfamily a, polypeptide 1
709	4.6	gnf1m08588_a_at	NM_177841	4932418E24	hypothetical protein
710	4.6	gnf1m34875_at	XM_908554		similar to Brain protein 44-like protein
711	4.6	gnf1m31200_a_at	NM_183181	1700095H12	Esterase/lipase/thioesterase family active site containing protein
712	4.6	gnf1m18179_at		A430076A20	ring finger protein 126
713	4.6	gnf1m16046_a_at	NM_027037	1700007K09	hypothetical protein
714	4.6	gnf1m18900_a_at	XM_911732	4930572D21	similar to unnamed protein product MDAC1 [Homo sapiens]
715	4.6	gnf1m04840_a_at	NM_026132	4930429J24	weakly similar to thioredoxin domain containing 8
716	4.6	gnf1m04027_a_at	NM_021311		piwi-like homolog 1 (Drosophila)
717	4.6	gnf1m15089_a_at	NM_030106	1700080C03	THYMOSIN BETA-LIKE PROTEIN [Rattus norvegicus]
718	4.6	gnf1m17702_a_at	NM_001029929	4932412N08	zinc finger, MYND-type containing 15
719	4.6	gnf1m01848_a_at	NM_009356	1700030B16	testicular serine protease 2
720	4.6	gnf1m31669_at	NM_001033766	4930596D02	weakly similar to hypothetical EF-hand/guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif containing protein [Mus musculus]
721	4.6	gnf1m14175_a_at		4933413D07	unclassifiable
722	4.6	gnf1m03831_at	NM_019873	B020003M05	FK506 binding protein-like
723	4.6	gnf1m09886_a_at	NM_053253	4022419B10	zinc finger, MYND domain containing 10
724	4.6	gnf1m30081_a_at	NM_029245	4930572N15	ankyrin repeat domain 53 (Ankrd53)
725	4.6	gnf1m15511_a_at	NM_027164	G430033H23	leucine rich repeat containing 27
726	4.6	gnf1m14180_a_at	XM_924040	4933413N12	hypothetical protein
727	4.6	gnf1m16760_a_at		1700007J06	leucine rich repeat containing 34
728	4.6	gnf1m31239_at	NM_029595		phosphatidylethanolamine binding protein 2
729	4.6	gnf1m30814_a_at	NM_027083	1700023H08	lysozyme-like 6
730	4.6	gnf1m29073_a_at	NM_027404	4930405J06	BCL2-associated athanogene 5
731	4.6	gnf1m07352_a_at	NM_153518	4933417K04	coiled-coil domain containing 65
732	4.6	gnf1m10539_at	NM_016915	I830139D09	phospholipase A2, group VI
733	4.6	gnf1m29781_a_at		4930534K13	IBR domain containing 3
734	4.6	gnf1m17307_a_at	XM_905388	1700016C15	hypothetical protein
735	4.6	gnf1m22576_a_at	NM_198299	E130303B06	weakly similar to sodium channel and clathrin linker 1 (Sclt1)

736	4.6	gnf1m05430_s_at	NM_029292	1700008F21	weakly similar to predicted coiled-coil domain containing 7 Mus musculus
737	4.6	gnf1m17138_a_at	NM_198224	1700060E18	membrane-spanning 4-domains, subfamily A, member 13 (Ms4a13), Mus musculus
738	4.6	gnf1m11494_a_at	NM_173023	4932415G16	CatSper channel subunit beta mRNA
739	4.6	gnf1m05314_a_at	NM_028502	4933403P17	Ubiquitin-conjugating enzyme E2-17 kDa 4 (EC 6.3.2.19) (Ubiquitin-protein ligase) (Ubiquitin carrier protein) (E2(17)KB 4) homolog [Rattus norvegicus]
740	4.6	gnf1m23608_at		4733401H18	nuclear protein E3-3
741	4.5	gnf1m03738_a_at	NM_019569		fascin homolog 3, actin-bundling protein, testicular (Strongylocentrotus purpuratus)
742	4.5	gnf1m28856_at	XM_923932	4932419B04	hypothetical protein
743	4.5	gnf1m00002_f_at	NM_009449	1700025I19	tubulin, alpha 3B (Tuba3b)
744	4.5	gnf1m11444_a_at	NM_020279	4921506E08	chemokine (C-C motif) ligand 28
745	4.5	gnf1m10583_a_at	NM_021714	6030486B17	WW domain binding protein 11
746	4.5	gnf1m13353_a_at		5133400G04	homologue TATA-binding protein-like factor-interacting protein isoform 2
747	4.5	gnf1m07927_a_at	NM_170671	4932408B01	Mycbp associated protein
748	4.5	gnf1m18803_a_at	XM_907218	4921518C22	tetratricopeptide repeat domain 18
749	4.5	gnf1m11143_a_at	NM_018811	B020003E02	abhydrolase domain containing 2 (Abhd2)
750	4.5	gnf1m29125_a_at	XM_909809	4931413A09	similar to coiled-coil domain containing 105 Homo sapiens
751	4.5	gnf1m11085_a_at	NM_029659	4922505N17	serine/threonine/tyrosine interacting-like 1
752	4.5	gnf1m29679_a_at	XM_924628	2900041A11	hypothetical protein
753	4.5	gnf1m04831_a_at	NM_026100	4930434I17	Tctex1 domain containing 1
754	4.5	gnf1m18691_a_at	NM_183108	4930479M11	hypothetical protein
755	4.5	gnf1m14745_a_at	XM_910021	1700020C07	hypothetical protein
756	4.5	gnf1m09990_a_at		1700003M02	hypothetical protein
757	4.5	gnf1m10388_a_at	NM_146074		transcription factor B1, mitochondrial
758	4.5	gnf1m13335_a_at		5330430P22	cytochrome P450, family 17, subfamily a, polypeptide 1
759	4.5	gnf1m13926_a_at	XM_181390	1700051I12	collagen, type XX, alpha 1
760	4.5	gnf1m04043_a_at	NM_021343	G830022G14	spermatogenesis associated 5
761	4.5	gnf1m19017_at			ri=1700054H16 hypothetical 2Fe-2S ferredoxin-like structure containing protein
762	4.5	gnf1m03884_a_at	NM_019995		DNA segment, Chr 3, ERATO Doi 300, expressed
763	4.5	gnf1m06357_a_at	NM_144547		anti-Mullerian hormone type 2 receptor
764	4.5	gnf1m07633_at	NM_175176	4922501L14	hypothetical protein
765	4.5	gnf1m15539_a_at	XM_912930	4933401F05	weakly similar to adrenal mitochondrial protease
766	4.5	gnf1m33946_at	XM_914511		gene model 591, (NCBI)
767	4.5	gnf1m16481_a_at		1700104P03	hypothetical protein
768	4.5	gnf1m05440_a_at	NM_029335	1700026D08	hypothetical protein
769	4.5	gnf1m31824_at			gametogenetin
770	4.5	gnf1m07947_a_at	NM_173771	4933406M09	N-ACETYLGLUCOSAMINYLTRANSFERASE VI [Gallus gallus]
771	4.5	gnf1m09736_at	NM_173384		SRY-box containing gene 30
772	4.5	gnf1m04458_a_at	NM_025290	1700007N08	weakly similar to testis specific gene A2 (MORN motif containing)
773	4.5	gnf1m29295_a_at	XM_924788	1700023D19	weakly similar to predicted SCRL protein variant 1
774	4.5	gnf1m09549_a_at	NM_029354	2610001E06	hypothetical protein
775	4.5	gnf1m05485_a_at	NM_029610	2310004B22	LYR motif containing 1 (Lyrm1)
776	4.5	gnf1m21656_a_at	NM_198624	4922504M18	hypothetical Ubiquitin domain containing protein
777	4.5	gnf1m05484_at	XM_891342	1700023A18	phosphatidylethanolamine binding protein 2
778	4.5	gnf1m22950_a_at	NM_001033465	1700120A01	Sperm flagellar protein 1 (LOC681930), Rattus norvegicus
779	4.5	gnf1m33278_at			SEC63 domain containing 1
780	4.5	gnf1m32514_at	XM_906877		similar to leucine rich repeat containing 45
781	4.5	gnf1m11459_s_at	NM_025657	4930405K06	similar to predicted leucine rich repeat containing 57
782	4.5	gnf1m11448_a_at	NM_023249	4921520K19	yippee-like 1 (Drosophila)
783	4.4	gnf1m08591_at	NM_172521	4932438M10	similar to nuclear protein in testis (predicted)
784	4.4	gnf1m32673_at	NM_001034858	C230012F14	armadillo repeat containing 2
785	4.4	gnf1m07613_a_at	NM_029150	4922501F22	spermatogenesis associated 16
786	4.4	gnf1m19221_a_at	NM_183307	4921511C16	coiled-coil domain containing 63 (Ccdc63)
787	4.4	gnf1m10532_a_at	NM_015789	1700011P15	dickkopf-like 1
788	4.4	gnf1m03205_a_at	NM_013638	4930502I03	RAN guanine nucleotide release factor (Rangrf)
789	4.4	gnf1m24904_a_at	NM_177594	I830061M19	myotubularin related protein 9
790	4.4	gnf1m23761_x_at	NM_001001450	4930533E22	hypothetical synovial sarcoma, X member B, breakpoint 2
791	4.4	gnf1m08863_a_at	NM_173449	4921523A10	Protein phosphatase 2C domain containing protein
792	4.4	gnf1m23679_a_at		4921506L10	hypothetical protein
793	4.4	gnf1m03380_a_at	NM_015768	4930455F09	prokineticin 2
794	4.4	gnf1m16751_at		2610318N02	hypothetical Proline-rich region profile containing protein
795	4.4	gnf1m16263_a_at	XM_920333	1700029F22	EF-hand domain (C-terminal) containing 1
796	4.4	gnf1m32046_at	NM_028377	4933402K21	Lysine-rich region containing protein
797	4.4	gnf1m13936_a_at	XM_129743	4933424G06	unclassifiable
798	4.4	gnf1m23858_at		4933408D05	hypothetical SUMO-1-specific protease mRNA, complete cds. [Mus musculus]
799	4.4	gnf1m17378_a_at		4932423M01	coiled-coil domain containing 83 (Ccdc83) Mus musculus
800	4.4	gnf1m30213_at	NM_001033296	4921501G24	weakly similar to sel-1 suppressor of lin-12-like 2 (C. elegans) (Sel1l2)
801	4.4	gnf1m13352_a_at	XM_922071	4933434I06	enkurin
802	4.4	gnf1m30554_a_at		1700126L10	CLG01 (DJ453C12.5) (P53 RESPONSE ELEMENT) [Homo sapiens]
803	4.4	gnf1m04480_a_at	NM_025329	1700112I01	DYnein Light chain (Tctex type] family member (dylt-2) Mus musculus
804	4.4	gnf1m29178_a_at	NM_010920	1700127P06	NK2 transcription factor related, locus 6 (Drosophila)
805	4.4	gnf1m18823_at		4932416M14	hypothetical protein
806	4.4	gnf1m04335_a_at	NM_023597	C230006K09	solute carrier family 25 (mitochondrial carrier, ornithine transporter) member 2
807	4.4	gnf1m32296_at	NM_027724	4922503N05	cancer antigen 1
808	4.4	gnf1m16235_at	XM_920780		leucine rich repeat containing 51
809	4.4	gnf1m16053_a_at	XM_907364	1700054F22	similar to unnamed protein product NIPSNAP4 PROTEIN (MGC:14553) (DKFZP564D177) (FLJ13953) (HSPC299) [Homo sapiens]
810	4.4	gnf1m32877_at	NM_001033775	4933422H20	similar to Butyrophylin-like/Zn-finger, B-box/SPla/RYanodine receptor SPRY/Zn-finger, RING containing protein
811	4.4	gnf1m29170_a_at	NM_028821	1700010H15	weakly similar to dynein, axonemal, light chain 1 (Dnalc1)
812	4.4	gnf1m03178_a_at	NM_013604	I420015J16	metaxin 1
813	4.4	gnf1m10285_a_at	NM_027485	C530035L23	zinc finger protein 438
814	4.4	gnf1m15939_at	XM_888419	1700014B07	hypothetical protein
815	4.4	gnf1m34313_at			ENSMUST00000062198 transcript (in rel.37.34e)
816	4.4	gnf1m17231_a_at	XM_914008	4930444P10	hypothetical Arginine-rich region containing protein
817	4.4	gnf1m02953_a_at	XM_356072	4932703D08	a disintegrin and metallopeptidase domain 25 (testase 2)
818	4.4	gnf1m16847_a_at	XM_916000	1700011E04	predicted GLI pathogenesis-related 1 like 1 (Glipr1l1)
819	4.4	gnf1m14779_a_at	XM_920709	4930529M09	HORMA domain containing 2
820	4.4	gnf1m18303_a_at		1700013D04	hypothetical coiled-coil domain containing 117, mRNA (cDNA cloneIMAGE:3597771). [Mus musculus]
821	4.4	gnf1m05497_a_at	NM_029661	1700027D21	hypothetical protein
822	4.4	gnf1m09744_a_at	XM_909329	F630050M23	Rsb-66 protein (Rsb66)
823	4.4	gnf1m06329_a_at	NM_139301		cation channel of sperm 1
824	4.4	gnf1m28413_a_at	XM_924976	E430036P15	X-ray radiation resistance associated 1
825	4.4	gnf1m10111_a_at	NM_024445	1700016K08	translin-associated factor X (Tsnax) interacting protein 1
826	4.4	gnf1m14697_a_at	XM_904855	4930544O15	hypothetical protein
827	4.4	gnf1m01785_a_at	NM_009241	1700003G22	sperm adhesion molecule 1
828	4.4	gnf1m10540_a_at	NM_016915	I830139D09	phospholipase A2, group VI
829	4.4	gnf1m17327_at	XM_907953	4933432M07	ring finger protein 148
830	4.4	gnf1m05722_a_at	NM_033079		DNA segment, Chr 6, Miriam Meisler 5, expressed
831	4.4	gnf1m00743_a_at	NM_153778	4933425C05	atonal homolog 8 (Drosophila)
832	4.3	gnf1m09652_a_at	NM_178378	I730086C16	IQ motif containing G
833	4.3	gnf1m33186_at	NM_198106	1700014P15	solute carrier family 9, member 10 (Slc9a10)
834	4.3	gnf1m21648_a_at	XM_920302	4921501M07	centrosomal protein 63 (Cep63)
835	4.3	gnf1m03234_a_at	NM_013688		t-complex-associated testis expressed 1
836	4.3	gnf1m17083_a_at	XM_912033	4930415O20	hypothetical protein
837	4.3	gnf1m15124_a_at		4930570E03	hypothetical protein
838	4.3	gnf1m07476_a_at	NM_026915	1810009N24	lysozyme-like 4
839	4.3	gnf1m17370_a_at	XM_920050	2410072D24	homologue proteasome (prosome, macropain) subunit, alpha type, 8 isoform 2
840	4.3	gnf1m23685_a_at	XM_922120	4921521O07	predicted coiled-coil domain containing 81 (Ccdc81) Mus musculus
841	4.3	gnf1m16233_a_at	NM_028484	4732409C05	hypothetical protein
842	4.3	gnf1m16596_at		1700062G21	neurexin I
843	4.3	gnf1m18898_a_at	NM_030025	4932413L18	hypothetical CLIP-190 CG5020-PB, isoform B like Macaca mulatta
844	4.3	gnf1m17179_a_at	NM_183097	1700067K01	hypothetical protein
845	4.3	gnf1m19220_a_at	NM_198655	4921509C19	weakly similar to Eukaryotic protein kinase containing protein
846	4.3	gnf1m17222_s_at	XM_915652	4933402N03	Cytochrome c heme-binding site containing protein
847	4.3	gnf1m31792_at			inferred: ref|XP_058620.1|(XM_058620) similar to SPLICING FACTOR, PROLINE-AND GLUTAMINE-RICH (POLYPYRIMIDINE TRACT-BINDING PROTEIN-ASSOCIATED SPLICING FACTOR) (PTB-ASSOCIATED SPLICING FACTOR) (PSF) (DNA-BINDING P52/P100 COMPLEX, 100 KDA SUBUNIT) (H. sapiens) [Homo sapiens] mCG52111
848	4.3	gnf1m10381_a_at	NM_175240	C820010C07	transmembrane protein 162 (Tmem162)
849	4.3	gnf1m15247_a_at		1700014J02	unclassifiable
850	4.3	gnf1m07312_a_at	NM_153162	A630069B14	prion protein dublet
851	4.3	gnf1m03015_a_at	NM_011902	1700021H01	tektin 2 (Tekt2)

852	4.3	gnf1m05029_a_at	NM_026634	A930018P22	coiled-coil domain containing 11
853	4.3	gnf1m31775_at	NM_183096		RIKEN cDNA 1700031F13 gene
854	4.3	gnf1m29259_a_at	NM_026739	F630110C03	MAD2 mitotic arrest deficient-like 2 (yeast)
855	4.3	gnf1m18930_a_at	XM_917165	4930548L10	Glutamine-rich region containing protein
856	4.3	gnf1m17242_a_at	XM_910887	4921505G21	hypothetical serine/threonine kinase 33
857	4.3	gnf1m13554_a_at	XM_919028	1700034F02	hypothetical ARM repeat structure containing protein
858	4.3	gnf1m31128_a_at	NM_025856	4930578M17	hypothetical SH3/Neutrophil cytosol factor 2/Src homology 3 (SH3) domain profile/Arginine-rich region profile containing protein homologue [Mus musculus]
859	4.3	gnf1m30342_a_at	XM_622687	1700026J12	weakly similar to CD47 antigen
860	4.3	gnf1m08594_a_at	NM_175350	4933402B14	transmembrane protein 146 (Tmem146)
861	4.3	gnf1m18683_a_at	XM_358794	4933416B22	hypothetical protein
862	4.3	gnf1m20339_at		A630001I11	poly A binding protein, cytoplasmic 2
863	4.3	gnf1m23862_a_at	XM_909128	4933415J19	ornithine transporter 2
864	4.3	gnf1m18488_a_at		3110023G01	homologue katanin p60 subunit A-like 2 (Katnal2)
865	4.3	gnf1m14608_a_at		4930511J24	unclassifiable
866	4.3	gnf1m23007_a_at	XM_910005	1700086D22	unclassifiable
867	4.3	gnf1m14122_at		4921513D11	hypothetical protein
868	4.3	gnf1m25228_s_at		E430035G08	elongation factor 1 homolog (ELF1, S. cerevisiae)
869	4.3	gnf1m14003_a_at	NM_001033148	1700029J07	hypothetical protein
870	4.3	gnf1m00675_s_at	NM_175240	1700042I18	transmembrane protein 162 (Tmem162)
871	4.3	gnf1m07915_a_at	NM_175672	4933417L03	hypothetical protein
872	4.3	gnf1m17027_a_at		4933424N20	unclassifiable
873	4.3	gnf1m28909_a_at	NM_001033299	4933431C08	zinc finger protein 217
874	4.3	gnf1m10081_a_at	NM_175091	C230076L23	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase
875	4.3	gnf1m04890_a_at	NM_026248	4930430A15	hypothetical Ankyrin repeat profile/Ankyrin-repeat/Ankyrin repeat region circular profile/Yeast DNA-binding domain containing protein
876	4.3	gnf1m23726_s_at		4930445I03	hypothetical protein
877	4.3	gnf1m08600_a_at	NM_177651	4933409G03	hypothetical protein
878	4.3	gnf1m09708_a_at	NM_031177	6030405E03	WD repeat domain 10
879	4.3	gnf1m05483_s_at	XM_894461	1700010D01	hypothetical protein
880	4.3	gnf1m18301_a_at		1700121N02	unclassifiable
881	4.3	gnf1m29905_a_at	XM_916034	4930584P19	DMRT-like family B with proline-rich C-terminal, 1
882	4.3	gnf1m14431_a_at	NM_028568	1700094E07	Dual specificity protein phosphatase containing protein
883	4.3	gnf1m07938_at	NM_173433	4932416A15	jumonji domain containing 2D
884	4.3	gnf1m15165_a_at		1700123M18	sialophorin, pseudogene
885	4.3	gnf1m07942_a_at	NM_176980	4932422E22	hypothetical Ankyrin repeat structure containing protein
886	4.3	gnf1m03347_a_at	NM_013908	4930533L09	F-box and WD-40 domain protein 5
887	4.3	gnf1m19228_at		4930526M03	weakly similar to predicted Ribosome-binding protein 1 (Ribosome receptor protein) (mRRp)
888	4.3	gnf1m33609_at		4922505K22	hypothetical protein
889	4.3	gnf1m08204_a_at		A330015D16	weakly similar to predicted Myosin heavy chain, fast skeletal muscle, embryonic
890	4.3	gnf1m17176_a_at	XM_915437	1700013B14	interleukin 31
891	4.2	gnf1m29417_a_at	NM_198033	A130090N03	amyotrophic lateral sclerosis 4 homolog (human)
892	4.2	gnf1m19278_at	NM_001024727	4932416H13	hypothetical protein
893	4.2	gnf1m21703_at		4933402M05	Adult male testis cDNA, RIKEN full-length enriched library, clone:4933402M05 product:serine/threonine kinase 33, full insert sequence
894	4.2	gnf1m27322_at	XM_900667	D030054G02	hypothetical protein
895	4.2	gnf1m19389_at		6030430N23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4
896	4.2	gnf1m16361_a_at	XM_905314	4933404O19	tetratricopeptide repeat domain 25
897	4.2	gnf1m09922_a_at	NM_026837	1700012A05	transmembrane protein 53 (Tmem53)
898	4.2	gnf1m30030_a_at	NM_199226	4933434J16	testicular haploid expressed gene
899	4.2	gnf1m03045_a_at	NM_011956	F630003D02	nucleotide binding protein 2
900	4.2	gnf1m35588_at	XM_904133		gene model 381, (NCBI)
901	4.2	gnf1m30176_a_at		1700023F06	hypothetical protein
902	4.2	gnf1m04244_a_at	NM_023043	A730048L21	alanine and arginine rich domain containing protein
903	4.2	gnf1m16560_a_at	NM_028129	2610020H08	exonuclease NEF-sp
904	4.2	gnf1m15246_a_at	XM_925564	1700020A23	hypothetical Serine phosphorylation site in HPr protein containing protein
905	4.2	gnf1m15384_a_at	NM_027032	1700008H23	Park2 co-regulated
906	4.2	gnf1m15103_at		1700104B16	hypothetical protein
907	4.2	gnf1m00084_a_at	NM_198223	E430007B19	similar to alveolar soft part sarcoma chromosome region, candidate 1 (human)
908	4.2	gnf1m29722_a_at	XM_924594	1700086L19	SERTA domain containing 4
909	4.2	gnf1m04060_a_at	NM_021372	4930439L04	SERTA domain containing 2
910	4.2	gnf1m04974_a_at	NM_026459	1700112P19	coiled-coil domain containing 70
911	4.2	gnf1m08351_a_at	NM_175503	B230381K07	cofactor required for Sp1 transcriptional activation, subunit 7
912	4.2	gnf1m13072_a_at	NM_009711	4930445K15	artemin
913	4.2	gnf1m30456_at	XM_886718		similar to solute carrier family 26, member 8 isoform a
914	4.2	gnf1m18789_a_at		1700016D18	similar to predicted testis-specific factor 1 (LOC631870), mRNA Length = 438 ref|XM_905802.1| Mus musculus
915	4.2	gnf1m34794_at	XM_904628		similar to heterogeneous nuclear ribonucleoprotein D-like
916	4.2	gnf1m09287_a_at	NM_029696	1700124B08	malate dehydrogenase 1B, NAD (soluble) (Mdh1b)
917	4.2	gnf1m11267_s_at	XM_916449	1700012D21	CBF1 INTERACTING COREPRESSOR CIR [Homo sapiens]
918	4.2	gnf1m14198_at		4933417D19	unclassifiable
919	4.2	gnf1m30490_at	NM_194269		MORN repeat containing 2
920	4.2	gnf1m08601_a_at	NM_172914	4933409I22	coiled-coil domain containing 113, mRNA (cDNA cloneMGC:74046 IMAGE:6705542), complete cds. [Mus musculus]
921	4.2	gnf1m29567_a_at		1700008J08	ankyrin repeat domain 48
922	4.2	gnf1m03665_a_at	NM_019396		cysteine and histidine rich 1
923	4.2	gnf1m07300_s_at	NM_153136	I530023E14	nudix (nucleoside diphosphate linked moiety X)-type motif 18
924	4.2	gnf1m16056_at			T-complex-associated testis expressed 2 /cds=UNKNOWN /gb=U46151 /gi=4097088 /len=1890 gnl|UG|Mm#S686001
925	4.2	gnf1m04036_s_at	NM_021329	5430416M17	HLA-B-associated transcript 3
926	4.2	gnf1m29619_a_at		4930567K20	unclassifiable
927	4.2	gnf1m13788_a_at		1700003P14	unclassifiable
928	4.2	gnf1m18102_a_at	XM_918858	1700021A20	unclassifiable
929	4.2	gnf1m28873_a_at	XM_909379	4930404K22	spermidine/spermine N1-acetyl transferase-like 1
930	4.2	gnf1m16754_a_at	NM_029326	1700018L24	Proline-rich region containing protein
931	4.2	gnf1m30720_a_at	NM_198107	E130314H02	mediator complex subunit 16 (Med16)
932	4.2	gnf1m25893_s_at	NM_029714	4932441M08	P-loop containing nucleotide triphosphate hydrolases structure containing protein Mus musculus
933	4.2	gnf1m15314_a_at	XM_924273	1700108H04	alkB, alkylation repair homolog 3 (E. coli)
934	4.1	gnf1m13294_a_at	NM_022981		zinc finger protein 110
935	4.1	gnf1m05025_a_at	NM_026628	1700120K04	hypothetical protein
936	4.1	gnf1m23056_a_at		1700095K22	unclassifiable
937	4.1	gnf1m34064_at	XM_911870		similar to Vacuolar ATP synthase subunit S1 precursor (V-ATPase S1 subunit) (V-ATPase S1 accessory protein) (V-ATPase Ac45 subunit) (C7-1 protein)
938	4.1	gnf1m21675_a_at	NM_207527	4930504O13	weakly similar to predicted olfactory receptor 30 like Macaca mulatta
939	4.1	gnf1m09413_s_at	XM_909844	I0C0045B19	polycomb group ring finger 4
940	4.1	gnf1m28952_s_at		4922504O05	similar to a disintegrin and metallopeptidase domain 4
941	4.1	gnf1m09379_a_at	NM_133689	4930579J09	IIIG9 LONG FORM homolog [Mus musculus]
942	4.1	gnf1m05431_a_at	NM_029295	1700001C14	chemokine-like factor
943	4.1	gnf1m04453_a_at	NM_025281	1700026C17	Ly1 antibody reactive clone
944	4.1	gnf1m13302_a_at	XM_923323	1700025M16	unclassifiable
945	4.1	gnf1m13366_a_at	XM_901672	4933406L18	serine (or cysteine) peptidase inhibitor, clade A, member 3A
946	4.1	gnf1m00055_a_at	NM_029916	C330007K24	serine threonine kinase 31
947	4.1	gnf1m17834_at		4632417E12	unclassifiable
948	4.1	gnf1m14138_a_at	XM_907780	4931431F19	hypothetical Ubiquitin domain containing protein
949	4.1	gnf1m17325_s_at	XM_900745	4930412B11	hypothetical protein
950	4.1	gnf1m05428_a_at	NM_029285	1700001C02	hypothetical protein
951	4.1	gnf1m21504_a_at		E130009J12	hypothetical protein
952	4.1	gnf1m18670_a_at		4921513J18	hypothetical Na+/H+ exchanger containing protein
953	4.1	gnf1m05040_a_at	NM_026652	4930547C10	weakly similar to predicted topoisomerase I binding, arginine/serine-rich-like [Macaca mulatta]
954	4.1	gnf1m06747_a_at	NM_146248		coiled-coil alpha-helical rod protein 1
955	4.1	gnf1m04782_a_at	NM_025977	4930548O08	ATP/GTP-binding site motif A (P-loop) containing protein
956	4.1	gnf1m06039_a_at	NM_133706	F830021L03	hypothetical transmembrane protein 97
957	4.1	gnf1m29010_at	XM_916311	4933400N17	similar to predicted DNA-binding protein RFX2
958	4.1	gnf1m14159_at		4933403G17	weakly similar to hormone-sensitive lipase testicular isoform mRNA Rattus norvegicus
959	4.1	gnf1m01774_x_at	NM_009220		spermiogenesis specific transcript on the Y 1
960	4.1	gnf1m33369_at	XM_129357		RIKEN cDNA 4930463G05 gene
961	4.1	gnf1m17158_a_at	XM_904138	1700011N24	Retroviral-type aspartic protease containing protein
962	4.1	gnf1m01825_a_at	NM_009319	G430108J08	TAR (HIV) RNA binding protein 2
963	4.1	gnf1m10515_a_at	NM_026789	1110020C03	kelch-like 10 (Drosophila)
964	4.1	gnf1m07618_a_at	NM_175161	4931422A03	unclassifiable
965	4.1	gnf1m14462_a_at		4930423M02	unclassifiable
966	4.1	gnf1m13646_at	NM_010029	4932703A03	hypothetical DEAD (Asp-Glu-Ala-Asp) box polypeptide 4
967	4.1	gnf1m17225_a_at	XM_917103	4921528O07	hypothetical ARM repeat structure containing protein
968	4.1	gnf1m29825_a_at	XM_924219	5033427P15	cystatin 8 (cystatin-related epididymal spermatogenic)
969	4.1	gnf1m29003_at	NM_001013783		similar to Hypothetical protein MGC26988
970	4.1	gnf1m14629_at		4930445B03	unclassifiable
971	4.1	gnf1m04684_at	NM_025763	4933436I01	hypothetical protein

972	4.1	gnf1m04919_a_at	NM_026319	1700029H06	intraflagellar transport 74 homolog (Chlamydomonas) (Ift74)
973	4.1	gnf1m29032_a_at	NM_009713	4931413D17	arylsulfatase A
974	4.1	gnf1m17230_at		4930444P10	hypothetical Arginine-rich region containing protein
975	4.1	gnf1m31545_at	XM_909116		gene model 1564, (NCBI)
976	4.1	gnf1m31677_at	NM_001033434	4931417M15	hypothetical Leucine-rich repeat/Leucine-rich repeat, typical subtype containing protein
977	4.1	gnf1m23725_at		4930445I03	hypothetical protein
978	4.1	gnf1m18605_a_at	XM_924252	E130217B17	coiled-coil domain containing 65
979	4.1	gnf1m33894_x_at			inferred: gb|AAA40527.1| (L04850) putative [Mus musculus] mCG116665
980	4.1	gnf1m10239_a_at	NM_028938	4933403H06	leucine rich repeat containing 44
981	4.1	gnf1m14404_a_at	XM_908365	1700041E20	homologue calcium and integrin binding family member 4
982	4.1	gnf1m04907_a_at	NM_026291	4930560N03	hypothetical protein
983	4.1	gnf1m16968_at		4933436F18	unclassifiable
984	4.1	gnf1m23164_a_at		1700010E23	spermatogenesis associated 6 (Spata6) (GO:0005524 InterPro|IPR001687) [Mus musculus]
985	4.1	gnf1m29423_a_at	XM_923476	1700011I03	hypothetical protein
986	4.0	gnf1m04841_x_at	NM_026136	4930449I24	weakly similar to predicted Ral guanine nucleotide dissociation stimulator (RalGEF) (RalGDS) [Mus musculus]
987	4.0	gnf1m12264_a_at	NM_019723	4933428J05	similar to predicted solute carrier family 22 (organic cation transporter), member 21
988	4.0	gnf1m05321_a_at	NM_028554	1700072E05	hypothetical protein
989	4.0	gnf1m23702_a_at	NM_181815	4930404C07	Glutamic acid-rich region containing proteinMus musculus
990	4.0	gnf1m00096_a_at	NM_172125	4922502O05	hypothetical a disintegrin and metallopeptidase domain 1b
991	4.0	gnf1m17206_a_at	XM_909594	1700121K02	similar to predicted PKD2 interactor, golgi and endoplasmic reticulum associated 1Rattus norvegicus
992	4.0	gnf1m12974_a_at	NM_025723	D630044H03	hypothetical S-adenosyl-L-methionine-dependent methyltransferases structure containing protein
993	4.0	gnf1m18366_at		1700001G11	hypothetical protein
994	4.0	gnf1m30927_a_at	NM_207275	4930517K23	hypothetical Barrier to autointegration factor (BAF) containing protein
995	4.0	gnf1m13538_a_at	XM_907646	4930557A04	hypothetical Histone-fold structure containing protein
996	4.0	gnf1m30249_s_at	NM_011516	4932419D11	synaptonemal complex protein 1
997	4.0	gnf1m19279_s_at	NM_001002775	4932416K20	weakly similar to retinitis pigmentosa GTPase regulator
998	4.0	gnf1m13551_a_at		4930519P11	hypothetical protein
999	4.0	gnf1m05234_a_at	NM_027963	1700019F09	WD repeat domain 16
1000	4.0	gnf1m33931_at	XM_924567		inferred: ref|NP_113644.1| (NM_031456) Charcot-Marie-Tooth duplicated region transcript 1 [Homo sapiens] mCG116106
1001	4.0	gnf1m04649_a_at	NM_025687	4921514K14	testis expressed gene 12
1002	4.0	gnf1m12431_a_at	NM_028661	G730044P08	hypothetical protein
1003	4.0	gnf1m23182_a_at		1700048O20	zinc finger protein 620
1004	4.0	gnf1m00044_a_at	NM_175667	4930570K13	weakly similar to predicted DNA binding protein with his-thr domain
1005	4.0	gnf1m15352_a_at	XM_924500	4933415I03	coiled-coil domain containing 11
1006	4.0	gnf1m05424_a_at	NM_029247	A630022F21	hypothetical protein
1007	4.0	gnf1m31032_at	XM_904650		RIKEN cDNA 4930455B06 gene
1008	4.0	gnf1m02369_a_at	NM_010443	I830091K06	heme oxygenase (decycling) 2
1009	4.0	gnf1m14719_a_at	NM_029232	4930563P21	hypothetical polyamine modulated factor 1 binding protein 1-like [Macaca mulatta]
1010	4.0	gnf1m10382_a_at	NM_029946	4931407K02	weakly similar to predicted EF-hand containing protein
1011	4.0	gnf1m22843_a_at		4930544N01	weakly simlar to adrenergic receptor, alpha 1d
1012	4.0	gnf1m01590_a_at	NM_008868		phospholipase A2, group IIC

No. 2, pancreas specific genes

#1	#2	#3	#4	#5	#6
1	6.4	gnf1m29691_a_at	XM_924840	1810044E12	chymotrypsin C (caldecrin)
2	6.2	gnf1m11115_a_at	NM_008387	1810027C14	insulin II
3	6.0	gnf1m30562_x_at			trypsinogen 16 trypsinogen 16 mCG124046
4	6.0	gnf1m11106_a_at	NM_023707	1810009J06	RIKEN cDNA 1810009J06 gene
5	5.9	gnf1m11109_a_at	NM_008386	C820020F18	insulin I
6	5.9	gnf1m27435_at		D130047M23	similar to HSPC009 (HSPC009 PROTEIN) [Homo sapiens]
7	5.9	gnf1m34778_at	NM_146523		olfactory receptor 850
8	5.8	gnf1m16788_a_at		1810063P13	RIKEN cDNA 1810028F09 gene
9	5.8	gnf1m01676_a_at	NM_009043	2010012A06	regenerating islet-derived 2
10	5.7	gnf1m31882_at	NM_146653		olfactory receptor 435
11	5.7	gnf1m27753_at		D530031E19	hypothetical protein
12	5.7	gnf1m18121_at		G630079N01	expressed sequence AI846148
13	5.6	gnf1m04787_a_at	NM_025989	2310046E09	glycoprotein 2 (zymogen granule membrane)
14	5.6	gnf1m29860_at			inferred: gb|AAH18205.1|AAH18205 (BC018205) Unknown (protein for IMAGE:3464710) [Homo sapiens] mCG12382
15	5.6	gnf1m10387_a_at	XM_906665	1810033M07	RIKEN cDNA 1810033M07 gene
16	5.6	gnf1m08517_a_at	XR_000394	D830038L22	cDNA sequence BC022713
17	5.6	gnf1m30530_at			RIKEN cDNA 2410080P20 gene RIKEN cDNA 2410080P20 gene mCG124898
18	5.6	gnf1m07563_at	NM_026743	G430064L22	tetraspanin 11
19	5.6	gnf1m23471_at		4430402N11	synuclein, alpha
20	5.6	gnf1m04836_a_at	NM_026109	1810045G11	RIKEN cDNA 1810008K16 gene
21	5.6	gnf1m16820_a_at	NM_026460	1810015G24	serine (or cysteine) peptidase inhibitor, clade I, member 2
22	5.6	gnf1m01501_a_at	NM_008703		neuromedin B receptor
23	5.5	gnf1m30890_at		F830010D04	epidermodysplasia verruciformis 2
24	5.5	gnf1m22733_at		F830021D11	RIKEN cDNA F830021D11 gene
25	5.5	gnf1m11000_s_at	NM_019428	I920099C09	ribonuclease P/MRP 30 subunit (human)
26	5.4	gnf1m27918_a_at		D930008N19	calcium channel, voltage dependent, alpha2/delta subunit 3
27	5.4	gnf1m23847_at		4932702M20	ATP/GTP binding protein-like 2
28	5.4	gnf1m02896_x_at	NM_011645	2010010O17	protease, serine, 3
29	5.4	gnf1m34364_at			inferred: ref|NP_032110.1| (NM_008084) glyceraldehyde-3-phosphate dehydrogenase [Mus musculus] mCG50539
30	5.4	gnf1m36029_x_at			inferred: ref|NP_297344.1| (NC_002488) hypothetical protein [Xylella fastidiosa 9a5c] mCG1030383
31	5.3	gnf1m24907_at		9430077P08	insulin-like growth factor I receptor
32	5.3	gnf1m28804_at	NM_001024698		similar to Carboxypeptidase A2 precursor
33	5.3	gnf1m35016_at			inferred: ref|NP_032278.1| (NM_008252) high mobility group protein 2 [Mus musculus] mCG50741
34	5.3	gnf1m25036_at		9630017N24	RIKEN cDNA 6530411M01 gene
35	5.3	gnf1m03336_a_at	NM_013893	1810046J24	regenerating islet-derived 3 delta
36	5.3	gnf1m02393_a_at	NM_010491		islet amyloid polypeptide
37	5.3	gnf1m33126_at			inferred: ref|XP_033313.1| (XM_033313) hypothetical protein FLJ10665 [Homo sapiens] mCG129432
38	5.3	gnf1m29526_a_at	XM_923427	0610025J13	RIKEN cDNA 0610025J13 gene
39	5.3	gnf1m29399_at			inferred: ref|XP_130814.1| (XM_130814) expressed sequence AI504870 [Mus musculus] mCG21890
40	5.3	gnf1m04279_a_at	NM_023182	2300003F21	chymotrypsin-like
41	5.2	gnf1m08774_a_at	NM_173022	F630002O11	cDNA sequence BC048403
42	5.2	gnf1m31711_at	NM_177587	1810012M12	aquaporin 12
43	5.2	gnf1m29511_at			inferred: ref|XP_051995.1| (XM_051995) KIAA1435 protein [Homo sapiens] mCG21671
44	5.2	gnf1m33879_x_at			inferred: ref|XP_060421.1| (XM_060421) similar to putative (H. sapiens) [Homo sapiens] mCG116890
45	5.2	gnf1m07537_a_at	NM_146150	6030449O20	nardilysin, N-arginine dibasic convertase, NRD convertase 1
46	5.2	gnf1m03841_a_at	NM_019917		vomeronasal 2, receptor, 1b
47	5.2	gnf1m08161_at	NM_176929	9930038B18	RIKEN cDNA 9930038B18 gene
48	5.2	gnf1m05089_a_at		1810007A24	pancreatic lipase
49	5.2	gnf1m17562_s_at	NM_147041		olfactory receptor 57
50	5.1	gnf1m11114_at	NM_008387	1810027C14	insulin II
51	5.1	gnf1m33580_x_at	XM_915048		similar to Polyadenylate-binding protein 4 (Poly(A)-binding protein 4) (PABP 4) (Inducible poly(A)-binding protein) (iPABP) (Activated-platelet protein 1) (APP-1)
52	5.1	gnf1m00107_a_at	NM_023333	2210010C04	RIKEN cDNA 2210010C04 gene
53	5.1	gnf1m21836_at		9230113A21	hypothetical protein
54	5.1	gnf1m23621_at		4831426I01	hypothetical protein
55	5.1	gnf1m01330_a_at	NM_008411	1810060I02	CUB and zona pellucida-like domains 1
56	5.1	gnf1m20122_at		A230068D05	unclassifiable
57	5.1	gnf1m34632_at			inferred: ref|NP_005792.1| (NM_005801) putative translation initiation factor [Homo sapiens] mCG1035752
58	5.1	gnf1m25033_at		9630016K09	RIKEN cDNA B930086A06 gene
59	5.1	gnf1m07677_at	NM_028623	6330505O07	cystatin E/M
60	5.1	gnf1m31567_at			inferred: ref|NP_060355.1| (NM_017885) hypothetical protein FLJ20568 [Homo sapiens] mCG8073
61	5.1	gnf1m07165_at	NM_147067		olfactory receptor 829
62	5.0	gnf1m24991_at		9530082L10	SIMILAR TO OXYSTEROL BINDING PROTEIN-LIKE 9 homolog [Mus musculus]
63	5.0	gnf1m35851_at	NM_001012269		olfactory receptor 1513
64	5.0	gnf1m35978_x_at			inferred: gb|AAL55824.1|AF318317_1 (AF318317) unknown [Homo sapiens] mCG1034126
65	5.0	gnf1m25665_a_at		A430108H20	RIKEN cDNA 1600023E10 gene
66	5.0	gnf1m33388_at	NM_001034873	9630059B11	kinase suppressor of ras 2
67	5.0	gnf1m21458_at		D930011H06	15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930011H06 product:hypothetical protein, full insert sequence
68	5.0	gnf1m04627_a_at	XM_919625	2510042J05	DAZ interacting protein 1
69	5.0	gnf1m33154_at			inferred: ref|NP_033956.1| (NM_009826) coiled coil forming protein 1 [Mus musculus] mCG129079
70	5.0	gnf1m29642_a_at			inferred: ref|XP_131932.1| (XM_131932) similar to ATP-

					binding cassette, sub-family F, member 2 [Mus musculus] mCG16473
71	5.0	gnf1m31256_s_at	XM_910652	A430098H07	jerky homolog-like (mouse)
72	5.0	gnf1m13375_a_at		4930533N22	RIKEN cDNA 4930533N22 gene
73	5.0	gnf1m23450_at		3830420C06	seryl-aminoacyl-tRNA synthetase
74	5.0	gnf1m25339_at		A130057L17	peroxisomal biogenesis factor 13
75	5.0	gnf1m14046_at		1810073G21	pancreatic lipase related protein 1
76	5.0	gnf1m33491_at			inferred: ref|NP_035698.1| (NM_011568) RNA and export factor binding protein 1; Tcra enhancer-binding factor interacting protein 1 [Mus musculus] mCG123687
77	5.0	gnf1m02120_a_at	NM_009885	1810019H12	carboxyl ester lipase
78	5.0	gnf1m29035_a_at	NM_175004	6030462P20	RIKEN cDNA A230072I16 gene
79	4.9	gnf1m35466_at			inferred: ref|NP_003810.1| (NM_003819) poly(A)-binding protein, cytoplasmic 4 (inducible form); inducible poly(A)-binding protein [Homo sapiens] mCG1031933
80	4.9	gnf1m34369_at			inferred: ref|NP_035229.1| (NM_011099) pyruvate kinase 3 [Mus musculus] mCG50497
81	4.9	gnf1m31639_at			Transcribed locus
82	4.9	gnf1m05219_a_at	NM_027883	9930003H07	DEAH (Asp-Glu-Ala-His) box polypeptide 34
83	4.9	gnf1m16696_at			Mouse partial mRNA for hypothetical protein (P4(21)n gene) /cds=UNKNOWN /gb=AJ242955 /gi=5042303 /len=1730 gnl|UG|Mm#S685684
84	4.9	gnf1m34902_at	XM_906410		similar to glycerol-3-phosphate dehydrogenase 1-like
85	4.9	gnf1m36040_at			uncharacterized Celera prediction mCG1029985
86	4.9	gnf1m10050_at	NM_080854		solute carrier family 34 (sodium phosphate), member 3
87	4.9	gnf1m14651_at	XM_901924	4930474H20	RIKEN cDNA 4930474H20 gene
88	4.9	gnf1m18557_at		2610510C17	RIKEN cDNA 2610510C17 gene
89	4.9	gnf1m07982_at	NM_177177	5930403N24	RIKEN cDNA 5930403N24 gene
90	4.9	gnf1m35063_at			inferred: ref|NP_058797.1| (NM_017101) peptidylprolyl isomerase A (cyclophilin A) [Rattus norvegicus] mCG49869
91	4.9	gnf1m12380_a_at	NM_027436	A930014F04	mitochondrial intermediate peptidase
92	4.9	gnf1m22102_at		C130099E04	Eph receptor B1
93	4.9	gnf1m07032_a_at	NM_146878		olfactory receptor 30
94	4.9	gnf1m30939_s_at	XM_906291	9330169N05	RIKEN cDNA C230040D10 gene
95	4.9	gnf1m16394_at	XM_914914	1810041F13	protein disulfide isomerase associated 2
96	4.9	gnf1m09104_a_at	XM_915356		similar to Olfactory receptor 5D13
97	4.9	gnf1m24376_at		6430520H06	RIKEN cDNA 4833422F24 gene
98	4.9	gnf1m32785_at			obsolete Celera prediction mCT136127
99	4.9	gnf1m31205_at	NM_001033448	G430025O10	RIKEN cDNA 1810058N15 gene
100	4.8	gnf1m08832_s_at	NM_178404	A230104G09	zinc finger CCCH type containing 6
101	4.8	gnf1m35967_x_at			uncharacterized Celera prediction mCG1034864
102	4.8	gnf1m20060_at		A130086G11	RIKEN cDNA A130086G11 gene
103	4.8	gnf1m05617_a_at	NM_030889		sortilin-related VPS10 domain containing receptor 2
104	4.8	gnf1m33768_x_at			inferred: ref|NP_032110.1| (NM_008084) glyceraldehyde-3-phosphate dehydrogenase [Mus musculus] mCG118656
105	4.8	gnf1m10363_at	NM_138674		polycystic kidney and hepatic disease 1-like 1
106	4.8	gnf1m02247_at	NM_010198		fibroblast growth factor 11
107	4.8	gnf1m31318_at			inferred: ref|NP_036302.1| (NM_012170) F-box only protein 22; hypothetical protein FLJ13986; F-box protein Fbx22 [Homo sapiens] mCG9673
108	4.8	gnf1m33666_at			inferred: ref|NP_080695.1| (NM_026419) elastase 3B, pancreatic [Mus musculus] mCG120450
109	4.8	gnf1m14292_at		4930513L20	RIKEN cDNA 4930513L20 gene
110	4.8	gnf1m33036_x_at			inferred: ref|NP_000963.1| (NM_000972) ribosomal protein L7a; 60S ribosomal protein L7a; surfeit 3; surfeit locus protein 3; PLA-X polypeptide; thyroid hormone receptor uncoupling protein [Homo sapiens] mCG12602
111	4.8	gnf1m23733_a_at	XM_916176	F730211G02	RIKEN cDNA 4930467M19 gene
112	4.8	gnf1m34525_at			inferred: gb|AAF81070.1|AF223427_1 (AF223427) RRM-containing protein SEB-4 [Xenopus laevis] mCG1043826
113	4.8	gnf1m23206_s_at	NM_029706	2210008M23	carboxypeptidase B1 (tissue)
114	4.8	gnf1m13602_at		1500017I17	RIKEN cDNA 1500017I17 gene
115	4.8	gnf1m31474_x_at			inferred: ref|NP_035420.1| (NM_011290) ribosomal protein L6 [Mus musculus] mCG8028
116	4.7	gnf1m18072_at		B930009L08	gene model 939, (NCBI)
117	4.7	gnf1m24193_a_at		6030438E01	polymerase (RNA) III (DNA directed) polypeptide F
118	4.7	gnf1m19676_at	NM_001024504	9330185P08	expressed sequence AW495713
119	4.7	gnf1m04959_a_at	NM_026419	2310074F01	elastase 3, pancreatic
120	4.7	gnf1m29606_s_at	XM_924600	B630013K15	centrosomal protein 350
121	4.7	gnf1m28965_a_at		A430024H01	secretory carrier membrane protein 4
122	4.7	gnf1m34247_at			inferred: gb|AAD29851.1| (AF079520) laminin gamma-3 chain precursor [Mus musculus] mCG17454
123	4.7	gnf1m25764_at		G370140P21	squalene epoxidase
124	4.7	gnf1m09129_at	NM_001011775		olfactory receptor 1419
125	4.7	gnf1m03988_at	NM_020612		cell matrix adhesion regulator
126	4.7	gnf1m35864_at			inferred: ref|NP_003878.1| (NM_003887) development- and differentiation-enhancing factor 2; PYK2 C terminus-associated protein [Homo sapiens] mCG1041697
127	4.7	gnf1m18730_at		1700001E18	RIKEN cDNA 1110058L19 gene
128	4.7	gnf1m14300_at		1700026M20	cDNA sequence BC051628
129	4.7	gnf1m22547_at		E030030I02	unclassifiable
130	4.7	gnf1m08478_at		D130057M20	hypothetical protein
131	4.7	gnf1m17507_at			gb=U69137 Mouse T2-cadherin mRNA, partial cds
132	4.7	gnf1m29038_a_at	NM_028055	6330586L13	RIKEN cDNA 1500005I02 gene
133	4.7	gnf1m30962_at	XM_924334		centromere autoantigen F
134	4.7	gnf1m23991_at		5730419A11	unclassifiable
135	4.7	gnf1m30976_a_at	NM_008100	C820020M20	glucagon
136	4.6	gnf1m28927_at	NM_001037752	1700012K18	similar to beta-defensin 123
137	4.6	gnf1m05504_a_at	NM_029747	2410137M14	RIKEN cDNA 2410137M14 gene
138	4.6	gnf1m28687_a_at	NM_029212	4930535E21	RIKEN cDNA 4930535E21 gene
139	4.6	gnf1m19259_at		4931419J09	Adult male testis cDNA, RIKEN full-length enriched library, clone:4931419J09 product:unclassifiable, full insert sequence
140	4.6	gnf1m25806_at		A630019K16	3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630019K16 product:paired box gene 1, full insert sequence
141	4.6	gnf1m31737_at			inferred: ref|NP_001817.1| (NM_001826) CDC28 protein kinase 1; CKS1(S. cerevisiae Cdc28/Cdc2 kinase subunit) homolog-1 [Homo sapiens] mCG6352
142	4.6	gnf1m27822_at		D630041E16	caspase 9
143	4.6	gnf1m34997_at			inferred: gb|AAB40653.1| (U66840) MAP kinase 3c [Homo sapiens] mCG51091
144	4.6	gnf1m31287_a_at		1700010L04	RIKEN cDNA 1700010L04 gene
145	4.6	gnf1m28150_at		E130208G24	S-adenosylhomocysteine hydrolase-like 1
146	4.6	gnf1m13748_at		4632415I09	HEAT SHOCK PROTEIN, 25 KDA
147	4.6	gnf1m07824_a_at	NM_172805	6430546I09	potassium voltage-gated channel, subfamily H (eag-related), member 5
148	4.6	gnf1m33663_at			inferred: ref|NP_035826.1| (NM_011696) voltage-dependent anion channel 3 [Mus musculus] mCG120473
149	4.6	gnf1m33853_at	XM_907687		similar to immunoglobulin superfamily, member 2
150	4.6	gnf1m23001_a_at		4930449M09	RIKEN cDNA 1700025L06 gene
151	4.6	gnf1m28420_a_at		E530001O09	unclassifiable
152	4.6	gnf1m13198_at		F730028L02	F730028L02 unclassifiable clone
153	4.6	gnf1m22907_at		9630038C06	unclassifiable
154	4.6	gnf1m13900_s_at	NM_199060		cDNA sequence AF067061
155	4.6	gnf1m31803_at			RIKEN cDNA 1110020J08 gene RIKEN cDNA 1110020J08 gene mCG5717
156	4.6	gnf1m32216_at	NM_001024645		cDNA sequence BC036313
157	4.6	gnf1m14412_at		1700040F17	RIKEN cDNA 1700040F17 gene
158	4.6	gnf1m30589_at			inferred: ref|NP_055518.1| (NM_014703) KIAA0800 gene product [Homo sapiens] mCG123324
159	4.6	gnf1m32669_at		9430075C07	expressed sequence AU042671
160	4.6	gnf1m28625_at	NM_001037957		dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1b
161	4.6	gnf1m10963_s_at	NM_023182	2300003F21	chymotrypsin-like
162	4.6	gnf1m12165_s_at		A230052M14	sacsin
163	4.6	gnf1m31818_at	XM_914444		similar to testicular acid phosphatase isoform a precursor
164	4.6	gnf1m14825_at		5830433M15	RIKEN cDNA 5830433M15 gene
165	4.6	gnf1m15847_at		0610010K06	RIKEN cDNA 0610010K06 gene
166	4.6	gnf1m15083_at		5330439K02	RIKEN cDNA 5330439K02 gene
167	4.6	gnf1m28495_at		F830016J06	pannexin 1
168	4.5	gnf1m04240_a_at	NM_022993	F630047I08	low-density lipoprotein receptor-related protein 10
169	4.5	gnf1m04545_a_at	NM_025458	1810057G13	transmembrane emp24 protein transport domain containing 6
170	4.5	gnf1m28022_at		E030022H18	unclassifiable
171	4.5	gnf1m17499_at		2610509C21	RIKEN cDNA 2610007O09 gene
172	4.5	gnf1m29551_at			inferred: ref|XP_109605.1| (XM_109605) proteasome (prosome, macropain) 26S subunit, ATPase 3, interacting protein [Mus musculus] mCG20202
173	4.5	gnf1m02308_at	NM_010340	3830420C14	G-protein-coupled receptor 50
174	4.5	gnf1m29324_a_at		6720465F12	ubiquitin-conjugating enzyme E2S
175	4.5	gnf1m09141_s_at	NM_001011785		olfactory receptor 987
176	4.5	gnf1m19231_at		4930415C24	gene model 1653, (NCBI)

177	4.5	gnf1m09082_a_at	NM_207149		olfactory receptor 1010
178	4.5	gnf1m32002_x_at	XM_912694		similar to putative pheromone receptor (Go-VN5)
179	4.5	gnf1m01890_at	NM_009430	0910001K11	protease, serine, 2
180	4.5	gnf1m19876_at		9830114D01	RIKEN cDNA 4933422E07 gene
181	4.5	gnf1m00432_a_at	NM_007491	4930443I07	ADP-ribosyltransferase 5
182	4.5	gnf1m17931_at		1700007N19	chondroitin sulfate proteoglycan 3
183	4.5	gnf1m09206_at	NM_181819		WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2
184	4.5	gnf1m28621_at			gb|BC018362.1| Mouse clone MGC:19264 IMAGE:3986648, mRNA, complete cds
185	4.5	gnf1m34842_at	NM_001033793	B020039L20	RIKEN cDNA B020006M18 gene
186	4.5	gnf1m09567_s_at	NM_011646	2210415M03	trypsin 4
187	4.5	gnf1m01117_a_at	NM_008005	6430536H17	fibroblast growth factor 18
188	4.5	gnf1m20905_at		B930055O11	unclassifiable
189	4.5	gnf1m35682_at			inferred: ref|XP_059133.1| (XM_059133) similar to ubiquinol-cytochrome c reductase hinge protein (H. sapiens) [Homo sapiens] mCG50773
190	4.5	gnf1m35798_x_at			inferred: gb|AAH16248.1|AAH16248 (BC016248) Similar to zinc finger protein 85 (HPF4, HTF1) [Mus musculus] mCG1044717
191	4.5	gnf1m18052_at		A630098M21	unclassifiable
192	4.5	gnf1m32971_at	NM_145853	G370028G22	two pore channel 1
193	4.5	gnf1m06755_s_at	NM_146267		olfactory receptor 769
194	4.5	gnf1m24653_at		9630042F02	UDP-Gal:betaGal beta 1,3-galactosyltransferase, polypeptide 6
195	4.5	gnf1m22439_a_at	NM_001013780	E030001G18	solute carrier family 25, member 34
196	4.5	gnf1m35624_x_at	XM_911459		hypothetical LOC545187
197	4.5	gnf1m31715_at			inferred: gb|AAL61305.1| (AY073642) olfactory receptor MOR256-29 [Mus musculus] mCG55158
198	4.5	gnf1m36013_at	XM_905701		similar to vomeronasal 1 receptor, D7
199	4.5	gnf1m17683_at			gb=U11548 Mouse TFIIi-associated transactivator factor p17 mRNA, complete cds
200	4.5	gnf1m17582_at			gb=X80430 Mouse tex267 mRNA (5'region)
201	4.5	gnf1m35633_at			inferred: ref|NP_000066.1| (NM_000075) cyclin-dependent kinase 4, isoform 1; cell division kinase 4; cutaneous malignant melanoma, 3 [Homo sapiens] mCG55481
202	4.5	gnf1m27846_at		D730022H23	RIKEN cDNA A730037C10 gene
203	4.5	gnf1m07233_at	NM_148947		lymphocyte antigen 6 complex, locus G5C
204	4.5	gnf1m11349_at	NM_031167	F630220G16	interleukin 1 receptor antagonist
205	4.5	gnf1m35511_at	XM_904498		similar to zinc finger protein 709
206	4.4	gnf1m27231_at		C820013I09	hypothetical PDZ domain (also known as DHR or GLGF) containing protein
207	4.4	gnf1m31456_at			expressed sequence AA987064 expressed sequence AA987064 mCG8570
208	4.4	gnf1m07472_a_at	NM_026716	0910001K16	syncollin
209	4.4	gnf1m28464_at	XM_922413	M5C1043P11	Crm, cramped-like (Drosophila)
210	4.4	gnf1m08526_at		E030024N20	RIKEN cDNA E030024N20 gene
211	4.4	gnf1m04601_a_at	NM_025583	9030613K09	chymotrypsinogen B1
212	4.4	gnf1m18224_at		9330186C21	unclassifiable
213	4.4	gnf1m03597_at	NM_018754		stratifin
214	4.4	gnf1m13222_at	XM_905316	G430074B03	chemokine (C-C motif) receptor 10
215	4.4	gnf1m31739_at	XM_909971		similar to oxoglutarate dehydrogenase-like
216	4.4	gnf1m00169_a_at	NM_178255	4930554N11	hyaluronan and proteoglycan link protein 3
217	4.4	gnf1m21935_at		A730040I02	unclassifiable
218	4.4	gnf1m08978_at	XM_923109		similar to olfactory receptor Olr804
219	4.4	gnf1m34883_at	NM_146518		olfactory receptor 523
220	4.4	gnf1m35688_at			inferred: ref|XP_059037.1| (XM_059037) similar to putative (H. sapiens) [Homo sapiens] mCG50591
221	4.4	gnf1m03655_a_at	NM_018874	1810032A23	pancreatic lipase related protein 1
222	4.4	gnf1m18520_a_at	XM_900600	6030442D07	similar to mitogen-activated protein kinase kinase kinase 13
223	4.4	gnf1m35863_at	XM_906995		gene model 252, (NCBI)
224	4.4	gnf1m19962_at		A130004F19	unclassifiable
225	4.4	gnf1m03189_s_at	NM_013618		olfactory receptor 64
226	4.4	gnf1m05681_a_at	NM_031408		PERQ amino acid rich, with GYF domain 1
227	4.4	gnf1m15556_at		E130116L18	RIKEN cDNA E130116L18 gene
228	4.4	gnf1m15817_at		3010034A12	f-box only protein 6a
229	4.4	gnf1m02655_a_at	NM_011128	2210004D24	pancreatic lipase-related protein 2
230	4.4	gnf1m13665_at	XM_915228		similar to T-cell receptor beta chain V region C5 precursor
231	4.4	gnf1m01060_a_at	NM_007919		elastase 2A
232	4.4	gnf1m17223_at		4930413G21	RIKEN cDNA 4930413G21 gene
233	4.4	gnf1m07019_s_at	NM_146862		olfactory receptor 9
234	4.4	gnf1m17302_at		4921532D01	RIKEN cDNA 4921532D01 gene
235	4.4	gnf1m13986_a_at	XM_905181	1190003K10	RIKEN cDNA 1190003K10 gene
236	4.4	gnf1m11515_at	NM_025725	4932416C18	RIKEN cDNA 4921513E08 gene
237	4.4	gnf1m27453_at		D130054H18	hypothetical protein
238	4.4	gnf1m33595_at			uncharacterized Celera prediction mCG121791
239	4.4	gnf1m25240_at		9930101A07	RIKEN cDNA 9930039A11 gene
240	4.4	gnf1m34266_at	XM_904475		similar to O-acyltransferase (membrane bound) domain containing 1
241	4.4	gnf1m07155_a_at	NM_147051		olfactory receptor 362
242	4.4	gnf1m20955_at		C030046L04	unclassifiable
243	4.4	gnf1m23297_at	XM_904933	2610002B11	RIKEN cDNA 2310002J21 gene
244	4.4	gnf1m34938_x_at	NM_146656		olfactory receptor 444
245	4.4	gnf1m03180_a_at	NM_013606	F430202K10	myxovirus (influenza virus) resistance 2
246	4.4	gnf1m33808_at	NM_207253		olfactory receptor 1371
247	4.4	gnf1m17189_at		2010007L08	RIKEN cDNA 2010007L08 gene
248	4.4	gnf1m35492_at			inferred: ref|NP_036099.1| (NM_011969) proteasome (prosome, macropain) subunit, alpha type 7 [Mus musculus] mCG18545
249	4.4	gnf1m19615_at		9230114N12	hypothetical Isoleucine-rich region containing protein
250	4.4	gnf1m35642_at			inferred: gb|AAC72797.1| (AF081106) ORF2 [Mus musculus domesticus] mCG54614
251	4.3	gnf1m18658_s_at		B230397F11	weakly similar to CELL DEATH REGULATOR AVEN [Homo sapiens]
252	4.3	gnf1m14135_at		4931407J08	RIKEN cDNA 4931407J08 gene
253	4.3	gnf1m09124_at			inferred: gb|AAL61316.1| (AY073653) olfactory receptor MOR257-3 [Mus musculus] mCG60446
254	4.3	gnf1m34017_at			inferred: gb|AAL50790.1|AF454056_1 (AF454056) se14-3r protein [Homo sapiens] mCG114715
255	4.3	gnf1m21623_at		4632407M08	hypothetical Phenylalanine-rich region profile/Serine-rich region profile containing protein
256	4.3	gnf1m23958_at		5330439L06	RIKEN cDNA 1300013D05 gene
257	4.3	gnf1m31563_x_at			inferred: ref|NP_037061.1| (NM_012929) procollagen II alpha 1 [Rattus norvegicus] mCG64250
258	4.3	gnf1m18259_at		9030022M04	unclassifiable
259	4.3	gnf1m35601_at			uncharacterized Celera prediction mCG60559
260	4.3	gnf1m28146_at		E130120L03	cytosolic acyl-CoA thioesterase 1
261	4.3	gnf1m17305_at		4930443G03	RIKEN cDNA 4930443G03 gene
262	4.3	gnf1m08715_at	NM_172761	C920004D05	cDNA sequence BC052066
263	4.3	gnf1m30124_a_at	NM_203319		DEAH (Asp-Glu-Ala-His) box polypeptide 37
264	4.3	gnf1m08724_s_at		D130060J02	RIKEN cDNA D130060J02 gene
265	4.3	gnf1m02645_a_at	NM_011107	2310012E07	phospholipase A2, group IB, pancreas
266	4.3	gnf1m06895_a_at	NM_146651		olfactory receptor 1403
267	4.3	gnf1m33059_at			glutamate receptor interacting protein 2
268	4.3	gnf1m32420_at	XM_914429		similar to 40S ribosomal protein S15 (RIG protein)
269	4.3	gnf1m07048_s_at	NM_146901		olfactory receptor 1217
270	4.3	gnf1m31198_at	NM_028317	D030046B15	RIKEN cDNA 2810030E01 gene
271	4.3	gnf1m29989_a_at	NM_033612	1810009A17	elastase 1, pancreatic
272	4.3	gnf1m14565_a_at		4833427F10	RIKEN cDNA 4833427F10 gene
273	4.3	gnf1m22445_at		D830039M14	RIKEN cDNA D830039M14 gene
274	4.3	gnf1m22055_at		C130048D21	unclassifiable
275	4.3	gnf1m19984_at		A130023H13	unclassifiable
276	4.3	gnf1m01675_a_at	NM_009042	5033401N17	regenerating islet-derived 1
277	4.3	gnf1m25364_at		A130078K13	unclassifiable
278	4.3	gnf1m26312_at		B230211D20	RIKEN cDNA F830001A07 gene
279	4.3	gnf1m36033_at	NM_206903		olfactory receptor 3
280	4.3	gnf1m31842_at			inferred: ref|NP_002625.1| (NM_002634) prohibitin [Homo sapiens] mCG51148
281	4.3	gnf1m16571_a_at		E130016D18	kelch-like 25 (Drosophila)
282	4.3	gnf1m23743_at		4930485C04	mutS homolog 4 (E. coli)
283	4.3	gnf1m30401_a_at	NM_001003405	2210415M03	RIKEN cDNA 1810049H19 gene
284	4.3	gnf1m08069_at		9230101H05	piwi-like homolog 4 (Drosophila)
285	4.3	gnf1m25663_at		A430107I06	proprotein convertase subtilisin/kexin type 3
286	4.3	gnf1m27571_at		D230023M10	unclassifiable
287	4.3	gnf1m35595_at			inferred: ref|NP_031817.1| (NM_007791) cysteine rich protein [Mus musculus] mCG61881
288	4.3	gnf1m19756_at		9430079A18	hypothetical protein
289	4.3	gnf1m25844_at		A630048I20	interleukin 15 receptor, alpha chain
290	4.3	gnf1m20560_at		A830048E23	calcium channel, voltage-dependent, gamma subunit 4
291	4.3	gnf1m07670_a_at	NM_175197	A630087P21	RIKEN cDNA 1700055D18 gene
292	4.3	gnf1m27751_at		D530020L18	zinc finger protein 36, C3H type-like 1
293	4.3	gnf1m11108_a_at	NM_011271	1810011N10	ribonuclease, RNase A family, 1 (pancreatic)
294	4.3	gnf1m35585_at			uncharacterized Celera prediction mCG63327
295	4.3	gnf1m08963_a_at	NM_146275		olfactory receptor 1402
296	4.3	gnf1m13423_a_at			CDNA clone MGC:6757 IMAGE:3594209
297	4.3	gnf1m31138_at	NM_028162	F630113I18	TBC1 domain family, member 5
298	4.3	gnf1m20080_at		A130098P13	CDNA FLJ10678 FIS, CLONE NT2RP2006472 homolog [Homo sapiens]
299	4.3	gnf1m21045_s_at		C130089K02	similar to mastermind-like 3
300	4.3	gnf1m22928_at		A230086C11	hypothetical protein LOC545410
301	4.2	gnf1m13817_s_at	NM_199060		cDNA sequence AF067061
302	4.2	gnf1m29833_s_at	XM_924663	9630025B04	M-phase phosphoprotein 9
303	4.2	gnf1m32621_at			inferred: ref|NP_036686.1| (NM_012554) enolase 1, alpha

					[Rattus norvegicus] mCG18926
304	4.2	gnf1m28392_a_at		E430024E22	NOL1/NOP2/Sun domain family 3
305	4.2	gnf1m32904_at	XM_917520		similar to Spectrin beta chain, brain 4 (Spectrin, non-erythroid beta chain 4) (Beta-V spectrin) (BSPECV)
306	4.2	gnf1m33610_at	XM_909794		similar to dead end homolog 1
307	4.2	gnf1m24513_at		6720482J09	aconitase 2, mitochondrial
308	4.2	gnf1m12237_a_at	NM_031187	A430103N06	tryptase alpha/beta 1
309	4.2	gnf1m35869_at			inferred: ref|XP_016001.1| (XM_016001) hypothetical protein XP_016001 [Homo sapiens] mCG1041621
310	4.2	gnf1m12329_s_at		B930075E15	hypothetical protein
311	4.2	gnf1m01241_at	NM_008238		forkhead box N1
312	4.2	gnf1m14021_a_at			RIKEN cDNA 2410024N13 gene
313	4.2	gnf1m36099_at			inferred: gb|AAF81417.1|AF239196_4 (AF239196) BCL1 lymphoma-derived single chain idiotype variable region [synthetic construct] mCG1025862
314	4.2	gnf1m34089_at			inferred: ref|XP_151046.1| (XM_151046) hypothetical protein XP_151046 [Mus musculus] mCG113690
315	4.2	gnf1m22281_at		D230007B16	unclassifiable
316	4.2	gnf1m29087_at			inferred: gb|AAH20488.1|AAH20488 (BC020488) Similar to protein with polyglutamine repeat; calcium (ca2+) homeostasis endoplasmic reticulum protein [Mus musculus] mCG5625
317	4.2	gnf1m25326_at		A130049D12	cryptochrome 2 (photolyase-like)
318	4.2	gnf1m32175_at	XM_912234		hypothetical protein LOC620642
319	4.2	gnf1m32528_at			uncharacterized Celera prediction mCG13775
320	4.2	gnf1m24170_at		6030413L20	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3
321	4.2	gnf1m10237_at	NM_029686	1810008A02	polycystic kidney disease 1 like 2
322	4.2	gnf1m19795_at		9530058P14	casein kinase 1, epsilon
323	4.2	gnf1m34035_at			inferred: ref|XP_131925.1| (XM_131925) similar to Rad50-interacting protein 1; hypothetical protein FLJ11785 [Mus musculus] NP 068749 NM 021930 Homo sapiens ref|NP_068749.2| (NM_021930) Rad50-interacting protein 1; hypothetical protein FLJ11785 [Homo sapiens] mCG114470
324	4.2	gnf1m19538_at		8030437B22	cyclic nucleotide gated channel alpha 3
325	4.2	gnf1m32939_at	NM_027745		coiled-coil domain containing 57
326	4.2	gnf1m17978_at		4933434K12	Transcribed locus
327	4.2	gnf1m25782_at		A630002C06	hypothetical Metallo-dependent phosphatases structure containing protein
328	4.2	gnf1m35410_s_at	XM_912587		gene model 41, (NCBI)
329	4.2	gnf1m12531_a_at	NM_177132	C130002K19	RIKEN cDNA 1520401A03 gene
330	4.2	gnf1m12367_at	NM_178766	A930004C23	RIKEN cDNA B230315F11 gene
331	4.2	gnf1m35501_at			inferred: ref|NP_034003.1| (NM_009873) cyclin-dependent kinase 6 [Mus musculus] mCG1028465
332	4.2	gnf1m17658_at		G430056N18	hypothetical YjeF-like structure containing protein
333	4.2	gnf1m33472_at	XM_908933	4930545J21	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4
334	4.2	gnf1m07219_a_at	NM_147221	I0C0014N20	GLIS family zinc finger 1
335	4.2	gnf1m26629_at		C030018L17	REGULATOR OF G-PROTEIN SIGNALING 20 (RGS20) (REGULATOR OF G-PROTEIN SIGNALING Z1) homolog [Mus musculus]
336	4.2	gnf1m15163_at		2210403E17	phosphofructokinase, liver, B-type
337	4.2	gnf1m09093_at	NM_178244		transmembrane epididymal protein 1
338	4.2	gnf1m31597_at	XM_924190		similar to Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 1 (GalNAc alpha-2,6-sialyltransferase I) (ST6GalNAc I) (Sialyltransferase 7A)
339	4.2	gnf1m08566_a_at	NM_172479	F930032P09	solute carrier family 38, member 5
340	4.2	gnf1m10964_a_at	NM_009363	0910001O22	trefoil factor 2 (spasmolytic protein 1)
341	4.2	gnf1m07029_at	NM_146875		olfactory receptor 895
342	4.2	gnf1m29817_a_at	NM_183180	6720430O15	tetraspanin 18
343	4.2	gnf1m34154_at			inferred: ref|NP_116095.1| (NM_032706) hypothetical protein MGC12966 [Homo sapiens] mCG113002
344	4.2	gnf1m27441_at		D130050K19	polyhomeotic-like 2 (Drosophila)
345	4.2	gnf1m08227_at	NM_173365	A430106B11	G protein-coupled receptor 20
346	4.2	gnf1m17244_at		4933421D24	RIKEN cDNA 4933421D24 gene
347	4.2	gnf1m12932_a_at	NM_009036	D430025K11	recombining binding protein suppressor of hairless-like (Drosophila)
348	4.2	gnf1m33356_at			uncharacterized Celera prediction mCG126184
349	4.2	gnf1m01257_a_at	NM_008266	5730469B06	homeo box B1
350	4.2	gnf1m16328_at		4930427C17	RIKEN cDNA 4930471M09 gene
351	4.2	gnf1m24106_a_at		E130302K06	RIKEN cDNA 4930459M12 gene
352	4.2	gnf1m25226_at		9930030P21	programmed cell death protein 11
353	4.2	gnf1m22882_at	NM_001024489	A630024D08	RIKEN cDNA 1700034H15 gene
354	4.1	gnf1m17811_at		6720475G09	unclassifiable
355	4.1	gnf1m09569_at	NM_175473		Fraser syndrome 1 homolog (human)
356	4.1	gnf1m30741_a_at		9430088F20	development and differentiation enhancing factor-like 1
357	4.1	gnf1m35793_at			inferred: ref|NP_006249.1| (NM_006258) protein kinase, cGMP-dependent, type I; Protein kinase, cGMP-dependent, regulatory, type I; cGKI; protein kinase, cGMP-dependent, regulatory, type I, beta [Homo sapiens] mCG1045202
358	4.1	gnf1m35378_x_at	XM_912339		similar to Ig kappa chain V-VI region NQ2-17.4.1
359	4.1	gnf1m03629_a_at	NM_018809	1810061H18	pancreas specific transcription factor, 1a
360	4.1	gnf1m03709_at	NM_019476		olfactory receptor 159
361	4.1	gnf1m22378_at		D530008I23	unclassifiable
362	4.1	gnf1m15673_at			tripartite motif-containing 41
363	4.1	gnf1m18115_at		6530411M01	RIKEN cDNA 6530411M01 gene
364	4.1	gnf1m09125_a_at	NM_146720		olfactory receptor 421
365	4.1	gnf1m07669_a_at	NM_177993	4732474A02	high mobility group box transcription factor 1
366	4.1	gnf1m32259_at			inferred: ref|NP_032110.1| (NM_008084) glyceraldehyde-3-phosphate dehydrogenase [Mus musculus] mCG21423
367	4.1	gnf1m33049_at			inferred: ref|NP_032110.1| (NM_008084) glyceraldehyde-3-phosphate dehydrogenase [Mus musculus] mCG130516
368	4.1	gnf1m22463_at		D930013C07	unclassifiable
369	4.1	gnf1m15808_at			Mouse anti-human CD37 antibody WR17 gamma heavy chain variable region mRNA, complete cds /cds=(0,365) /gb=AY058909 /gi=16902043 /len=375 gnl|UG|Mm#S2455815
370	4.1	gnf1m06996_at	NM_146827		olfactory receptor 983
371	4.1	gnf1m26743_at		C130048F06	RIKEN cDNA 4930429B21 gene
372	4.1	gnf1m19599_at		9130206J18	unclassifiable
373	4.1	gnf1m01728_a_at	NM_009137		chemokine (C-C motif) ligand 22
374	4.1	gnf1m02718_a_at	NM_011259	2010207I02	regenerating islet-derived 3 alpha
375	4.1	gnf1m33074_at			uncharacterized Celera prediction mCG130119
376	4.1	gnf1m25913_a_at		A630097D09	ankyrin repeat domain 10
377	4.1	gnf1m35861_at			uncharacterized Celera prediction mCG1042041
378	4.1	gnf1m27724_at		D430035C11	A kinase (PRKA) anchor protein (gravin) 12
379	4.1	gnf1m05794_at			Mouse heat shock 10 kDa protein 1 (chaperonin 10), pseudogene 2 (Hspe1-ps2), mRNA
380	4.1	gnf1m06770_x_at	NM_146291		olfactory receptor 1484
381	4.1	gnf1m19495_at		6720416O16	unclassifiable
382	4.1	gnf1m15927_at		5730446C15	RIKEN cDNA 5730446C15 gene
383	4.1	gnf1m08119_at		9530053H22	hypothetical protein 9530053H22
384	4.1	gnf1m21871_at		A130059I02	WW domain-containing oxidoreductase
385	4.1	gnf1m32959_at	XM_917812	F930017C10	SEC31-like 2 (S. cerevisiae)
386	4.1	gnf1m14769_a_at		4930463O16	RIKEN cDNA 4930463O16 gene
387	4.1	gnf1m29398_a_at	NM_029706	0910001A18	carboxypeptidase B1 (tissue)
388	4.1	gnf1m08765_at		D930030O05	RIKEN cDNA D930030O05 gene
389	4.1	gnf1m26973_at		C230094E01	TBC1 domain family, member 7
390	4.1	gnf1m34389_at			inferred: gb|AAH20169.1|AAH20169 (BC020169) Unknown (protein for IMAGE:3543815) [Homo sapiens] mCG50160
391	4.1	gnf1m35950_x_at			inferred: gb|AAL61498.1| (AY073835) olfactory receptor MOR135-5 [Mus musculus] mCG1036269
392	4.1	gnf1m29191_at			inferred: ref|NP_477388.1| (NM_058040) Faf-P1; Fly Fas-associated factor [Drosophila melanogaster] mCG4392
393	4.1	gnf1m21668_at		4930438B12	unclassifiable
394	4.1	gnf1m19092_at		2700007L21	peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase
395	4.1	gnf1m23125_at		1190005J19	motile sperm domain containing 3
396	4.1	gnf1m23569_at		4732471J01	RIKEN cDNA 4732471J01 gene
397	4.1	gnf1m34880_s_at	NM_146926		olfactory receptor 476
398	4.1	gnf1m26143_at		A930024K11	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 ALPHA KINASE 1 (FRAGMENT) homolog [Mus musculus]
399	4.1	gnf1m31450_at	XM_906597		FAT tumor suppressor homolog 3 (Drosophila)
400	4.1	gnf1m35754_at			inferred: ref|XP_070240.1| (XM_070240) similar to TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3) (H. sapiens) [Homo sapiens] mCG1047447
401	4.1	gnf1m02448_a_at	NM_010636		Kruppel-like factor 12
402	4.1	gnf1m15557_at		9530092J24	RIKEN cDNA 5430434F05 gene
403	4.1	gnf1m24099_at		5830496J19	solute carrier family 44, member 2
404	4.0	gnf1m18055_at		4930405E17	carboxypeptidase B2 (plasma)

405	4.0	gnf1m33088_at	XM_914704		UBX domain containing 7
406	4.0	gnf1m25702_at		A530029A01	CDNA FLJ30119 FIS, CLONE BRACE1000070 homolog [Homo sapiens]
407	4.0	gnf1m34402_x_at	XM_906834		similar to Ran-specific GTPase-activating protein (Ran binding protein 1) (RANBP1) (HpaII tiny fragments locus 9a protein)
408	4.0	gnf1m35302_s_at	NM_146437		olfactory receptor 1000
409	4.0	gnf1m29806_at			inferred: ref|XP_134089.1| (XM_134089) similar to BRF2, subunit of RNA polymerase III transcription initiation factor, BRF1-like; RNA polymerase III transcription initiation factor BRFU; transcription factor IIB-related factor, TFIIIB50 [Mus musculus] mCG2249
410	4.0	gnf1m32553_x_at			inferred: gb|AAL09445.1|AF309508_1 (AF309508) farnesyl pyrophosphate synthase [Mus musculus] mCG19081
411	4.0	gnf1m33796_s_at	XM_909258		gene model 392, (NCBI)
412	4.0	gnf1m09741_s_at	NM_033580		protocadherin gamma subfamily B, 8
413	4.0	gnf1m21288_at		D130067L24	unclassifiable
414	4.0	gnf1m27913_at		D930007D24	RIKEN cDNA 5430432N15 gene
415	4.0	gnf1m03926_a_at	NM_020289		olfactory receptor 544
416	4.0	gnf1m28299_at		E330019N15	SMAP-1 homolog [Homo sapiens]
417	4.0	gnf1m07464_at		4732497C06	MYOSIN-IC homolog [Homo sapiens]
418	4.0	gnf1m32455_at	NM_001033441	G270054A15	expressed sequence AU045404
419	4.0	gnf1m01833_a_at	NM_009328		transcription factor 15
420	4.0	gnf1m00045_a_at	NM_181420	9030012M21	cDNA sequence BC032265
421	4.0	gnf1m09529_s_at	XM_895716	6530401P13	RAS protein activator like 2
422	4.0	gnf1m33920_at			inferred: ref|XP_006959.3| (XM_006959) similar to glyceraldehyde-3-phosphate dehydrogenase (H. sapiens) [Homo sapiens] mCG116319
423	4.0	gnf1m19870_a_at		9630058G16	hypothetical gene supported by AK036329
424	4.0	gnf1m33604_at			regulator of sex-limitation candidate 24
425	4.0	gnf1m25020_at		9630006B12	hypothetical protein
426	4.0	gnf1m26962_at		I830082K10	Nfat activating molecule with ITAM motif 1
427	4.0	gnf1m26418_at		B330007M19	discs, large homolog 2 (Drosophila)
428	4.0	gnf1m02125_a_at	NM_009890	I830084M14	cholesterol 25-hydroxylase
429	4.0	gnf1m20903_at		B930053K13	hypothetical protein
430	4.0	gnf1m34527_at			inferred: ref|NP_001006.1| (NM_001015) ribosomal protein S11; 40S ribosomal protein S11 [Homo sapiens] mCG1043329
431	4.0	gnf1m23935_a_at		5330420D20	RIKEN cDNA 5330420D20 gene

No. 3, oocyte specific genes

#1	#2	#3	#4	#5	#6
1	6.5	gnf1m30961_a_at	XM_924334	4930486L02	centromere autoantigen F
2	6.2	gnf1m06748_a_at	NM_146250		G protein-coupled receptor 1
3	5.9	gnf1m31660_at	XM_904234		similar to PRAME family member 9
4	5.8	gnf1m02950_a_at	NM_011775	A430016G17	zona pellucida glycoprotein 2
5	5.7	gnf1m21586_at	NM_198674	E330012N03	similar to hypothetical protein E330023O18
6	5.6	gnf1m22601_a_at	NM_175011	E330017A01	RIKEN cDNA E330017A01 gene
7	5.5	gnf1m08554_a_at	NM_177690	E330007A02	NACHT, leucine rich repeat and PYD containing 2
8	5.5	gnf1m28886_a_at		L230001B22	LIM homeobox protein 8
9	5.4	gnf1m02951_a_at	NM_011776	2410001F05	zona pellucida glycoprotein 3
10	5.4	gnf1m30576_a_at		B930099F18	unclassifiable
11	5.4	gnf1m34191_at	NM_198960		transcription factor AP-2, epsilon
12	5.3	gnf1m28752_at	XM_920480		similar to Na+ dependent glucose transporter 1
13	5.3	gnf1m11368_at	NM_009757	B020029E15	bone morphogenetic protein 15
14	5.2	gnf1m01178_a_at	NM_008110	7420463G17	growth differentiation factor 9
15	5.2	gnf1m16093_at	NM_033320	1110017N23	glucuronyl C5-epimerase
16	5.2	gnf1m11848_a_at	NM_133353	7420700J01	oocyte secreted protein 1
17	5.2	gnf1m30527_at	NM_001033283	E330030M12	gene model 97, (NCBI)
18	5.2	gnf1m23490_at		4631433P05	vesicle transport through interaction with t-SNAREs 1 homolog
19	5.2	gnf1m08558_a_at	NM_173773	E330017M15	oogenesin 4
20	5.1	gnf1m21562_a_at	XM_920526	E130318K11	uracil DNA glycosylase 2
21	5.1	gnf1m15535_a_at	NM_026849	9430051D16	RIKEN cDNA 1110061O04 gene
22	5.1	gnf1m04710_a_at	NM_025819	1200016B10	RIKEN cDNA 1200016B10 gene
23	5.1	gnf1m31175_at		B020005F19	cDNA sequence BC052883
24	5.1	gnf1m02992_a_at	NM_011860	E330019F16	NACHT, leucine rich repeat and PYD containing 5
25	5.1	gnf1m13260_a_at		B020030M24	T-cell lymphoma breakpoint 1
26	5.1	gnf1m22609_a_at	NM_001033214	E330034G19	RIKEN cDNA E330034G19 gene
27	5.1	gnf1m01972_a_at			zona pellucida glycoprotein 1
28	5.1	gnf1m08559_a_at	NM_177571	E330017N17	hypothetical protein E330017N17
29	5.1	gnf1m09667_a_at	XM_917102	A430083E15	nucleoporin 214
30	5.0	gnf1m08557_a_at	NM_177598	E330017E16	F-box and WD-40 domain protein 13
31	5.0	gnf1m17214_s_at	NM_028387	4831410G10	RIKEN cDNA 2900006F19 gene
32	5.0	gnf1m08926_s_at	NM_175127	7420450G03	F-box protein 28
33	5.0	gnf1m09326_a_at	NM_178892	4632422G22	TCDD-inducible poly(ADP-ribose) polymerase
34	5.0	gnf1m32851_at			ENSMUST00000074244 transcript (in rel.37.34e)
35	5.0	gnf1m08149_a_at	NM_178736	C230098F24	ELMO domain containing 2
36	5.0	gnf1m00046_a_at	NM_175215	F830104M21	LysM, putative peptidoglycan-binding, domain containing 4
37	5.0	gnf1m16896_at		4930521G14	RIKEN cDNA 4930544M13 gene
38	5.0	gnf1m29971_a_at	XM_919543	A930002I23	RIKEN cDNA 4930487N19 gene
39	5.0	gnf1m06245_a_at	NM_138311	E330021E10	H1 histone family, member O, oocyte-specific
40	5.0	gnf1m03018_a_at	NM_011906	F830032K21	G protein-coupled receptor 175
41	5.0	gnf1m03110_a_at	NM_013479	I0C0031F16	Bcl2-like 10
42	5.0	gnf1m00312_a_at	NM_173737	8430410A17	RIKEN cDNA 8430410A17 gene
43	5.0	gnf1m33167_at			transmembrane protein 122
44	5.0	gnf1m12974_a_at	NM_025723	D630044H03	hypothetical S-adenosyl-L-methionine-dependent methyltransferases structure containing protein
45	5.0	gnf1m09902_a_at	NM_053254	F630026I01	transducin-like enhancer of split 6, homolog of Drosophila E(spl)
46	5.0	gnf1m07285_at	NM_153106	B020006J20	peptidyl arginine deiminase, type VI
47	4.9	gnf1m30913_a_at	NM_001037725	F630107I23	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 13 (human)
48	4.9	gnf1m08567_a_at	NM_181345	E330038E07	nucleophosmin/nucleoplasmin 2
49	4.9	gnf1m05952_at	NM_130869		OG2 homeobox gene
50	4.9	gnf1m05550_a_at	NM_030236	F830001G13	F-box only protein 34
51	4.9	gnf1m29341_a_at	NM_133225	8430407O11	acyl-Coenzyme A binding domain containing 3
52	4.9	gnf1m29887_a_at	NM_001004185	B430206J08	WAS protein homology region 2 domain containing 1
53	4.9	gnf1m12000_at	NM_026434	9530020N09	RNA binding motif protein 18
54	4.9	gnf1m23779_a_at		4930563O14	RIKEN cDNA 4931428L18 gene
55	4.9	gnf1m18955_a_at	XM_912265	C730042B03	trophinin associated protein
56	4.9	gnf1m11490_a_at	NM_018831	4930564M16	DNA cross-link repair 1A, PSO2 homolog (S. cerevisiae)
57	4.9	gnf1m29609_at	NM_001033452	D930032I15	gene model 1967, (NCBI)
58	4.9	gnf1m15784_a_at	NM_027149	I0C0032E22	RIKEN cDNA 2310040A13 gene
59	4.9	gnf1m10026_a_at	NM_134033		cDNA sequence BC018601
60	4.9	gnf1m10357_a_at	NM_146215	C730036L12	cDNA sequence BC025546
61	4.9	gnf1m31534_at	NM_174877		zygote arrest 1
62	4.9	gnf1m11064_a_at	XM_908461	I920051H06	polymerase (RNA) II (DNA directed) polypeptide C
63	4.9	gnf1m07288_a_at	NM_153110	E330039K03	tripartite motif-containing 61
64	4.9	gnf1m33923_at	XM_908019		hypothetical LOC544755
65	4.8	gnf1m30889_at	NM_198600	I830078N12	polymerase (DNA directed) sigma
66	4.8	gnf1m17493_a_at		6430525G20	zinc finger protein 108
67	4.8	gnf1m08922_a_at	NM_178741	C630033J19	kelch-like 8 (Drosophila)
68	4.8	gnf1m07815_a_at	NM_178657	E330030D17	oogenesin 1
69	4.8	gnf1m11391_a_at	NM_033541	9130230E18	2'-5' oligoadenylate synthetase 1C
70	4.8	gnf1m00719_a_at	NM_175542	6430703L12	rotatin
71	4.8	gnf1m08421_at	NM_175342	C330003B14	RIKEN cDNA C330003B14 gene
72	4.8	gnf1m06657_a_at	NM_145977	7420401D15	solute carrier family 45, member 3
73	4.8	gnf1m26416_a_at		B230385P13	inferred: transformed mouse 3T3 cell double minute 4
74	4.8	gnf1m18392_at	NM_138657	M5C1099J02	suppressor of cytokine signaling 7 (Socs7)
75	4.8	gnf1m25972_a_at		I420020M02	ubiquitin specific protease 19
76	4.8	gnf1m19345_a_at	NM_177869	5830457H01	expressed sequence AI847670
77	4.8	gnf1m04415_a_at	NM_024262	9430087D06	RIKEN cDNA 1200011M11 gene
78	4.8	gnf1m18629_a_at	NM_175031	4931409P07	serine/threonine kinase 36 (fused homolog, Drosophila)
79	4.8	gnf1m05690_a_at	NM_031870	4932427F05	mutS homolog 4 (E. coli)
80	4.8	gnf1m30352_at	XM_920772		helicase, mus308-like (Drosophila)
81	4.8	gnf1m09619_a_at		4022413I18	hypothetical Zn-finger, NF-X1 type/Zinc finger RING-type profile/Cysteine-rich region profile/Glycine-rich region profile/Zn-finger-like, PHD finger containing protein
82	4.8	gnf1m06095_at	NM_133910		TBC1 domain family, member 14
83	4.8	gnf1m21164_at		C730018N17	unclassifiable
84	4.8	gnf1m03279_a_at	NM_013773	7420471I21	T-cell leukemia/lymphoma 1B, 1
85	4.8	gnf1m06295_a_at	NM_138954	B020005E07	ret finger protein-like 4
86	4.8	gnf1m19491_at		6720407O05	unclassifiable
87	4.8	gnf1m30703_at	NM_001013776		hypothetical protein LOC382106
88	4.8	gnf1m09805_a_at	NM_026480	I1C0008P04	RIKEN cDNA 2410146L05 gene
89	4.8	gnf1m07508_a_at	NM_019493	B020039D12	B-cell translocation gene 4
90	4.8	gnf1m19037_a_at	XM_898196	9330189K18	AT rich interactive domain 1B (Swi1 like)
91	4.7	gnf1m29491_a_at	XM_910498	I830007N16	RIKEN cDNA 2700029M09 gene
92	4.7	gnf1m07705_a_at	NM_172815	E130304P21	R-spondin 2 homolog (Xenopus laevis)
93	4.7	gnf1m10718_a_at	NM_026123	4922505F15	unc-50 homolog (C. elegans)
94	4.7	gnf1m24532_at	XM_893519	7030405H07	RING1 and YY1 binding protein
95	4.7	gnf1m07955_at	NM_175017	4933427D06	RIKEN cDNA 4933427D06 gene
96	4.7	gnf1m22904_x_at		B020039I20	HD domain containing 3
97	4.7	gnf1m01197_a_at	NM_008154		G-protein coupled receptor 3
98	4.7	gnf1m26814_at		C130084O20	selected mouse cDNA on the X
99	4.7	gnf1m23266_at		F830027O21	chromodomain protein, Y chromosome-like
100	4.7	gnf1m08564_at	NM_172481	E330024M09	NACHT, leucine rich repeat and PYD containing 4B
101	4.7	gnf1m22590_a_at	NM_199036	E330001M05	F-box and WD-40 domain protein 15
102	4.7	gnf1m04662_a_at	NM_025722	4921524J17	RIKEN cDNA 4921524J17 gene
103	4.7	gnf1m33573_at	XM_908434		similar to RIKEN cDNA A430107P09 gene
104	4.7	gnf1m08561_a_at	NM_175527	E330021D16	RIKEN cDNA E330021D16 gene
105	4.7	gnf1m16575_at	XM_908442	2810012H18	coiled-coil domain containing 6
106	4.7	gnf1m28911_a_at	XM_910582	2810040O04	zinc fingerprotein 618
107	4.7	gnf1m10862_at	NM_012042	I920086F14	cullin 1
108	4.7	gnf1m03748_a_at	NM_019588	9530064F18	phospholipase C, epsilon 1
109	4.7	gnf1m13397_a_at		1500026F15	RIKEN cDNA 2810453I06 gene
110	4.7	gnf1m29470_a_at	XM_925577	I920020H01	protein tyrosine phosphatase, receptor type, f polypeptide

					(PTPRF), interacting protein, alpha 1
111	4.7	gnf1m05164_a_at	NM_027411	B020004G07	RIKEN cDNA 2600001J17 gene
112	4.7	gnf1m17612_s_at	XM_906226	A930011E11	RIKEN cDNA 1110065L07 gene
113	4.7	gnf1m09787_a_at	NM_027422	F630102P07	RIKEN cDNA 2700087H15 gene
114	4.7	gnf1m28697_a_at	NM_007562	E230006C08	basonuclin 1
115	4.7	gnf1m08592_at	NM_172705	4932439F05	PHD finger protein 13
116	4.6	gnf1m05052_a_at	NM_029794	1500000C01	DNA segment, Chr 11, ERATO Doi 636, expressed
117	4.6	gnf1m00615_a_at	NM_181417	E430020F17	cysteine and glycine-rich protein 2 binding protein
118	4.6	gnf1m00374_s_at	XM_897204		ring finger and WD repeat domain 2
119	4.6	gnf1m08562_at	NM_177187	E330023J07	DNA segment, Chr 5, ERATO Doi 577, expressed
120	4.6	gnf1m00395_at	NM_027802	7420700M11	oocyte specific homeobox 1
121	4.6	gnf1m13138_a_at	NM_008316	E430014O06	Hus1 homolog (S. pombe)
122	4.6	gnf1m32478_at	XM_915014		similar to transcription elongation factor B (SIII), polypeptide 2
123	4.6	gnf1m31294_a_at	XM_918100	B020004A05	oocyte maturation, beta
124	4.6	gnf1m00103_a_at	NM_010021	8030454H23	deleted in azoospermia-like
125	4.6	gnf1m23026_s_at		G730030D09	PAP associated domain containing 1
126	4.6	gnf1m30724_a_at	NM_001002894	4921520L01	NACHT, leucine rich repeat and PYD containing 14
127	4.6	gnf1m16358_at	XM_131719	2310047N01	D164 sialomucin-like 2
128	4.6	gnf1m20390_at		A630050C01	3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630050C01 product:unclassifiable, full insert sequence
129	4.6	gnf1m28846_a_at	NM_001024919	2310022M17	RIKEN cDNA 2310022M17 gene
130	4.6	gnf1m30531_at	XM_925541	6430548M15	TAO kinase 1
131	4.6	gnf1m29070_a_at	XM_916714	2700049A03	RIKEN cDNA 2700049A03 gene
132	4.6	gnf1m29306_at	NM_026579	I920095K20	DNA segment, Chr 10, Wayne State University 102, expressed
133	4.6	gnf1m28854_at	XM_914670	B020028L23	expressed sequence AU024076
134	4.6	gnf1m24830_at		9430024M13	bone morphogenetic protein 5
135	4.6	gnf1m13090_x_at	NM_178894	E330015L10	expressed sequence AA792892
136	4.6	gnf1m17453_at	NM_026127		RIKEN cDNA 4833420G17 gene
137	4.6	gnf1m06466_at	NM_145228		2'-5' oligoadenylate synthetase 1H
138	4.6	gnf1m13147_a_at	NM_025699	1700081J12	RIKEN cDNA 3230401D17 gene
139	4.6	gnf1m30080_a_at	NM_197992	2010002K04	polycomb group ring finger 1
140	4.6	gnf1m00998_a_at	NM_007810	E330007H14	cytochrome P450, family 19, subfamily a, polypeptide 1
141	4.6	gnf1m30873_a_at	XM_921247	C130001D11	C1q domain containing 1
142	4.6	gnf1m04413_a_at	NM_024242	I830082O20	RIO kinase 1 (yeast)
143	4.6	gnf1m08791_a_at	NM_177069	E330009P21	RIKEN cDNA E330009P21 gene
144	4.6	gnf1m30989_s_at		E230016M20	unclassifiable
145	4.6	gnf1m33640_at	NM_001033794	7420486K21	expressed sequence C85627
146	4.6	gnf1m29704_a_at	NM_175201	M5C1088B21	ring finger protein 38
147	4.5	gnf1m10238_a_at	NM_026758	1110001M01	M phase phosphoprotein 6
148	4.5	gnf1m05458_s_at	NM_029416	B020023K24	Kruppel-like factor 17
149	4.5	gnf1m00097_a_at	NM_007623	D030003P20	chromobox homolog 2 (Drosophila Pc class)
150	4.5	gnf1m02661_a_at	NM_011137	C230064N08	POU domain, class 2, transcription factor 1
151	4.5	gnf1m04400_a_at	NM_024213	I920062N18	anaphase promoting complex subunit 4
152	4.5	gnf1m29650_a_at	NM_027314	4933422F17	membrane-associated ring finger (C3HC4) 5
153	4.5	gnf1m25673_a_at		A430110I16	splicing factor 3b, subunit 3
154	4.5	gnf1m14863_at		6530413F01	rabphilin 3A-like (without C2 domains)
155	4.5	gnf1m10061_a_at	NM_024254	I920040K15	RIKEN cDNA 2410042D21 gene
156	4.5	gnf1m30810_at	NM_001024205		nuclear fragile X mental retardation protein interacting protein 2
157	4.5	gnf1m34888_at	NM_001025564		hypothetical LOC217066
158	4.5	gnf1m06037_a_at	NM_133701	I1C0020L10	RIKEN cDNA 2610031L17 gene
159	4.5	gnf1m10356_s_at	XM_900102	B020015A14	oocyte specific homeobox 1
160	4.5	gnf1m20977_a_at		E230001J08	unclassifiable
161	4.5	gnf1m11659_a_at	NM_026075	6820402F12	RIKEN cDNA 3110031B13 gene
162	4.5	gnf1m29621_at		C530010F03	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)
163	4.5	gnf1m00544_a_at	NM_172766	C630001A18	nuclear factor related to kappa B binding protein
164	4.5	gnf1m05520_a_at	NM_029846	5830475I01	autophagy-related 16-like 1 (yeast)
165	4.5	gnf1m13096_a_at	NM_177703	E330023O18	F-box and WD-40 domain protein 19
166	4.5	gnf1m33881_at			inferred: ref|XP_033028.2|(XM_033028) hypothetical protein XP_033028 [Homo sapiens] mCG116841
167	4.5	gnf1m32651_x_at	NM_001008428	7420476B15	F-box and WD-40 domain protein 12
168	4.5	gnf1m09601_a_at	XM_925665	6230429P11	inhibitor of Bruton agammaglobulinemia tyrosine kinase
169	4.5	gnf1m06558_a_at	NM_145546	I920073J21	general transcription factor IIB
170	4.5	gnf1m24244_a_at	NM_198010	A730093D16	ankyrin repeat domain 17
171	4.5	gnf1m16106_a_at	NM_028040	F830031C20	RNA pseudouridylate synthase domain containing 4
172	4.5	gnf1m04995_a_at	NM_026518	I920096N10	ring finger protein 146
173	4.5	gnf1m10030_a_at	NM_145355	I920064B12	ring finger protein 185
174	4.5	gnf1m30011_a_at	NM_026549	6030457N17	RIKEN cDNA 6030457N17 gene
175	4.5	gnf1m04980_a_at	NM_026479	F630001B12	zinc finger, CCHC domain containing 10
176	4.5	gnf1m05034_a_at	NM_026643	2810011I24	RIKEN cDNA 2410017P07 gene
177	4.5	gnf1m25771_at		A530093J23	immunoglobulin heavy chain 4 (serum IgG1)
178	4.5	gnf1m05945_a_at	NM_130796	2810421C03	sorting nexin associated golgi protein 1
179	4.5	gnf1m05268_a_at	NM_028106	7420443B10	zinc finger, BED domain containing 3
180	4.5	gnf1m28765_a_at		4932423E22	mbt domain containing 1
181	4.4	gnf1m30901_at	XM_918760	B020001O03	expressed sequence C87977
182	4.4	gnf1m01105_a_at	NM_007985	I920089C24	Fanconi anemia, complementation group C
183	4.4	gnf1m17498_a_at	NM_019921	C430003L11	A kinase (PRKA) anchor protein 10
184	4.4	gnf1m26841_at	XM_925276	C130097O10	cat eye syndrome chromosome region, candidate 2 homolog (human)
185	4.4	gnf1m15929_a_at		D130020G02	DNA segment, Chr 9, ERATO Doi 423, expressed
186	4.4	gnf1m03281_a_at	NM_013774		T-cell leukemia/lymphoma 1B, 4
187	4.4	gnf1m07986_a_at	NM_177475	6030407P18	suppressor of hairy wing homolog 2 (Drosophila)
188	4.4	gnf1m03899_a_at	NM_020021	4930571D16	Moloney sarcoma oncogene
189	4.4	gnf1m02798_a_at	NM_011420	I830076M14	survival motor neuron 1
190	4.4	gnf1m24615_s_at	NM_027804	G430007B02	ubiquitin specific peptidase 19
191	4.4	gnf1m29820_a_at	NM_028986	E130002P16	zinc finger protein 336
192	4.4	gnf1m10228_a_at	NM_027409	E430009I24	motile sperm domain containing 1
193	4.4	gnf1m30438_at			inferred: gb|AAH19796.1|AAH19796 (BC019796) Unknown (protein for IMAGE:4923005) [Mus musculus] mCG13475
194	4.4	gnf1m00322_a_at	NM_010786	1700007J15	transformed mouse 3T3 cell double minute 2
195	4.4	gnf1m03577_a_at	NM_017475	I830015H15	Ras-related GTP binding C
196	4.4	gnf1m04540_a_at	NM_025446	2010012K22	androgen-induced 1
197	4.4	gnf1m26226_a_at	NM_010804	M5C1026B14	myeloid/lymphoid or mixed lineage-leukemia translocation to 10 homolog (Drosophila)
198	4.4	gnf1m28277_at	NM_015793	I0C0037J19	F-box and WD-40 domain protein 14
199	4.4	gnf1m04652_a_at	NM_025706	4932416D24	TBC1 domain family, member 15
200	4.4	gnf1m03686_a_at	NM_019434	F430004B09	minichromosome maintenance deficient 3 (S. cerevisiae) associated protein
201	4.4	gnf1m16265_a_at	NM_027091	I1C0042E05	nucleoporin 35
202	4.4	gnf1m08496_a_at	NM_172631	D330030L18	DNA segment, Chr 18, ERATO Doi 653, expressed
203	4.4	gnf1m30830_at		I0C0042K12	NACHT, LRR and PYD containing protein 9c
204	4.4	gnf1m29271_at	XM_620267		similar to hypothetical protein FLJ20397
205	4.4	gnf1m28716_a_at	NM_001024135	1110008P08	kelch repeat and BTB (POZ) domain containing 7
206	4.4	gnf1m10172_a_at	NM_175311	F630008H06	zinc finger protein 513
207	4.4	gnf1m10001_a_at	XM_919590	I530009P20	establishment of cohesion 1 homolog 1 (S. cerevisiae)
208	4.4	gnf1m04940_a_at	NM_026371	I830028E01	loss of heterozygosity, 12, chromosomal region 1 homolog (human)
209	4.4	gnf1m01752_a_at		A930023B20	seven in absentia 2
210	4.4	gnf1m14492_a_at		0610033M10	RIKEN cDNA 0610033M10 gene
211	4.4	gnf1m19616_at		E330037N21	RIKEN cDNA 9230115E21 gene
212	4.4	gnf1m32413_at		C330012K05	gene model 1967, (NCBI)
213	4.4	gnf1m32052_at			OIP4 - RELATED (by Panther) mCG4511
214	4.4	gnf1m11620_a_at	NM_146170	B930024K20	expressed sequence C87436
215	4.4	gnf1m10590_at	NM_025482	G270079P12	tumor protein D52-like 2
216	4.4	gnf1m08924_a_at	NM_172615	F630032M11	RIKEN cDNA 1700021K19 gene
217	4.4	gnf1m04292_s_at	NM_023233	5730562C12	tripartite motif protein 13
218	4.4	gnf1m06456_a_at	NM_145210	E330025J23	2'-5' oligoadenylate synthetase 1E
219	4.4	gnf1m29561_a_at	XM_920199	2310030K10	ADP-ribosylation factor interacting protein 1
220	4.4	gnf1m10533_a_at	NM_007892	F830048D09	E2F transcription factor 5
221	4.4	gnf1m01750_a_at	NM_009173		seven in absentia 1B
222	4.3	gnf1m02052_a_at	NM_009765	4930451K22	breast cancer 2
223	4.3	gnf1m09271_a_at	NM_175290	C330026N02	NACHT, leucine rich repeat and PYD containing 4F
224	4.3	gnf1m23122_at		1190002G15	sorting nexin 9
225	4.3	gnf1m00510_a_at	NM_178375	4921517A06	zinc finger, SWIM domain containing 3
226	4.3	gnf1m09790_a_at	NM_133700	1110056N09	BTB (POZ) domain containing 10
227	4.3	gnf1m23273_at		2410038P04	suppressor of variegation 3-9 homolog 1 (Drosophila)
228	4.3	gnf1m01431_a_at	NM_008589	I920048L22	mesoderm posterior 2
229	4.3	gnf1m16922_a_at		2610312O17	RIKEN cDNA 1110054O05 gene
230	4.3	gnf1m08043_at	NM_172539	7420700F21	astacin-like metalloendopeptidase (M12 family)
231	4.3	gnf1m22236_at	XM_914443	D030047E23	RIKEN cDNA D230004J03 gene
232	4.3	gnf1m31151_at	NM_001024917	7420471K04	Bcl3 binding protein
233	4.3	gnf1m02110_a_at	NM_009862	I920087J24	cell division cycle 45 homolog (S. cerevisiae)-like
234	4.3	gnf1m10724_at	NM_008692		nuclear transcription factor-Y gamma
235	4.3	gnf1m11802_a_at	NM_026119	I1C0025D15	mediator of RNA polymerase II transcription, subunit 4 homolog (yeast)
236	4.3	gnf1m21764_at		7420441D12	ubiquitin specific peptidase 30
237	4.3	gnf1m12383_a_at	NM_011135	I920091F11	CCR4-NOT transcription complex, subunit 7
238	4.3	gnf1m31112_a_at	XM_921951		cell division cycle 27 homolog (S. cerevisiae)
239	4.3	gnf1m16919_a_at	NM_197988	1190005I06	RIKEN cDNA 1190005I06 gene
240	4.3	gnf1m22196_a_at	NM_001012517	I920184K22	fucosyltransferase 10
241	4.3	gnf1m26369_at		F630207G02	Btg3 associated nuclear protein
242	4.3	gnf1m17429_at		7420447K14	RIKEN cDNA 6330416L11 gene
243	4.3	gnf1m10284_a_at	NM_138585	G630022O12	calcium homeostasis endoplasmic reticulum protein
244	4.3	gnf1m30600_a_at	XM_909322	9630037P07	RIKEN cDNA 9630037P07 gene
245	4.3	gnf1m02902_a_at	NM_011657		tubby-like protein 3
246	4.3	gnf1m09991_a_at		C530022J18	hypothetical Lipocalin-related protein and Bos/Can/Equ allergen containing protein

247	4.3	gnf1m33427_at	XM_916262		gene model 527, (NCBI)
248	4.3	gnf1m17639_at		C730032N23	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)
249	4.3	gnf1m23284_at		2510005J23	peroxisome biogenesis factor 7
250	4.3	gnf1m29280_a_at	NM_080561	F630024P17	RIKEN cDNA 2810055G22 gene
251	4.3	gnf1m23463_a_at	NM_181650	4022401E08	PR domain containing 4
252	4.3	gnf1m10004_a_at	NM_027930	2610016C23	RIKEN cDNA 2610016C23 gene
253	4.3	gnf1m29158_at	NM_175025	B230348M20	ATPase, Ca++-sequestering
254	4.3	gnf1m22577_a_at	NM_001013377	E130306D19	RIKEN cDNA E130306D19 gene
255	4.3	gnf1m16871_a_at		F830023N07	nuclear transcription factor-Y alpha
256	4.3	gnf1m08574_a_at	NM_177088	4732496G21	coiled-coil domain containing 45
257	4.3	gnf1m30114_a_at	NM_172516	C230050J24	receptor interacting protein kinase 5
258	4.3	gnf1m22661_a_at		F630005A19	zinc finger protein 341
259	4.3	gnf1m16223_a_at	XM_917330	2810407P21	similar to Exocyst complex component Sec3
260	4.3	gnf1m30451_a_at	NM_180599	F630202N16	microfibrillar-associated protein 3
261	4.3	gnf1m28732_at			spastin
262	4.3	gnf1m32185_at			inferred: gb|AAH19848.1|AAH19848 (BC019848) Similar to cactin [Homo sapiens] mCG3280
263	4.3	gnf1m27008_at		C330045B02	unclassifiable
264	4.3	gnf1m12897_a_at	NM_172405	D230004N03	RIKEN cDNA 3830405G04 gene
265	4.2	gnf1m22595_a_at	NM_001033211	I0C0046K11	expressed sequence AU022751
266	4.2	gnf1m13695_at		E130119J07	RIKEN cDNA E130119J07 gene
267	4.2	gnf1m00710_a_at	NM_023729	4933400N19	ankyrin repeat, SAM and basic leucine zipper domain containing 1
268	4.2	gnf1m08318_a_at	NM_172746		HIRA interacting protein 3
269	4.2	gnf1m10411_a_at		G730029A12	peptidylprolyl isomerase (cyclophilin) like 5
270	4.2	gnf1m09585_a_at	NM_145576		Zinc finger protein 212
271	4.2	gnf1m32800_at			inferred: gb|AAH11820.1|AAH11820 (BC011820) Unknown (protein for IMAGE:3619501) [Homo sapiens] mCG12659
272	4.2	gnf1m27711_at		D430026H23	phospholipase A2, activating protein
273	4.2	gnf1m18473_at	XM_922117	C230071E20	RIKEN cDNA 4933421B21 gene
274	4.2	gnf1m09634_a_at	NM_029337	C820012F11	E1A binding protein p400
275	4.2	gnf1m06127_a_at	NM_134017	2410018D16	methionine adenosyltransferase II, beta
276	4.2	gnf1m00299_a_at	NM_030743	I830162O14	zinc finger protein 313
277	4.2	gnf1m31045_at		C130054M03	RIKEN cDNA A630007B06 gene
278	4.2	gnf1m02434_a_at	NM_010600	M5C1047E09	potassium voltage-gated channel, subfamily H (eag-related), member 1
279	4.2	gnf1m22176_at		C330011L24	DNA segment, Chr 8, ERATO Doi 587, expressed
280	4.2	gnf1m30307_at	XM_920356	B020013L18	IQ motif containing with AAA domain
281	4.2	gnf1m20990_s_at	XM_923034	C130034K06	RIKEN cDNA A430041B07 gene
282	4.2	gnf1m13082_a_at	NM_028730	I530018A10	peroxisome biogenesis factor 26
283	4.2	gnf1m16087_a_at	NM_027560	G630019P16	arrestin domain containing 2
284	4.2	gnf1m09291_a_at	NM_026780	1110018L13	SYF2 homolog, RNA splicing factor (S. cerevisiae)
285	4.2	gnf1m03255_a_at	NM_013719	2610011M03	eukaryotic translation initiation factor 2 alpha kinase 4
286	4.2	gnf1m09536_a_at	NM_027263	2810407L01	RIKEN cDNA 2610040C18 gene
287	4.2	gnf1m18666_a_at	NM_028916	4921508G15	EF-hand domain (C-terminal) containing 2
288	4.2	gnf1m05250_a_at	NM_028034	7420437I06	RIKEN cDNA 2410004F06 gene
289	4.2	gnf1m16623_at	XM_914303	2610024M03	protein phosphatase 1, regulatory subunit 3D
290	4.2	gnf1m05539_a_at	NM_030153	A330021G12	MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)
291	4.2	gnf1m30027_at	XM_924076		TAF4A RNA polymerase II, TATA box binding protein (TBP)-associated factor
292	4.2	gnf1m15775_a_at	NM_183149	A430092M15	zinc finger protein 598
293	4.2	gnf1m06473_a_at	NM_145371	E430003B07	eukaryotic translation initiation factor 2B, subunit 1 (alpha)
294	4.2	gnf1m16582_at		4930481B07	RIKEN cDNA 4930481B07 gene
295	4.2	gnf1m26268_a_at	NM_025747	B130055N05	RIKEN cDNA 4933411K20 gene
296	4.2	gnf1m08556_s_at	XM_898812	E330015L10	expressed sequence AA792892
297	4.2	gnf1m17779_s_at		B930054M11	unclassifiable
298	4.2	gnf1m06092_x_at	NM_133893	E330028E06	2'-5' oligoadenylate synthetase 1D
299	4.2	gnf1m03965_s_at	XM_913263		aurora kinase C
300	4.2	gnf1m31661_at	XM_910255		hypothetical protein LOC635251
301	4.2	gnf1m12239_a_at	NM_177672	K530042E13	DNA segment, Chr 4, ERATO Doi 429, expressed
302	4.2	gnf1m24029_at		5730547A05	nucleoporin 62
303	4.2	gnf1m29590_a_at		4631426G04	zinc finger CCCH type containing 6
304	4.2	gnf1m11119_at	NM_010754	1810047O14	MAD homolog 2 (Drosophila)
305	4.2	gnf1m05931_a_at	NM_080848	4432406L10	WD repeat domain 5
306	4.2	gnf1m27190_a_at		C730023J07	leucine rich repeat containing 28
307	4.2	gnf1m08745_at	NM_177450	D630009N02	carnosine dipeptidase 1 (metallopeptidase M20 family)
308	4.2	gnf1m31009_a_at	NM_013910	2810055D04	F-box and leucine-rich repeat protein 10
309	4.2	gnf1m30183_at			inferred: ref|XP_088331.1| (XM_088331) hypothetical protein XP_088331 [Homo sapiens] mCG2510
310	4.1	gnf1m02731_a_at	NM_011293		polymerase (RNA) II (DNA directed) polypeptide J
311	4.1	gnf1m21264_a_at	XM_913342	D130048N15	Similar to RIKEN cDNA B430319H21 gene
312	4.1	gnf1m16129_a_at	NM_011919	I1C0015D22	inhibitor of growth family, member 1
313	4.1	gnf1m01576_a_at	NM_008838	F630222N08	phosphatidylinositol glycan, class F
314	4.1	gnf1m13596_at		2310046A20	SUMO1/sentrin specific peptidase 1
315	4.1	gnf1m07475_a_at	NM_009764		breast cancer 1
316	4.1	gnf1m34058_x_at			inferred: ref|XP_033028.2| (XM_033028) hypothetical protein XP_033028 [Homo sapiens] mCG114037
317	4.1	gnf1m07227_a_at	NM_148932	F630037F14	nuclear pore membrane protein 121
318	4.1	gnf1m07979_a_at	NM_176953	G370012I03	ligase IV, DNA, ATP-dependent
319	4.1	gnf1m10740_a_at	NM_016812	F630207G02	Btg3 associated nuclear protein
320	4.1	gnf1m04731_a_at	NM_025853	1700022L09	RIKEN cDNA 1700022L09 gene
321	4.1	gnf1m30701_a_at	XM_884388	1700124P09	RIKEN cDNA 1700124P09 gene
322	4.1	gnf1m15204_at	XM_900053	D330023N06	IQ motif containing GTPase activating protein 3
323	4.1	gnf1m33239_at	XM_924746		DNA segment, Chr 16, ERATO Doi 519, expressed
324	4.1	gnf1m30159_a_at	NM_172151	6330570D04	zinc finger, DHHC domain containing 8
325	4.1	gnf1m02838_a_at	NM_011513	G730029C15	surfeit gene 5
326	4.1	gnf1m27845_a_at	NM_178640	I830149D05	UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 2
327	4.1	gnf1m30756_at	XM_887622		similar to chromosome 6 open reading frame 148
328	4.1	gnf1m29966_a_at	XM_917146		zinc finger protein 664
329	4.1	gnf1m03272_a_at	NM_013757	5330428N11	synaptotagmin-like 4
330	4.1	gnf1m01949_a_at	NM_009534	I920028O19	yes-associated protein 1
331	4.1	gnf1m10346_a_at	XM_911042	4930533G20	F-box protein 43
332	4.1	gnf1m28959_a_at	XM_908452		tripartite motif protein 33
333	4.1	gnf1m01799_a_at	NM_009269	6030452M19	serine palmitoyltransferase, long chain base subunit 1
334	4.1	gnf1m05891_a_at	NM_057173	5330410G07	LIM domain only 1
335	4.1	gnf1m17216_s_at	NM_019923	A530039D21	inositol 1,4,5-triphosphate receptor 2
336	4.1	gnf1m31649_at	NM_194056	I0C0021D08	NACHT, LRR and PYD containing protein 9a
337	4.1	gnf1m12593_a_at	NM_016769	C630019N20	MAD homolog 3 (Drosophila)
338	4.1	gnf1m03856_a_at	NM_019941		zinc finger protein 235
339	4.1	gnf1m24294_at		6330442G23	hypothetical Cysteine-rich region profile containing protein
340	4.1	gnf1m10565_a_at	NM_023153	I730099H06	RIKEN cDNA 0610040D20 gene
341	4.1	gnf1m21846_a_at	NM_175016	9530023G02	alkB, alkylation repair homolog 2 (E. coli)
342	4.1	gnf1m09548_a_at	NM_146068	I530027A02	RIKEN cDNA 2310008H04 gene
343	4.1	gnf1m16585_at	XM_906311	B230314J02	hexamthylene bis-acetamide inducible 2
344	4.1	gnf1m05274_a_at	NM_028142	2810405F18	NOL1/NOP2/Sun domain family, member 4
345	4.1	gnf1m23755_a_at		4930511P18	RIKEN cDNA G630039H03 gene
346	4.1	gnf1m03428_a_at	NM_016688	F630118J21	programmed cell death protein 7
347	4.1	gnf1m03280_s_at	NM_013775	B020004B10	T-cell leukemia/lymphoma 1B, 1
348	4.0	gnf1m11638_a_at	NM_023239	C530046P15	necdin-like 2
349	4.0	gnf1m05006_a_at	NM_026557	9030406D12	ring finger and CHY zinc finger domain containing 1
350	4.0	gnf1m11525_a_at	NM_053180	4932702G04	cell cycle related kinase
351	4.0	gnf1m06090_a_at	NM_133886	4933403J17	expressed sequence AU040320
352	4.0	gnf1m06007_at			Mouse expressed sequence AA407930 (AA407930), mRNA
353	4.0	gnf1m24959_a_at	NM_001001144	I920039J23	SREBP cleavage activating protein
354	4.0	gnf1m33641_at		7420420A09	similar to F-box- and WD40-repeat-containing protein
355	4.0	gnf1m11061_s_at	NM_026949	I830015C07	CCR4-NOT transcription complex, subunit 8
356	4.0	gnf1m06752_at	NM_146258		serologically defined colon cancer antigen 13
357	4.0	gnf1m11526_a_at	NM_025979	1700028B20	microtubule associated serine/threonine kinase-like
358	4.0	gnf1m12215_a_at	NM_144884	C430047K18	torsin family 1, member A (torsin A)
359	4.0	gnf1m30421_a_at	NM_178115	2700050L05	RIKEN cDNA 2700050L05 gene
360	4.0	gnf1m00567_a_at	NM_027654	F630119D13	polycomb group ring finger 6
361	4.0	gnf1m29753_a_at	NM_199196	E430023E10	suppressor of zeste 12 homolog (Drosophila)
362	4.0	gnf1m11045_at	NM_024183	C530024M13	FIP1 like 1 (S. cerevisiae)
363	4.0	gnf1m18741_s_at	NM_029334	C730029A09	RIKEN cDNA 2700069A02 gene
364	4.0	gnf1m26345_a_at		B230323K17	WD repeat domain 33
365	4.0	gnf1m06720_a_at	NM_146169		cDNA sequence BC017133
366	4.0	gnf1m26990_a_at	NM_015732	D330025A07	axin2
367	4.0	gnf1m01318_a_at	NM_008389	1700023J10	IAP promoted placental gene
368	4.0	gnf1m01059_a_at	NM_007916	I920024M01	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19a
369	4.0	gnf1m05140_a_at	NM_027213	F830011B05	mediator of RNA polymerase II transcription, subunit 6 homolog (yeast)
370	4.0	gnf1m15900_a_at	NM_177471	F630113O12	coiled-coil domain containing 69
371	4.0	gnf1m04859_a_at	NM_026173	I830013E02	RIKEN cDNA 1200014M14 gene

No. 4, fertilized egg specific genes

#1	#2	#3	#4	#5	#6
1	5.2	gnf1m30527_at	NM_001033283	E330030M12	gene model 97, (NCBI)
2	5.2	gnf1m01178_a_at	NM_008110	7420463G17	growth differentiation factor 9
3	5.2	gnf1m10718_a_at	NM_026123	4922505F15	unc-50 homolog (C. elegans)
4	5.2	gnf1m22609_a_at	NM_001033214	E330034G19	RIKEN cDNA E330034G19 gene
5	5.2	gnf1m13260_a_at		B020030M24	T-cell lymphoma breakpoint 1
6	5.2	gnf1m11848_a_at	NM_133353	7420700J01	oocyte secreted protein 1
7	5.1	gnf1m11620_a_at	NM_146170	B930024K20	expressed sequence C87436
8	5.1	gnf1m23026_s_at		G730030D09	PAP associated domain containing 1
9	5.1	gnf1m18955_a_at	XM_912265	C730042B03	trophinin associated protein
10	5.1	gnf1m29491_a_at	XM_910498	I830007N16	RIKEN cDNA 2700029M09 gene
11	5.1	gnf1m11659_a_at	NM_026075	6820402F12	RIKEN cDNA 3110031B13 gene
12	5.1	gnf1m09326_a_at	NM_178892	4632422G22	TCDD-inducible poly(ADP-ribose) polymerase
13	5.1	gnf1m11490_a_at	NM_018831	4930564M16	DNA cross-link repair 1A, PSO2

					homolog (S. cerevisiae)
14	5.0	gnf1m03110_a_at	NM_013479	I0C0031F16	Bcl2-like 10
15	5.0	gnf1m00312_a_at	NM_173737	8430410A17	RIKEN cDNA 8430410A17 gene
16	5.0	gnf1m24029_at		5730547A05	nucleoporin 62
17	5.0	gnf1m00046_a_at	NM_175215	F830104M21	LysM, putative peptidoglycan-binding, domain containing 4
18	5.0	gnf1m32413_at		C330012K05	gene model 1967, (NCBI)
19	5.0	gnf1m16358_at	XM_131719	2310047N01	D164 sialomucin-like 2
20	5.0	gnf1m30114_a_at	NM_172516	C230050J24	receptor interacting protein kinase 5
21	5.0	gnf1m06245_a_at	NM_138311	E330021E10	H1 histone family, member O, oocyte-specific
22	5.0	gnf1m01105_a_at	NM_007985	I920089C24	Fanconi anemia, complementation group C
23	5.0	gnf1m18392_at	NM_138657	M5C1099J02	suppressor of cytokine signaling 7 (Socs7)
24	5.0	gnf1m07288_a_at	NM_153110	E330039K03	tripartite motif-containing 61
25	5.0	gnf1m10026_a_at	NM_134033		cDNA sequence BC018601
26	5.0	gnf1m21562_a_at	XM_920526	E130318K11	uracil DNA glycosylase 2
27	5.0	gnf1m11368_at	NM_009757	B020029E15	bone morphogenetic protein 15
28	5.0	gnf1m06295_a_at	NM_138954	B020005E07	ret finger protein-like 4
29	4.9	gnf1m29609_at	NM_001033452	D930032I15	gene model 1967, (NCBI)
30	4.9	gnf1m31534_at	NM_174877		zygote arrest 1
31	4.9	gnf1m30576_a_at		B930099F18	unclassifiable
32	4.9	gnf1m04415_a_at	NM_024262	9430087D06	RIKEN cDNA 1200011M11 gene
33	4.9	gnf1m13397_a_at		1500026F15	RIKEN cDNA 2810453I06 gene
34	4.9	gnf1m14492_a_at		0610033M10	RIKEN cDNA 0610033M10 gene
35	4.9	gnf1m25972_a_at		I420020M02	ubiquitin specific protease 19
36	4.9	gnf1m03279_a_at	NM_013773	7420471I21	T-cell leukemia/lymphoma 1B, 1
37	4.9	gnf1m15784_a_at	NM_027149	I0C0032E22	RIKEN cDNA 2310040A13 gene
38	4.9	gnf1m30889_at	NM_198600	I830078N12	polymerase (DNA directed) sigma
39	4.9	gnf1m04794_a_at	NM_026000	I730094B12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9
40	4.9	gnf1m03281_a_at	NM_013774		T-cell leukemia/lymphoma 1B, 4
41	4.9	gnf1m00544_a_at	NM_172766	C630001A18	nuclear factor related to kappa B binding protein
42	4.9	gnf1m33916_at	XM_922102		cDNA sequence AK129128
43	4.9	gnf1m01752_a_at		A930023B20	seven in absentia 2
44	4.9	gnf1m00494_a_at	NM_020507	E970024A05	transducer of ERBB2, 2
45	4.8	gnf1m07815_a_at	NM_178657	E330030D17	oogenesin 1
46	4.8	gnf1m08149_a_at	NM_178736	C230098F24	ELMO domain containing 2
47	4.8	gnf1m11064_a_at	XM_908461	I920051H06	polymerase (RNA) II (DNA directed) polypeptide C
48	4.8	gnf1m07955_at	NM_175017	4933427D06	RIKEN cDNA 4933427D06 gene
49	4.8	gnf1m20390_at		A630050C01	3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630050C01 product:unclassifiable, full insert sequence
50	4.8	gnf1m02661_a_at	NM_011137	C230064N08	POU domain, class 2, transcription factor 1
51	4.8	gnf1m06657_a_at	NM_145977	7420401D15	solute carrier family 45, member 3
52	4.8	gnf1m10590_at	NM_025482	G270079P12	tumor protein D52-like 2
53	4.8	gnf1m05690_a_at	NM_031870	4932427F05	mutS homolog 4 (E. coli)
54	4.8	gnf1m23284_at		2510005J23	peroxisome biogenesis factor 7
55	4.8	gnf1m29341_a_at	NM_133225	8430407O11	acyl-Coenzyme A binding domain containing 3
56	4.8	gnf1m09787_a_at	NM_027422	F630102P07	RIKEN cDNA 2700087H15 gene
57	4.8	gnf1m10357_a_at	NM_146215	C730036L12	cDNA sequence BC025546
58	4.8	gnf1m02798_a_at	NM_011420	I830076M14	survival motor neuron 1
59	4.8	gnf1m28752_at	XM_920480		similar to Na+ dependent glucose transporter 1
60	4.8	gnf1m04710_a_at	NM_025819	1200016B10	RIKEN cDNA 1200016B10 gene
61	4.8	gnf1m26416_a_at		B230385P13	inferred: transformed mouse 3T3 cell double minute 4
62	4.8	gnf1m05891_a_at	NM_057173	5330410G07	LIM domain only 1
63	4.8	gnf1m33923_at	XM_908019		hypothetical LOC544755
64	4.8	gnf1m33573_at	XM_908434		similar to RIKEN cDNA A430107P09 gene
65	4.8	gnf1m16575_at	XM_908442	2810012H18	coiled-coil domain containing 6
66	4.8	gnf1m31175_at		B020005F19	cDNA sequence BC052883
67	4.8	gnf1m16093_at	NM_033320	1110017N23	glucuronyl C5-epimerase
68	4.8	gnf1m01318_a_at	NM_008389	1700023J10	IAP promoted placental gene
69	4.8	gnf1m17612_s_at	XM_906226	A930011E11	RIKEN cDNA 1110065L07 gene
70	4.7	gnf1m08558_a_at	NM_173773	E330017M15	oogenesin 4
71	4.7	gnf1m15929_a_at		D130020G02	DNA segment, Chr 9, ERATO Doi 423, expressed
72	4.7	gnf1m05458_s_at	NM_029416	B020023K24	Kruppel-like factor 17
73	4.7	gnf1m07508_a_at	NM_019493	B020039D12	B-cell translocation gene 4
74	4.7	gnf1m12000_at	NM_026434	9530020N09	RNA binding motif protein 18
75	4.7	gnf1m30989_s_at		E230016M20	unclassifiable
76	4.7	gnf1m08922_a_at	NM_178741	C630033J19	kelch-like 8 (Drosophila)
77	4.7	gnf1m30352_at	XM_920772		helicase, mus308-like (Drosophila)
78	4.7	gnf1m09619_a_at		4022413I18	hypothetical Zn-finger, NF-X1 type/Zinc finger RING-type profile/Cysteine-rich region profile/Glycine-rich region profile/Zn-finger-like, PHD finger containing protein
79	4.7	gnf1m08561_a_at	NM_175527	E330021D16	RIKEN cDNA E330021D16 gene
80	4.7	gnf1m09657_a_at	XM_924216	D030051D21	centrosomal protein 164
81	4.7	gnf1m24615_s_at	NM_027804	G430007B02	ubiquitin specific peptidase 19
82	4.7	gnf1m10061_a_at	NM_024254	I920040K15	RIKEN cDNA 2410042D21 gene
83	4.7	gnf1m04662_a_at	NM_025722	4921524J17	RIKEN cDNA 4921524J17 gene
84	4.7	gnf1m26369_at		F630207G02	Btg3 associated nuclear protein
85	4.7	gnf1m01431_a_at	NM_008589	I920048L22	mesoderm posterior 2
86	4.7	gnf1m22549_at		E030034H13	hypothetical protein
87	4.7	gnf1m10740_a_at	NM_016812	F630207G02	Btg3 associated nuclear protein
88	4.7	gnf1m10228_a_at	NM_027409	E430009I24	motile sperm domain containing 1
89	4.7	gnf1m03748_a_at	NM_019588	9530064F18	phospholipase C, epsilon 1
90	4.7	gnf1m00395_at	NM_027802	7420700M11	oocyte specific homeobox 1
91	4.7	gnf1m31294_a_at	XM_918100	B020004A05	oocyte maturation, beta
92	4.7	gnf1m05520_a_at	NM_029846	5830475I01	autophagy-related 16-like 1 (yeast)
93	4.6	gnf1m01506_a_at		E430013K21	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26
94	4.6	gnf1m00103_a_at	NM_010021	8030454H23	deleted in azoospermia-like
95	4.6	gnf1m24830_at		9430024M13	bone morphogenetic protein 5
96	4.6	gnf1m06037_a_at	NM_133701	I1C0020L10	RIKEN cDNA 2610031L17 gene
97	4.6	gnf1m17214_s_at	NM_028387	4831410G10	RIKEN cDNA 2900006F19 gene
98	4.6	gnf1m04753_a_at	NM_025909	3930401E05	OMA1 homolog, zinc metallopeptidase (S. cerevisiae)
99	4.6	gnf1m19491_at		6720407O05	unclassifiable
100	4.6	gnf1m11119_at	NM_010754	1810047O14	MAD homolog 2 (Drosophila)
101	4.6	gnf1m29470_a_at	XM_925577	I920020H01	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein, alpha 1
102	4.6	gnf1m29887_a_at	NM_001004185	B430206J08	WAS protein homology region 2 domain containing 1
103	4.6	gnf1m10862_at	NM_012042	I920086F14	cullin 1
104	4.6	gnf1m30080_a_at	NM_197992	2010002K04	polycomb group ring finger 1
105	4.6	gnf1m05268_a_at	NM_028106	7420443B10	zinc finger, BED domain containing 3
106	4.6	gnf1m03965_s_at	XM_913263		aurora kinase C
107	4.6	gnf1m02838_a_at	NM_011513	G730029C15	surfeit gene 5
108	4.6	gnf1m03577_a_at	NM_017475	I830015H15	Ras-related GTP binding C
109	4.6	gnf1m00299_a_at	NM_030743	I830162O14	zinc finger protein 313
110	4.6	gnf1m21164_at		C730018N17	unclassifiable
111	4.6	gnf1m05034_a_at	NM_026643	2810011I24	RIKEN cDNA 2410017P07 gene
112	4.6	gnf1m09585_a_at	NM_145576		Zinc finger protein 212
113	4.6	gnf1m28846_a_at	NM_001024919	2310022M17	RIKEN cDNA 2310022M17 gene
114	4.6	gnf1m28854_at	XM_914670	B020028L23	expressed sequence AU024076
115	4.6	gnf1m28886_a_at		L230001B22	LIM homeobox protein 8
116	4.6	gnf1m30451_a_at	NM_180599	F630202N16	microfibrillar-associated protein 3
117	4.6	gnf1m14736_at		2610028F08	R-spondin 2 homolog (Xenopus laevis)
118	4.6	gnf1m12383_a_at	NM_011135	I920091F11	CCR4-NOT transcription complex, subunit 7
119	4.5	gnf1m30159_a_at	NM_172151	6330570D04	zinc finger, DHHC domain containing 8
120	4.5	gnf1m02110_a_at	NM_009862	I920087J24	cell division cycle 45 homolog (S. cerevisiae)-like
121	4.5	gnf1m28971_a_at	XM_906868	2410012M07	RIKEN cDNA 2410012M07 gene
122	4.5	gnf1m08924_a_at	NM_172615	F630032M11	RIKEN cDNA 1700021K19 gene
123	4.5	gnf1m09601_a_at	XM_925665	6230429P11	inhibitor of Bruton agammaglobulinemia tyrosine kinase
124	4.5	gnf1m02992_a_at	NM_011860	E330019F16	NACHT, leucine rich repeat and PYD containing 5
125	4.5	gnf1m17498_a_at	NM_019921	C430003L11	A kinase (PRKA) anchor protein 10
126	4.5	gnf1m26345_a_at		B230323K17	WD repeat domain 33
127	4.5	gnf1m08559_a_at	NM_177571	E330017N17	hypothetical protein E330017N17
128	4.5	gnf1m10030_a_at	NM_145355	I920064B12	ring finger protein 185
129	4.5	gnf1m15204_at	XM_900053	D330023N06	IQ motif containing GTPase activating protein 3
130	4.5	gnf1m10238_a_at	NM_026758	1110001M01	M phase phosphoprotein 6
131	4.5	gnf1m13138_a_at	NM_008316	E430014O06	Hus1 homolog (S. pombe)
132	4.5	gnf1m16919_a_at	NM_197988	1190005I06	RIKEN cDNA 1190005I06 gene
133	4.5	gnf1m30011_a_at	NM_026549	6030457N17	RIKEN cDNA 6030457N17 gene
134	4.5	gnf1m22577_a_at	NM_001013377	E130306D19	RIKEN cDNA E130306D19 gene
135	4.5	gnf1m04995_a_at	NM_026518	I920096N10	ring finger protein 146
136	4.5	gnf1m02902_a_at	NM_011657		tubby-like protein 3
137	4.5	gnf1m29158_at	NM_175025	B230348M20	ATPase, Ca++-sequestering
138	4.5	gnf1m16181_at		1810034K18	polymerase (DNA directed), epsilon 3 (p17 subunit)
139	4.5	gnf1m08564_at	NM_172481	E330024M09	NACHT, leucine rich repeat and PYD containing 4B
140	4.5	gnf1m00228_a_at	NM_019441	0610007M19	palmitoyl-protein thioesterase 2
141	4.5	gnf1m27008_at		C330045B02	unclassifiable
142	4.5	gnf1m10356_s_at	XM_900102	B020015A14	oocyte specific homeobox 1
143	4.5	gnf1m01576_a_at	NM_008838	F630222N08	phosphatidylinositol glycan, class F
144	4.5	gnf1m04189_a_at	NM_022022	4931439M19	ubiquitination factor E4B, UFD2 homolog (S. cerevisiae)
145	4.5	gnf1m30703_at	NM_001013776		hypothetical protein LOC382106
146	4.5	gnf1m04413_a_at	NM_024242	I830082O20	RIO kinase 1 (yeast)
147	4.5	gnf1m05411_a_at	NM_029096	1110008J03	RIKEN cDNA 1110008J03 gene
148	4.5	gnf1m19616_at		E330037N21	RIKEN cDNA 9230115E21 gene
149	4.5	gnf1m09667_a_at	XM_917102	A430083E15	nucleoporin 214
150	4.5	gnf1m24244_a_at	NM_198010	A730093D16	ankyrin repeat domain 17
151	4.5	gnf1m11638_a_at	NM_023239	C530046P15	necdin-like 2
152	4.5	gnf1m08421_at	NM_175342	C330003B14	RIKEN cDNA C330003B14 gene
153	4.4	gnf1m09271_a_at	NM_175290	C330026N02	NACHT, leucine rich repeat and PYD containing 4F
154	4.4	gnf1m23490_at		4631433P05	vesicle transport through interaction with t-SNAREs 1 homolog
155	4.4	gnf1m30372_a_at		4833411O04	RIKEN cDNA 4833411O04 gene
156	4.4	gnf1m07705_a_at	NM_172815	E130304P21	R-spondin 2 homolog (Xenopus laevis)
157	4.4	gnf1m01750_a_at	NM_009173		seven in absentia 1B
158	4.4	gnf1m32052_at			OIP4 - RELATED (by Panther) mCG4511
159	4.4	gnf1m10049_a_at	NM_013699	I530025L12	upstream binding protein 1
160	4.4	gnf1m08592_at	NM_172705	4932439F05	PHD finger protein 13
161	4.4	gnf1m30863_a_at		6330441H01	unclassifiable
162	4.4	gnf1m30913_a_at	NM_001037725	F630107I23	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 13 (human)
163	4.4	gnf1m10001_a_at	XM_919590	I530009P20	establishment of cohesion 1 homolog 1 (S. cerevisiae)
164	4.4	gnf1m06558_a_at	NM_145546	I920073J21	general transcription factor IIB
165	4.4	gnf1m09548_a_at	NM_146068	I530027A02	RIKEN cDNA 2310008H04 gene
166	4.4	gnf1m29704_a_at	NM_175201	M5C1088B21	ring finger protein 38
167	4.4	gnf1m17639_at		C730032N23	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)
168	4.4	gnf1m04980_a_at	NM_026479	F630001B12	zinc finger, CCHC domain containing 10
169	4.4	gnf1m00719_a_at	NM_175542	6430703L12	rotatin

170	4.4	gnf1m29070_a_at	XM_916714	2700049A03	RIKEN cDNA 2700049A03 gene
171	4.4	gnf1m09790_a_at	NM_133700	1110056N09	BTB (POZ) domain containing 10
172	4.4	gnf1m28277_at	NM_015793	I0C0037J19	F-box and WD-40 domain protein 14
173	4.4	gnf1m33167_at			transmembrane protein 122
174	4.4	gnf1m29561_a_at	XM_920199	2310030K10	ADP-ribosylation factor interacting protein 1
175	4.4	gnf1m34191_at	NM_198960		transcription factor AP-2, epsilon
176	4.4	gnf1m32478_at	XM_915014		similar to transcription elongation factor B (SIII), polypeptide 2
177	4.4	gnf1m17429_at		7420447K14	RIKEN cDNA 6330416L11 gene
178	4.4	gnf1m11118_a_at	NM_009226	2810410O03	small nuclear ribonucleoprotein D1
179	4.4	gnf1m06473_a_at	NM_145371	E430003B07	eukaryotic translation initiation factor 2B, subunit 1 (alpha)
180	4.4	gnf1m00374_s_at	XM_897204		ring finger and WD repeat domain 2
181	4.4	gnf1m19037_a_at	XM_898196	9330189K18	AT rich interactive domain 1B (Swi1 like)
182	4.4	gnf1m10533_a_at	NM_007892	F830048D09	E2F transcription factor 5
183	4.3	gnf1m31543_at	XM_906832		hypothetical protein LOC623166
184	4.3	gnf1m04652_a_at	NM_025706	4932416D24	TBC1 domain family, member 15
185	4.3	gnf1m12239_a_at	NM_177672	K530042E13	DNA segment, Chr 4, ERATO Doi 429, expressed
186	4.3	gnf1m17449_at	NM_027839	9130012D09	CEA-related cell adhesion molecule 20
187	4.3	gnf1m30307_at	XM_920356	B020013L18	IQ motif containing with AAA domain
188	4.3	gnf1m29621_at		C530010F03	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)
189	4.3	gnf1m29971_a_at	XM_919543	A930002I23	RIKEN cDNA 4930487N19 gene
190	4.3	gnf1m29650_a_at	NM_027314	4933422F17	membrane-associated ring finger (C3HC4) 5
191	4.3	gnf1m17216_s_at	NM_019923	A530039D21	inositol 1,4,5-triphosphate receptor 2
192	4.3	gnf1m04779_a_at		2900001A12	ankyrin repeat domain 12
193	4.3	gnf1m16871_a_at		F830023N07	nuclear transcription factor-Y alpha
194	4.3	gnf1m28697_a_at	NM_007562	E230006C08	basonuclin 1
195	4.3	gnf1m12833_a_at			general transcription factor IIIC, polypeptide 2, beta
196	4.3	gnf1m22973_at	NM_025431	1190005P17	RIKEN cDNA 1190005P17 gene
197	4.3	gnf1m29271_at	XM_620267		similar to hypothetical protein FLJ20397
198	4.3	gnf1m03899_a_at	NM_020021	4930571D16	Moloney sarcoma oncogene
199	4.3	gnf1m05945_a_at	NM_130796	2810421C03	sorting nexin associated golgi protein 1
200	4.3	gnf1m12897_a_at	NM_172405	D230004N03	RIKEN cDNA 3830405G04 gene
201	4.3	gnf1m04940_a_at	NM_026371	I830028E01	loss of heterozygosity, 12, chromosomal region 1 homolog (human)
202	4.3	gnf1m06127_a_at	NM_134017	2410018D16	methionine adenosyltransferase II, beta
203	4.3	gnf1m13939_a_at		1700001P03	NK2 transcription factor related, locus 4 (Drosophila)
204	4.3	gnf1m29306_at	NM_026579	I920095K20	DNA segment, Chr 10, Wayne State University 102, expressed
205	4.3	gnf1m12593_a_at	NM_016769	C630019N20	MAD homolog 3 (Drosophila)
206	4.3	gnf1m01949_a_at	NM_009534	I920028O19	yes-associated protein 1
207	4.3	gnf1m31661_at	XM_910255		hypothetical protein LOC635251
208	4.3	gnf1m16301_a_at	XM_925135	1110069I23	F-box and leucine-rich repeat protein 17
209	4.3	gnf1m29960_a_at		F830114J03	folylpolyglutamyl synthetase
210	4.3	gnf1m02951_a_at	NM_011776	2410001F05	zona pellucida glycoprotein 3
211	4.3	gnf1m15775_a_at	NM_183149	A430092M15	zinc finger protein 598
212	4.3	gnf1m07986_a_at	NM_177475	6030407P18	suppressor of hairy wing homolog 2 (Drosophila)
213	4.3	gnf1m23101_at	NM_019570	1110027I23	REV1-like (S. cerevisiae)
214	4.2	gnf1m04303_a_at	NM_023290	6030446P03	makorin, ring finger protein, 2
215	4.2	gnf1m28700_a_at		9530062A14	RIKEN cDNA A630082K20 gene
216	4.2	gnf1m05006_a_at	NM_026557	9030406D12	ring finger and CHY zinc finger domain containing 1
217	4.2	gnf1m10172_a_at	NM_175311	F630008H06	zinc finger protein 513
218	4.2	gnf1m28732_at			spastin
219	4.2	gnf1m10724_at	NM_008692		nuclear transcription factor-Y gamma
220	4.2	gnf1m03609_a_at	NM_018775	C630001K10	TBC1 domain family, member 8
221	4.2	gnf1m23779_a_at		4930563O14	RIKEN cDNA 4931428L18 gene
222	4.2	gnf1m16106_a_at	NM_028040	F830031C20	RNA pseudouridylate synthase domain containing 4
223	4.2	gnf1m16623_at	XM_914303	2610024M03	protein phosphatase 1, regulatory subunit 3D
224	4.2	gnf1m06092_x_at	NM_133893	E330028E06	2'-5' oligoadenylate synthetase 1D
225	4.2	gnf1m12791_a_at	NM_026220	I920055O03	microfibrillar-associated protein 1
226	4.2	gnf1m21846_a_at	NM_175016	9530023G02	alkB, alkylation repair homolog 2 (E. coli)
227	4.2	gnf1m09902_a_at	NM_053254	F630026I01	transducin-like enhancer of split 6, homolog of Drosophila E(spl)
228	4.2	gnf1m18680_a_at		F420007A05	DNA-damage inducible protein 2
229	4.2	gnf1m19095_at		6330407P15	zinc finger protein 422
230	4.2	gnf1m06456_a_at	NM_145210	E330025J23	2'-5' oligoadenylate synthetase 1E
231	4.2	gnf1m30600_a_at	XM_909322	9630037P07	RIKEN cDNA 9630037P07 gene
232	4.2	gnf1m22595_a_at	NM_001033211	I0C0046K11	expressed sequence AU022751
233	4.2	gnf1m17144_s_at		4632430A05	aryl hydrocarbon receptor nuclear translocator-like 2
234	4.2	gnf1m28765_a_at		4932423E22	mbt domain containing 1
235	4.2	gnf1m26041_at		A830015L23	weakly similar to ACTIN-BINDING PROTEIN FRABIN-GAMMA [Mus musculus]
236	4.2	gnf1m10411_a_at		G730029A12	peptidylprolyl isomerase (cyclophilin) like 5
237	4.2	gnf1m00510_a_at	NM_178375	4921517A06	zinc finger, SWIM domain containing 3
238	4.2	gnf1m09301_a_at	NM_027212	I730042E14	thyroid hormone receptor associated protein 6
239	4.2	gnf1m29733_a_at	NM_201226	F630110M03	leucine rich repeat containing 47
240	4.2	gnf1m01799_a_at	NM_009269	6030452M19	serine palmitoyltransferase, long chain base subunit 1
241	4.2	gnf1m06095_at	NM_133910		TBC1 domain family, member 14
242	4.2	gnf1m33427_at	XM_916262		gene model 527, (NCBI)
243	4.2	gnf1m30438_at			inferred: gb|AAH19796.1|AAH19796 (BC019796) Unknown (protein for IMAGE:4923005) [Mus musculus] mCG13475
244	4.2	gnf1m00998_a_at	NM_007810	E330007H14	cytochrome P450, family 19, subfamily a, polypeptide 1
245	4.2	gnf1m29820_a_at	NM_028986	E130002P16	zinc finger protein 336
246	4.2	gnf1m30531_at	XM_925541	6430548M15	TAO kinase 1
247	4.2	gnf1m04292_s_at	NM_023233	5730562C12	tripartite motif protein 13
248	4.2	gnf1m24546_at		7420451F24	cleavage stimulation factor, 3' pre-RNA, subunit 1
249	4.2	gnf1m12282_s_at		F730045M14	zinc finger protein, subfamily 1A, 4 (Eos)
250	4.2	gnf1m28716_a_at	NM_001024135	1110008P08	kelch repeat and BTB (POZ) domain containing 7
251	4.2	gnf1m03255_a_at	NM_013719	2610011M03	eukaryotic translation initiation factor 2 alpha kinase 4
252	4.2	gnf1m11385_a_at	NM_009343	G730035E18	PHD finger protein 1
253	4.2	gnf1m14025_at		2500002E12	SAM and SH3 domain containing 1
254	4.2	gnf1m29590_a_at		4631426G04	zinc finger CCCH type containing 6
255	4.2	gnf1m03351_a_at	NM_013917	E430014I06	pituitary tumor-transforming 1
256	4.2	gnf1m05507_a_at	NM_029790	0610027B03	methyltransferase 5 domain containing 1
257	4.2	gnf1m09202_s_at	XM_908127		protein phosphatase 1, regulatory subunit 10
258	4.2	gnf1m11754_a_at	NM_007563	F830003N05	2,3-bisphosphoglycerate mutase
259	4.2	gnf1m08496_a_at	NM_172631	D330030L18	DNA segment, Chr 18, ERATO Doi 653, expressed
260	4.2	gnf1m08318_a_at	NM_172746		HIRA interacting protein 3
261	4.2	gnf1m30473_at	XM_923664		cDNA sequence BC066140
262	4.2	gnf1m13082_a_at	NM_028730	I530018A10	peroxisome biogenesis factor 26
263	4.1	gnf1m01097_a_at	NM_007970	F630047M06	enhancer of zeste homolog 1 (Drosophila)
264	4.1	gnf1m28911_a_at	XM_910582	2810040O04	zinc fingerprotein 618
265	4.1	gnf1m25413_a_at	NM_029998	I830054J11	RIKEN cDNA 6030458C11 gene
266	4.1	gnf1m16265_a_at	NM_027091	I1C0042E05	nucleoporin 35
267	4.1	gnf1m20990_s_at	XM_923034	C130034K06	RIKEN cDNA A430041B07 gene
268	4.1	gnf1m01059_a_at	NM_007916	I920024M01	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19a
269	4.1	gnf1m08043_at	NM_172539	7420700F21	astacin-like metalloendopeptidase (M12 family)
270	4.1	gnf1m23266_at		F830027O21	chromodomain protein, Y chromosome-like
271	4.1	gnf1m16087_a_at	NM_027560	G630019P16	arrestin domain containing 2
272	4.1	gnf1m03280_s_at	NM_013775	B020004B10	T-cell leukemia/lymphoma 1B, 1
273	4.1	gnf1m15535_a_at	NM_026849	9430051D16	RIKEN cDNA 1110061O04 gene
274	4.1	gnf1m13657_at		2410098H20	RUN and TBC1 domain containing 2
275	4.1	gnf1m26841_at	XM_925276	C130097O10	cat eye syndrome chromosome region, candidate 2 homolog (human)
276	4.1	gnf1m02777_s_at	NM_011378	8030498F03	transcriptional regulator, SIN3A (yeast)
277	4.1	gnf1m03272_a_at	NM_013757	5330428N11	synaptotagmin-like 4
278	4.1	gnf1m21764_at		7420441D12	ubiquitin specific peptidase 30
279	4.1	gnf1m29280_a_at	NM_080561	F630024P17	RIKEN cDNA 2810055G22 gene
280	4.1	gnf1m30027_at	XM_924076		TAF4A RNA polymerase II, TATA box binding protein (TBP)-associated factor
281	4.1	gnf1m09391_a_at	NM_173363		eukaryotic translation initiation factor 5
282	4.1	gnf1m09291_a_at	NM_026780	1110018L13	SYF2 homolog, RNA splicing factor (S. cerevisiae)
283	4.1	gnf1m05550_a_at	NM_030236	F830001G13	F-box only protein 34
284	4.1	gnf1m30830_at		I0C0042K12	NACHT, LRR and PYD containing protein 9c
285	4.1	gnf1m15590_at		4930406D14	RIKEN cDNA 4930406D14 gene
286	4.1	gnf1m24022_at		5730525N20	small nuclear ribonucleoprotein D1
287	4.1	gnf1m02731_a_at	NM_011293		polymerase (RNA) II (DNA directed) polypeptide J
288	4.1	gnf1m06313_a_at	NM_139218	7420498L12	developmental pluripotency-associated 3
289	4.1	gnf1m23802_at		4931413K24	SUMO/sentrin specific peptidase 8
290	4.1	gnf1m09991_a_at		C530022J18	hypothetical Lipocalin-related protein and Bos/Can/Equ allergen containing protein
291	4.1	gnf1m16922_a_at		2610312O17	RIKEN cDNA 1110054O05 gene
292	4.1	gnf1m27711_at		D430026H23	phospholipase A2, activating protein
293	4.1	gnf1m34058_x_at			inferred: ref|XP_033028.2| (XM_033028) hypothetical protein XP_033028 [Homo sapiens] mCG114037
294	4.1	gnf1m18914_at		4930406H16	RIKEN cDNA 4930406H16 gene
295	4.1	gnf1m00097_a_at	NM_007623	D030003P20	chromobox homolog 2 (Drosophila Pc class)
296	4.1	gnf1m22236_at	XM_914443	D030047E23	RIKEN cDNA D230004J03 gene
297	4.1	gnf1m15900_a_at	NM_177471	F630113O12	coiled-coil domain containing 69
298	4.1	gnf1m18473_at	XM_922117	C230071E20	RIKEN cDNA 4933421B21 gene
299	4.1	gnf1m11753_at	NM_007563	6330513J17	2,3-bisphosphoglycerate mutase
300	4.1	gnf1m09930_a_at	NM_026045	5330405H01	PRP18 pre-mRNA processing factor 18 homolog (yeast)
301	4.1	gnf1m00441_a_at	NM_178616	I730081G10	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11
302	4.1	gnf1m03608_a_at	NM_018774		polyhomeotic-like 2 (Drosophila)
303	4.1	gnf1m03275_a_at	NM_013764	9530009E09	deoxyguanosine kinase
304	4.1	gnf1m05565_a_at	NM_030564	4933435P17	ring finger protein 34
305	4.1	gnf1m29697_at	XM_907476		carbohydrate (chondroitin)

					synthase 1
306	4.1	gnf1m29443_a_at	XM_922388	F630107J06	RIKEN cDNA 4931433E08 gene
307	4.1	gnf1m30810_at	NM_001024205		nuclear fragile X mental retardation protein interacting protein 2
308	4.1	gnf1m19811_at		9530092E12	unclassifiable
309	4.0	gnf1m16223_a_at	XM_917330	2810407P21	similar to Exocyst complex component Sec3
310	4.0	gnf1m17453_at	NM_026127		RIKEN cDNA 4833420G17 gene
311	4.0	gnf1m03686_a_at	NM_019434	F430004B09	minichromosome maintenance deficient 3 (S. cerevisiae) associated protein
312	4.0	gnf1m29537_s_at	XM_909627	B830011O14	G protein-coupled receptor, family C, group 1, member B
313	4.0	gnf1m04771_s_at	XM_913852	2010100O12	RIKEN cDNA 2010100O12 gene
314	4.0	gnf1m31508_at			similar to hypothetical protein MGC42415
315	4.0	gnf1m14863_at		6530413F01	rabphilin 3A-like (without C2 domains)
316	4.0	gnf1m04731_a_at	NM_025853	1700022L09	RIKEN cDNA 1700022L09 gene
317	4.0	gnf1m33640_at	NM_001033794	7420486K21	expressed sequence C85627
318	4.0	gnf1m23128_at		M421020G19	jumonji, AT rich interactive domain 2
319	4.0	gnf1m12215_a_at	NM_144884	C430047K18	torsin family 1, member A (torsin A)
320	4.0	gnf1m17795_a_at		9630044M01	unclassifiable
321	4.0	gnf1m28358_a_at	NM_001039206	E430007J01	RIKEN cDNA 2410004P22 gene
322	4.0	gnf1m10469_a_at	NM_181570		cyclin-dependent kinase 8
323	4.0	gnf1m23831_at		4932427P06	angel homolog 2 (Drosophila)
324	4.0	gnf1m07475_a_at	NM_009764		breast cancer 1
325	4.0	gnf1m33977_s_at	XM_912011		similar to RIKEN cDNA A430107P09 gene
326	4.0	gnf1m11316_a_at	NM_053069	3632412H11	autophagy-related 5 (yeast)

No. 5, liver specific genes

#1	#2	#3	#4	#5	#6
1	7.1	gnf1m03553_a_at	NM_017371	I530016F13	hemopexin
2	6.9	gnf1m09228_a_at	NM_133653		methionine adenosyltransferase I, alpha
3	6.9	gnf1m03936_at	NM_020495		solute carrier organic anion transporter family, member 1b2
4	6.9	gnf1m16227_a_at	NM_013913	C730037J05	angiopoietin-like 3
5	6.9	gnf1m03107_a_at	NM_013475	2510008B09	apolipoprotein H
6	6.8	gnf1m20188_at		A330074B06	glutaminase 2 (liver, mitochondrial)
7	6.7	gnf1m01937_a_at	NM_009512		solute carrier family 27 (fatty acid transporter), member 5
8	6.7	gnf1m02170_s_at	NM_134144	1300015K14	cytochrome P450, family 2. subfamily c, polypeptide 37
9	6.7	gnf1m02481_a_at	NM_010702	2510008M19	leukocyte cell-derived chemotaxin 2
10	6.6	gnf1m33131_at	NM_001012310	C730001O18	expressed sequence AI132487
11	6.6	gnf1m15514_a_at	XM_904856	2510015E20	group specific component
12	6.6	gnf1m10769_a_at	NM_007385		apolipoprotein C-IV
13	6.6	gnf1m01597_a_at	NM_008877	3830402P08	plasminogen
14	6.6	gnf1m10614_x_at	NM_010005		cytochrome P450, family 2, subfamily d, polypeptide 10
15	6.6	gnf1m16140_a_at	XM_917766		cytochrome P450, family 2, subfamily c, polypeptide 44
16	6.6	gnf1m06740_a_at	NM_146214	C730030H13	tyrosine aminotransferase
17	6.5	gnf1m03115_at	NM_013485		complement component 9
18	6.5	gnf1m05812_a_at	NM_053176		histidine-rich glycoprotein
19	6.5	gnf1m05713_a_at	NM_032541		hepcidin antimicrobial peptide 1
20	6.4	gnf1m09699_s_at	XM_917532	G630093A09	murinoglobulin 1
21	6.4	gnf1m07245_a_at	NM_152811	1300012D20	UDP glucuronosyltransferase 2 family, polypeptide B1
22	6.4	gnf1m01355_a_at	NM_008455		kallikrein B, plasma 1
23	6.4	gnf1m13313_a_at		1300015B06	protein Z, vitamin K-dependent plasma glycoprotein
24	6.3	gnf1m06418_a_at	NM_144909	C730003B02	glucokinase regulatory protein
25	6.3	gnf1m10857_a_at	NM_133996	C730009L19	apolipoprotein N
26	6.3	gnf1m02235_a_at	NM_010168	I530018P09	coagulation factor II
27	6.2	gnf1m00901_a_at	NM_007618	I530005F24	serine (or cysteine) peptidase inhibitor, clade A, member 6
28	6.2	gnf1m23137_s_at	NM_011458	C730009L23	serine (or cysteine) peptidase inhibitor, clade A, member 3K
29	6.2	gnf1m04119_a_at	NM_021489		coagulation factor XII (Hageman factor)
30	6.2	gnf1m10551_a_at	NM_007972	F630223K11	coagulation factor X
31	6.2	gnf1m02425_a_at	NM_010582	5730412L20	inter-alpha trypsin inhibitor, heavy chain 2
32	6.2	gnf1m03437_a_at	NM_016702	C730009H22	alanine-glyoxylate aminotransferase
33	6.1	gnf1m01089_a_at	NM_007954		esterase 1
34	6.1	gnf1m00880_a_at	NM_007576	C730023F21	complement component 4 binding protein
35	6.1	gnf1m01326_a_at	NM_008406	C730026K04	inter-alpha trypsin inhibitor, heavy chain 1
36	6.0	gnf1m05225_a_at	NM_027918	1300017J02	RIKEN cDNA 1300017J02 gene
37	6.0	gnf1m13619_a_at	NM_007979	C730002C14	coagulation factor IX
38	6.0	gnf1m01913_a_at	NM_009474	C730047G18	urate oxidase
39	6.0	gnf1m03999_a_at	NM_021022	G630096B22	ATP-binding cassette, sub-family B (MDR/TAP), member 11
40	6.0	gnf1m16558_a_at	NM_199314	C730007J02	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 11
41	6.0	gnf1m12243_s_at	NM_010012	A530001C04	cytochrome P450, family 8, subfamily b, polypeptide 1
42	5.9	gnf1m30676_a_at	XM_922255	4732433M03	carbamoyl-phosphate synthetase 1
43	5.9	gnf1m15544_a_at		C730013F20	uridine phosphorylase 2
44	5.9	gnf1m10655_a_at	NM_007815	C730037L09	cytochrome P450, family 2, subfamily c, polypeptide 29
45	5.9	gnf1m03100_a_at	NM_013465	I530029B19	alpha-2-HS-glycoprotein
46	5.9	gnf1m03591_a_at	NM_018746	C730031O13	inter alpha-trypsin inhibitor, heavy chain 4
47	5.9	gnf1m01463_s_at	NM_008646	G630093A09	murinoglobulin 1
48	5.9	gnf1m00805_a_at	NM_007443	1300004O18	alpha 1 microglobulin/bikunin
49	5.8	gnf1m00930_a_at	NM_007686		complement component factor i
50	5.8	gnf1m28861_a_at	NM_133882	C730036I02	complement component 8, beta subunit
51	5.8	gnf1m00975_a_at	NM_007768	E430018L12	C-reactive protein, petaxin related
52	5.7	gnf1m16098_a_at	NM_027062	1700013L23	RIKEN cDNA 1700013L23 gene
53	5.7	gnf1m10786_a_at	NM_008819	5730405A09	phosphatidylethanolamine N-methyltransferase
54	5.7	gnf1m06340_s_at	XM_923552	C730026F11	esterase 31
55	5.7	gnf1m28632_at			solute carrier family 10 (sodium/bile acid cotransporter family), member 1
56	5.7	gnf1m02172_a_at	NM_010006	F530007D13	cytochrome P450, family 2, subfamily d, polypeptide 9
57	5.7	gnf1m00766_a_at	NM_007376		pregnancy zone protein
58	5.7	gnf1m05568_a_at	NM_030611	C730015J07	aldo-keto reductase family 1, member C6
59	5.6	gnf1m00257_a_at	NM_007818	C730009I07	cytochrome P450, family 3, subfamily a, polypeptide 11
60	5.6	gnf1m04260_a_at	NM_023114	2010015N05	apolipoprotein C-III
61	5.6	gnf1m01266_a_at	XM_925766		hydroxysteroid dehydrogenase-5, delta<5>-3-beta
62	5.6	gnf1m03106_a_at	NM_013474		apolipoprotein A-II
63	5.5	gnf1m07735_a_at	NM_175250	A530080C09	RIKEN cDNA 2810007J24 gene
64	5.5	gnf1m00022_a_at	NM_027552	4432411A05	kynureninase (L-kynurenine hydrolase)
65	5.5	gnf1m01233_a_at	NM_008223		serine (or cysteine) peptidase inhibitor, clade D, member 1
66	5.5	gnf1m10714_a_at	NM_011316		serum amyloid A 4
67	5.5	gnf1m29875_a_at	XM_907929	2610039N02	MOCO sulphurase C-terminal domain containing 1
68	5.5	gnf1m30148_at			inferred: gb|AAH11222.1|AAH11222 (BC011222) Similar to cytochrome P450, 2c37 [Mus musculus] mCG12494
69	5.5	gnf1m28772_at	NM_001029867	C730009A09	UDP glucuronosyltransferase 2 family, polypeptide B36
70	5.4	gnf1m10720_a_at	NM_011850	1300007F22	nuclear receptor subfamily 0, group B, member 2
71	5.4	gnf1m03576_a_at	NM_017473		retinol dehydrogenase 7
72	5.4	gnf1m28722_a_at			ENSMUST00000040807 transcript (in rel.37.34e)
73	5.3	gnf1m28781_a_at	NM_009654	C920028B14	albumin 1
74	5.3	gnf1m03395_a_at	NM_015799	F630312J08	transferrin receptor 2
75	5.3	gnf1m06019_s_at	XM_921598	C730027E20	cytochrome P450, family 2, subfamily a, polypeptide 12
76	5.3	gnf1m01005_a_at	NM_007822		cytochrome P450, family 4, subfamily a, polypeptide 14
77	5.3	gnf1m05714_s_at	NM_183257	2210420P15	hepcidin antimicrobial peptide 2
78	5.3	gnf1m05625_a_at	NM_031164	C730005G24	coagulation factor XIII, beta subunit
79	5.3	gnf1m16499_a_at	NM_001003893	C730007K24	mannan-binding lectin serine peptidase 2
80	5.2	gnf1m07216_a_at	NM_147218		ATP-binding cassette, sub-family A (ABC1), member 6
81	5.2	gnf1m02345_a_at	NM_010403	C730038I24	hydroxyacid oxidase 1, liver
82	5.2	gnf1m00372_a_at	NM_053096	1700019G17	camello-like 2
83	5.2	gnf1m02299_a_at	NM_010321	1810009D12	glycine N-methyltransferase
84	5.1	gnf1m01598_a_at	NM_008878	G630018H21	serine (or cysteine) peptidase inhibitor, clade F, member 2
85	5.1	gnf1m00290_a_at	NM_016668	4933406B07	betaine-homocysteine methyltransferase
86	5.1	gnf1m12777_a_at	NM_080844	C730035E04	serine (or cysteine) peptidase inhibitor, clade C (antithrombin), member 1
87	5.1	gnf1m01685_a_at	NM_009060	I920009B07	regucalcin
88	5.1	gnf1m17896_a_at			cDNA sequence BC023486
89	5.0	gnf1m06712_a_at	NM_146148	G630026A05	complement component 8, alpha polypeptide
90	5.0	gnf1m10456_a_at	NM_138951	G630090K23	cDNA sequence BC021608
91	5.0	gnf1m07281_at	NM_153100		eceptor transporter protein 3
92	5.0	gnf1m10709_a_at	NM_019911	3830418M10	tryptophan 2,3-dioxygenase
93	5.0	gnf1m00846_a_at	NM_007519	5830412M14	bile acid-Coenzyme A: amino acid N-acyltransferase
94	5.0	gnf1m10620_a_at	NM_007493		asialoglycoprotein receptor 2
95	5.0	gnf1m05929_a_at	NM_080845	F520008O15	formiminotransferase cyclodeaminase
96	5.0	gnf1m30360_a_at		I420028J16	sarcosine dehydrogenase
97	5.0	gnf1m17191_a_at	XM_908254	2210404A22	claudin 22
98	5.0	gnf1m01909_s_at	NM_133894	9430041C03	UDP glucuronosyltransferase 2 family, polypeptide B5
99	5.0	gnf1m33066_s_at	NM_010004	C730004C24	cytochrome P450, family 2, subfamily c, polypeptide 40
100	5.0	gnf1m03937_a_at	NM_020495		solute carrier organic anion transporter family, member 1b2
101	5.0	gnf1m12772_a_at	NM_007824	C730031G23	cytochrome P450, family 7, subfamily a, polypeptide 1
102	4.9	gnf1m03438_a_at	NM_016704		complement component 6
103	4.9	gnf1m29867_a_at	NM_181849	I920079K06	fibrinogen, B beta polypeptide
104	4.9	gnf1m30559_a_at	XM_925483	1110001J08	3-hydroxyanthranilate 3,4-dioxygenase
105	4.9	gnf1m28629_a_at	NM_001039544		major urinary protein 3
106	4.9	gnf1m06571_a_at	XM_908068	C730004F22	glycogen synthase 2
107	4.9	gnf1m30972_a_at	NM_019792	C730034H04	cytochrome P450, family 3, subfamily a, polypeptide 25
108	4.9	gnf1m09694_s_at	XM_915279	C730018O05	cytochrome P450, family 2. subfamily c, polypeptide 37
109	4.9	gnf1m06502_a_at	NM_145424	F530215H01	cDNA sequence BC089597
110	4.9	gnf1m05212_a_at	NM_027853	0610006F02	methyltransferase like 7B
111	4.9	gnf1m09873_a_at	NM_177406		cytochrome P450, family 4, subfamily a, polypeptide 12

112	4.9	gnf1m28543_a_at	XM_125854	G630005C23	amidohydrolase domain containing 1
113	4.9	gnf1m00339_a_at	NM_009803	C730009H01	nuclear receptor subfamily 1, group I, member 3
114	4.9	gnf1m08713_at	NM_172881	C730031G17	UDP glucuronosyltransferase 2 family, polypeptide B35
115	4.8	gnf1m11082_a_at	NM_023125	1600027I01	kininogen 1
116	4.8	gnf1m35115_at			inferred: gb|AAH16517.1|AAH16517 (BC016517) Unknown (protein for MGC:27756) [Mus musculus] mCG48945
117	4.8	gnf1m01789_a_at	NM_009253		serine (or cysteine) peptidase inhibitor, clade A, member 3M
118	4.8	gnf1m12767_a_at	NM_019546	C730020B03	proline dehydrogenase (oxidase) 2
119	4.8	gnf1m01541_a_at	NM_008777	I530004L01	phenylalanine hydroxylase
120	4.8	gnf1m01245_a_at	NM_008243	G730039B12	macrophage stimulating 1 (hepatocyte growth factor-like)
121	4.8	gnf1m27189_a_at		C730018L13	expressed sequence AI182371
122	4.8	gnf1m06501_at	NM_145424	F530215H01	cDNA sequence BC089597
123	4.7	gnf1m10784_at	NM_010565		inhibin beta-C
124	4.7	gnf1m01787_s_at	NM_009247	I920035F16	serine (or cysteine) peptidase inhibitor, clade A, member 1a
125	4.7	gnf1m03806_a_at	NM_019775	1110032P04	carboxypeptidase B2 (plasma)
126	4.7	gnf1m15585_a_at	NM_028454	F630230M15	transmembrane 7 superfamily member 2
127	4.7	gnf1m26223_a_at	NM_028788	C730023F16	RIKEN cDNA 1300002K09 gene
128	4.7	gnf1m10057_a_at	NM_178713		aldehyde dehydrogenase 8 family, member A1
129	4.7	gnf1m30458_s_at	XM_904752	0610011D16	cytochrome P450, family 4, subfamily a, polypeptide 10
130	4.7	gnf1m33004_at			inferred: gb|AAB94937.1| (AF039212) UDP-glucuronosyltransferase 1A7 [Rattus norvegicus] mCG131123
131	4.7	gnf1m25754_at		A530084B21	solute carrier family 21 (organic anion transporter), member 1
132	4.6	gnf1m10656_a_at	NM_008934		protein C
133	4.6	gnf1m10226_s_at	NM_170778	E330028L06	dihydropyrimidine dehydrogenase
134	4.6	gnf1m01185_a_at	NM_008124	1300008G06	gap junction membrane channel protein beta 1
135	4.6	gnf1m06122_a_at	NM_133997		apolipoprotein F
136	4.6	gnf1m29057_s_at	XM_886668	C730034H04	cytochrome P450, family 3, subfamily a, polypeptide 25
137	4.6	gnf1m09780_a_at	NM_133768	I920049G14	argininosuccinate lyase
138	4.6	gnf1m00522_a_at	NM_027902	1300008A22	transmembrane serine protease 6
139	4.6	gnf1m03147_s_at	NM_013547	0610012C11	homogentisate 1, 2-dioxygenase
140	4.6	gnf1m01807_x_at	NM_009286		sulfotransferase family 2A, dehydroepiandrosterone (DHEA)-preferring, member 2
141	4.6	gnf1m10748_a_at	NM_009202		solute carrier family 22 (organic cation transporter), member 1
142	4.6	gnf1m04864_a_at	NM_026180	1300003C16	ATP-binding cassette, sub-family G (WHITE), member 8
143	4.6	gnf1m10527_a_at	NR_002687	I920036P21	argininosuccinate synthetase 1
144	4.6	gnf1m05477_a_at	NM_029562	1300006E06	cytochrome P450, family 2, subfamily d, polypeptide 26
145	4.6	gnf1m06586_a_at	NM_145594		fibrinogen-like protein 1
146	4.5	gnf1m02031_a_at	NM_009714	4930534D09	asialoglycoprotein receptor 1
147	4.5	gnf1m09474_a_at	NM_026701	F530003P19	RIKEN cDNA 0610038K03 gene
148	4.5	gnf1m05361_a_at	NM_028772	1200014D15	dimethylglycine dehydrogenase precursor
149	4.5	gnf1m33119_at			inferred: gb|AAB47130.1| uMUP-VIII=18.695 kda major urinary protein [mice, Balb/c, urine, Peptide, 162 aa] mCG129513
150	4.5	gnf1m03388_a_at	NM_015780		complement component factor h-like 1
151	4.5	gnf1m18816_at		2610016E04	major urinary protein 1
152	4.5	gnf1m30104_a_at	XM_924654	5730470F19	RNA pseudouridylate synthase domain containing 3
153	4.5	gnf1m14294_at			carboxypeptidase N, polypeptide 2
154	4.5	gnf1m23907_at		5033417E09	arylacetamide deacetylase (esterase)
155	4.4	gnf1m10706_a_at	NM_009993	1300003J07	cytochrome P450, family 1, subfamily a, polypeptide 2
156	4.4	gnf1m02347_a_at	NM_010406		hemolytic complement
157	4.4	gnf1m05265_a_at	NM_028094	2010321J07	UDP glucuronosyltransferase 2 family, polypeptide A3
158	4.4	gnf1m10903_a_at	NM_144903	I530022M24	aldolase 2, B isoform
159	4.4	gnf1m10109_a_at	NM_146230	I530017M04	acetyl-Coenzyme A acyltransferase 1B
160	4.4	gnf1m03564_a_at	NM_017399	2010105C24	fatty acid binding protein 1, liver
161	4.4	gnf1m11783_a_at	NM_172465	6430508G22	zinc finger, DHHC domain containing 9
162	4.4	gnf1m05257_a_at	NM_028066	1600027G01	coagulation factor XI
163	4.4	gnf1m27195_at		C730026K03	coagulation factor V
164	4.4	gnf1m00425_a_at	NM_170778	E330028L06	dihydropyrimidine dehydrogenase
165	4.4	gnf1m10435_at	NM_170778		dihydropyrimidine dehydrogenase
166	4.4	gnf1m29794_s_at	XM_886540		cytochrome P450, family 3, subfamily a, polypeptide 25
167	4.4	gnf1m01414_a_at	NM_008555		mannan-binding lectin serine peptidase 1
168	4.4	gnf1m00400_a_at	NM_177789	A530061A11	V-set and immunoglobulin domain containing 4
169	4.4	gnf1m06018_a_at	NM_133657		cytochrome P450, family 2, subfamily a, polypeptide 12
170	4.4	gnf1m03664_a_at	NM_019395	C730030M09	fructose bisphosphatase 1
171	4.4	gnf1m00474_a_at	NM_027406	B230119O16	aldehyde dehydrogenase 1 family, member L1
172	4.3	gnf1m24247_a_at	XM_903848	4933417N20	ethanolamine kinase 2
173	4.3	gnf1m06341_a_at	NM_144512	C730037J22	solute carrier family 6 (neurotransmitter transporter, GABA), member 13
174	4.3	gnf1m03064_a_at	NM_011996		alcohol dehydrogenase 4 (class II), pi polypeptide
175	4.3	gnf1m05885_a_at	NM_054094	C730036G06	acyl-CoA synthetase medium-chain family member 1
176	4.3	gnf1m30358_x_at	NM_001029977		complement factor H-related protein
177	4.3	gnf1m10645_a_at	NM_008341		insulin-like growth factor binding protein 1
178	4.3	gnf1m00392_a_at	NM_178747	I530014P16	gulonolactone (L-) oxidase
179	4.3	gnf1m20528_a_at		E030046K17	eukaryotic translation initiation factor 3, subunit 10 (theta)
180	4.3	gnf1m06075_a_at	NM_133809		kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)
181	4.3	gnf1m29692_a_at	XM_915401	5033405N08	agmatine ureohydrolase (agmatinase)
182	4.3	gnf1m00023_a_at	NM_008256	1300004J23	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2
183	4.3	gnf1m05053_a_at	NM_026690	0610012D14	RIKEN cDNA 0610012D14 gene
184	4.3	gnf1m05586_a_at	NM_030703	0610011F20	carboxypeptidase N, polypeptide 1
185	4.3	gnf1m02513_a_at	NM_010776	C730024L16	mannose binding lectin (C)
186	4.3	gnf1m03414_a_at	XM_919150	I920184L23	S-adenosylhomocysteine hydrolase
187	4.3	gnf1m00366_a_at	NM_177002	D630035B04	RIKEN cDNA C730048C13 gene
188	4.2	gnf1m33353_at			inferred: gb|AAH05978.1|AAH05978 (BC005978) karyopherin alpha 2 (RAG cohort 1, importin alpha 1) [Homo sapiens] mCG126254
189	4.2	gnf1m02273_a_at	NM_010255	F930027M15	guanidinoacetate methyltransferase
190	4.2	gnf1m09901_a_at	NM_145565	C730010D03	serine dehydratase
191	4.2	gnf1m32875_at			inferred: ref|NP_032674.1| (NM_008648) major urinary protein 4 [Mus musculus] mCG132776
192	4.2	gnf1m01151_a_at	NM_008061	D630014N06	glucose-6-phosphatase, catalytic
193	4.2	gnf1m02169_a_at	NM_010000		cytochrome P450, family 2, subfamily b, polypeptide 9
194	4.2	gnf1m29287_a_at		0610005C13	RIKEN cDNA 0610005C13 gene
195	4.2	gnf1m11559_a_at	NM_145365	C730025L08	cAMP responsive element binding protein 3-like 3
196	4.2	gnf1m04231_a_at	NM_022884	I530012L08	betaine-homocysteine methyltransferase 2
197	4.2	gnf1m03693_a_at	NM_019447	G630096L04	hepatocyte growth factor activator
198	4.2	gnf1m09353_a_at	NM_053115		acyl-Coenzyme A oxidase 2, branched chain
199	4.2	gnf1m09846_a_at		C730040N12	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 7
200	4.2	gnf1m02339_a_at	NM_010391	1300010D05	histocompatibility 2, Q region locus 10
201	4.2	gnf1m06570_a_at	NM_145570		cDNA sequence BC014699
202	4.2	gnf1m15753_at	NM_175438		aldehyde dehydrogenase 4 family, member A1
203	4.2	gnf1m29873_a_at	NM_011255	I920187H11	retinol binding protein 4, plasma
204	4.2	gnf1m31676_at			inferred: gb|AAL61047.1| (AY073384) olfactory receptor MOR125-1 [Mus musculus] mCG56820
205	4.2	gnf1m34057_at	XM_906159		hypothetical protein LOC623919
206	4.1	gnf1m31926_x_at			inferred: gb|AAC27650.2| (AF078817) high mobility group protein [Spalax ehrenbergi] mCG49424
207	4.1	gnf1m12201_a_at	NM_134103	C730019B22	interleukin 1 receptor accessory protein
208	4.1	gnf1m02240_a_at	NM_010176	K430330E02	fumarylacetoacetate hydrolase
209	4.1	gnf1m21159_a_at	XM_918867	C730014M21	calcium and integrin binding family member 3
210	4.1	gnf1m35031_at			inferred: ref|NP_035424.1| (NM_011294) RNA polymerase II transcriptional coactivator [Mus musculus] mCG50416
211	4.1	gnf1m33092_at	XM_906759	M5C1068H14	apolipoprotein B
212	4.1	gnf1m01633_a_at	NM_008952	C730025C09	pipecolic acid oxidase
213	4.1	gnf1m32343_x_at			inferred: ref|NP_031808.1| (NM_007782) colony stimulating factor 3 receptor (granulocyte) [Mus musculus] mCG21155
214	4.1	gnf1m01376_a_at	NM_008490	C730023E10	lecithin cholesterol acyltransferase
215	4.1	gnf1m10416_a_at	NM_144845	F430112M20	UDP glycosyltransferases 3 family, polypeptide A2
216	4.1	gnf1m04032_a_at	XM_888081	C730002N09	peptidoglycan recognition protein 2
217	4.1	gnf1m00754_a_at	NR_002861		serine (or cysteine) peptidase inhibitor, clade A, member 4, pseudogene 1
218	4.1	gnf1m09764_a_at	NM_133943	I830015G06	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7
219	4.1	gnf1m02238_a_at	NM_010172	F730043B01	coagulation factor VII
220	4.1	gnf1m15567_at	NM_207216	F430101I22	UDP glycosyltransferases 3 family, polypeptide A1
221	4.1	gnf1m06112_at	NM_133969	1200012E24	cytochrome P450, family 4, subfamily v, polypeptide 3
222	4.1	gnf1m21309_at		D230014K18	unclassifiable
223	4.0	gnf1m30277_a_at			ENSMUST00000036050 transcript (in rel.37.34e)
224	4.0	gnf1m11914_a_at	NM_133960	9130231C15	carboxylesterase 6
225	4.0	gnf1m30667_at			uncharacterized Celera prediction mCG121657
226	4.0	gnf1m03979_a_at	NM_020598		olfactory receptor 17
227	4.0	gnf1m02742_a_at	NM_011318		serum amyloid P-component
228	4.0	gnf1m04407_a_at	NM_024229	B830039L18	phosphate cytidylyltransferase 2, ethanolamine
229	4.0	gnf1m12230_a_at	NM_026234	A930029E10	phosphatidylinositol glycan, class

					M
230	4.0	gnf1m22133_at		C230043N17	RIKEN cDNA C230043N17 gene
231	4.0	gnf1m12784_a_at	NM_053096	C730049C09	camello-like 2
232	4.0	gnf1m04099_a_at	NM_021456	C730013N07	carboxylesterase 1
233	4.0	gnf1m06234_at	NM_134246		acyl-CoA thioesterase 3

No. 6, thyroid specific genes

#1	#2	#3	#4	#5	#6
1	7.5	gnf1m13802_a_at	NM_008693	1700029O22	kallikrein 1-related peptidase b3
2	7.1	gnf1m00303_at	NM_010640		kallikrein 1-related peptidase b11
3	6.8	gnf1m03182_a_at	NM_013609	G730006F04	nerve growth factor, beta
4	6.7	gnf1m02570_a_at	NM_010915		kallikrein 1-related pepidase b4
5	6.6	gnf1m36056_at			uncharacterized Celera prediction mCG1028843
6	6.6	gnf1m03915_a_at	NM_020268		kallikrein 1-related peptidase b27
7	6.6	gnf1m02451_a_at	NM_010642	G430129N05	kallikrein 1-related peptidase b21
8	6.6	gnf1m01354_a_at	NM_008454		kallikrein 1-related peptidase b16
9	6.5	gnf1m02452_a_at	NM_010643		kallikrein 1-related peptidase b24
10	6.3	gnf1m34145_at	XM_906856		similar to axonemal dynein heavy chain 7
11	6.3	gnf1m02214_a_at	NM_010116		kallikrein 1-related peptidase b9
12	6.1	gnf1m14140_at		4931409D07	RIKEN cDNA 4931409D07 gene
13	6.0	gnf1m13193_a_at	NM_010645	F730016B20	kallikrein 1-related peptidase b1
14	6.0	gnf1m17641_at			gb=BC028546 Mouse clone IMAGE:1511509, mRNA, partial cds
15	6.0	gnf1m02453_x_at	NM_010644		kallikrein 1-related petidase b26
16	5.8	gnf1m01357_a_at	NM_008457		kallikrein 1-related peptidase b8
17	5.8	gnf1m35727_at	XM_909167		mucin 19
18	5.8	gnf1m01356_a_at	NM_008456		kallikrein 1-related peptidase b5
19	5.8	gnf1m24998_a_at		B230308C23	zinc finger protein 235
20	5.6	gnf1m25495_at		A230102K24	weakly similar to opioid receptor, kappa 1
21	5.5	gnf1m08232_at	XM_899454	C130026I21	RIKEN cNDA C130026I21 gene
22	5.4	gnf1m33515_x_at			ENSMUST00000087361 transcript (in rel.37.34e)
23	5.3	gnf1m35465_at			inferred: ref|NP_003810.1|(NM_003819) poly(A)-binding protein, cytoplasmic 4 (inducible form); inducible poly(A)-binding protein [Homo sapiens] mCG1031934
24	5.2	gnf1m03719_at			Mouse adaptor-related protein complex AP-4, beta 1 (Ap4b1), mRNA
25	5.2	gnf1m34040_at	XM_907779		dachsous 2 (Drosophila)
26	5.2	gnf1m03159_a_at	NM_013568		potassium voltage-gated channel, shaker-related, subfamily, member 6
27	5.1	gnf1m02501_a_at	NM_010748	F630019I07	lysosomal trafficking regulator
28	5.0	gnf1m22169_at		C230092H20	solute carrier family 39 (metal ion transporter), member 11
29	5.0	gnf1m02213_a_at	NM_010113	E430016A08	epidermal growth factor
30	5.0	gnf1m30017_at			uncharacterized Celera prediction mCG13130
31	4.9	gnf1m21910_at		A530052K18	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)
32	4.8	gnf1m33120_at			inferred: ref|XP_138032.1|(XM_138032) similar to glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - mouse [Mus musculus] mCG17415
33	4.8	gnf1m05516_at	NM_029831	1700127D06	RIKEN cDNA 1700127D06 gene
34	4.8	gnf1m01993_a_at	NM_009639		cysteine-rich secretory protein 3
35	4.8	gnf1m20450_at		A730012K24	7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730012K24 product:hypothetical protein, full insert sequence
36	4.8	gnf1m01462_a_at	NM_008644		mucin 10, submandibular gland salivary mucin
37	4.8	gnf1m14204_a_at		4933431I19	RIKEN cDNA 4933431I19 gene
38	4.8	gnf1m02856_at	NM_011564		sex determining region of Chr Y
39	4.8	gnf1m19382_at		6030416N07	unclassifiable
40	4.7	gnf1m20462_a_at		A730023A08	hypothetical protein
41	4.7	gnf1m22540_at		E030025L23	hypothetical protein
42	4.7	gnf1m36096_at	XM_905283		RIKEN cDNA 2410089E03 gene
43	4.7	gnf1m33654_at	XM_914541	6330416F17	hypothetical protein, MNCb-2457
44	4.7	gnf1m13714_at		8430406H22	RIKEN cDNA 8430406H22 gene
45	4.7	gnf1m32485_x_at			inferred: ref|NP_057177.1|(NM_016093) ribosomal protein L26-like 1; ribosomal protein L26 homolog; ribosomal protein L26 pseudogene 1 [Homo sapiens] mCG15495
46	4.7	gnf1m36116_at	XM_150341		hypothetical gene supported by AK016643
47	4.6	gnf1m33064_at	XM_906449		CDC42 binding protein kinase gamma (DMPK-like)
48	4.6	gnf1m20622_at		A930013N02	cDNA sequence BC028528
49	4.6	gnf1m34337_x_at			ENSMUST00000074721 transcript (in rel.37.34e)
50	4.6	gnf1m29377_a_at	XM_914595	D430036C22	RIKEN cDNA D430042O09 gene
51	4.6	gnf1m34495_at	XM_919562		fat tumor suppressor homolog (Drosophila)
52	4.6	gnf1m32670_at	NM_001029935		tripartite motif-containing 38
53	4.6	gnf1m19556_at		8030459P20	8030459P20 unclassifiable clone
54	4.6	gnf1m29401_s_at	NM_198927	4832442M15	submandibular gland protein C
55	4.5	gnf1m08352_a_at	NM_175502	B230382K22	transmembrane protein 74
56	4.5	gnf1m31699_x_at			inferred: gb|AAB04536.1|(U60820) anti-digoxin immunoglobulin heavy chain variable region precursor [Mus musculus] mCG55786
57	4.5	gnf1m32199_at			inferred: ref|NP_033298.1|(NM_009272) spermidine synthase [Mus musculus] mCG3374
58	4.5	gnf1m35249_at			inferred: ref|NP_032110.1|(NM_008084) glyceraldehyde-3-phosphate dehydrogenase [Mus musculus] mCG1042475
59	4.5	gnf1m22130_at		C230040D14	hypothetical protein C230040D14
60	4.5	gnf1m25547_at		A330071M14	RIKEN cDNA 2610033H07 gene
61	4.5	gnf1m33391_at	XM_913307		gene model 447, (NCBI)
62	4.5	gnf1m02074_a_at	NM_009802	4833414N20	carbonic anhydrase 6
63	4.4	AFFX-PheX-5_at			0
64	4.4	gnf1m22606_s_at	NM_173753	E330029L20	RIKEN cDNA A730024A03 gene
65	4.4	gnf1m18106_at		A230016A09	unclassifiable
66	4.4	gnf1m19521_at		6720485J18	12 days embryo male wolffian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone:6720485J18 product:hypothetical protein, full insert sequence
67	4.4	gnf1m21640_at		4832424I19	RIKEN cDNA 2310001A20 gene
68	4.4	gnf1m35312_at			inferred: gb|AAB60512.1|(U27186) Cys2/His2 zinc finger protein [Rattus norvegicus] mCG1039355
69	4.4	gnf1m33100_x_at			inferred: ref|XP_015366.1|(XM_015366) hypothetical protein XP_015366 [Homo sapiens] mCG129791
70	4.4	gnf1m18172_a_at		8030403L08	zinc finger protein 710
71	4.3	gnf1m13852_at		4930412F12	RIKEN cDNA 4930412F12 gene
72	4.3	gnf1m30216_a_at	NM_183088	2410018M08	RIKEN cDNA 2410018M08 gene
73	4.3	gnf1m18637_at		5430414B19	RIKEN cDNA 5430414B19 gene
74	4.3	gnf1m35399_x_at	XM_907226		similar to 60S ribosomal protein L39
75	4.3	gnf1m23485_at		4631416M11	hypothetical protein
76	4.3	gnf1m06481_a_at	NM_145386		cDNA sequence BC005655
77	4.3	gnf1m19119_at		1110035E08	unclassifiable
78	4.3	gnf1m35942_at	XM_911527		similar to Ig kappa chain V-I region HK102 precursor
79	4.3	gnf1m21125_at		C430017P18	erythrocyte protein band 4.1-like 3
80	4.3	gnf1m18697_at		D230039N12	RIKEN cDNA 4930505N22 gene
81	4.3	gnf1m33664_at	NM_001035243	F630006C01	transient receptor potential cation channel, subfamily M, member 3
82	4.3	gnf1m33795_at	XM_906846		similar to EC2-V2R pheromone receptor
83	4.3	gnf1m20823_a_at		B430302L04	hypothetical protein
84	4.3	gnf1m21683_a_at		4930558M01	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930558M01 product:unclassifiable, full insert sequence
85	4.3	gnf1m14689_at		4930526H09	RIKEN cDNA 4930526H09 gene
86	4.3	gnf1m18852_a_at		C030036D22	RIKEN cDNA C030036D22 gene
87	4.3	gnf1m27072_at		C530019H05	methyltransferase like 6
88	4.3	gnf1m15684_at			prolactin induced protein
89	4.2	gnf1m33013_at	XM_923091	3526401L13	SLIT-ROBO Rho GTPase activating protein 2
90	4.2	gnf1m15166_at		1700014P11	laminin gamma 3
91	4.2	gnf1m19325_at	NM_199365	5330438I03	RIKEN cDNA 5330438I03 gene
92	4.2	gnf1m15675_at	NM_009918		cyclic nucleotide gated channel alpha 3
93	4.2	gnf1m26156_at		A930030D01	similar to CDNA: FLJ22347 FIS, CLONE HRC06188 [Homo sapiens]
94	4.2	gnf1m23187_a_at	XM_914636	4930518P14	RIKEN cDNA 1700012B07 gene
95	4.2	gnf1m17894_at		F630105G17	ferritin heavy chain
96	4.2	gnf1m17808_at		6330410L21	RIKEN cDNA 6330410L21 gene
97	4.2	gnf1m21423_at	NM_001024720	D630034E04	similar to hemicentin
98	4.2	gnf1m32420_at	XM_914429		similar to 40S ribosomal protein S15 (RIG protein)
99	4.2	gnf1m27955_at		F730004C20	inhibitor of kappaB kinase beta
100	4.2	gnf1m12238_a_at	NM_178898	B230308L01	expressed sequence AI894139
101	4.2	gnf1m34160_at			inferred: gb|AAF36126.1|AF151040_1 (AF151040) HSPC206 [Homo sapiens] mCG112956
102	4.2	gnf1m34362_at			inferred: gb|AAH16558.1|AAH16558 (BC016558) Unknown (protein for IMAGE:3586350) [Mus musculus] mCG50624
103	4.2	gnf1m15606_at	XM_919237	5430426E14	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)
104	4.2	gnf1m11859_at		8030453O03	non MHC restricted killing associated
105	4.2	gnf1m05926_a_at	NM_080729		interleukin 17E
106	4.2	gnf1m35418_at			inferred: ref|NP_062310.1|(NM_019437) hypothetical protein [Mus musculus] mCG1034693
107	4.2	gnf1m28076_at		E130003L10	succinate-CoA ligase, GDP-forming, alpha subunit
108	4.2	gnf1m23193_at		1700120C01	capping protein (actin filament) muscle Z-line, beta
109	4.2	gnf1m30578_a_at	NM_027830	B430214B10	minichromosome maintenance deficient domain containing 1
110	4.2	gnf1m36031_at			uncharacterized Celera prediction mCG1030369
111	4.2	gnf1m12868_at		D130039I04	RIKEN cDNA D230012E17 gene
112	4.2	gnf1m34972_at	NM_146869		olfactory receptor 147
113	4.2	gnf1m19387_at		6030424J22	synaptotagmin VII
114	4.2	gnf1m31913_at			inferred: ref|NP_060548.1|

					(NM_018078) hypothetical protein FLJ10378 [Homo sapiens] mCG49707
115	4.1	gnf1m33791_at	XM_907417		similar to Cytochrome P450 2B20 (CYPIIB20) (P24)
116	4.1	gnf1m15079_at		5330434N09	frizzled homolog 5 (Drosophila)
117	4.1	gnf1m26575_at		B930060O04	unclassifiable
118	4.1	gnf1m21231_at	XM_902796	D130015I23	tetratricopeptide repeat domain 13
119	4.1	gnf1m11517_a_at	NM_026367	D030023G19	G patch domain containing 2
120	4.1	gnf1m30999_s_at	NM_009661	4732447A14	arachidonate 8-lipoxygenase
121	4.1	gnf1m07024_at	NM_146868		olfactory receptor 894
122	4.1	gnf1m10677_a_at	NM_008953	2310075K06	parotid secretory protein
123	4.1	gnf1m35463_at			inferred: ref|NP_114074.1| (NM_031868) protein phosphatase 1, catalytic subunit, alpha isoform [Mus musculus] mCG1032210
124	4.1	gnf1m17426_at		6430500D05	RIKEN cDNA 6430500D05 gene
125	4.1	gnf1m07617_at	NM_175161	4930420A19	RIKEN cDNA 4931422A03 gene
126	4.1	gnf1m11867_a_at	NM_013742	8030495L15	cysteinyl-tRNA synthetase
127	4.1	gnf1m10824_a_at	NM_138684	2300002A12	WAP four-disulfide core domain 12
128	4.1	gnf1m14145_at		4931412I15	RIKEN cDNA 4931412I15 gene
129	4.1	gnf1m07301_a_at	NM_153139		solute carrier family 36 (proton/amino acid symporter), member 1
130	4.1	gnf1m19103_at		4930579K13	ribosomal protein S6 kinase polypeptide 1
131	4.1	gnf1m25399_at		A230004G12	wingless related MMTV integration site 2b
132	4.1	gnf1m06209_at	NM_134219		vomeronasal 1 receptor, I2
133	4.1	gnf1m19154_at		4732418P20	TATA box binding protein-like 1
134	4.1	gnf1m14263_at		8430401P03	RIKEN cDNA 8430401P03 gene
135	4.1	gnf1m22963_at		A530031I11	hypothetical protein
136	4.1	gnf1m08210_s_at	NM_145486	E130018A02	membrane-associated ring finger (C3HC4) 2
137	4.1	gnf1m07782_a_at	NM_172587	C230071D10	CDC14 cell division cycle 14 homolog B (S. cerevisiae)
138	4.0	gnf1m35355_at			inferred: gb|AAH14745.1|AAH14745 (BC014745) Similar to RIKEN cDNA 5730591C18 gene [Mus musculus] mCG1037344
139	4.0	gnf1m00017_at	NM_021901		T-cell leukemia, homeobox 1
140	4.0	gnf1m26254_at		B130047P03	Cdc42 GTPase-activating protein
141	4.0	gnf1m17662_at		B430320O11	hypothetical protein
142	4.0	gnf1m02987_a_at	NM_011853	A530071G10	2'-5' oligoadenylate synthetase 1B
143	4.0	gnf1m18709_s_at	XM_921144	4930532L22	chromodomain helicase DNA binding protein 5
144	4.0	gnf1m23792_at		4930585K05	sperm associated antigen 16
145	4.0	gnf1m14247_a_at	NM_199055	5430438D01	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9
146	4.0	gnf1m19193_at		4831410D14	similar to TYROSINE-PROTEIN KINASE JAK3 (EC 2.7.1.112) (JANUS KINASE 3) (JAK-3) [Mus musculus]

No. 7, small intestine specific genes

#1	#2	#3	#4	#5	#6
1	6.9	gnf1m22975_a_at	NM_207658	2010320G05	RIKEN cDNA 2010016B13 gene
2	6.8	gnf1m31679_at	NM_001030291	I530028E15	ectonucleotide pyrophosphatase/phosphodiesterase 7
3	6.8	gnf1m04331_a_at	NM_023529	2010001N17	membrane-spanning 4-domains, subfamily A, member 10
4	6.8	gnf1m30350_at	XM_914093		lactase
5	6.8	gnf1m33685_at	XM_906199		RIKEN cDNA 2010204N08 gene
6	6.7	gnf1m04926_a_at	NM_026333	5033406B05	RIKEN cDNA 2010106E10 gene
7	6.4	gnf1m18409_a_at	XM_906199	2010204N08	RIKEN cDNA 2010204N08 gene
8	6.1	gnf1m30117_a_at	XM_906067	2010001C14	RIKEN cDNA 2010001C14 gene
9	6.0	gnf1m05445_a_at	NM_029360	2010003F10	transmembrane 4 superfamily member 5
10	5.9	gnf1m00085_s_at	NM_007844	2010319H24	defensin related sequence cryptdin peptide (paneth cells)
11	5.9	gnf1m32627_a_at	XM_907141	2010010B23	myosin IA
12	5.9	gnf1m30302_a_at		2010301M18	cytochrome P450, family 2, subfamily c, polypeptide 66
13	5.9	gnf1m04289_a_at	NM_023219	2010300P03	solute carrier family 5 (neutral amino acid transporters, system A), member 4b
14	5.7	gnf1m32637_at	NM_001004184		solute carrier family 28 (sodium-coupled nucleoside transporter), member 1
15	5.7	gnf1m08052_at	NM_177802	9030221C07	RIKEN cDNA 9030221C07 gene
16	5.7	gnf1m12505_a_at	NM_134420	B930010B04	solute carrier family 26, member 6
17	5.6	gnf1m01024_x_at	NM_007850		defensin related cryptdin 2
18	5.6	gnf1m01025_x_at	NM_007851		defensin related cryptdin 5
19	5.6	gnf1m33650_at	NM_001033199	9130019N24	expressed sequence AI747448
20	5.5	gnf1m09931_a_at	NM_153069		liver-expressed antimicrobial peptide 2
21	5.5	gnf1m10976_a_at	NM_009034	1110002L02	retinol binding protein 2, cellular
22	5.5	gnf1m34175_at	XM_909581		defensin related cryptdin 2
23	5.5	gnf1m05700_a_at	NM_031884	C730040P06	ATP-binding cassette, sub-family G (WHITE), member 5
24	5.4	gnf1m08281_a_at	NM_177182	A830053O21	RIKEN cDNA A830053O21 gene
25	5.4	gnf1m30198_a_at	NM_027286	C630041D11	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2
26	5.4	gnf1m04160_a_at	NM_021719	2210009B08	claudin 15
27	5.4	gnf1m02427_x_at	NM_010584		intelectin a
28	5.3	gnf1m15427_x_at			Mouse C3H/HeJ cryptdin-15 (Defcr15) mRNA, partial cds /cds=UNKNOWN /gb=U03065 /gi=437265 /len=119 gnl|UG|Mm#S2209
29	5.3	gnf1m04221_a_at	NM_022434	9130414F11	cytochrome P450, family 4, subfamily f, polypeptide 14
30	5.3	gnf1m01461_s_at	NM_008642	I920026D19	microsomal triglyceride transfer protein
31	5.3	gnf1m32536_at			inferred: ref|NP_113947.1| (NM_031759) N-acetylated alpha-linked acidic dipeptidase-like (ileal peptidase I100) [Rattus norvegicus] mCG11755
32	5.2	gnf1m23042_a_at	NM_183268	2010206A06	defensin related cryptdin 20
33	5.2	gnf1m05705_a_at	NM_032394		myosin VIIb
34	5.2	gnf1m04114_a_at	NM_021481	2210412M19	trehalase (brush-border membrane glycoprotein)
35	5.2	gnf1m00564_a_at	NM_181540	4933408I11	transmembrane 6 superfamily member 2
36	5.2	gnf1m30177_a_at	NM_001033364	G630055D06	cDNA sequence BC040758
37	5.1	gnf1m02718_a_at	NM_011259	2010207I02	regenerating islet-derived 3 alpha
38	5.1	gnf1m06690_a_at	NM_146064		sterol O-acyltransferase 2
39	5.0	gnf1m33688_at	XM_917712		similar to Serum amyloid P-component precursor (SAP)
40	5.0	gnf1m13288_a_at		F830007N10	cadherin 17
41	5.0	gnf1m11403_at	NM_026907	F430111H02	secreted and transmembrane 1
42	5.0	gnf1m05145_a_at	NM_027227	2010001H14	RIKEN cDNA 2010001H14 gene
43	5.0	gnf1m05494_a_at	NM_029638	I530028M11	amiloride binding protein 1 (amine oxidase, copper-containing)
44	5.0	gnf1m04014_a_at	NM_021291	D630032A02	solute carrier family 7 (cationic amino acid transporter, y+ system), member 9
45	5.0	gnf1m11133_a_at	NM_008119	2010305F10	gastric inhibitory polypeptide
46	4.9	gnf1m12324_a_at	NM_145494	F830020H14	malic enzyme 2, NAD(+)-dependent, mitochondrial
47	4.9	gnf1m30769_s_at	NM_207208	9130020L07	chloride channel calcium activated 6
48	4.9	gnf1m28989_a_at	XM_916703	4930516G09	mucin 3, intestinal
49	4.9	gnf1m00501_a_at	NM_207691	E130202O15	espin
50	4.9	gnf1m21825_a_at		9130221N23	NPC1-like 1
51	4.9	gnf1m03353_a_at	NM_013920	F430112P22	hepatocyte nuclear factor 4, gamma
52	4.9	gnf1m01003_a_at	NM_007819	C730041D17	cytochrome P450, family 3, subfamily a, polypeptide 13
53	4.9	gnf1m32430_at			inferred: ref|XP_139161.1| (XM_139161) similar to bA209J19.1.1 (GW112 protein) [Mus musculus] mCG19388
54	4.8	gnf1m00809_at			angiogenin, ribonuclease A family, member 3
55	4.8	gnf1m04210_a_at	NM_022411	C130087A09	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2
56	4.8	gnf1m15732_a_at	XM_907955	2010001E11	RIKEN cDNA 2010001E11 gene
57	4.8	gnf1m02605_a_at	NM_011036		pancreatitis-associated protein
58	4.8	gnf1m06515_a_at	NM_145449	1810023F06	RIKEN cDNA 1810023F06 gene
59	4.8	gnf1m05139_a_at	NM_027211	1810034H17	annexin A13
60	4.8	gnf1m29825_a_at	XM_924219	5033427P15	cystatin 8 (cystatin-related epididymal spermatogenic)
61	4.8	gnf1m10611_a_at	NM_007468	I920045H24	apolipoprotein A-IV
62	4.8	gnf1m01026_x_at	NM_007852		defensin related cryptdin 6
63	4.8	gnf1m06496_at	NM_145419	I530020L22	hexokinase domain containing 1
64	4.8	gnf1m11887_a_at	NM_019810	D630045H05	solute carrier family 5 (sodium/glucose cotransporter), member 1
65	4.7	gnf1m16545_at		2010306N10	unclassifiable
66	4.7	gnf1m04152_a_at	NM_021610		glycoprotein A33 (transmembrane)
67	4.7	gnf1m32791_at	XM_906210		similar to butyrophilin-like 8
68	4.7	gnf1m09647_a_at	NM_145932	I920191F06	RIKEN cDNA D630035O19 gene
69	4.7	gnf1m03142_a_at	NM_013542	K1C0001E01	granzyme B
70	4.7	gnf1m01429_a_at	NM_008586		meprin 1 beta
71	4.7	gnf1m22615_a_at		E330039G21	myosin XVB
72	4.7	gnf1m04296_a_at	NM_023256	9030623C06	RIKEN cDNA 9030623C06 gene
73	4.7	gnf1m02497_a_at	NM_010739	3830420G04	mucin 13, epithelial transmembrane
74	4.6	gnf1m00339_a_at	NM_009803	C730009H01	nuclear receptor subfamily 1, group I, member 3
75	4.6	gnf1m07637_a_at	NM_028069	1810074H01	mucin and cadherin like
76	4.6	gnf1m19589_at	NM_177744	9030421J09	RIKEN cDNA 9030421J09 gene
77	4.6	gnf1m04922_a_at	NM_026328	9130404O17	regenerating islet-derived family, member 4
78	4.6	gnf1m05969_a_at	NM_133184		solute carrier family 5, member 4a
79	4.6	gnf1m04542_a_at	NM_025453	5033426G15	transmembrane 4 L six family member 20
80	4.6	gnf1m11559_a_at	NM_145365	C730025L08	cAMP responsive element binding protein 3-like 3
81	4.6	gnf1m14304_at		2010003H20	RIKEN cDNA 2010003H20 gene
82	4.6	gnf1m30770_a_at		9130020L07	chloride channel calcium activated 6
83	4.6	gnf1m30972_a_at	NM_019792	C730034H04	cytochrome P450, family 3, subfamily a, polypeptide 25
84	4.6	gnf1m09954_at	NM_033039		oncomodulin
85	4.6	gnf1m00257_a_at	NM_007818	C730009I07	cytochrome P450, family 3, subfamily a, polypeptide 11
86	4.6	gnf1m06091_a_at	NM_133888	F630101B18	sphingomyelin phosphodiesterase, acid-like 3B
87	4.6	gnf1m22391_a_at	NM_001003915	D630044A17	solute carrier family 5 (sodium/glucose cotransporter), member 12
88	4.5	gnf1m30561_a_at	XM_922811	9030616M21	maltase-glucoamylase
89	4.5	gnf1m04260_a_at	NM_023114	2010015N05	apolipoprotein C-III
90	4.5	gnf1m13253_a_at	NM_007845		defensin related cryptdin, related sequence 10
91	4.5	gnf1m21818_at		9030006L09	Transcribed locus
92	4.5	gnf1m01102_a_at	NM_007980	2010000G01	fatty acid binding protein 2, intestinal
93	4.4	gnf1m34080_at			gene model 1123, (NCBI)
94	4.4	gnf1m30028_a_at	XM_905190	9130012O13	RIKEN cDNA 9130012O13 gene
95	4.4	gnf1m16792_a_at	NM_053103	M5C1032P19	ectonucleoside triphosphate diphosphohydrolase 7

96	4.4	gnf1m29693_at		1110046L06	Organic solute transporter beta
97	4.4	gnf1m09938_a_at	NM_134154	F630002E17	expressed sequence AW491445
98	4.4	gnf1m06554_a_at	NM_145539	C820008N10	transmembrane 4 superfamily member 4
99	4.3	gnf1m01219_a_at	NM_008191	0610009B03	guanylate cyclase activator 2b (retina)
100	4.3	gnf1m02861_a_at	NM_011575	2010306I07	trefoil factor 3, intestinal
101	4.3	gnf1m09020_at	NM_177544		angiogenin, ribonuclease A family, member 4
102	4.3	gnf1m01729_a_at	NM_009138	4921533C11	chemokine (C-C motif) ligand 25
103	4.3	gnf1m29464_a_at	XM_355937	2010110P09	RIKEN cDNA 2010110P09 gene
104	4.3	gnf1m13078_a_at	NM_019878	E230020O21	sulfotransferase family 1B, member 1
105	4.3	gnf1m00577_a_at	NM_178669	I920034J07	transmembrane protein 12
106	4.3	gnf1m00899_a_at	NM_007611	F630113J17	caspase 7
107	4.2	gnf1m06692_a_at	NM_146077	9130207B14	tripartite motif-containing 31
108	4.2	gnf1m03166_a_at	NM_013590		P lysozyme structural
109	4.2	gnf1m02627_a_at	NM_011076		ATP-binding cassette, sub-family B (MDR/TAP), member 1A
110	4.2	gnf1m28901_a_at	NM_145067		guanylate cyclase 2c
111	4.2	gnf1m31302_at	NM_001039241		similar to butyrophilin-like 7
112	4.2	gnf1m29057_s_at	XM_886668	C730034H04	cytochrome P450, family 3, subfamily a, polypeptide 25
113	4.2	gnf1m09793_at	NM_177580		BAI1-associated protein 2-like 2
114	4.2	gnf1m10618_a_at	NM_009178	2010310B14	ST3 beta-galactoside alpha-2,3-sialyltransferase 4
115	4.1	gnf1m19071_a_at	XM_908069	A430096B05	Fc fragment of IgG binding protein
116	4.1	gnf1m21823_a_at	XM_489685	9130004I05	hypothetical gene supported by AK078896
117	4.1	gnf1m02295_a_at	NM_010301	F430009P19	guanine nucleotide binding protein, alpha 11
118	4.1	gnf1m05288_a_at	NM_028270	I830157O10	aldehyde dehydrogenase 1 family, member B1
119	4.1	gnf1m13766_a_at	XM_908537	5033428B15	RIKEN cDNA 5033428B15 gene
120	4.1	gnf1m05263_a_at	NM_028085	2010013E14	ankyrin repeat and sterile alpha motif domain containing 4B
121	4.1	gnf1m29326_a_at	NM_027339	9130416C03	RIKEN cDNA 2210415F13 gene
122	4.1	gnf1m31481_x_at			uncharacterized Celera prediction mCG8654
123	4.1	gnf1m06112_at	NM_133969	1200012E24	cytochrome P450, family 4, subfamily v, polypeptide 3
124	4.1	gnf1m03564_a_at	NM_017399	2010105C24	fatty acid binding protein 1, liver
125	4.1	gnf1m05642_a_at	NM_031197	F520013J12	solute carrier family 2 (facilitated glucose transporter), member 2
126	4.0	gnf1m09607_a_at	NM_023493	1810018F03	camello-like 5
127	4.0	gnf1m24646_at		9130001H23	cytochrome P450, 2j6
128	4.0	gnf1m04616_a_at	NM_025622	2200008F12	lectin, galactose-binding, soluble 2
129	4.0	gnf1m28787_at	NM_001033879	7420443F16	tubulin, alpha-like 3
130	4.0	gnf1m06086_a_at	NM_133867	9130423G10	ESP8-like 3
131	4.0	gnf1m16117_a_at	NM_011463		serine peptidase inhibitor, Kazal type 4

No. 8, kidney specific genes

#1	#2	#3	#4	#5	#6
1	7.1	gnf1m01265_a_at	NM_008294	I920049K08	hydroxysteroid dehydrogenase-4, delta<5>-3-beta
2	7.0	gnf1m05348_at	NM_028746	F430105K03	solute carrier family 7, (cationic amino acid transporter, y+ system) member 13
3	6.9	gnf1m05523_a_at	NM_029901	9430025F20	aldo-keto reductase family 1, member C21
4	6.7	gnf1m16581_a_at	NM_183354		solute carrier family 12, member 1
5	6.7	gnf1m10283_a_at	NM_146197	F520004G19	acyl-CoA synthetase medium-chain family member 2
6	6.5	gnf1m10647_a_at	NM_009198	D630030E12	solute carrier family 17 (sodium phosphate), member 1
7	6.2	gnf1m02781_a_at	NM_011392	6430706P19	solute carrier family 34 (sodium phosphate), member 1
8	6.2	gnf1m15548_at		F530004J10	acyl-CoA synthetase medium-chain family member 2
9	6.1	gnf1m10887_a_at	NM_009203	D630047K05	solute carrier family 22 (organic anion/cation transporter), member 12
10	6.1	gnf1m10281_a_at	NM_009470	F530213L09	uromodulin
11	6.1	gnf1m30135_a_at	NM_026685		RIKEN cDNA 0610009B10 gene
12	5.9	gnf1m05349_a_at	NM_028747	F430111O10	RIKEN cDNA 0610012H03 gene
13	5.8	gnf1m00921_a_at	NM_007663	D330037K14	cadherin 16
14	5.8	gnf1m22177_at	NM_001033227	F530201E06	GRB2-related adaptor protein
15	5.7	gnf1m08749_at	NM_175330	D630029K05	RIKEN cDNA D630029K05 gene
16	5.6	gnf1m03998_a_at	NM_020626	0610008J07	transmembrane protein 27
17	5.5	gnf1m15565_a_at	XM_922809	0610012A11	RIKEN cDNA 0610012A11 gene
18	5.5	gnf1m03875_a_at	NM_019977	0610009I10	myo-inositol oxygenase
19	5.5	gnf1m26400_a_at	NM_001037842	B230368O20	camello-like 3
20	5.4	gnf1m06093_a_at	NM_133894	9430041C03	UDP glucuronosyltransferase 2 family, polypeptide B38
21	5.4	gnf1m28792_at	NM_001002900		YGHL1 homolog
22	5.4	gnf1m15567_at	NM_207216	F430101I22	UDP glycosyltransferases 3 family, polypeptide A1
23	5.4	gnf1m25247_at	NM_212444	9930122H11	glycerol kinase
24	5.3	gnf1m10665_at	NM_008585		meprin 1 alpha
25	5.3	gnf1m02432_a_at	NM_010594	D630002H20	kidney androgen regulated protein
26	5.3	gnf1m06115_a_at	NM_133980		solute carrier family 22 (organic cation transporter), member 13
27	5.3	gnf1m33110_at	XM_921174		low density lipoprotein receptor-related protein 2
28	5.3	gnf1m02978_a_at	NM_011834	F530204I17	aminoadipate aminotransferase
29	5.2	gnf1m10127_a_at	NM_029550	F530213F06	kidney expressed gene 1
30	5.2	gnf1m10456_a_at	NM_138951	G630090K23	cDNA sequence BC021608
31	5.1	gnf1m01151_a_at	NM_008061	D630014N06	glucose-6-phosphatase, catalytic
32	5.1	gnf1m03221_a_at	NM_013667		solute carrier family 22 (organic cation transporter), member 2
33	5.1	gnf1m10947_a_at	NM_009699	D630039I01	aquaporin 2
34	5.0	gnf1m10612_a_at	NM_027857	F430107N01	aspartoacylase (aminoacylase) 3
35	5.0	gnf1m07479_a_at	NM_027208	1810026B04	3-hydroxybutyrate dehydrogenase, type 2
36	5.0	gnf1m13413_at	NM_147025		olfactory receptor 380
37	5.0	gnf1m23136_a_at		2810406A16	transcription factor 2
38	4.9	gnf1m10416_a_at	NM_144845	F430112M20	UDP glycosyltransferases 3 family, polypeptide A2
39	4.9	gnf1m00366_a_at	NM_177002	D630035B04	RIKEN cDNA C730048C13 gene
40	4.9	gnf1m32547_at	NM_145548	F530013C01	cytochrome P450, family 2, subfamily j, polypeptide 13
41	4.9	gnf1m07320_a_at	NM_153193		hydroxysteroid dehydrogenase-2, delta<5>-3-beta
42	4.9	gnf1m02819_x_at	NM_011471		small proline-rich protein 2E
43	4.9	gnf1m00109_a_at	NM_019659	D630001P12	potassium inwardly-rectifying channel, subfamily J, member 1
44	4.9	gnf1m30458_s_at	XM_904752	0610011D16	cytochrome P450, family 4, subfamily a, polypeptide 10
45	4.9	gnf1m03307_a_at	NM_013823	6330501L09	klotho
46	4.8	gnf1m27802_at		D630032H21	solute carrier family 6 (neurotransmitter transporter), member 18
47	4.8	gnf1m00694_a_at	NM_009996	I420041M03	cytochrome P450, family 24, subfamily a, polypeptide 1
48	4.8	gnf1m18724_at	NM_001001444	0610030I09	defensin beta 29
49	4.8	gnf1m04866_a_at	NM_026183	2300007E21	RIKEN cDNA 1300013J15 gene
50	4.8	gnf1m10472_s_at	NM_007823	F530003M14	cytochrome P450, family 4, subfamily b, polypeptide 1
51	4.7	gnf1m04633_a_at	NM_025655	2310003K08	transmembrane and immunoglobulin domain containing
52	4.7	gnf1m04355_a_at	NM_023718	D630050M02	solute carrier organic anion transporter family, member 1a6
53	4.7	gnf1m27824_at		D630042G03	solute carrier family 12, member 1
54	4.7	gnf1m23067_at		0610042L23	phosphotriesterase related
55	4.7	gnf1m10057_a_at	NM_178713		aldehyde dehydrogenase 8 family, member A1
56	4.7	gnf1m09474_a_at	NM_026701	F530003P19	RIKEN cDNA 0610038K03 gene
57	4.7	gnf1m16362_at		F530203M14	cDNA sequence BC021785
58	4.7	gnf1m01765_a_at	NM_009205	D630006P08	solute carrier family 3, member 1
59	4.7	gnf1m03710_a_at	NM_019481	1500004P08	solute carrier family 13 (sodium/sulphate symporters), member 1
60	4.7	gnf1m10722_a_at	NM_023455	0610037O16	camello-like 4
61	4.7	gnf1m04775_a_at	NM_025956	1700112F08	RIKEN cDNA 1700011H14 gene
62	4.6	gnf1m22391_a_at	NM_001003915	D630044A17	solute carrier family 5 (sodium/glucose cotransporter), member 12
63	4.6	gnf1m27993_at		D930050K17	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3
64	4.6	gnf1m29179_a_at	NM_009968	5930429O16	crystallin, zeta
65	4.6	gnf1m10748_a_at	NM_009202		solute carrier family 22 (organic cation transporter), member 1
66	4.6	gnf1m01541_a_at	NM_008777	I530004L01	phenylalanine hydroxylase
67	4.6	gnf1m06364_a_at	NM_144785		solute carrier family 22 (organic anion transporter), member 19
68	4.6	gnf1m08059_at	NM_175305	F520011D01	leucine rich repeat containing 19
69	4.6	gnf1m01006_a_at	NM_007823	F530003M14	cytochrome P450, family 4, subfamily b, polypeptide 1
70	4.5	gnf1m10737_at	NM_010007	F530002C20	cytochrome P450, family 2, subfamily j, polypeptide 5
71	4.5	gnf1m04014_a_at	NM_021291	D630032A02	solute carrier family 7 (cationic amino acid transporter, y+ system), member 9
72	4.5	gnf1m10034_a_at	NM_133254		solute carrier family 5 (sodium/glucose cotransporter), member 2
73	4.5	gnf1m04185_a_at	NM_022017	K230039O04	transient receptor potential cation channel, subfamily V, member 4
74	4.4	gnf1m06398_a_at	NM_144856	F530004K04	solute carrier family 22 (organic anion transporter), member 7
75	4.4	gnf1m07954_a_at	NM_172378	4933425E16	cDNA sequence BC026439
76	4.4	gnf1m16161_a_at			Mouse Similar to xylulokinase homolog (H. influenzae), clone IMAGE:5043428, mRNA, partial cds /cds=UNKNOWN /gb=BC025442 /gi=19343553 /len=3173 gnl|UG|Mm#S2582558
77	4.4	gnf1m05625_a_at	NM_031164	C730005G24	coagulation factor XIII, beta subunit
78	4.4	gnf1m15710_a_at	NM_001033284	F520011L24	cDNA sequence BC026585
79	4.4	gnf1m12966_a_at	NM_177351	D630038A22	RIKEN cDNA C630028N24 gene
80	4.4	gnf1m03480_a_at	NM_016785	0610008H11	thiopurine methyltransferase
81	4.4	gnf1m10903_a_at	NM_144903	I530022M24	aldolase 2, B isoform
82	4.4	gnf1m16309_a_at	NM_010604	9130007L13	potassium inwardly-rectifying channel, subfamily J, member 16
83	4.3	gnf1m28622_a_at		6330575A10	D-amino acid oxidase 1
84	4.3	gnf1m01633_a_at	NM_008952	C730025C09	pipecolic acid oxidase
85	4.3	gnf1m04484_a_at	NM_025337	E130308C22	aldo-keto reductase family 7, member A5 (aflatoxin aldehyde reductase)
86	4.3	gnf1m01909_s_at	NM_133894	9430041C03	UDP glucuronosyltransferase 2 family, polypeptide B5
87	4.3	gnf1m15713_a_at	NM_010616	9130007B22	kinesin family member 12
88	4.2	gnf1m10719_a_at	NM_019701	I920067P16	chloride channel Kb
89	4.2	gnf1m10650_a_at	NM_008439	2010300P15	ketohexokinase
90	4.2	gnf1m01537_a_at	NM_008767	0610010E09	solute carrier family 22 (organic cation transporter), member 18
91	4.2	gnf1m09724_a_at	XM_923228	D030060O14	RAB11 family interacting protein 3 (class II)
92	4.2	gnf1m03664_a_at	NM_019395	C730030M09	fructose bisphosphatase 1
93	4.2	gnf1m06502_a_at	NM_145424	F530215H01	cDNA sequence BC089597
94	4.2	gnf1m08818_a_at	NM_144821	G430030G06	expressed sequence AI317395
95	4.2	gnf1m32466_at	NM_001033041	F530007C24	amino carboxymuconate semialdehyde decarboxylase
96	4.2	gnf1m11779_a_at	NM_013888	6430500P04	DnaJ (Hsp40) homolog, subfamily

					C, member 12
97	4.2	gnf1m12767_a_at	NM_019546	C730020B03	proline dehydrogenase (oxidase) 2
98	4.2	gnf1m03147_s_at	NM_013547	0610012C11	homogentisate 1, 2-dioxygenase
99	4.2	gnf1m09433_a_at	NM_054055	F430109H11	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3
100	4.1	gnf1m25504_a_at		A230106J09	crystallin, lamda 1
101	4.1	gnf1m06281_a_at	NM_138685	D630020P16	WAP four-disulfide core domain 15
102	4.1	gnf1m10651_a_at	NM_011731	F530202L21	solute carrier family 6 (neurotransmitter transporter), member 20
103	4.1	gnf1m05092_a_at	NM_026947	1810022C23	RIKEN cDNA 1810022C23 gene
104	4.1	gnf1m02677_a_at	NM_011172		proline dehydrogenase
105	4.1	gnf1m05772_a_at	NM_052824	1700101G12	FXYD domain-containing ion transport regulator 2
106	4.1	gnf1m00043_a_at	NM_016675	1300013G06	claudin 2
107	4.0	gnf1m15753_at	NM_175438		aldehyde dehydrogenase 4 family, member A1
108	4.0	gnf1m06071_a_at	NM_133797	I920194N11	RIKEN cDNA 4833439L19 gene
109	4.0	gnf1m10738_a_at	NM_010007	F530002C20	cytochrome P450, family 2, subfamily j, polypeptide 5
110	4.0	gnf1m06417_a_at	NM_144908	E430002F06	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11
111	4.0	gnf1m05748_a_at	NM_033564	9030404G22	Mpv17 transgene, kidney disease mutant-like

No. 9, salivary gland specific genes

#1	#2	#3	#4	#5	#6
1	6.7	gnf1m35496_at			inferred: gb|AAA03341.1| (U02032) ribosomal protein L23a [Homo sapiens] mCG1028615
2	6.6	gnf1m33423_s_at	XM_914430		similar to Gastric triacylglycerol lipase precursor (Gastric lipase) (GL)
3	6.5	gnf1m27768_at		D630008I05	unclassifiable
4	6.5	gnf1m33904_x_at			ENSMUST00000079849 transcript (in rel.37.34e)
5	6.5	gnf1m30523_at		F630048B04	expressed sequence AI747699
6	6.5	gnf1m03958_a_at	NM_020563		androgen-binding protein eta
7	6.4	gnf1m03750_at	NM_019628		proline-rich protein MP5
8	6.4	gnf1m31334_x_at	XM_914390		similar to pregastric esterase
9	6.1	gnf1m04075_a_at	NM_021405		cystatin 10 (chondrocytes)
10	6.0	gnf1m10354_at	NM_177446		androgen binding protein zeta
11	5.9	gnf1m01403_a_at	NM_008530		lymphocyte antigen 6 complex, locus F
12	5.9	gnf1m05715_at	NM_032542		seminal vesicle antigen-like 2
13	5.7	gnf1m31674_x_at	NM_001004160		similar to proline rich protein MP4
14	5.6	gnf1m02800_a_at	NM_011423		submaxillary gland androgen regulated protein 1
15	5.6	gnf1m01639_a_at	XM_905489		patched homolog 2
16	5.6	gnf1m28645_at	NM_021386		claudin 10
17	5.4	gnf1m09235_s_at	XM_910843	5530600L21	odorant binding protein Ia
18	5.4	gnf1m21380_at		D430009N09	hypothetical protein
19	5.4	gnf1m06481_a_at	NM_145386		cDNA sequence BC005655
20	5.4	gnf1m29944_at	XM_913838		lipocalin 11
21	5.4	gnf1m15684_at			prolactin induced protein
22	5.3	gnf1m35805_x_at			inferred: gb|AAH06770.1|AAH06770 (BC006770) Unknown (protein for MGC:8099) [Mus musculus] mCG1044483
23	5.3	gnf1m14047_at		2210017G18	RIKEN cDNA 2210017G18 gene
24	5.3	gnf1m22522_at		E030001I17	weakly similar to 2010003O02RIK PROTEIN [Mus musculus]
25	5.2	gnf1m11910_a_at	NM_011823	C030004I11	G protein-coupled receptor 34
26	5.2	gnf1m17149_a_at		4930505M18	RIKEN cDNA 4930505M18 gene
27	5.2	gnf1m17033_at		4933403M19	RIKEN cDNA 4933403M19 gene
28	5.2	gnf1m04280_a_at	NM_023186	2210020N23	chitinase, acidic
29	5.2	gnf1m21697_at		4933400A22	unclassifiable
30	5.1	gnf1m18973_at			gb=U35310 Mouse mel-13b transcript
31	5.1	gnf1m05897_a_at	NM_080420	5830499B15	lactoperoxidase
32	5.0	gnf1m32601_at	XM_910856		similar to odorant binding protein Ia
33	5.0	gnf1m01464_a_at	NM_008648		major urinary protein 4
34	4.9	gnf1m32966_at			inferred: ref|NP_079494.1| (NM_025218) UL16-binding protein 1 [Homo sapiens] mCG12640
35	4.9	gnf1m02190_a_at	NM_010061	F930025I20	deoxyribonuclease I
36	4.9	gnf1m20497_at		A730081N03	unclassifiable
37	4.9	gnf1m04197_a_at	NM_022313	E430010C01	Era (G-protein)-like 1 (E. coli)
38	4.9	gnf1m01532_a_at	NM_008754	5530600L21	odorant binding protein Ia
39	4.8	gnf1m35149_at	NM_183191		phospholipase C-like 3
40	4.8	gnf1m07515_at	NM_176925	A430057M04	RIKEN cDNA A430057M04 gene
41	4.8	gnf1m33455_at			similar to hypothetical protein
42	4.7	gnf1m11988_a_at	NM_023865	9530002B09	RIKEN cDNA 9530002B09 gene
43	4.7	gnf1m07388_a_at	NM_153590		killer cell lectin-like receptor family E member 1
44	4.7	gnf1m35679_s_at	NM_146492		olfactory receptor 724
45	4.7	gnf1m22868_at		4732461J20	keratin complex 1, acidic, gene 5
46	4.7	gnf1m32804_at	XM_892365		similar to actin 3 - fruit fly (Drosophila melanogaster) (fragments)
47	4.7	gnf1m17190_at	XM_908254	2210404A22	claudin 22
48	4.7	gnf1m10677_a_at	NM_008953	2310075K06	parotid secretory protein
49	4.6	gnf1m17920_at		C230081E04	unclassifiable
50	4.5	gnf1m07435_a_at	NM_010281	G430050D13	gamma-glutamyl hydrolase
51	4.5	gnf1m23958_at		5330439L06	RIKEN cDNA 1300013D05 gene
52	4.5	gnf1m25579_at		A430024D24	unclassifiable
53	4.5	gnf1m33927_x_at			ENSMUST00000077122 transcript (in rel.37.34e)
54	4.4	gnf1m03419_a_at	NM_016667		syntrophin, basic 1
55	4.4	gnf1m24395_at		6430540A14	hypothetical SAP domain containing protein
56	4.4	gnf1m01992_a_at	NM_009638	2310021L10	cysteine-rich secretory protein 1
57	4.3	gnf1m33762_x_at	XM_922194		similar to vomeronasal 2, receptor, 1
58	4.3	gnf1m31716_at			uncharacterized Celera prediction mCG55052
59	4.3	gnf1m35982_at			inferred: ref|NP_035731.1| (NM_011601) T lymphoma oncogene [Mus musculus] mCG1033795
60	4.3	gnf1m34974_at			inferred: ref|NP_058846.1| (NM_017150) ribosomal protein L29 [Rattus norvegicus] mCG51974
61	4.3	gnf1m02074_a_at	NM_009802	4833414N20	carbonic anhydrase 6
62	4.3	gnf1m35853_at	XM_906713		similar to 40S ribosomal protein S15 (RIG protein)
63	4.2	gnf1m13091_at	NM_054046	E330019N23	differentially expressed in FDCP 8
64	4.2	gnf1m15443_at		5730478J17	RIKEN cDNA 5730478J17 gene
65	4.2	gnf1m28813_a_at	XM_916698	2310050N11	RIKEN cDNA 2310050N11 gene
66	4.2	gnf1m34131_x_at	XM_906496		similar to zinc finger protein 709
67	4.2	gnf1m15534_at	NM_008649		major urinary protein 5
68	4.2	gnf1m00648_a_at	NM_010800	1810009C13	basic helix-loop-helix domain containing, class B, 8
69	4.2	gnf1m09073_a_at	NM_146345		olfactory receptor 1491
70	4.2	gnf1m34995_at			inferred: ref|XP_051580.1| (XM_051580) similar to HSPC070 protein (H. sapiens) [Homo sapiens] mCG51159
71	4.2	gnf1m26159_at		A930031C22	weakly similar to ZINC FINGER 202 M3 SPLICE VARIANT [Mus musculus]
72	4.2	gnf1m32586_at	XM_915478		hypothetical LOC432591
73	4.2	gnf1m24241_at		6030463O13	hypothetical Arginine-rich region containing protein
74	4.2	gnf1m25233_a_at		9930035M16	hypothetical protein
75	4.2	gnf1m17256_x_at	XM_904800		proline-rich protein BstNI subfamily 1
76	4.1	gnf1m27332_at	XM_922588	D030058M09	nucleotide binding protein-like
77	4.1	gnf1m34972_at	NM_146869		olfactory receptor 147
78	4.1	gnf1m27714_a_at		E030027O16	transforming growth factor beta 1 induced transcript 1
79	4.1	gnf1m14778_at		4930537H20	RIKEN cDNA 4930537H20 gene
80	4.1	gnf1m33012_at			inferred: gb|AAH12312.1|AAH12312 (BC012312) Similar to hypothetical protein DKFZp434G0522 [Mus musculus] mCG12506
81	4.1	gnf1m01271_a_at	NM_008313	C630046L14	5 hydroxytryptamine (serotonin) receptor 4
82	4.1	gnf1m22799_s_at		4930404J24	RIKEN cDNA 4930404J24 gene
83	4.1	gnf1m32388_at			Pseudogene for inferred: ref|NP_061280.1| (NM_018810) makorin, ring finger protein, 1 [Mus musculus] mCG21584
84	4.1	gnf1m18546_at	XM_904821	8030497G14	cyclin-dependent kinase inhibitor 3
85	4.1	gnf1m12980_a_at	NM_029682	1700095N21	Stam binding protein like 1
86	4.1	gnf1m20307_at		I920049I17	unclassifiable
87	4.1	gnf1m25253_at		A030006P04	syntrophin, acidic 1
88	4.1	gnf1m34839_at	NM_182714		olfactory receptor 91
89	4.0	gnf1m06318_s_at	NM_152802	9230103N16	defensin beta 12
90	4.0	gnf1m02210_a_at	NM_010099	9830138J21	ectodysplasin-A
91	4.0	gnf1m32602_at			inferred: gb|AAH03199.1|AAH03199 (BC003199) RIKEN cDNA 2310058A11 gene [Mus musculus] mCG16193
92	4.0	gnf1m15910_at		9430006E19	GA repeat binding protein, beta 2
93	4.0	gnf1m23087_a_at	NM_025304	1810004A15	leucine carboxyl methyltransferase 1
94	4.0	gnf1m24041_a_at		5830444H09	staufen (RNA binding protein) homolog 1 (Drosophila)
95	4.0	gnf1m33367_x_at			peptidylprolyl isomerase A pseudogene chr19_428.1

No. 10, eye specific genes

#1	#2	#3	#4	#5	#6
1	7.3	gnf1m00981_a_at	NM_007776		crystallin, gamma D
2	7.0	gnf1m00978_a_at	NM_007773	A930026B12	crystallin, beta B2
3	6.9	gnf1m00573_a_at	NM_012065	A930027A04	phosphodiesterase 6G, cGMP-specific, rod, gamma
4	6.9	gnf1m04351_s_at	NM_023695	E130317B02	crystallin, beta B1
5	6.8	gnf1m28078_at		E130006G23	retinal S-antigen
6	6.7	gnf1m17108_at	NM_144761	E130105D02	crystallin, gamma B
7	6.6	gnf1m30922_a_at		E630012K22	crystallin, alpha A
8	6.6	gnf1m11269_a_at	NM_021882	2810025C24	silver
9	6.6	gnf1m07393_at	NM_153601		glutamate-ammonia ligase (glutamine synthetase) domain containing 1
10	6.5	gnf1m15059_a_at	XM_917055	E130101O17	galectin-related inter-fiber protein
11	6.5	gnf1m04047_s_at	NM_021352	E130107C24	crystallin, beta B3
12	6.5	gnf1m02152_at	NM_009967	E130006E18	crystallin, gamma S
13	6.4	gnf1m30133_at		D130033I21	hypothetical protein
14	6.4	gnf1m06650_a_at	NM_145963	A930036I05	potassium inwardly-rectifying channel, subfamily J, member 14
15	6.4	gnf1m03369_a_at	NM_015745		retinol binding protein 3, interstitial
16	6.4	gnf1m04440_a_at	NM_024458	A930002E23	phosducin
17	6.3	gnf1m06379_at	NM_144813		solute carrier family 24 (sodium/potassium/calcium exchanger), member 1
18	6.3	gnf1m07891_a_at	NM_177693	I1C0020D18	lens intrinsic membrane protein 2
19	6.3	gnf1m01672_a_at	NM_009038		recoverin

20	6.3	gnf1m04045_a_at	NM_021351	6820402K11	crystallin, beta A4
21	6.3	gnf1m05528_a_at	NM_029987		retinal pigment epithelium 65
22	6.2	gnf1m04046_a_at	NM_021352		crystallin, beta B3
23	6.2	gnf1m29067_a_at		A930021D15	ankyrin repeat domain 33
24	6.2	gnf1m04142_a_at	NM_021541	E130107M19	crystallin, beta A2
25	6.1	gnf1m16702_at	NM_021478	D430040H24	tubby like protein 1
26	6.1	gnf1m05646_a_at	NM_031202	G370117C01	tyrosinase-related protein 1
27	6.1	gnf1m12896_a_at	NM_009965	D230003J06	crystallin, beta A1
28	6.1	gnf1m00980_a_at	NM_007775		crystallin, gamma C
29	5.9	gnf1m00703_a_at	NM_008140	A930002G18	guanine nucleotide binding protein, alpha transducing 1
30	5.9	gnf1m19361_at		5930422J03	tolloid-like
31	5.8	gnf1m00768_a_at	NM_007378	D830040G08	ATP-binding cassette, sub-family A (ABC1), member 4
32	5.8	gnf1m29957_a_at	NM_007723		cyclic nucleotide gated channel alpha 1
33	5.8	gnf1m08653_a_at	NM_145601	A930006A15	cDNA sequence BC016201
34	5.8	gnf1m13044_a_at	NM_008600	E130102N08	major intrinsic protein of eye lens fiber
35	5.8	gnf1m17874_a_at		E130218I03	RIKEN cDNA E130106C14 gene
36	5.7	gnf1m21962_a_at	XM_923785	A930011N13	cDNA sequence BC048943
37	5.6	gnf1m16693_at	NM_011302		retinoschisis 1 homolog (human)
38	5.6	gnf1m17433_a_at		A930007I01	aryl hydrocarbon receptor-interacting protein-like 1
39	5.5	gnf1m02175_a_at	NM_010024		dopachrome tautomerase
40	5.5	gnf1m06532_a_at	NM_145493	A930004D23	complexin 4
41	5.5	gnf1m06697_a_at	NM_146086	A630063G20	ribosomal protein S2
42	5.4	gnf1m01691_a_at	XM_925769	5033427A21	rod outer segment membrane protein 1
43	5.4	gnf1m29850_a_at		A830047P19	HEAT-like (PBS lyase) repeat containing 1
44	5.4	gnf1m10518_a_at	NM_011676	2410112J20	unc-119 homolog (C. elegans)
45	5.4	gnf1m06693_a_at	NM_146079	7530416I21	guanylate cyclase activator 1B
46	5.3	gnf1m02462_a_at	NM_010661	E130302L01	keratin complex 1, acidic, gene 12
47	5.3	gnf1m10785_a_at	NM_008189		guanylate cyclase activator 1a (retina)
48	5.2	gnf1m28079_a_at		E130006G23	retinal S-antigen
49	5.2	gnf1m13409_at	XM_914910		retinitis pigmentosa 1 homolog (human)-like 1
50	5.2	gnf1m12387_a_at	NM_145143	A930032J21	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)
51	5.2	gnf1m22179_at	NM_001004171	C330036H15	hypothetical gene supported by AK082832
52	5.1	gnf1m20604_a_at	NR_002873	A930007B02	Vax2 opposite strand transcript 1
53	5.1	gnf1m21792_at		6820439G08	syntaxin 3
54	5.1	gnf1m32629_a_at		6330574L03	beaded filament structural protein 2, phakinin
55	5.1	gnf1m12366_a_at	NM_023898	A930033D18	phosphodiesterase 6H, cGMP-specific, cone, gamma
56	5.1	gnf1m04350_a_at	NM_023695	E130317B02	crystallin, beta B1
57	5.1	gnf1m02049_a_at	NM_009751	E130307L19	beaded filament structural protein in lens-CP94
58	5.0	gnf1m13915_at			G protein-coupled receptpr kinase 1
59	5.0	gnf1m12390_a_at		E130109K18	nuclear receptor subfamily 2, group E, member 3
60	5.0	gnf1m01383_a_at	NM_008504		granzyme M (lymphocyte met-ase 1)
61	4.9	gnf1m03950_a_at	NM_020516	A030012J09	solute carrier family 16 (monocarboxylic acid transporters), member 8
62	4.9	gnf1m05099_a_at	NM_027010	3200002G02	crystallin, gamma F
63	4.9	gnf1m10704_a_at	NM_013877	A930021F10	calcium binding protein 5
64	4.9	gnf1m12208_a_at	NM_144929	A930015B08	RIKEN cDNA A330096I21 gene
65	4.9	gnf1m06746_a_at	NM_146245	A930028G01	leucine rich repeat containing 21
66	4.8	gnf1m06621_a_at	NM_145835	E130104I05	lactase-like
67	4.7	gnf1m30040_a_at	NM_011502		syntaxin 3
68	4.7	gnf1m01561_a_at	NM_008806	A930009G18	phosphodiesterase 6B, cGMP, rod receptor, beta polypeptide
69	4.6	gnf1m00940_a_at	NM_007701	7420434P22	C. elegans ceh-10 homeo domain containing homolog
70	4.6	gnf1m13745_a_at	XM_924558	A930034P04	melan-A
71	4.6	gnf1m31007_at			cDNA sequence BC048679
72	4.6	gnf1m01625_a_at	NM_008938	7530416B14	retinal degeneration, slow (retinitis pigmentosa 7)
73	4.6	gnf1m11167_a_at	NM_008141	3830432D16	guanine nucleotide binding protein, alpha transducing 2
74	4.6	gnf1m17195_a_at	XM_916650	2310043J07	RIKEN cDNA 2310043J07 gene
75	4.5	gnf1m22298_at		D230046H12	hypothetical protein
76	4.5	gnf1m06587_a_at	NM_145598	A930031O08	thioredoxin-like 6
77	4.5	gnf1m01995_a_at	NM_009644	F730207M15	aryl-hydrocarbon receptor repressor
78	4.5	gnf1m00726_a_at	NM_007770	E130106I11	cone-rod homeobox containing gene
79	4.4	gnf1m12378_a_at	NM_021340	A930029L15	retinal G protein coupled receptor
80	4.4	gnf1m26137_a_at	NM_001035246	D230020D17	transient receptor potential cation channel, subfamily M, member 3
81	4.3	gnf1m10693_a_at	NM_133205		arrestin 3, retinal
82	4.3	gnf1m07838_at	NM_175098	I420013G23	RIKEN cDNA 6330407D12 gene
83	4.2	gnf1m01159_a_at	NM_008075		gamma-aminobutyric acid (GABA-C) receptor, subunit rho 1
84	4.2	gnf1m21507_at	NM_174999	E130012K09	hypothetical protein E130012K09
85	4.1	gnf1m03006_a_at	NM_011881		G protein-coupled receptpr kinase 1
86	4.1	gnf1m01176_a_at	NM_008106		opsin 1 (cone pigments), medium-wave-sensitive (color blindness, deutan)
87	4.1	gnf1m15300_a_at	XM_925124	2610034M16	RIKEN cDNA 2610034M16 gene
88	4.1	gnf1m08295_at	NM_173418	A930010E21	leucine rich repeat containing 22
89	4.1	gnf1m08874_at		A930034K02	unclassifiable
90	4.0	gnf1m01343_a_at	NM_008438	D930012M16	keratocan
91	4.0	gnf1m10167_a_at	NM_173736	A930008A01	sterile alpha motif domain containing 11
92	4.0	gnf1m21871_at		A130059I02	WW domain-containing oxidoreductase
93	4.0	gnf1m08160_a_at	NM_177162	9930101B10	RIKEN cDNA 9930032O22 gene

No. 11, medial olfactory epithelium specific genes

#1	#2	#3	#4	#5	#6
1	7.0	gnf1m22599_a_at		E330010A04	hypothetical Bactericidal permeability-increasing protein, BPI structure containing protein
2	6.6	gnf1m17012_a_at	XM_489285	5730403I07	RIKEN cDNA 5730403I07 gene
3	6.5	gnf1m34200_at	NM_001034875	E330032E14	gene model 1006, (NCBI)
4	6.5	gnf1m00950_a_at	NM_007724	4832423E21	cyclic nucleotide gated channel alpha 2
5	6.5	gnf1m06812_s_at	NM_147068		olfactory receptor 168
6	6.3	gnf1m12913_s_at	NM_177087	K230038F04	RIKEN cDNA 4632412N22 gene
7	6.2	gnf1m05785_at	NM_053093		tachykinin 4
8	5.8	gnf1m17252_a_at	XM_486715	5430402E10	similar to Odorant-binding protein precursor (OBP)
9	5.8	gnf1m12708_a_at	NM_172898	C530042M23	kin of IRRE like 2 (Drosophila)
10	5.8	gnf1m31135_at	NM_194357	4833435C14	antimicrobial peptide RYA3
11	5.7	gnf1m07387_at	NM_153589	4930527E21	transmembrane protein 16B
12	5.7	gnf1m07056_s_at	NM_146913		olfactory receptor 1347
13	5.6	gnf1m20169_at		A330065M03	RIKEN cDNA A330043J11 gene
14	5.5	gnf1m03300_a_at	NM_013809	3110040K11	cytochrome P450, family 2, subfamily g, polypeptide 1
15	5.5	gnf1m13003_a_at	NM_010095	D930015N03	early B-cell factor 2
16	5.5	gnf1m30492_at	XM_924923		flavin containing monooxygenase 6
17	5.5	gnf1m09872_a_at	NM_053184	C130005L05	UDP glucuronosyltransferase 2 family, polypeptide A1
18	5.4	gnf1m27881_at	NM_010605	D830027N20	potassium inwardly-rectifying channel, subfamily J, member 5
19	5.4	gnf1m32233_at	NM_001033317	9230103C20	cyclic nucleotide gated channel alpha 4
20	5.3	gnf1m06848_x_at	NM_146555		olfactory receptor 805
21	5.3	gnf1m31720_at		A230090L09	cDNA sequence BC049352
22	5.3	gnf1m09505_at	NM_178414	3110085P20	cDNA sequence BC048390
23	5.3	gnf1m02739_a_at	NM_011312		S100 calcium binding protein A5
24	5.3	gnf1m32542_at	NM_001033443	F930014I06	cyclin-dependent kinase-like 4
25	5.2	gnf1m31310_at	XM_915303		gene model 693, (NCBI)
26	5.2	gnf1m17463_a_at	XM_908788	9230116B18	RIKEN cDNA 9230116B18 gene
27	5.2	gnf1m06978_at	NM_146807		olfactory receptor 136
28	5.2	gnf1m09153_a_at	NM_177465	A430096O08	uromodulin-like 1
29	5.2	gnf1m07624_a_at	NM_175167	4833413D08	RIKEN cDNA 5430413K10 gene
30	5.2	gnf1m21706_a_at	NM_207210	4933407K03	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4
31	5.1	gnf1m07309_a_at	NM_153156		stomatin (Epb7.2)-like 3
32	5.1	gnf1m10052_at	NM_178412		cDNA sequence BC051070
33	5.1	gnf1m30005_at	NM_198656	4022416J06	cadherin-like 26
34	5.1	gnf1m15487_at		9230110L08	Rho-guanine nucleotide exchange factor
35	5.0	gnf1m11843_a_at	NM_178214	I920051L22	histone 2, H2bb
36	5.0	gnf1m32183_at	XM_355976		secretoglobin, family 1C, member 1
37	5.0	gnf1m24421_at		6430579P05	calcium/calmodulin-dependent protein kinase II, delta
38	5.0	gnf1m29768_at	NM_183172	9830132D18	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)
39	5.0	gnf1m03130_a_at	NM_013515	I830025K05	stomatin
40	5.0	gnf1m32819_at	NM_198650		solute carrier family 22 (organic anion transporter), member 20
41	5.0	gnf1m08272_a_at	NM_146052	A730092P18	leucine rich repeat containing 3B
42	4.9	gnf1m03595_a_at	NM_018751		sulfotransferase family, cytosolic, 1C, member 1
43	4.9	gnf1m17426_at		6430500D05	RIKEN cDNA 6430500D05 gene
44	4.8	gnf1m07118_at	NM_146998		olfactory receptor 195
45	4.8	gnf1m06637_at	NM_145922		potassium voltage gated channel, Shaw-related subfamily, member 4
46	4.8	gnf1m02594_at	NM_011010	5430435H13	olfactory marker protein
47	4.8	gnf1m02885_a_at	XM_903827	D130020P04	target of myb1 homolog (chicken)
48	4.8	gnf1m08826_a_at	NM_175024	G630049C14	RIKEN cDNA G630049C14 gene
49	4.7	gnf1m18656_at	XM_144408	2310003L06	RIKEN cDNA 2310003L06 gene
50	4.7	gnf1m02208_a_at	NM_010096	C130014O03	early B-cell factor 3
51	4.7	gnf1m06516_a_at	NM_145451	1700020G18	glutathione peroxidase 6
52	4.7	gnf1m06327_a_at	NM_139296		monooxygenase, DBH-like 2
53	4.7	gnf1m07917_at	NM_001011800	4931403F16	olfactory receptor 212
54	4.7	gnf1m08422_a_at	NM_144917	D130076C22	RNA binding motif and ELMO domain 1
55	4.7	gnf1m03930_a_at	NM_020293		claudin 9
56	4.7	gnf1m20922_at	NM_001004151	B930086I10	receptor transporter protein 1
57	4.6	gnf1m35554_at			inferred: gb|AAL61047.1| (AY073384) olfactory receptor MOR125-1 [Mus musculus] mCG23021
58	4.6	gnf1m07945_s_at	NM_172865	4932703L02	mannosidase, endo-alpha
59	4.6	gnf1m12520_a_at	NM_178673	B930093L07	follistatin-like 5
60	4.6	gnf1m05817_a_at	NM_053188	A530024K02	steroid 5 alpha-reductase 2
61	4.6	gnf1m07993_at	NM_177350	6030447F07	gliomedin
62	4.5	gnf1m25556_s_at	XM_920918	A830087L05	RIKEN cDNA A730046J19 gene
63	4.5	gnf1m33178_at			expressed sequence AU021092
64	4.4	gnf1m10706_a_at	NM_009993	1300003J07	cytochrome P450, family 1, subfamily a, polypeptide 2
65	4.4	gnf1m24678_a_at		1700001O02	RIKEN cDNA 1700041C02 gene
66	4.4	gnf1m16746_a_at	XM_915229	1190003M12	RIKEN cDNA 1190003M12 gene
67	4.4	gnf1m03947_s_at	NM_020513		olfactory receptor 1507
68	4.4	gnf1m07372_a_at	NM_153558		lipocalin 13
69	4.4	gnf1m23372_a_at	NM_001007581	4933412J21	similar to mNori-2p
70	4.4	gnf1m18551_at		2610011C15	guanine nucleotide binding protein, alpha stimulating, olfactory type
71	4.3	gnf1m33892_at			inferred: ref|NP_057440.1| (NM_016356) RU2S [Homo sapiens] mCG116692
72	4.3	gnf1m33007_at	XM_913800		similar to odorant binding protein 2B

73	4.3	gnf1m02475_a_at	NM_010694		lipocalin 3
74	4.3	gnf1m24804_at		9330210P10	calmegin
75	4.2	gnf1m32690_at		B020010F16	elongation factor RNA polymerase II-like 3
76	4.2	gnf1m06968_s_at	NM_146794		olfactory receptor 1261
77	4.2	gnf1m10211_a_at	XM_919865		expressed sequence AI790298
78	4.2	gnf1m26901_at		C230053I05	Unc4.1 homeobox (C. elegans)
79	4.2	gnf1m03909_at	NM_020051		achaete-scute complex homolog-like 3 (Drosophila)
80	4.1	gnf1m03244_at	NM_013702		Unc4.1 homeobox (C. elegans)
81	4.1	gnf1m23699_x_at		4921536C22	1700091H14RIK PROTEIN homolog [Mus musculus]
82	4.1	gnf1m28034_at		E030027N17	hypothetical protein
83	4.1	gnf1m07867_a_at	NM_177822	4732467B22	cDNA sequence BC052484
84	4.0	gnf1m06411_a_at	NM_144890	E030027N05	cDNA sequence BC018465
85	4.0	gnf1m30647_a_at		1110069O07	RIKEN cDNA 1110069O07 gene
86	4.0	gnf1m12912_a_at	NM_177087	K230038F04	RIKEN cDNA 4632412N22 gene
87	4.0	gnf1m30608_x_at	NM_001007552		intelectin b

No. 12, blastocysts specific genes

#1	#2	#3	#4	#5	#6
1	7.4	gnf1m32207_at			preferentially expressed antigen in melanoma like 7
2	7.2	gnf1m10140_at	NM_178249		preferentially expressed antigen in melanoma like 6
3	6.9	gnf1m32993_x_at		I1C0037K09	unclassifiable
4	6.7	gnf1m09737_at	NM_178247	I1C0025M01	developmental pluripotency associated 1
5	6.7	gnf1m30349_at	NM_001034897	I1C0031F10	similar to protease
6	6.5	gnf1m05155_at	NM_027344	I0C0030P07	RIKEN cDNA 2310051M13 gene
7	6.5	gnf1m05279_a_at	NM_028218	2210409E12	RIKEN cDNA 2210409E12 gene
8	6.4	gnf1m29226_a_at	XM_915636	I1C0037D04	nuclear domain 10 protein 52
9	6.2	gnf1m32956_x_at	NM_001033638	I1C0031F22	Crx opposite strand transcript 1
10	6.2	gnf1m33449_x_at			inferred: ref|NP_034375.1| (NM_010245) Friend virus susceptibility 4 [Mus musculus] mCG124469
11	5.8	gnf1m31026_s_at		G630020J15	hypothetical LOC434126
12	5.8	gnf1m33860_at	NM_001025435	I1C0015P14	cDNA sequence BC053393
13	5.7	gnf1m22399_at		D630033B11	transient receptor potential cation channel, subfamily V, member 5
14	5.6	gnf1m13158_at	NM_011790	I1C0031E08	ariadne homolog 2 (Drosophila)
15	5.4	gnf1m35498_x_at			obsolete Celera prediction mCT146197
16	5.3	gnf1m33306_x_at			uncharacterized Celera prediction mCG126957
17	5.3	gnf1m08675_a_at	NM_177731	C130073F10	RIKEN cDNA C130073F10 gene
18	5.2	gnf1m00385_a_at	NM_133792	F630115J08	lysophospholipase 3
19	5.2	gnf1m07231_at	NM_148942		serine (or cysteine) peptidase inhibitor, clade B, member 6c
20	5.2	gnf1m03790_a_at	NM_019727	I920049H08	sorting nexin 1
21	5.1	gnf1m21099_at		C230095C13	unclassifiable
22	5.1	gnf1m18865_a_at	NM_013827	E330027A01	metal response element binding transcription factor 2
23	5.0	gnf1m16204_a_at	NM_028615	I1C0040O20	developmental pluripotency associated 2
24	5.0	gnf1m03897_at	NM_020018		melanoma antigen, family A, 5
25	4.9	gnf1m02130_a_at	NM_009903		claudin 4
26	4.9	gnf1m09355_s_at	NM_025274	I1C0038J20	developmental pluripotency associated 5
27	4.9	gnf1m16230_a_at	NM_015798	I1C0048I09	F-box protein 15
28	4.9	gnf1m30904_at	XM_918785		Unknown (protein for IMAGE:30033377)
29	4.8	gnf1m13938_a_at	NM_025890	I1C0007M13	RIKEN cDNA 2410004A20 gene
30	4.8	gnf1m29385_s_at	NM_010136	C130084G11	eomesodermin homolog (Xenopus laevis)
31	4.7	gnf1m08808_a_at	NM_172822	F630022B06	phosphatidylinositol glycan, class Z
32	4.7	gnf1m06235_a_at	NM_134248	5031400I12	hepatitis A virus cellular receptor 1
33	4.7	gnf1m19280_at	NM_001033321	4932417I16	RIKEN cDNA 4932417I16 gene
34	4.7	gnf1m09637_a_at	NM_152810	I920070H23	cell division cycle 5-like (S. pombe)
35	4.6	gnf1m12684_a_at	NM_007673	C430044A20	caudal type homeo box 2
36	4.6	gnf1m31183_a_at	XM_485202	C130020L13	zinc finger and BTB domain containing 10
37	4.6	gnf1m07339_at	NM_153417		transient receptor potential cation channel, subfamily M, member 6
38	4.6	gnf1m02280_a_at	NM_010269	I1C0017N07	ganglioside-induced differentiation-associated-protein 2
39	4.6	gnf1m12533_a_at	NM_029094	G430147P21	phosphatidylinositol 3-kinase, catalytic, beta polypeptide
40	4.6	gnf1m05056_a_at	NM_026728	I1C0025L16	enoyl Coenzyme A hydratase domain containing 2
41	4.6	gnf1m10775_a_at	NM_008624	C820001L23	muscle and microspikes RAS
42	4.6	gnf1m00324_a_at	NM_146093	4930455J02	DNA segment, Chr 19, ERATO Doi 721, expressed
43	4.6	gnf1m08503_a_at	NM_172758	D430050E18	cDNA sequence BC031853
44	4.6	gnf1m29738_at		I830072P10	RAB20, member RAS oncogene family
45	4.5	gnf1m16279_at	NM_134249	I1C0024G10	T-cell immunoglobulin and mucin domain containing 2
46	4.5	gnf1m12675_a_at	XM_922775	I1C0015J23	leucyl-tRNA synthetase
47	4.5	gnf1m09876_a_at	NM_145950	C230027H09	cDNA sequence BC010311
48	4.5	gnf1m10749_a_at	NM_180678	I730038J10	glycyl-tRNA synthetase
49	4.5	gnf1m03440_a_at	NM_181329	I730062F04	coilin
50	4.5	gnf1m17293_at		4833426J09	RIKEN cDNA 4833426J09 gene
51	4.5	gnf1m22649_at		E530001F21	RIKEN cDNA E530001F21 gene
52	4.4	gnf1m05466_a_at	NM_029456	E430019I11	SAPS domain family, member 3
53	4.4	gnf1m30025_s_at	XM_904497	6330513H14	Wilms' tumour 1-associating protein
54	4.4	gnf1m06099_a_at	NM_133937	1700020E14	RIKEN cDNA 6720456B07 gene
55	4.4	gnf1m10821_at	NM_011396	B930066D05	solute carrier family 22 (organic cation transporter), member 5
56	4.4	gnf1m31134_at	XM_903021	F630103C07	oxysterol binding protein-like 7
57	4.4	gnf1m02017_a_at	NM_009680		adaptor-related protein complex 3, beta 1 subunit
58	4.4	gnf1m04944_a_at	NM_026386	I830170H06	sorting nexin 2
59	4.3	gnf1m00986_s_at	NM_007782	G630018O10	colony stimulating factor 3 receptor (granulocyte)
60	4.3	gnf1m07661_s_at	NM_026693	C630001N14	gamma-aminobutyric acid (GABA-A) receptor-associated protein-like 2
61	4.3	gnf1m28675_at			RIKEN cDNA C430049B03 gene
62	4.3	gnf1m11974_a_at	NM_009752	I830127P19	galactosidase, beta 1
63	4.3	gnf1m01956_a_at	NM_009556		zinc finger protein 42
64	4.3	gnf1m00350_a_at	NM_026360	4930588A18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47
65	4.3	gnf1m13821_at			TEA domain family member 4
66	4.2	gnf1m09428_s_at	NM_025274	I1C0038J20	developmental pluripotency associated 5
67	4.2	gnf1m09759_a_at	NM_026678	F830220J20	biliverdin reductase A
68	4.2	gnf1m06713_a_at	NM_146149	2010309H15	cDNA sequence BC026682
69	4.2	gnf1m15871_a_at	NM_027450	G430030C05	GLI pathogenesis-related 2
70	4.2	gnf1m28768_a_at	XM_917740	A530057A03	similar to predicted similar to mitochondrial glycerol 3-phosphate acyltransferase
71	4.2	gnf1m07439_s_at	NM_008602	4930503N10	protein inhibitor of activated STAT 2
72	4.2	gnf1m04103_a_at	NM_021463	I730048G12	phosphoribosyl pyrophosphate synthetase 1
73	4.2	gnf1m04639_a_at	NM_025663	I920080F14	G patch domain containing 4
74	4.1	gnf1m30194_a_at	NM_001033310	F830006B07	cDNA sequence BC038311
75	4.1	gnf1m12990_a_at	XM_906312	E430002N06	phosphatidylserine synthase 1
76	4.1	gnf1m19147_a_at	NM_194344	I420001D24	SH3 domain and tetratricopeptide repeats 1
77	4.1	gnf1m28148_at		E130203M01	weakly similar to KIAA0042 PROTEIN [Homo sapiens]
78	4.1	gnf1m09348_a_at	NM_153548	E430025E21	RIKEN cDNA E430025E21 gene
79	4.1	gnf1m22820_a_at	NM_001025156	I420019J23	RIKEN cDNA 4633402D15 gene
80	4.1	gnf1m25585_at		A430033H03	inferred: RIKEN cDNA 4932432N11 gene
81	4.1	gnf1m28582_a_at		1500003O18	makorin, ring finger protein, 1
82	4.1	gnf1m12854_a_at	NM_080452	G730023G11	mitochondrial ribosomal protein S2
83	4.1	gnf1m00844_a_at	NM_007515	G730021I22	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3
84	4.0	gnf1m01735_a_at	XM_911233	I1C0050J07	stromal cell derived factor receptor 2
85	4.0	gnf1m29874_a_at	XM_908144	9430066F19	glutamyl-prolyl-tRNA synthetase

No. 13, placenta specific genes

#1	#2	#3	#4	#5	#6
1	7.2	gnf1m30798_at	NM_001033372	I920038K03	gene model 648, (NCBI)
2	7.1	gnf1m16016_a_at		1600012P17	RIKEN cDNA 1600012P17 gene
3	7.0	gnf1m03049_x_at	NM_011963		pregnancy specific glycoprotein 18
4	6.9	gnf1m32962_at	NM_001029987	G630014J02	diamine oxidase-like protein 2
5	6.7	gnf1m09648_a_at	NM_020261	1620401C02	pregnancy-specific glycoprotein 23
6	6.7	gnf1m04749_a_at	NM_025896	1600032A24	prolactin like protein I
7	6.7	gnf1m16800_at	NM_029355	1600014J19	prolactin-like protein N
8	6.6	gnf1m29570_at			inferred: ref|XP_065416.1| (XM_065416) similar to fibulin 1 isoform C precursor (H. sapiens) [Homo sapiens] mCG21007
9	6.5	gnf1m04964_a_at	NM_026429	I530008A16	trophoblast specific protein beta
10	6.5	gnf1m30794_at	XM_904271	I530030E10	pregnancy-specific glycoprotein 30
11	6.5	gnf1m05493_a_at	NM_029636	1600010J02	cathepsin Q
12	6.5	gnf1m33489_at	XM_916868		pappalysin 2
13	6.4	gnf1m32390_at			inferred: ref|XP_067564.1| (XM_067564) hypothetical protein XP_067564 [Homo sapiens] mCG21029
14	6.4	gnf1m33745_at	NM_054060		pregnancy-specific glycoprotein 25
15	6.3	gnf1m15571_a_at	XM_921301	1600014K23	RIKEN cDNA 1600014K23 gene
16	6.3	gnf1m02675_a_at	NM_011168	1600027O19	prolactin-like protein F
17	6.3	gnf1m05085_a_at	XM_895640	1600000I23	cathepsin 3
18	6.2	gnf1m04302_a_at	NM_023289	I530005M18	CEA-related cell adhesion molecule 11
19	6.2	gnf1m05868_x_at	NM_054063		pregnancy-specific glycoprotein 28
20	6.2	gnf1m11080_a_at	NM_012007	1600023H08	cathepsin J
21	6.2	gnf1m03882_a_at	NM_019991	1600012E17	prolactin-like protein M
22	6.1	gnf1m03922_a_at	NM_020284	3830409D04	cathepsin R
23	6.0	gnf1m04578_a_at	NM_025532	2310047B08	prolactin-like protein K
24	6.0	gnf1m18606_a_at	XM_904257	I530030E10	pregnancy-specific glycoprotein 30
25	5.9	gnf1m05311_at	NM_028477	1600017L04	prolactin like protein C delta
26	5.9	gnf1m17882_at		8030442B19	pregnancy specific glycoprotein 16
27	5.8	gnf1m07686_a_at	NM_023741	I530009E04	prolactin-like protein C 3
28	5.7	gnf1m04093_a_at	NM_021445	1600022N02	cathepsin 6
29	5.7	gnf1m11084_a_at	NM_009411	2610015G13	trophoblast specific protein alpha
30	5.7	gnf1m11083_a_at	XM_895696	1600027J17	cathepsin M
31	5.7	gnf1m08759_at	NM_173420	D930020E02	RIKEN cDNA D930020E02 gene
32	5.6	gnf1m05138_a_at	NM_028171	I530025P09	CEA-related cell adhesion molecule 13
33	5.5	gnf1m06261_a_at	NM_138648		oxidized low density lipoprotein (lectin-like) receptor 1
34	5.5	gnf1m11081_a_at	NM_008865	I530016N24	chorionic somatomammotropin hormone 2
35	5.5	gnf1m09346_s_at	NM_181852	I530023D16	proliferin
36	5.4	gnf1m04824_a_at	NM_026087	I530016C18	CEA-related cell adhesion molecule 12
37	5.3	gnf1m11077_a_at	NM_011167	1600017E04	prolactin-like protein C 1
38	5.3	gnf1m11078_a_at	NM_023332	1600019F10	prolactin-like protein C 2
39	5.3	gnf1m02746_a_at	NM_011328	I530009D06	secretin
40	5.2	gnf1m01850_a_at	NM_009364	3830413B11	tissue factor pathway inhibitor 2
41	5.2	gnf1m04776_a_at	NM_025957	1600025E09	CEA-related cell adhesion molecule 14
42	5.1	gnf1m01635_a_at	NM_008955	3830418K07	reproductive homeobox 6
43	5.0	gnf1m11071_a_at	NM_011455	1600002F03	serine (or cysteine) peptidase inhibitor, clade B, member 9f

44	5.0	gnf1m02650_x_at	NM_011118		proliferin 2
45	5.0	gnf1m19297_a_at	NM_001033424	I530025D16	RIKEN cDNA 5031408O05 gene
46	4.9	gnf1m30812_at	XM_907647		gene model 719, (NCBI)
47	4.9	gnf1m11543_a_at	NM_028958	4933438I11	TAF7-like RNA polymerase II, TATA box binding protein (TBP)-associated factor
48	4.8	gnf1m00926_a_at	NM_007677		pregnancy specific glycoprotein 17
49	4.8	gnf1m15536_at		4930486L24	RIKEN cDNA 4930486L24 gene
50	4.6	gnf1m16953_a_at	NM_027512	C430021A01	RIKEN cDNA 3830417A13 gene
51	4.6	gnf1m05252_at	NM_028045	1600014E20	RIKEN cDNA 1600014E20 gene
52	4.6	gnf1m19995_at		A130029G22	hypothetical protein
53	4.6	gnf1m11323_a_at	NM_011453	5031401I15	serine (or cysteine) peptidase inhibitor, clade B, member 9c
54	4.5	gnf1m17335_at	XM_919174	4933402E13	RIKEN cDNA 4933402E13 gene
55	4.5	AFFX-TransRecMur/X57349_5_at			0
56	4.5	gnf1m00788_a_at	NM_007423	I920085C12	alpha fetoprotein
57	4.5	gnf1m29081_s_at	XM_908287	I530025D16	RIKEN cDNA 5031408O05 gene
58	4.4	AFFX-TransRecMur/X57349_3_at			0
59	4.4	gnf1m02205_at	NM_010088	I530026J03	decidual/trophoblast prolactin-related protein
60	4.4	gnf1m09276_s_at	XM_895253	3830412A07	prolactin like protein O
61	4.4	gnf1m00108_at	NM_008764	I530030F10	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)
62	4.3	gnf1m02812_a_at	NM_011456	C430007E01	serine (or cysteine) peptidase inhibitor, clade B, member 9e
63	4.3	gnf1m05136_a_at	XM_904843	1600015I10	RIKEN cDNA 1600015I10 gene
64	4.3	gnf1m04385_a_at	NM_023894	1600026O01	reproductive homeobox 9
65	4.3	gnf1m05649_a_at	NM_031254	F730040N08	triggering receptor expressed on myeloid cells 2
66	4.3	gnf1m20286_s_at	NM_001005863	F430107K21	mitochondrial tumor suppressor 1
67	4.2	AFFX-TransRecMur/X57349_M_at			0
68	4.2	gnf1m05257_a_at	NM_028066	1600027G01	coagulation factor XI
69	4.2	gnf1m17336_a_at	XM_919174	4933402E13	RIKEN cDNA 4933402E13 gene
70	4.2	gnf1m03557_s_at	NM_017378	G630096J22	protocadherin 12
71	4.2	gnf1m19802_at		9530076L18	hypothetical protein 9530076L18
72	4.1	gnf1m33493_at	NM_054064	C430030O18	pregnancy-specific glycoprotein 29
73	4.1	gnf1m09438_s_at	NM_028455	E430007O20	RIKEN cDNA 3110043J09 gene
74	4.1	gnf1m34547_at	NM_001009549		zinc finger protein 36, C3H type-like 3
75	4.1	gnf1m02813_s_at	NM_011456	C430007E01	serine (or cysteine) peptidase inhibitor, clade B, member 9e
76	4.1	gnf1m30811_at	XM_907647		gene model 719, (NCBI)
77	4.0	gnf1m34992_at	XM_894724		VH coding region
78	4.0	gnf1m13239_a_at	NM_010720	I830071L07	lipase, endothelial
79	4.0	gnf1m06022_a_at	NM_133661		solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12
80	4.0	gnf1m01914_a_at	NM_009475		proline-rich acidic protein 1

No. 14, skeletal muscle specific genes

#1	#2	#3	#4	#5	#6
1	6.7	gnf1m03905_at	NM_020033	4833407M17	ankyrin repeat domain 2 (stretch responsive muscle)
2	6.4	gnf1m01571_a_at	NM_173021	B230365M07	phosphorylase kinase alpha 1
3	6.2	gnf1m07402_a_at	NM_153786	D930008K19	vestigial like 2 homolog (Drosophila)
4	5.9	gnf1m34804_x_at	NM_206870		alpha-interferon
5	5.8	gnf1m31922_at			ENSMUST00000087566 transcript (in rel.37.34e)
6	5.6	gnf1m30823_a_at		2310033H20	calcium channel, voltage-dependent, gamma subunit 6
7	5.6	gnf1m20338_a_at	NM_001013799	A530098C11	RIKEN cDNA A530098C11 gene
8	5.5	gnf1m05628_a_at	NM_031173	F630207K13	calcium channel, voltage-dependent, beta 1 subunit
9	5.4	gnf1m05245_a_at	NM_028001	2310032K21	RIKEN cDNA 2300003C06 gene
10	5.4	gnf1m11854_at	NM_026056	7630403A08	CAP, adenylate cyclase-associated protein, 2 (yeast)
11	5.3	gnf1m27133_at		C630012A10	DUAL-SPECIFICITY PHOSPHATASE TS-DSP1 homolog [Mus musculus]
12	5.2	gnf1m05911_a_at	NM_080466	A030001A14	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3
13	5.1	gnf1m30505_a_at		6030430B11	hypothetical Zinc finger, C2H2 type containing protein
14	5.1	gnf1m02082_a_at	NM_009813		calsequestrin 1
15	5.1	gnf1m31732_at			ENSMUST00000058085 transcript (in rel.37.34e)
16	5.0	gnf1m32501_at			inferred: ref|NP_031464.1| (NM_007438) aldolase 1, A isoform [Mus musculus] mCG20022
17	4.9	gnf1m00652_a_at	NM_177776	D830039B09	RIKEN cDNA D130058I21 gene
18	4.9	gnf1m05478_a_at	NM_029569	1110018D09	ankyrin repeat and SOCs box-containing protein 5
19	4.9	gnf1m09475_a_at	NM_133723	2310005F16	aspartate-beta-hydroxylase
20	4.8	gnf1m32144_x_at			ENSMUST00000071116 transcript (in rel.37.34e)
21	4.8	gnf1m03409_a_at	NM_015825		SH3-binding domain glutamic acid-rich protein
22	4.8	gnf1m35257_at	XM_911774		similar to Fructose-bisphosphate aldolase A (Muscle-type aldolase) (Aldolase 1)
23	4.8	gnf1m31500_at	NM_011652		titin
24	4.7	gnf1m23094_at		1110018A23	asparagine-linked glycosylation 2 homolog (yeast, alpha-1,3-mannosyltransferase)
25	4.7	gnf1m03011_a_at	NM_011892	4833420L09	sarcoglycan, gamma (dystrophin-associated glycoprotein)
26	4.7	gnf1m31979_at			similar to interferon inducible GTPase similar to interferon-inducible GTPase mCG6032
27	4.7	gnf1m35934_x_at			inferred: ref|XP_060406.1| (XM_060406) similar to diaphanous homologue (H. sapiens) [Homo sapiens] mCG1036717
28	4.7	gnf1m34324_at	XM_905672		gene model 1075, (NCBI)
29	4.6	gnf1m18462_a_at	NM_027551	I920029E19	RIKEN cDNA 4631423F02 gene
30	4.6	gnf1m32122_at	NM_001033042	I920022E05	expressed sequence AI595366
31	4.6	gnf1m03360_a_at	XM_924012	E970023J21	calcium channel, voltage-dependent, L type, alpha 1S subunit
32	4.6	gnf1m19063_at		A230005G17	ankyrin repeat and SOCS box-containing 16
33	4.6	gnf1m33481_at			inferred: ref|NP_058704.1| (NM_017008) glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus] mCG123870
34	4.6	gnf1m31103_at	XM_358900		rabphilin 3A-like (without C2 domains)
35	4.6	gnf1m14303_at		2310074I15	titin
36	4.6	gnf1m23260_at		2310058C22	myosin, heavy polypeptide 1, skeletal muscle, adult
37	4.5	gnf1m21860_a_at	XM_919342	9830004H17	myosin, light polypeptide kinase 2, skeletal muscle
38	4.5	gnf1m32807_at	NM_011652		titin
39	4.5	gnf1m32799_at	XM_912786		similar to tripartite motif-containing 63
40	4.4	gnf1m17057_at	XM_907184	2310015B20	RIKEN cDNA 2310015B20 gene
41	4.4	gnf1m33513_at	XM_905086		similar to Triosephosphate isomerase (TIM) (Triose-phosphate isomerase)
42	4.4	gnf1m08139_a_at	NM_177707	9830125E18	SH3 and cysteine rich domain 3
43	4.4	gnf1m11347_a_at	NM_080444	D830047D19	ankyrin repeat and SOCS box-containing protein 10
44	4.4	gnf1m25405_s_at	NM_172381	A730048I18	expressed sequence AI314180
45	4.4	gnf1m11169_a_at	NM_023784	2310016N21	Yip1 domain family, member 7
46	4.4	gnf1m22171_at		C230096H19	hypothetical protein
47	4.3	gnf1m31602_x_at			inferred: gb|AAK91790.1| (AY042194) MrgA4 RF-amide G protein-coupled receptor [Mus musculus] mCG62041
48	4.3	gnf1m01879_a_at	NM_009416	3302001K05	tropomyosin 2, beta
49	4.3	gnf1m12991_a_at	NM_080856	D830023M13	ankyrin repeat and SOCS box-containing protein 14
50	4.3	gnf1m19330_a_at	XM_916258	5430424A14	leiomodin 3 (fetal)
51	4.3	gnf1m30611_s_at	NM_009109	A630095L05	ryanodine receptor 1, skeletal muscle
52	4.3	gnf1m03459_a_at	NM_016749	4833439E12	myosin binding protein H
53	4.3	gnf1m18333_s_at	XM_905765	A330094N09	myopalladin
54	4.3	gnf1m34867_at			inferred: gb|AAL61273.1| (AY073610) olfactory receptor MOR256-19 [Mus musculus] mCG56478
55	4.3	gnf1m13416_a_at		1110058D09	ankyrin repeat domain 23
56	4.3	gnf1m32724_at	NM_001013013		dehydrogenase/reductase (SDR family) member 7C
57	4.2	gnf1m22074_at		C130073O12	16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130073O12 product:hypothetical protein, full insert sequence
58	4.2	gnf1m09174_a_at		4933417I20	aldolase 1, A isoform, pseudogene 2
59	4.2	gnf1m01743_a_at	NM_009161	2310066C16	sarcoglycan, alpha (dystrophin-associated glycoprotein)
60	4.2	gnf1m10776_a_at	NM_021508	A630045E02	myozenin 1
61	4.2	gnf1m16196_s_at	NM_011743	4832420E07	zinc finger protein 106
62	4.2	gnf1m31378_x_at			inferred: ref|NP_032110.1| (NM_008084) glyceraldehyde-3-phosphate dehydrogenase [Mus musculus] mCG8986
63	4.2	gnf1m30588_a_at	XM_905765	1110056A04	myopalladin
64	4.2	gnf1m26247_at		B130044G13	hypothetical protein
65	4.2	gnf1m10184_a_at	NM_139297	9030206D14	UDP-glucose pyrophosphorylase 2
66	4.2	gnf1m30069_at			inferred: ref|NP_059127.1| (NM_017431) protein kinase, AMP-activated, gamma 3 non-catalytic subunit [Homo sapiens] mCG133883
67	4.2	gnf1m02316_a_at	NM_010351		goosecoid
68	4.2	gnf1m12411_a_at	NM_175456	C130068O12	actin-binding Rho activating protein
69	4.1	gnf1m28960_at	NM_001033303	9830138J07	adenosine monophosphate deaminase 1 (isoform M)
70	4.1	gnf1m32530_at			inferred: ref|NP_032110.1| (NM_008084) glyceraldehyde-3-phosphate dehydrogenase [Mus musculus] mCG13844
71	4.1	gnf1m14380_at		3110004A18	5'-nucleotidase, cytosolic III
72	4.1	gnf1m21614_a_at	NM_001013826	1110056B09	similar to Dual specificity protein phosphatase 13 (Testis- and skeletal-muscle-specific DSP)
73	4.1	gnf1m02630_a_at			phosphorylase kinase gamma 1
74	4.1	gnf1m32115_x_at			inferred: ref|NP_032110.1| (NM_008084) glyceraldehyde-3-phosphate dehydrogenase [Mus musculus] mCG22107
75	4.1	gnf1m04580_a_at	NM_025535	2900019I22	SAR1 gene homolog B (S. cerevisiae)
76	4.1	gnf1m10852_a_at	XM_925724	5230400G09	hemochromatosis type 2 (juvenile) (human homolog)
77	4.1	gnf1m01021_x_at	NM_007846		defensin related cryptdin, related sequence 12
78	4.1	gnf1m03443_a_at	NM_016712	G630091I18	tropomodulin 4
79	4.0	gnf1m32134_at	NM_001013405		DNA segment, Chr 9, ERATO Doi 402, expressed

80	4.0	gnf1m32522_at	XM_906658	9830113L01	similar to triadin 95

No. 15, thymus specific genes

#1	#2	#3	#4	#5	#6
1	6.5	gnf1m22768_at		G630024G08	hypothetical protein
2	5.9	gnf1m04258_s_at	NM_023064	4930403I07	RIKEN cDNA 1700021K02 gene
3	5.8	gnf1m25105_a_at		9630050A10	unclassifiable
4	5.6	gnf1m13663_at		8230401J17	Stam binding protein like 1
5	5.6	gnf1m22627_a_at		E430014B02	RIKEN cDNA E430014B02 gene
6	5.6	gnf1m04257_a_at	NM_023064	E430019H22	RIKEN cDNA 1700021K02 gene
7	5.4	gnf1m20000_a_at		A130034K24	RIKEN cDNA A130034K24 gene
8	5.4	gnf1m16764_at		2810043O03	RIKEN cDNA 2810043O03 gene
9	5.4	gnf1m22098_at		C130095N07	unclassifiable
10	5.3	gnf1m13107_a_at	NM_009345	E430024C24	deoxynucleotidyltransferase, terminal
11	5.3	gnf1m01663_a_at	NM_009019	E430001F04	recombination activating gene 1
12	5.2	gnf1m17589_at			gb=X00439 Mouse thymocyte mRNA fragment for T-cell receptor pseudogene (86T3)
13	5.1	gnf1m20254_a_at		A430093H23	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430093H23 product:unclassifiable, full insert sequence
14	4.9	gnf1m00613_at	NM_009913	4632401H02	chemokine (C-C motif) receptor 9
15	4.9	gnf1m25913_a_at		A630097D09	ankyrin repeat domain 10
16	4.8	gnf1m25851_at		A630050N17	epsilon-tubulin 1
17	4.8	gnf1m27467_a_at		D130059J10	nuclear factor of activated T-cells, cytoplasmic 3
18	4.8	gnf1m25325_at		C920018K02	T-cell receptor beta, variable 13
19	4.8	gnf1m25811_at		A630024J20	CD3 antigen, epsilon polypeptide
20	4.8	gnf1m21369_at		D330030A04	unclassifiable
21	4.8	gnf1m21843_at		I830153K09	unclassifiable
22	4.7	gnf1m20488_at		A730051E03	unclassifiable
23	4.7	gnf1m11598_s_at	NM_133206	9630029E07	zinc and ring finger 1
24	4.7	gnf1m20046_at		A130077L17	transcription factor 7, T-cell specific
25	4.7	gnf1m08796_at	NM_178666	E430004N04	RIKEN cDNA E430004N04 gene
26	4.7	gnf1m13686_at		C630040K21	RIKEN cDNA C630040K21 gene
27	4.6	gnf1m20026_at		A130055N14	unclassifiable
28	4.6	gnf1m25793_at		A630007H13	T-cell receptor alpha chain precursor V-J region (TA72) (fragment) homolog [Mus musculus]
29	4.6	gnf1m03450_a_at	NM_016720	C730047I07	neuraminidase 3
30	4.6	gnf1m25650_at		A430104A14	special AT-rich sequence binding protein 1
31	4.6	gnf1m28074_at		E130002N09	RIKEN cDNA A430106G13 gene
32	4.6	gnf1m06569_at	NM_145566		HIV-1 Rev binding protein-like
33	4.6	gnf1m20228_at		A430046P16	hypothetical protein
34	4.6	gnf1m27019_at		C430005I18	cDNA sequence BC023882
35	4.5	gnf1m12132_at	XM_909371	A130010M04	RIKEN cDNA 5830406J20 gene
36	4.5	gnf1m18858_a_at	NM_198297	A430035I04	T cell receptor associated transmembrane adaptor 1
37	4.5	gnf1m28369_s_at		E430013N08	RIKEN cDNA 1110007A06 gene
38	4.4	gnf1m02686_a_at	NM_011195		pre T-cell antigen receptor alpha
39	4.4	gnf1m21857_a_at		9630045H20	RIKEN cDNA 9630045H20 gene
40	4.4	gnf1m01333_a_at	NM_008418		potassium voltage-gated channel, shaker-related subfamily, member 3
41	4.4	gnf1m13655_s_at		E430032M10	T-cell receptor gamma, variable 4
42	4.4	gnf1m20342_at		A630005I04	RIKEN cDNA A630005I04 gene
43	4.4	gnf1m14243_at		5530401D11	RIKEN cDNA 5530401D11 gene
44	4.4	gnf1m21085_a_at		E430002K11	RIKEN cDNA C230085N15 gene
45	4.4	gnf1m17830_at		C920008N22	RIKEN cDNA C920008N22 gene
46	4.4	gnf1m25080_at		9630042D24	unclassifiable
47	4.4	gnf1m19341_at		5830444F18	RIKEN cDNA 5830444F18 gene
48	4.3	gnf1m04270_a_at	NM_023137	2010309G22	ubiquitin D
49	4.3	gnf1m25648_at		A430103G07	inferred: Mouse (clone RAD11) T-cell receptor rearranged delta-chain mRNA V-D-J-C region, 3' end
50	4.3	gnf1m25146_at		9830125P17	myeloblastosis oncogene
51	4.3	gnf1m25878_at		A630074B15	nuclear receptor coactivator 6 interacting protein
52	4.3	gnf1m13884_at			Mouse T cell receptor mRNA /cds=UNKNOWN /gb=M97158 /gi=200865 /len=1093 gnl|UG|Mm#S121750
53	4.3	gnf1m21072_at	NM_207265	C230071H18	RIKEN cDNA C230071H18 gene
54	4.3	gnf1m27741_a_at		D430042L22	Adult male thymus cDNA, RIKEN full-length enriched library, clone:5830431N23 product:unclassifiable, full insert sequence
55	4.3	gnf1m27277_at		D030017L14	RAB14, member RAS oncogene family
56	4.3	gnf1m13116_a_at	NM_177194	E430003K09	RIKEN cDNA A130023I24 gene
57	4.2	gnf1m20047_at		A130077N19	unclassifiable
58	4.2	gnf1m07721_a_at		E430026B20	thyroid hormone receptor associated protein 2
59	4.2	gnf1m19347_at		5830468D02	unclassifiable
60	4.2	gnf1m25123_a_at		A130079G03	RIKEN cDNA A130001G05 gene
61	4.2	gnf1m19996_at		A130029H20	unclassifiable
62	4.2	gnf1m01729_a_at	NM_009138	4921533C11	chemokine (C-C motif) ligand 25
63	4.2	gnf1m18624_a_at		9030625I09	RIKEN cDNA 1700069O15 gene
64	4.2	gnf1m02324_a_at	NM_010364	I530030O21	general transcription factor II H, polypeptide 4
65	4.2	gnf1m24091_s_at		A130043E07	similar to T-cell receptor alpha chain V region CTL-F3 precursor [Mus musculus]
66	4.1	gnf1m20621_at	NM_001001497	A930013B10	RIKEN cDNA A930013B10 gene
67	4.1	gnf1m25293_at		A130022O15	protease, serine, 16 (thymus)
68	4.1	gnf1m29160_s_at		9230110J10	hypothetical protein
69	4.1	gnf1m20028_at		A130058I09	unclassifiable
70	4.1	gnf1m18427_a_at		E430019C18	RIKEN cDNA 2600010L24 gene
71	4.1	gnf1m23837_at		4932439N05	DIPEPTIDYL PEPTIDASE 8 homolog [Homo sapiens]
72	4.0	gnf1m27907_at		D930002G07	unclassifiable
73	4.0	gnf1m05850_a_at	NM_181664	A630014J17	cysteine-rich protein 3
74	4.0	gnf1m34314_at			similar to T-cell receptor beta chain VNDNJC precursor

No. 16, snout epidermis specific genes

#1	#2	#3	#4	#5	#6
1	6.8	gnf1m32364_at	XM_910151	7530403J15	similar to Serpinb6c protein
2	6.3	gnf1m05120_a_at	NM_027105	2310002B14	RIKEN cDNA 2310002B14 gene
3	5.8	gnf1m03864_a_at	NM_019956	1110055M01	keratin complex 2, basic, gene 6g
4	5.7	gnf1m03246_a_at	NM_013707		keratin associated protein 14
5	5.5	gnf1m03251_at	NM_013713		keratin associated protein 15
6	5.4	gnf1m02466_a_at	NM_010666	5430409L11	keratin complex-1, acidic, gene C29
7	5.4	gnf1m07746_a_at	NM_130857	A030006N06	keratin associated protein 16-5
8	5.3	gnf1m31127_a_at		I920089L09	ADP-ribosylhydrolase like 2
9	5.3	gnf1m12125_a_at	NM_175424	A030004J04	RIKEN cDNA A030004J04 gene
10	5.2	gnf1m33887_at	XM_906239		diacylglycerol O-acyltransferase 2-like 3
11	5.2	gnf1m03667_at	NM_019398		eosinophil-associated, ribonuclease A family, member 5
12	5.2	gnf1m05531_a_at	XM_919025	A030005L19	RIKEN cDNA A030005L19 gene
13	5.1	gnf1m02617_a_at	NM_011060		peptidyl arginine deiminase, type III
14	5.0	gnf1m08678_at	NM_177661	C130079G13	RIKEN cDNA C130079G13 gene
15	5.0	gnf1m31483_at			uncharacterized Celera prediction mCG2980
16	5.0	gnf1m02738_a_at	NM_011310	5430416K16	S100 calcium binding protein A3
17	4.9	gnf1m05210_a_at	NM_027844	4833428E21	keratin associated protein 5-2
18	4.9	gnf1m18889_at	XM_919033	A030014E15	RIKEN cDNA A030014E15 gene
19	4.8	gnf1m13773_at	XM_917709	5530401F02	keratin associated protein 8-1
20	4.8	gnf1m00244_a_at	NM_153108		defensin beta 8
21	4.8	gnf1m16351_at	XR_000508	A030006P16	RIKEN cDNA A030006P16 gene
22	4.8	gnf1m31507_at	XM_916083		similar to arylacetamide deacetylase
23	4.7	gnf1m03509_a_at	NM_016880	4833411P03	keratin complex 1, acidic, gene 24
24	4.7	gnf1m29350_a_at	XM_904709		keratin complex 1, acidic, gene 3
25	4.7	gnf1m13744_a_at	NM_010668	4732448G14	keratin complex 2, basic, gene 17
26	4.6	gnf1m05238_a_at	NM_027983	A030014I10	RIKEN cDNA 2310015J09 gene
27	4.6	gnf1m05741_at	NM_033478		lymphocyte antigen 6 complex, locus G6D
28	4.6	gnf1m04203_a_at	NM_022322	4833424O07	tenomodulin
29	4.6	gnf1m05207_a_at	NM_027819	9030405D14	gamma-glutamyltransferase 6
30	4.6	gnf1m13603_at		A030001H12	keratin associated protein 5-5
31	4.6	gnf1m05953_at	NM_130870		keratin associated protein 16-1
32	4.6	gnf1m02471_a_at	NM_010676		keratin associated protein 8-2
33	4.5	gnf1m11033_s_at	NM_007703	1300004I20	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 3
34	4.5	gnf1m16438_at		2310040C09	RIKEN cDNA 2310040C09 gene
35	4.5	gnf1m05873_at	NM_054074		defensin beta 6
36	4.5	gnf1m28699_a_at	NM_001033171	G830034J03	RIKEN cDNA 2310020F24 gene
37	4.5	gnf1m06689_a_at	NM_146063	4733401E22	cDNA sequence BC031593
38	4.4	gnf1m05849_a_at	NM_053249		keratin complex 2, basic, gene 20
39	4.4	gnf1m13354_a_at	XM_919110	5530401N06	RIKEN cDNA 5530401N06 gene
40	4.4	gnf1m32206_at			gene model 247, (NCBI)
41	4.4	gnf1m06048_a_at	NM_133730	4631426H08	RIKEN cDNA 4631426H08 gene
42	4.3	gnf1m03967_at	NM_020576	A030012F01	psoriasis susceptibility 1 candidate 2 (human)
43	4.3	gnf1m17405_a_at	NM_028973	5430427N11	leucine rich repeat containing 15
44	4.3	gnf1m17069_a_at	XM_894986	4632435A09	G protein-coupled receptor 115
45	4.2	gnf1m15703_at			keratin associated protein 16-9
46	4.2	gnf1m05066_at	NM_026807	1110033F04	RIKEN cDNA 1110033F04 gene
47	4.2	gnf1m21863_a_at	XM_919372	9930021F22	diacylglycerol O-acyltransferase 2-like 6
48	4.2	gnf1m08176_a_at	NM_177723	A030011M19	hypothetical protein A030011M19
49	4.2	gnf1m02463_a_at	NM_010663		keratin complex 1, acidic, gene 17
50	4.2	gnf1m06678_a_at	NM_146030	F630041G20	pleckstrin homology domain containing, family H (with MyTH4 domain) member 3
51	4.2	gnf1m11415_a_at	NM_008127	4733401H10	gap junction membrane channel protein beta 4
52	4.2	gnf1m29988_a_at	NM_010667	4732481L17	keratin complex 2, basic, gene 10
53	4.1	gnf1m30692_a_at		9130204L05	RIKEN cDNA 9130204L05 gene
54	4.1	gnf1m02470_a_at	NM_010673		keratin associated protein 6-2
55	4.1	gnf1m29164_a_at	XM_925719	2310051B22	X-ray repair complementing defective repair in Chinese hamster cells 1
56	4.1	gnf1m21868_at		A030010G24	6 days neonate skin cDNA, RIKEN full-length enriched library, clone:A030010G24 product:hypothetical protein, full insert sequence
57	4.1	gnf1m05184_a_at	NM_027563	4733401E01	keratin complex 1, acidic, gene 4
58	4.1	gnf1m21643_at	XM_905488	4833413O15	RIKEN cDNA 4833413O15 gene
59	4.1	gnf1m29218_a_at	XM_130987	5430417P09	retinoic acid receptor responder (tazarotene induced) 1
60	4.0	gnf1m06739_a_at	NM_146213	A030007M20	cDNA sequence BC026374
61	4.0	gnf1m14590_a_at	XM_916112	4930449A18	RIKEN cDNA 4930449A18 gene
62	4.0	gnf1m15601_at	NM_183189		keratin associated protein 13-1
63	4.0	gnf1m15672_at	NM_001013823		similar to keratin associated protein 4-10; keratin associated protein 4.10
64	4.0	gnf1m09801_s_at	NM_016879	4732459O18	keratin complex 2, basic, gene 18
65	4.0	gnf1m15543_at	XM_924606	1110030O19	kallikrein 5
66	4.0	gnf1m19951_at		A030004L08	gene model 312, (NCBI)
67	4.0	gnf1m05296_a_at		2810039D03	angiopoietin-like 1
68	4.0	gnf1m05946_a_at	NM_130856	1110002D05	keratin associated protein 16-8

No. 17, mammary gland (lact) specific genes

#1	#2	#3	#4	#5	#6
1	7.4	gnf1m10696_a_at	NM_133892	D730001H10	L-amino acid oxidase 1

2	7.1	gnf1m03113_a_at	NM_013483	D730003G03	butyrophilin, subfamily 1, member A1
3	7.1	gnf1m12986_a_at	NM_009973	D730045O16	casein delta
4	7.0	gnf1m02472_a_at	NM_010679		lactalbumin, alpha
5	6.7	gnf1m10796_a_at	NM_011709	D730001D15	whey acidic protein
6	6.7	gnf1m00987_a_at	NM_007784	D730016P16	casein alpha
7	6.5	gnf1m15416_a_at			casein kappa
8	6.5	gnf1m32098_at			inferred: ref|NP_055712.1|(NM_014897) KIAA0924 protein [Homo sapiens] mCG3800
9	6.3	gnf1m00588_a_at	NM_009972	D730049P05	casein beta
10	6.3	gnf1m33440_at	XM_904420		similar to Golgi autoantigen, golgin subfamily A member 2 (Golgi matrix protein GM130)
11	5.9	gnf1m27777_s_at	NM_199009	I420028O07	RIKEN cDNA 4632419K20 gene
12	5.9	gnf1m00988_at	NM_007785	D730050N06	casein gamma
13	5.8	gnf1m08137_at	NM_172732	9830005G06	C-type lectin domain family 9, member a
14	5.8	gnf1m30289_a_at		4732460E09	lysyl-tRNA synthetase, pseudogene 1
15	5.5	gnf1m02199_a_at			dentin sialophosphoprotein
16	5.5	gnf1m26737_at		C130045M15	expressed sequence AI197445
17	5.4	gnf1m05767_a_at	NM_033618		suppressor of Ty 16 homolog (S. cerevisiae)
18	5.3	gnf1m00179_at	NM_022317	G830037O11	solute carrier family 28 (sodium-coupled nucleoside transporter), member 3
19	5.2	gnf1m28323_at		E330031L19	RIKEN cDNA 4432405B04 gene
20	5.1	gnf1m26667_at		C130015N15	unclassifiable
21	5.1	gnf1m15655_x_at			Mouse Similar to L1 repeat, Tf subfamily, member 30, clone MGC:7372 IMAGE:3487559, mRNA, complete cds /cds=(1160,1303) /gb=BC007159 /gi=13938088 /len=2021 gnl|UG|Mm#S2050031
22	5.0	gnf1m35992_at			inferred: gb|AAC14131.1|(AF057564) putative retrovirus-related gag protein [Rattus norvegicus] mCG1032495
23	5.0	gnf1m13932_x_at			Mouse clone IMAGE:3674789, mRNA, partial cds /cds=UNKNOWN /gb=BC019591 /gi=18044323 /len=1114 gnl|UG|Mm#S2534025
24	4.9	gnf1m35483_at			inferred: ref|NP_035895.1|(NM_011765) zinc finger protein 97 [Mus musculus] mCG1029834
25	4.9	gnf1m06823_x_at	NM_146370		olfactory receptor 47
26	4.8	gnf1m27835_at		D730002K16	casein alpha
27	4.8	gnf1m18116_at		3732413O03	plasma membrane proteolipid
28	4.8	gnf1m28885_at	NM_175936		cDNA sequence AJ543404
29	4.7	gnf1m24682_at		9230118I10	ceruloplasmin
30	4.7	gnf1m21715_at		5031438A03	RIKEN cDNA 5031438A03 gene
31	4.6	gnf1m24385_at		6430528J02	hypothetical Ribosome recycling factor containing protein
32	4.6	gnf1m25197_at		9930001L01	cofactor required for Sp1 transcriptional activation, subunit 2
33	4.5	gnf1m01436_a_at	NM_008594	I830047G19	milk fat globule-EGF factor 8 protein
34	4.5	gnf1m17416_a_at	XM_905179	4933439G10	tetratricopeptide repeat domain 9
35	4.5	gnf1m16416_a_at		2810455O05	RIKEN cDNA 2810455O05 gene
36	4.4	gnf1m06955_at	NM_146779		olfactory receptor 196
37	4.4	gnf1m28950_a_at	XR_000481		gene model 566, (NCBI)
38	4.4	gnf1m34258_x_at			inferred: ref|NP_058797.1|(NM_017101) peptidylprolyl isomerase A (cyclophilin A) [Rattus norvegicus] mCG8332
39	4.3	gnf1m10367_a_at	NM_133709	1810022C01	chordin-like 2
40	4.3	gnf1m32837_at	XM_909329		OVO homolog-like 3 (Drosophila)
41	4.3	gnf1m09034_at	NM_001011525		olfactory receptor 1415
42	4.3	gnf1m05718_a_at	NM_033072	K430314N15	methyl-CpG binding domain protein 6
43	4.3	gnf1m27502_at	XM_925219	F830013L16	RIKEN cDNA 9430038I01 gene
44	4.3	gnf1m21947_at		A830015M10	unclassifiable
45	4.3	gnf1m14534_at		4933416A02	RIKEN cDNA 4933416A02 gene
46	4.2	gnf1m34962_at	XM_912363		similar to malate dehydrogenase, mitochondrial
47	4.2	gnf1m24652_s_at	XM_889153		hypothetical protein LOC624610
48	4.2	gnf1m28597_a_at		D730042M18	butyrophilin, subfamily 1, member A1
49	4.2	gnf1m31701_at			uncharacterized Celera prediction mCG55760
50	4.2	gnf1m15778_a_at	NM_008134	D730050C14	glycosylation dependent cell adhesion molecule 1
51	4.2	gnf1m00454_a_at	NM_013912	6030430G11	apelin
52	4.1	gnf1m32208_at			inferred: ref|NP_113808.1|(NM_031620) 3-phosphoglycerate dehydrogenase [Rattus norvegicus] mCG20679
53	4.1	gnf1m22440_a_at	NM_177135	D830030K20	RIKEN cDNA D830030K20 gene
54	4.1	gnf1m33450_at			uncharacterized Celera prediction mCG124428
55	4.1	gnf1m07399_a_at	NM_153782	E030006B12	cDNA sequence BC029169
56	4.1	gnf1m19455_at		6430537K16	RIKEN cDNA 6430537K16 gene
57	4.1	gnf1m11684_a_at	NM_007740	5930402D07	procollagen, type IX, alpha 1
58	4.1	gnf1m13007_at	NM_175280	D930025J04	RIKEN cDNA 4930529M08 gene
59	4.1	gnf1m09929_a_at	NM_145921	E230009B14	thioesterase domain containing 1
60	4.1	gnf1m20091_at		A230020D02	unclassifiable
61	4.0	gnf1m34500_at			inferred: ref|NP_080720.1|(NM_026444) citrate synthase [Mus musculus] mCG1049880
62	4.0	gnf1m21921_a_at		A630021E21	unclassifiable

No. 18, bone marrow specific genes

#1	#2	#3	#4	#5	#6
1	5.6	gnf1m28110_at		E130103H07	inferred: ADP-ribosylation factor-directed GTPase activating protein isoform b {Mus musculus}
2	5.4	gnf1m18248_a_at		E130213N17	unclassifiable
3	5.1	gnf1m14290_a_at	XR_000511	4930456L15	RIKEN cDNA 4930456L15 gene
4	5.1	gnf1m32867_x_at	XM_917898		similar to zinc finger protein 658
5	5.1	gnf1m27552_at		D230014K09	ARP10 actin-related protein 10 homolog (S. cerevisiae)
6	5.0	gnf1m33375_x_at			ENSMUST00000090609 transcript (in rel.37.34e)
7	5.0	gnf1m34742_at	NM_207621		olfactory receptor 553
8	4.8	gnf1m19694_a_at		A730034A12	RIKEN cDNA 9330209N08 gene
9	4.8	gnf1m32725_at	XM_908293		similar to glucagon-like peptide 2 receptor
10	4.7	gnf1m20333_at		A530095B06	hypothetical protein
11	4.7	gnf1m02136_at	NM_009921		cathelicidin antimicrobial peptide
12	4.7	gnf1m24540_at		7330411H24	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4
13	4.6	gnf1m19887_a_at	NM_001002786	9830134C10	RIKEN cDNA 9830134C10 gene
14	4.6	gnf1m15155_at		4833426L05	weakly similar to EUKARYOTIC TRANSLATION INITIATION FACTOR 2 ALPHA KINASE 1 (EC 2.7.1.-) (HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE) (HEME-REGULATED INHIBITOR) (HRI) (HEME-CONTROLLED REPRESSOR) (HCR) (HEMIN-SENSITIVE INITIATION FACTOR-2 ALPHA KINASE) [Mus musculus]
15	4.6	gnf1m08144_a_at	NM_145976	C330008G01	cDNA sequence BC027057
16	4.6	gnf1m21943_at		A730098E24	unclassifiable
17	4.6	gnf1m28319_at		E330031I18	Transcribed locus
18	4.5	gnf1m00065_at	NM_010369	I530023F06	glycophorin A
19	4.5	gnf1m02725_a_at	NM_011280	2510041F02	tripartite motif protein 10
20	4.5	gnf1m32940_at		F930043F05	RIKEN cDNA 2310033K02 gene
21	4.5	gnf1m27124_at		C630003M04	RAB27b, member RAS oncogene family
22	4.5	gnf1m28038_at		E030029M14	Transcribed locus
23	4.4	gnf1m10282_a_at		C730049K16	RIKEN cDNA C730027J19 gene
24	4.4	gnf1m28018_at		E030019E14	moesin
25	4.4	gnf1m23478_at		4631409B15	hypothetical protein
26	4.4	gnf1m10422_a_at	NM_027292	9830132N02	benzodiazapine receptor, peripheral-like 1
27	4.4	gnf1m05996_a_at	NM_133245	2510041L04	erythroid associated factor
28	4.4	gnf1m11882_s_at	NM_178611	A730095M18	leukocyte-associated Ig-like receptor 1
29	4.4	gnf1m03319_a_at	NM_013848	9830164O15	erythroblast membrane-associated protein
30	4.4	gnf1m25867_at		A630061O15	RNA guanylyltransferase and 5'-phosphatase
31	4.3	gnf1m01494_a_at	NM_008694	F420005O16	neutrophilic granule protein
32	4.3	gnf1m20848_at		B830028K19	unclassifiable
33	4.3	gnf1m07499_at		I1C0028I03	ATP synthase 6, mitochondrial
34	4.3	gnf1m34859_at			uncharacterized Celera prediction mCG56733
35	4.3	gnf1m25815_at		A630025C14	unclassifiable
36	4.3	gnf1m02787_a_at	NM_011403	K0C0005O03	solute carrier family 4 (anion exchanger), member 1
37	4.3	gnf1m01169_at	NM_008089	I920074C13	GATA binding protein 1
38	4.3	gnf1m28990_a_at	XM_917669	4930527A11	RIKEN cDNA 2410076I21 gene
39	4.3	gnf1m32465_at	XM_914211		similar to heat shock protein 1, beta
40	4.3	gnf1m13954_at		4933433G08	RIKEN cDNA 4933433G08 gene
41	4.2	gnf1m07500_at		0610041B20	cytochrome b, mitochondrial
42	4.2	gnf1m26753_at		C130052O19	demethyl-Q 7
43	4.2	gnf1m20788_at		B230350J17	unclassifiable
44	4.2	gnf1m20285_at		A530018P15	hypothetical protein
45	4.2	gnf1m02422_a_at	NM_010575	F930117J03	integrin alpha 2b
46	4.2	gnf1m28509_at		F830048D03	UVRAG (FRAGMENT) homolog [Mus musculus]
47	4.1	gnf1m09214_a_at	NM_146317		olfactory receptor 725
48	4.1	gnf1m00558_a_at	NM_026331	C730046J21	solute carrier family 25, member 37
49	4.1	gnf1m20379_at		A630042D17	hypothetical gene supported by AK040104
50	4.1	gnf1m33498_at			uncharacterized Celera prediction mCG123560
51	4.1	gnf1m23222_a_at		2010308F09	RIKEN cDNA 2010308F09 gene
52	4.1	gnf1m12064_at	NM_021384	9830001A05	radical S-adenosyl methionine domain containing 2
53	4.1	gnf1m15634_at			Mouse Similar to AD037 protein, clone MGC:27537 IMAGE:4459337, mRNA, complete cds /cds=(98,748) /gb=BC023245 /gi=23270958 /len=2817 gnl|UG|Mm#S2779056
54	4.1	gnf1m14798_at		4930572C08	RIKEN cDNA 4930572C08 gene
55	4.1	gnf1m15456_at		2610301H18	RIKEN cDNA 2610301H18 gene
56	4.1	gnf1m35431_at			inferred: gb|AAF91328.1|AF246633_1 (AF246633) protease [Mus musculus] mCG1034501
57	4.1	gnf1m02815_a_at	XM_904631	F430201D02	spectrin alpha 1
58	4.0	gnf1m05712_a_at	NM_032540	4432406O14	Kell blood group
59	4.0	gnf1m27280_at		D030019B03	kinesin-like 1
60	4.0	gnf1m31026_s_at		G630020J15	hypothetical LOC434126
61	4.0	gnf1m08210_s_at	NM_145486	E130018A02	membrane-associated ring finger (C3HC4) 2

No. 19, spleen specific genes

#1	#2	#3	#4	#5	#6
1	5.4	gnf1m20804_a_at	NM_183142	6030406L03	expressed sequence AI849156
2	5.3	gnf1m04279_a_at	NM_023182	2300003F21	chymotrypsin-like
3	5.2	gnf1m32666_at	XM_901323	A830029C13	SH3/ankyrin domain gene 2
4	5.1	gnf1m05089_a_at		1810007A24	pancreatic lipase
5	5.0	gnf1m34728_at	XM_908024		similar to melanoma antigen, family B, 2
6	4.9	gnf1m10963_s_at	NM_023182	2300003F21	chymotrypsin-like
7	4.9	gnf1m31687_at	NM_001033419	F930006J18	CEA-related cell adhesion molecule 16
8	4.8	gnf1m04959_a_at	NM_026419	2310074F01	elastase 3, pancreatic
9	4.8	gnf1m04601_a_at	NM_025583	9030613K09	chymotrypsinogen B1
10	4.8	gnf1m01890_at	NM_009430	0910001K11	protease, serine, 2
11	4.8	gnf1m32881_at	XM_906114		RIKEN cDNA 1700027L20 gene
12	4.7	gnf1m01435_a_at	NM_008593		forkhead box D2
13	4.7	gnf1m09567_s_at	NM_011646	2210415M03	trypsin 4
14	4.7	gnf1m30401_a_at	NM_001003405	2210415M03	RIKEN cDNA 1810049H19 gene
15	4.7	gnf1m29989_a_at	NM_033612	1810009A17	elastase 1, pancreatic
16	4.7	gnf1m01060_a_at	NM_007919		elastase 2A
17	4.7	gnf1m02120_a_at	NM_009885	1810019H12	carboxyl ester lipase
18	4.7	gnf1m28804_at	NM_001024698		similar to Carboxypeptidase A2 precursor
19	4.7	gnf1m01676_a_at	NM_009043	2010012A06	regenerating islet-derived 2
20	4.6	gnf1m23206_s_at	NM_029706	2210008M23	carboxypeptidase B1 (tissue)
21	4.6	gnf1m12930_at	NM_010101	D430018B13	endothelial differentiation, sphingolipid G-protein-coupled receptor, 3
22	4.6	gnf1m01675_a_at	NM_009042	5033401N17	regenerating islet-derived 1
23	4.6	gnf1m31774_at	XM_916785		disrupted in schizophrenia 1
24	4.5	gnf1m28562_at		G630034I07	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)
25	4.5	gnf1m24434_at		6430627B09	RIKEN cDNA 0610037L13 gene
26	4.5	gnf1m23254_a_at		A430061F24	zinc finger protein 99
27	4.5	gnf1m07472_a_at	NM_026716	0910001K16	syncollin
28	4.5	gnf1m35851_at	NM_001012269		olfactory receptor 1513
29	4.4	gnf1m14425_at		1700069L16	RIKEN cDNA 1700069L16 gene
30	4.4	gnf1m29398_a_at	NM_029706	0910001A18	carboxypeptidase B1 (tissue)
31	4.4	gnf1m24582_a_at		8030492B03	rad and gem related GTP binding protein 1
32	4.4	gnf1m11108_a_at	NM_011271	1810011N10	ribonuclease, RNase A family, 1 (pancreatic)
33	4.4	gnf1m09672_s_at	NM_134252	0610030P10	transient receptor potential cation channel, subfamily M, member 8
34	4.3	gnf1m04787_a_at	NM_025989	2310046E09	glycoprotein 2 (zymogen granule membrane)
35	4.3	gnf1m33491_at			inferred: ref|NP_035698.1| (NM_011568) RNA and export factor binding protein 1; Tcra enhancer-binding factor interacting protein 1 [Mus musculus] mCG123687
36	4.3	gnf1m07968_at		5330438O12	hypothetical protein
37	4.3	gnf1m23660_at		4833425M04	leucine rich repeat containing 17
38	4.2	gnf1m25786_at		I730057O13	interleukin 2 receptor, alpha chain
39	4.2	gnf1m07266_at	NM_153072	4930577G14	Hus1 homolog b (S. pombe)
40	4.2	gnf1m34431_at			inferred: ref|NP_001763.1| (NM_001772) CD33 antigen (gp67) [Homo sapiens] mCG49602
41	4.2	gnf1m10178_at	NM_177635		histocompatibility 2, M region locus 11
42	4.2	gnf1m11106_a_at	NM_023707	1810009J06	RIKEN cDNA 1810009J06 gene
43	4.2	gnf1m03655_a_at	NM_018874	1810032A23	pancreatic lipase related protein 1
44	4.2	gnf1m13718_at			Mouse RNA for 18.8 family from nasopharyngeal carcinoma tumour /cds=UNKNOWN /gb=X16301 /gi=50759 /len=1419 gnl|UG|Mm#S121968
45	4.1	gnf1m27587_at		D230033C05	similar to CDNA FLJ12949 FIS, CLONE NT2RP2005336, WEAKLY SIMILAR TO TRICHOHYALIN [Homo sapiens]
46	4.1	gnf1m32704_at			inferred: ref|NP_032645.1| (NM_008619) Moloney leukemia virus 10 [Mus musculus] mCG18552
47	4.1	gnf1m24972_at		9530065C24	smoothelin
48	4.1	gnf1m32018_at	XM_907327	G630062J21	dpy-19-like 4 (C. elegans)
49	4.1	gnf1m11686_a_at	XM_915769	F430010A04	similar to E2F transcription factor 7
50	4.1	gnf1m22573_a_at	NM_207252	E130006D01	RIKEN cDNA E130006D01 gene
51	4.1	gnf1m21862_a_at	XM_911566	9830166G18	glycoprotein 6 (platelet)
52	4.1	gnf1m25386_at		A130093M04	inferred: HYPOTHETICAL PROTEIN KIAA0310 (FRAGMENT). [Human] {Homo sapiens}
53	4.1	gnf1m21898_at		A430092C21	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430092C21 product:hypothetical protein, full insert sequence
54	4.1	gnf1m27700_a_at	NM_024241	D430019P19	kinesin family member 24
55	4.1	gnf1m30562_x_at			trypsinogen 16 trypsinogen 16 mCG124046
56	4.0	gnf1m31920_at	XM_910134		cerebellar degeneration-related protein 2-like
57	4.0	gnf1m23200_at		1810012N22	similar to MITOCHONDRIAL 39S RIBOSOMAL PROTEIN L18 (MRP-L18) [Homo sapiens]
58	4.0	gnf1m28805_a_at	NM_025350	1810004B15	carboxypeptidase A1
59	4.0	gnf1m02010_a_at	XM_911199	9130414I10	amylase 2, pancreatic
60	4.0	gnf1m08234_a_at		A530045M11	weakly similar to KIAA1751 PROTEIN (FRAGMENT) [Homo sapiens]

No. 20, tongue specific genes

#1	#2	#3	#4	#5	#6
1	6.6	gnf1m15482_a_at	NM_001033177	9930024P18	RIKEN cDNA 2310001L23 gene
2	6.4	gnf1m05889_a_at	NM_054100	2310034C09	RIKEN cDNA 2310034C09 gene
3	6.3	gnf1m16827_a_at	XM_911145	2300002O18	RIKEN cDNA 2300002O18 gene
4	6.3	gnf1m05131_a_at	NM_027170	2310057N15	RIKEN cDNA 2310057N15 gene
5	6.2	gnf1m25803_at		A630017J09	adenosine deaminase
6	6.2	gnf1m19077_a_at		1110013A16	serine (or cysteine) peptidase inhibitor, clade B, member 3C
7	5.9	gnf1m02469_a_at	NM_010671	1110029H15	keratin associated protein 13
8	5.6	gnf1m14009_at		2310079G19	RIKEN cDNA 2310079G19 gene
9	5.5	gnf1m17002_at	XM_917616	2310061N02	RIKEN cDNA 2310061N02 gene
10	5.4	gnf1m01854_s_at	NM_009374	9930009I11	transglutaminase 3, E polypeptide
11	5.3	gnf1m32664_at	XM_911927		similar to protein kinase Bsk146
12	5.2	gnf1m05243_a_at	NM_027997	2310014L03	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 9
13	5.2	gnf1m15568_at	XM_914283	2310008B01	kallikrein 12
14	5.2	gnf1m11157_a_at	NM_019728	2310011K19	defensin beta 4
15	4.9	gnf1m23262_a_at		4833442E01	keratin complex 1, acidic, gene 13
16	4.8	gnf1m05116_a_at	NM_027087	2300006N05	RIKEN cDNA 2300006N05 gene
17	4.8	gnf1m04342_a_at	NM_023631	2310003G12	aldehyde oxidase 4
18	4.8	gnf1m00001_at	NM_009126		serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3A
19	4.8	gnf1m18383_at	XM_918929	2310001H18	hypothetical LOC545549
20	4.8	gnf1m16119_at	NM_008474		keratin complex 2, basic, gene 16
21	4.8	gnf1m32331_s_at	NM_198680	1110013A16	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3B
22	4.8	gnf1m05236_a_at	NM_027971	A530016D18	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 12
23	4.7	gnf1m13841_at		2310043M15	RIKEN cDNA 2310043M15 gene
24	4.7	gnf1m31812_at			inferred: ref|NP_032502.1| (NM_008476) keratin complex 2, gene 6a; 60-kDa keratin; keratin complex 2, basic, gene 6c [Mus musculus] mCG51665
25	4.7	gnf1m16876_at	XM_918693	4732468B01	keratin complex 1, acidic, gene 5
26	4.7	gnf1m03271_a_at	NM_013756		defensin beta 3
27	4.6	gnf1m02005_a_at	NM_009659	2310043I18	arachidonate 12-lipoxygenase, 12R type
28	4.6	gnf1m28862_a_at	XM_485520	8430427K15	myomesin family, member 3
29	4.6	gnf1m28723_a_at	XM_915395	2310002L13	RIKEN cDNA 2310002L13 gene
30	4.6	gnf1m08163_a_at	NM_175148	9930102M17	RIKEN cDNA 2300002M23 gene
31	4.6	gnf1m01366_a_at	NM_008475		keratin complex 2, basic, gene 4
32	4.6	gnf1m02795_a_at	NM_011414	2310075E18	secretory leukocyte peptidase inhibitor
33	4.5	gnf1m02825_a_at	NM_011478		small proline-rich protein 3
34	4.5	gnf1m15481_at		2310046K23	RIKEN cDNA 2310046K23 gene
35	4.5	gnf1m01363_a_at	NM_008470		keratin complex 1, acidic, gene 16
36	4.5	gnf1m04788_s_at	NM_025990	2310075A07	RIKEN cDNA 2310021H06 gene
37	4.5	gnf1m33717_at	NM_001013756		expressed sequence AI561912
38	4.5	gnf1m10998_a_at	NM_019450	1110033G16	interleukin 1 family, member 6
39	4.5	gnf1m10266_a_at	NM_145369	2310042O12	WAP four-disulfide core domain 5
40	4.5	gnf1m02467_s_at	NM_010669	9930033J10	keratin complex 2, basic, gene 6a
41	4.4	gnf1m06043_a_at	NM_133712	2300002A13	kallikrein 10
42	4.4	gnf1m01721_a_at	NM_009126		serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3A
43	4.3	gnf1m32304_at	NM_199422		S100 calcium binding protein A15
44	4.3	gnf1m04564_a_at	NM_025501	2310007F04	RIKEN cDNA 2310007F04 gene
45	4.3	gnf1m08395_a_at	NM_181490	C130046K08	claudin 17
46	4.3	gnf1m13300_at		1810006M18	envoplakin
47	4.3	gnf1m32847_at	NM_001039042		kallikrein 13
48	4.2	gnf1m01707_a_at	NM_009100	2310079L14	repetin
49	4.1	gnf1m21550_at		E130203F07	unclassifiable
50	4.1	gnf1m29163_a_at	XM_921005	2210418J09	cornifelin
51	4.1	gnf1m29248_a_at	XM_914186	2210412E05	RIKEN cDNA 2210412E05 gene
52	4.1	gnf1m31108_a_at	XM_911951	5430402E13	RIKEN cDNA 2310047D13 gene
53	4.1	gnf1m12016_at	NM_181320	9530081F05	dual specificity phosphatase 16
54	4.1	gnf1m19078_at	XM_902000	4831413C10	similar to keratin associated protein 9-1
55	4.1	gnf1m18385_at		2310002A05	RIKEN cDNA 2310002A05 gene
56	4.0	gnf1m23241_a_at	NM_008476	2310065C01	keratin complex 2, basic, gene 6a
57	4.0	gnf1m15965_at		5530401L02	homologue to ultra-high-sulfur keratin - mouse, complete

No. 21, B220+ B-cells specific genes

#1	#2	#3	#4	#5	#6
1	5.4	gnf1m02337_a_at	NM_010388	F630111I02	histocompatibility 2, class II, locus Mb1
2	5.1	gnf1m12081_a_at	NM_133211	F830106P16	toll-like receptor 7
3	5.1	gnf1m13203_a_at	NM_009835	F830010E07	chemokine (C-C motif) receptor 6
4	4.9	gnf1m03091_a_at	NM_012057	I830045P17	interferon regulatory factor 5
5	4.8	gnf1m32949_at	XM_912889		similar to Ig kappa chain V-IV region B17 precursor
6	4.8	gnf1m32461_at			inferred: gb|AAH17134.1|AAH17134 (BC017134) Unknown (protein for MGC:27649) [Mus musculus] mCG19339
7	4.8	gnf1m13210_a_at	NM_007549	F830045C23	B lymphoid kinase
8	4.7	gnf1m11826_a_at	NM_010387	6720426H23	histocompatibility 2, class II, locus Mb1
9	4.7	gnf1m01290_a_at	NM_008348	I830123K10	interleukin 10 receptor, alpha
10	4.7	gnf1m02101_a_at	NM_009845	F830115L07	CD22 antigen
11	4.7	gnf1m08758_s_at	NM_172681	F630107L10	RIKEN cDNA D930015E06 gene
12	4.6	gnf1m19299_a_at	NM_198642	F630103B16	RIKEN cDNA 5031414D18 gene
13	4.6	gnf1m05259_a_at	NM_028075	F830206F13	tumor necrosis factor receptor superfamily, member 13c

14	4.6	gnf1m11131_a_at	NM_031373	G530131O21	opioid growth factor receptor
15	4.6	gnf1m13807_at		F630206K19	tumor necrosis factor receptor superfamily, member 13b
16	4.6	gnf1m10519_a_at	NM_010386	I920078O06	histocompatibility 2, class II, locus DMa
17	4.5	gnf1m13615_a_at	NM_007758	1810013M23	complement receptor 2
18	4.5	gnf1m16327_a_at		A530066G20	hypothetical protein
19	4.5	gnf1m28507_at		F830036K21	complement receptor 2
20	4.5	gnf1m17260_at	NM_019866		Spi-B transcription factor (Spi-1/PU.1 related)
21	4.5	gnf1m16740_at	NM_181734	F830034J19	RIKEN cDNA 5830472M02 gene
22	4.5	gnf1m13502_s_at	XM_912724		similar to Ig kappa chain V-V region MOPC 21 precursor
23	4.5	gnf1m16986_at	NM_009302	I920052L14	SWA-70 protein
24	4.5	gnf1m02841_a_at	NM_011518	F420003H05	spleen tyrosine kinase
25	4.5	gnf1m05658_a_at	NM_031376	I830174K10	phosphoinositide-3-kinase adaptor protein 1
26	4.4	gnf1m03393_a_at	NM_015790	A630008D12	icos ligand
27	4.4	gnf1m29681_a_at	NM_030098	A230056F18	ribonuclease, RNase A family, 6
28	4.4	gnf1m02495_a_at	NM_010735	F830035M07	lymphotoxin A
29	4.3	gnf1m03132_a_at	NM_013517		Fc receptor, IgE, low affinity II, alpha polypeptide
30	4.3	gnf1m12072_a_at	NM_178165	A230020G22	Fc receptor-like 1
31	4.3	gnf1m32629_a_at		6330574L03	beaded filament structural protein 2, phakinin
32	4.3	gnf1m01227_a_at	NM_008206	F630118D21	histocompatibility 2, O region alpha locus
33	4.3	gnf1m12099_a_at	NM_172900	F830048K03	sialic acid binding Ig-like lectin G
34	4.3	gnf1m10418_a_at	NM_145141	F830204N13	ubiquinol-cytochrome c reductase binding protein
35	4.2	gnf1m34612_at			inferred: gb|AAC18780.1|(M23690) immunoglobulin light chain kappa [Mus musculus] mCG1036442
36	4.2	gnf1m10984_a_at	NM_010745	1110007J13	lymphocyte antigen 86
37	4.2	gnf1m09406_a_at	NM_010407	I830077E17	hemopoietic cell kinase
38	4.2	gnf1m06625_a_at	NM_181318	G430095K03	RasGEF domain family, member 1B
39	4.2	gnf1m34194_at	NM_207246		RAS, guanyl releasing protein 3
40	4.2	gnf1m12131_a_at	NM_028809	A130004L09	actin related protein 2/3 complex, subunit 5-like
41	4.2	gnf1m01929_a_at	NM_009500		Vav2 oncogene
42	4.2	gnf1m11147_a_at	NM_009514	2210401P05	pre-B lymphocyte gene 3
43	4.2	gnf1m04438_a_at	NM_024444	1810054N16	cytochrome P450, family 4, subfamily f, polypeptide 18
44	4.2	gnf1m08243_at	NM_177584	A630002H24	B and T lymphocyte associated
45	4.2	gnf1m02660_a_at	NM_011136	E430020O13	POU domain, class 2, associating factor 1
46	4.1	gnf1m35384_s_at	XM_911979		immunoglobulin kappa chain variable 34 (V34)
47	4.1	gnf1m27099_at		C530043A01	B-cell CLL/lymphoma 11A (zinc finger protein)
48	4.1	gnf1m00864_a_at	NM_007551	F830112L05	Burkitt lymphoma receptor 1
49	4.1	gnf1m10735_a_at	NM_178087	F830014J16	promyelocytic leukemia
50	4.1	gnf1m04527_a_at	NM_025423	1110059E24	RIKEN cDNA 1110059E24 gene
51	4.0	gnf1m00599_a_at	NM_025340	1110008I16	SHANK-associated RH domain interacting protein
52	4.0	gnf1m28628_at	NM_011306	I420027M12	retinoid X receptor beta
53	4.0	gnf1m12251_a_at	NM_172842	E430019B13	lymphocyte transmembrane adaptor 1
54	4.0	gnf1m03379_a_at	NM_015766	F730317H01	Epstein-Barr virus induced gene 3
55	4.0	gnf1m23499_at		4632409G01	unclassifiable
56	4.0	gnf1m26221_a_at	NM_199198	E430029A03	histone deacetylase 10

No. 22, large intestine specific genes

#1	#2	#3	#4	#5	#6
1	7.1	gnf1m05146_a_at	NM_027239	1810065E05	RIKEN cDNA 1810065E05 gene
2	6.7	gnf1m05208_a_at	NM_027832	9130404C18	seminal vesicle antigen-like 1
3	6.4	gnf1m04551_s_at	XM_904677	1810073D07	RIKEN cDNA 1810030J14 gene
4	6.3	gnf1m01218_a_at	NM_008190	2010007F09	guanylate cyclase activator 2a (guanylin)
5	6.0	gnf1m02976_a_at	NM_011831		insulin-like 5
6	5.8	gnf1m04382_a_at		9030012B21	resistin like beta
7	5.7	gnf1m09735_a_at	NM_145474		cDNA sequence BC018285
8	5.7	gnf1m00809_at			angiogenin, ribonuclease A family, member 3
9	5.6	gnf1m13814_at	NM_009880		caudal type homeo box 1
10	5.6	gnf1m16178_at	NM_027220		protease, serine, 32
11	5.4	gnf1m21823_a_at	XM_489685	9130004I05	hypothetical gene supported by AK078896
12	5.4	gnf1m05264_a_at	NM_028089	2010318C06	cytochrome P450, family 2, subfamily c, polypeptide 55
13	5.3	gnf1m30028_a_at	XM_905190	9130012O13	RIKEN cDNA 9130012O13 gene
14	5.2	gnf1m19589_at	NM_177744	9030421J09	RIKEN cDNA 9030421J09 gene
15	5.1	gnf1m09020_at	NM_177544		angiogenin, ribonuclease A family, member 4
16	5.1	gnf1m04467_a_at	NM_025308	2010104G20	RIKEN cDNA 1810007E14 gene
17	5.1	gnf1m10609_a_at	NM_023154	0610025L15	ethylmalonic encephalopathy 1
18	5.0	gnf1m16117_a_at	NM_011463		serine peptidase inhibitor, Kazal type 4
19	4.9	gnf1m28989_a_at	XM_916703	4930516G09	mucin 3, intestinal
20	4.9	gnf1m29326_a_at	NM_027339	9130416C03	RIKEN cDNA 2210415F13 gene
21	4.9	gnf1m00681_a_at	NM_007500	C230040F02	atonal homolog 1 (Drosophila)
22	4.9	gnf1m24650_at		9130013M11	solute carrier family 26, member 3
23	4.9	gnf1m04542_a_at	NM_025453	5033426G15	transmembrane 4 L six family member 20
24	4.8	gnf1m04112_a_at	NM_021475	F830031L06	ADAM-like, decysin 1
25	4.8	gnf1m31167_a_at		4930403C10	RIKEN cDNA 4930403C10 gene
26	4.8	gnf1m34080_at			gene model 1123, (NCBI)
27	4.8	gnf1m08067_a_at	NM_178899	C820005A15	expressed sequence AI987662
28	4.8	gnf1m18855_a_at	XM_922730	C330008K14	RIKEN cDNA C330008K14 gene
29	4.7	gnf1m02497_a_at	NM_010739	3830420G04	mucin 13, epithelial transmembrane
30	4.7	gnf1m22615_a_at		E330039G21	myosin XVB
31	4.7	gnf1m04152_a_at	NM_021610		glycoprotein A33 (transmembrane)
32	4.7	gnf1m00241_s_at	NM_013921	2010015P21	transmembrane protease, serine 8 (intestinal)
33	4.7	gnf1m13512_a_at		C230008K20	cDNA sequence BC023744
34	4.6	gnf1m13126_a_at	NM_027988	E430007K11	NADPH oxidase organizer 1
35	4.5	gnf1m30976_a_at	NM_008100	C820020M20	glucagon
36	4.5	gnf1m04218_a_at	NM_022430	2010004L09	membrane-spanning 4-domains, subfamily A, member 8A
37	4.4	gnf1m02627_a_at	NM_011076		ATP-binding cassette, sub-family B (MDR/TAP), member 1A
38	4.4	gnf1m04633_a_at	NM_025655	2310003K08	transmembrane and immunoglobulin domain containing
39	4.4	gnf1m02779_a_at	NM_011388		solute carrier family 10, member 2
40	4.4	gnf1m30177_a_at	NM_001033364	G630055D06	cDNA sequence BC040758
41	4.4	gnf1m13288_a_at		F830007N10	cadherin 17
42	4.3	gnf1m15280_at		1190002B21	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5
43	4.3	gnf1m02861_a_at	NM_011575	2010306I07	trefoil factor 3, intestinal
44	4.3	gnf1m30033_a_at		2210021I22	glucosaminyl (N-acetyl) transferase 3, mucin type
45	4.2	gnf1m01164_a_at	NM_008081		beta-1,4-N-acetyl-galactosaminyl transferase 2
46	4.2	gnf1m10113_a_at	NM_145435	C820007C10	peptide YY
47	4.2	gnf1m00826_a_at	NM_007474	I920039O06	aquaporin 8
48	4.1	gnf1m19593_at		9030624O13	solute carrier family 9 (sodium/hydrogen exchanger), member 3
49	4.1	gnf1m30770_a_at		9130020L07	chloride channel calcium activated 6
50	4.1	gnf1m30769_s_at	NM_207208	9130020L07	chloride channel calcium activated 6
51	4.1	gnf1m07377_a_at	NM_153568	D230014F07	cDNA sequence BC031901
52	4.0	gnf1m30529_a_at	NM_201256	1110004O12	eukaryotic translation initiation factor 4E binding protein 3
53	4.0	gnf1m19071_a_at	XM_908069	A430096B05	Fc fragment of IgG binding protein
54	4.0	gnf1m03908_a_at	NM_020049	9030613J17	solute carrier family 6 (neurotransmitter transporter), member 14
55	4.0	gnf1m32627_a_at	XM_907141	2010010B23	myosin IA

No. 23, stomach specific genes

#1	#2	#3	#4	#5	#6
1	6.9	gnf1m11150_a_at	NM_009362	2310075I07	trefoil factor 1
2	6.8	gnf1m23236_a_at		9130006K20	annexin A10
3	6.5	gnf1m04780_a_at	NM_025973	2210416O16	progastricsin (pepsinogen C)
4	6.4	gnf1m02036_a_at	NM_009724	2310065K03	ATPase, H+/K+ exchanging, beta polypeptide
5	6.4	gnf1m10234_a_at	NM_030181	4930405J24	V-set and immunoglobulin domain containing 1
6	6.4	gnf1m04549_a_at	NM_025467	2210419G06	RIKEN cDNA 1810036H07 gene
7	6.4	gnf1m28611_a_at		2310038I05	ATPase, H+/K+ exchanging, alpha polypeptide
8	6.3	gnf1m11149_a_at	NM_021488	2210408M22	ghrelin
9	6.3	gnf1m07731_a_at	NM_029727	2210006M16	RIKEN cDNA 2210006M16 gene
10	6.2	gnf1m11904_a_at	NM_008118	9130204L19	gastric intrinsic factor
11	5.9	gnf1m16988_at		2210005L13	mucin 5, subtypes A and C, tracheobronchial/gastric
12	5.8	gnf1m16746_a_at	XM_915229	1190003M12	RIKEN cDNA 1190003M12 gene
13	5.7	gnf1m18350_a_at		1810010D01	RIKEN cDNA 1810010D01 gene
14	5.6	gnf1m11146_a_at	NM_011922	I920046M24	annexin A10
15	5.4	gnf1m04548_a_at	NM_025466	2210420L15	gastrokine 1
16	5.2	gnf1m06150_a_at	NM_134110	2200002I16	potassium voltage-gated channel, Isk-related subfamily, gene 2
17	5.2	gnf1m03951_a_at	NM_020518	2210413P10	V-set and immunoglobulin domain containing 2
18	4.9	gnf1m10041_a_at	NM_026935	G630025A20	sulfotransferase family, cytosolic, 1C, member 2
19	4.9	gnf1m06355_a_at	NM_144544		RIKEN cDNA 2210407C18 gene
20	4.9	gnf1m08742_at	NM_172737	D430041B17	RIKEN cDNA D430041B17 gene
21	4.8	gnf1m13073_a_at	NM_021453	I920065H02	pepsinogen 5, group I
22	4.7	gnf1m27088_at	NM_178280	C530030G16	sal-like 3 (Drosophila)
23	4.5	gnf1m18901_at		4930572F24	RIKEN cDNA 2610528E23 gene
24	4.5	gnf1m04280_a_at	NM_023186	2210020N23	chitinase, acidic
25	4.4	gnf1m10569_a_at	NM_007799	I530011F11	cathepsin E
26	4.4	gnf1m11152_a_at	NM_025620	2210417D09	RIKEN cDNA 2210417D09 gene
27	4.4	gnf1m04616_a_at	NM_025622	2200008F12	lectin, galactose-binding, soluble 2
28	4.3	gnf1m05278_a_at	NM_028216	2210408B04	prostate stem cell antigen
29	4.3	gnf1m01108_a_at	NM_007989		forkhead box H1
30	4.3	gnf1m32773_at	XM_914516		gene model 935, (NCBI)
31	4.3	gnf1m02645_a_at	NM_011107	2310012E07	phospholipase A2, group IB, pancreas
32	4.3	gnf1m21557_a_at	NM_001005477	E130309B19	RIKEN cDNA E130309B19 gene
33	4.3	gnf1m33973_at			uncharacterized Celera prediction mCG115317
34	4.3	gnf1m09755_at	NM_181729		mucin 6, gastric
35	4.2	gnf1m01766_a_at	NM_009207		solute carrier family 4 (anion exchanger), member 2
36	4.2	gnf1m11141_a_at	NM_023709	2200003B16	calpain 9 (nCL-4)
37	4.2	gnf1m09966_a_at	NM_145209	I830016G04	2'-5' oligoadenylate synthetase-like 1
38	4.2	gnf1m04545_a_at	NM_025458	1810057G13	transmembrane emp24 protein transport domain containing 6
39	4.1	gnf1m32563_at			aldehyde dehydrogenase family 7 member A1 aldehyde dehydrogenase family 7, member A1 mCG16296
40	4.1	gnf1m30502_a_at		9530083L01	fer-1-like 4 (C. elegans)
41	4.1	gnf1m09844_a_at	NM_172469	5730466J16	chloride intracellular channel 6
42	4.1	gnf1m33051_at			inferred: gb|AAH12778.1|AAH12778 (BC012778) Unknown (protein for IMAGE:3939659) [Homo sapiens] mCG130493

43	4.1	gnf1m00852_a_at	NM_007526		BarH-like homeobox 1
44	4.1	gnf1m35002_at			inferred: ref|NP_036064.1| (NM_011934) estrogen related receptor, beta; estrogen receptor related 2 [Mus musculus] mCG50969
45	4.0	gnf1m05364_a_at	NM_028775	A330069N14	cytochrome P450, family 2, subfamily s, polypeptide 1
46	4.0	gnf1m03816_a_at	NM_019815		claudin 18
47	4.0	gnf1m10964_a_at	NM_009363	0910001O22	trefoil factor 2 (spasmolytic protein 1)
48	4.0	gnf1m34830_x_at	NM_146636		olfactory receptor 1487

No. 24, prostate specific genes

#1	#2	#3	#4	#5	#6
1	7.2	gnf1m03978_a_at	NM_020597		beta-microseminoprotein
2	6.7	gnf1m13650_at	NM_009300	9230116E14	seminal vesicle protein 2
3	6.6	gnf1m01816_a_at	NM_009301	1700125I06	seminal vesicle secretion 5
4	6.5	gnf1m03575_a_at	NM_017471	9830120G21	probasin
5	6.2	gnf1m11992_a_at	NM_020264	9530004K16	seminal vesicle protein, secretion 7
6	6.1	gnf1m11564_a_at	NM_008267	5033401H24	homeo box B13
7	6.0	gnf1m27244_at		C920006B11	HISTONE H2A.F GENE (FRAGMENT) homolog [Gallus gallus]
8	6.0	gnf1m08117_at	NM_177911	9530008N10	transglutaminase 4 (prostate)
9	6.0	gnf1m11987_a_at	NM_017390	G630066O15	seminal vesicle protein, secretion 2
10	5.9	gnf1m15728_a_at		G430099L10	DnaJ (Hsp40) homolog, subfamily C, member 10
11	5.8	gnf1m02575_a_at	NM_010921	9530090D16	NK-3 transcription factor, locus 1 (Drosophila)
12	5.8	gnf1m11994_a_at	NM_030718	9530006M03	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase, transferase B, alpha 1-3-galactosyltransferase)
13	5.6	gnf1m35116_at	XM_904194		similar to calmodulin 1
14	5.6	gnf1m29041_a_at	XM_906807	2610025P07	cDNA sequence BC025076
15	5.6	gnf1m02743_a_at	XM_914346	9530039G05	spermine binding protein
16	5.5	gnf1m02997_a_at	NM_011867		solute carrier family 26, member 4
17	5.2	gnf1m24987_a_at		9530079O21	expressed sequence BB123696
18	5.2	gnf1m29298_at		I830091H05	FGF receptor activating protein 1
19	5.1	gnf1m11988_a_at	NM_023865	9530002B09	RIKEN cDNA 9530002B09 gene
20	5.1	gnf1m14622_at	XM_356334	4930408F14	RIKEN cDNA 4930408F14 gene
21	5.1	gnf1m14007_at	NM_027128	2310011G06	RIKEN cDNA 2310011G06 gene
22	4.9	gnf1m09912_a_at	NM_025610	4933423N16	asparaginase like 1
23	4.8	gnf1m08118_a_at	NM_177911	9530008N10	transglutaminase 4 (prostate)
24	4.8	gnf1m07623_at	NM_175166	9530082P11	RIKEN cDNA 5430419D17 gene
25	4.7	gnf1m07724_a_at	NM_172426	C630015N03	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2
26	4.7	gnf1m03486_a_at	NM_016845	4921539N17	proacrosin binding protein
27	4.7	gnf1m29297_a_at		I830091H05	FGF receptor activating protein 1
28	4.5	gnf1m31210_a_at	NM_146682		olfactory receptor 76
29	4.4	gnf1m03975_a_at	NM_020588	I830087K14	RIKEN cDNA 1300007B12 gene
30	4.4	gnf1m10772_at	NM_007843		defensin beta 1
31	4.3	gnf1m02008_s_at	NM_009665	I920063F03	S-adenosylmethionine decarboxylase 1
32	4.3	gnf1m11713_a_at	NM_008604	6030454K05	membrane metallo endopeptidase
33	4.3	gnf1m22192_at		C530028E13	unclassifiable
34	4.2	gnf1m35415_x_at	XM_917952		similar to nuclear localized factor 1
35	4.2	gnf1m02996_a_at	NM_011864	9930024B13	3'-phosphoadenosine 5'-phosphosulfate synthase 2
36	4.1	gnf1m09372_s_at	NM_027203		leukocyte receptor cluster (LRC) member 1
37	4.1	gnf1m08394_at		C130036J11	RIKEN cDNA D930028F11 gene
38	4.1	gnf1m09797_a_at	NM_181048	C030010L06	RIKEN cDNA A130010J15 gene
39	4.1	gnf1m01462_a_at	NM_008644		mucin 10, submandibular gland salivary mucin
40	4.1	gnf1m25386_at		A130093M04	inferred: HYPOTHETICAL PROTEIN KIAA0310 (FRAGMENT). [Human] {Homo sapiens}
41	4.0	gnf1m10631_a_at	NM_013891	9030406H20	SAM pointed domain containing ets transcription factor
42	4.0	gnf1m30009_a_at	XM_909954	1700127F16	WAP four-disulfide core domain 3
43	4.0	gnf1m05777_at			melanophilin
44	4.0	gnf1m23974_at		5730402C02	RIKEN cDNA 5330420D20 gene
45	4.0	gnf1m06134_a_at	NM_134052		acireductone dioxygenase 1

No. 25, vomeralnasal organ specific genes

#1	#2	#3	#4	#5	#6
1	6.5	gnf1m01928_s_at	XM_620407		vomeronasal 2, receptor, 4
2	6.5	gnf1m32795_at	XM_912696	A430104B10	similar to Uromodulin precursor (Tamm-Horsfall urinary glycoprotein) (THP)
3	6.5	gnf1m01923_x_at	NM_009487		vomeronasal 2, receptor, 10
4	6.2	gnf1m06175_a_at	NM_134180		vomeronasal 1 receptor, C25
5	5.9	gnf1m02475_a_at	NM_010694		lipocalin 3
6	5.6	gnf1m02476_at	NM_010695		lipocalin 4
7	5.6	gnf1m25839_a_at		A630091H24	lipocalin 4
8	5.6	gnf1m12375_a_at	NM_009141	F830049O18	chemokine (C-X-C motif) ligand 5
9	5.5	gnf1m35337_at			inferred: gb|AAF72554.1|AF269232_1 (AF269232) butyrophilin-like protein BUTR-1 [Mus musculus] mCG1038007
10	5.4	gnf1m07884_at	NM_134170	4831417D05	vomeronasal 1 receptor, C15
11	5.3	gnf1m33873_x_at			inferred: ref|NP_033519.1| (NM_009493) vomeronasal 2, receptor, 4; vomeronasal organ family 2, receptor, 4 [Mus musculus] 033515 009489 14 ref|NP_033515.1| (NM_009489) vomeronasal 2, receptor, 14; vomeronasal organ family 2, receptor, 14 [Mus musculus] mCG56771
12	5.3	gnf1m33007_at	XM_913800		similar to odorant binding protein 2B
13	5.3	gnf1m15428_a_at	XM_920036		vomeronasal 2, receptor, 13
14	5.2	gnf1m33575_at	XM_912883		S100 calcium binding protein, zeta
15	5.0	gnf1m13290_s_at	NM_019918		tissue-type vomeronasal neurons putative pheromone receptor V2R2
16	5.0	gnf1m12051_at	NM_178749	9630050F05	serine/threonine kinase 32A
17	5.0	gnf1m01927_x_at	NM_009492		vomeronasal 2, receptor, 12
18	4.9	gnf1m31642_at	XM_914529		induced in fatty liver dystrophy 3
19	4.9	gnf1m30476_at			inferred: ref|XP_143284.1| (XM_143284) similar to tissue-type vomeronasal neurons putative pheromone receptor V2 [Mus musculus] mCG126038
20	4.9	gnf1m07372_a_at	NM_153558		lipocalin 13
21	4.9	gnf1m17488_at		A430105L04	transient receptor potential cation channel, subfamily C, member 2
22	4.8	gnf1m07344_at	NM_153422		phosphodiesterase 5A, cGMP-specific
23	4.7	gnf1m09872_a_at	NM_053184	C130005L05	UDP glucuronosyltransferase 2 family, polypeptide A1
24	4.7	gnf1m02571_a_at	NM_010916		nescient helix loop helix 1
25	4.7	gnf1m01924_x_at	NM_009489		vomeronasal 2, receptor, 14
26	4.6	gnf1m24697_a_at		A330015F06	osmotic stress protein
27	4.6	gnf1m32713_at	XM_925590	F930032F14	solute carrier family 4, sodium bicarbonate transporter-like, member 11
28	4.5	gnf1m34943_at	XM_915884		similar to olfactory receptor 365
29	4.3	gnf1m07446_a_at	NM_011644	A430105L04	transient receptor potential cation channel, subfamily C, member 2
30	4.3	gnf1m25038_at		9630019I16	hypothetical protein
31	4.3	gnf1m21784_at		6720465N03	RIKEN cDNA 9430071P14 gene
32	4.3	gnf1m09963_a_at	NM_010320	G730009J10	guanine nucleotide binding protein (G protein), gamma 8 subunit
33	4.2	gnf1m12520_a_at	NM_178673	B930093L07	follistatin-like 5
34	4.2	gnf1m16364_at		2810405F17	RIKEN cDNA 2810405F17 gene
35	4.2	gnf1m01925_x_at	NM_009490		vomeronasal 2, receptor, 15
36	4.2	gnf1m17463_a_at	XM_908788	9230116B18	RIKEN cDNA 9230116B18 gene
37	4.1	gnf1m11843_a_at	NM_178214	I920051L22	histone 2, H2bb
38	4.1	gnf1m07341_a_at	NM_153418	I920034C14	cDNA sequence U46068
39	4.1	gnf1m33679_x_at			ENSMUST00000071760 transcript (in rel.37.34e)
40	4.0	gnf1m05950_a_at	NM_130861	4930486M03	solute carrier organic anion transporter family, member 1a5
41	4.0	gnf1m30271_a_at		4933403L16	calreticulin 4
42	4.0	gnf1m17391_x_at	NM_009485		vomeronasal 2, receptor, 1

No. 26, heart specific genes

#1	#2	#3	#4	#5	#6
1	6.1	gnf1m31874_x_at			inferred: ref|NP_113808.1| (NM_031620) 3-phosphoglycerate dehydrogenase [Rattus norvegicus] mCG50387
2	6.0	gnf1m30834_at	NM_008725	I920194N08	natriuretic peptide precursor type A
3	5.8	gnf1m08513_s_at	NM_175441	I920041I20	RIKEN cDNA D830007F02 gene
4	5.7	gnf1m01466_a_at	NM_008653	I920180J22	myosin binding protein C, cardiac
5	5.5	gnf1m08732_a_at	NM_172750	D330008N11	ADP-ribosylhydrolase like 1
6	5.5	gnf1m24218_a_at		F420007B19	RIKEN cDNA D830007F02 gene
7	5.3	gnf1m00526_a_at	NM_023129	0610013B18	phospholamban
8	5.2	gnf1m10923_a_at	NM_009406	I920092G04	troponin I, cardiac
9	5.1	gnf1m17989_at		6030406G17	unclassifiable
10	5.0	gnf1m02083_a_at	NM_009814	3110082J19	calsequestrin 2
11	5.0	gnf1m10871_a_at	NM_013468	I920078A07	ankyrin repeat domain 1 (cardiac muscle)
12	4.9	gnf1m23903_a_at		I420023L02	Ras-related associated with diabetes
13	4.9	gnf1m00672_s_at	XM_919974	D830041H11	triadin
14	4.9	gnf1m11169_a_at	NM_023784	2310016N21	Yip1 domain family, member 7
15	4.8	gnf1m02252_a_at	NM_010212	I920089C03	four and a half LIM domains 2
16	4.8	gnf1m31518_at	NM_001033208	I920069H02	expressed sequence AA407270
17	4.8	gnf1m27893_at		D830041H11	unclassifiable
18	4.8	gnf1m33637_at	XM_925036		TNNI3 interacting kinase
19	4.6	gnf1m11516_at	NM_013868	4932416D13	heat shock protein family, member 7 (cardiovascular)
20	4.6	gnf1m01866_a_at	NM_009393		troponin C, cardiac/slow skeletal
21	4.5	gnf1m02884_a_at	NM_011619	I920078H23	troponin T2, cardiac
22	4.5	gnf1m00171_a_at	NM_178869	I920085F07	tubulin tyrosine ligase-like 1
23	4.5	gnf1m17296_a_at		1110018J23	RIKEN cDNA 1110018J23 gene
24	4.5	gnf1m27860_a_at		D830005K03	RIKEN cDNA A530058N18 gene
25	4.5	gnf1m10968_a_at	NM_013808	2610029O20	cysteine and glycine-rich protein 3
26	4.4	gnf1m16562_a_at	NM_028838	4933431K03	leucine rich repeat containing 2
27	4.4	gnf1m21353_at		D330008I21	13 days embryo heart cDNA, RIKEN full-length enriched library, clone:D330008I21 product:hypothetical protein, full insert sequence
28	4.4	gnf1m02546_s_at	NM_080728		myosin, heavy polypeptide 6, cardiac muscle, alpha
29	4.2	gnf1m16193_a_at	NM_053098	I920184N14	leiomodin 2 (cardiac)
30	4.2	gnf1m03502_a_at	NM_016869	1700001A04	corin
31	4.1	gnf1m06744_a_at	NM_146242	D830007J05	leucine rich repeat containing 10
32	4.1	gnf1m02547_a_at	NM_010861	I920040L18	myosin, light polypeptide 2, regulatory, cardiac, slow
33	4.1	gnf1m10927_a_at	NM_024179	2310016M19	RIKEN cDNA 0610009O20 gene
34	4.1	gnf1m19766_s_at	NM_028004	9430093B17	titin
35	4.1	gnf1m09315_a_at	NM_138601	1110020K04	DNA segment, Chr 10, Johns Hopkins University 81 expressed
36	4.0	gnf1m29489_a_at	NM_010859	I920078F11	myosin, light polypeptide 3
37	4.0	gnf1m23084_a_at		2310022E02	PDZ and LIM domain 5
38	4.0	gnf1m04125_a_at	NM_021503	1110012I24	myozenin 2

No. 27, umbilical cord specific genes

#1	#2	#3	#4	#5	#6
1	6.6	gnf1m11333_a_at	NM_130866	4631413D08	olfactory receptor 78
2	5.7	gnf1m05451_a_at	NM_029394	5730433I16	sorting nexing 24
3	5.4	gnf1m14049_at		2900002J02	RIKEN cDNA 2900002J02 gene
4	5.2	gnf1m12286_a_at	NM_007925	A630042I19	elastin
5	5.2	gnf1m02242_a_at	XM_925733		fibrillin 2
6	4.8	gnf1m26869_s_at		D430042D24	unclassifiable
7	4.8	gnf1m01110_a_at	NM_007992	I920045J03	fibulin 2
8	4.7	gnf1m12409_a_at	NM_023653	I530025P16	wingless-related MMTV integration site 2
9	4.7	gnf1m02492_a_at	NM_010728	D530004C15	lysyl oxidase
10	4.7	gnf1m21789_at		6820427D17	12 days embryo female mullerian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone:6820427D17 product:unclassifiable, full insert sequence
11	4.7	gnf1m04457_a_at	NM_025288	3300001H20	stefin A3
12	4.5	gnf1m17195_a_at	XM_916650	2310043J07	RIKEN cDNA 2310043J07 gene
13	4.5	gnf1m29592_at	NM_007603		calpain 6
14	4.5	gnf1m28615_at			gb|BC014809.1| Mouse Similar to tropomyosin 2 (beta), clone MGC:18587 IMAGE:3497670, mRNA, complete cds
15	4.4	gnf1m09632_a_at	NM_011708	6820430P06	Von Willebrand factor homolog
16	4.4	gnf1m18863_s_at	XM_917316	E130118M10	dynamin 3, opposite strand
17	4.4	gnf1m28851_a_at	NM_175643	A430089F14	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 2
18	4.3	gnf1m27516_at		D130080F22	unclassifiable
19	4.3	gnf1m15836_at		D330012K20	pleiomorphic adenoma gene-like 1
20	4.3	gnf1m16666_a_at	XM_912539	I830027K07	collagen triple helix repeat containing 1
21	4.3	gnf1m27680_at	NM_007737	D330045B21	procollagen, type V, alpha 2
22	4.3	gnf1m29165_a_at	XM_911929	1110008I14	RIKEN cDNA 1110008I14 gene
23	4.2	gnf1m10663_a_at	NM_008771	9530013F18	purinergic receptor P2X, ligand-gated ion channel, 1
24	4.2	gnf1m13904_a_at	NM_007736	4931421N12	procollagen, type IV, alpha 5
25	4.2	gnf1m02749_at	NM_011333	I830170B21	chemokine (C-C motif) ligand 2
26	4.2	gnf1m35865_at			inferred: ref|NP_033376.1| (NM_009350) testis nuclear RNA binding protein; testis nuclear RNA-binding protein [Mus musculus] mCG1041679
27	4.2	gnf1m03502_a_at	NM_016869	1700001A04	corin
28	4.2	gnf1m18190_at		D630022B14	unclassifiable
29	4.1	gnf1m18382_a_at		8430429I17	amyloid beta (A4) precursor protein-binding, family B, member 2
30	4.1	gnf1m03646_a_at	NM_018857	I920057I12	mesothelin
31	4.1	gnf1m02878_a_at	NM_011607	A430071G16	tenascin C
32	4.1	gnf1m00003_f_at	NM_010649	G930001N01	killer cell lectin-like receptor, subfamily A, member 4
33	4.1	gnf1m08280_at	NM_177182	A830053O21	RIKEN cDNA A830053O21 gene
34	4.1	gnf1m04396_a_at	NM_024198	F420010N11	glutathione peroxidase 7
35	4.0	gnf1m20925_at		B930086P04	unclassifiable
36	4.0	gnf1m11549_at	NM_011526	5031408O12	transgelin

No. 28, adrenal gland specific genes

#1	#2	#3	#4	#5	#6
1	7.3	gnf1m32266_at	XM_908062	D530008O11	hematopoietic cell transcript 1
2	7.1	gnf1m01606_at	NM_008890		phenylethanolamine-N-methyltransferase
3	6.5	gnf1m02165_a_at	NM_009995	I920026N02	cytochrome P450, family 21, subfamily a, polypeptide 1
4	6.2	gnf1m01114_at	NM_007997	5830428C01	ferredoxin reductase
5	6.1	gnf1m06470_at	NM_145364		aldo-keto reductase family 1, member D1
6	5.9	gnf1m30620_at		3732409I16	dopamine beta hydroxylase
7	5.8	gnf1m11856_a_at	NM_008560	8030422J23	melanocortin 2 receptor
8	5.8	gnf1m02040_a_at	NM_009731	G270033F23	aldo-keto reductase family 1, member B7
9	5.5	gnf1m13099_at	NM_011485	E330028H19	steroidogenic acute regulatory protein
10	5.5	gnf1m29915_a_at	NM_182783	F530001K16	cDNA sequence BC030183
11	5.5	gnf1m09458_a_at	NM_138942	3732409I16	dopamine beta hydroxylase
12	5.4	gnf1m24541_at		7330411N07	cytochrome P450, 11a, cholesterol side chain cleavage
13	5.3	gnf1m06298_a_at	NM_139051	G630046C19	nuclear receptor subfamily 5, group A, member 1
14	5.3	gnf1m00665_a_at	NM_133902	4432411H13	serine dehydratase-like
15	5.3	gnf1m05817_a_at	NM_053188	A530024K02	steroid 5 alpha-reductase 2
16	5.2	gnf1m26434_at		I1C0019M08	scavenger receptor class B, member 1
17	5.0	gnf1m27678_a_at	NM_010608	D330042M19	potassium channel, subfamily K, member 3
18	4.7	gnf1m16539_at		4930426D05	RIKEN cDNA 4930426D05 gene
19	4.7	gnf1m03123_a_at	NM_013498	4930469D11	cAMP responsive element modulator
20	4.7	gnf1m13443_a_at	NM_010608		potassium channel, subfamily K, member 3
21	4.6	gnf1m02162_a_at	NM_009991		cytochrome P450, family 11, subfamily b, polypeptide 2
22	4.6	gnf1m04424_a_at	NM_024283	C630001B03	RIKEN cDNA 1500015O10 gene
23	4.5	gnf1m07622_a_at	NM_178058	G270015M23	apoptosis-inducing factor (AIF)-like mitochondrion-associated inducer of death
24	4.5	gnf1m29142_a_at	NM_028782	I420047M08	protease, serine, 15
25	4.4	gnf1m01264_a_at	NM_008293	I920176L22	hydroxysteroid dehydrogenase-1, delta<5>-3-beta
26	4.4	gnf1m28333_at		E330036N16	ferredoxin 1
27	4.3	gnf1m14814_at		5033417F24	RIKEN cDNA 5033417F24 gene
28	4.3	gnf1m00547_a_at	NM_177322		angiotensin II receptor, type 1a
29	4.3	gnf1m05187_a_at	NM_027582	4921521F21	RIKEN cDNA 4921521F21 gene
30	4.2	gnf1m01113_a_at	NM_007996	G370022H24	ferredoxin 1
31	4.2	gnf1m15214_at	NM_030150		DNA segment, Chr 11, Lothar Hennighausen 2, expressed
32	4.1	gnf1m10757_a_at	NM_026358	1700025H02	RIKEN cDNA 4930583H14 gene
33	4.1	gnf1m19709_a_at	NM_201361	A830036I20	expressed sequence AW061290
34	4.0	gnf1m24231_at		6030456M03	cytochrome P450, 11a, cholesterol side chain cleavage
35	4.0	gnf1m11540_a_at	NM_134076	4933431E19	abhydrolase domain containing 4

No. 29, digits specific genes

#1	#2	#3	#4	#5	#6
1	6.0	gnf1m31751_at			inferred: gb|AAH13651.1|AAH13651 (BC013651) serine protease inhibitor 2-2 [Mus musculus] mCG54087
2	6.0	gnf1m11374_at	NM_177717	4732456N10	RIKEN cDNA 4732456N10 gene
3	5.5	gnf1m13744_a_at	NM_010668	4732448G14	keratin complex 2, basic, gene 17
4	5.3	gnf1m18320_at		1110025L11	keratin associated protein 6-1
5	5.1	gnf1m01001_a_at	NM_007814		cytochrome P450, family 2, subfamily b, polypeptide 19
6	5.0	gnf1m17069_a_at	XM_894986	4632435A09	G protein-coupled receptor 115
7	5.0	gnf1m04072_a_at	XM_355243	C730019K03	proteoglycan 4 (megakaryocyte stimulating factor, articular superficial zone protein)
8	4.9	gnf1m16490_at			keratin associated protein 6-3
9	4.9	gnf1m29400_a_at		2300005B03	RIKEN cDNA 2300005B03 gene
10	4.8	gnf1m02470_a_at	NM_010673		keratin associated protein 6-2
11	4.8	gnf1m05183_a_at	NM_027562	4632413B12	C-type lectin domain family 2, member g
12	4.8	gnf1m08170_at	NM_173024	A030003A19	RIKEN cDNA A030003A19 gene
13	4.8	gnf1m10992_at	NM_028621	1110017B05	keratin associated protein 21-1
14	4.8	gnf1m32912_at	XM_916075		similar to arylacetamide deacetylase
15	4.8	gnf1m33581_at	XM_911236		HtrA serine peptidase 4
16	4.8	gnf1m19125_a_at	NM_001013797	1190026I17	similar to protease inhibitor H; acrosin inhibitor
17	4.6	gnf1m13271_a_at		A030011K22	keratin associated protein 6-1
18	4.6	gnf1m14245_a_at		5430433J05	RIKEN cDNA 5430433J05 gene
19	4.6	gnf1m10259_a_at	NM_030061	9230117E20	RIKEN cDNA 9230117E20 gene
20	4.6	gnf1m10126_a_at	NM_212483	2410129K01	RIKEN cDNA 2410039E07 gene
21	4.5	gnf1m05946_a_at	NM_130856	1110002D05	keratin associated protein 16-8
22	4.4	gnf1m13773_at	XM_917709	5530401F02	keratin associated protein 8-1
23	4.4	gnf1m05129_at	NM_027157	2310043L02	RIKEN cDNA 2310043L02 gene
24	4.4	gnf1m30645_a_at	XM_911236	B430206E18	HtrA serine peptidase 4
25	4.3	gnf1m16824_a_at	XM_924011	E130120J09	RIKEN cDNA 2310058N18 gene
26	4.1	gnf1m29350_a_at	XM_904709		keratin complex 1, acidic, gene 3
27	4.1	gnf1m07833_a_at	NM_144943		CD 207 antigen
28	4.1	gnf1m01045_a_at	NM_007882		desmocollin 3
29	4.1	gnf1m23564_at	NM_009334	4732469D10	transcription factor AP-2 beta
30	4.1	gnf1m16229_a_at	XM_904796	1110001M24	RIKEN cDNA 1110001M24 gene
31	4.0	gnf1m06689_a_at	NM_146063	4733401E22	cDNA sequence BC031593
32	4.0	gnf1m13307_a_at	XM_904773	2310050C09	RIKEN cDNA 2310050C09 gene

No. 30, bone specific genes

#1	#2	#3	#4	#5	#6
1	6.0	gnf1m31485_at	NM_207131	F420002G12	CCAAT/enhancer binding protein (C/EBP), epsilon
2	5.6	gnf1m03387_a_at	NM_015779		elastase 2, neutrophil
3	5.6	gnf1m29315_a_at		A330075D07	weakly similar to INTERFERON-INDUCED TRANSMEMBRANE PROTEIN 2 (INTERFERON-INDUCIBLE PROTEIN 1-8D) [Homo sapiens]
4	5.5	gnf1m00134_a_at	XM_894904	A630006E24	sclerostin
5	5.4	gnf1m01494_a_at	NM_008694	F420005O16	neutrophilic granule protein
6	5.3	gnf1m02138_a_at	NM_009926	1110017L07	procollagen, type XI, alpha 2
7	5.2	gnf1m02679_at	NM_011178		proteinase 3
8	5.2	gnf1m15355_a_at	XM_915869	2510006A02	ficolin B
9	5.2	gnf1m11209_a_at	NM_008920	F830043J06	proteoglycan 2, bone marrow
10	5.1	gnf1m00993_at	NM_007800		cathepsin G
11	5.0	gnf1m00955_a_at	NM_007729	B130009K01	procollagen, type XI, alpha 1
12	5.0	gnf1m02136_at	NM_009921		cathelicidin antimicrobial peptide
13	5.0	gnf1m02534_a_at	NM_010824	2700059B01	myeloperoxidase
14	5.0	gnf1m01136_a_at	NM_008039	E330010I07	formyl peptide receptor, related sequence 2
15	4.9	gnf1m04076_a_at	NM_021407	9830128F02	triggering receptor expressed on myeloid cells 3
16	4.9	gnf1m13191_a_at	NM_008611	F730319L09	matrix metallopeptidase 8
17	4.7	gnf1m02725_a_at	NM_011280	2510041F02	tripartite motif protein 10
18	4.7	gnf1m30116_a_at	NM_001002842	4632424B03	PML-RAR alpha-regulated adaptor molecule 1
19	4.6	gnf1m05977_a_at	NM_133209		paired immunoglobin-like type 2 receptor beta
20	4.6	gnf1m18359_a_at	XM_904446	E030028I19	RIKEN cDNA 1810033B17 gene
21	4.5	gnf1m33526_at	XM_909906		RIKEN cDNA I830127L07 gene
22	4.5	gnf1m01441_a_at	NM_008607	I830091A16	matrix metallopeptidase 13
23	4.4	gnf1m12091_a_at	NM_008405	F930031G18	integrin beta 2-like
24	4.3	gnf1m01273_at	NM_008318		integrin binding sialoprotein
25	4.3	gnf1m26364_a_at	XM_911496	B230337H21	apolipoprotein L, 2
26	4.2	gnf1m00065_at	NM_010369	I530023F06	glycophorin A
27	4.2	gnf1m05656_s_at	NM_031368	C130067M06	bone gamma-carboxyglutamate protein, related sequence 1
28	4.1	gnf1m05996_a_at	NM_133245	2510041L04	erythroid associated factor
29	4.1	gnf1m12074_a_at	NM_133246	9830113C01	membrane-spanning 4-domains, subfamily A, member 3
30	4.1	gnf1m03319_a_at	NM_013848	9830164O15	erythroblast membrane-associated protein
31	4.0	gnf1m11207_a_at	NM_020504	2500004B14	claudin 13

No. 31, lung specific genes

#1	#2	#3	#4	#5	#6

1	6.7	gnf1m07220_at	NM_147779		surfactant associated protein B
2	6.3	gnf1m00790_a_at	NM_007425	1200016F14	advanced glycosylation end product-specific receptor
3	6.3	gnf1m02764_a_at	NM_011359		surfactant associated protein C
4	5.6	gnf1m13985_at		1110050K14	RIKEN cDNA 1110050K14 gene
5	5.5	gnf1m02753_a_at	NM_011339	E030017H13	chemokine (C-X-C motif) ligand 15
6	5.4	gnf1m03156_s_at	NM_013565	A930004K02	integrin alpha 3
7	5.2	gnf1m26239_at	XM_483915	B130039D23	pleckstrin homology domain containing, family K member 1
8	5.1	gnf1m24301_at		6330501C04	ERG PROTEIN homolog [Mus musculus]
9	4.9	gnf1m09808_a_at	NM_028306		heat shock protein 12B
10	4.9	gnf1m09513_a_at	NM_029928	M5C1105K07	protein tyrosine phosphatase, receptor type, B
11	4.9	gnf1m06553_at	NM_145536		cDNA sequence BC020535
12	4.8	gnf1m13225_a_at	NM_025437	G430080G23	eukaryotic translation initiation factor 1A, Y-linked
13	4.8	gnf1m05862_a_at	NM_054038	8430440N01	secretoglobin, family 3A, member 2
14	4.8	gnf1m00353_a_at	NM_181444		G protein-coupled receptor, family C, group 5, member A
15	4.7	gnf1m02912_a_at	NM_011681	I530005I22	secretoglobin, family 1A, member 1 (uteroglobin)
16	4.7	gnf1m02745_a_at	NM_011326	F530014I17	sodium channel, nonvoltage-gated 1 gamma
17	4.7	gnf1m34849_at	NM_001001807		olfactory receptor 234
18	4.7	gnf1m02786_a_at	NM_011402	I1C0020L19	solute carrier family 34 (sodium phosphate), member 2
19	4.6	gnf1m03236_a_at	NM_013690		endothelial-specific receptor tyrosine kinase
20	4.6	gnf1m11873_a_at	NM_177356	8430417I16	lysosomal-associated membrane protein 3
21	4.5	gnf1m24246_a_at		6030475M24	unclassifiable
22	4.4	gnf1m01742_a_at	NM_009160		surfactant associated protein D
23	4.3	gnf1m01885_a_at	NM_009425	A630004M21	tumor necrosis factor (ligand) superfamily, member 10
24	4.2	gnf1m03816_a_at	NM_019815		claudin 18
25	4.2	gnf1m07350_a_at	NM_153513		cDNA sequence BC028528
26	4.2	gnf1m15595_a_at	NM_033525	K230315E09	nephronectin
27	4.2	gnf1m28929_a_at	NM_007695	F630225K06	chitinase 3-like 1
28	4.1	gnf1m00030_a_at	NM_018881	2310042I22	flavin containing monooxygenase 2
29	4.0	gnf1m02347_a_at	NM_010406		hemolytic complement
30	4.0	gnf1m10888_a_at	NM_011182	I920035G16	pleckstrin homology, Sec7 and coiled-coil domains 3
31	4.0	gnf1m05988_a_at	NM_133229	A630004L20	Down syndrome critical region homolog 6 (human)

No. 32, cerebellum specific genes

#1	#2	#3	#4	#5	#6
1	6.3	gnf1m01156_a_at	NM_008068	9630012C19	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 6
2	5.6	gnf1m23531_at		4732433A03	aspartate-beta-hydroxylase
3	5.6	gnf1m19471_a_at	NM_176952	C630040G20	RIKEN cDNA 6430573F11 gene
4	5.1	gnf1m02315_a_at	NM_010350	M5C1026K02	glutamate receptor, ionotropic, NMDA2C (epsilon 3)
5	5.1	gnf1m24456_at		6530411F08	glutamate receptor, ionotropic, delta 2
6	5.0	gnf1m01379_s_at	NM_008498	C230045C03	LIM homeobox protein 1
7	5.0	gnf1m25400_at		A230008P07	unclassifiable
8	4.8	gnf1m09707_a_at	XM_907237	I1C0004A05	protein phosphatase 1, regulatory subunit 10
9	4.7	gnf1m03541_s_at	NM_054079	1500012D04	interleukin 22
10	4.7	gnf1m02223_a_at	NM_010134		engrailed 2
11	4.6	gnf1m08920_a_at	NM_026380	6530413N01	regulator of G-protein signaling 8
12	4.6	gnf1m13918_a_at	NM_007592	1300004E06	carbonic anhydrase 8
13	4.5	gnf1m12517_a_at	NM_019820	B930083H17	cerebellin 3 precursor protein
14	4.5	gnf1m18269_a_at		A630033B20	unclassifiable
15	4.5	gnf1m08292_at	NM_177790	A930006D11	RIKEN cDNA A930006D11Rik gene
16	4.5	gnf1m13274_at		K230334G01	neurogenic differentiation 2
17	4.5	gnf1m01762_a_at	NM_009200	I420008D08	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6
18	4.4	gnf1m18590_at		2900083I11	RIKEN cDNA 2900083I11 gene
19	4.4	gnf1m11812_a_at	NM_011153	6530401M09	G substrate
20	4.4	gnf1m03749_a_at	NM_019626	K430357H14	cerebellin 1 precursor protein
21	4.4	gnf1m30730_at	XM_925385		Src homology 2 domain containing F
22	4.4	gnf1m14886_at		6330436F06	RIKEN cDNA 6330436F06 gene
23	4.4	gnf1m26901_at		C230053I05	Unc4.1 homeobox (C. elegans)
24	4.3	gnf1m17757_at		B230312E22	B230312E22 unclassifiable clone
25	4.3	gnf1m03701_a_at	NM_019465	B930098P10	cytotoxic and regulatory T cell molecule
26	4.3	gnf1m26515_at		B930002F08	zinc finger protein of the cerebellum 4
27	4.3	gnf1m32347_at			glutamate receptor, metabotropic 4
28	4.2	gnf1m19820_at		9630009A21	unclassifiable
29	4.1	gnf1m30665_at	NM_023543		chimerin (chimaerin) 2
30	4.1	gnf1m25038_at		9630019I16	hypothetical protein

No. 33, embryo day 6.5 specific genes

#1	#2	#3	#4	#5	#6
1	5.5	gnf1m11382_a_at	NM_010203	4732467I02	fibroblast growth factor 5
2	5.4	gnf1m12921_at	NM_009004	D330036L06	kinesin family member 20A
3	5.3	gnf1m03276_a_at	NM_013766	4921529H02	prolactin-like protein I
4	5.3	gnf1m03727_a_at	NM_019540	C430005G24	pore forming protein-like
5	5.2	gnf1m32200_at			inferred: gb|AAH18387.1|AAH18387 (BC018387) Similar to RIKEN cDNA 2700091N06 gene [Mus musculus] mCG20935
6	5.1	gnf1m10359_a_at	NM_172156	C430027I15	chorionic somatomammotropin hormone 1
7	4.9	gnf1m17824_at	NR_002862	C230040C07	poly(A)-binding protein, cytoplasmic pseudogene
8	4.7	gnf1m05787_a_at	NM_053095		interleukin 24
9	4.7	gnf1m09080_at	NM_001011811		olfactory receptor 487
10	4.7	gnf1m08880_at	NM_032006	C430029P05	matrix metallopeptidase 1a (interstitial collagenase)
11	4.6	gnf1m09471_a_at	NM_019539	5630400J12	cathepsin 7
12	4.6	gnf1m02205_at	NM_010088	I530026J03	decidual/trophoblast prolactin-related protein
13	4.5	gnf1m15786_a_at	NM_008554	2410083I15	achaete-scute complex homolog-like 2 (Drosophila)
14	4.5	gnf1m09640_a_at		4631401O15	myosin 1H
15	4.4	gnf1m07087_at	NM_146961		olfactory receptor 539
16	4.3	gnf1m34478_x_at			inferred: gb|AAH12655.1|AAH12655 (BC012655) Unknown (protein for IMAGE:3669867) [Mus musculus] mCG48637
17	4.3	gnf1m11820_at	NM_010499	F630103G03	immediate early response 2
18	4.3	gnf1m33507_at			inferred: ref|NP_058593.1| (NM_016897) translocase of inner mitochondrial membrane 23 homolog (yeast); translocase of inner mitochondrial membrane [Mus musculus] mCG123348
19	4.2	gnf1m13268_a_at		F930102P07	histocompatibility 2, class II antigen E alpha
20	4.2	gnf1m26254_at		B130047P03	Cdc42 GTPase-activating protein
21	4.2	gnf1m15908_at	NM_001013825		similar to hypothetical protein FLJ14345
22	4.2	gnf1m16840_at		5730442A01	tumor rejection antigen gp96
23	4.1	gnf1m02674_a_at	NM_011166		prolactin-like protein B
24	4.1	gnf1m30449_at			expressed sequence AI427833 expressed sequence AI427833 mCG126575
25	4.1	gnf1m21118_at	XM_914594	C430002N04	CEA-related cell adhesion molecule 15
26	4.0	gnf1m01922_a_at	NM_009482	2410026A04	undifferentiated embryonic cell transcription factor 1
27	4.0	gnf1m01893_a_at	NM_009434	2400006G02	pleckstrin homology-like domain, family A, member 2
28	4.0	gnf1m26996_at		C330022A02	tripartite motif protein 27

No. 34, pituitary specific genes

#1	#2	#3	#4	#5	#6
1	7.2	gnf1m16838_at	NM_008045	5730420N04	follicle stimulating hormone beta
2	6.5	gnf1m01892_a_at	NM_009432		thyroid stimulating hormone, beta subunit
3	6.3	gnf1m02124_a_at	NM_009889		glycoprotein hormones, alpha subunit
4	5.7	gnf1m01297_a_at	NM_008355		interleukin 13
5	5.6	gnf1m23424_a_at		3110047H05	hypothetical protein
6	5.6	gnf1m17959_at		A430027H14	potassium channel, subfamily K, member 2
7	5.6	gnf1m18099_a_at		2810449D17	RIKEN cDNA 2810449D17 gene
8	5.5	gnf1m30143_a_at		4732455E07	mitogen activated protein kinase kinase 7
9	5.5	gnf1m11611_a_at	NM_008895	5730420K11	pro-opiomelanocortin-alpha
10	5.3	gnf1m01378_a_at	NM_008497	A230101A12	luteinizing hormone beta
11	4.9	gnf1m23937_a_at	NM_001003685	5330422G23	growth hormone releasing hormone receptor
12	4.8	gnf1m01580_a_at			ENSMUST00000075861 transcript (in rel.37.34e)
13	4.8	gnf1m18480_a_at	XM_922596	D030058A04	zinc finger, RAN-binding domain containing 3
14	4.5	gnf1m03198_a_at	NM_013628		proprotein convertase subtilisin/kexin type 1
15	4.4	gnf1m19291_at	NM_001004168	4933413G10	hypothetical gene supported by AK030184
16	4.4	gnf1m26869_s_at		D430042D24	unclassifiable
17	4.4	gnf1m02672_a_at	NM_011164	5730421F19	prolactin
18	4.4	gnf1m10439_a_at	NM_183336	5530402E03	immunoglobulin superfamily, member 1
19	4.3	gnf1m26987_at	XM_900840	C330007E15	RIKEN cDNA C330024D21 gene
20	4.2	gnf1m21014_at		C130048C12	similar to L1 RETROTRANSPOSON, TF SUBFAMILY L1MD-TF18, PARTIAL SEQUENCE [Mus musculus domesticus]
21	4.2	gnf1m09621_a_at	NM_008117	5730422D01	growth hormone
22	4.2	gnf1m12417_at		B130049A16	RAD23a homolog (S. cerevisiae)
23	4.2	gnf1m03930_a_at	NM_020293		claudin 9
24	4.1	gnf1m29363_a_at		1110011K07	RIKEN cDNA 1110014L17 gene
25	4.1	gnf1m22826_at		4930519F09	RIKEN cDNA 4930519F09 gene
26	4.0	gnf1m32192_at	XM_924616		hypothetical protein LOC623757

No. 35, brown fat specific genes

#1	#2	#3	#4	#5	#6
1	5.6	gnf1m27192_at		C730025J11	adrenergic receptor, alpha 1a, ALPHA 1A-ADRENOCEPTOR
2	4.9	gnf1m23653_at		4833405B16	uncoupling protein 1, mitochondrial
3	4.9	gnf1m15492_at		5430410E06	RIKEN cDNA 5430410E06 gene
4	4.8	gnf1m08231_at	NM_178139	A530025J20	otopetrin 1
5	4.6	gnf1m18802_at	NM_029690	B930042O03	actin related protein M1
6	4.6	gnf1m20070_at		A130094L10	16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130094L10 product:unclassifiable, full insert sequence
7	4.6	gnf1m29715_at	NM_181857	4930565H06	DNA polymerase N
8	4.5	gnf1m27636_at		D330011I06	unclassifiable
9	4.5	gnf1m11432_a_at	NM_009463	4833405B16	uncoupling protein 1 (mitochondrial, proton carrier)

10	4.5	gnf1m35999_at			inferred: ref|NP_032529.2| (NM_008503) ribosomal protein S2; repeat family 3 gene [Mus musculus] mCG1032252
11	4.4	gnf1m26432_at		B430117C13	Fc receptor, IgG, low affinity IIb
12	4.3	gnf1m00326_s_at	NM_134093	K230305F10	LETM1 domain containing 1
13	4.3	gnf1m08622_at	XM_906543	6030441H18	RIKEN cDNA 6030441H18 gene
14	4.3	gnf1m07163_a_at	NM_147063		olfactory receptor 520
15	4.2	gnf1m20409_at		A630064P09	hypothetical protein
16	4.2	gnf1m06879_at	NM_146590		olfactory receptor 1085
17	4.2	gnf1m17413_at		2610042G18	tetraspanin 18
18	4.2	gnf1m26429_at		F630017G06	lipoprotein lipase
19	4.1	gnf1m18155_at		A130098A21	unclassifiable
20	4.1	gnf1m34713_x_at	XM_888474	I1C0046E08	cDNA sequence BC052688
21	4.1	gnf1m34388_x_at	XM_911502		similar to ribosomal protein L7-like 1
22	4.1	gnf1m19577_at		8430406N14	unclassifiable
23	4.0	gnf1m18547_at		A630019I02	hypothetical LOC408254

No. 36, bladder specific genes

#1	#2	#3	#4	#5	#6
1	6.6	gnf1m01915_a_at	NM_009476		uroplakin 2
2	6.3	gnf1m04323_a_at	NM_023478	1110017C07	uroplakin 3A
3	5.6	gnf1m28162_at		E130303A22	GATA binding protein 3
4	5.3	gnf1m29262_a_at	NM_026815	1110031P12	uroplakin 1A
5	4.9	gnf1m10663_a_at	NM_008771	9530013F18	purinergic receptor P2X, ligand-gated ion channel, 1
6	4.9	gnf1m06333_a_at	NM_139306	9530014B21	N-acylsphingosine amidohydrolase 3-like
7	4.8	gnf1m11546_at	NM_010935	5031404D23	neuropeptide Y receptor Y6
8	4.8	gnf1m27709_a_at	NM_009170	D430024L03	sonic hedgehog
9	4.6	gnf1m25707_a_at	NM_029018	A530032A05	CD200 receptor 3
10	4.5	gnf1m24933_at		9530006G20	synaptopodin 2
11	4.4	gnf1m28221_a_at	NM_001024619	E230008G13	leucine rich repeat containing 54
12	4.4	gnf1m18386_a_at		2310002D06	RIKEN cDNA 2310002D06 gene
13	4.2	gnf1m13875_at			Mouse clone IMAGE:3989034, mRNA /cds=UNKNOWN /gb=BC012717 /gi=15706467 /len=1655 gnl|UG|Mm#S2204884
14	4.2	gnf1m11144_a_at	NM_018802	2210012D01	synaptotagmin VIII
15	4.2	gnf1m12734_a_at	NM_178924	C630013E24	uroplakin 1B
16	4.1	gnf1m25748_a_at		A530078I09	inferred: actin, alpha 2, smooth muscle, aorta
17	4.1	gnf1m02263_a_at	NM_010232	I920090I12	flavin containing monooxygenase 5
18	4.1	gnf1m08900_a_at	NM_025712	9530003D19	RIKEN cDNA 4631426E05 gene
19	4.1	gnf1m01781_at	NM_009235	2410119O10	SRY-box containing gene 15
20	4.0	gnf1m01331_a_at	NM_008412		involucrin
21	4.0	gnf1m06028_a_at	NM_133675	1110032A04	RIKEN cDNA 1110032A04 gene

No. 37, dorsal root ganglia specific genes

#1	#2	#3	#4	#5	#6
1	5.4	gnf1m05878_at	NM_054084		calcitonin-related polypeptide, beta
2	5.3	gnf1m13444_s_at	XM_912838	4930555K19	leucine rich repeat and sterile alpha motif containing 1
3	5.1	gnf1m09535_s_at	NM_009134		sodium channel, voltage-gated, type X, alpha
4	5.0	gnf1m31984_at	NM_198860	4022402K14	expressed sequence AI646023
5	4.9	gnf1m03008_a_at	NM_011887		sodium channel, voltage-gated, type XI, alpha
6	4.9	gnf1m33299_at	XM_916337		gene model 765, (NCBI)
7	4.8	gnf1m03206_a_at	NM_013639	7120476M05	peripherin 1
8	4.7	gnf1m16713_at	NM_001033954		calcitonin/calcitonin-related polypeptide, alpha
9	4.6	gnf1m04997_a_at	NM_026523	3110023K12	neuromedin B
10	4.6	gnf1m01989_a_at	NM_009635	F730316L09	advillin
11	4.5	gnf1m02805_a_at	NM_011430	C530045H03	synuclein, gamma
12	4.5	gnf1m00748_at	NM_021369	A930003O18	cholinergic receptor, nicotinic, alpha polypeptide 6
13	4.5	gnf1m13492_a_at	NM_033217	A030014A01	nerve growth factor receptor (TNFR superfamily, member 16)
14	4.4	gnf1m08103_a_at		C530048O08	RIKEN cDNA 9430031J16 gene
15	4.4	gnf1m01988_at	NM_009635		advillin
16	4.3	gnf1m33690_at	XM_916777		diacylglycerol kinase, eta
17	4.1	gnf1m12600_at	NM_008309	C130095B09	5-hydroxytryptamine (serotonin) receptor 1D
18	4.1	gnf1m16660_a_at		2700049H19	hypothetical LOC228584
19	4.1	gnf1m17918_a_at		4833429M11	Bcl-associated death promoter
20	4.1	gnf1m16507_at		5830411H19	solute carrier family 36 (proton/amino acid symporter), member 1

No. 38, olfactory bulb specific genes

#1	#2	#3	#4	#5	#6
1	6.1	gnf1m28883_s_at	NM_001037750	6430524C05	gene model 1533, (NCBI)
2	5.5	gnf1m04065_a_at	NM_021390		sal-like 1 (Drosophila)
3	5.1	gnf1m02185_a_at	NM_010053	6430538C22	distal-less homeobox 1
4	4.8	gnf1m19621_at		A530051K19	cytoplasmic polyadenylation element binding protein 3
5	4.7	gnf1m13651_a_at	NM_010025	2610028K20	doublecortin
6	4.7	gnf1m26184_at		B130002G13	similar to somatotropin intron-related protein RDE.25 (fragment) [Rattus norvegicus]
7	4.7	gnf1m14373_at		2900073C17	RIKEN cDNA 2900073C17 gene
8	4.6	gnf1m33170_at	NM_001034898	E530011F12	gene model 1286, (NCBI)
9	4.6	gnf1m09450_s_at	XM_922114	A830081I04	echinoderm microtubule associated protein like 5
10	4.4	gnf1m20130_at		A230077E20	unclassifiable
11	4.3	gnf1m26452_at		B430214E22	unclassifiable
12	4.3	gnf1m19658_at		9330169N05	RIKEN cDNA C230040D10 gene
13	4.3	gnf1m12430_at	NM_008310	B230106O20	5-hydroxytryptamine (serotonin) receptor 1F
14	4.3	gnf1m00656_a_at	NM_011216		protein tyrosine phosphatase, receptor type, O
15	4.2	gnf1m19216_at		4833442A19	unclassifiable
16	4.2	gnf1m11804_a_at	NM_080644	A930104B02	calcium channel, voltage-dependent, gamma subunit 5
17	4.2	gnf1m32315_at	XM_905651		similar to transmembrane protein 46
18	4.1	gnf1m01135_a_at	NM_008036		FBJ osteosarcoma oncogene B
19	4.1	gnf1m02246_a_at	NM_010195	4022446J01	leucine rich repeat containing G protein coupled receptor 5
20	4.0	gnf1m21985_at		B930068K11	RIKEN cDNA B930068K11 gene

No. 39, trachea specific genes

#1	#2	#3	#4	#5	#6
1	5.6	gnf1m05861_a_at	NM_170727	1110030K16	secretoglobin, family 3A, member 1
2	5.4	gnf1m05862_a_at	NM_054038	8430440N01	secretoglobin, family 3A, member 2
3	5.1	gnf1m02825_a_at	NM_011478		small proline-rich protein 3
4	4.8	gnf1m02912_a_at	NM_011681	I530005I22	secretoglobin, family 1A, member 1 (uteroglobin)
5	4.8	gnf1m29223_a_at	XM_923104	4930443F05	cytokine like 1
6	4.7	gnf1m23262_a_at		4833442E01	keratin complex 1, acidic, gene 13
7	4.6	gnf1m27118_at	NM_001024478	C630001B07	RIKEN cDNA 1110049B09 gene
8	4.5	gnf1m11157_a_at	NM_019728	2310011K19	defensin beta 4
9	4.5	gnf1m29986_a_at	NM_177369		myosin, heavy polypeptide 8, skeletal muscle, perinatal
10	4.4	gnf1m01366_a_at	NM_008475		keratin complex 2, basic, gene 4
11	4.3	gnf1m02795_a_at	NM_011414	2310075E18	secretory leukocyte peptidase inhibitor
12	4.3	gnf1m18383_at	XM_918929	2310001H18	hypothetical LOC545549
13	4.2	gnf1m34138_at	XM_904952		cDNA sequence BC038167
14	4.1	gnf1m00789_a_at	NM_007424		aggrecan 1
15	4.1	gnf1m18385_at		2310002A05	RIKEN cDNA 2310002A05 gene

No. 40, CD4+T-cells specific genes

#1	#2	#3	#4	#5	#6
1	6.0	gnf1m05717_a_at	NM_033042	A430110L22	tumor necrosis factor receptor superfamily, member 25
2	5.7	gnf1m01869_a_at	NM_009400	C130084C11	tumor necrosis factor receptor superfamily, member 18
3	4.7	gnf1m04233_a_at	NM_022888	0910001L11	folate receptor 4 (delta)
4	4.6	gnf1m32609_at	XM_909582		immunoglobulin heavy chain variable region
5	4.5	gnf1m00913_a_at	NM_007650	F430014J22	CD5 antigen
6	4.5	gnf1m04349_a_at	NM_023684	F830221O09	Lck interacting transmembrane adaptor 1
7	4.5	gnf1m31021_a_at	NM_175258	E330007P07	Rap guanine nucleotide exchange factor (GEF) 6
8	4.4	gnf1m34314_at			similar to T-cell receptor beta chain VNDNJC precursor
9	4.4	gnf1m08477_a_at	NM_172293	D130052A12	cDNA sequence BC038822
10	4.3	gnf1m22690_a_at	NM_177320	G530023B10	phosphoinositide-3-kinase, regulatory subunit 5, p101
11	4.3	gnf1m08249_a_at	NM_173766	E430020L17	RIKEN cDNA A630023P12 gene
12	4.1	gnf1m24046_a_at	XM_915161	5830405F06	similar to T-cell receptor beta chain V region 86T1 precursor
13	4.1	gnf1m02904_a_at	NM_011659		tumor necrosis factor receptor superfamily, member 4
14	4.0	gnf1m10816_a_at	NM_009539	E430037O03	zeta-chain (TCR) associated protein kinase

No. 41, epidermis specific genes

#1	#2	#3	#4	#5	#6
1	5.0	gnf1m21641_at		4832428G11	RIKEN cDNA 4832428G11 gene
2	4.9	gnf1m28593_at	NM_030601	5830469K03	chloride channel calcium activated 2
3	4.8	gnf1m07746_a_at	NM_130857	A030006N06	keratin associated protein 16-5
4	4.7	gnf1m20436_a_at	XM_912879	A630098G03	RIKEN cDNA A630098G03 gene
5	4.6	gnf1m02471_a_at	NM_010676		keratin associated protein 8-2
6	4.4	gnf1m05953_at	NM_130870		keratin associated protein 16-1
7	4.3	gnf1m04524_a_at	NM_025420	4833420N21	late cornified envelope 5A
8	4.2	gnf1m11849_a_at	NM_024450	7530414A03	stearoyl-coenzyme A desaturase 3
9	4.2	gnf1m15703_at			keratin associated protein 16-9
10	4.1	gnf1m03251_at	NM_013713		keratin associated protein 15
11	4.1	gnf1m19913_at	NM_001013804	9930021H12	filaggrin 2
12	4.0	gnf1m19028_at		4733401I12	RIKEN cDNA 4733401I12 gene

No. 42, preoptic specific genes

#1	#2	#3	#4	#5	#6
1	5.4	gnf1m10962_a_at	NM_011025	0710008H05	oxytocin
2	5.3	gnf1m02041_at	NM_009732	A230025O05	arginine vasopressin
3	5.3	gnf1m12931_a_at	NM_177121	D430022H10	RIKEN cDNA B930095G15 gene
4	4.9	gnf1m13910_at		6330406O05	RIKEN cDNA 6330406O05 gene
5	4.8	gnf1m30112_a_at	XM_619443		RIKEN cDNA 0610007P22 gene
6	4.5	gnf1m30314_a_at	NM_029971	A230109K23	pro-melanin-concentrating hormone
7	4.4	gnf1m02349_a_at	NM_010410		hypocretin
8	4.3	gnf1m10035_a_at	XM_918655	D630008O05	dynein, axonemal, heavy chain 1
9	4.1	gnf1m01886_a_at	NM_009426	2410044F19	thyrotropin releasing hormone
10	4.1	gnf1m00887_a_at	NM_007588	A230103M05	calcitonin receptor

No. 43, adipose tissue specific genes

#1	#2	#3	#4	#5	#6
1	6.3	gnf1m11918_a_at	NM_008324	9230107E06	indoleamine-pyrrole 2,3 dioxygenase
2	5.4	gnf1m04226_a_at	NM_022814	9430006B19	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1
3	5.0	gnf1m10602_a_at	NM_009704	9130206K13	amphiregulin
4	4.9	gnf1m16461_a_at		2310076O14	apolipoprotein L, 6
5	4.8	gnf1m03098_at			ENSMUST00000038079 transcript (in rel.37.34e)
6	4.3	gnf1m11678_a_at	NM_008493	D730002G04	leptin
7	4.2	gnf1m26921_at	NM_011994	C230066M19	ATP-binding cassette, sub-family D (ALD), member 2
8	4.1	gnf1m23821_a_at	NM_010719	4932412K13	lipase, hormone sensitive

9	4.1	gnf1m05871_a_at	NM_054071		fibroblast growth factor receptor-like 1

No. 44, embryo day 7.5 specific genes

#1	#2	#3	#4	#5	#6
1	5.8	gnf1m02673_a_at	NM_011165	C430019L15	prolactin-like protein A
2	5.0	gnf1m01983_at	NM_009627	G730018N16	adrenomedullin
3	4.9	gnf1m03727_a_at	NM_019540	C430005G24	pore forming protein-like
4	4.8	gnf1m03030_a_at	NM_011927		CEA-related cell adhesion molecule 9
5	4.8	gnf1m10359_a_at	NM_172156	C430027I15	chorionic somatomammotropin hormone 1
6	4.1	gnf1m09471_a_at	NM_019539	5630400J12	cathepsin 7
7	4.1	gnf1m02264_a_at	NM_010235	G830028K10	fos-like antigen 1
8	4.1	gnf1m02650_x_at	NM_011118		proliferin 2
9	4.1	gnf1m08880_at	NM_032006	C430029P05	matrix metallopeptidase 1a (interstitial collagenase)

No. 45, CD8+T-cells specific genes

#1	#2	#3	#4	#5	#6
1	5.9	gnf1m32844_at		F830032L03	G protein-coupled receptor 114
2	5.2	gnf1m33464_at	XM_204856	5830463C22	similar to apolipoprotein L, 3 (predicted)
3	4.8	gnf1m22690_a_at	NM_177320	G530023B10	phosphoinositide-3-kinase, regulatory subunit 5, p101
4	4.7	gnf1m02458_a_at	NM_010654	A430011E14	killer cell lectin-like receptor, subfamily D, member 1
5	4.5	gnf1m31021_a_at	NM_175258	E330007P07	Rap guanine nucleotide exchange factor (GEF) 6
6	4.3	gnf1m05592_a_at		E430004O20	chemokine (C-X-C motif) receptor 6
7	4.1	gnf1m11208_a_at	NM_024253	E430014G21	natural killer cell group 7 sequence
8	4.1	gnf1m15860_a_at	XM_915243		T-cell receptor beta, variable 13

No. 46, trigeminal specific genes

#1	#2	#3	#4	#5	#6
1	5.3	gnf1m07822_a_at	NM_153105	F530003O17	claudin 19
2	5.1	gnf1m06563_a_at	NM_145555	I530014I18	RIKEN cDNA A330049M08 gene
3	4.3	gnf1m01989_a_at	NM_009635	F730316L09	advillin
4	4.3	gnf1m03206_a_at	NM_013639	7120476M05	peripherin 1
5	4.3	gnf1m09535_s_at	NM_009134		sodium channel, voltage-gated, type X, alpha
6	4.1	gnf1m16713_at	NM_001033954		calcitonin/calcitonin-related polypeptide, alpha
7	4.1	gnf1m29643_a_at	NM_183000	3830432N09	amiloride-sensitive cation channel 3
8	4.0	gnf1m09621_a_at	NM_008117	5730422D01	growth hormone

No. 47, uterus specific genes

#1	#2	#3	#4	#5	#6
1	6.0	gnf1m02820_at	NM_011472		small proline-rich protein 2F
2	5.8	gnf1m11079_a_at	NM_019511	1600021K13	receptor (calcitonin) activity modifying protein 3
3	5.6	gnf1m02616_a_at	NM_011059	A030006O20	peptidyl arginine deiminase, type I
4	4.7	gnf1m05781_a_at	NM_053085	5031404B19	transcription factor 23
5	4.4	gnf1m01564_a_at	XM_915139	F630107K01	peptidyl arginine deiminase, type II
6	4.2	gnf1m28608_a_at		F630204G22	hydroxysteroid 11-beta dehydrogenase 2
7	4.2	gnf1m32206_at			gene model 247, (NCBI)
8	4.1	gnf1m29898_a_at	NM_008381	4022431B02	inhibin beta-B

No. 48, embryo day 10.5 specific genes

#1	#2	#3	#4	#5	#6
1	4.4	gnf1m23332_at		2700008K06	unclassifiable
2	4.4	gnf1m11633_a_at	NM_010405	5730460L13	hemoglobin X, alpha-like embryonic chain in Hba complex
3	4.4	gnf1m16677_a_at	NM_009234	6230403H02	SRY-box containing gene 11
4	4.3	gnf1m22972_at		1110038H03	SRY-box containing gene 11
5	4.1	gnf1m01653_a_at	NM_008988	D030056K15	putative neuronal cell adhesion molecule
6	4.1	gnf1m12588_a_at	NM_172412	C530010J15	glypican 2 (cerebroglycan)
7	4.0	gnf1m03436_a_at	NM_016701	1190008F12	nestin

No. 49, hippocampus specific genes

#1	#2	#3	#4	#5	#6
1	6.4	gnf1m08348_at	NM_178887	B230372M18	fibrinogen C domain containing 1
2	5.3	gnf1m08349_a_at	NM_178887	B230372M18	fibrinogen C domain containing 1
3	5.1	gnf1m15269_at		8030496P19	glycoprotein m6b
4	5.0	gnf1m08380_a_at	NM_177193	B930052A04	immunoglobulin superfamily containing leucine-rich repeat 2
5	4.6	gnf1m07985_at	NM_177854	6030405A18	RIKEN cDNA 6030405A18 gene
6	4.6	gnf1m24427_at		6430587E11	similar to COPINE VII [Homo sapiens]
7	4.2	gnf1m26520_a_at		D930018L04	glutamate receptor, ionotropic, NMDA2A (epsilon 1)

No. 50, hypothalamus specific genes

#1	#2	#3	#4	#5	#6
1	4.8	gnf1m30314_a_at	NM_029971	A230109K23	pro-melanin-concentrating hormone
2	4.6	gnf1m11894_a_at	NM_178896	9030622J04	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)
3	4.5	gnf1m02041_at	NM_009732	A230025O05	arginine vasopressin
4	4.2	gnf1m25410_at		A230027G02	adenylate cyclase activating polypeptide 1
5	4.1	gnf1m18631_at	XM_909450	1110017D07	PDZ domain containing RING finger 4
6	4.0	gnf1m02349_a_at	NM_010410		hypocretin
7	4.0	gnf1m00792_a_at	NM_007427	A430075H22	agouti related protein

No. 51, lymph node specific genes

#1	#2	#3	#4	#5	#6
1	6.0	gnf1m00984_s_at	NM_007781	I830081A20	colony stimulating factor 2 receptor, beta 1, low-affinity (granulocyte-macrophage)
2	4.4	gnf1m00985_a_at	NM_007781		colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage)
3	4.4	gnf1m02509_a_at	NM_010766	I920095G17	macrophage receptor with collagenous structure
4	4.2	gnf1m25017_at		9630004O19	unclassifiable
5	4.2	gnf1m03009_at	NM_011888	G630025K01	chemokine (C-C motif) ligand 19
6	4.1	gnf1m02647_a_at	NM_011109		phospholipase A2, group IID
7	4.0	gnf1m30032_at	NM_026972	A530056D21	CD209b antigen

No. 52, ovary specific genes

#1	#2	#3	#4	#5	#6
1	6.0	gnf1m16904_a_at	NM_007696		oviductal glycoprotein 1
2	5.4	gnf1m13270_a_at	NM_010564		inhibin alpha
3	4.9	gnf1m21820_at		9030017N01	unclassifiable
4	4.5	gnf1m00997_a_at	NM_007809	6030448H16	hypothetical cytochrome P450, family 17, subfamily a, polypeptide 1
5	4.5	gnf1m19802_at		9530076L18	hypothetical protein 9530076L18
6	4.4	gnf1m05187_a_at	NM_027582	4921521F21	RIKEN cDNA 4921521F21 gene
7	4.2	gnf1m28954_a_at	NM_001012434		potassium channel tetramerisation domain containing 14

No. 53, dorsal striatum specific genes

#1	#2	#3	#4	#5	#6
1	4.3	gnf1m29979_at	NM_197945	5730599K07	ProSAPiP1 protein
2	4.2	gnf1m02144_a_at	NM_009946		complexin 2
3	4.2	gnf1m04217_a_at	NM_022427		G-protein coupled receptor 88
4	4.1	gnf1m34682_at		A830030P14	G protein-coupled receptor 6
5	4.1	gnf1m02722_a_at	NM_011268		regulator of G-protein signaling 9

No. 54, embryo day 8.5 specific genes

#1	#2	#3	#4	#5	#6
1	4.6	gnf1m04647_a_at	NM_025684	5730557A08	RIKEN cDNA 5730521E12 gene
2	4.3	gnf1m13899_a_at		G630096F14	carbonic anhydrase 7
3	4.2	gnf1m11633_a_at	NM_010405	5730460L13	hemoglobin X, alpha-like embryonic chain in Hba complex
4	4.0	gnf1m11262_a_at	NM_008219	2810007M22	hemoglobin Z, beta-like embryonic chain

No. 55, embryo day 9.5 specific genes

#1	#2	#3	#4	#5	#6
1	4.6	gnf1m22666_at	NM_198605	F630043A04	RIKEN cDNA F630043A04 gene
2	4.3	gnf1m28731_a_at		0610016J10	RIKEN cDNA 0610016J10 gene
3	4.2	gnf1m11633_a_at	NM_010405	5730460L13	hemoglobin X, alpha-like embryonic chain in Hba complex
4	4.1	gnf1m19351_at		5930402A21	crumbs homolog 2 (Drosophila)

No. 56, spinal cord lower specific genes

#1	#2	#3	#4	#5	#6
1	5.6	gnf1m03022_a_at	NM_011910		urotensin 2
2	4.3	gnf1m24400_at		6430545K04	glycine receptor, alpha 1 subunit
3	4.1	gnf1m20806_a_at		B230397M16	glycine receptor, alpha 1 subunit

No. 57, substantia nigra specific genes

#1	#2	#3	#4	#5	#6
1	5.2	gnf1m02174_a_at	NM_010020	9330165P06	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3
2	4.3	gnf1m23556_a_at		A130081F14	inferred: protein associating with small stress protein PASS1 {Rattus norvegicus}
3	4.1	gnf1m08549_at	NM_177057	E230015B07	RIKEN cDNA E230015B07 gene

No. 58, amygdala specific genes

#1	#2	#3	#4	#5	#6
1	4.8	gnf1m31999_at	XM_907532		cadherin 9
2	4.1	gnf1m16736_at			LIM domain only 3

No. 59, cerebral cortex specific genes

#1	#2	#3	#4	#5	#6
1	4.3	gnf1m08380_a_at	NM_177193	B930052A04	immunoglobulin superfamily containing leucine-rich repeat 2

No. 60, frontal cortex specific genes

#1	#2	#3	#4	#5	#6
1	4.3	gnf1m30549_at	NM_182839	C630015P20	RIKEN cDNA 2900041A09 gene

No. 61, spinal cord upper specific genes

#1	#2	#3	#4	#5	#6
1	4.1	gnf1m25497_a_at		A230103O17	glial fibrillary acidic protein

Appendix Table 2a. Testis-specificity of the genes, representative 8-mer and annotation

Data of the 1st to the 634th testis-specific genes.

#1 Expression level ranking in this group as determined by testis specificity.

#2 Classification of the representative 8-mer.

#3 Testis-specificity level.

#1	Microarray ID	#2	Representative 8-mer	Clone ID	#3	Gene Ontology Classification			Annotation
						Molecular function	Biological process	Cellular component	
1	gnf1m18736_a_at	C3	GGGCGGGG	1700015G11	7.30				unclassifiable
2	gnf1m07925_a_at	A13*	TCACAGAG	4931432L23	7.16	binding	physiological process, cellular process	cell part	hypothetical Zn-finger, B-box/Zinc finger B-box type profile containing protein Mus musculus
3	gnf1m11104_a_at	C3	GGGCGGGG	4930544H24	7.14	catalytic activity, binding	regulation of biological process	cell part	lactate dehydrogenase C (Ldhc)
4	gnf1m04918_a_at	C1	GGGAGGGG	4930551D19	7.11	catalytic activity, binding	regulation of biological process	cell part	hypothetical Serine proteases, trypsin family containing protein
5	gnf1m03878_a_at	C2*	GCCCCGCC	1700008H15	7.10				testis expressed gene 101
6	gnf1m16565_a_at	A1*	TGACATCA	1700018C11	7.08				hypothetical protein
7	gnf1m04973_a_at	A3	ATGTCACA	1700086N05	7.07				testis-specific leucine zipper protein nurit
8	gnf1m18408_at	B15	AAAAAAAA	1700007F22	7.04	enzyme regulator activity	response to stimulus	organelle, cell part	serine peptidase inhibitor, Kazal type 2
9	gnf1m02827_a_at	A1*	TGACATCA	1700010L20	7.03	binding	cellular process, physiological process	organelle, cell part	zinc and ring finger 4
10	gnf1m01622_a_at	A13*	TCACAGAG	1700007K08	7.02	binding	cellular process, physiological process, reproduction, development	cell part	protamine 2
11	gnf1m04562_a_at	A1	TGATGTCA	1700025H18	7.02				hypothetical protein
12	gnf1m05640_a_at	A13*	TCACAGAG	4933431I08	7.00	catalytic activity, binding	physiological process, cellular process	cell part	phosphoglycerate kinase 2
13	gnf1m14004_a_at	A1	TGATGTCA	1700029I08	7.00	structural molecule activity, binding	physiological process, cellular process	cell part	hypothetical Actin-like ATPase domain structure containing protein
14	gnf1m05106_a_at	B35	CTCTCTCT	1700008P20	6.98	binding	physiological process, cellular process	cell part, organelle part, protein complex, organelle	Tescalcin (TSC)
15	gnf1m02291_a_at	B6	CAGCCAAT	4922501K24	6.93	catalytic activity, binding	cellular process, reproduction, development, physiological process	cell part	glycerol kinase-like 1
16	gnf1m08571_a_at	B10	GGCAGCTG	1700049L16	6.93				hematological and neurological expressed 1-like Mus musculus
17	gnf1m05233_a_at	A10	ACATCACA	1700018F16	6.93	catalytic activity, binding	physiological process, cellular process	cell part	dipeptidase 3
18	gnf1m29029_a_at	C3	GGGCGGGG	4930553D05	6.90				unclassifiable
19	gnf1m01872_a_at	A1	TGATGTCA	1700029H23	6.89	binding	physiological process, cellular process, regulation of biological process	cell part	hypothetical transition protein 1
20	gnf1m14508_a_at	A2*	CATTGTGA	1700095G12	6.89	catalytic activity, binding	cellular process, physiological process	cell part	C-5 cytosine-specific DNA methylase containing protein
21	gnf1m04031_a_at	B27	CCTCTCTC	1700027G07	6.87	binding, transcription regulator activity	physiological process, cellular process	extracellular region, extracellular region part	hypothetical activator of CREM in testis
22	gnf1m08595_a_at	B15	AAAAAAAA	NM_177901	6.87				hypothetical protein
23	gnf1m23057_a_at	B5	TGGGAGGA	1700112D12	6.86				unclassifiable
24	gnf1m21680_a_at	C3	GGGCGGGG	4930526D03	6.86				PUTATIVE NOVEL PROTEIN (FRAGMENT) [Homo sapiens]
25	gnf1m18731_a_at	B37	TGGGCGGG	1700007H20	6.85				predicted heat shock protein, alpha-crystallin-related, B9
26	gnf1m02317_a_at	A26	GAGCTCTG	1700025C22	6.84				germ cell-specific gene 1
27	gnf1m03620_a_at	A2	TCACAATG	1700007I14	6.84	binding	response to stimulus	cell part, organelle, protein complex, organelle part	histone H1-like protein in spermatids 1
28	gnf1m29482_a_at	B39	CCCCACCC	4933409I12	6.82	catalytic activity, binding	regulation of biological process	cell part, organelle	gametogenetin binding protein 1
29	gnf1m02157_a_at	B33*	TGTGTGTG	1700027J17	6.82	enzyme regulator activity	reproduction, development, cellular process	cell part	cystatin 9
30	gnf1m16813_a_at	C3	GGGCGGGG	1700003F12	6.81				Bcl-2-like protein
31	gnf1m16162_a_at	A9*	CTTTGTGA	1700001F04	6.81				cysteine-rich perinuclear theca 12
32	gnf1m13969_a_at	A37	CAGAGAGA	4933433O19	6.81				unclassifiable
33	gnf1m18818_a_at	A1	TGATGTCA	1700015E13	6.80				unclassifiable
34	gnf1m07713_at	C3*	CCCCGCCC	4930583E11	6.80				TATA-binding protein-like factor-interacting protein isoform 1
35	gnf1m05107_a_at	A22	TCTGAGGC	4930403C08	6.80	binding	physiological	organelle, cell	EF-hand containing protein

							process, cellular process, reproduction	part	
36	gnf1m21688_a_at	A1	TGATGTCA	4930571K11	6.79				hypothetical protein LOC629141
37	gnf1m07749_a_at	A16*	TGAGGTCA	4930503O21	6.78	transporter activity, catalytic activity	regulation of biological process, physiological process, cellular process	cell part, organelle, protein complex, organelle part	cytochrome c oxidase subunit VIIb2
38	gnf1m01424_a_at	A1	TGATGTCA	4933417G15	6.76				sperm mitochondria-associated cysteine-rich protein
39	gnf1m14498_a_at	A2	TCACAATG	1700011F03	6.75				hypothetical protein
40	gnf1m10448_a_at	A44	CTCTGTCT	1700001N01	6.75				spermatogenesis associated 4
41	gnf1m05189_a_at	B15	AAAAAAAA	4921509E07	6.70				hypothetical protein
42	gnf1m04371_a_at	B38*	GGGGTGGG	1700012M14	6.69				hypothetical Yeast DNA-binding domain containing protein
43	gnf1m03516_a_at	A2	TCACAATG	4930567P17	6.68	enzyme regulator activity, binding	interaction between organisms	organelle, cell part	ornithine decarboxylase antizyme 3 (Oaz3)
44	gnf1m05703_a_at	B12	GCCTCCTG	4930402K08	6.67	catalytic activity, binding	response to stimulus, interaction between organisms, physiological process	cell part, organelle, protein complex, organelle part	testis-specific serine kinase 6
45	gnf1m05614_a_at	A1*	TGACATCA	NM_030744	6.66	enzyme regulator activity, binding			ropporin, rhophilin associated protein 1 (Ropn1)
46	gnf1m30318_a_at	A48	CTCCCAGA	1700122B10	6.65				ATPase, Class I, type 8B, member 3
47	gnf1m05024_a_at	A26	GAGCTCTG	4930470K20	6.65	binding	regulation of biological process	cell part	weakly similar to LATE HISTONE H2A.1 [Psammechinus miliaris]
48	gnf1m15067_a_at	A16*	TGAGGTCA	4930571C24	6.63				hypothetical Proline-rich region profile containing protein
49	gnf1m05319_at	A34	TGCCCAGG	1700052K11	6.60	catalytic activity	development, regulation of biological process	organelle, cell part	tousled-like kinase 2 (Arabidopsis)
50	gnf1m17380_at	A46	AGGAGCAG	NM_183103	6.59	catalytic activity			similar to testis-specific serine protease-6 (Tessp6)
51	gnf1m04906_a_at	B1	TGCCTCTG	1700006G11	6.58				hypothetical ARM repeat structure containing protein
52	gnf1m05831_a_at	B3	CTCTTCCT	1700102P08	6.54				hypothetical protein
53	gnf1m28824_a_at	B7	TGACGTCA	1700021P22	6.54				hypothetical protein
54	gnf1m05103_at	B5	TGGGAGGA	4922505K21	6.54	binding, transcription regulator activity	physiological process, cellular process	cell part, protein complex, organelle part, organelle	CKLF-like MARVEL transmembrane domain containing 2A
55	gnf1m31282_a_at	A2*	CATTGTGA	4922505E12	6.54				beta tubulin containing protein (Fragment) Mus musculus
56	gnf1m29239_s_at	A49	TCTCAGCC	1700051A02	6.52				weakly similar to Phosphatidylethanolamine binding protein [Homo sapiens]
57	gnf1m22667_a_at	A1	TGATGTCA	4930550F01	6.51	binding, catalytic activity	physiological process, cellular process	organelle part, organelle, cell part	immunity-related GTPase family, cinema 1
58	gnf1m29365_a_at	A34	TGCCCAGG	1700001P01	6.51				hypothetical protein
59	gnf1m17232_a_at	C1*	CCCCTCCC	1700019A02	6.50				Glutamic acid-rich region containing protein
60	gnf1m16484_a_at	A16	TGACCTCA	1700015M15	6.50				PLAC8-like 1
61	gnf1m18668_a_at	B25	CCTTCCTC	4921521J18	6.50	transporter activity	regulation of biological process, physiological process, cellular process	cell part, protein complex	hypothetical solute carrier organic anion transporter family, member 6c1
62	gnf1m30974_a_at	B6	CAGCCAAT	1700007F21	6.50				predicted cytochrome c oxidase, subunit VIIIc
63	gnf1m19018_a_at	C3	GGGCGGGG	1700067P11	6.48	transporter activity, catalytic activity	physiological process, cellular process	extracellular region part	cytochrome c oxidase subunit VIb polypeptide 2
64	gnf1m05191_a_at	B2	AGGAAGAA	NM_027617	6.47				spermatogenesis associated 1 (Spata1)
65	gnf1m05036_a_at	B7	TGACGTCA	4933406G04	6.47				IQ motif containing F3
66	gnf1m16969_a_at	A32	TCTCTGTG	1700011H22	6.46				hypothetical protein
67	gnf1m18161_at	A13*	TCACAGAG	1700036B12	6.46				unclassifiable
68	gnf1m04422_a_at	A1	TGATGTCA	1700094C09	6.45				hypothetical protein
69	gnf1m01267_a_at	B11	AGCAGCTG	1700007A15	6.45	binding	physiological process, cellular process, reproduction, development	extracellular region	DnaJ (Hsp40) homolog, subfamily B, member 3
70	gnf1m11095_a_at	B39	CCCCACCC	1700020D05	6.43				weakly similar to predicted mage-g2 protein
71	gnf1m23194_a_at	A12	CTGTGACA	1700123E07	6.42	binding	response to stimulus, development, regulation of biological process, physiological process, cellular process	cell part, organelle	protamine 1
72	gnf1m16837_a_at	C3	GGGCGGGG	4932435D11	6.42	binding, catalytic activity	physiological process, cellular process	cell part, organelle	a disintegrin and metallopeptidase domain 2
73	gnf1m05482_at	A1	TGATGTCA	1700012A03	6.40				hypothetical protein
74	gnf1m30466_a_at	C2	GGCGGGGC	4933407K12	6.40	transcription regulator activity, binding	regulation of biological process, physiological process, cellular process	cell part	zinc finger protein 597
75	gnf1m03233_a_at	A40	CTGAGGCT	1700025P05	6.40				weakly similar to t-complex protein 11
76	gnf1m01645_a_at	A28	GGTCCTCT	NM_008978	6.40	catalytic activity			protein tyrosine phosphatase, non-receptor type 20 (Ptpn20)
77	gnf1m04833_a_at	A16*	TGAGGTCA	1700093K21	6.39				hypothetical protein
78	gnf1m14421_at	C1	GGGAGGGG	1700056P15	6.38	catalytic activity, binding	physiological process, cellular	organelle, cell part	thioredoxin domain containing 3 (spermatozoa)

							process		
79	gnf1m15372_a_at	C3	GGGCGGGG	1700006F03	6.37	enzyme regulator activity	physiological process, cellular process, reproduction	cell part, organelle	predicted cystatin 12
80	gnf1m00200_a_at	A44	CTCTGTCT	4930425N13	6.36				similar to hexosaminidase A
81	gnf1m16785_at	A1	TGATGTCA	1700012F11	6.34				weakly similar to predicted late cornified envelope-like proline-rich 1-like [Macaca mulatta]
82	gnf1m13528_a_at	B16	CAGGCTGG	4930553D19	6.32				MAS20 protein import receptor signature containing protein
83	gnf1m11098_a_at	A2*	CATTGTGA	1700027M20	6.31	transcription regulator activity, binding	physiological process, cellular process	cell part	spermatogenic Zip 1
84	gnf1m13649_a_at	A37	CAGAGAGA	4933424C13	6.29	binding	reproduction, development	cell part, protein complex, organelle	weakly similar to SH2 domain containing 6, transcript variant 3
85	gnf1m16782_a_at	B35	CTCTCTCT	1700030E15	6.29				PMP22 claudin domain-containing protein (Pmp22cd)
86	gnf1m03152_a_at	C3	GGGCGGGG	NM_013558	6.29	binding			heat shock protein 1-like (Hspa1l)
87	gnf1m03870_a_at	A3	ATGTCACA	1700016F14	6.28	binding	physiological process, cellular process	organelle, cell part	DnaJ (Hsp40) homolog, subfamily B, member 8
88	gnf1m23680_a_at	C2*	GCCCCGCC	4921515A04	6.27	binding, transcription regulator activity	physiological process, cellular process	cell part	septin 10
89	gnf1m22992_a_at	A44	CTCTGTCT	4933402H05	6.26	binding	physiological process, cellular process	cell part	hypothetical G-protein beta WD-40 repeats containing protein
90	gnf1m05022_a_at	A2	TCACAATG	4931415M17	6.23	structural molecule activity, binding	physiological process, cellular process	cell part, organelle part, organelle	hypothetical protein
91	gnf1m07572_a_at	A13*	TCACAGAG	4930579G22	6.23				predicted Nuclear protein 1 (Protein p8) (Candidate of metastasis 1) Canis familiaris
92	gnf1m23028_a_at	B39*	GGGTGGGG	1700025B10	6.22				unclassifiable
93	gnf1m11087_a_at	A1	TGATGTCA	1700007A05	6.22	binding, transporter activity	regulation of biological process	organelle, cell part	transition protein 2
94	gnf1m18372_a_at	A9*	CTTTGTGA	1700006H02	6.22				cysteine-rich perinuclear theca 3 (Cypt3)
95	gnf1m03522_a_at	B9	CTGAGCCA	1700003P16	6.22	catalytic activity, binding	reproduction, development, cellular process	extracellular region, cell part	protein phosphatase 1D magnesium-dependent, delta isoform
96	gnf1m30439_a_at	C2	GGCGGGGC	1700047N01	6.21				nucleoporin 50-like, homologue [Rattus norvegicus]
97	gnf1m21699_a_at	A1	TGATGTCA	4933400K24	6.21				ubiquilin 3
98	gnf1m04674_a_at	A2*	CATTGTGA	NM_025743	6.21	binding			weakly similar to F-actin capping protein subunit alpha 1
99	gnf1m09684_a_at	A1	TGATGTCA	1700029K01	6.21				weakly similar to coiled-coil domain containing 46
100	gnf1m09290_s_at	A1	TGATGTCA	1700001F09	6.20				hypothetical Cytochrome c family heme-binding site containing protein
101	gnf1m16418_a_at	A16	TGACCTCA	1700047I16	6.19				aldehyde dehydrogenase family 5, subfamily A1
102	gnf1m21711_at	C4	GGGGCGGG	4933433K01	6.18	catalytic activity	development, physiological process, cellular process	cell part, protein complex, organelle part, organelle	hypothetical Phospholipase D/nuclease structure containing protein
103	gnf1m11535_a_at	B15	AAAAAAAA	1700021F12	6.16	binding	physiological process, cellular process	cell part	DnaJ (Hsp40) homolog, subfamily B, member 7
104	gnf1m31557_at	A41	GAGGCCAG	4933416C03	6.16				TATA box binding protein-associated factor, RNA polymerase II, Q
105	gnf1m04827_a_at	B26	AAAACAAA	1700038F02	6.16	catalytic activity	physiological process, cellular process	cell part	lysozyme-like 1
106	gnf1m13309_a_at	A2	TCACAATG	4933411K16	6.15				unclassifiable
107	gnf1m28993_at	B1	TGCCTCTG	4932432C05	6.15				similar to hypothetical P-loop containing nucleotide triphosphate hydrolases structure containing protein Mus musculus
108	gnf1m04975_a_at	A2	TCACAATG	1700129C05	6.14				hypothetical protein
109	gnf1m13089_a_at	A1*	TGACATCA	4933432H20	6.13	catalytic activity	response to stimulus, regulation of biological process	organelle, cell part	tubby-like protein 2
110	gnf1m04681_a_at	B6	CAGCCAAT	1700027I20	6.12	catalytic activity	physiological process, cellular process	cell part, organelle	aldolase 1, A isoform, pseudogene 1
111	gnf1m29783_a_at	A2	TCACAATG	1700125D06	6.11				basic proline-rich protein [Sus scrofa]
112	gnf1m05339_a_at	A15	GGTTGCTA	4930432H15	6.11				hypothetical protein
113	gnf1m29197_a_at	C3	GGGCGGGG	4921523C20	6.11				hypothetical protein
114	gnf1m01836_a_at	B15*	TTTTTTTT	4921503O11	6.11	signal transducer activity, catalytic activity, binding	physiological process, cellular process	cell part	t-complex protein 10a
115	gnf1m18379_a_at	A1*	TGACATCA	1700028F16	6.10				transmembrane and coiled-coil domains 2
116	gnf1m04828_a_at	C2*	GCCCCGCC	1700065E01	6.10				ATPase, Class I, type 8B, member 3
117	gnf1m03186_a_at	A13	CTCTGTGA	NM_013615	6.10	structural molecule activity			outer dense fiber of sperm tails 2
118	gnf1m29413_a_at	C3	GGGCGGGG	4922505A09	6.10				unnamed protein product putative GE36-like
119	gnf1m16899_a_at	C3	GGGCGGGG	4921508H09	6.10				IQ motif containing H
120	gnf1m17304_a_at	A46	AGGAGCAG	1700029M20	6.10				unclassifiable
121	gnf1m02292_a_at	B28	GCAGCTGC	1700037H23	6.09	catalytic activity, binding	cellular process, physiological process, reproduction, development	cell part, organelle part, organelle	glycerol kinase 2
122	gnf1m05467_a_at	A44	CTCTGTCT	NM_029472	6.07	catalytic activity			glutathione S-transferase, theta 4 (Gstt4)

123	gnf1m28744_a_at	A41	GAGGCCAG	1700001J03	6.06	enzyme regulator activity	physiological process	extracellular region, extracellular region part	Ras GEF structure containing protein
124	gnf1m10484_a_at	B15*	TTTTTTTT	NM_029019	6.06	binding, transporter activity			hypothetical StAR-related lipid transfer (START) domain containing 6
125	gnf1m04449_a_at	A1*	TGACATCA	1700051E21	6.06	structural molecule activity, binding	physiological process, cellular process, regulation of biological process	cell part	weakly similar to hypothetical actin-like 7b
126	gnf1m17100_a_at	A50	CCTGGCTG	4921517L17	6.06				Cyclic nucleotide-binding domain/cAMP/cGMP binding motif profile containing protein, [Mus musculus]
127	gnf1m13320_a_at	A14	TTGTGAGG	1700058G18	6.05				hypothetical protein
128	gnf1m18464_x_at	B39	CCCCACCC	4933402N22	6.04				spermatogenesis associated glutamate (E)-rich protein 1, pseudogene 1
129	gnf1m03507_a_at	A27	AGGTTCTG	4930590O05	6.04	translation regulator activity, binding	cellular process, physiological process, reproduction, development, regulation of biological process	cell part	Y box protein 2
130	gnf1m13535_a_at	A1	TGATGTCA	1700006E09	6.02				hypothetical protein
131	gnf1m29281_a_at	B15	AAAAAAAA	4930560D22	6.01	binding	physiological process, cellular process	cell part	leucine rich repeat containing 36
132	gnf1m00010_at	A2	TCACAATG	G630012H19	6.00	catalytic activity, binding		organelle, cell part	testis specific protein kinase 1
133	gnf1m18469_a_at	A18	TCTGTGAG	4922502J23	6.00				putative unnamed protein product
134	gnf1m13311_a_at	A1	TGATGTCA	4933436O18	6.00				similar to ankyrin repeat and SOCS box-containing protein 17
135	gnf1m05152_a_at	A4	GATGTCAC	NM_027304	5.99	binding			H1 histone family, member N, testis-specific (H1fnt)
136	gnf1m05413_a_at	A13	CTCTGTGA	4930500C14	5.98	transporter activity, catalytic activity	response to stimulus, physiological process, cellular process	extracellular region, extracellular region part	ATPase, H+ transporting, lysosomal V1 subunit E2
137	gnf1m15286_a_at	A13	CTCTGTGA	1700054J20	5.97				hypothetical protein
138	gnf1m17051_a_at	A5	ATGTCATA	1700034O15	5.97				hypothetical protein
139	gnf1m17239_a_at	B34	GGCAGAGG	1700016M24	5.97				ARM repeat structure containing protein
140	gnf1m04675_a_at	B28	GCAGCTGC	4933415F23	5.97	enzyme regulator activity, binding	physiological process, cellular process	cell part, organelle part, organelle	protein phosphatase 1, regulatory (inhibitor) subunit 14B (Ppp1r14b) Mus musculus
141	gnf1m02858_a_at	A32	TCTCTGTG	4930512O07	5.96	structural molecule activity	cellular process, physiological process	cell part, organelle	tektin 1
142	gnf1m04830_a_at	A26	GAGCTCTG	1700124G06	5.95				hypothetical protein
143	gnf1m13343_at	A1*	TGACATCA	1700007N18	5.95				coiled-coil domain containing 54
144	gnf1m14497_at	B16	CAGGCTGG	1700016H13	5.93				hypothetical protein
145	gnf1m09323_a_at	A13	CTCTGTGA	1700030B07	5.93				hypothetical protein
146	gnf1m16460_a_at	A2	TCACAATG	4930558A17	5.92				unclassifiable
147	gnf1m04659_a_at	A32	TCTCTGTG	4921504I05	5.92				hypothetical Lysine-rich region profile containing protein
148	gnf1m01977_a_at	A1	TGATGTCA	1700038F08	5.92	structural molecule activity, binding	physiological process, cellular process	cell part, organelle	actin-like 7a
149	gnf1m16879_a_at	C3	GGGCGGGG	1700028D05	5.91				coiled-coil domain containing 19
150	gnf1m11727_a_at	B4	AGGGAGGC	1700120K02	5.90	catalytic activity	physiological process, cellular process	cell part, organelle, protein complex, organelle part	ubiquitin-conjugating enzyme E2, J1
151	gnf1m00890_a_at	A46	AGGAGCAG	4930590H21	5.90	binding, catalytic activity	physiological process, cellular process	organelle, cell part	centrin 1
152	gnf1m32036_at	B39	CCCCACCC	4922503O18	5.89				hypothetical Proline-rich region profile containing protein
153	gnf1m11092_a_at	A47	AGAGAGAC	4922504H01	5.89				phosducin-like 2
154	gnf1m05047_a_at	C3	GGGCGGGG	4930400A03	5.88	binding	physiological process, cellular process	cell part, protein complex, organelle	weakly similar to Suppressor Of Clr family member (soc-2) [Macaca mulatta]
155	gnf1m16355_a_at	A35	TCCAGGAG	1700110M21	5.87				gamma-aminobutyric acid (GABA-B) receptor binding protein
156	gnf1m00498_a_at	A17	CCTAGCAA	NM_026314	5.87	binding			dyslexia susceptibility 1 candidate 1 homolog (human)
157	gnf1m23054_a_at	A1	TGATGTCA	1700119N03	5.86				unclassifiable
158	gnf1m16867_a_at	B28	GCAGCTGC	1700025F22	5.85				hypothetical protein
159	gnf1m13851_a_at	C3	GGGCGGGG	1700023E05	5.84				similar to testicular haploid expressed gene product isoform 2 Rattus norvegicus
160	gnf1m16809_a_at	A1*	TGACATCA	1700029J11	5.84				hypothetical protein
161	gnf1m17150_a_at	A16*	TGAGGTCA	1700017N19	5.83				zinc finger CCCH type containing 11A (MGC134438) Bos taurus
162	gnf1m15272_a_at	A1	TGATGTCA	1700106J16	5.82				hypothetical protein
163	gnf1m17672_at	A51	CAGAGATG	1700080P15	5.82				protocadherin 8
164	gnf1m04678_a_at	A2*	CATTGTGA	4933411N24	5.82				hypothetical protein
165	gnf1m04672_a_at	A2*	CATTGTGA	4931420D14	5.81				Cysteine-rich region containing protein
166	gnf1m09776_a_at	A48	CTCCCAGA	4933402P03	5.81				hypothetical protein
167	gnf1m11493_a_at	A13	CTCTGTGA	4930594D03	5.81	binding	physiological process, cellular process	cell part	capping protein (actin filament) muscle Z-line, alpha 3
168	gnf1m02095_a_at	A23	TGCTTTCC	4922503G10	5.79	binding	physiological process, cellular process	organelle part, cell part	chaperonin subunit 6b (zeta)
169	gnf1m08603_a_at	B3	CTCTTCCT	4933414G08	5.79	binding	physiological process, cellular process,	cell part	spermatogenesis associated 21 (GO:0005509 InterPro|IPR002048)

							regulation of biological process		
170	gnf1m34593_at	A46	AGGAGCAG	4932412L17	5.78				SH3/Fibronectin, type III/Src homology 3 (SH3) domain profile/Fibronectin, type III-like fold containing protein
171	gnf1m15591_a_at	A37	CAGAGAGA	6030447N09	5.78	enzyme regulator activity	physiological process, cellular process	cell part, organelle part, organelle	hypothetical cystatin 8 (cystatin-related epididymal spermatogenic)
172	gnf1m18367_a_at	A1	TGATGTCA	1700001K23	5.77				hypothetical protein
173	gnf1m04557_a_at	A13*	TCACAGAG	1700093C11	5.77				keratin type II (fragment) [Ovis sp.]
174	gnf1m13765_a_at	A2	TCACAATG	1700023B23	5.77				TSC22-related inducible leucine zipper protein 2 homolog [Mus musculus]
175	gnf1m05914_a_at	A39	TTTAAAAA	4921519C19	5.77	binding	cellular process, physiological process, reproduction, development	cell part, organelle part	similar to ring finger protein 36
176	gnf1m08509_a_at	A1*	TGACATCA	4930517I12	5.76				Sad1 and UNC84 domain containing 1
177	gnf1m09369_a_at	B11	AGCAGCTG	1700129L13	5.76	transporter activity	physiological process, cellular process	cell part, protein complex	host cell factor C2
178	gnf1m05019_a_at	C4	GGGGCGGG	1700111D04	5.76	catalytic activity	regulation of biological process	cell part, organelle	glutathione S-transferase omega 2
179	gnf1m29993_a_at	A2*	CATTGTGA	1700057K13	5.76				hypothetical protein
180	gnf1m09975_a_at	A1*	TGACATCA	1700108M19	5.75				hypothetical protein
181	gnf1m16805_a_at	C2	GGCGGGGC	1700017D11	5.75				zona pellucida binding protein 2
182	gnf1m07901_a_at	C2*	GCCCCGCC	4921539K22	5.75	binding	physiological process, cellular process	cell part, organelle, protein complex, organelle part	F-box and leucine-rich repeat protein 13
183	gnf1m16786_at	A1	TGATGTCA	1700034E13	5.74				hypothetical Zinc finger, C2H2 type containing protein
184	gnf1m14533_a_at	B17	CAGAGCAG	4933426G20	5.74				P-loop containing nucleotide triphosphate hydrolases structure containing protein
185	gnf1m18623_a_at	A9*	CTTTGTGA	4933413L02	5.73	motor activity, binding	physiological process, cellular process	cell part	kinesin family member 2B
186	gnf1m05111_a_at	B15	AAAAAAAA	1700013G24	5.73				hypothetical protein
187	gnf1m05805_a_at	A1*	TGACATCA	1700012B22	5.73	catalytic activity	physiological process, cellular process	extracellular region, extracellular region part	allantoicase
188	gnf1m14505_at	A16	TGACCTCA	1700084J23	5.72	binding	physiological process	cell part	spermatogenesis and centriole associated 1
189	gnf1m23842_s_at	A36	TTCTGGAA	4932442C03	5.72				hypothetical KIAA1211 protein
190	gnf1m18943_a_at	A1	TGATGTCA	1700026H02	5.72	catalytic activity	reproduction, development, cellular process	organelle, cell part	similar to AMP-dependent synthetase and ligase containing protein
191	gnf1m16848_at	B14	AGAGAAAG	1700010B08	5.71				hypothetical protein
192	gnf1m23721_a_at	A12	CTGTGACA	1700026A08	5.70				potassium channel tetramerisation domain containing 16
193	gnf1m07836_s_at	A3*	TGTGACAT	4932703D08	5.69	catalytic activity, binding	physiological process	organelle, cell part	a disintegrin and metallopeptidase domain 25 (testase 2)
194	gnf1m17137_a_at	A13	CTCTGTGA	4922505M08	5.69				EP300 interacting inhibitor of differentiation 3 (Eid3) Mus musculus
195	gnf1m05102_a_at	B33	CACACACA	1700011O04	5.68				outer dense fiber of sperm tails 3
196	gnf1m00905_a_at	C2*	GCCCCGCC	4933406P14	5.68	enzyme regulator activity, binding	cellular process, physiological process, development, regulation of biological process	cell part	cyclin A1
197	gnf1m04090_a_at	A1	TGATGTCA	4921507E16	5.68				testis specific protein, Ddc8
198	gnf1m29211_at	A1*	TGACATCA	NM_198673	5.67				outer dense fiber of sperm tails 3-like 1
199	gnf1m14454_a_at	A3*	TGTGACAT	4930404H21	5.66				hypothetical protein
200	gnf1m04909_a_at	B41	CCTCCCTC	1700025O14	5.66	binding, catalytic activity	regulation of biological process, physiological process, cellular process	organelle, cell part	RHO GTPASE (FRAGMENT) homolog [Platichthys flesus]
201	gnf1m11503_a_at	A40	CTGAGGCT	4931440G22	5.65	structural molecule activity, binding	physiological process, cellular process	cell part	actin-related protein T2
202	gnf1m04667_a_at	B39	CCCCACCC	4921526K24	5.65	catalytic activity	physiological process, cellular process	cell part, organelle, organelle part	HRAS-like suppressor family, member 5
203	gnf1m19286_s_at	B37	TGGGCGGG	4933401K09	5.64				coiled-coil domain containing 67 (Ccdc67)
204	gnf1m11500_a_at	A9*	CTTTGTGA	4931430D02	5.64				hypothetical Serine-rich region profile containing protein Mus musculus
205	gnf1m29836_a_at	A40	CTGAGGCT	1700013F07	5.64				hypothetical protein
206	gnf1m29816_a_at	A1*	TGACATCA	1700092M07	5.63				unclassifiable
207	gnf1m06632_a_at	A13*	TCACAGAG	1700000A07	5.62	enzyme regulator activity	physiological process, cellular process	cell part	ropporin 1-like
208	gnf1m23688_at	B6	CAGCCAAT	4921523E13	5.61				testicular cell adhesion molecule 1
209	gnf1m04680_s_at	B39	CCCCACCC	1700021A04	5.61				hypothetical protein
210	gnf1m00717_a_at	C2*	GCCCCGCC	1700006J14	5.61				hypothetical protein
211	gnf1m04829_a_at	A5	ATGTCATA	1700054O13	5.60	binding	physiological process, cellular process	cell part, organelle part, organelle	HUNTINGTIN INTERACTING PROTEIN HYPM (FRAGMENT) [Homo sapiens]
212	gnf1m29329_a_at	A27	AGGTTCTG	1700013E09	5.60				weakly similar to arrestin domain containing 5
213	gnf1m05108_a_at	A1*	TGACATCA	1700001F22	5.59	binding	response to stimulus	cell part, organelle	high-mobility group box 4
214	gnf1m05415_a_at	C3	GGGCGGGG	4930511M11	5.59	signal transducer activity	regulation of biological process	extracellular region	glutamate receptor Gr1 [Bombyx mori]
215	gnf1m18640_a_at	A5	ATGTCATA	4930414N22	5.59				hypothetical protein
216	gnf1m04194_a_at	A13	CTCTGTGA	4933401C12	5.59	catalytic activity	reproduction, development, cellular process	cell part, organelle, organelle part	3-oxoacid CoA transferase 2A

217	gnf1m09496_a_at	A44	CTCTGTCT	NM_029597	5.58				hypothetical protein
218	gnf1m16801_a_at	A3	ATGTCACA	1700034G24	5.57				unclassifiable
219	gnf1m04835_a_at	A3	ATGTCACA	4921518O14	5.56	catalytic activity	physiological process, cellular process	organelle, cell part	haloacid dehalogenase-like hydrolase domain
220	gnf1m08596_at	A17	CCTAGCAA	4933402O15	5.56	catalytic activity	physiological process, cellular process, regulation of biological process	organelle, cell part	lactate dehydrogenase A-like 6B
221	gnf1m04774_a_at	B24	CTCTGCCT	1700095P10	5.56				hypothetical protein
222	gnf1m04609_a_at	A1	TGATGTCA	4933405L11	5.56				hypothetical protein
223	gnf1m16762_at	A8	TCTGTGAC	1700024P04	5.55	binding	cellular process	cell part, extracellular region, organelle	HISTONE H2B
224	gnf1m17287_a_at	A3	ATGTCACA	4930509B16	5.54	structural molecule activity	physiological process, cellular process	cell part	motile sperm domain containing 4
225	gnf1m02604_a_at	B15	AAAAAAAA	4933413O15	5.54	binding	physiological process, cellular process, regulation of biological process	cell part	poly A binding protein, cytoplasmic 2
226	gnf1m02518_a_at	C3	GGGCGGGG	NM_010787	5.53				male enhanced antigen 1
227	gnf1m00135_a_at	B3	CTCTTCCT	4921522D01	5.52	transporter activity, binding	cellular process	organelle, cell part	cation channel, sperm associated 3
228	gnf1m28600_a_at	A8	TCTGTGAC	4930414P16	5.52	binding, enzyme regulator activity	physiological process, cellular process	cell part	proacrosin binding protein
229	gnf1m15462_at	A46	AGGAGCAG	1700031F10	5.51				hypothetical DnaJ (Hsp40) homolog, subfamily B, member 8
230	gnf1m11486_s_at	B7	TGACGTCA	4930554N06	5.51				hypothetical protein
231	gnf1m15497_a_at	B15	AAAAAAAA	1700021J15	5.51				hypothetical adenylate kinase 3
232	gnf1m29059_a_at	A38	CTTCCAGA	1700109H08	5.51	binding	physiological process, cellular process	cell part, organelle part, organelle	EF-hand containing protein
233	gnf1m16931_a_at	B3	CTCTTCCT	1700034K16	5.50				hypothetical Leucine-rich repeat/Leucine-rich repeat, typical subtype containing protein
234	gnf1m14420_at	A13	CTCTGTGA	1700055M20	5.50				similar to testis/prostate/placenta-expressed protein (Tepp), Rattus norvegicus
235	gnf1m22181_at	A39	TTTAAAAA	NM_198421	5.49	catalytic activity, binding			ubiquitin specific peptidase 49
236	gnf1m30109_a_at	C3	GGGCGGGG	4930403E08	5.49				hypothetical protein
237	gnf1m04912_a_at	A37	CAGAGAGA	4930549C01	5.48				hypothetical Arginine-rich region containing protein
238	gnf1m17481_a_at	B28	GCAGCTGC	4933402A08	5.48	binding, transcription regulator activity	reproduction, development, cellular process	cell part, organelle part, protein complex, organelle	weakly similar to ANKYRIN MOTIF [Homo sapiens]
239	gnf1m07933_a_at	A32*	CACAGAGA	4932412H11	5.47	binding	physiological process, cellular process	cell part, extracellular matrix, extracellular region part	Leucine-rich repeat/Leucine-rich repeat, typical subtype containing protein
240	gnf1m05432_a_at	B15*	TTTTTTTT	1700001L23	5.47				spermatogenesis associated 19
241	gnf1m17365_a_at	A24	CCATGGCA	1700104L12	5.47				unclassifiable
242	gnf1m18797_at	A44	CTCTGTCT	1700096P12	5.46				hypothetical protein
243	gnf1m03390_s_at	B11	AGCAGCTG	4921520L14	5.45				zona pellucida binding protein
244	gnf1m02854_s_at	B18	TCTCTTCC	1700026A18	5.45	binding	regulation of biological process, physiological process, cellular process	cell part	t-complex-associated testis expressed 3
245	gnf1m04665_a_at	A37	CAGAGAGA	4933430B12	5.44	binding, transporter activity	reproduction, development, cellular process	cell part	kelch-like 10 (Drosophila)
246	gnf1m07331_a_at	A35	TCCAGGAG	1700008E04	5.44	catalytic activity, binding	physiological process, cellular process	cell part, extracellular region part	a disintegrin and metallopeptidase domain 32
247	gnf1m04911_a_at	B24	CTCTGCCT	1700016A07	5.44				intraflagellar transport 172 homolog (Chlamydomonas)
248	gnf1m08607_a_at	B33	CACACACA	4933421C08	5.43				hypothetical protein
249	gnf1m04668_a_at	B15	AAAAAAAA	4933434E03	5.43	binding, transcription regulator activity	physiological process, cellular process	cell part, organelle	Ankyrin repeat profile/Ankyrin-repeat/Ankyrin repeat region circular profile/Yeast DNA-binding domain containing protein
250	gnf1m05232_at	A13	CTCTGTGA	1700017G21	5.42	binding	regulation of biological process	cell part	weakly similar to GERM CELL-LESS 1 PROTEIN [Mus musculus]
251	gnf1m04565_a_at	C2*	GCCCCGCC	1700121E04	5.41	catalytic activity	physiological process, cellular process	cell part, protein complex, organelle part, organelle	NEURONAL PROTEIN 15.6 [Mus musculus]
252	gnf1m12700_at	B39	CCCCACCC	NM_029992	5.41				similar to trichoplein, keratin filament binding
253	gnf1m28807_a_at	A50	CCTGGCTG	1700016K02	5.41				hypothetical protein
254	gnf1m29282_a_at	A50	CCTGGCTG	4931428F04	5.41				hypothetical protein
255	gnf1m04663_a_at	A13*	TCACAGAG	4921510H08	5.40				Glutamic acid-rich region containing protein
256	gnf1m08585_a_at	A26	GAGCTCTG	4932411A10	5.40	binding	reproduction, development, cellular process	cell part, protein complex, organelle part, organelle	hypothetical microrchidia 2B
257	gnf1m05313_a_at	A9*	CTTTGTGA	4931430J05	5.39				weakly similar to unnamed protein product putative DC44 [Homo sapiens]
258	gnf1m17372_a_at	B15	AAAAAAAA	4921510J17	5.38	binding	regulation of biological process, physiological process, cellular	cell part, organelle	hypothetical EF-hand containing protein

							process		
259	gnf1m05104_a_at	B15	AAAAAAAA	1700006D24	5.37	binding	physiological process, cellular process	cell part	leucine rich repeat containing 46
260	gnf1m21705_at	B24*	AGGCAGAG	4933406N18	5.36	binding	physiological process, cellular process, regulation of biological process	organelle, cell part	selenoprotein W
261	gnf1m01900_s_at	B39	CCCCACCC	4922505K03	5.36	structural molecule activity, binding, catalytic activity	regulation of biological process	organelle, cell part, extracellular region part	tubulin, alpha 3
262	gnf1m04115_a_at	C4	GGGGCGGG	1700016O14	5.36				weakly similar to synaptogyrin 4
263	gnf1m16886_a_at	B33	CACACACA	1700011E24	5.36				hypothetical protein
264	gnf1m12062_a_at	C3	GGGCGGGG	4922505M13	5.35				predicted spermatogenesis associated 7
265	gnf1m22798_a_at	A1	TGATGTCA	4930544D05	5.34				cholinergic receptor, nicotinic, epsilon polypeptide
266	gnf1m21707_a_at	A9*	CTTTGTGA	4933407P14	5.34	catalytic activity	physiological process, cellular process	organelle, cell part	intramembrane protease 5 Rattus norvegicus
267	gnf1m16055_a_at	A50	CCTGGCTG	4933407G07	5.33	structural molecule activity	regulation of biological process, physiological process, cellular process	cell part, organelle, protein complex	tektin 3
268	gnf1m02761_a_at	C3	GGGCGGGG	1700008J04	5.33				small EDRK-rich factor 1
269	gnf1m09361_a_at	A43	GGCTGTGG	8030492M19	5.32				melanoma associated antigen (mutated) 1
270	gnf1m00690_a_at	A35	TCCAGGAG	4930513F16	5.32	binding	physiological process, cellular process	cell part	hypothetical IQ calmodulin-binding motif containing protein
271	gnf1m18944_a_at	A9*	CTTTGTGA	1700085A12	5.31				similar to partial Cypt15 gene for putative cysteine-rich perinuclear theca protein Mus musculus
272	gnf1m16949_a_at	A1*	TGACATCA	1700020N01	5.31	binding	physiological process, cellular process, development	cell part	weakly similar to ZINC FINGER PROTEIN (FRAGMENT) [Homo sapiens]
273	gnf1m17145_a_at	A48	CTCCCAGA	1700058C13	5.31	binding	physiological process, cellular process	organelle part, cell part	weakly similar to Short palate, lung and nasal epithelium carcinoma-associated protein 3 homolog precursor Rattus norvegicus
274	gnf1m13380_a_at	C2*	GCCCCGCC	4933427K18	5.30	enzyme regulator activity	physiological process, cellular process	cell part	PROTEIN PHOSPHATASE INHIBITOR 2 (IPP-2) [Rattus norvegicus]
275	gnf1m04972_a_at	A1	TGATGTCA	4930599B21	5.30	catalytic activity	cellular process, regulation of biological process	cell part	hypothetical Glycosyl transferase, family 2/Microbodies C-terminal targeting signal containing protein
276	gnf1m18365_a_at	A13	CTCTGTGA	4930584F24	5.29				hypothetical protein
277	gnf1m14127_a_at	A9*	CTTTGTGA	4921539E11	5.29				hypothetical protein
278	gnf1m18795_at	B2	AGGAAGAA	1700099I09	5.29				unclassifiable
279	gnf1m10020_a_at	A36	TTCTGGAA	NM_178387	5.28				spermatogenesis associated 18 (Spata18)
280	gnf1m17067_a_at	A1*	TGACATCA	1700008A04	5.28				hypothetical protein
281	gnf1m04901_a_at	A7	GTGATGTC	1700021J16	5.28				similar to sterile alpha motif domain containing 8
282	gnf1m16472_a_at	B7	TGACGTCA	4930578N16	5.28				SH2 domain containing 4B Macaca mulatta
283	gnf1m04878_a_at	C3	GGGCGGGG	1700027I10	5.28				hypothetical protein
284	gnf1m09173_s_at	A48	CTCCCAGA	4930506L13	5.27				tetratricopeptide repeat domain 30A1 (Ttc30a1) homologue [Mus musculus]
285	gnf1m13810_a_at	C2*	GCCCCGCC	4932700H03	5.27	catalytic activity	physiological process	cell part, organelle part, organelle	a disintegrin and metalloprotease domain 5
286	gnf1m23031_a_at	A2	TCACAATG	4930558C23	5.26				unclassifiable
287	gnf1m00213_at	C3	GGGCGGGG	4930577M16	5.26				transmembrane protein 56
288	gnf1m18610_a_at	B7	TGACGTCA	1700031M16	5.25				unclassifiable
289	gnf1m21700_a_at	A46	AGGAGCAG	4933401F02	5.25				weakly similar to hypothetical Cysteine-rich region profile/Lysine-rich region profile containing protein
290	gnf1m18956_a_at	A39	TTTAAAAA	8030402F09	5.24				Retroviral matrix proteins structure containing protein
291	gnf1m05322_a_at	B15	AAAAAAAA	1700095H13	5.24	binding	physiological process, response to stimulus, cellular process	extracellular region, extracellular region part	methyl-CpG binding domain protein 3-like 1
292	gnf1m02161_a_at	B6	CAGCCAAT	1700048D19	5.24	binding, catalytic activity	physiological process, cellular process	cell part	hypothetical cytochrome c, testis
293	gnf1m14679_a_at	A17	CCTAGCAA	4930505A04	5.23				hypothetical protein
294	gnf1m08609_at	A9	TCACAAAG	4933430J11	5.23	signal transducer activity, binding	physiological process, cellular process	organelle, cell part	anthrax toxin receptor-like (Antxrl) Mus musculus
295	gnf1m04025_a_at	C3	GGGCGGGG	NM_021308	5.23	binding			piwi-like homolog 2 (Drosophila)
296	gnf1m14102_a_at	A13	CTCTGTGA	4921511I05	5.23	transporter activity	physiological process, cellular process	cell part, organelle	solute carrier organic anion transporter family, member 6d1
297	gnf1m01563_a_at	A46	AGGAGCAG	4930458G11	5.23	catalytic activity	regulation of biological process, physiological process, cellular process	cell part	pyruvate dehydrogenase E1 alpha 2
298	gnf1m13386_a_at	A50	CCTGGCTG	4932411E05	5.22	binding, transcription regulator activity	reproduction, physiological process, cellular process	cell part, protein complex, organelle	similar to predicted restin-like 2
299	gnf1m30782_a_at	A50	CCTGGCTG	1700006H03	5.22				hypothetical protein
300	gnf1m05324_a_at	B35	CTCTCTCT	1700080E11	5.22	binding, catalytic activity	development, regulation of biological process, physiological process, cellular process	cell part	Nucleoside diphosphate-linked moiety X motif 16 (Nudix motif 16) like [Rattus norvegicu]

301	gnf1m07926_a_at	B7	TGACGTCA	4931433A13	5.21				hypothetical TESTIS DEVELOPMENT PROTEIN NYD-SP29 [Homo sapiens]
302	gnf1m05446_s_at	A5	ATGTCATA	1700025E21	5.21				hypothetical protein
303	gnf1m04669_a_at	A1*	TGACATCA	4921530L21	5.21	binding	physiological process, cellular process	cell part, organelle	ATP/GTP-binding site motif A (P-loop) containing protein Mus musculus
304	gnf1m05221_s_at	B20	CCTGGGCT	NM_027891	5.21	binding, transcription regulator activity, catalytic activity			leucine-rich repeats and WD repeat domain containing 1 (Lrwd1)
305	gnf1m22978_a_at	A19	CCTTAGCT	1700027K06	5.21				hypothetical protein
306	gnf1m05023_a_at	A1*	TGACATCA	1700067P10	5.21				hypothetical protein
307	gnf1m23745_s_at	B30	GAAAAAAA	4930469D11	5.20	binding, transcription regulator activity	physiological process, cellular process	cell part	cAMP responsive element modulator
308	gnf1m16802_a_at	B1	TGCCTCTG	4933406J07	5.20	binding	physiological process, cellular process, regulation of biological process, growth	cell part	synaptonemal complex central element protein 1
309	gnf1m01842_a_at	A22	TCTGAGGC	NM_009350	5.20	binding, catalytic activity			adenosine deaminase domain containing 1 (testis specific) (Adad1)
310	gnf1m04883_a_at	A39	TTTAAAAA	4932702K14	5.20	binding	physiological process, cellular process	organelle, cell part	POLY A BINDING PROTEIN, CYTOPLASMIC 1 homolog [Mus musculus]
311	gnf1m11470_s_at	A9*	CTTTGTGA	4930487F03	5.19	catalytic activity, binding	response to stimulus	extracellular region part, cell part	testis-specific serine kinase 1
312	gnf1m23825_at	A35	TCCAGGAG	4932413P05	5.19	binding, catalytic activity	regulation of biological process, physiological process, cellular process	cell part	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type II)
313	gnf1m16041_a_at	B39	CCCCACCC	1700020N15	5.19				hypothetical protein
314	gnf1m07614_at	A37	CAGAGAGA	4921517C16	5.19				similar to predicted Myosin heavy chain A (MHC A) Rattus norvegicus
315	gnf1m28992_s_at	B1	TGCCTCTG	4932441M08	5.19				P-loop containing nucleotide triphosphate hydrolases structure containing protein Mus musculus
316	gnf1m08576_at	A52	AGGCTGTG	4922503E23	5.18				DnaJ (Hsp40) homolog, subfamily C, member 5 gamma
317	gnf1m11501_at	A11	TGTGAGGT	4931433M19	5.18	binding	regulation of biological process	cell part, extracellular region part	Leucine-rich repeat containing protein
318	gnf1m15086_a_at	A1	TGATGTCA	4930471G03	5.18				unclassifiable
319	gnf1m04283_s_at	A8	TCTGTGAC	NM_023197	5.18				weakly similar to unnamed protein product TSG118.1 [Mus musculus]
320	gnf1m10438_a_at	A13	CTCTGTGA	1700112P14	5.17	binding, catalytic activity	physiological process, cellular process	extracellular region part, cell part	ring finger and FYVE like domain containing protein
321	gnf1m23188_a_at	A16	TGACCTCA	1700085B22	5.16				hypothetical ELAFIN-LIKE PROTEIN I [Mus musculus]
322	gnf1m07706_at	B15	AAAAAAAA	NM_029294	5.16	catalytic activity, binding			phosphoribosyl pyrophosphate synthetase 1-like 1 (Prps1l1)
323	gnf1m05113_a_at	A1	TGATGTCA	1700019M22	5.16				weakly similar to Lysine-rich region containing protein
324	gnf1m14022_a_at	B39*	GGGTGGGG	1700028J19	5.16	binding	physiological process, cellular process	cell part, organelle part, organelle	RNA-binding region RNP-1 (RNA recognition motif) containing protein
325	gnf1m21712_a_at	A27	AGGTTCTG	4933440E22	5.15				similar to Salivary glue protein Sgs-4 precursor
326	gnf1m04602_a_at	B13	GCTCTGGG	1700016J15	5.15				hypothetical protein
327	gnf1m18790_a_at	C2*	GCCCCGCC	1700023L04	5.14				hypothetical protein
328	gnf1m08593_at	A8*	GTCACAGA	4933400C05	5.14				hypothetical protein
329	gnf1m13575_a_at	A1*	TGACATCA	1700055J15	5.13				IQ motif containing F1
330	gnf1m04869_a_at	C3*	CCCCGCCC	4921527B01	5.13				hypothetical protein
331	gnf1m16237_at	B14	AGAGAAAG	4930555P18	5.11				ring finger protein 139
332	gnf1m17677_a_at	A13	CTCTGTGA	4921509H06	5.11				ribophorin II
333	gnf1m16806_a_at	A13	CTCTGTGA	1700001D09	5.11				adenosine A3 receptor (Adora3), transcript variant 2
334	gnf1m07287_a_at	A1*	TGACATCA	4930524L02	5.11	binding, transcription regulator activity	physiological process, cellular process	cell part	TGIF homeobox 1
335	gnf1m29009_s_at	A25	TGAGAAGG	1700001J11	5.10				RING FINGER PROTEIN 19 (XY BODY PROTEIN) (XYBP) (GAMETOGENESIS EXPRESSED PROTEIN GEG-154) (UBCM4-INTERACTING PROTEIN 117) (UIP117) [Mus musculus]
336	gnf1m23019_a_at	A8	TCTGTGAC	1700096M17	5.09				unclassifiable
337	gnf1m05230_a_at	C3	GGGCGGGG	1700010P14	5.09	binding	physiological process, cellular process	cell part, organelle part	PHD finger protein 7
338	gnf1m05869_a_at	A2	TCACAATG	1700041H07	5.09	signal transducer activity, catalytic activity	cellular process, reproduction, development, regulation of biological process, physiological process	cell part, organelle	phospholipase C, zeta 1
339	gnf1m29533_a_at	B29	TGCTGGGA	1700026M06	5.09				mesoderm posterior 1
340	gnf1m14871_a_at	A16	TGACCTCA	1700111I05	5.08				Williams-Beuren syndrome chromosome region 28 Mus musculus
341	gnf1m04825_at	A1*	TGACATCA	1700042N06	5.08	catalytic activity	physiological process	cell part	IQ motif containing F4
342	gnf1m14121_a_at	A36	TTCTGGAA	4930412D12	5.08				hypothetical protein
343	gnf1m08583_a_at	A37	CAGAGAGA	4931408E15	5.07				hypothetical Glutamine-rich region profile containing protein Mus musculus
344	gnf1m04671_a_at	C3	GGGCGGGG	4931417E11	5.06				JNK1-associated membrane protein, transcript variant 2 Pan troglodytes
345	gnf1m06454_a_at	A42	GGCCAGCC	4930563B01	5.06	transporter	physiological	cell part	similar to predicted defensin beta 19

						activity	process, cellular process		
346	gnf1m00611_a_at	B5	TGGGAGGA	4930563A13	5.05				XAP-5-LIKE PROTEIN homolog [Mus musculus]
347	gnf1m03287_a_at	A9	TCACAAAG	NM_013783	5.04	catalytic activity, binding			mel transforming oncogene-like 1
348	gnf1m30047_a_at	A1	TGATGTCA	1700026P12	5.04				eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
349	gnf1m08258_a_at	B5	TGGGAGGA	NM_175477	5.02	binding, transcription regulator activity			weakly similar to zinc finger protein 574
350	gnf1m05026_a_at	A1	TGATGTCA	1700067M22	5.02				DJ1028D15.4 (NOVEL PROTEIN) [Homo sapiens]
351	gnf1m09678_a_at	A1*	TGACATCA	4930540L03	5.02				similar to sperm acrosome membrane protein
352	gnf1m08579_a_at	A8	TCTGTGAC	4930503F14	5.01				hypothetical protein
353	gnf1m10425_a_at	A16	TGACCTCA	1700029H01	5.01				spermatogenesis associated 3
354	gnf1m00518_a_at	A40	CTGAGGCT	1700008K17	5.01				calcium homeostasis endoplasmic reticulum protein like
355	gnf1m29254_a_at	A23	TGCTTTCC	1700010G02	5.01				weakly similar to predicted 5-oxoprolinase (ATP-hydrolysing)
356	gnf1m04677_a_at	B1	TGCCTCTG	4933409D10	5.01				zinc finger protein 474
357	gnf1m10164_a_at	B7	TGACGTCA	4933417P13	5.00				ring finger protein 39
358	gnf1m30510_at	A43	GGCTGTGG	4922505P07	5.00	catalytic activity	physiological process, cellular process	cell part	hypothetical tyrosine specific protein phosphatase and dual specificity protein phosphatase family containing protein (Fragment) homolog [Mus musculus]
359	gnf1m03538_a_at	B6	CAGCCAAT	NM_016964	4.99				stromal antigen 3 (Stag3)
360	gnf1m17780_a_at	B3	CTCTTCCT	4921530L18	4.98				unclassifiable
361	gnf1m08599_a_at	A13*	TCACAGAG	4933406A14	4.98	binding	physiological process, cellular process	cell part	schlafen like 1
362	gnf1m11446_a_at	A1	TGATGTCA	4921514H13	4.97	catalytic activity, binding	cellular process, physiological process, reproduction, development	cell part, extracellular region part	5'-nucleotidase, cytosolic IB
363	gnf1m21698_a_at	A16	TGACCTCA	4933400F01	4.97	catalytic activity	regulation of biological process	cell part	Ly6/Plaur domain containing 4
364	gnf1m13868_a_at	B23	AGAGGCAG	4933409F16	4.97				hypothetical protein
365	gnf1m18614_at	B1	TGCCTCTG	1700036D21	4.97	catalytic activity	physiological process, cellular process	cell part, organelle	SERINE PROTEASE-LIKE 1 homolog [Mus musculus]
366	gnf1m07703_at	A9*	CTTTGTGA	4930429C23	4.96				hypothetical protein
367	gnf1m17299_a_at	A12	CTGTGACA	NM_183113	4.96				hypothetical protein
368	gnf1m10318_a_at	A9*	CTTTGTGA	1700116D15	4.96	catalytic activity, binding	physiological process, cellular process	organelle, cell part	preproacrosin
369	gnf1m29406_a_at	A1	TGATGTCA	4933406A08	4.96	catalytic activity	regulation of biological process, physiological process, cellular process	cell part, organelle part, organelle	hyaluronoglucosaminidase 5
370	gnf1m19292_a_at	C3	GGGCGGGG	4933417A14	4.96	binding	physiological process, cellular process	extracellular region	calicin
371	gnf1m01239_a_at	A31	CCTGAGCA	4932442B12	4.96				hepatoma derived growth factor-like 1
372	gnf1m05200_a_at	A13*	TCACAGAG	4933432K11	4.96	binding	physiological process, cellular process	cell part, protein complex, organelle part, organelle	fibrous sheath-interacting protein 1
373	gnf1m09001_a_at	B24*	AGGCAGAG	NM_172789	4.95				hypothetical protein
374	gnf1m07673_a_at	A7	GTGATGTC	4921537E06	4.95				amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 11 (human)
375	gnf1m05904_a_at	A10	ACATCACA	4930594I21	4.95	catalytic activity, binding	regulation of biological process	cell part, organelle	testis-specific serine kinase 3
376	gnf1m26405_a_at	B25	CCTTCCTC	1700093L14	4.95	transporter activity	response to stimulus, regulation of biological process, physiological process, cellular process	organelle, cell part	karyopherin (importin) alpha 6
377	gnf1m15241_at	B24*	AGGCAGAG	1700024G10	4.94				hypothetical Cytochrome c family heme-binding site containing protein
378	gnf1m13484_a_at	C2*	GCCCCGCC	1700021C14	4.93				SSTK-INTERACTING PROTEIN VARIANT (SIMILAR TO RIKEN CDNA 1700021C14 GENE) [Homo sapiens]
379	gnf1m07910_at	A32	TCTCTGTG	NM_176965	4.93	binding			EF-hand calcium binding domain 5 (Efcab5)
380	gnf1m01668_a_at	B25	CCTTCCTC	1700025K02	4.92	binding, signal transducer activity, catalytic activity	physiological process, cellular process	cell part, organelle	RAS-like, family 2, locus 9
381	gnf1m13378_a_at	C1*	CCCCTCCC	4930488L21	4.91				unclassifiable
382	gnf1m03933_a_at	B22	CAGGAAGT	1700023E12	4.91	catalytic activity	cellular process, physiological process, development, regulation of biological process	cell part, organelle	protease, serine, 21
383	gnf1m08598_a_at	B6	CAGCCAAT	G630083P15	4.91	binding		cell part	maelstrom homolog (Drosophila)
384	gnf1m03696_a_at	B28	GCAGCTGC	4933408D12	4.91	binding	physiological process, cellular process	organelle, cell part	leucine rich repeat containing 6 (testis)
385	gnf1m30255_at	A1*	TGACATCA	4933411H15	4.91	catalytic activity, binding	physiological process, development, cellular process,	cell part, organelle	zinc finger, DHHC domain containing 19

							regulation of biological process		
386	gnf1m04832_a_at	A30	CTGTTGCT	1700095F04	4.90				transmembrane and coiled-coil domains 5
387	gnf1m11445_a_at	A41	GAGGCCAG	NM_020330	4.90	catalytic activity, binding			a disintegrin and metallopeptidase domain 21 (Adam21)
388	gnf1m05105_a_at	A2*	CATTGTGA	1700011M07	4.90				ankyrin repeat and SOCS box-containing protein 9
389	gnf1m16749_a_at	B25	CCTTCCTC	1700025C14	4.88				unclassifiable
390	gnf1m29721_a_at	A41	GAGGCCAG	4930403N07	4.88				Centromeric protein E (CENP-E protein) like Rattus norvegicus
391	gnf1m23783_a_at	B11	AGCAGCTG	4930568O20	4.88				hypothetical leucine rich repeat containing 9 (Lrrc9)
392	gnf1m04559_at	A1	TGATGTCA	1700010M22	4.88	catalytic activity, binding	regulation of biological process, physiological process, cellular process	cell part, protein complex, organelle part, organelle	hypothetical SCP-2 sterol transfer domain containing protein
393	gnf1m21616_a_at	A9*	CTTTGTGA	1700020H15	4.88	catalytic activity	reproduction, physiological process, cellular process	cell part	hypothetical Serine proteases, trypsin family containing protein
394	gnf1m18718_s_at	C3	GGGCGGGG	4921517J08	4.88	binding	physiological process, cellular process	cell part	weakly similar to predicted speedy homolog 1 (Drosophila)
395	gnf1m29853_a_at	C3	GGGCGGGG	1700028O09	4.87				testis expressed gene 22
396	gnf1m00618_a_at	A50	CCTGGCTG	4933405E16	4.87	transporter activity	physiological process, cellular process	cell part, organelle	component of oligomeric golgi complex 6
397	gnf1m30687_a_at	B14	AGAGAAAG	1700006L23	4.86	binding, transcription regulator activity	regulation of biological process, physiological process, cellular process, response to stimulus	cell part, organelle, protein complex, organelle part	DnaJ (Hsp40) homolog, subfamily B, member 6
398	gnf1m01426_a_at	C3	GGGCGGGG	1700122H24	4.86	binding	physiological process, cellular process, regulation of biological process	cell part, organelle part, organelle	meiosis expressed gene 1
399	gnf1m02204_a_at	A39	TTTAAAAA	4932412H23	4.85	catalytic activity, binding	cellular process	cell part	a disintegrin and metallopeptidase domain 24 (testase 1)
400	gnf1m03853_a_at	A3*	TGTGACAT	1700065B04	4.85				sperm tail associated protein
401	gnf1m04341_a_at	A33	TTTCTCCA	1700011N16	4.84	transcription regulator activity, binding	reproduction, development, cellular process	extracellular region, extracellular region part	general transcription factor II A, 1-like factor
402	gnf1m30845_a_at	A27	AGGTTCTG	4930408G06	4.84				unclassifiable
403	gnf1m16811_a_at	A9	TCACAAAG	1700006C19	4.84	enzyme regulator activity	physiological process	extracellular region, extracellular region part	similar to predicted cystatin 13
404	gnf1m00515_a_at	A1	TGATGTCA	1700021O15	4.83				sperm associated antigen 4-like
405	gnf1m04153_a_at	C1*	CCCCTCCC	NM_021611	4.83	binding, motor activity			myosin light chain 2, precursor lymphocyte-specific (Mylc2pl)
406	gnf1m04624_a_at	C3	GGGCGGGG	1700027L03	4.81	binding, catalytic activity	physiological process, cellular process	cell part	hypothetical AAA ATPase superfamily containing protein
407	gnf1m21663_at	B24*	AGGCAGAG	4930415L07	4.81				similar to hypothetical protein LOC546166
408	gnf1m29447_a_at	C3	GGGCGGGG	1700010A17	4.81				MORN motif containing protein
409	gnf1m03440_a_at	C4	GGGGCGGG	NM_181329	4.80	catalytic activity, binding			coilin
410	gnf1m05185_a_at	B39	CCCCACCC	4921507P07	4.80	transporter activity	cellular process	organelle, cell part	hypothetical Bacterial extracellular solute-binding protein, family 1 containing protein
411	gnf1m00465_a_at	B24*	AGGCAGAG	1700023J02	4.78	transporter activity, catalytic activity	physiological process, cellular process	cell part, organelle	aquaporin 11
412	gnf1m08260_a_at	B24*	AGGCAGAG	NM_172755	4.78	binding, catalytic activity			splicing factor, arginine/serine-rich 14
413	gnf1m13863_a_at	A1	TGATGTCA	4933413G11	4.78	binding	physiological process, cellular process	cell part, organelle	heat shock transcription factor, Y linked 2
414	gnf1m17727_a_at	A54	CTCCAGAG	4930421J07	4.76				hypothetical protein
415	gnf1m16168_at	A40	CTGAGGCT	1700029F09	4.76	catalytic activity	physiological process, cellular process	cell part, organelle, protein complex, organelle part	Esterase/lipase/thioesterase family active site containing protein
416	gnf1m04664_a_at	B9	CTGAGCCA	4921522P10	4.76				hypothetical protein
417	gnf1m13957_at	B11	AGCAGCTG	4930518C04	4.76				unclassifiable
418	gnf1m32587_at	A37	CAGAGAGA	4930408K01	4.76	enzyme regulator activity	regulation of biological process	organelle part, cell part	cystatin-like 1
419	gnf1m17050_at	B7	TGACGTCA	1700007L12	4.76				IQ motif containing F5
420	gnf1m03716_a_at	B36	CTTCCTGG	4921526M11	4.75	catalytic activity, signal transducer activity, binding	physiological process, cellular process	protein complex, organelle part, cell part	G protein-coupled receptor kinase 2, groucho gene related (Drosophila)
421	gnf1m16360_a_at	B11	AGCAGCTG	1700030H21	4.75	transporter activity, binding	cellular process	extracellular region, extracellular region part	vitelliform macular dystrophy 2 homolog (human)
422	gnf1m05464_a_at	A13	CTCTGTGA	4930511H01	4.75				Trp-Asp (WD) repeats profile/Trp-Asp (WD) repeats circular profile/G-protein beta WD-40 repeats containing protein
423	gnf1m05443_a_at	A27	AGGTTCTG	1700030K01	4.75				hypothetical spermatogenesis associated 9 (Spata9)
424	gnf1m23751_s_at	A26	GAGCTCTG	1700065F16	4.74				IQ calmodulin-binding motif containing protein
425	gnf1m15253_a_at	A20	AGGTCACA	1700003E16	4.73				short-chain dehydrogenase/reductase Homo sapiens
426	gnf1m03674_s_at	C3	GGGCGGGG	4930570K13	4.73	binding, transcription	physiological process, cellular	cell part	weakly similar to predicted DNA binding protein with his-thr domain

						regulator activity	process		
427	gnf1m11488_a_at	A40	CTGAGGCT	4930557G02	4.72				forty-two-three domain containing 1
428	gnf1m07481_a_at	A13	CTCTGTGA	4922505I06	4.72	binding, structural molecule activity, enzyme regulator activity	regulation of biological process	extracellular region, extracellular region part	calcium-binding tyrosine-(Y)-phosphorylation regulated (fibrousheathin 2)
429	gnf1m12672_a_at	C2*	GCCCCGCC	4933428M04	4.72	binding	response to stimulus, reproduction, development, cellular process	cell part	diablo homolog (Drosophila)
430	gnf1m11483_a_at	A8	TCTGTGAC	NM_026296	4.72				hypothetical protein
431	gnf1m09582_s_at	B11	AGCAGCTG	1700026G17	4.72				unclassifiable
432	gnf1m05317_a_at	B5	TGGGAGGA	1700013O04	4.71	binding	reproduction, development, cellular process	cell part	CKLF-like MARVEL transmembrane domain containing 2B
433	gnf1m21689_at	A2	TCACAATG	4930580A02	4.71				hypothetical protein
434	gnf1m00673_a_at	B15	AAAAAAAA	4921511E02	4.71				hypothetical FAD/NAD(P)-binding domain structure containing protein
435	gnf1m11491_a_at	A50	CCTGGCTG	4930570A05	4.71				coiled-coil domain containing 38
436	gnf1m16043_at	A50	CCTGGCTG	4930518J20	4.70				unclassifiable
437	gnf1m23757_a_at	A1	TGATGTCA	4930523O13	4.70				unclassifiable
438	gnf1m04696_a_at	C3	GGGCGGGG	4930588C21	4.70				radial spokehead-like 2
439	gnf1m23030_a_at	B6	CAGCCAAT	4930517G24	4.70				unclassifiable
440	gnf1m15504_at	C1*	CCCCTCCC	1700085L02	4.69				antizyme inhibitor 1
441	gnf1m32897_at	A44	CTCTGTCT	4930569G22	4.69	transporter activity	physiological process, cellular process	organelle, cell part	hypothetical Sodium:neurotransmitter symporter/Sodium:neurotransmitter symporter family profile containing protein, full insert sequence
442	gnf1m02810_a_at	C3	GGGCGGGG	1700000E13	4.68	enzyme regulator activity	cellular process	cell part, extracellular region part	sperm autoantigenic protein 17
443	gnf1m30953_a_at	A12*	TGTCACAG	4933437F05	4.68	catalytic activity	physiological process, cellular process, development	cell part, organelle part, protein complex, organelle	NAD(P)-binding Rossmann-fold domains structure containing protein
444	gnf1m28689_a_at	A13*	TCACAGAG	4921511K06	4.68				hypothetical sarcolemma associated protein isoform 5
445	gnf1m30975_at	A16	TGACCTCA	4933412E13	4.68	enzyme regulator activity	physiological process, cellular process	extracellular region, extracellular region part, cell part	hypothetical SEC7-like domain/SEC7 domain profile containing protein
446	gnf1m07701_a_at	A9	TCACAAAG	1700049P18	4.68				unclassifiable
447	gnf1m08597_a_at	B15	AAAAAAAA	4933403D14	4.66	binding	physiological process, cellular process, regulation of biological process	organelle part, cell part, protein complex	Domain in various gamma-carboxylases and other proteins containing protein
448	gnf1m05872_at	B15*	TTTTTTTT	1700023D02	4.66				hypothetical testis specific gene A13
449	gnf1m14537_a_at	B6	CAGCCAAT	4933427G17	4.65				hypothetical protein
450	gnf1m09247_a_at	A32	TCTCTGTG	4930511O11	4.64	catalytic activity	cellular process, physiological process	cell part	ubiquitin specific peptidase 50
451	gnf1m17163_a_at	A44	CTCTGTCT	1700061J05	4.64				hypothetical protein
452	gnf1m17712_a_at	A53	CCAGGGAG	1700120B22	4.64				hypothetical protein LOC621121
453	gnf1m04730_a_at	A50	CCTGGCTG	NM_025851	4.63				hypothetical protein
454	gnf1m09400_a_at	A1	TGATGTCA	4933408H04	4.63				weakly similar to predicted Acr formation associated factor Pan troglodytes
455	gnf1m14422_at	C2	GGCGGGGC	1700064D17	4.63				hypothetical protein
456	gnf1m04070_a_at	A50	CCTGGCTG	4930524C15	4.62	binding, transcription regulator activity	cellular process, physiological process, reproduction, development	cell part	zinc finger and BTB domain containing 32
457	gnf1m17313_at	A6	TTGTGATG	4930432K09	4.62				hypothetical protein
458	gnf1m11086_a_at	C3	GGGCGGGG	1700003B04	4.62	binding	regulation of biological process	cell part, organelle	hypothetical insulin-like 6
459	gnf1m29012_a_at	B7	TGACGTCA	4921528H16	4.62	binding, catalytic activity	reproduction, regulation of biological process, physiological process, cellular process	cell part, extracellular region part, organelle	RNI-like structure containing protein
460	gnf1m08625_a_at	B39	CCCCACCC	1700129C13	4.61	binding, catalytic activity	physiological process, cellular process	extracellular region	centrin 4
461	gnf1m00997_a_at	A50	CCTGGCTG	6030448H16	4.61	catalytic activity	physiological process, cellular process	cell part, organelle	hypothetical cytochrome P450, family 17, subfamily a, polypeptide 1
462	gnf1m08588_a_at	B38	CCCACCCC	4932418E24	4.61				hypothetical protein
463	gnf1m31200_a_at	A9*	CTTTGTGA	1700095H12	4.61	catalytic activity	physiological process, cellular process	cell part, organelle	Esterase/lipase/thioesterase family active site containing protein
464	gnf1m16046_a_at	A1	TGATGTCA	1700007K09	4.60				hypothetical protein
465	gnf1m18900_a_at	A25	TGAGAAGG	4930572D21	4.60				similar to unnamed protein product MDAC1 [Homo sapiens]
466	gnf1m04840_a_at	A1	TGATGTCA	4930429J24	4.60				weakly similar to thioredoxin domain containing 8
467	gnf1m15089_a_at	A1	TGATGTCA	1700080C03	4.60				THYMOSIN BETA-LIKE PROTEIN [Rattus norvegicus]
468	gnf1m17702_a_at	B6	CAGCCAAT	4932412N08	4.59	binding, signal transducer activity	physiological process, cellular process, response to stimulus, development	organelle, cell part	zinc finger, MYND-type containing 15
469	gnf1m31669_at	B31	AGAGGAAG	4930596D02	4.59	enzyme regulator activity, binding	cellular process, reproduction, development, physiological process	cell part, extracellular matrix, extracellular region part	weakly similar to hypothetical EF-hand/guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif containing protein [Mus musculus]

470	gnf1m03831_at	B3	CTCTTCCT	NM_019873	4.58	binding			FK506 binding protein-like
471	gnf1m09886_a_at	A5	ATGTCATA	NM_053253	4.58	binding			zinc finger, MYND domain containing 10
472	gnf1m16760_a_at	B15	AAAAAAAA	1700007J06	4.57	binding	cellular process, physiological process, reproduction, development, regulation of biological process	cell part	leucine rich repeat containing 34
473	gnf1m30814_a_at	A1	TGATGTCA	1700023H08	4.57	catalytic activity	reproduction	cell part, protein complex, organelle part, organelle	lysozyme-like 6
474	gnf1m29073_a_at	C2	GGCGGGGC	4930405J06	4.57	binding	regulation of biological process	cell part	BCL2-associated athanogene 5
475	gnf1m07352_a_at	B15	AAAAAAAA	4933417K04	4.57				coiled-coil domain containing 65
476	gnf1m29781_a_at	B6	CAGCCAAT	4930534K13	4.56				IBR domain containing 3
477	gnf1m05430_s_at	B10	GGCAGCTG	1700008F21	4.56				weakly similar to predicted coiled-coil domain containing 7 Mus musculus
478	gnf1m17138_a_at	B23	AGAGGCAG	1700060E18	4.56				membrane-spanning 4-domains, subfamily A, member 13 (Ms4a13), Mus musculus
479	gnf1m11494_a_at	B11	AGCAGCTG	4932415G16	4.55				CatSper channel subunit beta mRNA
480	gnf1m05314_a_at	B32	AAACAAAA	4933403P17	4.55	catalytic activity, binding	physiological process, cellular process	cell part	Ubiquitin-conjugating enzyme E2-17 kDa 4 (EC 6.3.2.19) (Ubiquitin- protein ligase) (Ubiquitin carrier protein) (E2(17)KB 4) homolog [Rattus norvegicus]
481	gnf1m28856_at	C3	GGGCGGGG	4932419B04	4.55				hypothetical protein
482	gnf1m00002_f_at	B35	CTCTCTCT	NM_009449	4.54	structural molecule activity, binding, catalytic activity			tubulin, alpha 3B (Tuba3b)
483	gnf1m10583_a_at	B34	GGCAGAGG	6030486B17	4.54	binding	physiological process, regulation of biological process, cellular process	cell part, organelle	WW domain binding protein 11
484	gnf1m07927_a_at	B7	TGACGTCA	4932408B01	4.53				Mycbp associated protein
485	gnf1m18803_a_at	B15*	TTTTTTTT	4921518C22	4.53				tetratricopeptide repeat domain 18
486	gnf1m11143_a_at	C3	GGGCGGGG	NM_018811	4.53	catalytic activity			abhydrolase domain containing 2 (Abhd2)
487	gnf1m29125_a_at	A26	GAGCTCTG	4931413A09	4.53				similar to coiled-coil domain containing 105 Homo sapiens
488	gnf1m11085_a_at	B7	TGACGTCA	4922505N17	4.53	catalytic activity	physiological process, cellular process	cell part, organelle, protein complex, organelle part	serine/threonine/tyrosine interacting-like 1
489	gnf1m04831_a_at	A3*	TGTGACAT	4930434I17	4.52				Tctex1 domain containing 1
490	gnf1m18691_a_at	A2*	CATTGTGA	4930479M11	4.52				hypothetical protein
491	gnf1m14745_a_at	A3*	TGTGACAT	1700020C07	4.52				hypothetical protein
492	gnf1m09990_a_at	B3	CTCTTCCT	1700003M02	4.52				hypothetical protein
493	gnf1m07633_at	A2	TCACAATG	NM_175176	4.50				hypothetical protein
494	gnf1m16481_a_at	C3	GGGCGGGG	1700104P03	4.50				hypothetical protein
495	gnf1m05440_a_at	C1	GGGAGGGG	1700026D08	4.50				hypothetical protein
496	gnf1m07947_a_at	C1	GGGAGGGG	4933406M09	4.49				N-ACETYLGLUCOSAMINYLTRANSFERASE VI [Gallus gallus]
497	gnf1m04458_a_at	C4	GGGGCGGG	1700007N08	4.49				weakly similar to testis specific gene A2 (MORN motif containing)
498	gnf1m09549_a_at	B19	GCCAATCA	NM_029354	4.48				hypothetical protein
499	gnf1m05485_a_at	C3	GGGCGGGG	NM_029610	4.48				LYR motif containing 1 (Lyrm1)
500	gnf1m21656_a_at	A1*	TGACATCA	4922504M18	4.47				hypothetical Ubiquitin domain containing protein
501	gnf1m22950_a_at	C2*	GCCCCGCC	1700120A01	4.46				Sperm flagellar protein 1 (LOC681930), Rattus norvegicus
502	gnf1m11459_s_at	B15	AAAAAAAA	4930405K06	4.46				similar to predicted leucine rich repeat containing 57
503	gnf1m11448_a_at	C3	GGGCGGGG	4921520K19	4.45	catalytic activity	regulation of biological process	cell part	yippee-like 1 (Drosophila)
504	gnf1m08591_at	C1*	CCCCTCCC	NM_172521	4.45				similar to nuclear protein in testis (predicted)
505	gnf1m07613_a_at	C3	GGGCGGGG	4922501F22	4.45	binding	physiological process, cellular process	organelle, cell part, extracellular region, extracellular region part	spermatogenesis associated 16
506	gnf1m19221_a_at	A40	CTGAGGCT	NM_183307	4.44				coiled-coil domain containing 63 (Ccdc63)
507	gnf1m10532_a_at	A34	TGCCCAGG	1700011P15	4.44				dickkopf-like 1
508	gnf1m23761_x_at	A35	TCCAGGAG	4930533E22	4.44	binding	physiological process, cellular process	cell part	hypothetical synovial sarcoma, X member B, breakpoint 2
509	gnf1m08863_a_at	B15	AAAAAAAA	4921523A10	4.44	catalytic activity	physiological process, cellular process	cell part	Protein phosphatase 2C domain containing protein
510	gnf1m23679_a_at	A26	GAGCTCTG	4921506L10	4.43				hypothetical protein
511	gnf1m03380_a_at	B17	CAGAGCAG	4930455F09	4.43				prokineticin 2
512	gnf1m16263_a_at	B28	GCAGCTGC	1700029F22	4.42	binding	physiological process, cellular process	cell part, organelle	EF-hand domain (C-terminal) containing 1
513	gnf1m32046_at	C2*	GCCCCGCC	4933402K21	4.42				Lysine-rich region containing protein
514	gnf1m13936_a_at	A37	CAGAGAGA	4933424G06	4.42				unclassifiable
515	gnf1m23858_at	A16*	TGAGGTCA	4933408D05	4.42	catalytic activity	regulation of biological process, physiological process, cellular process	cell part	hypothetical SUMO-1-specific protease mRNA, complete cds. [Mus musculus]
516	gnf1m17378_a_at	A45	CTCCTCTT	4932423M01	4.41				coiled-coil domain containing 83 (Ccdc83) Mus musculus

517	gnf1m30213_at	B31	AGAGGAAG	4921501G24	4.41	binding	physiological process, cellular process	cell part	weakly similar to sel-1 suppressor of lin-12-like 2 (C. elegans) (Sel1l2)
518	gnf1m13352_a_at	A17	CCTAGCAA	4933434I06	4.41	binding	physiological process, cellular process	extracellular region	enkurin
519	gnf1m30554_a_at	A1	TGATGTCA	1700126L10	4.40				CLG01 (DJ453C12.5) (P53 RESPONSE ELEMENT) [Homo sapiens]
520	gnf1m04480_a_at	B15	AAAAAAAA	1700112I01	4.40				DYnein Light chain (Tctex type) family member (dylt-2) Mus musculus
521	gnf1m29178_a_at	A2	TCACAATG	1700127P06	4.40	binding, transcription regulator activity	physiological process	extracellular region, extracellular region part	NK2 transcription factor related, locus 6 (Drosophila)
522	gnf1m16053_a_at	A1*	TGACATCA	1700054F22	4.40				similar to unnamed protein product NIPSNAP4 PROTEIN (MGC:14553) (DKFZP564D177) (FLJ13953) (HSPC299) [Homo sapiens]
523	gnf1m32877_at	A1*	TGACATCA	4933422H20	4.40	binding, signal transducer activity	cellular process, reproduction, development, regulation of biological process, physiological process	cell part, organelle	similar to Butyrophylin-like/Zn-finger, B-box/SPla/RYanodine receptor SPRY/Zn-finger, RING containing protein
524	gnf1m29170_a_at	A17	CCTAGCAA	1700010H15	4.40	motor activity, binding	regulation of biological process	extracellular region part	weakly similar to dynein, axonemal, light chain 1 (Dnalc1)
525	gnf1m03178_a_at	C2*	GCCCCGCC	NM_013604	4.39	transporter activity			metaxin 1
526	gnf1m14779_a_at	A35	TCCAGGAG	4930529M09	4.38				HORMA domain containing 2
527	gnf1m18303_a_at	C2*	GCCCCGCC	1700013D04	4.38				hypothetical coiled-coil domain containing 117, mRNA (cDNA cloneIMAGE:3597771). [Mus musculus]
528	gnf1m05497_a_at	A10	ACATCACA	1700027D21	4.38				hypothetical protein
529	gnf1m10111_a_at	C3	GGGCGGGG	1700016K08	4.37	binding	physiological process, cellular process	cell part	translin-associated factor X (Tsnax) interacting protein 1
530	gnf1m01785_a_at	A1	TGATGTCA	1700003G22	4.36	catalytic activity, binding	cellular process	cell part, protein complex, organelle	sperm adhesion molecule 1
531	gnf1m10540_a_at	C3	GGGCGGGG	NM_016915	4.36	catalytic activity, nutrient reservoir activity			phospholipase A2, group VI
532	gnf1m17327_at	A1	TGATGTCA	4933432M07	4.35	binding, catalytic activity	cellular process, physiological process	cell part, organelle	ring finger protein 148
533	gnf1m00743_a_at	A21	CAAAGCCC	4933425C05	4.35	binding	physiological process, cellular process	cell part, extracellular region part	atonal homolog 8 (Drosophila)
534	gnf1m21648_a_at	C4	GGGGCGGG	4921501M07	4.35				centrosomal protein 63 (Cep63)
535	gnf1m17083_a_at	A13	CTCTGTGA	4930415O20	4.34				hypothetical protein
536	gnf1m23685_a_at	A17	CCTAGCAA	4921521O07	4.33				predicted coiled-coil domain containing 81 (Ccdc81) Mus musculus
537	gnf1m18898_a_at	B15*	TTTTTTTT	4932413L18	4.33				hypothetical CLIP-190 CG5020-PB, isoform B like Macaca mulatta
538	gnf1m19220_a_at	A9	TCACAAAG	4921509C19	4.33	catalytic activity, binding	response to stimulus, regulation of biological process	cell part	weakly similar to Eukaryotic protein kinase containing protein
539	gnf1m17222_s_at	A2	TCACAATG	4933402N03	4.32	binding	physiological process, cellular process	cell part, synapse part, synapse	Cytochrome c heme-binding site containing protein
540	gnf1m10381_a_at	B7	TGACGTCA	NM_175240	4.32				transmembrane protein 162 (Tmem162)
541	gnf1m15247_a_at	C3	GGGCGGGG	1700014J02	4.32				unclassifiable
542	gnf1m03015_a_at	B28	GCAGCTGC	NM_011902	4.32	structural molecule activity			tektin 2 (Tekt2)
543	gnf1m18930_a_at	A6	TTGTGATG	4930548L10	4.31				Glutamine-rich region containing protein
544	gnf1m17242_a_at	A29	CCTCACAG	4921505G21	4.31	catalytic activity, binding	physiological process, cellular process	cell part, protein complex, organelle part, organelle	hypothetical serine/threonine kinase 33
545	gnf1m31128_a_at	C3	GGGCGGGG	4930578M17	4.31				hypothetical SH3/Neutrophil cytosol factor 2/Src homology 3 (SH3) domain profile/Arginine-rich region profile containing protein homologue [Mus musculus]
546	gnf1m08594_a_at	A40	CTGAGGCT	NM_175350	4.31				transmembrane protein 146 (Tmem146)
547	gnf1m18683_a_at	A2	TCACAATG	4933416B22	4.30				hypothetical protein
548	gnf1m23862_a_at	A32*	CACAGAGA	4933415J19	4.30	binding, transporter activity	cellular process, regulation of biological process, physiological process	cell part	ornithine transporter 2
549	gnf1m23007_a_at	C2*	GCCCCGCC	1700086D22	4.30				unclassifiable
550	gnf1m14122_at	B33	CACACACA	4921513D11	4.30				hypothetical protein
551	gnf1m14003_a_at	B7	TGACGTCA	1700029J07	4.29				hypothetical protein
552	gnf1m28909_a_at	A34	TGCCCAGG	4933431C08	4.29	transcription regulator activity, binding	physiological process	cell part	zinc finger protein 217
553	gnf1m04890_a_at	A39	TTTAAAAA	4930430A15	4.28	binding, transcription regulator activity	physiological process, cellular process, regulation of biological process	cell part, organelle	hypothetical Ankyrin repeat profile/Ankyrin-repeat/Ankyrin repeat region circular profile/Yeast DNA-binding domain containing protein
554	gnf1m23726_s_at	A1*	TGACATCA	4930445I03	4.27				hypothetical protein
555	gnf1m08600_a_at	A16	TGACCTCA	NM_177651	4.27				hypothetical protein
556	gnf1m09708_a_at	B39	CCCCACCC	6030405E03	4.27				WD repeat domain 10
557	gnf1m05483_s_at	A1	TGATGTCA	1700010D01	4.27				hypothetical protein
558	gnf1m18301_a_at	A32	TCTCTGTG	1700121N02	4.27				unclassifiable

559	gnf1m29905_a_at	B21	CAGCCTCC	4930584P19	4.27				DMRT-like family B with proline-rich C-terminal, 1
560	gnf1m14431_a_at	A3*	TGTGACAT	1700094E07	4.27	catalytic activity	regulation of biological process	cell part	Dual specificity protein phosphatase containing protein
561	gnf1m07938_at	A48	CTCCCAGA	4932416A15	4.26	binding, catalytic activity	physiological process, cellular process	cell part, organelle part, organelle	jumonji domain containing 2D
562	gnf1m15165_a_at	A13	CTCTGTGA	1700123M18	4.26				sialophorin, pseudogene
563	gnf1m07942_a_at	C2	GGCGGGGC	4932422E22	4.26	binding, transcription regulator activity	regulation of biological process	cell part, organelle	hypothetical Ankyrin repeat structure containing protein
564	gnf1m03347_a_at	A37	CAGAGAGA	4930533L09	4.26				F-box and WD-40 domain protein 5
565	gnf1m33609_at	A4*	GTGACATC	4922505K22	4.25				hypothetical protein
566	gnf1m17176_a_at	A9	TCACAAAG	1700013B14	4.25	binding	physiological process, cellular process, reproduction, development	cell part	interleukin 31
567	gnf1m16361_a_at	B37	TGGGCGGG	4933404O19	4.24	binding	cellular process, physiological process	cell part, organelle part, organelle	tetratricopeptide repeat domain 25
568	gnf1m09922_a_at	C2*	GCCCCGCC	NM_026837	4.23				transmembrane protein 53 (Tmem53)
569	gnf1m30030_a_at	A18	TCTGTGAG	4933434J16	4.23	binding	physiological process, cellular process	cell part, organelle	testicular haploid expressed gene
570	gnf1m03045_a_at	B15	AAAAAAAA	NM_011956	4.23	binding			nucleotide binding protein 2
571	gnf1m15246_a_at	A2	TCACAATG	1700020A23	4.23				hypothetical Serine phosphorylation site in HPr protein containing protein
572	gnf1m15384_a_at	C4	GGGGCGGG	1700008H23	4.23				Park2 co-regulated
573	gnf1m15103_at	C2*	GCCCCGCC	1700104B16	4.22				hypothetical protein
574	gnf1m00084_a_at	C4	GGGGCGGG	NM_198223	4.22	binding			similar to alveolar soft part sarcoma chromosome region, candidate 1 (human)
575	gnf1m29722_a_at	A49	TCTCAGCC	1700086L19	4.22				SERTA domain containing 4
576	gnf1m04060_a_at	C3	GGGCGGGG	4930439L04	4.21	transcription regulator activity, binding	cellular process, reproduction, development, physiological process	organelle, cell part, organelle part	SERTA domain containing 2
577	gnf1m04974_a_at	A8	TCTGTGAC	1700112P19	4.21				coiled-coil domain containing 70
578	gnf1m13072_a_at	C3	GGGCGGGG	4930445K15	4.20	binding	cellular process	organelle, cell part	artemin
579	gnf1m18789_a_at	A1	TGATGTCA	1700016D18	4.20				similar to predicted testis-specific factor 1 (LOC631870), mRNA Length = 438 ref|XM_905802.1| Mus musculus
580	gnf1m09287_a_at	A38	CTTCCAGA	NM_029696	4.19	catalytic activity, binding			malate dehydrogenase 1B, NAD (soluble) (Mdh1b)
581	gnf1m11267_s_at	A3	ATGTCACA	1700012D21	4.19	transcription regulator activity, binding	physiological process	cell part, extracellular region part	CBF1 INTERACTING COREPRESSOR CIR [Homo sapiens]
582	gnf1m08601_a_at	B39	CCCCACCC	4933409I22	4.18				coiled-coil domain containing 113, mRNA (cDNA cloneMGC:74046 IMAGE:6705542), complete cds. [Mus musculus]
583	gnf1m29619_a_at	A44	CTCTGTCT	4930567K20	4.18				unclassifiable
584	gnf1m13788_a_at	A1	TGATGTCA	1700003P14	4.17				unclassifiable
585	gnf1m18102_a_at	B3	CTCTTCCT	1700021A20	4.16				unclassifiable
586	gnf1m16754_a_at	A1	TGATGTCA	1700018L24	4.16				Proline-rich region containing protein
587	gnf1m15314_a_at	A1	TGATGTCA	1700108H04	4.15				alkB, alkylation repair homolog 3 (E. coli)
588	gnf1m05025_a_at	A26	GAGCTCTG	1700120K04	4.15				hypothetical protein
589	gnf1m23056_a_at	A2*	CATTGTGA	1700095K22	4.15				unclassifiable
590	gnf1m21675_a_at	C3	GGGCGGGG	4930504O13	4.14				weakly similar to predicted olfactory receptor 30 like Macaca mulatta
591	gnf1m28952_s_at	B1	TGCCTCTG	4922504O05	4.14	catalytic activity	development, regulation of biological process	extracellular region, extracellular region part	similar to a disintegrin and metallopeptidase domain 4
592	gnf1m09379_a_at	A15	GGTTGCTA	4930579J09	4.13				IIIG9 LONG FORM homolog [Mus musculus]
593	gnf1m05431_a_at	B15	AAAAAAAA	1700001C14	4.13	binding	cellular process	cell part, organelle, organelle part	chemokine-like factor
594	gnf1m04453_a_at	C1	GGGAGGGG	1700026C17	4.13	binding	reproduction	organelle, cell part	Ly1 antibody reactive clone
595	gnf1m13302_a_at	A1*	TGACATCA	1700025M16	4.13				unclassifiable
596	gnf1m13366_a_at	A40	CTGAGGCT	4933406L18	4.13	enzyme regulator activity	regulation of biological process, physiological process, cellular process	cell part, organelle part, organelle	serine (or cysteine) peptidase inhibitor, clade A, member 3A
597	gnf1m14138_a_at	A16	TGACCTCA	4931431F19	4.13				hypothetical Ubiquitin domain containing protein
598	gnf1m05428_a_at	A14	TTGTGAGG	1700001C02	4.13				hypothetical protein
599	gnf1m18670_a_at	B15	AAAAAAAA	4921513J18	4.12	transporter activity	physiological process, cellular process	protein complex, cell part	hypothetical Na+/H+ exchanger containing protein
600	gnf1m05040_a_at	B27	CCTCTCTC	4930547C10	4.12				weakly similar to predicted topoisomerase I binding, arginine/serine-rich-like [Macaca mulatta]
601	gnf1m04782_a_at	A13	CTCTGTGA	4930548O08	4.10	binding	physiological process, cellular process	organelle, cell part	ATP/GTP-binding site motif A (P-loop) containing protein
602	gnf1m06039_a_at	C4	GGGGCGGG	NM_133706	4.10				hypothetical transmembrane protein 97
603	gnf1m14159_at	C3	GGGCGGGG	4933403G17	4.10				weakly similar to hormone-sensitive lipase testicular isoform mRNA Rattus norvegicus
604	gnf1m17158_a_at	A44	CTCTGTCT	1700011N24	4.09	catalytic activity	physiological process, cellular process	cell part, organelle	Retroviral-type aspartic protease containing protein
605	gnf1m01825_a_at	C3	GGGCGGGG	NM_009319	4.09	binding			TAR (HIV) RNA binding protein 2
606	gnf1m07618_a_at	B8	TTTATTTT	4931422A03	4.09				unclassifiable
607	gnf1m13646_at	C4	GGGGCGGG	4932703A03	4.09	catalytic activity,	physiological	organelle part,	hypothetical DEAD (Asp-Glu-Ala-

						binding	process, cellular process	cell part	Asp) box polypeptide 4
608	gnf1m17225_a_at	B40	CCCTCCTC	4921528O07	4.09				hypothetical ARM repeat structure containing protein
609	gnf1m04684_at	A1	TGATGTCA	4933436I01	4.08				hypothetical protein
610	gnf1m04919_a_at	A1*	TGACATCA	NM_026319	4.08				intraflagellar transport 74 homolog (Chlamydomonas) (Ift74)
611	gnf1m29032_a_at	B6	CAGCCAAT	4931413D17	4.07				arylsulfatase A
612	gnf1m10239_a_at	A26	GAGCTCTG	4933403H06	4.06	binding	cellular process	cell part, protein complex, organelle part, organelle	leucine rich repeat containing 44
613	gnf1m04907_a_at	A1*	TGACATCA	4930560N03	4.06				hypothetical protein
614	gnf1m23164_a_at	A1	TGATGTCA	1700010E23	4.05	binding	physiological process, cellular process	organelle, cell part	spermatogenesis associated 6 (Spata6) (GO:0005524 InterPro|IPR001687) [Mus musculus]
615	gnf1m29423_a_at	A13	CTCTGTGA	1700011I03	4.05				hypothetical protein
616	gnf1m04841_x_at	A41	GAGGCCAG	4930449I24	4.05	enzyme regulator activity	reproduction, development, regulation of biological process, cellular process	cell part	weakly similar to predicted Ral guanine nucleotide dissociation stimulator (RalGEF) (RalGDS) [Mus musculus]
617	gnf1m12264_a_at	A22	TCTGAGGC	4933428J05	4.05	transporter activity, binding	cellular process, physiological process	cell part	similar to predicted solute carrier family 22 (organic cation transporter), member 21
618	gnf1m23702_a_at	B31	AGAGGAAG	4930404C07	4.04				Glutamic acid-rich region containing proteinMus musculus
619	gnf1m00096_a_at	A3*	TGTGACAT	4922502O05	4.04	catalytic activity, binding	physiological process, cellular process	cell part, organelle	hypothetical a disintegrin and metallopeptidase domain 1b
620	gnf1m17206_a_at	A2*	CATTGTGA	1700121K02	4.04				similar to predicted PKD2 interactor, golgi and endoplasmic reticulum associated 1Rattus norvegicus
621	gnf1m18366_at	A46	AGGAGCAG	1700001G11	4.03				hypothetical protein
622	gnf1m30927_a_at	A1	TGATGTCA	4930517K23	4.03	binding	development	organelle, cell part	hypothetical Barrier to autointegration factor (BAF) containing protein
623	gnf1m13538_a_at	A1*	TGACATCA	4930557A04	4.03	binding	reproduction, physiological process, cellular process	protein complex, organelle part, cell part	hypothetical Histone-fold structure containing protein
624	gnf1m30249_s_at	A35	TCCAGGAG	4932419D11	4.03	binding	physiological process, cellular process, regulation of biological process	cell part	synaptonemal complex protein 1
625	gnf1m19279_s_at	B7	TGACGTCA	NM_001002775	4.03				weakly similar to retinitis pigmentosa GTPase regulator
626	gnf1m13551_a_at	C1	GGGAGGGG	4930519P11	4.03				hypothetical protein
627	gnf1m05234_a_at	A32	TCTCTGTG	1700019F09	4.02	signal transducer activity	physiological process, cellular process	extracellular region	WD repeat domain 16
628	gnf1m04649_a_at	A23	TGCTTTCC	4921514K14	4.02				testis expressed gene 12
629	gnf1m23182_a_at	A13*	TCACAGAG	1700048O20	4.01				zinc finger protein 620
630	gnf1m15352_a_at	C3	GGGCGGGG	4933415I03	4.01				coiled-coil domain containing 11
631	gnf1m05424_a_at	C3	GGGCGGGG	NM_029247	4.01				hypothetical protein
632	gnf1m14719_a_at	B39	CCCCACCC	4930563P21	4.01				hypothetical polyamine modulated factor 1 binding protein 1-like [Macaca mulatta]
633	gnf1m10382_a_at	C3	GGGCGGGG	4931407K02	4.01	binding	response to stimulus	organelle, cell part	weakly similar to predicted EF-hand containing protein
634	gnf1m22843_a_at	A32*	CACAGAGA	4930544N01	4.01				weakly simlar to adrenergic receptor, alpha 1d

Appendix Table 2b. Testis-specificity and annotation of the genes whose regulatory regions were not completely sequenced or overlapped with other regulatory regions

Data of 85 testis-specific genes whose regulatory regions were not completely sequenced or whose regulatory regions overlapped with other regulatory regions.

#1 Expression level ranking in this group as determined by testis specificity.

#2 Testis-specificity level.

#1	Microarray ID	Clone ID	#2	Gene Ontology Classification			Annotation
				Molecular function	Biological process	Cellular component	
1	gnf1m21655_at	NM_199034	7.32	binding			weakly similar to predicted CD69 antigen (p60, early T-cell activation antigen)
2	gnf1m31778_at	2410022A04	7.04	binding	physiological process, cellular process		glutamine rich 2 (Qrich2)
3	gnf1m12377_a_at	A930013E12	6.87	transcription regulator activity, binding	regulation of biological process, physiological process, cellular process	organelle, cell part	coiled-coil domain containing 60 (Ccdc60)
4	gnf1m04821_a_at	NM_026084	6.65				hypothetical protein
5	gnf1m13831_a_at	4921511C04	6.59				Peptidase, eukaryotic cysteine peptidase active site containing protein
6	gnf1m03322_a_at	E030006L06	6.50	binding			Janus kinase 3
7	gnf1m18722_a_at	4930597B14	6.42	binding	reproduction, development, regulation of biological process, cellular process	cell part	leucine rich repeat containing 56
8	gnf1m30191_s_at	I920062J18	6.13				hypothetical Proline-rich region profile containing protein
9	gnf1m06267_a_at	M5C1099J02	6.11	binding	cellular process, regulation of biological process, physiological process	cell part	suppressor of cytokine signaling 7 (Socs7)
10	gnf1m08368_a_at	D330025M16	6.08	binding		organelle, cell part	zinc finger, HIT domain containing 2
11	gnf1m16052_a_at	1700081D17	6.00			organelle, cell part	similar to PEBP family protein precursor
12	gnf1m10564_at	3830408C23	5.91	binding, catalytic activity	response to stimulus, regulation of biological process, physiological process, cellular process	cell part, organelle	ankyrin repeat and SOCS box-containing protein 17
13	gnf1m29416_a_at	F630225G14	5.88				testis specific protein kinase 1
14	gnf1m07900_a_at	NM_177765	5.83	catalytic activity	physiological process, cellular process		tubulin tyrosine ligase-like family, member 13 (Ttll13)
15	gnf1m30626_at	G630078G02	5.75			extracellular region	maelstrom homolog (Drosophila)
16	gnf1m16137_a_at	1190002A17	5.75	catalytic activity, binding	physiological process, cellular process		hypothetical Adenylate kinase containing protein
17	gnf1m16775_a_at	NM_011516	5.72	binding	physiological process, cellular process	cell part, organelle part, organelle	atonal homolog 8 (Drosophila)
18	gnf1m22221_a_at	C920025L08	5.66	binding		cell part	sperm mitochondria-associated cysteine-rich protein
19	gnf1m16828_a_at	2410015A16	5.59			extracellular region	ring finger protein 148
20	gnf1m27335_a_at	D030060E19	5.58				hypothetical S-adenosyl-L-methionine-dependent methyltransferases structure containing protein
21	gnf1m13456_at	4930432J16	5.55				coiled-coil domain containing 116
22	gnf1m17690_at	A630039F22	5.49				spermatogenesis associated 21
23	gnf1m13287_a_at	F630042F15	5.40	binding, catalytic activity, transcription regulator activity	regulation of biological process, physiological process, cellular process	cell part, protein complex, organelle part, organelle	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20 (Ddx20)
24	gnf1m11136_s_at	I920045M18	5.34	catalytic activity, binding	physiological process, cellular process, regulation of biological process	cell part, organelle, organelle part	MYST histone acetyltransferase 1
25	gnf1m08962_s_at	C130098D09	5.33				ATP/GTP binding protein-like 5 (Agbl5), transcript variant 3
26	gnf1m31215_s_at	4933439H17	5.31	catalytic activity	physiological process, cellular process		hypothetical Peptidase, eukaryotic cysteine peptidase active site containing protein
27	gnf1m18853_a_at	5930422B18	5.30				unclassifiable
28	gnf1m30265_a_at	I920019O09	5.20	catalytic activity, binding	physiological process, cellular process	organelle, cell part	ribonuclease H2, large subunit
29	gnf1m04978_s_at	1700062C23	5.19	binding			zinc finger protein 217
30	gnf1m28680_a_at	1810037J08	5.18				phosphoglycerate kinase 2
31	gnf1m05239_a_at	G530145B18	5.16		regulation of biological process, physiological process, cellular process		MAD2 mitotic arrest deficient-like 2 (yeast) (Mad2l2)
32	gnf1m00466_a_at	E430037N03	5.08	binding	regulation of biological process, physiological process, cellular process	organelle, cell part	WD repeat domain 62
33	gnf1m09512_a_at	A630082B21	5.07	binding			regulatory factor X, 2 (influences HLA class II expression)
34	gnf1m04905_at	4930465K10	5.03				asteroid homolog 1 (Drosophila)
35	gnf1m09987_s_at	F630205N16	5.00	catalytic activity, binding	physiological process, cellular process		6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 (Pfkfb4)
36	gnf1m11605_a_at	5430408G21	5.00	catalytic activity, binding			WW domain binding protein 11
37	gnf1m07602_a_at	5730427C23	4.96	binding			melanoma associated antigen (mutated) 1
38	gnf1m13975_a_at	4930432J01	4.96				unclassifiable
39	gnf1m16773_a_at	1110017D15	4.96				diablo homolog (Drosophila)

40	gnf1m05337_a_at	1110014P06	4.92		cellular process	organelle, cell part	solute carrier family 22 (organic cation transporter), member 21
41	gnf1m13937_a_at	C920013G19	4.80			cell part	hypothetical protein
42	gnf1m30004_a_at	7120447D04	4.80	binding, catalytic activity	physiological process, cellular process, regulation of biological process	cell part, protein complex, organelle	thioredoxin reductase 3
43	gnf1m30753_at	4922504L10	4.80			organelle, cell part	similar to Salivary glue protein Sgs-4 precursor
44	gnf1m31291_a_at	2010109A12	4.79		physiological process, cellular process		fibrous sheath-interacting protein 1
45	gnf1m29201_at	I0C0026C19	4.78				hypothetical protein
46	gnf1m02430_a_at	E430014A10	4.76	catalytic activity, binding, signal transducer activity	cellular process, physiological process, development, regulation of biological process	cell part, organelle	AN1, ubiquitin-like, homolog (Xenopus laevis)
47	gnf1m15242_at	I920045P05	4.74	enzyme regulator activity	physiological process, cellular process, regulation of biological process		cyclin K
48	gnf1m31664_at	F630047G17	4.71	binding		cell part, organelle	X-ray radiation resistance associated 1 protein
49	gnf1m18101_at	9930109I05	4.67				kinesin family member 2B
50	gnf1m30390_a_at	4930453N24	4.63	catalytic activity	physiological process, cellular process		hypothetical Peptidase, eukaryotic cysteine peptidase active site containing protein
51	gnf1m32280_a_at	M5C1026A22	4.62	catalytic activity	physiological process, cellular process	cell part	glycosyltransferase 8 domain containing 3
52	gnf1m18179_at	A430076A20	4.61				ring finger protein 126
53	gnf1m22576_a_at	E130303B06	4.56				weakly similar to sodium channel and clathrin linker 1 (Sclt1)
54	gnf1m23608_at	4733401H18	4.55			organelle, cell part	nuclear protein E3-3
55	gnf1m29679_a_at	2900041A11	4.53				hypothetical protein
56	gnf1m13335_a_at	5330430P22	4.51				cytochrome P450, family 17, subfamily a, polypeptide 1
57	gnf1m04043_a_at	G830022G14	4.51	binding, catalytic activity	reproduction, development, cellular process	cell part, organelle	spermatogenesis associated 5
58	gnf1m03205_a_at	4930502I03	4.44	binding	cellular process, reproduction, development, physiological process	cell part, organelle, protein complex, organelle part	RAN guanine nucleotide release factor (Rangrf)
59	gnf1m24904_a_at	I830061M19	4.44	catalytic activity, enzyme regulator activity, binding	physiological process, cellular process		myotubularin related protein 9
60	gnf1m16751_at	2610318N02	4.43				hypothetical Proline-rich region profile containing protein
61	gnf1m04335_a_at	C230006K09	4.40	signal transducer activity, transporter activity, catalytic activity	physiological process, cellular process	cell part	solute carrier family 25 (mitochondrial carrier, ornithine transporter) member 2
62	gnf1m10285_a_at	C530035L23	4.39	binding, transcription regulator activity	regulation of biological process, physiological process, cellular process	organelle, cell part	zinc finger protein 438
63	gnf1m09744_a_at	F630050M23	4.38	catalytic activity			Rsb-66 protein (Rsb66)
64	gnf1m28413_a_at	E430036P15	4.37				X-ray radiation resistance associated 1
65	gnf1m17370_a_at	2410072D24	4.34	catalytic activity	physiological process, cellular process	cell part, protein complex	homologue proteasome (prosome, macropain) subunit, alpha type, 8 isoform 2
66	gnf1m16233_a_at	4732409C05	4.33				hypothetical protein
67	gnf1m07312_a_at	A630069B14	4.32	catalytic activity, antioxidant activity	cellular process, physiological process	cell part	prion protein dublet
68	gnf1m05029_a_at	A930018P22	4.31				coiled-coil domain containing 11
69	gnf1m29259_a_at	F630110C03	4.31				MAD2 mitotic arrest deficient-like 2 (yeast)
70	gnf1m20339_at	A630001I11	4.30				poly A binding protein, cytoplasmic 2
71	gnf1m18488_a_at	3110023G01	4.30	binding			homologue katanin p60 subunit A-like 2 (Katnal2)
72	gnf1m25228_s_at	E430035G08	4.30				elongation factor 1 homolog (ELF1, S. cerevisiae)
73	gnf1m04244_a_at	A730048L21	4.23	binding	physiological process, cellular process	cell part	alanine and arginine rich domain containing protein
74	gnf1m16560_a_at	2610020H08	4.23	catalytic activity			exonuclease NEF-sp
75	gnf1m08351_a_at	B230381K07	4.20				cofactor required for Sp1 transcriptional activation, subunit 7
76	gnf1m07300_s_at	I530023E14	4.18	binding, catalytic activity			nudix (nucleoside diphosphate linked moiety X)-type motif 18
77	gnf1m04036_s_at	5430416M17	4.18	enzyme regulator activity, binding	physiological process, cellular process	cell part, organelle part, organelle	HLA-B-associated transcript 3
78	gnf1m30720_a_at	E130314H02	4.16	signal transducer activity	physiological process, cellular process, regulation of biological process	cell part, protein complex, organelle part, organelle	mediator complex subunit 16 (Med16)
79	gnf1m09413_s_at	I0C0045B19	4.14	binding, transcription regulator activity, catalytic activity	physiological process, development, cellular process, regulation of biological process	cell part, organelle part, protein complex, organelle	polycomb group ring finger 4
80	gnf1m10515_a_at	1110020C03	4.09				kelch-like 10 (Drosophila)
81	gnf1m29825_a_at	5033427P15	4.09			cell part	cystatin 8 (cystatin-related epididymal spermatogenic)
82	gnf1m18605_a_at	E130217B17	4.06				coiled-coil domain containing 65
83	gnf1m12974_a_at	D630044H03	4.04				hypothetical S-adenosyl-L-methionine-dependent methyltransferases structure containing protein
84	gnf1m12431_a_at	G730044P08	4.02				hypothetical protein
85	gnf1m02369_a_at	I830091K06	4.01	catalytic activity, binding	physiological process, cellular process	cell part, organelle	heme oxygenase (decycling) 2

Appendix Table 2c. Testis-specificity and annotation of the genes which were not supported to cover the intact 5'-ends

Data of 157 testis-specific genes that have no experimental evidence to cover the intact 5′-ends.

#1 Expression level ranking in this group as determined by testis specificity.

#2 Testis-specificity level.

#1	Microarray ID	Clone ID	#2	Gene Ontology Classification			Annotation
				Molecular function	Biological process	Cellular component	
1	gnf1m31206_a_at	1700019B01	7.01				weakly similar to predicted coiled-coil domain containing 89 (Ccdc89)
2	gnf1m29756_a_at	1700021F07	6.94				similar to low in lung cancer 1
3	gnf1m16054_a_at	1700009N14	6.90	binding, transporter activity, catalytic activity	cellular process, physiological process, regulation of biological process	cell part, organelle part, protein complex, organelle	weakly similar to RAN protein
4	gnf1m18742_a_at	1700022P22	6.87				hypothetical protein
5	gnf1m17312_a_at	4933405J11	6.75				hypothetical protein
6	gnf1m30572_a_at	4933413C15	6.72				weakly similar to coiled-coil domain containing 67 (Ccdc67)
7	gnf1m05112_s_at	1700018F24	6.71				hypothetical Ras GEF structure containing protein
8	gnf1m31877_at	4933439L02	6.56				hypothetical protein
9	gnf1m08577_a_at	4922504H04	6.53	transporter activity, binding	physiological process, cellular process	cell part, protein complex	potassium channel tetramerisation domain containing 19
10	gnf1m28686_a_at	1700095K08	6.53				TBC1 domain family, member 21
11	gnf1m31096_a_at	1700003O08	6.51				unclassifiable
12	gnf1m16159_a_at	1700025M08	6.48	catalytic activity	physiological process, cellular process	cell part, extracellular region, organelle	sperm acrosome associated 3
13	gnf1m18375_a_at	1700016G14	6.47				unclassifiable
14	gnf1m02714_a_at	4930569O14	6.46	binding		organelle, cell part	RNA binding motif protein, Y chromosome, family 1, member A1
15	gnf1m18660_at	1700108N11	6.44				ovo-like 2 (Drosophila)
16	gnf1m17095_a_at	4930579F01	6.43				similar to predicted stromal protein associated with thymii and lymph nodes isoform 2
17	gnf1m23185_a_at	1700056E22	6.40				hypothetical protein
18	gnf1m30605_a_at	4930467B22	6.32				ATP-binding cassette, sub-family C (CFTR/MRP), member 12
19	gnf1m17234_a_at	1700049K14	6.30	catalytic activity	physiological process, cellular process	cell part	weakly similar to predicted Plasma kallikrein precursor (Plasma prekallikrein) (Kininogenin) (Fletcher factor)
20	gnf1m17328_a_at	4933432N21	6.29	structural molecule activity	physiological process, cellular process	cell part, organelle	homologue testis specific 10 (Tsga10)
21	gnf1m13976_a_at	4930570O04	6.24				unclassifiable
22	gnf1m29757_a_at	1810013N20	6.24				testis specific 10 interacting protein (Tsga10ip)
23	gnf1m17352_a_at	4921530D09	6.24				hypothetical protein
24	gnf1m13790_a_at	1700056A17	6.19				melanoma antigen, family B, 5
25	gnf1m05414_a_at	4930503E14	6.13				weakly similar to alpha12-takusan
26	gnf1m23650_at	4833401A03	6.11	transporter activity	cellular process, physiological process	cell part	polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like
27	gnf1m16285_at	4930571K23	6.10				unclassifiable
28	gnf1m23176_x_at	1700029H17	6.02		reproduction		similar to predicted Ssty2 protein isoform 1
29	gnf1m25487_at	A230094D06	6.00	signal transducer activity, binding	cellular process	cell part, extracellular region part	G protein-coupled receptor 106
30	gnf1m14468_at	4930405A07	5.99				unclassifiable
31	gnf1m21682_at	4930551J12	5.99				unclassifiable
32	gnf1m31099_a_at	1700027A15	5.99				hypothetical protein
33	gnf1m30571_a_at	3300001K11	5.87				tektin 5 (Tekt5)
34	gnf1m14530_a_at	4933422M21	5.86	binding	physiological process, cellular process	cell part	ADP-ribosylation factor-like 13
35	gnf1m22995_a_at	4933425D22	5.83				unclassifiable
36	gnf1m21654_a_at	4922501K12	5.78				hypothetical protein
37	gnf1m16440_at	4930442P07	5.77				unclassifiable
38	gnf1m14460_a_at	4930415F15	5.74				hypothetical protein
39	gnf1m30457_a_at	1700019G24	5.72				unclassifiable
40	gnf1m07557_at	A930027N24	5.70				cDNA sequence BC049715
41	gnf1m09162_s_at	1700023A18	5.70	binding, enzyme regulator activity		cell part	phosphatidylethanolamine binding protein 2
42	gnf1m16079_a_at	6330543E12	5.64				IQ motif and WD repeats 1
43	gnf1m31171_a_at	3526402J02	5.63	catalytic activity			ataxia telangiectasia and rad3 related
44	gnf1m19128_at	1700042K15	5.62	catalytic activity, binding	physiological process, cellular process		ring finger protein 133
45	gnf1m18415_a_at	1700030G11	5.62				weakly similar to novel protein containing an anlyrin domain
46	gnf1m21667_at	4930427O07	5.56				hypothetical protein
47	gnf1m19258_at	4931412E05	5.53				zinc finger protein 148, pseudogene 1
48	gnf1m13500_a_at	1700113H08	5.53				hypothetical protein
49	gnf1m30831_a_at	1700012C08	5.45				unclassifiable
50	gnf1m18455_at	3830402K23	5.45				synaptonemal complex protein 2 (Sycp2)

51	gnf1m23022_a_at	1700108A15	5.44				unclassifiable
52	gnf1m23777_at	4930555L03	5.40				IBR domain containing 3
53	gnf1m23355_a_at	2810017G21	5.38	binding, transcription regulator activity	development, regulation of biological process, physiological process, cellular process	cell part, protein complex, organelle part, organelle	homeo box A4
54	gnf1m16866_a_at	4930527E24	5.36				weakly similar to Xlr-like
55	gnf1m13830_a_at	1700023A16	5.35				hypothetical protein
56	gnf1m14298_a_at	4930535E05	5.35				weakly similar to predicted T-cell activation Rho GTPase-activating protein isoform b
57	gnf1m13520_at	4930452G13	5.34				unclassifiable
58	gnf1m17104_at	4933438K21	5.31				unclassifiable
59	gnf1m28768_a_at	A530057A03	5.30	catalytic activity	physiological process, cellular process	cell part	similar to predicted similar to mitochondrial glycerol 3-phosphate acyltransferase
60	gnf1m18414_at	1700030L20	5.27				developmentally regulated repeat element-containing transcript 1a
61	gnf1m30921_s_at	4921509O09	5.27				weakly similar to predicted Sycp3 like Y-linked
62	gnf1m23872_at	4933434I20	5.25	catalytic activity	physiological process	extracellular region, extracellular region part, cell part	hypothetical Prokaryotic membrane lipoprotein lipid attachment site containing protein
63	gnf1m11101_a_at	6030488D03	5.23				hypothetical protein
64	gnf1m13832_a_at	4921509B22	5.21	binding, transcription regulator activity	regulation of biological process	organelle, cell part	hypothetical Leucine-rich repeat/bZIP (Basic-leucine zipper) transcription factor family/Leucine-rich repeat, typical subtype containing protein
65	gnf1m13833_at	4930449C09	5.18				unclassifiable
66	gnf1m23167_a_at	1700018G05	5.17				unclassifiable
67	gnf1m18868_a_at	4933440C21	5.14	binding		cell part	DC-STAMP domain containing 1
68	gnf1m14147_at	4932703K07	5.12				heat shock protein 1, alpha
69	gnf1m30771_a_at	4930578E11	5.11				unclassifiable
70	gnf1m13328_a_at	4933422B16	5.11				hypothetical Tetratricopeptide repeat (TPR) structure containing protein
71	gnf1m18620_a_at	1700048O14	5.10				unclassifiable
72	gnf1m16843_s_at	4921511M17	5.09			cell part	hypothetical protein
73	gnf1m16116_a_at	3110013H01	5.08	catalytic activity	physiological process	organelle, cell part	proline-rich polypeptide 6
74	gnf1m18655_at	4931438A05	5.08				weakly similar to predicted vitamin A-deficient testicular protein 11-like
75	gnf1m17085_a_at	4930435E18	5.08				unclassifiable
76	gnf1m13998_a_at	1700017D01	5.07				hypothetical protein
77	gnf1m28673_a_at	4930469G21	5.06				hypothetical protein
78	gnf1m17273_a_at	1700063H04	5.06				hypothetical protein
79	gnf1m11449_at	4921521M13	5.03	binding, catalytic activity	reproduction, development, cellular process	cell part, organelle	DNA segment, Chr 1, Pasteur Institute 1
80	gnf1m29797_a_at	2900092C05	4.94				hypothetical protein
81	gnf1m23957_a_at	5330437G15	4.93				serine/threonine kinase 33
82	gnf1m30296_at	3632444A02	4.93				tetratricopeptide repeat domain 21B
83	gnf1m13582_a_at	1700013H16	4.93				hypothetical protein
84	gnf1m18132_a_at	1700003H21	4.92				EF hand calcium binding protein 1
85	gnf1m19031_at	4933404M19	4.89				weakly similar to predicted proline-rich cyclin A1-interacting protein isoform 1
86	gnf1m05196_a_at	4933411G06	4.89	catalytic activity, binding	physiological process, cellular process, response to stimulus, regulation of biological process	cell part, organelle part, protein complex, organelle	weakly similar to SMT3 suppressor of mif two 3 homolog 1 isoform b precursor
87	gnf1m14178_a_at	4933422A05	4.88				unclassifiable
88	gnf1m09828_a_at	F830031M20	4.87				intraflagellar transport 140 homolog (Chlamydomonas)
89	gnf1m05434_a_at	1700012P12	4.85	transporter activity, binding	physiological process, cellular process	cell part, organelle	profilin 3
90	gnf1m16015_at	4933429H19	4.85	signal transducer activity, transporter activity	physiological process, cellular process	cell part	hypothetical TonB-dependent receptor protein containing protein
91	gnf1m17688_at	4931436F15	4.82				hypothetical protein
92	gnf1m14866_at	1700003F17	4.81				hypothetical protein
93	gnf1m05419_a_at	4930542N07	4.81			cell part	hypothetical protein
94	gnf1m16980_a_at	4933434G05	4.78				coiled-coil domain containing 57 (Ccdc57)
95	gnf1m13323_a_at	4930433I05	4.77			organelle part, cell part	cylicin, basic protein of sperm head cytoskeleton 1
96	gnf1m03386_a_at	1700021G14	4.76	enzyme regulator activity, binding	physiological process, cellular process	cell part	immunoglobulin (CD79A) binding protein 1b
97	gnf1m29246_s_at	9230104I23	4.75				tripartite motif-containing 36
98	gnf1m33184_at	1700014P15	4.74	transporter activity, binding	physiological process, cellular process, reproduction, development	cell part, organelle	solute carrier family 9, member 10 (Slc9a10)
99	gnf1m16929_at	1700024J04	4.73	signal transducer activity			hypothetical TNFR/CD27/30/40/95 cysteine-rich region/von Willebrand factor, type C repeat containing protein
100	gnf1m23708_at	4930408P03	4.72	binding	physiological process, cellular process	cell part, organelle, protein complex, organelle part	HISTONE H2B (FRAGMENT) homolog [Mus musculus]
101	gnf1m29612_a_at	1700020H17	4.71	catalytic activity			molybdenum cofactor synthesis 3
102	gnf1m31156_a_at	C330017P09	4.67				hypothetical protein
103	gnf1m14489_at	4933412L11	4.66				unclassifiable
104	gnf1m14693_a_at	4930527J03	4.64				hypothetical Alanine-rich region containing protein

105	gnf1m23738_s_at	4930476G21	4.62	binding			ring finger protein 17
106	gnf1m14207_at	4933435G04	4.61				hypothetical protein
107	gnf1m01848_a_at	1700030B16	4.59	catalytic activity	physiological process, cellular process		testicular serine protease 2
108	gnf1m14175_a_at	4933413D07	4.58				unclassifiable
109	gnf1m30081_a_at	4930572N15	4.58	binding, transcription regulator activity	regulation of biological process		ankyrin repeat domain 53 (Ankrd53)
110	gnf1m15511_a_at	G430033H23	4.58				leucine rich repeat containing 27
111	gnf1m14180_a_at	4933413N12	4.58				hypothetical protein
112	gnf1m17307_a_at	1700016C15	4.56				hypothetical protein
113	gnf1m11444_a_at	4921506E08	4.54	binding	physiological process, response to stimulus, cellular process	extracellular region, extracellular region part	chemokine (C-C motif) ligand 28
114	gnf1m13353_a_at	5133400G04	4.53		reproduction, development, cellular process	cell part	homologue TATA-binding protein-like factor-interacting protein isoform 2
115	gnf1m13926_a_at	1700051I12	4.51	structural molecule activity	cellular process		collagen, type XX, alpha 1
116	gnf1m15539_a_at	4933401F05	4.50	catalytic activity	physiological process, cellular process	cell part	weakly similar to adrenal mitochondrial protease
117	gnf1m29295_a_at	1700023D19	4.49				weakly similar to predicted SCRL protein variant 1
118	gnf1m32673_at	C230012F14	4.45	binding			armadillo repeat containing 2
119	gnf1m18823_at	4932416M14	4.40				hypothetical protein
120	gnf1m32296_at	4922503N05	4.40				cancer antigen 1
121	gnf1m15939_at	1700014B07	4.39				hypothetical protein
122	gnf1m17231_a_at	4930444P10	4.39				hypothetical Arginine-rich region containing protein
123	gnf1m16847_a_at	1700011E04	4.38			extracellular region part	predicted GLI pathogenesis-related 1 like 1 (Glipr1l1)
124	gnf1m14697_a_at	4930544O15	4.37			cell part	hypothetical protein
125	gnf1m09652_a_at	I730086C16	4.35				IQ motif containing G
126	gnf1m15124_a_at	4930570E03	4.34				hypothetical protein
127	gnf1m07476_a_at	1810009N24	4.34	catalytic activity	physiological process, cellular process	extracellular region, extracellular region part	lysozyme-like 4
128	gnf1m16596_at	1700062G21	4.33				neurexin I
129	gnf1m17179_a_at	1700067K01	4.33				hypothetical protein
130	gnf1m13554_a_at	1700034F02	4.31				hypothetical ARM repeat structure containing protein
131	gnf1m30342_a_at	1700026J12	4.31		cellular process	cell part	weakly similar to CD47 antigen
132	gnf1m14608_a_at	4930511J24	4.30				unclassifiable
133	gnf1m07915_a_at	4933417L03	4.29				hypothetical protein
134	gnf1m17027_a_at	4933424N20	4.29				unclassifiable
135	gnf1m10081_a_at	C230076L23	4.29	binding, catalytic activity, transcription regulator activity	physiological process, cellular process, regulation of biological process, growth		tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase
136	gnf1m19228_at	4930526M03	4.26				weakly similar to predicted Ribosome-binding protein 1 (Ribosome receptor protein) (mRRp)
137	gnf1m08204_a_at	A330015D16	4.25				weakly similar to predicted Myosin heavy chain, fast skeletal muscle, embryonic
138	gnf1m29417_a_at	A130090N03	4.25				amyotrophic lateral sclerosis 4 homolog (human)
139	gnf1m19278_at	4932416H13	4.25				hypothetical protein
140	gnf1m21703_at	4933402M05	4.25				Adult male testis cDNA, RIKEN full-length enriched library, clone:4933402M05 product:serine/threonine kinase 33, full insert sequence
141	gnf1m27322_at	D030054G02	4.25				hypothetical protein
142	gnf1m19389_at	6030430N23	4.24				DEAD (Asp-Glu-Ala-Asp) box polypeptide 4
143	gnf1m30176_a_at	1700023F06	4.23				hypothetical protein
144	gnf1m14198_at	4933417D19	4.19				unclassifiable
145	gnf1m29567_a_at	1700008J08	4.18				ankyrin repeat domain 48
146	gnf1m28873_a_at	4930404K22	4.16	catalytic activity			spermidine/spermine N1-acetyl transferase-like 1
147	gnf1m00055_a_at	C330007K24	4.13				serine threonine kinase 31
148	gnf1m17834_at	4632417E12	4.13	binding, transcription regulator activity	regulation of biological process		unclassifiable
149	gnf1m17325_s_at	4930412B11	4.13				hypothetical protein
150	gnf1m21504_a_at	E130009J12	4.12				hypothetical protein
151	gnf1m29010_at	4933400N17	4.10	binding	regulation of biological process		similar to predicted DNA-binding protein RFX2
152	gnf1m14462_a_at	4930423M02	4.09				unclassifiable
153	gnf1m14629_at	4930445B03	4.08				unclassifiable
154	gnf1m31677_at	4931417M15	4.07				hypothetical Leucine-rich repeat/Leucine-rich repeat, typical subtype containing protein
155	gnf1m14404_a_at	1700041E20	4.06	binding			homologue calcium and integrin binding family member 4
156	gnf1m16968_at	4933436F18	4.05				unclassifiable
157	gnf1m05321_a_at	1700072E05	4.05			cell part	hypothetical protein

Appendix Table 2d. Testis specificity and annotation of 18 testis-specific genes whose clone IDs were duplicated with other genes shown in Appendix Table 2a, b, and c

Data of 18 testis-specific genes whose clone IDs were duplicated with other genes shown in Appendix Table 2a, b, and c.

#1 Expression level ranking in this group as determined by testis specificity.

#2 Testis-specificity level.

				Gene Ontology Classification			
#1	**Calibri**	**Clone ID**	**#2**	**Molecular function**	**Biological process**	**Cellular component**	**Annotation**
1	gnf1m05228_s_at	1700001F09	6.26				hypothetical Cytochrome c family heme-binding site containing protein
2	gnf1m30192_a_at	I920062J18	5.97				Proline-rich region profile containing protein
3	gnf1m16354_at	1700110M21	5.59				gamma-aminobutyric acid (GABA-B) receptor binding protein
4	gnf1m14433_s_at	4930551J12	5.30				unclassifiable
5	gnf1m18537_s_at	1700001J11	5.14				RING FINGER PROTEIN 19 (XY BODY PROTEIN) (XYBP) (GAMETOGENESIS EXPRESSED PROTEIN GEG-154) (UBCM4-INTERACTING PROTEIN 117) (UIP117) [Mus musculus]
6	gnf1m13049_s_at	4930414P16	5.10	binding, enzyme regulator activity	physiological process, cellular process	cell part	proacrosin binding protein
7	gnf1m08682_a_at	C130098D09	4.86				ATP/GTP binding protein-like 5 (Agbl5), transcript variant 3
8	gnf1m17184_a_at	4921517J08	4.85	binding	physiological process, cellular process	cell part	weakly similar to predicted speedy homolog 1 (Drosophila)
9	gnf1m16842_a_at	4921511M17	4.72			cell part	hypothetical protein
10	gnf1m10539_at	NM_016915	4.57	catalytic activity, nutrient reservoir activity			phospholipase A2, group VI
11	gnf1m05484_at	1700023A18	4.47	binding, enzyme regulator activity		cell part	phosphatidylethanolamine binding protein 2
12	gnf1m02953_a_at	4932703D08	4.39	catalytic activity, binding	physiological process	organelle, cell part	a disintegrin and metallopeptidase domain 25 (testase 2)
13	gnf1m33186_at	1700014P15	4.35	transporter activity, binding	physiological process, cellular process, reproduction, development	cell part, organelle	solute carrier family 9, member 10 (Slc9a10)
14	gnf1m00675_s_at	NM_175240	4.29				transmembrane protein 162 (Tmem162)
15	gnf1m25893_s_at	4932441M08	4.16				P-loop containing nucleotide triphosphate hydrolases structure containing protein Mus musculus
16	gnf1m17230_at	4930444P10	4.07				hypothetical Arginine-rich region containing protein
17	gnf1m23725_at	4930445I03	4.06				hypothetical protein
18	gnf1m00044_a_at	4930570K13	4.01	binding, transcription regulator activity	physiological process, cellular process	cell part	weakly similar to predicted DNA binding protein with his-thr domain

Appendix Table 2e. Testis-specificity of the genes whose clone IDs were not available

Data of 118 testis-specific genes whose clone IDs were not available.

#1 Expression level ranking in this group as determined by testis specificity in this group.

#2 Testis-specificity level.

#1	Microarray ID	#2
1	gnf1m01980_a_at	7.21
2	gnf1m01166_at	7.07
3	gnf1m07353_a_at	7.04
4	gnf1m09241_a_at	7.00
5	gnf1m01533_a_at	6.95
6	gnf1m28688_at	6.87
7	gnf1m01973_a_at	6.85
8	gnf1m04179_a_at	6.85
9	gnf1m31560_x_at	6.83
10	gnf1m29198_at	6.78
11	gnf1m02000_a_at	6.70
12	gnf1m32513_at	6.69
13	gnf1m02899_a_at	6.65
14	gnf1m31337_at	6.64
15	gnf1m31231_s_at	6.62
16	gnf1m01847_a_at	6.61
17	gnf1m32279_at	6.46
18	gnf1m06613_at	6.39
19	gnf1m31104_at	6.30
20	gnf1m30747_at	6.25
21	gnf1m32681_at	6.19
22	gnf1m01883_a_at	6.18
23	gnf1m35021_at	6.05
24	gnf1m04122_a_at	6.02
25	gnf1m31219_at	6.02
26	gnf1m15984_a_at	5.99
27	gnf1m33287_at	5.95
28	gnf1m13524_at	5.94
29	gnf1m35156_at	5.90
30	gnf1m30644_at	5.85
31	gnf1m03857_at	5.85
32	gnf1m10353_at	5.79
33	gnf1m30330_at	5.79
34	gnf1m34052_at	5.78
35	gnf1m31382_at	5.78
36	gnf1m32047_at	5.74
37	gnf1m01946_x_at	5.68
38	gnf1m01894_a_at	5.65
39	gnf1m31519_at	5.58
40	gnf1m31638_at	5.58
41	gnf1m33591_at	5.55
42	gnf1m31460_at	5.54
43	gnf1m03383_a_at	5.53
44	gnf1m32251_at	5.52
45	gnf1m05913_a_at	5.50
46	gnf1m34195_at	5.50
47	gnf1m30329_at	5.50
48	gnf1m17628_s_at	5.48
49	gnf1m02371_a_at	5.42
50	gnf1m34642_at	5.39
51	gnf1m29752_a_at	5.39
52	gnf1m35671_at	5.38
53	gnf1m29143_at	5.36
54	gnf1m31738_at	5.29
55	gnf1m02318_a_at	5.28
56	gnf1m09049_at	5.27
57	gnf1m00344_s_at	5.27
58	gnf1m15214_at	5.27
59	gnf1m01899_x_at	5.26
60	gnf1m32619_at	5.25
61	gnf1m33789_x_at	5.21
62	gnf1m34257_at	5.18
63	gnf1m33886_at	5.12
64	gnf1m01008_a_at	5.08
65	gnf1m31643_at	5.05
66	gnf1m31572_at	5.04
67	gnf1m32037_at	5.00
68	gnf1m33866_at	4.96
69	gnf1m30625_at	4.94
70	gnf1m31344_at	4.93
71	gnf1m34001_at	4.93
72	gnf1m15387_a_at	4.92
73	gnf1m32998_at	4.88
74	gnf1m31891_at	4.87
75	gnf1m33005_at	4.87
76	gnf1m31390_at	4.83
77	gnf1m34576_at	4.83
78	gnf1m34600_at	4.80
79	gnf1m31889_at	4.77
80	gnf1m33206_at	4.69
81	gnf1m07302_a_at	4.65
82	gnf1m34875_at	4.61
83	gnf1m04027_a_at	4.60
84	gnf1m31239_at	4.57
85	gnf1m03738_a_at	4.55
86	gnf1m10388_a_at	4.52
87	gnf1m19017_at	4.51
88	gnf1m03884_a_at	4.50
89	gnf1m06357_a_at	4.50
90	gnf1m33946_at	4.50
91	gnf1m31824_at	4.50
92	gnf1m09736_at	4.49
93	gnf1m33278_at	4.46
94	gnf1m32514_at	4.46
95	gnf1m16235_at	4.40
96	gnf1m34313_at	4.39
97	gnf1m06329_a_at	4.37
98	gnf1m05722_a_at	4.35
99	gnf1m03234_a_at	4.34
100	gnf1m31792_at	4.32
101	gnf1m31775_at	4.31
102	gnf1m35588_at	4.23
103	gnf1m30456_at	4.20
104	gnf1m34794_at	4.20
105	gnf1m30490_at	4.19
106	gnf1m03665_a_at	4.18
107	gnf1m16056_at	4.18
108	gnf1m13294_a_at	4.15
109	gnf1m34064_at	4.14
110	gnf1m06747_a_at	4.12
111	gnf1m01774_x_at	4.10
112	gnf1m33369_at	4.09
113	gnf1m29003_at	4.09
114	gnf1m31545_at	4.07
115	gnf1m33894_x_at	4.06
116	gnf1m33931_at	4.02
117	gnf1m31032_at	4.01
118	gnf1m01590_a_at	4.00

PUBLICATIONS

Main paper:

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