



Title	Detection of tissue-specific genes and computational analysis of testis-specific gene expression regulatory regions
Author(s)	山下, 明史
Citation	大阪大学, 2009, 博士論文
Version Type	VoR
URL	https://hdl.handle.net/11094/2599
rights	
Note	

The University of Osaka Institutional Knowledge Archive : OUKA

<https://ir.library.osaka-u.ac.jp/>

The University of Osaka

**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

Akifumi Yamashita

Department of Genome Informatics,
Genome Information Research Center,
Research Institute for Microbial Diseases,
Osaka University, 3-1 Yamadaoka, Suita,
Osaka 565-0871, Japan

February, 2009

Contents

LIST of ABBREVIATIONS	5
ABSTRACT	6
1 INTRODUCTION	7
2 METHODS	10
2.1 Detection of tissue-specific genes	10
2.2 Annotation of tissue-specific genes	10
2.3 Extracting the 5'-regulatory regions	11
2.4 Selection of over-represented 8-mers	11
2.5 Comparison of the 8-mer frequency within regulatory regions of testis-specific genes with those of non-testis-specific genes.	13
3 RESULTS	14
3.1 Detection of tissue-specific genes	14
3.2 Selection of testis-specific genes which can be used for the following analysis	14
3.3 Classification of the over-represented 8-mers	15
3.4 Conservations of the flanking region of highlighted 8-mers	16

4 DISCUSSION	18
ACKNOWLEDGEMENTS	23
REFERENCES	24
TABLES	27
Table 1 - Number of tissue-specific genes	27
Table 2 - Classification of 117 representative 8-mers on the basis of their testis association level	28
Table 3 - 8-mers which appeared near by the other 8-mers	31
FIGURES	32
Fig. 1 - Number of tissue-specific genes	32
Fig. 2 - Identification of testis-specific genes and their 5'-regulatory regions	33
Fig. 3 - Profiling of 634 testis-specific genes	35
Fig. 4 - Conservations of flanking region of the highlighted 8-mers in testis-specific and non-testis-specific regulatory regions	36

APPENDIX TABLES	40
Appendix Table 1 - List of tissue specific genes	40
Appendix Table 2a - Testis-specificity of the genes, representative 8-mer and annotation	75
Appendix Table 2b - Testis-specificity and annotation of the genes whose regulatory regions were not completely sequenced or overlapped with other regulatory regions	90
Appendix Table 2c - Testis-specificity and annotation of the genes which were not supported to cover the intact 5'-ends	92
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	95
Appendix Table 2e - Testis-specificity of the genes whose clone IDs were not available	96
PUBLICATIONS	97

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- <i>O</i> -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 61 tissues, 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:

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

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

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

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

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, $\bar{x}_i$ 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:

$$Z_i = (O_i - \lambda_i) / \sqrt{\lambda_i} \text{ and}$$

$$\lambda_i = nP_i$$

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)RGYAAAC-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'-AAACCATGACATTCACAGAG-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 ($-2 \leq \text{testis association level} \leq 2$). 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 tgTGAXxTCa (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 ngTGATGTCa, while within non-testis-specific regulatory regions, it conserves only gTGATGTCa (**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 tgTG_{Axx}TC_{Aca} (xx= CA, CC, GG, and CG) only within testis-specific regulatory regions (**Fig. 4B-E**). CRE-like A1 conserves ngTCATGTCA_{Aca} 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 (TG_{Axx}TCA; 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 (tgTG_{Axx}TC_{Aca}; 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 (TTGTTGATG) 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'-AAACCATGACATTCACAGAG-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.

ACKNOWLEDGEMENTS

The author would like to express his sincerest gratitude to Professor Teruo Yasunaga for introducing him to the field of bioinformatics, for useful suggestions and discussions during the course of the study, and continuous encouragements during his graduate course. The author would like to express his sincerest gratitude to Dr. Kazunori Shimada for introducing him to the theme of this study, for useful suggestions, discussions and encouragements during the course of the study. The author thanks to Dr Naohisa Goto and Dr. Seiji Nishiguchi for useful suggestions and discussions during the course of the study. The author thanks to Dr. Tatsuya Takagi and Dr. Kousuke Okada for valuable suggestions and discussions especially about statistics. The author thanks to Dr Etsuro Yamanishi and Dr. Masaya Kawase for his constant support and encouragement. The author thanks to his parents, Dr. Takashi Yamashita and Dr. Hiroko Yamashita for constant support and encouragement. The author also thanks to all members of Department of Genome Informatics for their helpful discussions and encouragements. The author thanks the National Center for Biotechnology Information, USA; Genomics Institute of the Novartis Research Foundation, USA; DNA Data Bank of Japan; Genome Bioinformatics Group of the University of California, Santa Cruz; and the Ensembl, the Wellcome Trust Sanger Institute, UK, for permitting access to their network servers. The author is grateful to the Genome Information Research Center, Research Institute for Microbial Diseases, Osaka University, Japan for use of their computer systems.

REFERENCES

- Altschul, S.F., Madden, T.L., Schaffer, A.A., Zhang, J., Zhang, Z., Miller, W., Lipman, D.J., 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res.* 25, 3389-3402.
- Bono, H., et al., 2003. Systematic expression profiling of the mouse transcriptome using RIKEN cDNA microarrays. *Genome Res.* 13, 1318-1323.
- Carninci, P., et al., 2005. The transcriptional landscape of the mammalian genome. *Science* 309, 1559-1563.
- Dedrick, R.L., Jones, P.P., 1990. Sequence Elements Required for Activity of a Murine Major Histocompatibility Complex Class II Promoter Bind Common and Cell-Type-Specific Nuclear Factors. *Mol. Cell. Biol.* 10, 593-604.
- Dhar, M., Mascareno, M.M., and Siddiqui, M.A.Q., 1997. Two Distinct Factor-binding DNA Elements in Cardiac Myosin Light Chain 2 Gene Are Essential for Repression of Its Expression in Skeletal Muscle. *J. Biol. Chem.* 272, 18490-18497.
- FitzGerald, P.C., Shlyakhtenko, A., Mir, A.A., Vinson, C., 2004. Clustering of DNA sequences in human promoters. *Genome Res.* 14, 1562-1574.
- Flemington, E., Speck, S.H., 1990. Identification of phorbol ester response elements in the promoter of Epstein-Barr virus putative lytic switch gene BZLF1. *J. Virol.* 64, 1217-1226.
- Hong, S., Choi, I., Woo, J.M., Oh, J., Kim, T., Choi, E., Kim, T.W., Jung, Y.K., Kim, do H., Sun, C.H., Yi, G.S., Eddy, E.M., Cho, C., 2005. Identification and integrative analysis of 28 novel genes specifically expressed and developmentally regulated in murine spermatogenic cells. *J. Biol. Chem.* 280, 7685-7693.

- Iwakoshi, N.N., Lee, A.H., Glimcher, L.H., 2003. The X-box binding protein-1 transcription factor is required for plasma cell differentiation and the unfolded protein response. *Immunological Reviews* 194, 29–38.
- Karolchik, D., et al., 2003. The UCSC Genome Browser Database. *Nucleic Acids Res.* 31, 51-54.
- Letovsky, J., Dynan, W.S., 1989. Measurement of the binding of transcription factor Sp1 to a single GC box recognition sequence. *Nucleic Acids Res.* 17, 2639-2653.
- Matsumoto, M., Nishimura, T., 1998. Mersenne Twister: a 623-dimensionally equidistributed uniform pseudorandom number generator. *ACM Trans. Modeling and Computer Simulation* 8, 3-30.
- Mayr, B., Montminy, M., 2001. Transcriptional regulation by the phosphorylation-dependent factor CREB. *Nat. Rev. Mol. Cell Biol.* 2, 599-609.
- Rozenberg, J.M., Shlyakhtenko, A., Glass, K., Rishi, V., Myakishev, M.V., FitzGerald, P.C., and Vinson, C., 2008. All and only CpG containing sequences are enriched in promoters abundantly bound by RNA polymerase II in multiple tissues. *BMC Genomics*, 9, 67.
- Saffer, J.D., Jackson, S.P., Annarella, M.B., 1991. Developmental expression of SP1 in the mouse. *Mol. Cell Biol.* 11, 2189-2199.
- Sassone-Corsi, P., 1998. CREM: a master-switch governing male germ cell differentiation and apoptosis. *Cell. Dev. Biol.*, 9, 475-482.
- Smith, B., Fang, H., Pan, Y., Walker, P.R., Famili, A.F., Sikorska, M., 2007. Evolution of motif variants and positional bias of the cyclic-AMP response element. *BMC Evol. Biol.* 7, S15.

- Su, A.I., Wiltshire, T., Batalov, S., Lapp, H., Ching, K.A., Block, D., Zhang, J., Soden, R., Hayakawa, M., Kreiman, G., Cooke, M.P., Walker, J.R., Hogenesch, J.B., 2004. A gene atlas of the mouse and human protein-encoding transcriptomes. *Proc. Natl. Acad. Sci. USA* 101, 6062-6067.
- Suzuki, Y., Yamashita, R., Sugano, S., Nakai, K., 2004. DBTSS, DataBase of Transcriptional Start Sites: progress report 2004. *Nucleic Acids Res.* 32, D78-81.
- vanWert, J.M., Panek, H.R., Wolfe, S.A., Grimes, S.R., 1998. The TE promoter element of the histone H1t gene is essential for transcription in transgenic mouse primary spermatocytes. *Biol. Reprod.* 59, 704–710.
- vanWert, J.M., Wolfe, S.A., Grimes, S.R., 2008. Binding of RFX2 and NF-Y to the Testis-Specific Histone H1t Promoter May be Required for Transcriptional Activation in Primary Spermatocytes. *J. Cell. Biochem.*, 104, 1087-1101.
- Wolgemuth, D.J., Wartrin, F., 1991. List of cloned mouse genes with unique expression patterns during spermatogenesis. *Mamm. Genome* 1, 283-288.
- Zhang, X., et al., 2005. Genome-wide analysis of cAMP-response element binding protein occupancy, phosphorylation, and target gene activation in human tissues. *Proc. Natl. Acad. Sci. USA* 102, 4459-4464.

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	vomerolnasal 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	CTTCACAG	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	GAAAAAAAA	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](http://www.gen-info.osaka-u.ac.jp/~uhmin/study/others/tissue_specific/SupplementaryTable1.xlsx)

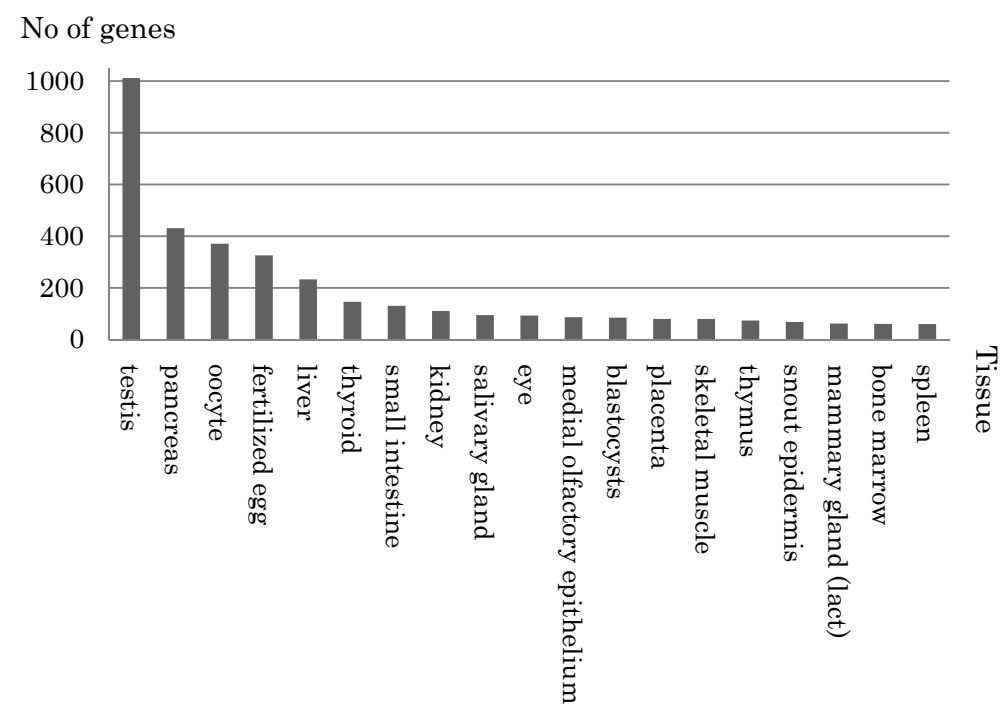
Table 3. 8-mers which appeared nearby other representative 8-mers

CRE-like 1. 5 genes. GTGATGTC (A7) TGATGTCA (A1) GATGTCAC (A4) ATGTCACA (A3) TGTCACAG (A12*)	8. 5 genes. TGAGGTCA (A16*) AGGTCACA (A20) GTCACAGA (A8*) TCACAGAG (A13*)	Sp1 binding site (group C) 16. 4 genes. GGGCGGGG (C3) GGCGGGGC (C2) GGGGCGGG (C4) GGGCGGGG (C3) GGCGGGGC (C2)	25. 8 genes. AGGCTGTG (A52) GGCTGTGG (A43)
2. 4 genes. TGATGTCA (A1) GATGTCAC (A4) ATGTCACA (A3) TCACAATG (A2)	9. 10 genes. TGTGAGGT (A11) TGAGGTCA (A16*)	17. 6 genes. GGGGCGGG (C4) GGGCGGGG (C3) GGCGGGGC (C2) GGGGCGGG (C4) GGGCGGGG (C3)	26. 5 genes. GAGGCCAG (A41) GGCCAGCC (A42)
3. 4 genes. CTTTGTGA (A9*) TTGTGATG (A6) GTGATGTC (A7) TGATGTCA (A1)	Partial ZII 10. 6 genes. TCTCTGTG (A32) CTCTGTGA (A13) TCTGTGAC (A8)	18. 19 genes. TGGGCGGG (B37) GGGCGGGG (C3) GGCGGGGC (C2)	27. 5 genes. TCTGTGAG (A18) TGTGAGGT (A11)
4. 12 genes. TGATGTCA (A1) ATGTCATA (A5)	11. 4 genes. TCTCTGTG (A32) CTCTGTGA (A13) TCTGTGAG (A18)	19. 4 genes. ATGTCACA (A3) TGTCACAG (A12*) GTCACAGA (A8*)	28. 11 genes. TCTCTTCC (B18) CTCTTCCT (B3)
5. 5 genes. CTGTGACA (A12) TGTGACAT (A3*) GTGACATC (A4*) TGACATCA (A1*) ACATCACA (A10)	12. 4 genes. CTCTGTGA (A13) TCTGTGAC (A8) CTGTGACA (A12)	Others 20. 5 genes. CTTTGTGA (A9*) TTGTGAGG (A14) TGTGAGGT (A11)	29. 5 genes. TCTGAGGC (A22) CTGAGGCT (A40)
6. 6 genes. TCTGTGAC (A8) CTGTGACA (A12) TGTGACAT (A3*) GTGACATC (A4*) TGACATCA (A1*)	13. 5 genes. CCTCACAG (A29) TCACAGAG (A13*)	21. 6 genes. GAGCTCTG (A26) GCTCTGGG (B13)	30. 4 genes. TGCCCTCTG (B1) CTCTGCCCT (B24)
7. 4 genes. TGACCTCA (A16) CCTCACAG (A29)	14. 4 genes. TCACAGAG (A13*) CACAGAGA (A32*)	22. 4 genes. CCCTCCTC (B40) CTCCTCTT (A45)	31. 9 genes. GGCAGCTG (B10) GCAGCTGC (B28)
	Partial CSS A 15. 4 genes. CATTGTGA (A2*) TTGTGATG (A6)	23. 6 genes. AGCAGCTG (B11) GCAGCTGC (B28)	32. 6 genes. CAGAGAGA (A37) AGAGAGAC (A47)
		24. 6 genes. CAGCCAAT (B6) GCCAATCA (B19)	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.

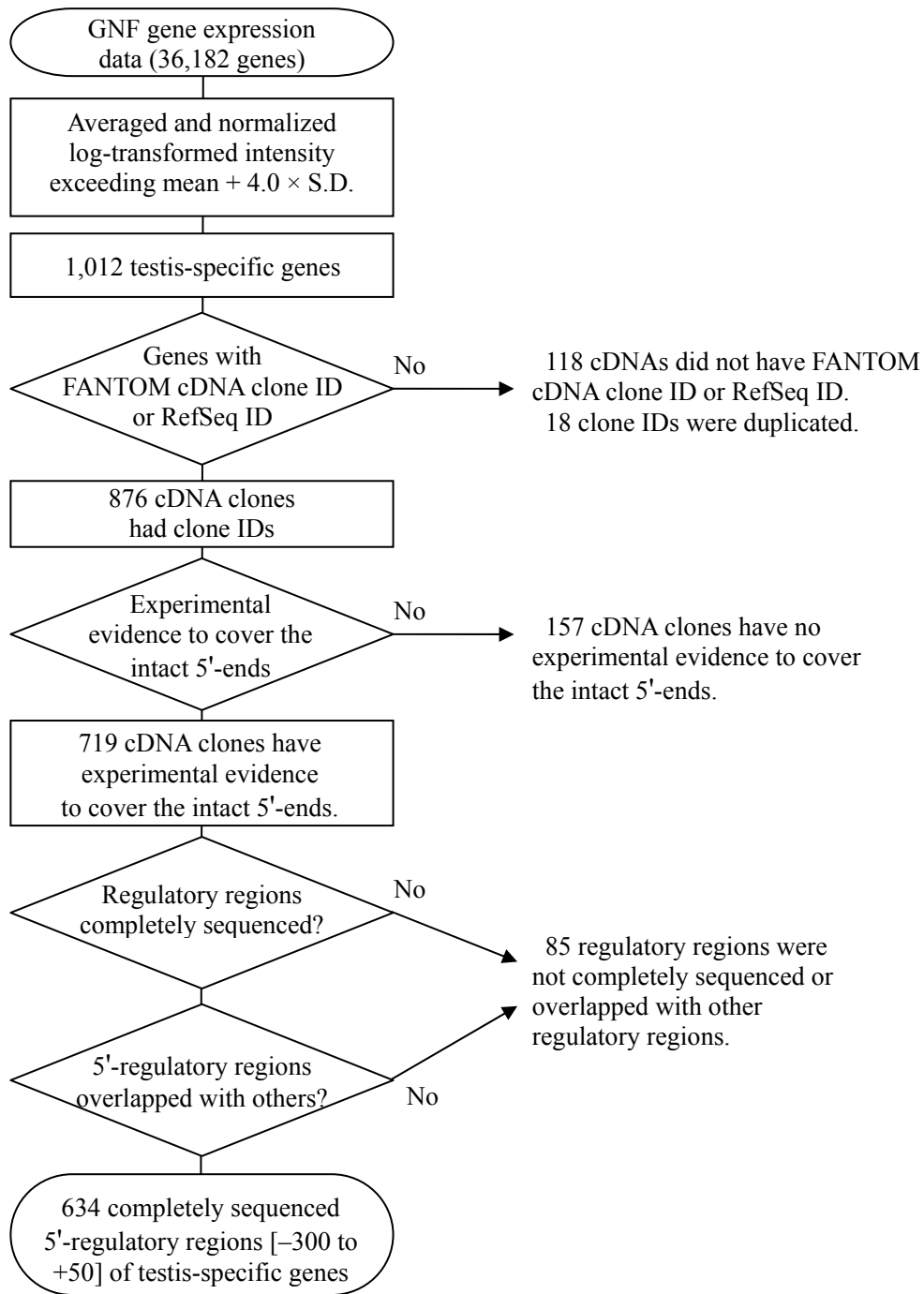
Figures

Fig. 1. Number of tissue-specific genes



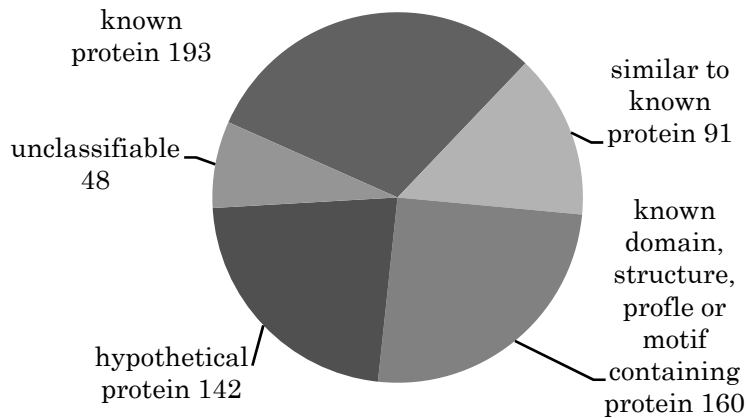
Number of tissue-specific genes for top 20 tissues that most abundantly exhibit their specific genes is shown. Horizontal axis represents the name of tissues, and vertical axis represents the number of tissue-specific gene.

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



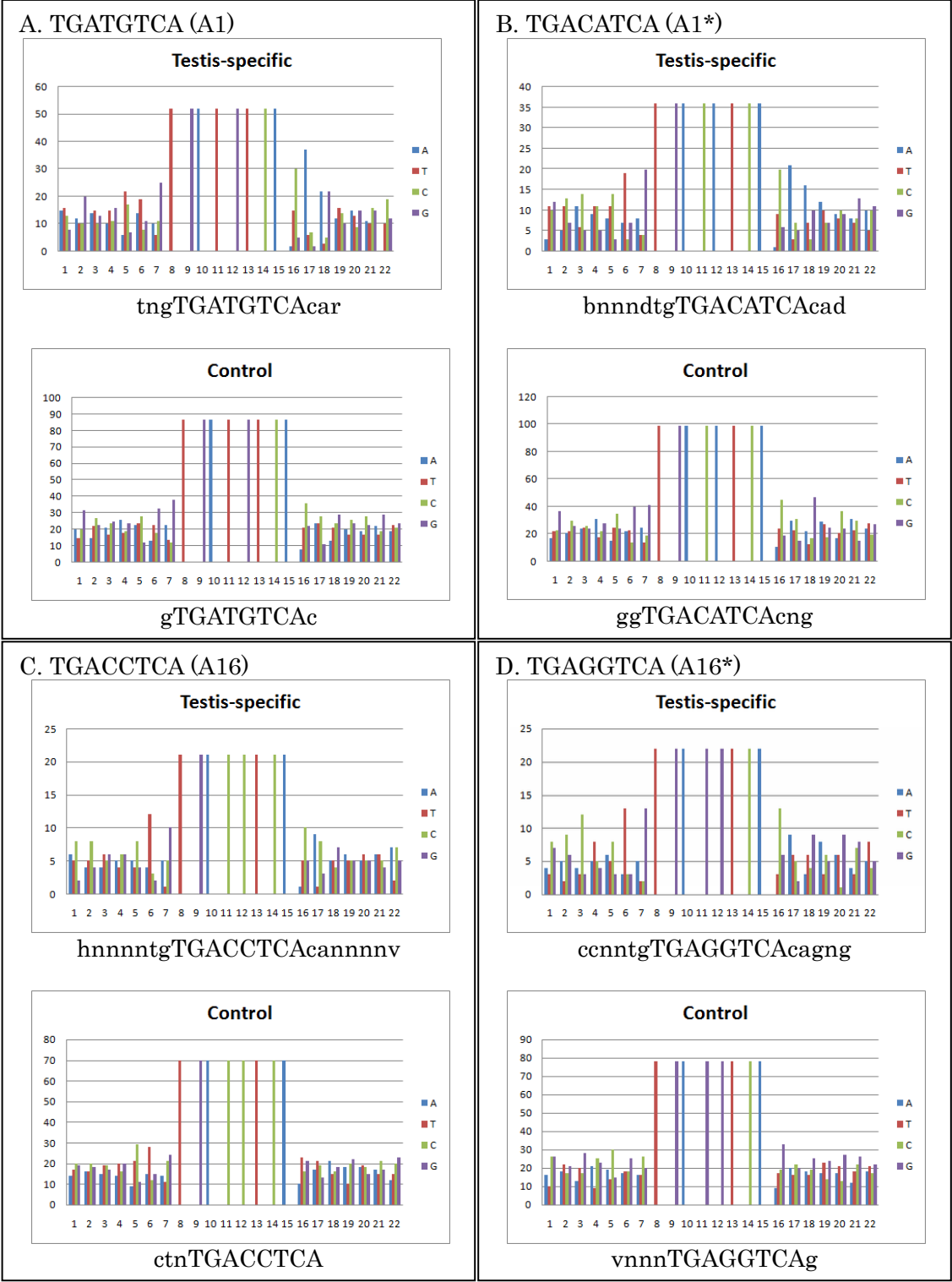
Starting from the GNF gene expression data of 36,182 genes, we obtained 1,012 testis-specific cDNAs. Of these, we excluded 118 cDNAs because they were not linked to either the FANTOM cDNA clone ID or RefSeq ID. Further, 18 clone IDs were found to be duplicated. Thus, of the 1,012 testis-specific cDNAs, 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

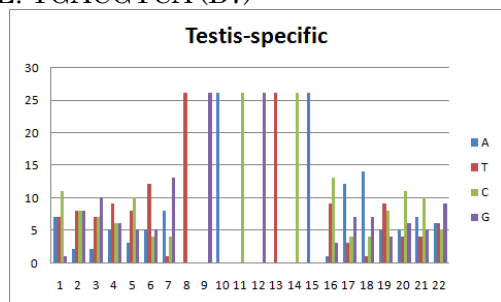


The selected 634 testis-specific genes were annotated and categorized into the following 5 groups on the basis of our knowledge about their functions: known proteins; similar to known proteins; known domain-, structure-, profile-, or motif-containing proteins; hypothetical proteins; and unclassifiable 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.

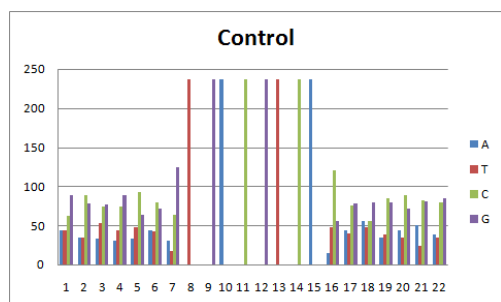
Fig. 4. Conservations of flanking region of the highlighted 8-mers in testis-specific and non-testis-specific regulatory regions
CRE-like



E. TGACGTCA (B7)



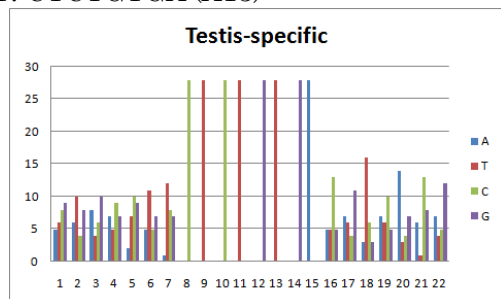
cbbnbtgTGACGTCAaa



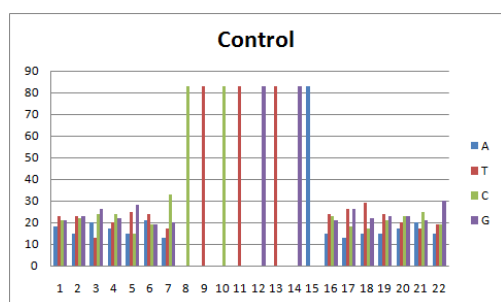
gTGACGTCAcnnnnv

Partial ZII

F. CTCTGTGA (A13)

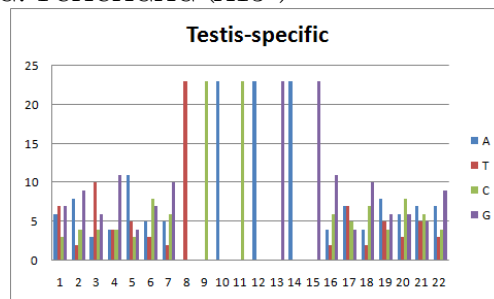


bntCTCTGTGAcntnacg

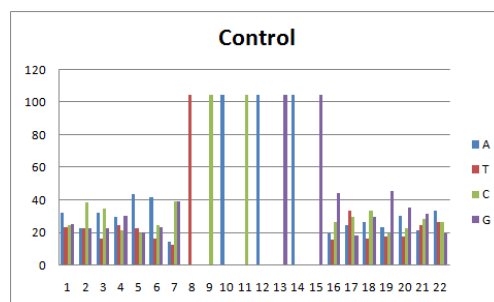


CTCTGTGA

G. TCACAGAG (A13*)

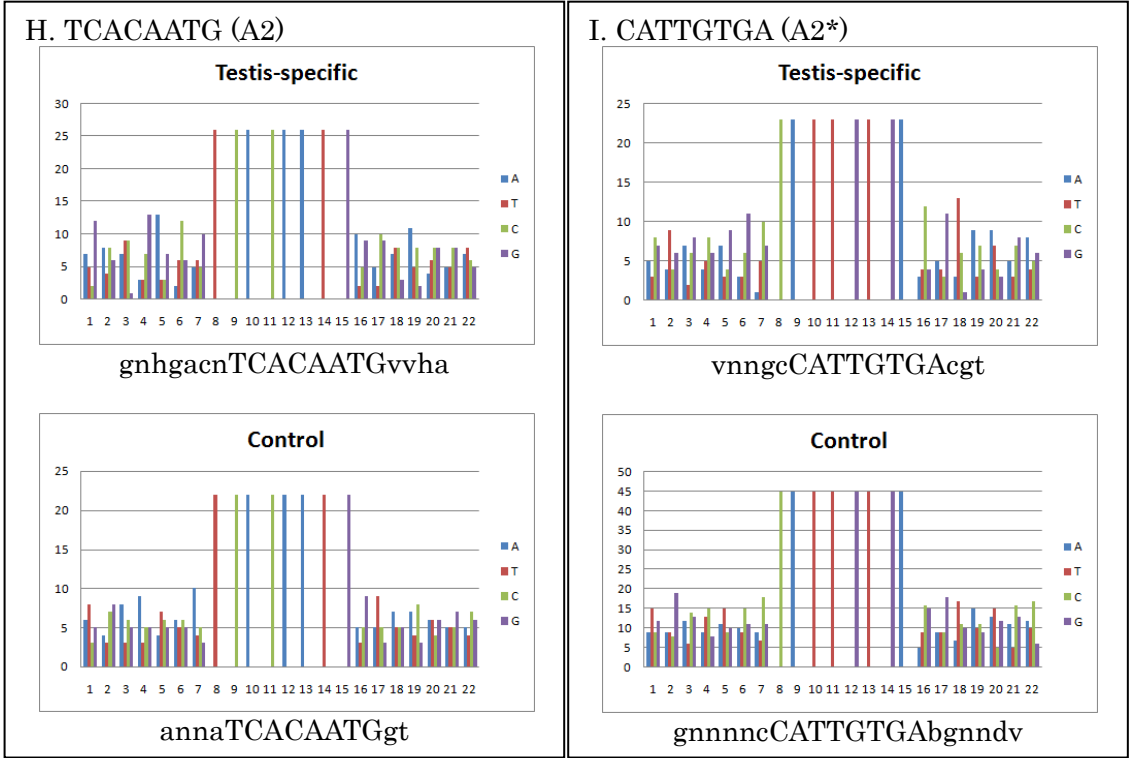


vtgangTCACAGAGgng

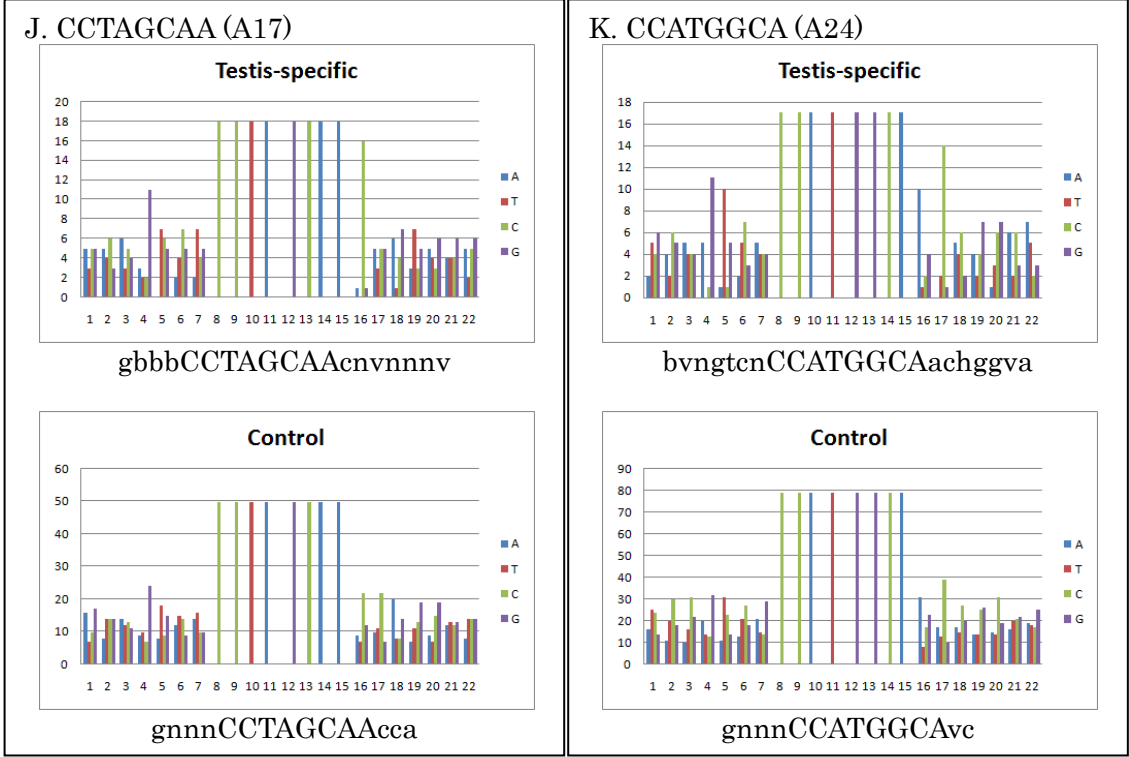


anvTCACAGAGgng

Partial CSS-A



Partial X-box



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.

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

#2 Tissue specificity level.

#4 RefSeq ID.

#6 Annotation.

ACKNOWLEDGMENTS

40/97

41/97

42/97

372	5.4	gnf1m08607_a_at	NM_177738	4933421C08	homolog (Chlamydomonas)	432	5.3	gnf1m00344_s_at	NM_011973	renal tumor antigen
373	5.4	gnf1m04668_a_at	NM_025732	4933434E03	hypothetical protein	433	5.3	gnf1m15214_at	NM_030150	DNA segment, Chr 11, Lothar Hennighausen 2, expressed
					Ankyrin repeat profile/Ankyrin-repeat/Ankyrin repeat region circular profile/Yeast DNA-binding domain containing protein	434	5.3	gnf1m13810_a_at	4932700H03	a disintegrin and metalloprotease domain 5
374	5.4	gnf1m05232_at	XM_895197	1700017G21	weakly similar to GERM CELL-LESS 1 PROTEIN [Mus musculus]	435	5.3	gnf1m30921_s_at	4921509O09	weakly similar to predicted Sycp3 like Y-linked
375	5.4	gnf1m02371_a_at	NM_010445		H6 homeo box 1	436	5.3	gnf1m23031_a_at	4930558C23	unclassifiable
376	5.4	gnf1m04565_a_at	NM_025503	1700121E04	NEURONAL PROTEIN 15.6 [Mus musculus]	437	5.3	gnf1m01899_x_at	NM_009446	tubulin, alpha 3
377	5.4	gnf1m12700_at	NM_029992	C530035A16	similar to trichoplein, keratin filament binding	438	5.3	gnf1m00213_at	NM_178936	transmembrane protein 56
378	5.4	gnf1m28807_a_at		1700016K02	hypothetical protein	439	5.3	gnf1m23872_at	4933434I20	hypothetical Prokaryotic membrane lipoprotein lipid attachment site containing protein
379	5.4	gnf1m29282_a_at	NM_028888	4931428F04	hypothetical protein	440	5.2	gnf1m18610_a_at	XM_923498	unclassifiable
380	5.4	gnf1m04663_a_at	NM_025724	4921510H08	Glutamic acid-rich region containing protein	441	5.2	gnf1m21700_at	NM_001001177	weakly similar to hypothetical Cysteine-rich region profile/Lysine-rich region profile containing protein
381	5.4	gnf1m23777_at		4930555L03	IBR domain containing 3	442	5.2	gnf1m32619_at		RIKEN cDNA 1700023F06 gene
382	5.4	gnf1m08585_a_at	NM_177719	4932411A10	hypothetical microcrhidia 2B	443	5.2	gnf1m18956_a_at	8030402F09	Retroviral matrix proteins structure containing protein
383	5.4	gnf1m13287_a_at	NM_017397	F630042F15	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20 (Ddx20)	444	5.2	gnf1m05322_a_at	NM_028557	methyl-CpG binding domain protein 3-like 1
384	5.4	gnf1m34642_at	XM_916095		RIKEN cDNA 1700001J11 gene ring finger protein 17	445	5.2	gnf1m02161_a_at	NM_009989	hypothetical cytochrome c, testis
385	5.4	gnf1m29752_a_at	NM_001033043		weakly similar to unnamed protein product putative DC44 [Homo sapiens]	446	5.2	gnf1m14679_a_at	XM_919213	hypothetical protein
386	5.4	gnf1m05313_a_at	NM_028494	4931430J05		447	5.2	gnf1m08609_at	NM_172808	anthrax toxin receptor-like (Antxrl) Mus musculus
387	5.4	gnf1m17372_a_at	XM_922004	4921510J17	hypothetical EF-hand containing protein	448	5.2	gnf1m04025_a_at	NM_021308	piwi-like homolog 2 (Drosophila)
388	5.4	gnf1m23355_a_at	NM_008265	2810017G21	homeo box A4	449	5.2	gnf1m11101_a_at	6030488D03	hypothetical protein
389	5.4	gnf1m35671_at	XM_909608		similar to IQ motif containing F4	450	5.2	gnf1m14102_a_at	XM_910370	solute carrier organic anion transporter family, member 6d1
390	5.4	gnf1m05104_a_at	NM_027026	1700006D24	leucine rich repeat containing 46	451	5.2	gnf1m01563_a_at	NM_008811	pyruvate dehydrogenase E1 alpha 2
391	5.4	gnf1m21705_at	NM_175033	4933406N18	selenoprotein W	452	5.2	gnf1m13386_a_at	4932411E05	similar to predicted restin-like 2
392	5.4	gnf1m01900_s_at	NM_009449	4922505K03	tubulin, alpha 3	453	5.2	gnf1m30782_a_at	XM_924920	hypothetical protein
393	5.4	gnf1m29143_at	NM_001039114		acyl-CoA synthetase bubblegum family member 2	454	5.2	gnf1m05324_a_at	NM_028562	Nucleoside diphosphate-linked moiety X motif 16 (Nudix motif 16) like [Rattus norvegicus]
394	5.4	gnf1m04115_a_at	NM_021482	1700016O14	weakly similar to synaptogyrin 4	455	5.2	gnf1m07926_a_at	NM_172864	hypothetical TESTIS DEVELOPMENT PROTEIN NYD-SP29 [Homo sapiens]
395	5.4	gnf1m16886_a_at	XM_917213	1700011E24	hypothetical protein	456	5.2	gnf1m05446_s_at	NM_029373	hypothetical protein
396	5.4	gnf1m16866_a_at	XM_621008	4930527E24	weakly similar to Xlr-like	457	5.2	gnf1m13832_a_at	XM_924281	hypothetical Leucine-rich repeat/bZIP (Basic-leucine zipper) transcription factor family/Leucine-rich repeat, typical subtype containing protein
397	5.4	gnf1m13830_a_at	XM_132958	1700023A16	hypothetical protein	458	5.2	gnf1m04669_a_at	NM_025733	ATP/GTP-binding site motif A (P-loop) containing protein Mus musculus
398	5.4	gnf1m14298_a_at	XM_913910	4930535E05	weakly similar to predicted T-cell activation Rho GTPase-activating protein isoform b	459	5.2	gnf1m05221_s_at	NM_027891	I1C0027N22 leucine-rich repeats and WD repeat domain containing 1 (Lrwd1)
399	5.4	gnf1m12062_a_at	NM_178914	4922505M13	predicted spermatogenesis associated 7	460	5.2	gnf1m22978_a_at	NM_183254	hypothetical protein
400	5.3	gnf1m22798_a_at		4930544D05	cholinergic receptor, nicotinic, epsilon polypeptide	461	5.2	gnf1m05023_a_at	NM_026625	hypothetical protein
401	5.3	gnf1m11136_s_at	NM_026370	I920045M18	MYST histone acetyltransferase 1	462	5.2	gnf1m33789_x_at	XM_920110	similar to spermatogenesis associated glutamate (E)-rich protein 2
402	5.3	gnf1m21707_a_at	NM_199019	4933407P14	intramembrane protease 5 Rattus norvegicus	463	5.2	gnf1m30265_a_at	XM_912989	ribonuclease H2, large subunit cAMP responsive element modulator
403	5.3	gnf1m13520_at		4930452G13	unclassifiable	464	5.2	gnf1m23745_s_at	XM_916850	synaptonemal complex central element protein 1
404	5.3	gnf1m16055_a_at	NM_027660	4933407G07	tektin 3	465	5.2	gnf1m16802_a_at	XM_916850	adenosine deaminase domain containing 1 (testis specific) (Ada1)
405	5.3	gnf1m02761_a_at	NM_011353	1700008J04	small EDRK-rich factor 1	466	5.2	gnf1m01842_a_at	NM_009350	POLY A BINDING PROTEIN, CYTOPLASMIC 1 homolog [Mus musculus]
406	5.3	gnf1m08962_s_at	NM_177759	C130098D09	ATP/GTP binding protein-like 5 (Aglb5), transcript variant 3 melanoma associated antigen (mutated) 1	467	5.2	gnf1m04883_a_at	NM_026226	zinc finger protein 217
407	5.3	gnf1m09361_a_at	NM_023431	8030492M19	hypothetical IQ calmodulin-binding motif containing protein	468	5.2	gnf1m04978_s_at	NM_026470	testis-specific serine kinase 1
408	5.3	gnf1m00690_a_at	NM_028848	4930513F16	similar to partial Cyp15 gene for putative cysteine-rich perinuclear theca protein Mus musculus	469	5.2	gnf1m11470_s_at	NM_009435	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type II)
409	5.3	gnf1m18944_a_at		1700085A12	unclassifiable	470	5.2	gnf1m23825_at	NM_001004025	hypothetical protein
410	5.3	gnf1m17104_at		4933438K21	weakly similar to ZINC FINGER PROTEIN (FRAGMENT) [Homo sapiens]	471	5.2	gnf1m16041_a_at	NM_027616	similar to predicted Myosin heavy chain A (MHC A) Rattus norvegicus
411	5.3	gnf1m16949_a_at		1700020N01	weakly similar to ZINC FINGER PROTEIN (FRAGMENT) [Homo sapiens]	472	5.2	gnf1m07614_at		P-loop containing nucleotide triphosphate hydrolases structure containing protein Mus musculus
412	5.3	gnf1m31215_s_at	XM_917051	4933439H17	hypothetical Peptidase, eukaryotic cysteine peptidase active site containing protein	473	5.2	gnf1m28992_s_at	NM_029714	phosphoglycerate kinase 2
413	5.3	gnf1m17145_a_at		1700058C13	weakly similar to Short palate, lung and nasal epithelium carcinoma-associated protein 3 homolog precursor Rattus norvegicus	474	5.2	gnf1m28680_a_at	XM_917134	DnaJ (Hsp40) homolog, subfamily C, member 5 gamma
414	5.3	gnf1m13380_a_at	XM_910715	4933427K18	PROTEIN PHOSPHATASE INHIBITOR 2 (IPP-2) [Rattus norvegicus]	475	5.2	gnf1m08576_at	NM_177677	Leucine-rich repeat containing protein
415	5.3	gnf1m18853_a_at	NM_029939	5930422B18	unclassifiable	476	5.2	gnf1m11501_at		unclassifiable
416	5.3	gnf1m04972_a_at	NM_026449	4930599B21	hypothetical Glycosyl transferase, family 2/Microbodies C-terminal targeting signal containing protein	477	5.2	gnf1m13833_at	XM_908619	similar to testis derived transcript isoform 1
417	5.3	gnf1m14433_s_at		4930551J12	unclassifiable	478	5.2	gnf1m34257_at		unclassifiable
418	5.3	gnf1m28768_a_at	XM_917740	A530057A03	similar to predicted similar to mitochondrial glycerol 3-phosphate acyltransferase	479	5.2	gnf1m15086_a_at	NM_030089	weakly similar to unnamed protein product TSG118.1 [Mus musculus]
419	5.3	gnf1m18365_a_at	XM_131958	4930584F24	hypothetical protein	480	5.2	gnf1m04283_s_at	NM_023197	unclassifiable
420	5.3	gnf1m31738_at	XM_910141		hypothetical LOC433757	481	5.2	gnf1m23167_a_at		ring finger and FYVE like domain containing protein
421	5.3	gnf1m14127_a_at	XM_915378	4921539E11	hypothetical protein	482	5.2	gnf1m10438_a_at	NM_026097	MAD2 mitotic arrest deficient-like 2 (yeast) (Mad2l2)
422	5.3	gnf1m18795_at		1700099I09	unclassifiable	483	5.2	gnf1m05239_a_at	NM_027985	hypothetical ELAFIN-LIKE PROTEIN I [Mus musculus]
423	5.3	gnf1m10020_a_at	NM_178387	1700067I02	spermatogenesis associated 18 (Spata18)	484	5.2	gnf1m23188_a_at	NM_183271	phosphoribosyl pyrophosphate synthetase 1-like 1 (Prps11)
424	5.3	gnf1m17067_a_at		1700008A04	hypothetical protein	485	5.2	gnf1m07706_at	NM_029294	weakly similar to Lysine-rich region containing protein
425	5.3	gnf1m04901_a_at	NM_026283	1700021J16	similar to sterile alpha motif domain containing 8	486	5.2	gnf1m05113_a_at	NM_027076	RNA-binding region RNP-1 (RNA recognition motif) containing protein
426	5.3	gnf1m02318_a_at	NM_010353		germ cell-specific gene 2	487	5.2	gnf1m14022_a_at	XM_924671	
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					

488	5.2	gnf1m21712_a_at	NM_001007591	4933440E22	similar to Salivary glue protein Sgs-4 precursor						precursor (ACE-T) (Dipeptidyl carboxypeptidase I) (Kininase II)
489	5.1	gnf1m04602_a_at	NM_025585	1700016J15	hypothetical protein	547	5.0	gnf1m03538_a_at	NM_016964	1530012K17	stromal antigen 3 (Stag3)
490	5.1	gnf1m18790_a_at	XM_485737	1700023L04	hypothetical protein	548	5.0	gnf1m17780_a_at		4921530L18	unclassifiable
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]	549	5.0	gnf1m08599_a_at	NM_177570	4933406A14	schlafen like 1
						550	5.0	gnf1m11446_a_at	NM_027588	4921514H13	5'-nucleotidase, cytosolic 1B
						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]
											phosphatidylglycerophosphate synthase 1
492	5.1	gnf1m18868_a_at	XM_912521	4933440C21	DC-STAMP domain containing 1	554	5.0	gnf1m33866_at	XM_911493		
493	5.1	gnf1m08593_at	NM_177801	4933400C05	hypothetical protein	555	5.0	gnf1m07703_at	NM_029252	4930429C23	hypothetical protein
494	5.1	gnf1m13575_a_at	XM_909321	1700055J15	IQ motif containing F1	556	5.0	gnf1m17299_a_at	NM_183113	4932414N04	hypothetical protein
495	5.1	gnf1m04869_a_at	NM_026188	4921527B01	hypothetical protein	557	5.0	gnf1m10318_a_at	NM_013455	1700116D15	preproacrosin
496	5.1	gnf1m14147_at		4932703K07	heat shock protein 1, alpha	558	5.0	gnf1m29406_a_at	NM_028957	4933406A08	hyaluronoglucosaminidase 5
497	5.1	gnf1m33886_at			RIKEN cDNA D030041N04 gene	559	5.0	gnf1m19292_a_at	NM_001002787	4933417A14	calicin
498	5.1	gnf1m16237_at		4930555P18	ring finger protein 139	560	5.0	gnf1m07602_a_at	NM_153777	5730427C23	melanoma associated antigen (mutated) 1
499	5.1	gnf1m17677_at	NM_001039557	4921509H06	ribophorin II						
500	5.1	gnf1m16806_a_at	NM_027025	1700001D09	adenosine A3 receptor (Adora3), transcript variant 2	561	5.0	gnf1m01239_a_at	NM_008232	4932442B12	hepatoma derived growth factor-like 1
					TGIF homeobox 1	562	5.0	gnf1m13975_a_at		4930432J01	unclassifiable
501	5.1	gnf1m07287_a_at	NM_153109	4930524L02	unclassifiable	563	5.0	gnf1m05200_a_at	XM_917400	4933432K11	fibrous sheath-interacting protein 1
502	5.1	gnf1m30771_a_at		4930578E11	unclassifiable	564	5.0	gnf1m16773_a_at	XM_921987	1110017D15	diablo homolog (Drosophila)
503	5.1	gnf1m13328_a_at	XM_916685	4933422B16	hypothetical Tetratricopeptide repeat (TPR) structure containing protein	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)
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]	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
505	5.1	gnf1m18620_a_at		1700048O14	unclassifiable	570	4.9	gnf1m29797_a_at	NM_028434	2900092C05	hypothetical protein
506	5.1	gnf1m13049_s_at	NM_016845	4930414P16	proacrosin binding protein	571	4.9	gnf1m30625_at	NM_198628		gene model 711, (NCBI)
507	5.1	gnf1m23019_a_at	XM_925014	1700096M17	unclassifiable	572	4.9	gnf1m13484_a_at		1700021C14	SSTK-INTERACTING PROTEIN VARIANT (SIMILAR TO RIKEN CDNA 1700021C14 GENE)
508	5.1	gnf1m05230_a_at	NM_027949	1700010P14	PHD finger protein 7						[Homo sapiens]
509	5.1	gnf1m05869_a_at	NM_054066	1700041H07	phospholipase C, zeta 1						PREDICTED: Mus musculus similar to hypothetical protein LOC84070 (LOC545136)
510	5.1	gnf1m16843_s_at	XM_910844	4921511M17	hypothetical protein	573	4.9	gnf1m31344_at			
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	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
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	576	4.9	gnf1m07910_at	NM_176965	4930563A03	EF-hand calcium binding domain 5 (Efcab5)
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	577	4.9	gnf1m34001_at	XM_910563		tudor domain containing 6
						578	4.9	gnf1m13582_a_at	XM_914306	1700013H16	hypothetical protein
518	5.1	gnf1m17085_a_at		4930435E18	unclassifiable	579	4.9	gnf1m01668_a_at	NM_009028	1700025K02	RAS-like, family 2, locus 9
519	5.1	gnf1m00466_a_at	NM_170777	E430037N03	WD repeat domain 62	580	4.9	gnf1m15387_a_at	NM_028672		RIKEN cDNA 4930430E16 gene
520	5.1	gnf1m13998_a_at	XM_908598	1700017D01	hypothetical protein	581	4.9	gnf1m05337_a_at	NM_028634	1110014P06	solute carrier family 22 (organic cation transporter), member 21
521	5.1	gnf1m08583_a_at	NM_177616	4931408E15	hypothetical Glutamine-rich region profile containing protein Mus musculus	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
522	5.1	gnf1m09512_a_at	NM_144528	A630082B21	regulatory factor X, 2 (influences HLA class II expression)	585	4.9	gnf1m08598_a_at	NM_175296	G630083P15	maelstrom homolog (Drosophila)
523	5.1	gnf1m04671_a_at	NM_025737	4931417E11	JNK1-associated membrane protein, transcript variant 2 Pan troglodytes	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
524	5.1	gnf1m06454_a_at	NM_145157	4930563B01	similar to predicted defensin beta 19	588	4.9	gnf1m04832_a_at	NM_026104	1700095F04	transmembrane and coiled-coil domains 5
525	5.1	gnf1m28673_a_at	XM_917268	4930469G21	hypothetical protein	589	4.9	gnf1m11445_a_at	NM_020330	4921506L22	a disintegrin and metallopeptidase domain 21 (Adam21)
526	5.1	gnf1m17273_a_at		1700063H04	hypothetical protein						
527	5.0	gnf1m00611_a_at		4930563A13	XAP-5-LIKE PROTEIN homolog [Mus musculus]	590	4.9	gnf1m05105_a_at	NM_027027	1700011M07	ankyrin repeat and SOCS box-containing protein 9
528	5.0	gnf1m31643_at	XM_909045		similar to solute carrier organic anion transporter family, member 6c1	591	4.9	gnf1m19031_at	XM_147508	4933404M19	weakly similar to predicted proline-rich cyclin A1-interacting protein isoform 1
529	5.0	gnf1m03287_a_at	NM_013783	F630024E10	mel transforming oncogene-like 1	592	4.9	gnf1m05196_a_at	XM_911175	4933411G06	weakly similar to SMT3 suppressor of mif two 3 homolog 1 isoform b precursor
530	5.0	gnf1m30047_a_at	NM_029663	1700026P12	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	593	4.9	gnf1m16749_a_at		1700025C14	unclassifiable
					ENSMUST00000017126 transcript (in rel.37.34e)	594	4.9	gnf1m32998_at			uncharacterized Celera prediction mCG131172
531	5.0	gnf1m31572_at				595	4.9	gnf1m29721_a_at	XM_916831	4930403N07	Centromeric protein E (CENP-E protein) like Rattus norvegicus
532	5.0	gnf1m11449_at	NM_033077	4921521M13	DNA segment, Chr 1, Pasteur Institute 1	596	4.9	gnf1m14178_a_at		4933422A05	unclassifiable
533	5.0	gnf1m04905_at		4930465K10	asteroid homolog 1 (Drosophila)	597	4.9	gnf1m23783_a_at		4930568O20	hypothetical leucine rich repeat containing 9 (Lrrc9)
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]	598	4.9	gnf1m04559_at	NM_025490	1700010M22	hypothetical SCP-2 sterol transfer domain containing protein
536	5.0	gnf1m09678_a_at	NM_026293	4930540L03	similar to sperm acrosome membrane protein	599	4.9	gnf1m21616_a_at	NM_175020	1700020H15	hypothetical Serine proteases, trypsin family containing protein
537	5.0	gnf1m08579_a_at	NM_177567	4930503F14	hypothetical protein	600	4.9	gnf1m18718_s_at	XM_925327	4921517J08	weakly similar to predicted speedy homolog 1 (Drosophila)
538	5.0	gnf1m10425_a_at	NM_027300	1700029H01	spermatogenesis associated 3	601	4.9	gnf1m29853_a_at	NM_029381	1700028O09	testis expressed gene 22
539	5.0	gnf1m00518_a_at	NM_026359	1700008K17	calcium homeostasis endoplasmic reticulum protein like	602	4.9	gnf1m09828_a_at	NM_134126	F830031M20	intraflagellar transport 140 homolog (Chlamydomonas)
540	5.0	gnf1m29254_a_at		1700010G02	weakly similar to predicted 5-oxoprolinase (ATP-hydrolysing)	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
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)	604	4.9	gnf1m33005_at	XM_906387	4933405E16	RIKEN cDNA 6430706D22 gene
543	5.0	gnf1m10164_a_at	NM_029602	4933417P13	ring finger protein 39	605	4.9	gnf1m00618_a_at	NM_026225	4933405E16	component of oligomeric golgi complex 6
544	5.0	gnf1m11605_a_at	NM_025651	5430408G21	WW domain binding protein 11	606	4.9	gnf1m30687_a_at	NM_001037941	1700006L23	DnaJ (Hsp40) homolog, subfamily B, member 6
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]	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 (Aglb5), transcript variant 3
546	5.0	gnf1m32037_at	XM_907217		similar to Angiotensin-converting enzyme, testis-specific isoform						

609	4.9	gnf1m17184_a_at		4921517J08	weakly similar to predicted speedy homolog 1 (Drosophila)	671	4.7	gnf1m00673_a_at	XM_924684	4921511E02	associated 1 protein
610	4.8	gnf1m02204_a_at	NM_010086	4932412H23	a disintegrin and metallopeptidase domain 24 (testase 1)						hypothetical FAD/NAD(P)-binding domain structure containing protein
611	4.8	gnf1m05434_a_at	NM_029303	1700012P12	profilin 3	672	4.7	gnf1m11491_a_at	NM_175488	4930570A05	coiled-coil domain containing 38
612	4.8	gnf1m16015_at		4933429H19	hypothetical TonB-dependent receptor protein containing protein	673	4.7	gnf1m16043_at		4930518J20	unclassifiable
613	4.8	gnf1m03853_a_at	NM_019938	1700065B04	sperm tail associated protein	674	4.7	gnf1m23757_a_at		4930523O13	unclassifiable
614	4.8	gnf1m04341_a_at	NM_023630	1700011N16	general transcription factor II A, 1-like factor	675	4.7	gnf1m04696_a_at	NM_025789	4930588C21	radial spokehead-like 2
						676	4.7	gnf1m23030_a_at		4930517G24	unclassifiable
615	4.8	gnf1m30845_a_at	XM_908035	4930408G06	unclassifiable	677	4.7	gnf1m15504_at		1700085L02	antizyme inhibitor 1
616	4.8	gnf1m16811_a_at	NM_027024	1700006C19	similar to predicted cystatin 13	678	4.7	gnf1m32897_at	NM_001033176	4930569G22	hypothetical
617	4.8	gnf1m00515_a_at	NM_029599	1700021O15	sperm associated antigen 4-like						Sodium:neurotransmitter symporter/Sodium:neurotransmitter symporter family profile containing protein, full insert sequence
618	4.8	gnf1m04153_a_at	NM_021611	1700027I08	myosin light chain 2, precursor lymphocyte-specific (Mylc2pl)	679	4.7	gnf1m33206_at	XM_916318		TATA element modulatory factor 1
619	4.8	gnf1m31390_at	XM_904650		RIKEN cDNA 4930455B06 gene	680	4.7	gnf1m02810_a_at	NM_011449	1700000E13	sperm autoantigenic protein 17
620	4.8	gnf1m34576_at			PREDICTED: Mus musculus similar to hypothetical protein MGC44505 (LOC544830)	681	4.7	gnf1m30953_a_at	XM_907160	4933437F05	NAD(P)-binding Rossmann-fold domains structure containing protein
											hypothetical sarcolemma associated protein isoform 5
621	4.8	gnf1m17688_at		4931436F15	hypothetical protein	682	4.7	gnf1m28689_a_at	XM_908853	4921511K06	hypothetical SEC7-like domain/SEC7 domain profile containing protein
622	4.8	gnf1m04624_a_at	NM_025636	1700027L03	hypothetical AAA ATPase superfamily containing protein similar to hypothetical protein LOC546166	683	4.7	gnf1m30975_at	NM_177698	4933412E13	unclassifiable
623	4.8	gnf1m21663_at	NM_001024730	4930415L07	hypothetical protein	684	4.7	gnf1m07701_a_at	NM_029200	1700049P18	hypothetical protein
624	4.8	gnf1m14866_at		1700003F17	hypothetical protein	685	4.7	gnf1m31156_a_at	XM_922719	C330017P09	kinesin family member 2B
625	4.8	gnf1m05419_a_at	NM_029199	4930542N07	hypothetical protein	686	4.7	gnf1m18101_at		9930109I05	unclassifiable
626	4.8	gnf1m29447_a_at	NM_029309	1700010A17	MORN motif containing protein	687	4.7	gnf1m14489_at		4933412L11	Domain in various gamma-carboxylases and other proteins containing protein
627	4.8	gnf1m34600_at	NM_183174		homeodomain leucine zipper-encoding gene	688	4.7	gnf1m08597_a_at	NM_177742	4933403D14	hypothetical testis specific gene A13
628	4.8	gnf1m03440_a_at	NM_181329	I730062F04	coilin						hypothetical protein
629	4.8	gnf1m13937_a_at	NM_001039244	C920013G19	hypothetical protein	689	4.7	gnf1m05872_at	NM_054073	1700023D02	gametogenetin binding protein 2
630	4.8	gnf1m30004_a_at		7120447D04	thioredoxin reductase 3	690	4.7	gnf1m14537_a_at	XM_923591	4933427G17	ubiquitin specific peptidase 50
631	4.8	gnf1m30753_at	NM_001033246	4922504L10	similar to Salivary glue protein Sgs-4 precursor	691	4.7	gnf1m07302_a_at	NM_153144	4930511O11	hypothetical Alanine-rich region containing protein
632	4.8	gnf1m05185_a_at	NM_027564	4921507P07	hypothetical Bacterial extracellular solute-binding protein, family 1 containing protein	692	4.6	gnf1m09247_a_at	XM_919429	4930527J03	hypothetical protein
						693	4.6	gnf1m14693_a_at		1700061J05	hypothetical protein
633	4.8	gnf1m31291_a_at		2010109A12	fibrous sheath-interacting protein 1	694	4.6	gnf1m17163_a_at	XM_911673	1700120B22	hypothetical protein LOC621121
634	4.8	gnf1m16980_a_at	NM_027745	4933434G05	coiled-coil domain containing 57 (Ccdc57)	695	4.6	gnf1m17712_a_at	XM_905792	1700010I14	hypothetical protein
635	4.8	gnf1m29201_at	XM_914515	I0C0026C19	hypothetical protein	696	4.6	gnf1m04730_a_at	NM_025851	4933408H04	weakly similar to predicted Acr formation associated factor Pan troglodytes
636	4.8	gnf1m00465_a_at	NM_175105	1700023J02	aquaporin 11	697	4.6	gnf1m09400_a_at	NM_027089		hypothetical Peptidase, eukaryotic cysteine peptidase active site containing protein
637	4.8	gnf1m08260_a_at	NM_172755	A630079E18	splicing factor, arginine/serine-rich 14						hypothetical protein
638	4.8	gnf1m13863_a_at	NM_027661	4933413G11	heat shock transcription factor, Y linked 2	698	4.6	gnf1m30390_a_at	XM_917051	4930453N24	zinc finger and BTB domain containing 32
639	4.8	gnf1m31889_at	XM_913655		similar to fibrous sheath interacting protein 2	699	4.6	gnf1m14422_at		4930524C15	hypothetical protein
640	4.8	gnf1m13323_a_at	XM_909141	4930433I05	cylicin, basic protein of sperm head cytoskeleton 1	700	4.6	gnf1m04070_a_at	NM_021397	4930524C15	zinc finger and BTB domain containing 32
641	4.8	gnf1m17727_a_at		4930421J07	hypothetical protein	701	4.6	gnf1m17313_at	NM_028648	4930432K09	hypothetical protein
642	4.8	gnf1m16168_at		1700029F09	Esterase/lipase/thioesterase family active site containing protein	702	4.6	gnf1m11086_a_at	NM_013754	4930003B04	hypothetical insulin-like 6
643	4.8	gnf1m04664_a_at	NM_025726	4921522P10	hypothetical protein	703	4.6	gnf1m29012_a_at	XM_910825	4921528H16	RNI-like structure containing protein
644	4.8	gnf1m02430_a_at	NM_010589	E430014A10	AN1, ubiquitin-like, homolog (Xenopus laevis)	704	4.6	gnf1m23738_s_at	NM_001033043	4930476G21	ring finger protein 17
645	4.8	gnf1m13957_at		4930518C04	unclassifiable	705	4.6	gnf1m32280_a_at	XM_909681	MSC1026A22	glycosyltransferase 8 domain containing 3
646	4.8	gnf1m32587_at	NM_177655	4930408K01	cystatin-like 1					4933435G04	hypothetical protein
647	4.8	gnf1m17050_at	XM_909493	1700007L12	IQ motif containing F5	706	4.6	gnf1m14207_at		1700129C13	centrin 4
648	4.8	gnf1m03386_a_at	NM_015777	1700021G14	immunoglobulin (CD79A) binding protein 1b	707	4.6	gnf1m08625_a_at	NM_145825	6030448H16	hypothetical cytochrome P450, family 17, subfamily a, polypeptide 1
649	4.8	gnf1m29246_s_at	NM_178872	9230104I23	tripartite motif-containing 36	708	4.6	gnf1m00997_a_at	NM_007809		hypothetical protein
650	4.8	gnf1m03716_a_at	NM_019497	4921526M11	G protein-coupled receptor kinase 2, groucho gene related (Drosophila)	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
651	4.8	gnf1m16360_a_at	XM_908211	1700030H21	vitelliform macular dystrophy 2 homolog (human)	711	4.6	gnf1m31200_a_at	NM_183181	1700095H12	Esterase/lipase/thioesterase family active site containing protein
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	712	4.6	gnf1m18179_at		A430076A20	ring finger protein 126
						713	4.6	gnf1m16046_a_at	NM_027037	1700007K09	hypothetical protein
653	4.7	gnf1m05443_a_at	NM_029343	1700030K01	hypothetical spermatogenesis associated 9 (Spat9)	714	4.6	gnf1m18900_a_at	XM_911732	4930572D21	similar to unnamed protein product MDAC1 [Homo sapiens]
654	4.7	gnf1m23751_s_at		1700065F16	IQ calmodulin-binding motif containing protein	715	4.6	gnf1m04840_a_at	NM_026132	4930429J24	weakly similar to thioredoxin domain containing 8
655	4.7	gnf1m33184_at		1700014P15	solute carrier family 9, member 10 (Slc9a10)	716	4.6	gnf1m04027_a_at	NM_021311		piwi-like homolog 1 (Drosophila)
656	4.7	gnf1m15242_at	NM_009832	I920045P05	cyclin K	717	4.6	gnf1m15089_a_at	NM_030106	1700080C03	THYMOSIN BETA-LIKE PROTEIN [Rattus norvegicus]
657	4.7	gnf1m15253_a_at	XM_922616	1700003E16	short-chain dehydrogenase/reductase Homo sapiens	718	4.6	gnf1m17702_a_at	NM_001029929	4932412N08	zinc finger, MYND-type containing 15
658	4.7	gnf1m16929_at		1700024J04	hypothetical TNFR/CD27/30/40/95 cysteine-rich region/von Willebrand factor, type C repeat containing protein	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]
659	4.7	gnf1m03674_s_at	NM_175667	4930570K13	weakly similar to predicted DNA binding protein with his-thr domain	721	4.6	gnf1m14175_a_at		4933413D07	unclassifiable
660	4.7	gnf1m11488_a_at	NM_027226	4930557G02	forty-two-three domain containing 1	722	4.6	gnf1m03831_at	NM_019873	B020003M05	FK506 binding protein-like
661	4.7	gnf1m07481_a_at	NM_181731	4922505I06	calcium-binding tyrosine-(Y)-phosphorylation regulated (fibrousheathin 2)	723	4.6	gnf1m09886_a_at	NM_053253	4022419B10	zinc finger, MYND domain containing 10
662	4.7	gnf1m12672_a_at	NM_023232	4933428M04	diablo homolog (Drosophila)	724	4.6	gnf1m30081_a_at	NM_029245	4930572N15	ankyrin repeat domain 53 (Ankrd53)
663	4.7	gnf1m23708_at		4930408P03	HISTONE H2B (FRAGMENT) homolog [Mus musculus]	725	4.6	gnf1m15511_a_at	NM_027164	G430033H23	leucine rich repeat containing 27
664	4.7	gnf1m11483_a_at	NM_026296	4933406G10	hypothetical protein	726	4.6	gnf1m14180_a_at	XM_924040	4933413N12	hypothetical protein
665	4.7	gnf1m16842_a_at	XM_910844	4921511M17	hypothetical protein	727	4.6	gnf1m16760_a_at		1700007J06	leucine rich repeat containing 34
666	4.7	gnf1m09582_s_at	NM_025744	1700026G17	unclassifiable	728	4.6	gnf1m31239_at	NM_029595		phosphatidylethanolamine binding protein 2
667	4.7	gnf1m05317_a_at	NM_028524	1700013O04	CKLF-like MARVEL transmembrane domain containing 2B	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
668	4.7	gnf1m29612_a_at	XM_911841	1700020H17	molybdenum cofactor synthesis 3	731	4.6	gnf1m07352_a_at	NM_153518	4933417K04	coiled-coil domain containing 65
669	4.7	gnf1m21689_at	NM_001004158	4930580A02	hypothetical protein	732	4.6	gnf1m10539_at	NM_016915	1830139D09	phospholipase A2, group VI
670	4.7	gnf1m31664_at	XM_905323	F630047G17	X-ray radiation resistance	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	gnflm05430_s_at	NM_029292	1700008F21	weakly similar to predicted coiled-coil domain containing 7 Mus musculus	799	4.4	gnflm17378_a_at		4932423M01	[Mus musculus] coiled-coil domain containing 83 (Cdc83) Mus musculus
737	4.6	gnflm17138_a_at	NM_198224	1700060E18	membrane-spanning 4-domains, subfamily A, member 13 (Ms4a13). Mus musculus	800	4.4	gnflm30213_at	NM_001033296	4921501G24	weakly similar to sel-1 suppressor of lin-12-like 2 (C. elegans) (Sel12)
738	4.6	gnflm11494_a_at	NM_173023	4932415G16	CatSper channel subunit beta mRNA	801	4.4	gnflm13352_a_at	XM_922071	4933434I06	enkurin
739	4.6	gnflm05314_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]	802	4.4	gnflm30554_a_at		1700126L10	CLG01 (DJ453C12.5) (P53 RESPONSE ELEMENT) [Homo sapiens]
740	4.6	gnflm23608_at		4733401H18	nuclear protein E3-3	803	4.4	gnflm04480_a_at	NM_025329	1700112I01	DYnein Light chain (Tctex type) family member (dylt-2) Mus musculus
741	4.5	gnflm03738_a_at	NM_019569		fascin homolog 3, actin-bundling protein, testicular (Strongylocentrotus purpuratus)	804	4.4	gnflm29178_a_at	NM_010920	1700127P06	NK2 transcription factor related, locus 6 (Drosophila)
742	4.5	gnflm28856_at	XM_923932	4932419B04	hypothetical protein	805	4.4	gnflm18823_at		4932416M14	hypothetical protein
743	4.5	gnflm00002_f_at	NM_009449	1700025I19	tubulin, alpha 3B (Tuba3b)	806	4.4	gnflm04335_a_at	NM_023597	C230006K09	solute carrier family 25 (mitochondrial carrier, ornithine transporter) member 2
744	4.5	gnflm11444_a_at	NM_020279	4921506E08	chemokine (C-C motif) ligand 28	807	4.4	gnflm32296_at	NM_027724	4922503N05	cancer antigen 1
745	4.5	gnflm10583_a_at	NM_021714	6030486B17	WW domain binding protein 11	808	4.4	gnflm16235_at	XM_920780		leucine rich repeat containing 51
746	4.5	gnflm13353_a_at		5133400G04	homologue TATA-binding protein-like factor-interacting protein isoform 2	809	4.4	gnflm16053_a_at	XM_907364	1700054F22	similar to unnamed protein product NIPSNAP4 PROTEIN (MGC:14553) (DKFZP564D177) (FLJ13953) (HSPC299) [Homo sapiens]
747	4.5	gnflm07927_a_at	NM_170671	4932408B01	Mycbp associated protein						similar to Butyrophylin-like/Zn-finger, B-box/SPla/Ryanodine receptor SPRY/Zn-finger, RING containing protein
748	4.5	gnflm18803_a_at	XM_907218	4921518C22	tetratricopeptide repeat domain 18						weakly similar to dynein, axonemal, light chain 1 (Dnalc1)
749	4.5	gnflm11143_a_at	NM_018811	B020003E02	abhydrolase domain containing 2 (Abhd2)	810	4.4	gnflm32877_at	NM_001033775	4933422H20	metaxin 1
750	4.5	gnflm29125_a_at	XM_909809	4931413A09	similar to coiled-coil domain containing 105 Homo sapiens	811	4.4	gnflm29170_a_at	NM_028821	1700010H15	zinc finger protein 438
751	4.5	gnflm11085_a_at	NM_029659	4922505N17	serine/threonine/tyrosine interacting-like 1	812	4.4	gnflm03178_a_at	NM_013604	1420015I16	hypothetical protein
752	4.5	gnflm29679_a_at	XM_924628	2900041A11	hypothetical protein	813	4.4	gnflm10285_a_at	NM_027485	C530035L23	ENSMUST00000062198 transcript (in ref.37.34e)
753	4.5	gnflm04831_a_at	NM_026100	4930434I17	Tctex1 domain containing 1	814	4.4	gnflm15939_at	XM_888419	1700014B07	hypothetical Arginine-rich region containing protein
754	4.5	gnflm18691_a_at	NM_183108	4930479M11	hypothetical protein	815	4.4	gnflm134313_at			a disintegrin and metallopeptidase domain 25 (testase 2)
755	4.5	gnflm14745_a_at	XM_910021	1700020C07	hypothetical protein						predicted GLI pathogenesis-related 1 like 1 (Gliplr11)
756	4.5	gnflm09990_a_at		1700003M02	hypothetical protein						HORMA domain containing 2
757	4.5	gnflm10388_a_at	NM_146074		transcription factor B1, mitochondrial	816	4.4	gnflm17231_a_at	XM_914008	4930444P10	hypothetical coiled-coil domain containing 117, mRNA (cDNA cloneIMAGE:3597771). [Mus musculus]
758	4.5	gnflm13335_a_at		5330430P22	cytochrome P450, family 17, subfamily a, polypeptide 1	817	4.4	gnflm02953_a_at	XM_356072	4932703D08	hypothetical protein
759	4.5	gnflm13926_a_at	XM_181390	1700051I12	collagen, type XX, alpha 1	818	4.4	gnflm16847_a_at	XM_916000	1700011E04	Rsb-66 protein (Rsb66)
760	4.5	gnflm04043_a_at	NM_021343	G830022G14	spermatogenesis associated 5	819	4.4	gnflm14779_a_at	XM_920709	4930529M09	cation channel of sperm 1
761	4.5	gnflm19017_at			ri=1700054H16 hypothetical 2Fe-2S ferredoxin-like structure containing protein	820	4.4	gnflm18303_a_at		1700013D04	X-ray radiation resistance associated 1
762	4.5	gnflm03884_a_at	NM_019995		DNA segment, Chr 3, ERATO Doi 300, expressed	821	4.4	gnflm05497_a_at	NM_029661	1700027D21	translin-associated factor X (Tsnax) interacting protein 1
763	4.5	gnflm06357_a_at	NM_144547		anti-Mullerian hormone type 2 receptor	822	4.4	gnflm09744_a_at	XM_909329	F630050M23	hypothetical protein
764	4.5	gnflm07633_at	NM_175176	4922501L14	hypothetical protein	823	4.4	gnflm06329_a_at	XM_139301		phospholipase A2, group VI
765	4.5	gnflm15539_a_at	XM_912930	4933401F05	weakly similar to adrenal mitochondrial protease gene model 591, (NCBI)	824	4.4	gnflm28413_a_at	XM_924976	E430036P15	ring finger protein 148
766	4.5	gnflm33946_at	XM_914511	1700104P03	hypothetical protein	825	4.4	gnflm10111_a_at	NM_024445	1700016K08	DNA segment, Chr 6, Miriam Meisler 5, expressed
767	4.5	gnflm16481_a_at		1700026D08	hypothetical protein	826	4.4	gnflm14697_a_at	XM_904855	4930544O15	atonal homolog 8 (Drosophila)
768	4.5	gnflm05440_a_at	NM_029335		gametogenetin	827	4.4	gnflm01785_a_at	NM_009241	1700003G22	IQ motif containing G
769	4.5	gnflm31824_at			N-ACETYLGLUCOSAMINYLTRANSFERASE VI [Gallus gallus]	828	4.4	gnflm10540_a_at	NM_016915	1830139D09	solute carrier family 9, member 10 (Slc9a10)
770	4.5	gnflm07947_a_at	NM_173771	4933406M09	SRY-box containing gene 30	829	4.4	gnflm17327_at	XM_907953	4933432M07	centrosomal protein 63 (Cep63) t-complex-associated testis expressed 1
771	4.5	gnflm09736_at	NM_173384		weakly similar to testis specific gene A2 (MORN motif containing)	830	4.4	gnflm05722_a_at	NM_033079		hypothetical protein
772	4.5	gnflm04458_a_at	NM_025290	1700007N08	weakly similar to predicted SCRL protein variant 1	831	4.4	gnflm00743_a_at	NM_153778	4933425C05	hypothetical protein
773	4.5	gnflm29295_a_at	XM_924788	1700023D19	hypothetical protein	832	4.3	gnflm09652_a_at	NM_178378	1730086C16	lysozyme-like 4
774	4.5	gnflm09549_a_at	NM_029354	2610001E06	hypothetical protein	833	4.3	gnflm33186_at	NM_198106	1700014P15	homologue proteasome (prosome, macropain) subunit, alpha type, 8 isoform 2
775	4.5	gnflm05485_a_at	NM_029610	2310004B22	LYR motif containing 1 (Lyrn1)	834	4.3	gnflm21648_a_at	XM_920302	4921501M07	predicted coiled-coil domain containing 81 (Ccdc81) Mus musculus
776	4.5	gnflm21656_a_at	NM_198624	4922504M18	hypothetical Ubiquitin domain containing protein	835	4.3	gnflm03234_a_at	XM_013688		hypothetical protein
777	4.5	gnflm05484_at	XM_891342	1700023A18	phosphatidylethanolamine binding protein 2	836	4.3	gnflm17083_a_at	XM_912033	4930415O20	neurexin I
778	4.5	gnflm22950_a_at	NM_001033465	1700120A01	Sperm flagellar protein 1 (LOC681930). Rattus norvegicus	837	4.3	gnflm15124_a_at		1700062G21	hypothetical CLIP-190 CG5020-PB, isoform B like Macaca mulatta
779	4.5	gnflm33278_at			SEC63 domain containing 1	838	4.3	gnflm07476_a_at	NM_026915	1810009N24	hypothetical protein
780	4.5	gnflm32514_at	XM_906877		similar to leucine rich repeat containing 45	839	4.3	gnflm17370_a_at	XM_920050	2410072D24	weakly similar to Eukaryotic protein kinase containing protein
781	4.5	gnflm11459_s_at	NM_025657	4930405K06	similar to predicted leucine rich repeat containing 57	840	4.3	gnflm23685_a_at	XM_922120	4921521O07	Cytochrome c heme-binding site containing protein
782	4.5	gnflm11448_a_at	NM_023249	4921520K19	yippee-like 1 (Drosophila)	841	4.3	gnflm16233_a_at	NM_028484	4732409C05	inferred: ref XP_058620.1 (XM_058620) similar to
783	4.4	gnflm08591_at	NM_172521	4932438M10	similar to nuclear protein in testis (predicted)	842	4.3	gnflm16596_at		4932413L18	SPLICING FACTOR, PROLINE- AND GLUTAMINE-RICH (POLYPYRIMIDINE TRACT-BINDING PROTEIN- ASSOCIATED SPLICING FACTOR) (PTB-ASSOCIATED SPLICING FACTOR) (PSF)
784	4.4	gnflm32673_at	NM_001034858	C230012F14	armadillo repeat containing 2	843	4.3	gnflm18898_a_at	NM_030025		(DNA-BINDING P52/P100 COMPLEX, 100 KDA SUBUNIT) (H. sapiens) [Homo sapiens] mCG52111
785	4.4	gnflm07613_a_at	NM_029150	4922501F22	spermatogenesis associated 16	844	4.3	gnflm17179_a_at	NM_183097	1700067K01	transmembrane protein 162 (Tmem162)
786	4.4	gnflm19221_a_at	NM_183307	4921511C16	coiled-coil domain containing 63 (Ccdc63)	845	4.3	gnflm19220_a_at	NM_198655	4921509C19	unclassifiable
787	4.4	gnflm10532_a_at	NM_015789	1700011P15	dickkopf-like 1	846	4.3	gnflm17222_s_at	XM_915652		prion protein dublet
788	4.4	gnflm03205_a_at	NM_013638	4930502I03	RAN guanine nucleotide release factor (Rangrf)	851	4.3	gnflm31792_at			tek2n 2 (Tek2)
789	4.4	gnflm24904_a_at	NM_177594	I830061M19	myotubularin related protein 9						
790	4.4	gnflm23761_x_at	NM_001001450	4930533E22	hypothetical synovial sarcoma, X member B, breakpoint 2						
791	4.4	gnflm08863_a_at	NM_173449	4921523A10	Protein phosphatase 2C domain containing protein						
792	4.4	gnflm23679_a_at		4921506L10	hypothetical protein						
793	4.4	gnflm03380_a_at	NM_015768	4930455F09	prokineticin 2						
794	4.4	gnflm16751_at		2610318N02	hypothetical Proline-rich region profile containing protein						
795	4.4	gnflm16263_a_at	XM_920333	1700029F22	EF-hand domain (C-terminal) containing 1						
796	4.4	gnflm32046_at	NM_028377	4933402K21	Lysine-rich region containing protein	848	4.3	gnflm10381_a_at	NM_175240	C820010C07	unclassifiable
797	4.4	gnflm13936_a_at	XM_129743	4933424G06	unclassifiable	849	4.3	gnflm15247_a_at		1700014J02	unclassifiable
798	4.4	gnflm23858_at		4933408D05	hypothetical SUMO-1-specific protease mRNA, complete cds.	850	4.3	gnflm07312_a_at	NM_153162	A630069B14	prion protein dublet
						851	4.3	gnflm03015_a_at	NM_011902	1700021H01	tek2n 2 (Tek2)

852	4.3	gnf1m05029_a_at	NM_026634	A930018P22	coiled-coil domain containing 11	914	4.2	gnf1m18789_a_at		1700016D18	similar to predicted testis-specific factor 1 (LOC631870), mRNA
853	4.3	gnf1m31775_at	NM_183096		RIKEN cDNA 1700031F13 gene						Length = 438 ref XM_905802.1
854	4.3	gnf1m29259_a_at	NM_026739	F630110C03	MAD2 mitotic arrest deficient-like 2 (yeast)						Mus musculus
855	4.3	gnf1m18930_a_at	XM_917165	4930548L10	Glutamine-rich region containing protein	915	4.2	gnf1m34794_at	XM_904628		similar to heterogeneous nuclear ribonucleoprotein D-like
856	4.3	gnf1m17242_a_at	XM_910887	4921505G21	hypothetical serine/threonine kinase 33	916	4.2	gnf1m09287_a_at	NM_029696	1700124B08	malate dehydrogenase 1B, NAD (soluble) (Mdh1b)
857	4.3	gnf1m13554_a_at	XM_919028	1700034F02	hypothetical ARM repeat structure containing protein	917	4.2	gnf1m11267_s_at	XM_916449	1700012D21	CBF1 INTERACTING COREPRESSOR CIR [Homo sapiens]
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]	918	4.2	gnf1m14198_at		4933417D19	unclassifiable
					weakly similar to CD47 antigen transmembrane protein 146 (Tmem146)	919	4.2	gnf1m30490_at	NM_194269		MORN repeat containing 2
859	4.3	gnf1m30342_a_at	XM_622687	1700026J12		920	4.2	gnf1m08601_a_at	NM_172914	4933409I22	coiled-coil domain containing 113, mRNA (cDNA cloneMGC:74046 IMAGE:6705542), complete cds. [Mus musculus]
860	4.3	gnf1m08594_a_at	NM_175350	4933402B14							
861	4.3	gnf1m18683_a_at	XM_358794	4933416B22	hypothetical protein	921	4.2	gnf1m29567_a_at		1700008J08	ankyrin repeat domain 48
862	4.3	gnf1m20339_at		A630001I11	poly A binding protein, cytoplasmic 2	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
863	4.3	gnf1m23862_a_at	XM_909128	4933415J19	ornithine transporter 2	924	4.2	gnf1m16056_at			T-complex-associated testis expressed 2 /cds=UNKNOWN /gb=U46151 /gi=4097088 /len=1890 gnl UG Mm#S686001
864	4.3	gnf1m18488_a_at		3110023G01	homologue katanin p60 subunit A-like 2 (Katnal2)						HLA-B-associated transcript 3
865	4.3	gnf1m14608_a_at		4930511J24	unclassifiable	925	4.2	gnf1m04036_s_at	NM_021329	5430416M17	unclassifiable
866	4.3	gnf1m23007_a_at	XM_910005	1700086D22	unclassifiable	926	4.2	gnf1m29619_a_at		4930567K20	unclassifiable
867	4.3	gnf1m14122_at		4921513D11	hypothetical protein	927	4.2	gnf1m13788_a_at		1700003P14	unclassifiable
868	4.3	gnf1m25228_s_at		E430035G08	elongation factor 1 homolog (ELF1, S. cerevisiae)	928	4.2	gnf1m18102_a_at	XM_918858	1700021A20	unclassifiable
869	4.3	gnf1m14003_a_at	NM_001033148	1700029J07	hypothetical protein	929	4.2	gnf1m28873_a_at	XM_909379	4930404K22	spermidine/spermine N1-acetyl transferase-like 1
870	4.3	gnf1m00675_s_at	NM_175240	1700042I18	transmembrane protein 162 (Tmem162)	930	4.2	gnf1m16754_a_at	NM_029326	1700018L24	Proline-rich region containing protein
871	4.3	gnf1m07915_a_at	NM_175672	4933417L03	hypothetical protein	931	4.2	gnf1m30720_a_at	NM_198107	E130314H02	mediator complex subunit 16 (Med16)
872	4.3	gnf1m17027_a_at		4933424N20	unclassifiable	932	4.2	gnf1m25893_s_at	NM_029714	4932441M08	P-loop containing nucleotide triphosphate hydrolases structure containing protein Mus musculus
873	4.3	gnf1m28909_a_at	NM_001033299	4933431C08	zinc finger protein 217						alkB, alkylation repair homolog 3 (E. coli)
874	4.3	gnf1m10081_a_at	NM_175091	C230076L23	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	933	4.2	gnf1m15314_a_at	XM_924273	1700108H04	zinc finger protein 110
875	4.3	gnf1m04890_a_at	NM_026248	4930430A15	hypothetical Ankyrin repeat profile/Ankyrin repeat region circular profile/Yeast DNA-binding domain containing protein	934	4.1	gnf1m13294_a_at	NM_022981		hypothetical protein
						935	4.1	gnf1m05025_a_at	NM_026628	1700120K04	unclassifiable
876	4.3	gnf1m23726_s_at		4930445I03	hypothetical protein	936	4.1	gnf1m23056_a_at		1700095K22	similar to Vacuolar ATP synthase subunit S1 precursor (V-ATPase S1 subunit) (V-ATPase S1 accessory protein) (V-ATPase A c45 subunit) (C7-1 protein)
877	4.3	gnf1m08600_a_at	NM_177651	4933409G03	hypothetical protein	937	4.1	gnf1m34064_at	XM_911870		weakly similar to predicted olfactory receptor 30 like Macaca mulatta
878	4.3	gnf1m09708_a_at	NM_031177	6030405E03	WD repeat domain 10	939	4.1	gnf1m09413_s_at	XM_909844	10C0045B19	polycomb group ring finger 4
879	4.3	gnf1m05483_s_at	XM_894461	1700010D01	hypothetical protein	940	4.1	gnf1m28952_s_at		4922504O05	similar to a disintegrin and metallopeptidase domain 4
880	4.3	gnf1m18301_a_at		1700121N02	unclassifiable	941	4.1	gnf1m09379_a_at	NM_133689	4930579J09	IIIG9 LONG FORM homolog [Mus musculus]
881	4.3	gnf1m29905_a_at	XM_916034	4930584P19	DMRT-like family B with proline-rich C-terminal, 1	942	4.1	gnf1m05431_a_at	NM_029295	1700001C14	chemokine-like factor
882	4.3	gnf1m14431_a_at	NM_028568	1700094E07	Dual specificity protein phosphatase containing protein	943	4.1	gnf1m04453_a_at	NM_025281	1700026C17	Lyl1 antibody reactive clone
883	4.3	gnf1m07938_at	NM_173433	4932416A15	jumonji domain containing 2D	944	4.1	gnf1m13302_a_at	XM_923323	1700025M16	unclassifiable
884	4.3	gnf1m15165_a_at		1700123M18	sialophorin, pseudogene	945	4.1	gnf1m13366_a_at	XM_901672	4933406L18	serine (or cysteine) peptidase inhibitor, clade A, member 3A
885	4.3	gnf1m07942_a_at	NM_176980	4932422E22	hypothetical Ankyrin repeat structure containing protein	946	4.1	gnf1m00055_a_at	NM_029916	C330007K24	serine threonine kinase 31
886	4.3	gnf1m03347_a_at	NM_013908	4930533L09	F-box and WD-40 domain protein 5	947	4.1	gnf1m17834_at		4632417E12	unclassifiable
887	4.3	gnf1m19228_at		4930526M03	weakly similar to predicted Ribosome-binding protein 1 (Ribosome receptor protein) (mRRp)	948	4.1	gnf1m14138_a_at	XM_907780	4931431F19	hypothetical Ubiquitin domain containing protein
888	4.3	gnf1m33609_at		4922505K22	hypothetical protein	949	4.1	gnf1m17325_s_at	XM_900745	4930412B11	hypothetical protein
889	4.3	gnf1m08204_a_at		A330015D16	weakly similar to predicted Myosin heavy chain, fast skeletal muscle, embryonic	950	4.1	gnf1m05428_a_at	NM_029285	1700001C02	hypothetical protein
890	4.3	gnf1m17176_a_at	XM_915437	1700013B14	interleukin 31	951	4.1	gnf1m21504_a_at		E130009I12	hypothetical protein
891	4.2	gnf1m29417_a_at	NM_198033	A130090N03	amyotrophic lateral sclerosis 4 homolog (human)	952	4.1	gnf1m18670_a_at		4921513J18	hypothetical Na ⁺ /H ⁺ exchanger containing protein
892	4.2	gnf1m19278_at	NM_001024727	4932416H13	hypothetical protein	953	4.1	gnf1m05040_a_at	NM_026652	4930547C10	weakly similar to predicted topoisomerase I binding, arginine/serine-rich-like [Macaca mulatta]
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	954	4.1	gnf1m06747_a_at	NM_146248		coiled-coil alpha-helical rod protein 1
894	4.2	gnf1m27322_at	XM_900667	D030054G02	hypothetical protein	955	4.1	gnf1m04782_a_at	NM_025977	4930548O08	ATP/GTP-binding site motif A (P-loop) containing protein
895	4.2	gnf1m19389_at		6030430N23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	956	4.1	gnf1m06039_a_at	NM_133706	F830021L03	hypothetical transmembrane protein 97
896	4.2	gnf1m16361_a_at	XM_905314	4933404O19	tetratricopeptide repeat domain 25	957	4.1	gnf1m29010_at	XM_916311	4933400N17	similar to predicted DNA-binding protein RFX2
897	4.2	gnf1m09922_a_at	NM_026837	1700012A05	transmembrane protein 53 (Tmem53)	958	4.1	gnf1m14159_at		4933403G17	weakly similar to hormone-sensitive lipase testicular isoform mRNA Rattus norvegicus
898	4.2	gnf1m30030_a_at	NM_199226	4933434J16	testicular haploid expressed gene	959	4.1	gnf1m01774_x_at	NM_009220		spermiogenesis specific transcript on the Y 1
899	4.2	gnf1m03045_a_at	NM_011956	F630003D02	nucleotide binding protein 2 gene model 381, (NCBI)	960	4.1	gnf1m33369_at	XM_129357		RIKEN cDNA 4930463G05 gene
900	4.2	gnf1m33588_at	XM_904133	1700104B16	hypothetical protein	961	4.1	gnf1m17158_a_at	XM_904138	1700011N24	Retroviral-type aspartic protease containing protein
901	4.2	gnf1m30176_a_at		1700023F06	alanine and arginine rich domain containing protein	962	4.1	gnf1m01825_a_at	NM_009319	G430108J08	TAR (HIV) RNA binding protein 2
902	4.2	gnf1m04244_a_at	NM_023043	A730048L21		963	4.1	gnf1m10515_a_at	NM_026789	1110020C03	kelch-like 10 (Drosophila)
903	4.2	gnf1m16560_a_at	NM_028129	2610020H08	exonuclease NEF-sp	964	4.1	gnf1m07618_a_at	NM_175161	4931422A03	unclassifiable
904	4.2	gnf1m15246_a_at	XM_925564	1700020A23	hypothetical Serine phosphorylation site in HPr protein containing protein	965	4.1	gnf1m14462_a_at		4930423M02	unclassifiable
905	4.2	gnf1m15384_a_at	NM_027032	1700008H23	Park2 co-regulated	966	4.1	gnf1m13646_at	NM_010029	4932703A03	hypothetical DEAD (Asp-Glu-Ala-Asp) box polypeptide 4
906	4.2	gnf1m15103_at		1700104B16	hypothetical protein	967	4.1	gnf1m17225_a_at	XM_917103	4921528O07	hypothetical ARM repeat structure containing protein
907	4.2	gnf1m00084_a_at	NM_198223	E430007B19	similar to alveolar soft part sarcoma chromosom region, candidate 1 (human)	968	4.1	gnf1m29825_a_at	XM_924219	5033427P15	cystatin 8 (cystatin-related epididymal spermatogenic) similar to Hypothetical protein MGC26988
908	4.2	gnf1m29722_a_at	XM_924594	1700086L19	SERTA domain containing 4	969	4.1	gnf1m29003_at	NM_001013783		unclassifiable
909	4.2	gnf1m04060_a_at	NM_021372	4930439L04	SERTA domain containing 2	970	4.1	gnf1m14629_at		4930445B03	hypothetical protein
910	4.2	gnf1m04974_a_at	NM_026459	1700112P19	coiled-coil domain containing 70	971	4.1	gnf1m04684_at	NM_025763	4933436I01	
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						

972	4.1	gnf1m04919_a_at	NM_026319	1700029H06	intraflagellar transport 74 homolog (Chlamydomonas) (Ift74)	18	5.6	gnf1m07563_at	NM_026743	G430064L22	mCG124898
973	4.1	gnf1m29032_a_at	NM_009713	4931413D17	arylsulfatase A	19	5.6	gnf1m23471_at		4430402N11	tetraspanin 11
974	4.1	gnf1m17230_at		4930444P10	hypothetical Arginine-rich region containing protein	20	5.6	gnf1m04836_a_at	NM_026109	1810045G11	synuclein, alpha
975	4.1	gnf1m31545_at	XM_909116		gene model 1564, (NCBI)	21	5.6	gnf1m16820_a_at	NM_026460	1810015G24	RIKEN cDNA 1810008K16 gene
976	4.1	gnf1m31677_at	NM_001033434	4931417M15	hypothetical Leucine-rich repeat/Leucine-rich repeat, typical subtype containing protein	22	5.6	gnf1m01501_a_at	NM_008703		serine (or cysteine) peptidase inhibitor, clade I, member 2
					hypothetical protein	23	5.5	gnf1m30890_at		F830010D04	neuromedin B receptor
977	4.1	gnf1m23725_at		4930445I03	coiled-coil domain containing 65	24	5.5	gnf1m22733_at			epidermodysplasia verruciformis 2
978	4.1	gnf1m18605_a_at	XM_924252	E130217B17	inferred: gb AAA40527.1 (L04850) putative [Mus musculus]	25	5.5	gnf1m11000_s_at	NM_019428	F830021D11	RIKEN cDNA F830021D11 gene
979	4.1	gnf1m33894_x_at			mCG116665					I920099C09	ribonuclease P/MRP 30 subunit (human)
					leucine rich repeat containing 44	26	5.4	gnf1m27918_a_at		D930008N19	calcium channel, voltage dependent, alpha2/delta subunit 3
980	4.1	gnf1m10239_a_at	NM_028938	4933403H06	homologue calcium and integrin binding family member 4	27	5.4	gnf1m23847_at		4932702M20	ATP/GTP binding protein-like 2
981	4.1	gnf1m14404_a_at	XM_908365	1700041E20	hypothetical protein	28	5.4	gnf1m02896_x_at	NM_011645	2010010O17	protease, serine, 3
					hypothetical protein	29	5.4	gnf1m34364_at			inferred: ref NP_032110.1 (NM_008084) glyceraldehyde-3-phosphate dehydrogenase [Mus musculus] mCG50539
982	4.1	gnf1m04907_a_at	NM_026291	4930560N03	hypothetical protein						inferred: ref NP_297344.1 (NC_002488) hypothetical protein [Xylella fastidiosa 9a5c] mCG1030383
983	4.1	gnf1m16968_at		4933436F18	unclassifiable						insulin-like growth factor I receptor similar to Carboxypeptidase A2 precursor
984	4.1	gnf1m23164_a_at		1700010E23	spermatogenesis associated 6 (Spata6) (GO:0005524 InterPro IPR001687) [Mus musculus]	30	5.4	gnf1m36029_x_at			inferred: ref NP_032278.1 (NM_008252) high mobility group protein 2 [Mus musculus] mCG50741
					weakly similar to predicted Ral guanine nucleotide dissociation stimulator (RalGEF) (RalGDS) [Mus musculus]	31	5.3	gnf1m24907_at		9430077P08	RIKEN cDNA 6530411M01 gene
					similar to predicted solute carrier family 22 (organic cation transporter), member 21	32	5.3	gnf1m28804_at	NM_001024698	1810046J24	regenerating islet-derived 3 delta islet amyloid polypeptide
987	4.0	gnf1m12264_a_at	NM_019723	4933428J05	hypothetical protein	33	5.3	gnf1m35016_at			inferred: ref XP_033313.1 (XM_033313) hypothetical protein FLJ10665 [Homo sapiens] mCG129432
					hypothetical protein	34	5.3	gnf1m25036_at		9630017N24	RIKEN cDNA 6530411M01 gene
988	4.0	gnf1m05321_a_at	NM_028554	1700072E05	hypothetical protein	35	5.3	gnf1m03336_a_at	NM_013893		regenerating islet-derived 3 delta
989	4.0	gnf1m23702_a_at	NM_181815	4930404C07	Glutamic acid-rich region containing proteinMus musculus	36	5.3	gnf1m02393_a_at	NM_010491		islet amyloid polypeptide
					hypothetical a disintegrin and metallopeptidase domain 1b	37	5.3	gnf1m33126_at			inferred: ref XP_033313.1 (XM_033313) hypothetical protein FLJ10665 [Homo sapiens] mCG129432
					similar to predicted PKD2 interactor, golgi and endoplasmic reticulum associated 1Rattus norvegicus	38	5.3	gnf1m29526_a_at	XM_923427	0610025J13	RIKEN cDNA 0610025J13 gene
					hypothetical S-adenosyl-L-methionine-dependent methyltransferases structure containing protein	39	5.3	gnf1m29399_at			inferred: ref XP_130814.1 (XM_130814) expressed sequence AI504870 [Mus musculus] mCG21890
993	4.0	gnf1m18366_at		1700001G11	hypothetical protein	40	5.3	gnf1m04279_a_at	NM_023182	2300003F21	chymotrypsin-like
994	4.0	gnf1m30927_a_at	NM_207275	4930517K23	hypothetical Barrier to autointegration factor (BAF) containing protein	41	5.2	gnf1m08774_a_at	NM_173022	F630002O11	cDNA sequence BC048403
					hypothetical Histone-fold structure containing protein	42	5.2	gnf1m31711_at	NM_177587	1810012M12	aquaporin 12
995	4.0	gnf1m13538_a_at	XM_907646	4930557A04	hypothetical Histone-fold structure containing protein	43	5.2	gnf1m29511_at			inferred: ref XP_051995.1 (XM_051995) KIAA1435 protein [Homo sapiens] mCG21671
					synaptonemal complex protein 1	44	5.2	gnf1m33879_x_at			inferred: ref XP_060421.1 (XM_060421) similar to putative (H. sapiens) [Homo sapiens] mCG116890
996	4.0	gnf1m30249_s_at	NM_011516	4932419D11	weakly similar to retinitis pigmentosa GTPase regulator						nardilysin, N-arginine dibasic convertase, NRD convertase 1
997	4.0	gnf1m19279_s_at	NM_001002775	4932416K20	WD repeat domain 16	45	5.2	gnf1m07537_a_at	NM_146150	6030449O20	vomerolysin, 2, receptor, 1b
					inferred: ref NP_113644.1 (NM_031456) Charcot-Marie-Tooth duplicated region transcript 1 [Homo sapiens] mCG116106	46	5.2	gnf1m03841_a_at	NM_019917		RIKEN cDNA 9930038B18 gene
998	4.0	gnf1m13551_a_at		4930519P11	hypothetical protein	47	5.2	gnf1m08161_at	NM_176929	9930038B18	pancreatic lipase
999	4.0	gnf1m05234_a_at	NM_027963	1700019F09	hypothetical protein	48	5.2	gnf1m05089_a_at		1810007A24	olfactory receptor 57
1000	4.0	gnf1m33931_at	XM_924567		testis expressed gene 12	49	5.2	gnf1m17562_s_at	NM_147041		insulin II
					hypothetical protein	50	5.1	gnf1m11114_at	NM_008387	1810027C14	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)
1001	4.0	gnf1m04649_a_at	NM_025687	4921514K14	hypothetical protein	51	5.1	gnf1m33580_x_at	XM_915048		RIKEN cDNA 2210010C04 gene
1002	4.0	gnf1m12431_a_at	NM_028661	G730044P08	hypothetical protein	52	5.1	gnf1m00107_a_at	NM_023333	2210010C04	hypothetical protein
1003	4.0	gnf1m23182_a_at		1700048O20	zinc finger protein 620	53	5.1	gnf1m21836_at		9230113A21	hypothetical protein
1004	4.0	gnf1m00044_a_at	NM_175667	4930570K13	weakly similar to predicted DNA binding protein with his-thr domain	54	5.1	gnf1m23621_at		4831426I01	hypothetical protein
					coiled-coil domain containing 11	55	5.1	gnf1m01330_a_at	NM_008411	1810060I02	CUB and zona pellucida-like domains 1
1005	4.0	gnf1m15352_a_at	XM_924500	4933415I03	coiled-coil domain containing 11	56	5.1	gnf1m20122_at		A230068D05	unclassifiable
1006	4.0	gnf1m05424_a_at	NM_029247	A630022F21	hypothetical protein	57	5.1	gnf1m34632_at			inferred: ref NP_005792.1 (NM_005801) putative translation initiation factor [Homo sapiens] mCG1035752
1007	4.0	gnf1m31032_at	XM_904650	RIKEN cDNA 4930455B06 gene	heme oxygenase (decycling) 2						RIKEN cDNA B930086A06 gene
1008	4.0	gnf1m02369_a_at	NM_010443	I830091K06	hypothetical polyamine modulated factor 1 binding protein 1-like [Macaca mulatta]	58	5.1	gnf1m25033_at		9630016K09	cystatin E/M
1009	4.0	gnf1m14719_a_at	NM_029232	4930563P21	weakly similar to predicted EF-hand containing protein	59	5.1	gnf1m07677_at	NM_028623	6330505O07	inferred: ref NP_060355.1 (NM_017885) hypothetical protein FLJ20568 [Homo sapiens] mCG8073
					weakly similar to adrenergic receptor, alpha 1d	60	5.1	gnf1m31567_at			inferred: ref NP_060355.1 (NM_017885) hypothetical protein FLJ20568 [Homo sapiens] mCG8073
1010	4.0	gnf1m10382_a_at	NM_029946	4931407K02	phospholipase A2, group IIC						olfactory receptor 829
1011	4.0	gnf1m22843_a_at		4930544N01						9530082L10	SIMILAR TO OXYSTEROL BINDING PROTEIN-LIKE 9 homolog [Mus musculus]
1012	4.0	gnf1m01590_a_at	NM_008868								olfactory receptor 1513
No. 2, pancreas specific genes											inferred: gb AAL55824.1 AF318317.1 (AF318317) unknown [Homo sapiens] mCG1034126
#1	#2	#3	#4	#5	#6						RIKEN cDNA 1600023E10 gene
1	6.4	gnf1m29691_a_at	XM_924840	1810044E12	chymotrypsin C (caldecrin)	61	5.1	gnf1m07165_at	NM_147067		kinase suppressor of ras 2
2	6.2	gnf1m11115_a_at	NM_008387	1810027C14	insulin II	62	5.0	gnf1m24991_at		D930011H06	15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930011H06
3	6.0	gnf1m30562_x_at			trypsinogen 16 trypsinogen 16 mCG124046						product: hypothetical protein, full insert sequence
4	6.0	gnf1m11106_a_at	NM_023707	1810009J06	RIKEN cDNA 1810009J06 gene						DAZ interacting protein 1
5	5.9	gnf1m11109_a_at	NM_008386	C820020F18	insulin I					A430108H20	inferred: ref NP_033956.1 (NM_009826) coiled coil forming protein 1 [Mus musculus] mCG129079
6	5.9	gnf1m27435_at		D130047M23	similar to HSPC009 (HSPC009 PROTEIN) [Homo sapiens]	63	5.0	gnf1m35851_at	NM_001012269		inferred: ref XP_131932.1 (XM_131932) similar to ATP-
7	5.9	gnf1m34778_at	NM_146523		olfactory receptor 850	64	5.0	gnf1m35978_x_at			
8	5.8	gnf1m16788_a_at		1810063P13	RIKEN cDNA 1810028F09 gene						
9	5.8	gnf1m01676_a_at	NM_009043	2010012A06	regenerating islet-derived 2	65	5.0	gnf1m25665_a_at		9630059B11	kinase suppressor of ras 2
10	5.7	gnf1m31882_at	NM_146653		olfactory receptor 435	66	5.0	gnf1m33388_at	NM_001034873		15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930011H06
11	5.7	gnf1m27753_at		D530031E19	hypothetical protein	67	5.0	gnf1m21458_at			product: hypothetical protein, full insert sequence
12	5.7	gnf1m18121_at		G630079N01	expressed sequence AI846148						DAZ interacting protein 1
13	5.6	gnf1m04787_a_at	NM_025989	2310046E09	glycoprotein 2 (zymogen granule membrane)						inferred: ref NP_033956.1 (NM_009826) coiled coil forming protein 1 [Mus musculus] mCG129079
					inferred: gb AAH18205.1 AAH18205 (BC018205) Unknown (protein for IMAGE:3464710) [Homo sapiens] mCG12382	68	5.0	gnf1m04627_a_at	XM_919625	2510042J05	inferred: ref XP_131932.1 (XM_131932) similar to ATP-
15	5.6	gnf1m10387_a_at	XM_906665	1810033M07	RIKEN cDNA 1810033M07 gene	69	5.0	gnf1m33154_at			
16	5.6	gnf1m08517_a_at	XR_000394	D830038L22	cDNA sequence BC022713						
17	5.6	gnf1m30530_at			RIKEN cDNA 2410080P20 gene	70	5.0	gnf1m29642_a_at			
					RIKEN cDNA 2410080P20 gene						

					binding cassette, sub-family F, member 2 [Mus musculus] mCG16473	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
71	5.0	gnf1m31256_s_at	XM_910652	A430098H07	jerky homolog-like (mouse)				inferred: gb AAD29851.1
72	5.0	gnf1m13375_a_at		4930533N22	RIKEN cDNA 4930533N22 gene	122 4.7 gnf1m34247_at			(AF079520) laminin gamma-3 chain precursor [Mus musculus] mCG17454
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	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
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	127 4.7 gnf1m18730_at		1700001E18	RIKEN cDNA 1110058L19 gene
					inferred: ref NP_035229.1 (NM_011099) pyruvate kinase 3 [Mus musculus] mCG50497	128 4.7 gnf1m14300_at		1700026M20	cDNA sequence BC051628
					Transcribed locus	129 4.7 gnf1m22547_at		E030030I02	unclassifiable
					DEAH (Asp-Glu-Ala-His) box polypeptide 34	130 4.7 gnf1m08478_at		D130057M20	hypothetical protein
81	4.9	gnf1m31639_at			Mouse partial mRNA for hypothetical protein (P4(21)n gene) /cds=UNKNOWN /gb=AJ242955 /gi=5042303 /len=1730 gnl UG Mm#5685684	131 4.7 gnf1m17507_at			gb=U69137 Mouse T2-cadherin mRNA, partial cds
82	4.9	gnf1m05219_a_at	NM_027883	9930003H07	similar to glycerol-3-phosphate dehydrogenase 1-like uncharacterized Celera prediction mCG1029985				RIKEN cDNA 1500005I02 gene centromere autoantigen F
83	4.9	gnf1m16696_at			solute carrier family 34 (sodium phosphate), member 3	132 4.7 gnf1m29038_a_at	NM_028055	6330586L13	unclassifiable
					RIKEN cDNA 4930474H20 gene	133 4.7 gnf1m30962_at	XM_924334	5730419A11	unclassifiable
					RIKEN cDNA 2610510C17 gene	134 4.7 gnf1m23991_at		C820020M20	glucagon
					RIKEN cDNA 5930403N24 gene	135 4.7 gnf1m30976_a_at	NM_008100	1700012K18	similar to beta-defensin 123
					inferred: ref NP_058797.1 (NM_017101) peptidylprolyl isomerase A (cyclophilin A) [Rattus norvegicus] mCG49869	136 4.6 gnf1m28927_at	NM_001037752	2410137M14	RIKEN cDNA 2410137M14 gene
					mitochondrial intermediate peptidase	137 4.6 gnf1m05504_a_at	NM_029747	4930535E21	RIKEN cDNA 4930535E21 gene
					Eph receptor B1	138 4.6 gnf1m28687_a_at	NM_029212	4931419J09	Adult male testis cDNA, RIKEN full-length enriched library, clone:4931419J09
					olfactory receptor 30	139 4.6 gnf1m19259_at			product:unclassifiable, full insert sequence
					RIKEN cDNA C230040D10 gene			A630019K16	3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630019K16 product:paired box gene 1, full insert sequence
					protein disulfide isomerase associated 2	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
					similar to Olfactory receptor 5D13			D630041E16	caspace 9
91	4.9	gnf1m12380_a_at	NM_027436	A930014F04	RIKEN cDNA 4833422F24 gene	142 4.6 gnf1m27822_at			inferred: gb AAB40653.1 (U66840) MAP kinase 3c [Homo sapiens] mCG51091
92	4.9	gnf1m22102_at			obsolete Celera prediction mCT136127	143 4.6 gnf1m34997_at			RIKEN cDNA 1700010L04 gene
93	4.9	gnf1m07032_a_at	NM_146878	C130099E04	RIKEN cDNA 1810058N15 gene				S-adenosylhomocysteine hydrolase-like 1
94	4.9	gnf1m18557_at	XM_906291	9330169N05	zinc finger CCCC type containing 6	144 4.6 gnf1m31287_a_at		1700010L04	HEAT SHOCK PROTEIN, 25 KDa
95	4.9	gnf1m16394_at	XM_914914	1810041F13	uncharacterized Celera prediction mCG1034864	145 4.6 gnf1m28150_at		E130208G24	potassium voltage-gated channel, subfamily H (eag-related), member 5
96	4.9	gnf1m09104_a_at	XM_915356	6430520H06	RIKEN cDNA A130086G11 gene				inferred: ref NP_035826.1 (NM_016696) voltage-dependent anion channel 3 [Mus musculus] mCG120473
97	4.9	gnf1m24376_at			RIKEN cDNA A130086G11 gene	146 4.6 gnf1m13748_at		4632415I09	similar to immunoglobulin superfamily, member 2
98	4.9	gnf1m32785_at			sortilin-related VPS10 domain containing receptor 2	147 4.6 gnf1m07824_a_at	NM_172805	6430546I09	RIKEN cDNA 1700025L06 gene
99	4.9	gnf1m31205_at	NM_001033448	G430025O10	inferred: ref NP_032110.1 (NM_008084) glyceraldehyde-3-phosphate dehydrogenase [Mus musculus] mCG118656	148 4.6 gnf1m33663_at			unclassifiable
100	4.8	gnf1m08832_s_at	NM_178404	A230104G09	polycystic kidney and hepatic disease 1-like 1				unclassifiable clone
101	4.8	gnf1m35967_x_at			fibroblast growth factor 11	149 4.6 gnf1m33853_at	XM_907687	9630038C06	cDNA sequence AF067061
102	4.8	gnf1m20060_at			inferred: ref NP_036302.1 (NM_012170) F-box only protein 22; hypothetical protein FLJ13986; F-box protein Fbx22 [Homo sapiens] mCG9673	150 4.6 gnf1m23001_a_at			RIKEN cDNA 1110020J08 gene
103	4.8	gnf1m05617_a_at	NM_030889	A130086G11	inferred: ref NP_080695.1 (NM_026419) elastase 3B, pancreatic [Mus musculus] mCG120450	151 4.6 gnf1m28420_a_at			RIKEN cDNA 1110020J08 gene mCG5717
104	4.8	gnf1m33768_x_at			RIKEN cDNA 4930513L20 gene	152 4.6 gnf1m13198_at			cDNA sequence BC036313
					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	153 4.6 gnf1m22907_at		1700040F17	RIKEN cDNA 1700040F17 gene
105	4.8	gnf1m10363_at	NM_138674		RIKEN cDNA 4930467M19 gene	154 4.6 gnf1m13900_s_at	NM_199060		inferred: ref NP_05518.1 (NM_014703) KIAA0800 gene product [Homo sapiens] mCG123324
106	4.8	gnf1m02247_at	NM_010198		inferred: gb AAF81070.1 AF223427_1 (AF223427) RRM-containing protein SEB-4 [Xenopus laevis] mCG1043826	155 4.6 gnf1m31803_at		9430075C07	expressed sequence AU042671 dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1b
107	4.8	gnf1m31318_at			carboxypeptidase B1 (tissue)				chymotrypsin-like
108	4.8	gnf1m33666_at			RIKEN cDNA 1500017I17 gene	156 4.6 gnf1m32216_at		2300003F21	sacsin
109	4.8	gnf1m14292_at			inferred: ref NP_035420.1 (NM_011290) ribosomal protein L6 [Mus musculus] mCG8028	157 4.6 gnf1m14412_at		A230052M14	similar to testicular acid phosphatase isoform a precursor
110	4.8	gnf1m33036_x_at			gene model 939, (NCBI)	158 4.6 gnf1m30589_at			RIKEN cDNA 5830433M15 gene
					polymerase (RNA) III (DNA directed) polypeptide F			5830433M15	RIKEN cDNA 5830433M15 gene
					expressed sequence AW495713			0610010K06	RIKEN cDNA 0610010K06 gene
111	4.8	gnf1m23733_a_at	XM_916176	F730211G02				5330439K02	RIKEN cDNA 5330439K02 gene
112	4.8	gnf1m34525_at						F830016J06	pannexin 1
								F630047I08	low-density lipoprotein receptor-related protein 10
								1810057G13	transmembrane emp24 protein transport domain containing 6
113	4.8	gnf1m23206_s_at	NM_029706	2210008M23	carboxypeptidase B1 (tissue)	169 4.5 gnf1m04545_a_at	NM_025458		unclassifiable
114	4.8	gnf1m13602_at			RIKEN cDNA 1500017I17 gene	170 4.5 gnf1m28022_at		E030022H18	unclassifiable
115	4.8	gnf1m31474_x_at			inferred: ref NP_035420.1 (NM_011290) ribosomal protein L6 [Mus musculus] mCG8028	171 4.5 gnf1m17499_at		2610509C21	RIKEN cDNA 2610007O09 gene
116	4.7	gnf1m18072_at			gene model 939, (NCBI)	172 4.5 gnf1m29551_at			inferred: ref XP_109605.1 (XM_109605) proteasome (prosome, macropain) 26S subunit, ATPase 3, interacting protein [Mus musculus] mCG20202
117	4.7	gnf1m24193_a_at			polymerase (RNA) III (DNA directed) polypeptide F			3830420C14	G-protein-coupled receptor 50
118	4.7	gnf1m19676_at	NM_001024504	9330185P08	expressed sequence AW495713			6720465F12	ubiquitin-conjugating enzyme E2S
								4930415C24	olfactory receptor 987 gene model 1653, (NCBI)

177	4.5	gnflm09082_a_at	NM_207149		olfactory receptor 1010	240	4.4	gnflm34266_at	XM_904475	similar to O-acyltransferase (membrane bound) domain containing 1
178	4.5	gnflm32002_x_at	XM_912694		similar to putative pheromone receptor (Go-VN5)					
179	4.5	gnflm01890_at	NM_009430	0910001K11	protease, serine, 2	241	4.4	gnflm07155_a_at	NM_147051	olfactory receptor 362
180	4.5	gnflm19876_at		9830114D01	RIKEN cDNA 4933422E07 gene	242	4.4	gnflm20955_at	C030046L04	unclassifiable
181	4.5	gnflm00432_a_at	NM_007491	4930443I07	ADP-ribosyltransferase 5	243	4.4	gnflm23297_at	XM_904933	RIKEN cDNA 2310002J21 gene
182	4.5	gnflm17931_at		1700007N19	chondroitin sulfate proteoglycan 3	244	4.4	gnflm34938_x_at	NM_146656	olfactory receptor 444
183	4.5	gnflm09206_at	NM_181819		WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2	245	4.4	gnflm03180_a_at	NM_013606	myxovirus (influenza virus) resistance 2
184	4.5	gnflm28621_at			gb BC018362.1 Mouse clone MGC:19264 IMAGE:3986648, mRNA, complete cds	246	4.4	gnflm33808_at	NM_207253	olfactory receptor 1371
185	4.5	gnflm34842_at	NM_001033793	B020039L20	RIKEN cDNA B020006M18 gene	247	4.4	gnflm17189_at		RIKEN cDNA 2010007L08 gene
186	4.5	gnflm09567_s_at	NM_011646	2210415M03	trypsin 4	248	4.4	gnflm135492_at		inferred: ref NP_036099.1 (NM_011969) proteasome (prosome, macropain) subunit, alpha type 7 [Mus musculus] mCG18545
187	4.5	gnflm001117_a_at	NM_008005	6430536H17	fibroblast growth factor 18					
188	4.5	gnflm20905_at		B930055O11	unclassifiable	249	4.4	gnflm19615_at		9230114N12 hypothetical Isoleucine-rich region containing protein
189	4.5	gnflm35682_at			inferred: ref XP_059133.1 (XM_059133) similar to ubiquinol-cytochrome c reductase hinge protein (H. sapiens) [Homo sapiens] mCG50773	250	4.4	gnflm35642_at		inferred: gb AAC72797.1 (AF081106) ORF2 [Mus musculus domesticus] mCG54614
190	4.5	gnflm35798_x_at			inferred: gb AAH16248.1 AAH16248 (BC016248) Similar to zinc finger protein 85 (HPF4, HTF1) [Mus musculus] mCG1044717	251	4.3	gnflm18658_s_at	B230397F11	weakly similar to CELL DEATH REGULATOR AVEN [Homo sapiens]
191	4.5	gnflm18052_at		A630098M21	unclassifiable	252	4.3	gnflm14135_at		RIKEN cDNA 4931407J08 gene
192	4.5	gnflm32971_at	NM_145853	G370028G22	two pore channel 1	253	4.3	gnflm09124_at		inferred: gb AAL61316.1 (AY073653) olfactory receptor MOR257-3 [Mus musculus] mCG60446
193	4.5	gnflm06755_s_at	NM_146267		olfactory receptor 769	254	4.3	gnflm34017_at		inferred: gb AAL50790.1 AF454056_1 (AF454056) se14-3r protein [Homo sapiens] mCG114715
194	4.5	gnflm24653_at		9630042F02	UDP-Gal:betaGal beta 1,3-galactosyltransferase, polypeptide 6	255	4.3	gnflm21623_at		4632407M08 hypothetical Phenylalanine-rich region profile/Serine-rich region profile containing protein
195	4.5	gnflm22439_a_at	NM_001013780	E030001G18	solute carrier family 25, member 34	256	4.3	gnflm23958_at		RIKEN cDNA 1300013D05 gene
196	4.5	gnflm35624_x_at	XM_911459		hypothetical LOC545187	257	4.3	gnflm31563_x_at		inferred: ref NP_037061.1 (NM_012929) procollagen II alpha 1 [Rattus norvegicus] mCG64250
197	4.5	gnflm31715_at			inferred: gb AAL61305.1 (AY073642) olfactory receptor MOR256-29 [Mus musculus] mCG55158	258	4.3	gnflm18259_at		unclassifiable
198	4.5	gnflm36013_at	XM_905701		similar to vomeronasal 1 receptor, D7	259	4.3	gnflm35601_at		uncharacterized Celera prediction mCG60559
199	4.5	gnflm17683_at			gb=U11548 Mouse TFIIi-associated transactivator factor p17 mRNA, complete cds	260	4.3	gnflm28146_at	E130120L03	cytosolic acyl-CoA thioesterase 1
200	4.5	gnflm17582_at			gb=X80430 Mouse tex267 mRNA (5'region)	261	4.3	gnflm17305_at	4930443G03	RIKEN cDNA 4930443G03 gene
201	4.5	gnflm35633_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	262	4.3	gnflm08715_at	NM_172761	C920004D05 cDNA sequence BC052066
202	4.5	gnflm27846_at		D730022H23	RIKEN cDNA A730037C10 gene	263	4.3	gnflm30124_a_at	NM_203319	DEAH (Asp-Glu-Ala-His) box polypeptide 37
203	4.5	gnflm07233_at	NM_148947		lymphocyte antigen 6 complex, locus G5C	264	4.3	gnflm08724_s_at	D13006J02	RIKEN cDNA D13006J02 gene
204	4.5	gnflm11349_at	NM_031167	F630220G16	interleukin 1 receptor antagonist	265	4.3	gnflm02645_a_at	2310012E07	phospholipase A2, group IB, pancreas
205	4.5	gnflm35511_at	XM_904498		similar to zinc finger protein 709	266	4.3	gnflm06895_a_at	NM_146651	olfactory receptor 1403
206	4.4	gnflm27231_at		C820013I09	hypothetical PDZ domain (also known as DHR or GLGF) containing protein	267	4.3	gnflm33059_at		glutamate receptor interacting protein 2
207	4.4	gnflm31456_at			expressed sequence AA987064 expressed sequence AA987064 mCG8570	268	4.3	gnflm32420_at	XM_914429	similar to 40S ribosomal protein S15 (RIG protein)
208	4.4	gnflm07472_a_at	NM_026716	0910001K16	syncollin	269	4.3	gnflm07048_s_at	NM_146901	olfactory receptor 1217
209	4.4	gnflm28464_a_at	XM_922413	M5C1043P11	Crm, cramped-like (Drosophila)	270	4.3	gnflm31198_at	NM_028317	RIKEN cDNA 2810030E01 gene
210	4.4	gnflm08526_at		E030024N20	RIKEN cDNA E030024N20 gene	271	4.3	gnflm29989_a_at	NM_033612	1810009A17 elastase 1, pancreatic
211	4.4	gnflm04601_a_at	NM_025583	9030613K09	chymotrypsinogen B1	272	4.3	gnflm14565_a_at		4833427F10 RIKEN cDNA 4833427F10 gene
212	4.4	gnflm18224_at		9330186C21	unclassifiable	273	4.3	gnflm22445_at		D830039M14 RIKEN cDNA D830039M14 gene
213	4.4	gnflm03597_at	NM_018754		stratifin	274	4.3	gnflm22055_at	C130048D21	unclassifiable
214	4.4	gnflm13222_at	XM_905316	G430074B03	chemokine (C-C motif) receptor 10	275	4.3	gnflm19984_at	A130023H13	unclassifiable
215	4.4	gnflm31739_at	XM_909971		similar to oxoglutarate dehydrogenase-like	276	4.3	gnflm01675_a_at	NM_009042	503340A1N7 regenerating islet-derived 1
216	4.4	gnflm00169_a_at	NM_178255	4930554N11	hyaluronan and proteoglycan link protein 3	277	4.3	gnflm25364_at	A130078K13	unclassifiable
217	4.4	gnflm21935_at		A730040I02	unclassifiable	278	4.3	gnflm26312_at	B230211D20	RIKEN cDNA F830001A07 gene
218	4.4	gnflm08978_at	XM_923109		similar to olfactory receptor Olr804	279	4.3	gnflm36033_at		olfactory receptor 3
219	4.4	gnflm34883_at	NM_146518		olfactory receptor 523	280	4.3	gnflm31842_at		inferred: ref NP_002625.1 (NM_002634) prohibitin [Homo sapiens] mCG51148
220	4.4	gnflm35688_at			inferred: ref XP_059037.1 (XM_059037) similar to putative (H. sapiens) [Homo sapiens] mCG50591	281	4.3	gnflm16571_a_at	E130016D18	kelch-like 25 (Drosophila)
221	4.4	gnflm03655_a_at	NM_018874	1810032A23	pancreatic lipase related protein 1	282	4.3	gnflm23743_at	4930485C04	mutS homolog 4 (E. coli)
222	4.4	gnflm18520_a_at	XM_900600	6030442D07	similar to mitogen-activated protein kinase kinase kinase 13	283	4.3	gnflm30401_a_at	NM_001003405	2210415M03 RIKEN cDNA 1810049H19 gene
223	4.4	gnflm35863_at	XM_906995	A130004F19	gene model 252, (NCBI)	284	4.3	gnflm08069_at		9230101H05 piwi-like homolog 4 (Drosophila)
224	4.4	gnflm19962_at			unclassifiable	285	4.3	gnflm25663_at	A430107I06	proprotein convertase subtilisin/kexin type 3
225	4.4	gnflm03189_s_at	NM_013618		olfactory receptor 64	286	4.3	gnflm27571_at	D230023M10	unclassifiable
226	4.4	gnflm05681_a_at	NM_031408		PERQ amino acid rich, with GYF domain 1	287	4.3	gnflm35595_at		inferred: ref NP_031817.1 (NM_007791) cysteine rich protein [Mus musculus] mCG61881
227	4.4	gnflm15556_at		E130116L18	RIKEN cDNA E130116L18 gene	288	4.3	gnflm19756_at	9430079A18	hypothetical protein
228	4.4	gnflm15817_at		3010034A12	f-box only protein 6a	289	4.3	gnflm25844_at	A630048I20	interleukin 15 receptor, alpha chain
229	4.4	gnflm02655_a_at	NM_011128	2210004D24	pancreatic lipase-related protein 2	290	4.3	gnflm20560_at	A830048E23	calcium channel, voltage-dependent, gamma subunit 4
230	4.4	gnflm13665_at	XM_915228		similar to T-cell receptor beta chain V region C5 precursor	291	4.3	gnflm07670_a_at	NM_175197	RIKEN cDNA 1700055D18 gene
231	4.4	gnflm01060_a_at	NM_007919	4930413G21	RIKEN cDNA 4930413G21 gene	292	4.3	gnflm27751_at		zinc finger protein 36, C3H type-like 1
232	4.4	gnflm17223_at			olfactory receptor 9	293	4.3	gnflm11108_a_at	NM_011271	1810011N10 ribonuclease, RNase A family, 1 (pancreatic)
233	4.4	gnflm07019_s_at	NM_146862		RIKEN cDNA 4921532D01 gene	294	4.3	gnflm35585_at		uncharacterized Celera prediction mCG63327
234	4.4	gnflm17302_at		4921532D01	RIKEN cDNA 1190003K10 gene	295	4.3	gnflm08963_a_at	NM_146275	olfactory receptor 1402
235	4.4	gnflm13986_a_at	XM_905181	1190003K10	RIKEN cDNA 1190003K10 gene	296	4.3	gnflm13423_a_at		CDNA clone MGC:6757 IMAGE:3594209
236	4.4	gnflm11515_at	NM_025725	4932416C18	RIKEN cDNA 4921513E08 gene	297	4.3	gnflm31138_at	NM_028162	TBC1 domain family, member 5
237	4.4	gnflm27453_at		D130054H18	hypothetical protein	298	4.3	gnflm20080_at	A130098P13	CDNA FLJ10678 FIS, CLONE NT2RP2006472 homolog [Homo sapiens]
238	4.4	gnflm33595_at			uncharacterized Celera prediction mCG121791	299	4.3	gnflm21045_s_at	C130089K02	similar to mastermind-like 3
239	4.4	gnflm25240_at		9930101A07	RIKEN cDNA 9930039A11 gene	300	4.3	gnflm22928_at	A230086C11	hypothetical protein LOC545410
						301	4.2	gnflm13817_s_at	NM_199060	cDNA sequence AF067061
						302	4.2	gnflm29833_s_at	XM_924663	9630025B04 M-phase phosphoprotein 9
						303	4.2	gnflm32621_at		inferred: ref NP_036686.1 (NM_012554) enolase 1, alpha

304	4.2	gnf1m28392_a_at	XM_917520	E430024E22	[Rattus norvegicus] mCG18926 NOL1/NOP2/Sun domain family 3 similar to Spectrin beta chain, brain 4 (Spectrin, non-erythroid beta chain 4) (Beta-V spectrin) (BSPECV)	351	4.2	gnf1m24106_a_at	NM_001024489	E130302K06 9930030P21 A630024D08 6720475G09	RIKEN cDNA 4930459M12 gene programmed cell death protein 11 RIKEN cDNA 1700034H15 gene unclassifiable Fraser syndrome 1 homolog (human)			
305	4.2	gnf1m32904_at				352	4.2	gnf1m25226_at				353	4.2	gnf1m22882_at
306	4.2	gnf1m33610_at	XM_909794	6720482J09 A430103N06	similar to dead end homolog 1 aconitase 2, mitochondrial tryptase alpha/beta 1 inferred: ref XP_016001.1 (XM_016001) hypothetical protein XP_016001 [Homo sapiens] mCG1041621	356	4.1	gnf1m30741_a_at	NM_175473	9430088F20	development and differentiation enhancing factor-like 1 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 similar to Ig kappa chain V-VI region NQ2-17.4.1 pancreas specific transcription factor, 1a olfactory receptor 159 unclassifiable tripartite motif-containing 41 RIKEN cDNA 6530411M01 gene olfactory receptor 421 high mobility group box transcription factor 1 inferred: ref NP_032110.1 (NM_008084) glyceraldehyde-3-phosphate dehydrogenase [Mus musculus] mCG21423 inferred: ref NP_032110.1 (NM_008084) glyceraldehyde-3-phosphate dehydrogenase [Mus musculus] mCG130516			
307	4.2	gnf1m24513_at				357	4.1	gnf1m35793_at				358	4.1	gnf1m35378_x_at
308	4.2	gnf1m12237_a_at	NM_031187	B930075E15	hypothetical protein forkhead box N1 RIKEN cDNA 2410024N13 gene inferred: gb AAF81417.1 AF239196_4 (AF239196) BCL1 lymphoma-derived single chain idiotype variable region [synthetic construct] mCG1025862 inferred: ref XP_151046.1 (XM_151046) hypothetical protein XP_151046 [Mus musculus] mCG113690	359	4.1	gnf1m03629_a_at	NM_019476	D530008I23				
309	4.2	gnf1m35869_at				360	4.1	gnf1m03709_at			361	4.1	gnf1m22378_at	NM_146720
310	4.2	gnf1m12329_s_at	NM_008238	D230007B16	unclassifiable inferred: gb AAH20488.1 AAH20488 (BC020488) Similar to protein with polyglutamine repeat; calcium (ca2+) homeostasis endoplasmic reticulum protein [Mus musculus] mCG5625	362	4.1	gnf1m15673_at	NM_177993	6530411M01				
311	4.2	gnf1m01241_at				363	4.1	gnf1m18115_at			364	4.1	gnf1m09125_a_at	NM_146720
312	4.2	gnf1m14021_a_at	XM_912234	A130049D12	cryptochrome 2 (photolyase-like) hypothetical protein LOC620642 uncharacterized Celera prediction mCG13775	365	4.1	gnf1m07669_a_at	NM_177993	D530008I23				
313	4.2	gnf1m36099_at				366	4.1	gnf1m32259_at			367	4.1	gnf1m33049_at	NM_177993
314	4.2	gnf1m34089_at	NM_029686	6030413L20	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 polycystic kidney disease 1 like 2 casein kinase 1, epsilon 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	368	4.1	gnf1m22463_at	NM_177993	6530411M01				
315	4.2	gnf1m22281_at				369	4.1	gnf1m15808_at			370	4.1	gnf1m06996_at	NM_177993
316	4.2	gnf1m29087_at	NM_029686	1810008A02 9530058P14	cyclic nucleotide gated channel alpha 3 coiled-coil domain containing 57 Transcribed locus hypothetical Metallo-dependent phosphatases structure containing protein gene model 41, (NCBI) RIKEN cDNA 1520401A03 gene RIKEN cDNA B230315F11 gene inferred: ref NP_034003.1 (NM_009873) cyclin-dependent kinase 6 [Mus musculus] mCG1028465	371	4.1	gnf1m26743_at	NM_177993	6530411M01				
317	4.2	gnf1m25326_at				372	4.1	gnf1m19599_at			373	4.1	gnf1m01728_a_at	NM_177993
318	4.2	gnf1m32175_at	XM_912234	A130049D12	cryptochrome 2 (photolyase-like) hypothetical protein LOC620642 uncharacterized Celera prediction mCG13775	374	4.1	gnf1m02718_a_at	NM_177993	6530411M01				
319	4.2	gnf1m32528_at				375	4.1	gnf1m33074_at			376	4.1	gnf1m25913_a_at	NM_177993
320	4.2	gnf1m24170_at	NM_029686	1810008A02 9530058P14	cyclic nucleotide gated channel alpha 3 coiled-coil domain containing 57 Transcribed locus hypothetical Metallo-dependent phosphatases structure containing protein gene model 41, (NCBI) RIKEN cDNA 1520401A03 gene RIKEN cDNA B230315F11 gene inferred: ref NP_034003.1 (NM_009873) cyclin-dependent kinase 6 [Mus musculus] mCG1028465	377	4.1	gnf1m35861_at	NM_177993	6530411M01				
321	4.2	gnf1m10237_at				378	4.1	gnf1m27724_at			379	4.1	gnf1m05794_at	NM_177993
322	4.2	gnf1m19795_at	NM_029686	1810008A02 9530058P14	cyclic nucleotide gated channel alpha 3 coiled-coil domain containing 57 Transcribed locus hypothetical Metallo-dependent phosphatases structure containing protein gene model 41, (NCBI) RIKEN cDNA 1520401A03 gene RIKEN cDNA B230315F11 gene inferred: ref NP_034003.1 (NM_009873) cyclin-dependent kinase 6 [Mus musculus] mCG1028465	380	4.1	gnf1m06770_x_at	NM_177993	6530411M01				
323	4.2	gnf1m34035_at				381	4.1	gnf1m19495_at			382	4.1	gnf1m15927_at	NM_177993
324	4.2	gnf1m19538_at	NM_027745	4933434K12 A630002C06	coiled-coil domain containing 57 Transcribed locus hypothetical Metallo-dependent phosphatases structure containing protein gene model 41, (NCBI) RIKEN cDNA 1520401A03 gene RIKEN cDNA B230315F11 gene inferred: ref NP_034003.1 (NM_009873) cyclin-dependent kinase 6 [Mus musculus] mCG1028465	383	4.1	gnf1m08119_at	NM_177993	6530411M01				
325	4.2	gnf1m32939_at				384	4.1	gnf1m21871_at			385	4.1	gnf1m32959_at	NM_177993
326	4.2	gnf1m17978_at	XM_912587	C130002K19	RIKEN cDNA 1520401A03 gene RIKEN cDNA B230315F11 gene inferred: ref NP_034003.1 (NM_009873) cyclin-dependent kinase 6 [Mus musculus] mCG1028465	386	4.1	gnf1m14769_a_at	NM_177993	6530411M01				
327	4.2	gnf1m25782_at				387	4.1	gnf1m29398_a_at			388	4.1	gnf1m08765_at	NM_177993
328	4.2	gnf1m35410_s_at	XM_912587	C130002K19	RIKEN cDNA 1520401A03 gene RIKEN cDNA B230315F11 gene inferred: ref NP_034003.1 (NM_009873) cyclin-dependent kinase 6 [Mus musculus] mCG1028465	389	4.1	gnf1m26973_at	NM_177993	6530411M01				
329	4.2	gnf1m12531_a_at				390	4.1	gnf1m34389_at			391	4.1	gnf1m35950_x_at	NM_177993
330	4.2	gnf1m12367_at	NM_178766	A930004C23	hypothetical Yjef-F-like structure containing protein NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4 GLIS family zinc finger 1 REGULATOR OF G-PROTEIN SIGNALING 20 (RGS20) (REGULATOR OF G-PROTEIN SIGNALING Z1) homolog [Mus musculus]	392	4.1	gnf1m29191_at	NM_177993	6530411M01				
331	4.2	gnf1m35501_at				393	4.1	gnf1m21668_at			394	4.1	gnf1m19092_at	NM_177993
332	4.2	gnf1m17658_at	XM_908933	4930545J21	hypothetical Yjef-F-like structure containing protein NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4 GLIS family zinc finger 1 REGULATOR OF G-PROTEIN SIGNALING 20 (RGS20) (REGULATOR OF G-PROTEIN SIGNALING Z1) homolog [Mus musculus]	395	4.1	gnf1m23125_at	NM_177993	6530411M01				
333	4.2	gnf1m33472_at				396	4.1	gnf1m23569_at			397	4.1	gnf1m34880_s_at	NM_177993
334	4.2	gnf1m07219_a_at	NM_147221	I0C0014N20 C030018L17	phosphofructokinase, liver, B-type transmembrane epididymal protein 1 similar to Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 1 (GalNAc alpha-2,6-sialyltransferase I) (ST6GalNAc I) (Sialyltransferase 7A) solute carrier family 38, member 5 trefoil factor 2 (spasmolytic protein 1) olfactory receptor 895 tetraspanin 18 inferred: ref NP_116095.1 (NM_032706) hypothetical protein MGC12966 [Homo sapiens] mCG113002	398	4.1	gnf1m26143_at	NM_177993	6530411M01				
335	4.2	gnf1m26629_at				399	4.1	gnf1m31450_at			400	4.1	gnf1m35754_at	NM_177993
336	4.2	gnf1m15163_at	NM_178244	2210403E17	phosphofructokinase, liver, B-type transmembrane epididymal protein 1 similar to Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 1 (GalNAc alpha-2,6-sialyltransferase I) (ST6GalNAc I) (Sialyltransferase 7A) solute carrier family 38, member 5 trefoil factor 2 (spasmolytic protein 1) olfactory receptor 895 tetraspanin 18 inferred: ref NP_116095.1 (NM_032706) hypothetical protein MGC12966 [Homo sapiens] mCG113002	401	4.1	gnf1m02448_a_at	NM_177993	6530411M01				
337	4.2	gnf1m09093_at				402	4.1	gnf1m15557_at			403	4.1	gnf1m24099_at	NM_177993
338	4.2	gnf1m31597_at	XM_924190	4930545J21	hypothetical Yjef-F-like structure containing protein NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4 GLIS family zinc finger 1 REGULATOR OF G-PROTEIN SIGNALING 20 (RGS20) (REGULATOR OF G-PROTEIN SIGNALING Z1) homolog [Mus musculus]	404	4.0	gnf1m18055_at	NM_177993	6530411M01				
339	4.2	gnf1m08566_a_at				405	4.1	gnf1m23125_at			406	4.1	gnf1m23569_at	NM_177993
340	4.2	gnf1m10964_a_at	NM_172479	F930032P09 0910001O22	solute carrier family 38, member 5 trefoil factor 2 (spasmolytic protein 1) olfactory receptor 895 tetraspanin 18 inferred: ref NP_116095.1 (NM_032706) hypothetical protein MGC12966 [Homo sapiens] mCG113002	407	4.1	gnf1m23569_at	NM_177993	6530411M01				
341	4.2	gnf1m07029_at				408	4.1	gnf1m23569_at			409	4.1	gnf1m23569_at	NM_177993
342	4.2	gnf1m29817_a_at	NM_183180	6720430O15	hypothetical protein MGC12966 [Homo sapiens] mCG113002	410	4.1	gnf1m23569_at	NM_177993	6530411M01				
343	4.2	gnf1m34154_at				411	4.1	gnf1m23569_at			412	4.1	gnf1m23569_at	NM_177993
344	4.2	gnf1m27441_at	NM_173365	D130050K19 A430106B11	polyhomeotic-like 2 (Drosophila) G protein-coupled receptor 20 RIKEN cDNA 4933421D24 gene recombining binding protein suppressor of hairless-like (Drosophila) uncharacterized Celera prediction mCG126184	413	4.1	gnf1m23569_at	NM_177993	6530411M01				
345	4.2	gnf1m08227_at				414	4.1	gnf1m23569_at			415	4.1	gnf1m23569_at	NM_177993
346	4.2	gnf1m17244_at	NM_009036	D430025K11	uncharacterized Celera prediction mCG126184	416	4.1	gnf1m23569_at	NM_177993	6530411M01				
347	4.2	gnf1m12932_a_at				417	4.1	gnf1m23569_at			418	4.1	gnf1m23569_at	NM_177993
348	4.2	gnf1m33356_at	NM_008266	5730469B06 4930427C17	homeo box B1 RIKEN cDNA 4930471M09 gene	419	4.1	gnf1m23569_at	NM_177993	6530411M01				
349	4.2	gnf1m01257_a_at				420	4.1	gnf1m23569_at			421	4.1	gnf1m23569_at	NM_177993
350	4.2	gnf1m16328_at	NM_008266	5730469B06 4930427C17	homeo box B1 RIKEN cDNA 4930471M09 gene	422	4.1	gnf1m23569_at	NM_177993	6530411M01				
						423	4.1	gnf1m23569_at			424	4.1	gnf1m23569_at	NM_177993
			NM_008266	5730469B06 4930427C17	homeo box B1 RIKEN cDNA 4930471M09 gene	425	4.1	gnf1m23569_at	NM_177993	6530411M01				
						426	4.1	gnf1m23569_at			427	4.1	gnf1m23569_at	NM_177993
			NM_008266	5730469B06 4930427C17	homeo box B1 RIKEN cDNA 4930471M09 gene	428	4.1	gnf1m23569_at	NM_177993	6530411M01				
						429	4.1	gnf1m23569_at			430	4.1	gnf1m23569_at	NM_177993
			NM_008266	5730469B06 4930427C17	homeo box B1 RIKEN cDNA 4930471M09 gene	431	4.1	gnf1m23569_at	NM_177993	6530411M01				
						432	4.1	gnf1m23569_at			433	4.1	gnf1m23569_at	NM_177993
			NM_008266	5730469B06 4930427C17	homeo box B1 RIKEN cDNA 4930471M09 gene	434	4.1	gnf1m23569_at	NM_177993	6530411M01				
						435	4.1	gnf1m23569_at			436	4.1	gnf1m23569_at	NM_177993
			NM_008266	5730469B06 4930427C17	homeo box B1 RIKEN cDNA 4930471M09 gene	437	4.1	gnf1m23569_at	NM_177993	6530411M01				
						438	4.1	gnf1m23569_at			439	4.1	gnf1m23569_at	NM_177993
			NM_008266	5730469B06 4930427C17	homeo box B1 RIKEN cDNA 4930471M09 gene	440	4.1	gnf1m23569_at	NM_177993	6530411M01				
						441	4.1	gnf1m23569_at			442	4.1	gnf1m23569_at	NM_177993
			NM_008266	5730469B06 4930427C17	homeo box B1 RIKEN cDNA 4930471M09 gene	443	4.1	gnf1m23569_at	NM_177993	6530411M01				
						444	4.1	gnf1m23569_at			445	4.1	gnf1m23569_at	NM_177993
			NM_008266	5730469B06 4930427C17	homeo box B1 RIKEN cDNA 4930471M09 gene	446	4.1	gnf1m23569_at	NM_177993	6530411M01				
						447	4.1	gnf1m23569_at			448	4.1	gnf1m23569_at	NM_177993
			NM_008266	5730469B06 4930427C17	homeo box B1 RIKEN cDNA 4930471M09 gene	449	4.1	gnf1m23569_at	NM_177993	6530411M01				
						450	4.1	gnf1m23569_at			451	4.1	gnf1m23569_at	NM_177993
			NM_008266	5730469B06 4930427C17	homeo box B1 RIKEN cDNA 4930471M09 gene	452	4.1	gnf1m23569_at	NM_177993	6530411M01				
						453	4.1	gnf1m23569_at			454	4.1	gnf1m23569_at	NM_177993
			NM_008266	5730469B06 4930427C17	homeo box B1 RIKEN cDNA 4930471M09 gene	455	4.1	gnf1m23569_at	NM_177993	6530411M01				
						456	4.1	gnf1m23569_at			457	4.1	gnf1m23569_at	NM_177993
			NM_008266	5730469B06 4930427C17	homeo box B1 RIKEN cDNA 4930471M09 gene	458	4.1	gnf1m23569_at	NM_177993	6530411M01				
						459	4.1	gnf1m23569_at			460	4.1	gnf1m23569_at	NM_177993
			NM_008266	5730469B06 4930427C17	homeo box B1 RIKEN cDNA 4930471M09 gene	461	4.1	gnf1m23569						

405	4.0	gnf1m33088_at	XM_914704	A530029A01	UBX domain containing 7	35	5.0	gnf1m08149_a_at	NM_178736	C230098F24	ELMO domain containing 2
406	4.0	gnf1m25702_at			CDNA FLJ30119 FIS, CLONE BRACE1000070 homolog [Homo sapiens]	36	5.0	gnf1m00046_a_at	NM_175215	F830104M21	LysM, putative peptidoglycan-binding, domain containing 4
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) olfactory receptor 1000	37	5.0	gnf1m16896_at		4930521G14	RIKEN cDNA 4930544M13 gene
408	4.0	gnf1m35302_s_at	NM_146437		inferred: ref XP_134089.1 (XM_134089) similar to BRF2, subunit of RNA polymerase III	38	5.0	gnf1m29971_a_at	XM_919543	A930002I23	RIKEN cDNA 4930487N19 gene
409	4.0	gnf1m29806_at			transcription initiation factor, BRF1-like; RNA polymerase III transcription initiation factor BRFU; transcription factor IIB-related factor, TFIIB50 [Mus musculus] mCG2249	39	5.0	gnf1m06245_a_at	NM_138311	E330021E10	H1 histone family, member O, oocyte-specific
410	4.0	gnf1m32553_x_at			inferred: gb AA109445.1 AF309508_1 (AF309508) farnesyl pyrophosphate synthase [Mus musculus] mCG19081	40	5.0	gnf1m03018_a_at	NM_011906	F830032K21	G protein-coupled receptor 175
411	4.0	gnf1m33796_s_at	XM_909258		gene model 392, (NCBI)	41	5.0	gnf1m03110_a_at	NM_013479	10C0031F16	Bcl2-like 10
412	4.0	gnf1m09741_s_at	NM_033580		protocadherin gamma subfamily B, 8	42	5.0	gnf1m00312_a_at	NM_173737	8430410A17	RIKEN cDNA 8430410A17 gene
413	4.0	gnf1m21288_at		D130067L24	unclassifiable	43	5.0	gnf1m33167_at		D630044H03	transmembrane protein 122
414	4.0	gnf1m27913_at		D930007D24	RIKEN cDNA 5430432N15 gene	44	5.0	gnf1m12974_a_at	NM_025723		hypothetical S-adenosyl-L-methionine-dependent methyltransferases structure containing protein
415	4.0	gnf1m03926_a_at	NM_020289	E330019N15	SMAP-1 homolog [Homo sapiens]	45	5.0	gnf1m09902_a_at	NM_053254	F630026I01	transducin-like enhancer of split 6, homolog of Drosophila E(spl)
416	4.0	gnf1m28299_at		4732497C06	MYOSIN-IC homolog [Homo sapiens]	46	5.0	gnf1m07285_at	NM_153106	B020006J20	peptidyl arginine deiminase, type VI
417	4.0	gnf1m07464_at			expressed sequence AU045404	47	4.9	gnf1m30913_a_at	NM_001037725	F630107I23	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 13 (human)
418	4.0	gnf1m32455_at	NM_001033441	G270054A15	transcription factor 15	48	4.9	gnf1m08567_a_at	NM_181345	E330038E07	nucleophosmin/nucleoplasmin 2
419	4.0	gnf1m01833_a_at	NM_009328		cDNA sequence BC032265	49	4.9	gnf1m05952_at	NM_130869		OG2 homeobox gene
420	4.0	gnf1m00045_a_at	NM_181420	9030012M21	RAS protein activator like 2	50	4.9	gnf1m05550_a_at	NM_030236	F830001G13	F-box only protein 34
421	4.0	gnf1m09529_s_at	XM_895716	6530401P13	inferred: ref NP_006959.3 (XM_006959) similar to glyceraldehyde-3-phosphate dehydrogenase (H. sapiens) [Homo sapiens] mCG116319	51	4.9	gnf1m29341_a_at	NM_133225	8430407O11	acyl-Coenzyme A binding domain containing 3
422	4.0	gnf1m33920_at			hypothetical gene supported by AK036329	52	4.9	gnf1m29887_a_at	NM_001004185	B430206J08	WAS protein homology region 2 domain containing 1
423	4.0	gnf1m19870_a_at		9630058G16	regulator of sex-limitation candidate 24	53	4.9	gnf1m12000_at	NM_026434	9530020N09	RNA binding motif protein 18
424	4.0	gnf1m33604_at			hypothetical protein	54	4.9	gnf1m23779_a_at		4930563O14	RIKEN cDNA 4931428L18 gene
425	4.0	gnf1m25020_at		9630006B12	Nfat activating molecule with ITAM motif 1	55	4.9	gnf1m18955_a_at	XM_912265	C730042B03	trophinin associated protein
426	4.0	gnf1m26962_at		I830082K10	discs, large homolog 2 (Drosophila)	56	4.9	gnf1m11490_a_at	NM_018831	4930564M16	DNA cross-link repair 1A, PSO2 homolog (S. cerevisiae)
427	4.0	gnf1m26418_at		B330007M19	cholesterol 25-hydroxylase	57	4.9	gnf1m29609_at	NM_001033452	D930032I15	gene model 1967, (NCBI)
428	4.0	gnf1m02125_a_at	NM_009890	I830084M14	hypothetical protein	58	4.9	gnf1m15784_a_at	NM_027149	10C0032E22	RIKEN cDNA 2310040A13 gene
429	4.0	gnf1m20903_at		B930053K13	inferred: ref NP_001006.1 (NM_001015) ribosomal protein S11; 40S ribosomal protein S11 [Homo sapiens] mCG1043329	59	4.9	gnf1m10026_a_at	NM_134033		cDNA sequence BC025546
430	4.0	gnf1m34527_at			RIKEN cDNA 5330420D20 gene	60	4.9	gnf1m10357_a_at	NM_146215	C730036L12	zygote arrest 1
431	4.0	gnf1m23935_a_at		5330420D20		61	4.9	gnf1m31534_at	NM_174877		polymerase (RNA) II (DNA directed) polypeptide C
No. 3, oocyte specific genes						62	4.9	gnf1m11064_a_at	XM_908461	I920051H06	tripartite motif-containing 61
#1	#2	#3	#4	#5	#6	63	4.9	gnf1m07288_a_at	NM_153110	E330039K03	hypothetical LOC544755
1	6.5	gnf1m30961_a_at	XM_924334	4930486L02	centromere autoantigen F	64	4.9	gnf1m33923_at	XM_908019		polymerase (DNA directed) sigma
2	6.2	gnf1m06748_a_at	NM_146250		G protein-coupled receptor 1	65	4.8	gnf1m30889_at	NM_198600	I830078N12	zinc finger protein 108
3	5.9	gnf1m31660_at	XM_904234		similar to PRAME family member 9	66	4.8	gnf1m17493_a_at		6430525G20	kelch-like 8 (Drosophila)
4	5.8	gnf1m02950_a_at	NM_011775	A430016G17	zona pellucida glycoprotein 2	67	4.8	gnf1m08922_a_at	NM_178741	C330033D17	oogenesis 1
5	5.7	gnf1m21586_at	NM_198674	E330012N03	similar to hypothetical protein E330023O18	68	4.8	gnf1m07815_a_at	NM_178657	E130230E18	2'-5' oligoadenylate synthetase 1C
6	5.6	gnf1m22601_a_at	NM_175011	E330017A01	RIKEN cDNA E330017A01 gene	69	4.8	gnf1m11391_a_at	NM_033541	6430703L12	rotatin
7	5.5	gnf1m08554_a_at	NM_177690	E330007A02	NACHT, leucine rich repeat and PYD containing 2	70	4.8	gnf1m00719_a_at	NM_175542	C330003B14	RIKEN cDNA C330003B14 gene
8	5.5	gnf1m28886_a_at		L230001B22	LIM homeobox protein 8	71	4.8	gnf1m08421_a_at	NM_175342	7420401D15	solute carrier family 45, member 3
9	5.4	gnf1m02951_a_at	NM_011776	2410001F05	zona pellucida glycoprotein 3	72	4.8	gnf1m06657_a_at	NM_145977	B230385P13	inferred: transformed mouse 3T3 cell double minute 4
10	5.4	gnf1m30576_a_at		B930099F18	unclassifiable	73	4.8	gnf1m26416_a_at			suppressor of cytokine signaling 7 (Socs7)
11	5.4	gnf1m34191_a_at	NM_198960		transcription factor AP-2, epsilon	74	4.8	gnf1m18392_at	NM_138657	MSC1099J02	ubiquitin specific protease 19
12	5.3	gnf1m28752_at	XM_920480		similar to Na+ dependent glucose transporter 1	75	4.8	gnf1m25972_a_at		5830457H01	expressed sequence A1847670
13	5.3	gnf1m11368_at	NM_009757	B020029E15	bone morphogenetic protein 15	76	4.8	gnf1m19345_a_at	NM_177869	9430087D06	RIKEN cDNA 1200011M11 gene
14	5.2	gnf1m01178_a_at	NM_008110	7420463G17	growth differentiation factor 9	77	4.8	gnf1m04415_a_at	NM_024262	4931409P07	serine/threonine kinase 36 (fused homolog, Drosophila)
15	5.2	gnf1m16093_at	NM_033320	1110017N23	glucuronyl C5-epimerase	78	4.8	gnf1m18629_a_at	NM_175031	4932427F05	mutS homolog 4 (E. coli)
16	5.2	gnf1m11848_a_at	NM_133353	7420700J01	oocyte secreted protein	79	4.8	gnf1m05690_a_at	NM_031870	4022413I18	helicase, mus308-like (Drosophila)
17	5.2	gnf1m30527_at	NM_001033283	E330030M12	gene model 97, (NCBI)	80	4.8	gnf1m30352_at	XM_920772		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
18	5.2	gnf1m23490_at		4631433P05	vesicle transport through interaction with t-SNAREs 1 homolog	81	4.8	gnf1m09619_a_at			TBC1 domain family, member 14 unclassifiable
19	5.2	gnf1m08558_a_at	NM_173773	E330017M15	oogenesis 4	82	4.8	gnf1m06095_at	NM_133910	C730018N17	T-cell leukemia/lymphoma 1B, 1
20	5.1	gnf1m21562_a_at	XM_920526	E130318K11	uracil DNA glycosylase 2	83	4.8	gnf1m21164_at		7420471I21	ret finger protein-like 4
21	5.1	gnf1m15535_a_at	NM_026849	9430051D16	RIKEN cDNA 1110061O04 gene	84	4.8	gnf1m03279_a_at	NM_013773	B020005E07	unclassifiable
22	5.1	gnf1m04710_a_at	NM_025819	1200016B10	RIKEN cDNA 1200016B10 gene	85	4.8	gnf1m06295_a_at	NM_138954	6720407O05	hypothetical protein LOC382106
23	5.1	gnf1m31175_at		B020005F19	cDNA sequence BC052883	86	4.8	gnf1m19491_at		11C0008P04	RIKEN cDNA 2410146L05 gene
24	5.1	gnf1m02992_a_at	NM_011860	E330019F16	NACHT, leucine rich repeat and PYD containing 5	87	4.8	gnf1m30703_at	NM_001013776	B020039D12	B-cell translocation gene 4
25	5.1	gnf1m13260_a_at		B020030M24	T-cell lymphoma breakpoint 1	88	4.8	gnf1m09805_a_at	NM_026480	9330189K18	AT rich interactive domain 1B (Swi1 like)
26	5.1	gnf1m22609_a_at	NM_001033214	E330034G19	RIKEN cDNA E330034G19 gene	89	4.8	gnf1m07508_a_at	NM_019493		selected mouse cDNA on the X chromosome-like
27	5.1	gnf1m01972_a_at			zona pellucida glycoprotein 1	90	4.8	gnf1m19037_at	XM_898196	E330024M09	NACHT, leucine rich repeat and PYD containing 4B
28	5.1	gnf1m08559_a_at	NM_177571	E330017N17	hypothetical protein E330017N17	91	4.7	gnf1m29491_a_at	XM_910498	E330001M05	F-box and WD-40 domain protein 15
29	5.1	gnf1m09667_a_at	XM_917102	A430083E15	nucleoporin 214	92	4.7	gnf1m07705_a_at	NM_172815	4921524I17	RIKEN cDNA 4921524I17 gene
30	5.0	gnf1m08557_a_at	NM_177598	E330017E16	F-box and WD-40 domain protein 13	93	4.7	gnf1m10718_a_at	NM_026123	4921524I17	RIKEN cDNA 4921524I17 gene
31	5.0	gnf1m17214_s_at	NM_028387	4831410G10	RIKEN cDNA 2900006F19 gene	94	4.7	gnf1m24532_at	XM_893519	E330021D16	RIKEN cDNA E330021D16 gene
32	5.0	gnf1m08926_s_at	NM_175127	7420450G03	F-box protein 28	95	4.7	gnf1m07955_at	XM_175017	2810012H18	coiled-coil domain containing 6
33	5.0	gnf1m09326_a_at	NM_178892	4632422G22	TCDD-inducible poly(ADP-ribose) polymerase	96	4.7	gnf1m22904_x_at		2810040O04	zinc fingerprotein 618
34	5.0	gnf1m32851_at			ENSMUST00000074244 transcript (in rel.37.34e)	97	4.7	gnf1m01197_a_at	NM_008154	1920086F14	cullin 1
						98	4.7	gnf1m26814_at		9530064F18	phospholipase C, epsilon 1
						99	4.7	gnf1m23266_at		1500026F15	RIKEN cDNA 2810453I06 gene
						100	4.7	gnf1m08564_at	NM_172481	I920020H01	protein tyrosine phosphatase, receptor type, f polypeptide
						101	4.7	gnf1m22590_a_at	NM_199036		
						102	4.7	gnf1m04662_a_at	NM_025722		
						103	4.7	gnf1m33573_at	XM_908434		
						104	4.7	gnf1m08561_a_at	NM_175527		
						105	4.7	gnf1m16575_at	XM_908442		
						106	4.7	gnf1m28911_a_at	XM_910582		
						107	4.7	gnf1m10862_at	NM_012042		
						108	4.7	gnf1m03748_a_at	NM_019588		
						109	4.7	gnf1m13397_a_at			
						110	4.7	gnf1m29470_a_at	XM_925577		

				(PTPRF), interacting protein, alpha 1	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
111	4.7	gnf1m05164_a_at	NM_027411	B020004G07	RIKEN cDNA 2600001J17 gene				C430003L11	A kinase (PRKA) anchor protein 10
112	4.7	gnf1m17612_s_at	XM_906226	A930011E11	RIKEN cDNA 1110065L07 gene				C130097O10	cat eye syndrome chromosome region, candidate 2 homolog (human)
113	4.7	gnf1m09787_a_at	NM_027422	F630102P07	RIKEN cDNA 2700087H15 gene	183	4.4	gnf1m17498_a_at	NM_019921	
114	4.7	gnf1m28697_a_at	NM_007562	E230006C08	basoonclin 1	184	4.4	gnf1m26841_at	XM_925276	
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	185	4.4	gnf1m15929_a_at		D130020G02
117	4.6	gnf1m00615_a_at	NM_181417	E430020F17	cysteine and glycine-rich protein 2 binding protein	186	4.4	gnf1m03281_a_at	NM_013774	2010012K22
118	4.6	gnf1m00374_s_at	XM_897204		ring finger and WD repeat domain 2	187	4.4	gnf1m07986_a_at	NM_177475	6030407P18
119	4.6	gnf1m08562_at	NM_177187	E330023J07	DNA segment, Chr 5, ERATO Doi 577, expressed	188	4.4	gnf1m03899_a_at	NM_020021	4930571D16
120	4.6	gnf1m00395_at	NM_027802	7420700M11	oocyte specific homeobox 1	189	4.4	gnf1m02798_a_at	NM_011420	1830076M14
121	4.6	gnf1m13138_a_at	NM_008316	E430014O06	Hus1 homolog (S. pombe)	190	4.4	gnf1m24615_s_at	NM_027804	G430007B02
122	4.6	gnf1m32478_at	XM_915014		similar to transcription elongation factor B (SIII), polypeptide 2	191	4.4	gnf1m29820_a_at	NM_028986	E130002P16
123	4.6	gnf1m31294_a_at	XM_918100	B020004A05	oocyte maturation, beta	192	4.4	gnf1m10228_a_at	NM_027409	E430009I24
124	4.6	gnf1m00103_a_at	NM_010021	8030454H23	deleted in azoospermia-like	193	4.4	gnf1m30438_at		
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	194	4.4	gnf1m00322_a_at	NM_010786	1700007J15
127	4.6	gnf1m16358_at	XM_131719	2310047N01	D164 sialomucin-like 2	195	4.4	gnf1m03577_a_at	NM_017475	I830015H15
128	4.6	gnf1m20390_at		A630050C01	3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630050C01	196	4.4	gnf1m04540_a_at	NM_025446	2010012K22
					product:unclassifiable, full insert sequence	197	4.4	gnf1m26226_a_at	NM_010804	M5C1026B14
129	4.6	gnf1m28846_a_at	NM_001024919	2310022M17	RIKEN cDNA 2310022M17 gene	198	4.4	gnf1m28277_at	NM_015793	10C0037J19
130	4.6	gnf1m30531_at	XM_925541	6430548M15	TAO kinase 1	199	4.4	gnf1m04652_a_at	NM_025706	4932416D24
131	4.6	gnf1m29070_a_at	XM_916714	2700049A03	RIKEN cDNA 2700049A03 gene	200	4.4	gnf1m03686_a_at	NM_019434	F430004B09
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	201	4.4	gnf1m16265_a_at	NM_027091	I1C0042E05
134	4.6	gnf1m24830_at		9430024M13	bone morphogenetic protein 5	202	4.4	gnf1m08496_a_at	NM_172631	D330030L18
135	4.6	gnf1m13090_x_at	NM_178894	E330015L10	expressed sequence AA792892					
136	4.6	gnf1m17453_at	NM_026127		RIKEN cDNA 4833420G17 gene	203	4.4	gnf1m30830_at		10C0042K12
137	4.6	gnf1m06466_at	NM_145228		2'-5' oligoadenylate synthetase 1H					
138	4.6	gnf1m13147_at	NM_025699	1700081J12	RIKEN cDNA 3230401D17 gene	204	4.4	gnf1m29271_at	XM_620267	
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	205	4.4	gnf1m28716_a_at	NM_001024135	1110008P08
141	4.6	gnf1m30873_a_at	XM_921247	C130001D11	C1q domain containing 1	206	4.4	gnf1m10172_a_at	NM_175311	F630008H06
142	4.6	gnf1m04413_a_at	NM_024242	I830082O20	RIO kinase 1 (yeast)	207	4.4	gnf1m10001_a_at	XM_919590	I530009P20
143	4.6	gnf1m08791_a_at	NM_177069	E330009P21	RIKEN cDNA E330009P21 gene					
144	4.6	gnf1m30989_s_at		E230016M20	unclassifiable	208	4.4	gnf1m04940_a_at	NM_026371	I830028E01
145	4.6	gnf1m33640_at	NM_001033794	7420486K21	expressed sequence C85627					
146	4.6	gnf1m29704_a_at	NM_175201	M5C1088B21	ring finger protein 38	209	4.4	gnf1m01752_a_at		A930023B20
147	4.5	gnf1m10238_a_at	NM_026758	1110001M01	M phase phosphoprotein 6	210	4.4	gnf1m14492_a_at		0610033M10
148	4.5	gnf1m05458_s_at	NM_029416	B020023K24	Kruppel-like factor 17	211	4.4	gnf1m19616_at		E330037N21
149	4.5	gnf1m00097_a_at	NM_007623	D030003P20	chromobox homolog 2 (Drosophila Pc class)	212	4.4	gnf1m32413_at		E330012K05
150	4.5	gnf1m02661_a_at	NM_011137	C230064N08	POU domain, class 2, transcription factor 1	213	4.4	gnf1m32052_at		
151	4.5	gnf1m04400_a_at	NM_024213	I920062N18	anaphase promoting complex subunit 4	214	4.4	gnf1m11620_a_at	NM_146170	B930024K20
152	4.5	gnf1m29650_a_at	NM_027314	4933422F17	membrane-associated ring finger (C3HC4) 5	215	4.4	gnf1m10590_a_at	NM_025482	G270079P12
153	4.5	gnf1m25673_a_at		A430110I16	splicing factor 3b, subunit 3	216	4.4	gnf1m08924_a_at	NM_172615	F630032M11
154	4.5	gnf1m14863_at		6530413F01	rabphilin 3A-like (without C2 domains)	217	4.4	gnf1m04292_s_at	NM_023233	5730562C12
155	4.5	gnf1m10061_a_at	NM_024254	I920040K15	RIKEN cDNA 2410042D21 gene	218	4.4	gnf1m06456_a_at	NM_145210	E330025J23
156	4.5	gnf1m30810_at	NM_001024205		nuclear fragile X mental retardation protein interacting protein 2	219	4.4	gnf1m29561_a_at	XM_920199	2310030K10
157	4.5	gnf1m34888_at	NM_001025564		hypothetical LOC217066	220	4.4	gnf1m10533_a_at	NM_007892	F830048D09
158	4.5	gnf1m06037_a_at	NM_133701	I1C0020L10	RIKEN cDNA 2610031L17 gene	221	4.4	gnf1m01750_a_at	NM_009173	
159	4.5	gnf1m10356_s_at	XM_900102	B020015A14	oocyte specific homeobox 1	222	4.3	gnf1m02052_a_at	NM_009765	4930451K22
160	4.5	gnf1m20977_a_at		E230001J08	unclassifiable	223	4.3	gnf1m09271_a_at	NM_175290	C330026N02
161	4.5	gnf1m11659_a_at	NM_026075	6820402F12	RIKEN cDNA 3110031B13 gene	224	4.3	gnf1m23122_at		1190002G15
162	4.5	gnf1m29621_at		C530010F03	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	225	4.3	gnf1m00510_a_at	NM_178375	4921517A06
163	4.5	gnf1m00544_a_at	NM_172766	C630001A18	nuclear factor related to kappa B binding protein	226	4.3	gnf1m09790_a_at	NM_133700	1110056N09
164	4.5	gnf1m05520_a_at	NM_029846	5830475I01	autophagy-related 16-like 1 (yeast)	227	4.3	gnf1m23273_at		2410038P04
165	4.5	gnf1m13096_a_at	NM_177703	E330023O18	F-box and WD-40 domain protein 19	228	4.3	gnf1m01431_a_at	NM_008589	I920048L22
166	4.5	gnf1m33881_at			inferred: ref XP_033028.2 (XM_033028) hypothetical protein XP_033028 [Homo sapiens]	229	4.3	gnf1m16922_a_at		2610312O17
167	4.5	gnf1m32651_x_at	NM_001008428	7420476B15	F-box and WD-40 domain protein 12	230	4.3	gnf1m08043_at	NM_172539	7420700F21
168	4.5	gnf1m09601_a_at	XM_925665	6230429P11	inhibitor of Bruton agammaglobulinemia tyrosine kinase	231	4.3	gnf1m22236_at	XM_914443	D030047E23
169	4.5	gnf1m06558_a_at	NM_145546	I920073J21	general transcription factor IIB	232	4.3	gnf1m31151_at	NM_001024917	7420471K04
170	4.5	gnf1m24244_a_at	NM_198010	A730093D16	ankyrin repeat domain 17	233	4.3	gnf1m02110_a_at	NM_009862	I920087J24
171	4.5	gnf1m16106_a_at	NM_028040	F830031C20	RNA pseudouridylylate synthase domain containing 4	234	4.3	gnf1m10724_at	NM_008692	
172	4.5	gnf1m04995_a_at	NM_026518	I920096N10	ring finger protein 146	235	4.3	gnf1m11802_a_at	NM_026119	I1C0025D15
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	236	4.3	gnf1m21764_at		7420444D12
175	4.5	gnf1m04980_a_at	NM_026479	F630001B12	zinc finger, CCHC domain containing 10	237	4.3	gnf1m12383_a_at	NM_011135	I920091F11
176	4.5	gnf1m05034_a_at	NM_026643	2810011I24	RIKEN cDNA 2410017P07 gene	238	4.3	gnf1m31112_a_at	XM_921951	
177	4.5	gnf1m25771_at		A530093J23	immunoglobulin heavy chain 4 (serum IgG1)	239	4.3	gnf1m16919_a_at	NM_197988	1190005I06
178	4.5	gnf1m05945_a_at	NM_130796	2810421C03	sorting nexin associated golgi protein 1	240	4.3	gnf1m22196_a_at	NM_001012517	I920184K22
179	4.5	gnf1m05268_a_at	NM_028106	7420443B10	zinc finger, BED domain containing 3	241	4.3	gnf1m26369_at		F630207C02
						242	4.3	gnf1m17429_at		G430047K14
						243	4.3	gnf1m10284_a_at	NM_138585	G630022O12
						244	4.3	gnf1m30600_a_at	XM_909322	9630037P07
						245	4.3	gnf1m02902_a_at	NM_011657	
						246	4.3	gnf1m09991_a_at		C530022J18
										hypothetical Lipocalin-related protein and Bos/Can/Equ allergen containing protein

247	4.3	gnflm33427_at	XM_916262	gene model 527, (NCBI)	314	4.1	gnflm13596_at	2310046A20	SUMO1/sentrin specific peptidase 1	
248	4.3	gnflm17639_at		C730032N23 ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	315	4.1	gnflm07475_a_at	NM_009764	breast cancer 1	
249	4.3	gnflm23284_at		2510005J23 peroxisome biogenesis factor 7	316	4.1	gnflm34058_x_at		inferred: ref XP_033028.2 (XM_033028) hypothetical protein XP_033028 [Homo sapiens] mCG114037	
250	4.3	gnflm29280_a_at	NM_080561	F630024P17 RIKEN cDNA 2810055G22 gene						
251	4.3	gnflm23463_a_at	NM_181650	4022401E08 PR domain containing 4						
252	4.3	gnflm10004_a_at	NM_027930	2610016C23 RIKEN cDNA 2610016C23 gene						
253	4.3	gnflm29158_at	NM_175025	B230348M20 ATPase, Ca++-sequestering	317	4.1	gnflm07227_a_at	NM_148932	F630037F14 nuclear pore membrane protein 121	
254	4.3	gnflm22577_a_at	NM_001013377	E130306D19 RIKEN cDNA E130306D19 gene	318	4.1	gnflm07979_a_at	NM_176953	G370012I03 ligase IV, DNA, ATP-dependent	
255	4.3	gnflm16871_a_at		F830023N07 nuclear transcription factor-Y alpha	319	4.1	gnflm10740_a_at	NM_016812	F630207G02 Btg3 associated nuclear protein	
256	4.3	gnflm08574_a_at	NM_177088	4732496G21 coiled-coil domain containing 45	320	4.1	gnflm04731_a_at	NM_025853	1700022L09 RIKEN cDNA 1700022L09 gene	
257	4.3	gnflm30114_a_at	NM_172516	C230050J24 receptor interacting protein kinase 5	321	4.1	gnflm30701_a_at	XM_884388	1700124P09 RIKEN cDNA 1700124P09 gene	
258	4.3	gnflm22661_a_at		F630005A19 zinc finger protein 341	322	4.1	gnflm15204_at	XM_900053	D330023N06 IQ motif containing GTPase activating protein 3	
259	4.3	gnflm16223_a_at	XM_917330	2810407P21 similar to Exocyst complex component Sec3	323	4.1	gnflm33239_at	XM_924746	DNA segment, Chr 16, ERATO Doi 519, expressed	
260	4.3	gnflm30451_a_at	NM_180599	F630202N16 microfilibrillar-associated protein 3 spastin	324	4.1	gnflm30159_a_at	NM_172151	6330570D04 zinc finger, DHHC domain containing 8	
261	4.3	gnflm28732_at		inferred: gb AAH19848.1 AAH19848 (BC019848) Similar to cactin [Homo sapiens] mCG3280	325	4.1	gnflm02838_a_at	NM_011513	G730029C15 surfeit gene 5	
262	4.3	gnflm32185_at			326	4.1	gnflm27845_a_at	NM_178640	I830149D05 UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 2	
263	4.3	gnflm27008_at		C330045B02 unclassifiable	327	4.1	gnflm30756_at	XM_887622	similar to chromosome 6 open reading frame 148	
264	4.3	gnflm12897_a_at	NM_172405	D230004N03 RIKEN cDNA 3830405G04 gene	328	4.1	gnflm29966_a_at	XM_917146	zinc finger protein 664	
265	4.2	gnflm22595_a_at	NM_001033211	I0C0046K11 expressed sequence A022751	329	4.1	gnflm03272_a_at	NM_013757	5330428N11 synaptotagmin-like 4	
266	4.2	gnflm13695_at		E130119J07 RIKEN cDNA E130119J07 gene	330	4.1	gnflm01949_a_at	NM_009534	I920028O19 yes-associated protein 1	
267	4.2	gnflm00710_a_at	NM_023729	4933400N19 ankyrin repeat, SAM and basic leucine zipper domain containing 1	331	4.1	gnflm10346_a_at	XM_911042	4930533G20 F-box protein 43	
268	4.2	gnflm08318_a_at	NM_172746	G730029A12 peptidylprolyl isomerase (cyclophilin) like 5	332	4.1	gnflm28959_a_at	XM_908452	tripartite motif protein 33	
269	4.2	gnflm10411_a_at		Zinc finger protein 212	333	4.1	gnflm01799_a_at	NM_009269	6030452M19 serine palmitoyltransferase, long chain base subunit 1	
270	4.2	gnflm09585_a_at	NM_145576	inferred: gb AAH11820.1 AAH11820 (BC011820) Unknown (protein for IMAGE:3619501) [Homo sapiens] mCG12659	334	4.1	gnflm05891_a_at	NM_057173	5330410G07 LIM domain only 1	
271	4.2	gnflm32800_at			335	4.1	gnflm17216_s_at	NM_019923	A530039D21 inositol 1,4,5-triphosphate receptor 2	
					336	4.1	gnflm31649_at	NM_194056	I0C0021D08 NACHT, LRR and PYD containing protein 9a	
					337	4.1	gnflm12593_a_at	NM_016769	C630019N20 MAD homolog 3 (Drosophila)	
272	4.2	gnflm27711_at		D430026H23 phospholipase A2, activating protein	338	4.1	gnflm03856_a_at	NM_019941	zinc finger protein 235	
273	4.2	gnflm18473_at	XM_922117	C230071E20 RIKEN cDNA 4933421B21 gene	339	4.1	gnflm24294_at		6330442G23 hypothetical Cysteine-rich region profile containing protein	
274	4.2	gnflm09634_a_at	NM_029337	C820012F11 E1A binding protein p400	340	4.1	gnflm10565_a_at	NM_023153	1730099H06 RIKEN cDNA 0610040D20 gene	
275	4.2	gnflm06127_a_at	NM_134017	2410018D16 methionine adenosyltransferase II, beta	341	4.1	gnflm21846_a_at	NM_175016	9530023G02 alkB, alkylation repair homolog 2 (E. coli)	
276	4.2	gnflm00299_a_at	NM_030743	I830162O14 zinc finger protein 313	342	4.1	gnflm09548_a_at	NM_146068	I530027A02 RIKEN cDNA 2310008H04 gene	
277	4.2	gnflm31045_at		C130054M03 RIKEN cDNA A630007B06 gene	343	4.1	gnflm16585_at	XM_906311	B230314J02 hexamethylene bis-acetamide inducible 2	
278	4.2	gnflm02434_a_at	NM_010600	M5C1047E09 potassium voltage-gated channel, subfamily H (eag-related), member 1	344	4.1	gnflm05274_a_at	NM_028142	2810405F18 NOL1/NOP2/Sun domain family, member 4	
279	4.2	gnflm22176_at		C330011L24 DNA segment, Chr 8, ERATO Doi 587, expressed	345	4.1	gnflm23755_a_at		4930511P18 RIKEN cDNA G630039H03 gene	
280	4.2	gnflm30307_at	XM_920356	B020013L18 IQ motif containing with AAA domain	346	4.1	gnflm03428_a_at	NM_016688	F630118J21 programmed cell death protein 7	
281	4.2	gnflm20990_s_at	XM_923034	C130034K06 RIKEN cDNA A430041B07 gene	347	4.1	gnflm03280_s_at	NM_013775	B020004B10 T-cell leukemia/lymphoma 1B, 1	
282	4.2	gnflm13082_a_at	NM_028730	I530018A10 peroxisome biogenesis factor 26	348	4.0	gnflm11638_a_at	NM_023239	C530046P15 necdin-like 2	
283	4.2	gnflm16087_a_at	NM_027560	G630019P16 arrestin domain containing 2	349	4.0	gnflm05006_a_at	NM_026557	9030406D12 ring finger and CHY zinc finger domain containing 1	
284	4.2	gnflm09291_a_at	NM_026780	1110018L13 SYF2 homolog, RNA splicing factor (S. cerevisiae)	350	4.0	gnflm11525_a_at	NM_053180	4932702G04 cell cycle related kinase	
285	4.2	gnflm03255_a_at	NM_013719	2610011M03 eukaryotic translation initiation factor 2 alpha kinase 4	351	4.0	gnflm06090_a_at	NM_133886	4933403J17 expressed sequence AU040320	
286	4.2	gnflm09536_a_at	NM_027263	2810407L01 RIKEN cDNA 2610040C18 gene	352	4.0	gnflm06007_at		Mouse expressed sequence AA407930 (AA407930), mRNA	
287	4.2	gnflm18666_a_at	NM_028916	4921508G15 EF-hand domain (C-terminal) containing 2	353	4.0	gnflm24959_a_at	NM_001001144	I920039J23 SREBP cleavage activating protein	
288	4.2	gnflm05250_a_at	NM_028034	7420437I06 RIKEN cDNA 2410004F06 gene	354	4.0	gnflm33641_at		7420420A09 similar to F-box- and WD40-repeat-containing protein	
289	4.2	gnflm16623_at	XM_914303	2610024M03 protein phosphatase 1, regulatory subunit 3D	355	4.0	gnflm11061_s_at	NM_026949	I830015C07 CCR4-NOT transcription complex, subunit 8	
290	4.2	gnflm05539_a_at	NM_030153	A330021G12 MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)	356	4.0	gnflm06752_at	NM_146258	serologically defined colon cancer antigen 13	
291	4.2	gnflm30027_at	XM_924076	TAF4A RNA polymerase II, TATA box binding protein (TBP)-associated factor	357	4.0	gnflm11526_a_at	NM_025979	1700028B20 microtubule associated serine/threonine kinase-like	
292	4.2	gnflm15775_a_at	NM_183149	A430092M15 zinc finger protein 598	358	4.0	gnflm12215_a_at	NM_144884	C430047K18 torsin family 1, member A (torsin A)	
293	4.2	gnflm06473_a_at	NM_145371	E430003B07 eukaryotic translation initiation factor 2B, subunit 1 (alpha)	359	4.0	gnflm30421_a_at	NM_178115	2700050L05 RIKEN cDNA 2700050L05 gene	
294	4.2	gnflm16582_at		4930481B07 RIKEN cDNA 4930481B07 gene	360	4.0	gnflm00567_a_at	NM_027654	F630119D13 polycomb group ring finger 6	
295	4.2	gnflm26268_a_at	NM_025747	B130055N05 RIKEN cDNA 4933411K20 gene	361	4.0	gnflm29753_a_at	NM_199196	E430023E10 suppressor of zeste 12 homolog (Drosophila)	
296	4.2	gnflm08556_s_at	XM_898812	E330015L10 expressed sequence AA792892	362	4.0	gnflm11045_at	NM_024183	C530024M13 FIP1 like 1 (S. cerevisiae)	
297	4.2	gnflm17779_s_at		B930054M11 unclassifiable	363	4.0	gnflm18741_s_at	NM_029334	C730029A09 RIKEN cDNA 2700069A02 gene	
298	4.2	gnflm06092_x_at	NM_133893	E330028E06 2'-5' oligoadenylate synthetase 1D	364	4.0	gnflm26345_a_at		B230323K17 WD repeat domain 33	
299	4.2	gnflm03965_s_at	XM_913263	hypothetical protein LOC635251	365	4.0	gnflm06720_a_at	NM_146169	cDNA sequence BC017133	
300	4.2	gnflm31661_at	XM_910255	aurora kinase C	366	4.0	gnflm26990_a_at	NM_015732	D330025A07 axin2	
301	4.2	gnflm12239_a_at	NM_177672	K530042E13 DNA segment, Chr 4, ERATO Doi 429, expressed	367	4.0	gnflm01318_a_at	NM_008389	I700023J10 IAP promoted placental gene	
302	4.2	gnflm24029_at		5730547A05 nucleoporin 62	368	4.0	gnflm01059_a_at	NM_007916	I920024M01 DEAD (Asp-Glu-Ala-Asp) box polypeptide 19a	
303	4.2	gnflm29590_a_at		4631426G04 zinc finger CCCC type containing 6	369	4.0	gnflm05140_a_at	NM_027213	F830011B05 mediator of RNA polymerase II transcription, subunit 6 homolog (yeast)	
304	4.2	gnflm11119_at	NM_010754	1810047O14 MAD homolog 2 (Drosophila)	370	4.0	gnflm15900_a_at	NM_177471	F630113O12 coiled-coil domain containing 69	
305	4.2	gnflm05931_a_at	NM_080848	4432406L10 WD repeat domain 5	371	4.0	gnflm04859_a_at	NM_026173	I830013E02 RIKEN cDNA 1200014M14 gene	
306	4.2	gnflm27190_a_at		C730023J07 leucine rich repeat containing 28	No. 4, fertilized egg specific genes					
307	4.2	gnflm08745_at	NM_177450	D630009N02 carnosine dipeptidase 1 (metallopeptidase M20 family)	#1	#2	#3	#4	#5	#6
308	4.2	gnflm31009_a_at	NM_013910	2810055D04 F-box and leucine-rich repeat protein 10	1	5.2	gnflm30527_at	NM_001033283	E330030M12 gene model 97, (NCBI)	
309	4.2	gnflm30183_at		inferred: ref XP_088331.1 (XM_088331) hypothetical protein XP_088331 [Homo sapiens] mCG2510	2	5.2	gnflm01178_a_at	NM_008110	7420463G17 growth differentiation factor 9	
					3	5.2	gnflm10718_a_at	NM_026123	4922505F15 unc-50 homolog (C. elegans)	
					4	5.2	gnflm22609_a_at	NM_001033214	E330034G19 RIKEN cDNA E330034G19 gene	
					5	5.2	gnflm13260_a_at		B020030M24 T-cell lymphoma breakpoint 1	
					6	5.2	gnflm11848_a_at	NM_133353	7420700J01 oocyte secreted protein 1	
					7	5.1	gnflm11620_a_at	NM_146170	B930024K20 expressed sequence C87436	
					8	5.1	gnflm23026_s_at		G730030D09 PAP associated domain containing 1	
310	4.1	gnflm02731_a_at	NM_011293	polymerase (RNA) II (DNA directed) polypeptide J	9	5.1	gnflm18955_a_at	XM_912265	C730042B03 trophinin associated protein	
311	4.1	gnflm21264_a_at	XM_913342	D130048N15 Similar to RIKEN cDNA B430319H21 gene	10	5.1	gnflm29491_a_at	XM_910498	I830007N16 RIKEN cDNA 2700029M09 gene	
312	4.1	gnflm16129_a_at	NM_011919	I1C0015D22 inhibitor of growth family, member 1	11	5.1	gnflm11659_a_at	NM_026075	6820402F12 RIKEN cDNA 3110031B13 gene	
313	4.1	gnflm01576_a_at	NM_008838	F630222N08 phosphatidylinositol glycan, class F	12	5.1	gnflm09326_a_at	NM_178892	4632422G22 TCDD-inducible poly(ADP-ribose) polymerase	
					13	5.1	gnflm11490_a_at	NM_018831	4930564M16 DNA cross-link repair 1A, PSO2	

55/97

170	4.4	gnflm29070_a_at	XM_916714	2700049A03	RIKEN cDNA 2700049A03 gene	240	4.2	gnflm01799_a_at	NM_009269	6030452M19	serine palmitoyltransferase, long chain base subunit 1
171	4.4	gnflm09790_a_at	NM_133700	1110056N09	BTB (POZ) domain containing 10	241	4.2	gnflm06095_at	NM_133910		TBC1 domain family, member 14
172	4.4	gnflm28277_at	NM_015793	I0C0037J19	F-box and WD-40 domain protein 14	242	4.2	gnflm33427_at	XM_916262		gene model 527, (NCBI)
173	4.4	gnflm33167_at			transmembrane protein 122	243	4.2	gnflm30438_at			inferred:
174	4.4	gnflm29561_a_at	XM_920199	2310030K10	ADP-ribosylation factor interacting protein 1						gb AAH19796.1 AAH19796
175	4.4	gnflm34191_at	NM_198960		transcription factor AP-2, epsilon	244	4.2	gnflm00998_a_at	NM_007810	E330007H14	cytochrome P450, family 19,
176	4.4	gnflm32478_at	XM_915014		similar to transcription elongation factor B (SIII), polypeptide 2	245	4.2	gnflm29820_a_at	NM_028986	E130002P16	subfamily a, polypeptide 1
177	4.4	gnflm17429_at		7420447K14	RIKEN cDNA 6330416L11 gene	246	4.2	gnflm30531_at	XM_925541	6430548M15	zinc finger protein 336
178	4.4	gnflm11118_a_at	NM_009226	2810410O03	small nuclear ribonucleoprotein D1	247	4.2	gnflm04292_s_at	NM_023233	5730562C12	TAO kinase 1
179	4.4	gnflm06473_a_at	NM_145371	E430003B07	eukaryotic translation initiation factor 2B, subunit 1 (alpha)	248	4.2	gnflm24546_at		7420451F24	tripartite motif protein 13
180	4.4	gnflm00374_s_at	XM_897204		ring finger and WD repeat domain 2	249	4.2	gnflm12282_s_at		F730045M14	cleavage stimulation factor, 3' pre-RNA, subunit 1
181	4.4	gnflm19037_a_at	XM_898196	9330189K18	AT rich interactive domain 1B (Swi1 like)	250	4.2	gnflm28716_a_at	NM_001024135	1110008P08	zinc finger protein, subfamily 1A, 4 (Eos)
182	4.4	gnflm10533_a_at	NM_007892	F830048D09	E2F transcription factor 5	251	4.2	gnflm03255_a_at	NM_013719	2610011M03	kelch repeat and BTB (POZ) domain containing 7
183	4.3	gnflm31543_at	XM_906832		hypothetical protein LOC623166	252	4.2	gnflm11385_a_at	NM_009343	G730035E18	eukaryotic translation initiation factor 2 alpha kinase 4
184	4.3	gnflm04652_a_at	NM_025706	4932416D24	TBC1 domain family, member 15	253	4.2	gnflm14025_at		2530002E12	PHD finger protein 1
185	4.3	gnflm12239_a_at	NM_177672	K530042E13	DNA segment, Chr 4, ERATO Doi 429, expressed	254	4.2	gnflm29590_a_at		4631426G04	SAM and SH3 domain containing 1
186	4.3	gnflm17449_at	NM_027839	9130012D09	CEA-related cell adhesion molecule 20	255	4.2	gnflm03351_a_at	NM_013917	E430014I06	zinc finger CCHC type containing 6
187	4.3	gnflm30307_at	XM_920356	B020013L18	IQ motif containing with AAA domain	256	4.2	gnflm05507_a_at	NM_029790	0610027B03	pituitary tumor-transforming 1 methyltransferase 5 domain containing 1
188	4.3	gnflm29621_at		C530010F03	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	257	4.2	gnflm09202_s_at	XM_908127		protein phosphatase 1, regulatory subunit 10
189	4.3	gnflm29971_a_at	XM_919543	A930002I23	RIKEN cDNA 4930487N19 gene	258	4.2	gnflm11754_a_at	NM_007563	F830003N05	2,3-bisphosphoglycerate mutase
190	4.3	gnflm29650_a_at	NM_027314	4933422F17	membrane-associated ring finger (C3HC4) 5	259	4.2	gnflm08496_a_at	NM_172631	D330030L18	DNA segment, Chr 18, ERATO Doi 653, expressed
191	4.3	gnflm17216_s_at	NM_019923	A530039D21	inositol 1,4,5-triphosphate receptor 2	260	4.2	gnflm08318_a_at	NM_172746		HIRA interacting protein 3
192	4.3	gnflm04779_a_at		2900001A12	ankyrin repeat domain 12	261	4.2	gnflm30473_at	XM_923664		cDNA sequence BC066140
193	4.3	gnflm16871_a_at		F830023N07	nuclear transcription factor-Y alpha	262	4.2	gnflm13082_a_at	XM_028730	I530018A10	peroxisome biogenesis factor 26
194	4.3	gnflm28697_a_at	NM_007562	E230006C08	basoonclin 1	263	4.1	gnflm01097_a_at	NM_007970	F630047M06	enhancer of zeste homolog 1 (Drosophila)
195	4.3	gnflm12833_a_at			general transcription factor IIIC, polypeptide 2, beta	264	4.1	gnflm28911_a_at	XM_910582	2810040O04	zinc fingerprotein 618
196	4.3	gnflm22973_at	NM_025431	1190005P17	RIKEN cDNA 1190005P17 gene	265	4.1	gnflm25413_a_at	XM_029998	I830054I11	RIKEN cDNA 6030458C11 gene
197	4.3	gnflm29271_at	XM_620267		similar to hypothetical protein FLJ20397	266	4.1	gnflm16265_a_at	NM_027091	I1C0042E05	nucleoporin 35
198	4.3	gnflm03899_a_at	NM_020021	4930517D16	Moloney sarcoma oncogene	267	4.1	gnflm20990_s_at	XM_923034	C130034K06	RIKEN cDNA A430041B07 gene
199	4.3	gnflm05945_a_at	NM_130796	2810421C03	sorting nexin associated golgi protein 1	268	4.1	gnflm01059_a_at	XM_007916	I920024M01	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19a
200	4.3	gnflm12897_a_at	NM_172405	D230004N03	RIKEN cDNA 3830405G04 gene	269	4.1	gnflm08043_at	NM_172539	7420700F21	astacin-like metalloendopeptidase (M12 family)
201	4.3	gnflm04940_a_at	NM_026371	I830028E01	loss of heterozygosity, 12, chromosomal region 1 homolog (human)	270	4.1	gnflm23266_at		F830027O21	chromodomain protein, Y chromosome-like
202	4.3	gnflm06127_a_at	NM_134017	2410018D16	methionine adenosyltransferase II, beta	271	4.1	gnflm16087_a_at	NM_027560	G630019P16	arrestin domain containing 2
203	4.3	gnflm13939_a_at		1700001P03	NK2 transcription factor related, locus 4 (Drosophila)	272	4.1	gnflm03280_s_at	NM_013775	B020004B10	T-cell leukemia/lymphoma 1B, 1
204	4.3	gnflm29306_at	NM_026579	I920095K20	DNA segment, Chr 10, Wayne State University 102, expressed	273	4.1	gnflm15535_a_at	NM_026849	9430051D16	RIKEN cDNA 1110061O04 gene
205	4.3	gnflm12593_a_at	NM_016769	C630019N20	MAD homolog 3 (Drosophila)	274	4.1	gnflm13657_at		2410098H20	RUN and TBC1 domain containing 2
206	4.3	gnflm01949_a_at	NM_009534	I920028O19	yes-associated protein 1	275	4.1	gnflm26841_at	XM_925276	C130097O10	cat eye syndrome chromosome region, candidate 2 homolog (human)
207	4.3	gnflm31661_a_at	XM_910255		hypothetical protein LOC635251	276	4.1	gnflm02777_s_at	NM_011378	8030498F03	transcriptional regulator, SIN3A (yeast)
208	4.3	gnflm16301_a_at	XM_925135	1110069I23	F-box and leucine-rich repeat protein 17	277	4.1	gnflm03272_a_at	NM_013757	5330428N11	synaptotagmin-like 4
209	4.3	gnflm29960_a_at		F830114J03	folypolylglutamyl synthetase	278	4.1	gnflm21764_at		7420441D12	ubiquitin specific peptidase 30
210	4.3	gnflm02951_a_at	NM_011776	2410001F05	zona pellucida glycoprotein 3	279	4.1	gnflm29280_a_at	NM_080561	F630024P17	RIKEN cDNA 2810055G22 gene
211	4.3	gnflm15775_a_at	NM_183149	A430092M15	zinc finger protein 598	280	4.1	gnflm30027_at	XM_924076		TAF4A RNA polymerase II, TATA box binding protein (TBP)-associated factor
212	4.3	gnflm07986_a_at	NM_177475	6030407P18	suppressor of hairy wing homolog 2 (Drosophila)	281	4.1	gnflm09391_a_at	NM_173363		eukaryotic translation initiation factor 5
213	4.3	gnflm23101_at	NM_019570	1110027I23	REV1-like (S. cerevisiae)	282	4.1	gnflm09291_a_at	NM_026780	1110018L13	SYF2 homolog, RNA splicing factor (S. cerevisiae)
214	4.2	gnflm04303_a_at	NM_023290	6030446P03	makorin, ring finger protein, 2	283	4.1	gnflm05550_a_at	NM_030236	F830001G13	F-box only protein 34
215	4.2	gnflm28700_a_at		9530062A14	RIKEN cDNA A630082K20 gene	284	4.1	gnflm30830_at		I0C0042K12	NACHT, LRR and PYD containing protein 9c
216	4.2	gnflm05006_a_at	NM_026557	9030406D12	ring finger and CHY zinc finger domain containing 1	285	4.1	gnflm15590_at		4930406D14	RIKEN cDNA 4930406D14 gene
217	4.2	gnflm10172_a_at	NM_175311	F630008H06	zinc finger protein 513	286	4.1	gnflm24022_at		5730525N20	small nuclear ribonucleoprotein D1
218	4.2	gnflm28732_at			spastin	287	4.1	gnflm02731_a_at	NM_011293		polymerase (RNA) II (DNA directed) polypeptide J
219	4.2	gnflm10724_at	NM_008692		nuclear transcription factor-Y gamma	288	4.1	gnflm06313_a_at	NM_139218	7420498L12	developmental pluripotency-associated 3
220	4.2	gnflm03609_a_at	NM_018775	C630001K10	TBC1 domain family, member 8	289	4.1	gnflm23802_at		4931413K24	SUMO/sentrin specific peptidase 8
221	4.2	gnflm23779_a_at		4930563O14	RIKEN cDNA 4931428L18 gene	290	4.1	gnflm09991_a_at		C530022J18	hypothetical Lipocalin-related protein and Bos/Can/Equ allergen containing protein
222	4.2	gnflm16106_a_at	NM_028040	F830031C20	RNA pseudouridylate synthase domain containing 4	291	4.1	gnflm16922_a_at		2610312O17	RIKEN cDNA 1110054O05 gene
223	4.2	gnflm16623_at	XM_914303	2610024M03	protein phosphatase 1, regulatory subunit 3D	292	4.1	gnflm27711_at		D430026H23	phospholipase A2, activating protein
224	4.2	gnflm06092_x_at	NM_133893	E330028E06	2'-5' oligoadenylate synthetase 1D	293	4.1	gnflm34058_x_at			inferred: ref XP_033028.2 (XM_033028) hypothetical protein XP_033028 [Homo sapiens]
225	4.2	gnflm12791_a_at	NM_026220	I920055O03	microfibrillar-associated protein 1	294	4.1	gnflm18914_at		4930406H16	RIKEN cDNA 4930406H16 gene
226	4.2	gnflm21846_a_at	NM_175016	9530023G02	alkB, alkylation repair homolog 2 (E. coli)	295	4.1	gnflm00097_a_at	NM_007623	D030003P20	chromobox homolog 2 (Drosophila Pc class)
227	4.2	gnflm09902_a_at	NM_053254	F630026I01	transducin-like enhancer of split 6, homolog of Drosophila E(spl)	296	4.1	gnflm22236_at	XM_914443	D030047E23	RIKEN cDNA D230004J03 gene
228	4.2	gnflm18680_a_at		F420007A05	DNA-damage inducible protein 2	297	4.1	gnflm15900_a_at	NM_177471	F630113O12	coiled-coil domain containing 69
229	4.2	gnflm19095_at		6330407P15	zinc finger protein 422	298	4.1	gnflm18473_at	XM_922117	C230071E20	RIKEN cDNA 4933421B21 gene
230	4.2	gnflm06456_a_at	NM_145210	E330025J23	2'-5' oligoadenylate synthetase 1E	299	4.1	gnflm11753_at	NM_007563	6330513J17	2,3-bisphosphoglycerate mutase
231	4.2	gnflm30600_a_at	XM_909322	9630037P07	RIKEN cDNA 9630037P07 gene	300	4.1	gnflm09930_a_at	NM_026045	5330405H01	PRP18 pre-mRNA processing factor 18 homolog (yeast)
232	4.2	gnflm22595_a_at	NM_001033211	I0C0046K11	expressed sequence AU022751	301	4.1	gnflm00441_a_at	NM_178616	I730081G10	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11
233	4.2	gnflm17144_s_at		4632430A05	aryl hydrocarbon receptor nuclear translocator-like 2	302	4.1	gnflm03608_a_at	NM_018774		polyhomeotic-like 2 (Drosophila)
234	4.2	gnflm28765_a_at		4932423E22	mbt domain containing 1	303	4.1	gnflm03275_a_at	NM_013764	9530009E09	deoxyguanosine kinase
235	4.2	gnflm26041_at		A830015L23	weakly similar to ACTIN-BINDING PROTEIN FRABIN-GAMMA [Mus musculus]	304	4.1	gnflm05565_a_at	NM_030564	4933435P17	ring finger protein 34
236	4.2	gnflm10411_a_at		G730029A12	peptidylprolyl isomerase (cyclophilin) like 5	305	4.1	gnflm29697_at	XM_907476		carbohydrate (chondroitin)
237	4.2	gnflm00510_a_at	NM_178375	4921517A06	zinc finger, SWIM domain containing 3						
238	4.2	gnflm09301_a_at	NM_027212	I730042E14	thyroid hormone receptor associated protein 6						
239	4.2	gnflm29733_a_at	NM_201226	F630110M03	leucine rich repeat containing 47						

306	4.1	gnf1m29443_a_at	XM_922388	F630107J06	synthase 1	47	5.9	gnf1m01463_s_at	NM_008646	G630093A09	chain 4
307	4.1	gnf1m30810_at	NM_001024205	RIKEN cDNA 4931433E08 gene	nuclear fragile X mental retardation	48	5.9	gnf1m00805_a_at	NM_007443	1300004O18	murinoglobulin 1
					protein interacting protein 2	49	5.8	gnf1m00930_a_at	NM_007686		alpha 1 microglobulin/bikunin
308	4.1	gnf1m19811_at		9530092E12	unclassifiable	50	5.8	gnf1m28861_a_at	NM_133882	C730036J02	complement component factor i
309	4.0	gnf1m16223_a_at	XM_917330	2810407P21	similar to Exocyst complex						complement component 8, beta
					component Sec3						subunit
310	4.0	gnf1m17453_at	NM_026127	RIKEN cDNA 4833420G17 gene	RIKEN cDNA 4833420G17 gene	51	5.8	gnf1m00975_a_at	NM_007768	E430018L12	C-reactive protein, petaxin related
311	4.0	gnf1m03686_a_at	NM_019434	F430004B09	minichromosome maintenance	52	5.7	gnf1m16098_a_at	NM_027062	1700013L23	RIKEN cDNA 1700013L23 gene
					deficient 3 (S. cerevisiae)	53	5.7	gnf1m10786_a_at	NM_008819	5730405A09	phosphatidylethanolamine N-
					associated protein						methyltransferase
312	4.0	gnf1m29537_s_at	XM_909627	B830011O14	G protein-coupled receptor, family	54	5.7	gnf1m06340_s_at	XM_923552	C730026F11	esterase 31
					C, group 1, member B	55	5.7	gnf1m28632_at			solute carrier family 10
313	4.0	gnf1m04771_s_at	XM_913852	2010100O12	RIKEN cDNA 2010100O12 gene						(sodium/bile acid cotransporter
314	4.0	gnf1m31508_at			similar to hypothetical protein	56	5.7	gnf1m02172_a_at	NM_010006	F530007D13	family), member 1
					MGC42415						cytochrome P450, family 2,
315	4.0	gnf1m14863_at		6530413F01	rabphilin 3A-like (without C2	57	5.7	gnf1m00766_a_at	NM_007376		subfamily d, polypeptide 9
					domains)	58	5.7	gnf1m00568_a_at	NM_030611	C730015J07	pregnancy zone protein
316	4.0	gnf1m04731_a_at	NM_025853	1700022L09	RIKEN cDNA 1700022L09 gene	59	5.6	gnf1m00257_a_at	NM_007818	C730009I07	aldo-keto reductase family 1,
317	4.0	gnf1m33640_at	NM_001033794	7420486K21	expressed sequence C85627						member C6
318	4.0	gnf1m23128_at		M421020G19	jumonji, AT rich interactive domain	60	5.6	gnf1m04260_a_at	NM_023114	2010015N05	cytochrome P450, family 3,
					2	61	5.6	gnf1m01266_a_at	NM_925766		subfamily a, polypeptide 11
319	4.0	gnf1m12215_a_at	NM_144884	C430047K18	torsin family 1, member A (torsin						apolipoprotein C-III
					A)						hydroxysteroid dehydrogenase-5,
320	4.0	gnf1m17795_a_at		9630044M01	unclassifiable	62	5.6	gnf1m03106_a_at	NM_013474		delta<5>-3-beta
321	4.0	gnf1m28358_a_at	NM_001039206	E430007J01	RIKEN cDNA 2410004P22 gene	63	5.5	gnf1m07735_a_at	NM_175250	A530080C09	apolipoprotein A-II
322	4.0	gnf1m10469_a_at	NM_181570	4932427P06	cyclin-dependent kinase 8	64	5.5	gnf1m00022_a_at	NM_027552	4432411A05	RIKEN cDNA 2810007J24 gene
323	4.0	gnf1m23831_at			angel homolog 2 (Drosophila)						kynureninase (L-kynurenine
324	4.0	gnf1m07475_a_at	NM_009764		breast cancer 1	65	5.5	gnf1m01233_a_at	NM_008223		hydrolase)
325	4.0	gnf1m33977_s_at	NM_912011		similar to RIKEN cDNA	66	5.5	gnf1m10714_a_at	NM_011316		serine (or cysteine) peptidase
					A430107P09 gene	67	5.5	gnf1m29875_a_at	XM_907929	2610039N02	inhibitor, clade D, member 1
326	4.0	gnf1m11316_a_at	NM_053069	3632412H11	autophagy-related 5 (yeast)						serum amyloid A 4
						68	5.5	gnf1m30148_at			MOCO sulphurase C-terminal
											domain containing 1
No. 5, liver specific genes											inferred:
#1	#2	#3	#4	#5	#6						gb AAH11222.1 AAH11222
1	7.1	gnf1m03553_a_at	NM_017371	I530016F13	hemopexin						(BC011222) Similar to cytochrome
2	6.9	gnf1m09228_a_at	NM_133653		methionine adenosyltransferase I,						P450, 2c37 [Mus musculus]
					alpha						mCG12494
3	6.9	gnf1m03936_at	NM_020495		solute carrier organic anion	69	5.5	gnf1m28772_at	NM_001029867	C730009A09	UDP glucuronosyltransferase 2
					transporter family, member 1b2						family, polypeptide B36
4	6.9	gnf1m16227_a_at	NM_013913	C730037J05	angiotensin-like 3	70	5.4	gnf1m10720_a_at	NM_011850	1300007F22	nuclear receptor subfamily 0, group
5	6.9	gnf1m03107_a_at	NM_013475	2510008B09	apolipoprotein H						B, member 2
6	6.8	gnf1m20188_at		A330074B06	glutaminase 2 (liver,	71	5.4	gnf1m03576_a_at	NM_017473		retinol dehydrogenase 7
					mitochondrial)	72	5.4	gnf1m28722_a_at			ENSMUST00000040807 transcript
7	6.7	gnf1m01937_a_at	NM_009512		solute carrier family 27 (fatty acid						(in rel.37.34e)
					transporter), member 5	73	5.3	gnf1m28781_a_at	NM_009654	C920028B14	albumin 1
8	6.7	gnf1m02170_s_at	NM_134144	1300015K14	cytochrome P450, family 2,	74	5.3	gnf1m03395_a_at	NM_015799	F630312J08	transferrin receptor 2
					subfamily c, polypeptide 37	75	5.3	gnf1m06019_s_at	XM_921598	C730027E20	cytochrome P450, family 2,
9	6.7	gnf1m02481_a_at	NM_010702	2510008M19	leukocyte cell-derived chemotaxin						subfamily a, polypeptide 12
					2						cytochrome P450, family 4,
10	6.6	gnf1m33131_at	NM_001012310	C730001O18	expressed sequence A1132487						subfamily a, polypeptide 14
11	6.6	gnf1m15514_a_at	XM_904856	2510015E20	group specific component	77	5.3	gnf1m05714_s_at	NM_183257	2210420P15	hepcidin antimicrobial peptide 2
12	6.6	gnf1m10769_a_at	NM_007385		apolipoprotein C-IV	78	5.3	gnf1m05625_a_at	NM_031164	C730005G24	coagulation factor XIII, beta
13	6.6	gnf1m01597_a_at	NM_008877	3830402P08	plasminogen						subunit
14	6.6	gnf1m10614_x_at	NM_010005		cytochrome P450, family 2,	79	5.3	gnf1m16499_a_at	NM_001003893	C730007K24	mannan-binding lectin serine
					subfamily d, polypeptide 10						peptidase 2
15	6.6	gnf1m16140_a_at	XM_917766		cytochrome P450, family 2,	80	5.2	gnf1m07216_a_at	NM_147218		ATP-binding cassette, sub-family A
					subfamily c, polypeptide 44						(ABC1), member 6
16	6.6	gnf1m06740_a_at	NM_146214	C730030H13	tyrosine aminotransferase	81	5.2	gnf1m02345_a_at	NM_010403	C730038J24	hydroxyacid oxidase 1, liver
17	6.5	gnf1m03115_at	NM_013485		complement component 9	82	5.2	gnf1m00372_a_at	NM_053096	1700019C17	camello-like 2
18	6.5	gnf1m05812_a_at	NM_053176		histidine-rich glycoprotein	83	5.2	gnf1m02299_a_at	NM_010321	1810009D12	glycine N-methyltransferase
19	6.5	gnf1m05713_a_at	NM_032541		hepcidin antimicrobial peptide 1	84	5.1	gnf1m01598_a_at	NM_008878	G630018H21	serine (or cysteine) peptidase
20	6.4	gnf1m09699_s_at	XM_917532	G630093A09	murinoglobulin 1						inhibitor, clade F, member 2
21	6.4	gnf1m07245_a_at	NM_152811	1300012D20	UDP glucuronosyltransferase 2	85	5.1	gnf1m00290_a_at	NM_016668	4933406B07	betaine-homocysteine
					family, polypeptide B1						methyltransferase
22	6.4	gnf1m01355_a_at	NM_008455		kallikrein B, plasma 1	86	5.1	gnf1m12777_a_at	NM_080844	C730035E04	serine (or cysteine) peptidase
23	6.4	gnf1m13313_a_at		1300015B06	protein Z, vitamin K-dependent						inhibitor, clade C (antithrombin),
					plasma glycoprotein						member 1
24	6.3	gnf1m06418_a_at	NM_144909	C730003B02	glucokinase regulatory protein	87	5.1	gnf1m01685_a_at	NM_009060	I920009B07	regucalcin
25	6.3	gnf1m10857_a_at	NM_013396	C730009L19	apolipoprotein H	88	5.1	gnf1m17896_a_at	NM_153100		cDNA sequence BC023486
26	6.3	gnf1m02235_a_at	NM_010168	I530018P09	coagulation factor II	89	5.0	gnf1m06712_a_at	NM_146148	G630026A05	complement component 8, alpha
27	6.2	gnf1m00901_a_at	NM_007618	I530005F24	serine (or cysteine) peptidase						polypeptide
					inhibitor, clade A, member 6	90	5.0	gnf1m10456_a_at	NM_138951	G630090K23	cDNA sequence BC021608
28	6.2	gnf1m23137_s_at	NM_011458	C730009L23	serine (or cysteine) peptidase	91	5.0	gnf1m07281_a_at	NM_153100		ceptor transporter protein 3
					inhibitor, clade A, member 3K	92	5.0	gnf1m10709_a_at	NM_019911	3830418M10	tryptophan 2,3-dioxygenase
29	6.2	gnf1m04119_a_at	NM_021489		coagulation factor XII (Hageman	93	5.0	gnf1m00846_a_at	NM_007519	5830412M14	bile acid-Coenzyme A: amino acid
					factor)						N-acyltransferase
30	6.2	gnf1m10551_a_at	NM_007972	F630223K11	coagulation factor X	94	5.0	gnf1m10620_a_at	NM_007493		asialoglycoprotein receptor 2
31	6.2	gnf1m02425_a_at	NM_010582	5730412L20	inter-alpha trypsin inhibitor, heavy	95	5.0	gnf1m05929_a_at	NM_080845	F520008O15	formiminotransferase
					chain 2						cyclodeaminase
32	6.2	gnf1m03437_a_at	NM_016702	C730009H22	alanine-glyoxylate	96	5.0	gnf1m30360_a_at		1420028J16	sarcosine dehydrogenase
					aminotransferase	97	5.0	gnf1m17191_a_at	XM_908254	2210404A22	claudin 22
33	6.1	gnf1m01089_a_at	NM_007954		esterase 1	98	5.0	gnf1m01909_s_at	NM_133894	9430041C03	UDP glucuronosyltransferase 2
34	6.1	gnf1m00880_a_at	NM_007576	C730023F21	complement component 4 binding						family, polypeptide B5
					protein	99	5.0	gnf1m33066_s_at	NM_010004	C730004C24	cytochrome P450, family 2,
35	6.1	gnf1m01326_a_at	NM_008406	C730026K04	inter-alpha trypsin inhibitor, heavy						subfamily c, polypeptide 40
					chain 1	100	5.0	gnf1m03937_a_at	NM_020495		solute carrier organic anion
36	6.0	gnf1m05225_a_at	NM_027918	1300017J02	RIKEN cDNA 1300017J02 gene						transporter family, member 1b2
37	6.0	gnf1m13619_a_at	NM_007979	C730002C14	coagulation factor IX	101	5.0	gnf1m12772_a_at	NM_007824	C730031G23	cytochrome P450, family 7,
38	6.0	gnf1m01913_a_at	NM_009474	C730047G18	urate oxidase						subfamily a, polypeptide 1
39	6.0	gnf1m03999_a_at	NM_021022	G630096B22	ATP-binding cassette, sub-family B	102	4.9	gnf1m03438_a_at	NM_016704		complement component 6
					(MDR/TAP), member 11	103	4.9	gnf1m29867_a_at	NM_181849	I920079K06	fibrinogen, B beta polypeptide
40	6.0	gnf1m16558_a_at	NM_199314	C730007J02	serine (or cysteine) peptidase	104	4.9	gnf1m30559_a_at	XM_925483	1110001J08	3-hydroxyanthranilate 3,4-
					inhibitor, clade A (alpha-1						dioxygenase
					antiproteinase, antitrypsin),	105	4.9	gnf1m28629_a_at	NM_001039544		major urinary protein 3
					member 11	106	4.9	gnf1m06571_a_at	XM_908068	C730004F22	glycogen synthase 2
41	6.0	gnf1m12243_s_at	NM_010012	A530001C04	cytochrome P450, family 8,	107	4.9	gnf1m30972_a_at	NM_019792	C730034H04	cytochrome P450, family 3,
					subfamily b, polypeptide 1						subfamily a, polypeptide 25
42	5.9	gnf1m30676_a_at	XM_922255	4732433M03	carbamoyl-phosphate synthetase 1	108	4.9	gnf1m09694_s_at	XM_915279	C730018C05	cytochrome P450, family 2,
43	5.9	gnf1m15544_a_at		C730013F20	uridine phosphorylase 2						subfamily c, polypeptide 37
44	5.9	gnf1m10655_a_at	NM_007815	C730037L09	cytochrome P450, family 2,	109	4.9	gnf1m06502_a_at	NM_145424	F530215H01	cDNA sequence BC089597
					subfamily c, polypeptide 29	110	4.9	gnf1m05212_a_at	NM_027853	0610006F02	methyltransferase like 7B
45	5.9	gnf1m03100_a_at	NM_013465	I530029B19	alpha-2-HS-glycoprotein	111	4.9	gnf1m09873_a_at	NM_177406		cytochrome P450, family 4,
46	5.9	gnf1m03591_a_at	NM_018746	C730031O13	inter alpha-trypsin inhibitor, heavy						subfamily a, polypeptide 12

112	4.9	gnf1m28543_a_at	XM_125854	G630005C23	amidohydrolase domain containing 1	174	4.3	gnf1m03064_a_at	NM_011996		alcohol dehydrogenase 4 (class II), pi polypeptide				
113	4.9	gnf1m00339_a_at	NM_009803	C730009H01	nuclear receptor subfamily 1, group I, member 3	175	4.3	gnf1m05885_a_at	NM_054094	C730036G06	acyl-CoA synthetase medium-chain family member 1				
114	4.9	gnf1m08713_at	NM_172881	C730031G17	UDP glucuronosyltransferase 2 family, polypeptide B35	176	4.3	gnf1m30358_x_at	NM_001029977		complement factor H-related protein				
115	4.8	gnf1m11082_a_at	NM_023125	1600027I01	kininogen 1	177	4.3	gnf1m10645_a_at	NM_008341		insulin-like growth factor binding protein 1				
116	4.8	gnf1m35115_at			inferred: gb AAH16517.1 AAH16517 (BC016517) Unknown (protein for MGC:27756) [Mus musculus] mCG48945	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)				
117	4.8	gnf1m01789_a_at	NM_009253		serine (or cysteine) peptidase inhibitor, clade A, member 3M	180	4.3	gnf1m06075_a_at	NM_133809		kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)				
118	4.8	gnf1m12767_a_at	NM_019546	C730020B03	proline dehydrogenase (oxidase) 2	181	4.3	gnf1m29692_a_at	XM_915401	5033405N08	agmatine ureohydrolase (agmatinase)				
119	4.8	gnf1m01541_a_at	NM_008777	I530004L01	phenylalanine hydroxylase	182	4.3	gnf1m00023_a_at	NM_008256	1300004J23	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2				
120	4.7	gnf1m01245_a_at	NM_008243	G730039B12	macrophage stimulating 1 (hepatocyte growth factor-like)	183	4.3	gnf1m05053_a_at	NM_026690	0610012D14	RIKEN cDNA 0610012D14 gene				
121	4.8	gnf1m27189_a_at		C730018L13	expressed sequence A1182371	184	4.3	gnf1m05586_a_at	NM_030703	0610011F20	carboxypeptidase N, polypeptide 1				
122	4.8	gnf1m06501_at	NM_145424	F530215H01	cDNA sequence BC089597	185	4.3	gnf1m02513_a_at	NM_010776	C730024L16	mannose binding lectin (C)				
123	4.7	gnf1m10784_at	NM_010565		inhibin beta-C	186	4.3	gnf1m03414_a_at	XM_919150	I920184L23	S-adenosylhomocysteine hydrolase				
124	4.7	gnf1m01787_s_at	NM_009247	I920035F16	serine (or cysteine) peptidase inhibitor, clade A, member 1a	187	4.3	gnf1m00366_a_at	NM_177002	D630035B04	RIKEN cDNA C730048C13 gene				
					carboxypeptidase B2 (plasma)	188	4.2	gnf1m33353_at			inferred: gb AAH05978.1 AAH05978 (BC005978) karyopherin alpha 2 (RAG cohort 1, importin alpha 1) [Homo sapiens] mCG126254				
125	4.7	gnf1m03806_a_at	NM_019775	1110032P04	transmembrane 7 superfamily member 2					F930027M15	guanidinoacetate methyltransferase				
126	4.7	gnf1m15585_a_at	NM_028454	F630230M15						C730010D03	serine dehydratase				
127	4.7	gnf1m26223_a_at	NM_028788	C730023F16	RIKEN cDNA 1300002K09 gene	189	4.2	gnf1m02273_a_at	NM_010255		inferred: ref NP_032674.1 (NM_008648) major urinary protein 4 [Mus musculus] mCG132776				
128	4.7	gnf1m10057_a_at	NM_178713		aldehyde dehydrogenase 8 family, member A1	190	4.2	gnf1m09901_a_at	NM_145565						
129	4.7	gnf1m30458_s_at	XM_904752	0610011D16	cytochrome P450, family 4, subfamily a, polypeptide 10	191	4.2	gnf1m32875_at							
130	4.7	gnf1m33004_at			inferred: gb AAB94937.1 (AF039212) UDP-glucuronosyltransferase 1A7 [Rattus norvegicus] mCG131123	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				
131	4.7	gnf1m25754_at		A530084B21	solute carrier family 21 (organic anion transporter), member 1	194	4.2	gnf1m29287_a_at		0610005C13	RIKEN cDNA 0610005C13 gene				
132	4.6	gnf1m10656_a_at	NM_008934		protein C	195	4.2	gnf1m11559_a_at	NM_145365	C730025L08	cAMP responsive element binding protein 3-like 3				
133	4.6	gnf1m10226_s_at	NM_170778	E330028L06	dihydropyrimidine dehydrogenase	196	4.2	gnf1m04231_a_at	NM_022884	I530012L08	betaine-homocysteine methyltransferase 2				
134	4.6	gnf1m01185_a_at	NM_008124	1300008G06	gap junction membrane channel protein beta 1	197	4.2	gnf1m03693_a_at	NM_019447	G630096L04	hepatocyte growth factor activator				
135	4.6	gnf1m06122_a_at	NM_133997		apolipoprotein F	198	4.2	gnf1m09353_a_at	NM_053115		acyl-Coenzyme A oxidase 2, branched chain				
136	4.6	gnf1m29057_s_at	XM_886668	C730034H04	cytochrome P450, family 3, subfamily a, polypeptide 25	199	4.2	gnf1m09846_a_at		C730040N12	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiprotease, antitrypsin), member 7				
137	4.6	gnf1m09780_a_at	NM_133768	I920049G14	argininosuccinate lyase						histocompatibility 2, Q region locus 10				
138	4.6	gnf1m00522_a_at	NM_027902	1300008A22	transmembrane serine protease 6	201	4.2	gnf1m06570_a_at	NM_145570		cDNA sequence BC014699				
139	4.6	gnf1m03147_s_at	NM_013547	0610012C11	homogentisate 1, 2-dioxygenase	202	4.2	gnf1m15753_at	NM_175438		aldehyde dehydrogenase 4 family, member A1				
140	4.6	gnf1m01807_x_at	NM_009286		sulfotransferase family 2A, dehydroepiandrosterone (DHEA)-preferring, member 2	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				
141	4.6	gnf1m10748_a_at	NM_009202		solute carrier family 22 (organic cation transporter), member 1	205	4.2	gnf1m34057_at	XM_906159		hypothetical protein LOC623919				
142	4.6	gnf1m04864_a_at	NM_026180	1300003C16	ATP-binding cassette, sub-family G (WHITE), member 8	206	4.1	gnf1m31926_x_at			inferred: gb AAC27650.2 (AF078817) high mobility group protein [Spalax ehrenbergi] mCG49424				
143	4.6	gnf1m10527_a_at	NR_002687	I920036P21	argininosuccinate synthetase 1					207	4.1	gnf1m12201_a_at	NM_134103	C730019B22	interleukin 1 receptor accessory protein
144	4.6	gnf1m05477_a_at	NM_029562	1300006E06	cytochrome P450, family 2, subfamily d, polypeptide 26					208	4.1	gnf1m02240_a_at	NM_010176	K43033E02	fumarylacetoacetate hydrolase
145	4.6	gnf1m06586_a_at	NM_145594		fibrinogen-like protein 1					209	4.1	gnf1m21159_a_at	XM_918867	C730014M21	calcium and integrin binding family member 3
146	4.5	gnf1m02031_a_at	NM_009714	4930534D09	asialoglycoprotein receptor 1					210	4.1	gnf1m35031_at			inferred: ref NP_035424.1 (NM_011294) RNA polymerase II transcriptional coactivator [Mus musculus] mCG50416
147	4.5	gnf1m09474_a_at	NM_026701	F530003P19	RIKEN cDNA 0610038K03 gene	211	4.1	gnf1m33092_at	XM_906759	M5C1068H14	apolipoprotein B				
148	4.5	gnf1m05361_a_at	NM_028772	1200014D15	dimethylglycine dehydrogenase precursor	212	4.1	gnf1m01633_a_at	NM_008952	C730025C09	pipecolic acid oxidase				
					inferred: gb AAB47130.1 uMUP-VIII=18.695 kda major urinary protein [mice, Balb/c, urine, Peptide, 162 aa] mCG129513	213	4.1	gnf1m32343_x_at			inferred: ref NP_031808.1 (NM_007782) colony stimulating factor 3 receptor (granulocyte) [Mus musculus] mCG21155				
149	4.5	gnf1m33119_at			complement component factor h-like 1	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				
150	4.5	gnf1m03388_a_at	NM_015780		major urinary protein 1	216	4.1	gnf1m04032_a_at	XM_888081	C730002N09	peptidoglycan recognition protein 2				
151	4.5	gnf1m18816_at		2610016E04	RNA pseudouridylate synthase domain containing 3	217	4.1	gnf1m00754_a_at	NR_002861		serine (or cysteine) peptidase inhibitor, clade A, member 4, pseudogene 1				
152	4.5	gnf1m30104_a_at	XM_924654	5730470F19	carboxypeptidase N, polypeptide 2	218	4.1	gnf1m09764_a_at	NM_133943	I830015G06	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7				
153	4.5	gnf1m14294_at		5033417E09	arylacetamide deacetylase (esterase)	219	4.1	gnf1m02238_a_at	NM_010172	F730043B01	coagulation factor VII				
154	4.5	gnf1m23907_at		1300003J07	cytochrome P450, family 1, subfamily a, polypeptide 2	220	4.1	gnf1m15567_at	NM_207216	F430101I22	UDP glycosyltransferases 3 family, polypeptide A1				
155	4.4	gnf1m10706_a_at	NM_009993		hemolytic complement	221	4.1	gnf1m06112_at	NM_133969	1200012E24	cytochrome P450, family 4, subfamily v, polypeptide 3				
156	4.4	gnf1m02347_a_at	NM_010406	2010321J07	UDP glucuronosyltransferase 2 family, polypeptide A3	222	4.1	gnf1m21309_at		D230014K18	unclassifiable				
157	4.4	gnf1m05265_a_at	NM_028094	I530022M24	aldolase 2, B isoform	223	4.0	gnf1m30277_a_at			ENSMUST00000036050 transcript (in rel.37.34e)				
158	4.4	gnf1m10903_a_at	NM_144903	I530017M04	acetyl-Coenzyme A acyltransferase 1B	224	4.0	gnf1m11914_a_at	NM_133960	9130231C15	carboxylesterase 6				
159	4.4	gnf1m10109_a_at	NM_146230		fatty acid binding protein 1, liver	225	4.0	gnf1m30667_at			uncharacterized Celera prediction mCG121657				
160	4.4	gnf1m03564_a_at	NM_017399	2010105C24	zinc finger, DHHC domain containing 9	226	4.0	gnf1m03979_a_at	NM_020598		olfactory receptor 17				
161	4.4	gnf1m11783_a_at	NM_172465	6430508G22	coagulation factor XI	227	4.0	gnf1m02742_a_at	NM_011318	B830039L18	serum amyloid P-component				
162	4.4	gnf1m05257_a_at	NM_028066	1600027G01	coagulation factor V	228	4.0	gnf1m04407_a_at	NM_024229		phosphate cytidylyltransferase 2, ethanalamine				
163	4.4	gnf1m27195_at		C730026K03	dihydropyrimidine dehydrogenase	229	4.0	gnf1m12230_a_at	NM_026234	A930029E10	phosphatidylinositol glycan, class				
164	4.4	gnf1m00425_a_at	NM_170778	E330028L06	dihydropyrimidine dehydrogenase										
165	4.4	gnf1m10435_at	NM_170778		cytochrome P450, family 3, subfamily a, polypeptide 25										
166	4.4	gnf1m29794_s_at	XM_886540		mannan-binding lectin serine peptidase 1										
167	4.4	gnf1m01414_a_at	NM_008555		V-set and immunoglobulin domain containing 4										
168	4.4	gnf1m00400_a_at	NM_177789	A530061A11	cytochrome P450, family 2, subfamily a, polypeptide 12										
169	4.4	gnf1m06018_a_at	NM_133657		fructose biphosphatase 1										
170	4.4	gnf1m03664_a_at	NM_019395	C730030M09	aldehyde dehydrogenase 1 family, member L1										
171	4.4	gnf1m00474_a_at	NM_027406	B230119O16	ethanolamine kinase 2										
172	4.3	gnf1m24247_a_at	XM_903848	4933417N20	solute carrier family 6 (neurotransmitter transporter, GABA), member 13										
173	4.3	gnf1m06341_a_at	NM_144512	C730037J22											

59/97

					(NM_018078) hypothetical protein FLI10378 [Homo sapiens] mCG49707		30	5.3	gnf1m01461_s_at	NM_008642	I920026D19	subfamily f, polypeptide 14 microsomal triglyceride transfer protein inferred: ref NP_113947.1 (NM_031759) N-acetylated alpha-linked acidic dipeptidase-like (ileal peptidase I100) [Rattus norvegicus] mCG11755
115	4.1	gnf1m33791_at	XM_907417		similar to Cytochrome P450 2B20 (CYP11B20) (P24)		31	5.3	gnf1m32536_at			
116	4.1	gnf1m15079_at			frizzled homolog 5 (Drosophila)							
117	4.1	gnf1m26575_at			unclassifiable							
118	4.1	gnf1m21231_at	XM_902796		D130015I23 tetra-ricopeptide repeat domain 13							
119	4.1	gnf1m11517_a_at	NM_026367		D030023G19 G patch domain containing 2		32	5.2	gnf1m23042_a_at	NM_183268	2010206A06	defensein related cryptdin 20
120	4.1	gnf1m30999_s_at	NM_009661		4732447A14 arachidonate 8-lipoxygenase		33	5.2	gnf1m05705_a_at	NM_032394		myosin VIIb
121	4.1	gnf1m07024_at	NM_146868		olfactory receptor 894		34	5.2	gnf1m04114_a_at	NM_021481	2210412M19	trehalase (brush-border membrane glycoprotein)
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		35	5.2	gnf1m00564_a_at	NM_181540	4933408I11	transmembrane 6 superfamily member 2
					RIKEN cDNA 6430500D05 gene		36	5.2	gnf1m30177_a_at	NM_001033364	G630055D06	cDNA sequence BC040758
124	4.1	gnf1m17426_at			4930420A19 RIKEN cDNA 4931422A03 gene		37	5.1	gnf1m02718_a_at	NM_011259	2010207J02	regenerating islet-derived 3 alpha sterol O-acetyltransferase 2
125	4.1	gnf1m07617_at	NM_175161		8030495L15 cysteinyl-tRNA synthetase		38	5.1	gnf1m06690_a_at	NM_146064		similar to Serum amyloid P-component precursor (SAP)
126	4.1	gnf1m11867_a_at	NM_013742		2300002A12 WAP four-disulfide core domain 12		39	5.0	gnf1m33688_at	XM_917712	F830007N10	cadherin 17
127	4.1	gnf1m10824_a_at	NM_138684		4931412I15 RIKEN cDNA 4931412I15 gene		40	5.0	gnf1m13288_a_at		F430111H02	secreted and transmembrane 1
128	4.1	gnf1m14145_at			solute carrier family 36 (proton/amino acid symporter), member 1		41	5.0	gnf1m11403_at	NM_026907	2010001H14	RIKEN cDNA 2010001H14 gene
129	4.1	gnf1m07301_a_at	NM_153139		4930579K13 ribosomal protein S6 kinase polypeptide 1		42	5.0	gnf1m05145_a_at	NM_027227	I530028M11	amiloride binding protein 1 (amine oxidase, copper-containing)
					A230004G12 wingless related MMTV integration site 2b		43	5.0	gnf1m05494_a_at	NM_029638	D630032A02	solute carrier family 7 (cationic amino acid transporter, y+ system), member 9
130	4.1	gnf1m19103_at			4732418P20 TATA box binding protein-like 1		44	5.0	gnf1m04014_a_at	NM_021291	2010305F10	gastric inhibitory polypeptide malic enzyme 2, NAD(+)-dependent, mitochondrial
131	4.1	gnf1m25399_at			8430401P03 RIKEN cDNA 8430401P03 gene		45	5.0	gnf1m11133_a_at	NM_008119	F830020H14	chloride channel calcium activated 6
132	4.1	gnf1m06209_at	NM_134219		A530031I11 hypothetical protein		46	4.9	gnf1m12324_a_at	NM_145494	9130020L07	mucin 3, intestinal
133	4.1	gnf1m19154_at			E130018A02 membrane-associated ring finger (C3HC4) 2		47	4.9	gnf1m30769_s_at	NM_207208	E130202O15	espin
134	4.1	gnf1m14263_at			C230071D10 CDC14 cell division cycle 14 homolog B (S. cerevisiae)		48	4.9	gnf1m28989_a_at	XM_916703	9130221N23	NPCL1-like 1
135	4.1	gnf1m22963_at			inferred: gb AAH14745.1 AAH14745 (BC014745) Similar to RIKEN cDNA 5730591C18 gene [Mus musculus] mCG1037344		49	4.9	gnf1m00501_a_at	NM_207691	F430112P22	hepatocyte nuclear factor 4, gamma
136	4.1	gnf1m08210_s_at	NM_145486		T-cell leukemia, homeobox 1		50	4.9	gnf1m21825_a_at	NM_013920	C730041D17	cytochrome P450, family 3, subfamily a, polypeptide 13
137	4.1	gnf1m07782_a_at	NM_172587		B130047P03 Cdc42 GTPase-activating protein		51	4.9	gnf1m03353_a_at	NM_007819		inferred: ref XP_139161.1 (XM_139161) similar to bA209J19.1.1 (GW112 protein) [Mus musculus] mCG19388
138	4.0	gnf1m35355_at			A530071G10 2'-5' oligoadenylate synthetase 1B		52	4.9	gnf1m32430_at		4930516G09	angiogenin, ribonuclease A family, member 3
					4930532L22 chromodomain helicase DNA binding protein 5		53	4.8	gnf1m00809_at	NM_022411	C130087A09	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2
139	4.0	gnf1m00017_at	NM_021901		4930585K05 sperm associated antigen 16		54	4.8	gnf1m00809_at		2010001E11	RIKEN cDNA 2010001E11 gene
140	4.0	gnf1m26254_at			5430438D01 carbohydrate (N-acetyl)galactosamine 4-0)		55	4.8	gnf1m04210_a_at	NM_022411	1810023F06	pancreatitis-associated protein
141	4.0	gnf1m17662_at			4831410D14 similar to TYROSINE-PROTEIN KINASE JAK3 (EC 2.7.1.112) [JANUS KINASE 3] (JAK-3) [Mus musculus]		56	4.8	gnf1m15732_a_at	XM_907955	1810023F06	RIKEN cDNA 1810023F06 gene
142	4.0	gnf1m02987_a_at	NM_011853				57	4.8	gnf1m02605_a_at	NM_011036	1810034H17	RIKEN cDNA 1810023F06 gene
143	4.0	gnf1m18709_s_at	XM_921144				58	4.8	gnf1m06515_a_at	NM_145449	5033427P15	annexin A13
							59	4.8	gnf1m05139_a_at	NM_027211		cystatin 8 (cystatin-related epididymal spermatogenic)
144	4.0	gnf1m23792_at					60	4.8	gnf1m29825_a_at	XM_924219	I920045H24	apolipoprotein A-IV
145	4.0	gnf1m14247_a_at	NM_199055				61	4.8	gnf1m10611_a_at	NM_007468	D630045H05	defensein related cryptdin 6
							62	4.8	gnf1m1026_x_at	NM_007852	I530020L22	hexokinase domain containing 1
146	4.0	gnf1m19193_at					63	4.8	gnf1m06496_at	NM_145419		solute carrier family 5 (sodium/glucose cotransporter), member 1
							64	4.8	gnf1m11887_a_at	NM_019810	2010306N10	unclassifiable glycoprotein A33 (transmembrane) similar to butyrophilin-like 8
							65	4.7	gnf1m16545_at		I920191F06	RIKEN cDNA D630035O19 gene
							66	4.7	gnf1m04152_a_at	NM_021610	K1C0001E01	granzyme B
							67	4.7	gnf1m32791_at	XM_906210		myosin I beta
3	6.8	gnf1m04331_a_at	NM_023529		2010001N17 membrane-spanning 4-domains, subfamily A, member 10		68	4.7	gnf1m09647_a_at	NM_145932	E330039G21	myosin XVb
4	6.8	gnf1m30350_at	XM_914093				69	4.7	gnf1m03142_a_at	NM_013542	9030623C06	RIKEN cDNA 9030623C06 gene
5	6.8	gnf1m33685_at	XM_906199				70	4.7	gnf1m01429_a_at	NM_008586	3830420G04	mucin 13, epithelial transmembrane
6	6.7	gnf1m04926_a_at	NM_026333		5033406B05 RIKEN cDNA 2010204N08 gene		71	4.7	gnf1m22615_a_at	NM_023256	C730009H01	nuclear receptor subfamily 1, group I, member 3
7	6.4	gnf1m18409_a_at	XM_906199		2010204N08 RIKEN cDNA 2010204N08 gene		72	4.7	gnf1m04296_a_at	NM_023256	1810074H01	mucin and cadherin like
8	6.1	gnf1m30117_a_at	XM_906067		2010001C14 RIKEN cDNA 2010001C14 gene		73	4.7	gnf1m02497_a_at	NM_010739	9030421J09	RIKEN cDNA 9030421J09 gene
9	6.0	gnf1m05445_a_at	NM_029360		2010003F10 transmembrane 4 superfamily member 5		74	4.6	gnf1m00339_a_at	NM_009803	9130404O17	regenerating islet-derived family, member 4
10	5.9	gnf1m00085_s_at	NM_007844		2010319H24 defensein related sequence cryptdin peptide (paneth cells)		75	4.6	gnf1m07637_a_at	NM_028069	5033426G15	solute carrier family 5, member 4a
11	5.9	gnf1m32627_a_at	XM_907141		2010010B23 myosin IA		76	4.6	gnf1m19589_at	NM_177744	C730025L08	transmembrane 4 L six family member 20
12	5.9	gnf1m30302_a_at			2010301M18 cytochrome P450, family 2, subfamily c, polypeptide 66		77	4.6	gnf1m04922_a_at	NM_026328	2010003H20	CAMP responsive element binding protein 3-like 3
13	5.9	gnf1m04289_a_at	NM_023219		2010300P03 solute carrier family 5 (neutral amino acid transporters, system A), member 4b		78	4.6	gnf1m05969_a_at	NM_133184	9130020L07	RIKEN cDNA 2010003H20 gene
14	5.7	gnf1m32637_at	NM_001004184				79	4.6	gnf1m04542_a_at	NM_025453		chloride channel calcium activated 6
							80	4.6	gnf1m11559_a_at	NM_145365	C730034H04	cytochrome P450, family 3, subfamily a, polypeptide 25
15	5.7	gnf1m08052_at	NM_177802		9030221C07 RIKEN cDNA 9030221C07 gene		81	4.6	gnf1m14304_at		C730009I07	oncomodulin
16	5.7	gnf1m12505_a_at	NM_134420		B930010B04 solute carrier family 26, member 6		82	4.6	gnf1m30770_a_at	NM_019792	9030616M21	cytochrome P450, family 3, subfamily a, polypeptide 11
17	5.6	gnf1m01024_x_at	NM_007850				83	4.6	gnf1m30972_a_at	NM_019792	F630101B18	spingomyelin phosphodiesterase, acid-like 3B
18	5.6	gnf1m01025_x_at	NM_007851				84	4.6	gnf1m09954_at	NM_033039	D630044A17	solute carrier family 5 (sodium/glucose cotransporter), member 12
19	5.6	gnf1m33650_at	NM_001033199		9130019N24 expressed sequence AI747448		85	4.6	gnf1m00257_a_at	NM_007818	9030616M21	maltese glycoamylase
20	5.5	gnf1m09931_a_at	NM_153069				86	4.6	gnf1m06091_a_at	NM_133888	2010015N05	apolipoprotein C-II
							87	4.6	gnf1m22391_a_at	NM_001003915		defensein related cryptdin, related sequence 10
21	5.5	gnf1m10976_a_at	NM_009034		1110002L02 retinol binding protein 2, cellular		88	4.5	gnf1m30561_a_at	XM_922811	9030006L09	Transcribed locus
22	5.5	gnf1m34175_at	XM_909581				89	4.5	gnf1m30028_a_at	NM_023314	2010000G01	fatty acid binding protein 2, intestinal
23	5.5	gnf1m05700_a_at	NM_031884		C730040P06 ATP-binding cassette, sub-family G (WHITE), member 5		90	4.5	gnf1m32523_a_at	NM_007845		gene model 1123, (NCBI)
24	5.4	gnf1m08281_a_at	NM_177182		A830053O21 RIKEN cDNA A830053O21 gene		91	4.5	gnf1m21818_at		9130012O13	RIKEN cDNA 9130012O13 gene
25	5.4	gnf1m30198_a_at	NM_027286		C630041D11 angiotensin I converting enzyme (peptidyl-di-peptidase A) 2		92	4.5	gnf1m01102_a_at	NM_007980	M5C1032P19	ectonucleoside triphosphate diaphosphorylase 7
							93	4.4	gnf1m34080_at	XM_905190		
26	5.4	gnf1m04160_a_at	NM_021719		2210009B08 claudin 15		94	4.4	gnf1m30028_a_at	XM_905190		
27	5.4	gnf1m02427_x_at	NM_010584				95	4.4	gnf1m16792_a_at	NM_053103		
28	5.3	gnf1m15427_x_at			intelectin a Mouse C3H/HeJ cryptdin-15 (Defcr15) mRNA, partial cds /gi=437265 /len=119							
					U G J							

61/97

62/97

20	6.3	gnf1m04045_a_at	NM_021351	6820402K11	crystallin, beta A4	92	4.0	gnf1m21871_at		A130059I02	WW domain-containing
21	6.3	gnf1m05528_a_at	NM_029987		retinal pigment epithelium 65						oxidoreductase
22	6.2	gnf1m04046_a_at	NM_021352		crystallin, beta B3	93	4.0	gnf1m08160_a_at	NM_177162	9930101B10	RIKEN cDNA 9930032O22 gene
23	6.2	gnf1m29067_a_at		A930021D15	ankyrin repeat domain 33	No. 11, medial olfactory epithelium specific genes					
24	6.2	gnf1m04142_a_at	NM_021541	E130107M19	crystallin, beta A2	#1	#2	#3	#4	#5	#6
25	6.1	gnf1m16702_at	NM_021478	D430040H24	tubby like protein 1	1	7.0	gnf1m22599_a_at		E330010A04	hypothetical Bactericidal
26	6.1	gnf1m05646_a_at	NM_031202	G370117C01	tyrosinase-related protein 1						permeability-increasing protein,
27	6.1	gnf1m12896_a_at	NM_009965	D230003J06	crystallin, beta A1						BPI structure containing protein
28	6.1	gnf1m00980_a_at	NM_007775		crystallin, gamma C	2	6.6	gnf1m17012_a_at	XM_489285	5730403I07	RIKEN cDNA 5730403I07 gene
29	5.9	gnf1m00703_a_at	NM_008140	A930002G18	guanine nucleotide binding protein, alpha transducing 1	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
30	5.9	gnf1m19361_at		5930422J03	tolloid-like						alpha 2
31	5.8	gnf1m00768_a_at	NM_007378	D830040G08	ATP-binding cassette, sub-family A (ABC1), member 4	5	6.5	gnf1m06812_s_at	NM_147068		olfactory receptor 168
						6	6.3	gnf1m12913_s_at	NM_177087	K230038F04	RIKEN cDNA 4632412N22 gene
32	5.8	gnf1m29957_a_at	NM_007723		cyclic nucleotide gated channel alpha 1	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)
33	5.8	gnf1m08653_a_at	NM_145601	A930006A15	cDNA sequence BC016201	9	5.8	gnf1m12708_a_at	NM_172898	C530042M23	kin of IRRE like 2 (Drosophila)
34	5.8	gnf1m13044_a_at	NM_008600	E130102N08	major intrinsic protein of eye lens fiber	10	5.8	gnf1m31135_at	NM_194357	4833435C14	antimicrobial peptide RYA3
						11	5.7	gnf1m07387_at	NM_153589	4930527E21	transmembrane protein 16B
35	5.8	gnf1m17874_a_at		E130218I03	RIKEN cDNA E130106C14 gene	12	5.7	gnf1m07056_s_at	NM_146913		olfactory receptor 1347
36	5.7	gnf1m21962_a_at	XM_923785	A930011N13	cDNA sequence BC048943	13	5.6	gnf1m20169_at		A330065M03	RIKEN cDNA A330043J11 gene
37	5.6	gnf1m16693_at	NM_011302		retinosis 1 homolog (human)	14	5.5	gnf1m03300_a_at	NM_013809	3110040K11	cytochrome P450, family 2, subfamily g, polypeptide 1
38	5.6	gnf1m17433_a_at		A930007I01	aryl hydrocarbon receptor-interacting protein-like 1	15	5.5	gnf1m13003_a_at	NM_010095	D930015N03	early B-cell factor 2
					dopachrome tautomerase	16	5.2	gnf1m30492_at	NM_029423		flavin containing monooxygenase 6
39	5.5	gnf1m02175_a_at	NM_010024	A930004D23	complexin 4	17	5.5	gnf1m09872_a_at	NM_053184	C130005L05	UDP glucuronosyltransferase 2 family, polypeptide A1
40	5.5	gnf1m06532_a_at	NM_145493	A630063G20	ribosomal protein S2						
41	5.5	gnf1m06697_a_at	NM_146086	5033427A21	rod outer segment membrane protein 1	18	5.4	gnf1m27881_at	NM_010605	D830027N20	potassium inwardly-rectifying channel, subfamily J, member 5
42	5.4	gnf1m01691_a_at	XM_925769								cyclic nucleotide gated channel alpha 4
						19	5.4	gnf1m32233_at	NM_001033317	9230103C20	olfactory receptor 805
43	5.4	gnf1m29850_a_at		A830047P19	HEAT-like (PBS lyase) repeat containing 1	20	5.3	gnf1m06848_x_at	NM_146555		cDNA sequence BC049352
44	5.4	gnf1m10518_a_at	NM_011676	2410112J20	unc-119 homolog (C. elegans)	21	5.3	gnf1m31720_at		A230090L09	cDNA sequence BC048390
45	5.4	gnf1m06693_a_at	NM_146079	7530416I21	guanylate cyclase activator 1B	22	5.3	gnf1m09505_at	NM_178414	3110085P20	S100 calcium binding protein A5
46	5.3	gnf1m02462_a_at	NM_010661	E130302L01	keratin complex 1, acidic, gene 12	23	5.3	gnf1m02739_a_at	NM_011312		cyclin-dependent kinase-like 4 gene model 693, (NCBI)
47	5.3	gnf1m10785_a_at	NM_008189		guanylate cyclase activator 1a (retina)	24	5.3	gnf1m32542_at	NM_001033443	F930014I06	RIKEN cDNA 9230116B18 gene
						25	5.2	gnf1m31310_at	XM_915303		olfactory receptor 136
48	5.2	gnf1m28079_a_at		E130006G23	retinal S-antigen	26	5.2	gnf1m17463_a_at	XM_908788	9230116B18	uromodulin-like 1
49	5.2	gnf1m13409_at	XM_914910		retinitis pigmentosa 1 homolog (human)-like 1	27	5.2	gnf1m06978_at	NM_146807		RIKEN cDNA 5430413K10 gene
						28	5.2	gnf1m09153_a_at	NM_177465	A430096O08	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4
50	5.2	gnf1m12387_a_at	NM_145143	A930032J21	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)	29	5.2	gnf1m07624_a_at	NM_175167	4833413D08	stomatatin (Epb7.2)-like 3
						30	5.2	gnf1m21706_a_at	NM_207210	4933407K03	cDNA sequence BC051070
51	5.2	gnf1m22179_at	NM_001004171	C330036H15	hypothetical gene supported by AK082832	31	5.1	gnf1m07309_a_at	NM_153156		cadherin-like 26
52	5.1	gnf1m20604_a_at	NR_002873	A930007B02	Vax2 opposite strand transcript 1	32	5.1	gnf1m10052_at	NM_178412		Rho-guanine nucleotide exchange factor
53	5.1	gnf1m21792_at		6820439G08	syntaxin 3	33	5.1	gnf1m30005_at	NM_198656	4022416J06	histone 2, H2bb
54	5.1	gnf1m32629_a_at		6330574L03	beaded filament structural protein 2, phakinin	34	5.1	gnf1m15487_at		9230110L08	secretoglobin, family 1C, member 1
55	5.1	gnf1m12366_a_at	NM_023898	A930033D18	phosphodiesterase 6H, cGMP-specific, cone, gamma	35	5.0	gnf1m11843_a_at	NM_178214	1920051L22	calcium/calmodulin-dependent protein kinase II, delta
56	5.1	gnf1m04350_a_at	NM_023695	E130317B02	crystallin, beta B1	36	5.0	gnf1m32183_at	XM_355976		resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)
57	5.1	gnf1m02049_a_at	NM_009751	E130307L19	beaded filament structural protein in lens-FP94	37	5.0	gnf1m24421_at		6430579P05	stomatatin
					G protein-coupled receptpr kinase 1	38	5.0	gnf1m29768_at	NM_183172	9830132D18	solute carrier family 22 (organic anion transporter), member 20
58	5.0	gnf1m13915_at				39	5.0	gnf1m03130_a_at	NM_013515	1830025K05	leucine rich repeat containing 3B
59	5.0	gnf1m12390_a_at		E130109K18	nuclear receptor subfamily 2, group E, member 3	40	5.0	gnf1m32819_at	NM_198650		sulfotransferase family, cytosolic, 1C, member 1
60	5.0	gnf1m01383_a_at	NM_008504		granzyme M (lymphocyte met-ase 1)	41	5.0	gnf1m08272_a_at	NM_146052	A730092P18	RIKEN cDNA 6430500D05 gene
						42	4.9	gnf1m03595_a_at	NM_018751		olfactory receptor 195
62	4.9	gnf1m05099_a_at	NM_027010	3200002G02	crystallin, gamma F	43	4.9	gnf1m17426_a_at		6430500D05	potassium voltage gated channel, Shaw-related subfamily, member 4
63	4.9	gnf1m10704_a_at	NM_013877	A930021F10	calcium binding protein 5	44	4.8	gnf1m07118_at	NM_146998		olfactory marker protein
64	4.9	gnf1m12208_a_at	NM_144929	A930015B08	RIKEN cDNA A330096I21 gene	45	4.8	gnf1m06637_at	NM_145922		target of myb1 homolog (chicken)
65	4.9	gnf1m06746_a_at	NM_146245	A930028G01	leucine rich repeat containing 21	46	4.8	gnf1m02594_at	NM_011010	G630049C14	RIKEN cDNA G630049C14 gene
66	4.8	gnf1m06621_a_at	NM_145835	E130104I05	lactase-like	47	4.8	gnf1m08826_a_at	NM_175024	2310003L06	RIKEN cDNA 2310003L06 gene
67	4.7	gnf1m30040_a_at	NM_011502		syntaxin 3	48	4.7	gnf1m18656_at	NM_144408	C130014A03	early B-cell factor 3
68	4.7	gnf1m01561_a_at	NM_008806	A930009G18	phosphodiesterase 6B, cGMP, rod receptor, beta polypeptide	49	4.7	gnf1m02208_a_at	NM_010096	1700020G18	glutathione peroxidase 6
						50	4.7	gnf1m06516_a_at	NM_145451		monooxygenase, DBH-like 2
69	4.6	gnf1m00940_a_at	NM_007701	7420434P22	C. elegans ceh-10 homeo domain containing homolog	51	4.7	gnf1m06327_a_at	NM_139296	4931403F16	olfactory receptor 212
70	4.6	gnf1m13745_a_at	XM_924558	A930034P04	melan-A	52	4.7	gnf1m07917_at	NM_001011800	D130076C22	RNA binding motif and ELMO domain 1
71	4.6	gnf1m31007_at			cDNA sequence BC048679	53	4.7	gnf1m08422_a_at	NM_144917		claudin 9
72	4.6	gnf1m01625_a_at	NM_008938	7530416B14	retinal degeneration, slow (retinitis pigmentosa 7)	54	4.7	gnf1m03930_a_at	NM_020293	B930086I10	receptor transporter protein 1
											inferred: gb AAL61047.1 (AY073384) olfactory receptor MOR125-1 [Mus musculus] mCG23021
73	4.6	gnf1m11167_a_at	NM_008141	3830432D16	guanine nucleotide binding protein, alpha transducing 2	55	4.7	gnf1m20922_at	NM_001004151		mannosidase, endo-alpha
74	4.6	gnf1m17195_a_at	XM_916650	2310043J07	RIKEN cDNA 2310043J07 gene	56	4.7	gnf1m35554_at			folliculin-like 5
75	4.5	gnf1m22298_at		D230046H12	hypothetical protein	60	4.6	gnf1m05817_a_at	NM_053188	A530024K02	steroid 5 alpha-reductase 2
76	4.5	gnf1m06587_a_at	NM_145598	A930031O08	thioredoxin-like 6	61	4.6	gnf1m07993_at	NM_177350	6030447F07	gluomedin
77	4.5	gnf1m01995_a_at	NM_009644	F730207M15	aryl-hydrocarbon receptor repressor	62	4.5	gnf1m25556_s_at	XM_920918	A830087L05	RIKEN cDNA A730046J19 gene
						63	4.5	gnf1m33178_at			expressed sequence AU021092
78	4.5	gnf1m00726_a_at	NM_007770	E130106I11	cone-rod homeobox containing gene	64	4.4	gnf1m10706_a_at	NM_009993	1300003J07	cytochrome P450, family 1, subfamily a, polypeptide 2
79	4.4	gnf1m12378_a_at	NM_021340	A930029L15	retinal G protein coupled receptor	65	4.4	gnf1m24678_a_at		1700001O02	RIKEN cDNA 1700041C02 gene
80	4.4	gnf1m26137_a_at	NM_001035246	D230020D17	transient receptor potential cation channel, subfamily M, member 3	66	4.4	gnf1m16746_a_at	XM_915229	1190003M12	RIKEN cDNA 1190003M12 gene
						67	4.4	gnf1m03947_s_at	NM_020513		olfactory receptor 1507
81	4.3	gnf1m10693_a_at	NM_133205	I420013G23	RIKEN cDNA 6330407D12 gene	68	4.4	gnf1m07372_a_at	NM_153558		lipocalin 13
82	4.3	gnf1m07838_at	NM_175098		gamma-aminobutyric acid (GABA-C) receptor, subunit rho 1	69	4.4	gnf1m23372_a_at	NM_001007581	4933412J21	similar to mNori-2p
83	4.2	gnf1m01159_a_at	NM_008075			70	4.4	gnf1m18551_at		2610011C15	guanine nucleotide binding protein, alpha stimulating, olfactory type
											inferred: ref NP_057440.1 (NM_016356) RU25 [Homo sapiens] mCG116692
84	4.2	gnf1m21507_at	NM_174999	E130012K09	hypothetical protein E130012K09						similar to odorant binding protein 2B
85	4.1	gnf1m03006_a_at	NM_011881		G protein-coupled receptpr kinase 1	71	4.3	gnf1m33892_at			
86	4.1	gnf1m01176_a_at	NM_008106		opsin 1 (cone pigments), medium-wave-sensitive (color blindness, deutan)	72	4.3	gnf1m33007_at	XM_913800		
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						

73	4.3	gnf1m02475_a_at	NM_010694		lipocalin 3	57	4.4	gnf1m02017_a_at	NM_009680		adaptor-related protein complex 3, beta 1 subunit
74	4.3	gnf1m24804_at		9330210P10	calmegin	58	4.4	gnf1m04944_a_at	NM_026386	I830170H06	sorting nexin 2
75	4.2	gnf1m32690_at		B020010F16	elongation factor RNA polymerase II-like 3	59	4.3	gnf1m00986_s_at	NM_007782	G630018O10	colony stimulating factor 3 receptor (granulocyte)
76	4.2	gnf1m06968_s_at	NM_146794		olfactory receptor 1261	60	4.3	gnf1m07661_s_at	NM_026693	C630001N14	gamma-aminobutyric acid (GABA-A) receptor-associated protein-like 2
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)	61	4.3	gnf1m28675_at			RIKEN cDNA C430049B03 gene
80	4.1	gnf1m03244_at	NM_013702		Unc4.1 homeobox (C. elegans)	62	4.3	gnf1m11974_a_at	NM_009752	I830127P19	galactosidase, beta 1
81	4.1	gnf1m23699_x_at		4921536C22	1700091H14RIK PROTEIN homolog [Mus musculus]	63	4.3	gnf1m01956_a_at	NM_009556		zinc finger protein 42
82	4.1	gnf1m28034_at		E030027N17	hypothetical protein	64	4.3	gnf1m00350_a_at	NM_026360	4930588A18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47
83	4.1	gnf1m07867_a_at	NM_177822	4732467B22	cDNA sequence BC052484	65	4.3	gnf1m13821_at			TEA domain family member 4
84	4.0	gnf1m06411_a_at	NM_144890	E030027N05	cDNA sequence BC018465	66	4.2	gnf1m09428_s_at	NM_025274	I1C0038J20	developmental pluripotency associated 5
85	4.0	gnf1m30647_x_at		1110069O07	RIKEN cDNA 1110069O07 gene	67	4.2	gnf1m09759_a_at	NM_026678	F830220J20	biliverdin reductase A
86	4.0	gnf1m12912_a_at	NM_177087	K230038F04	RIKEN cDNA 4632412N22 gene	68	4.2	gnf1m06713_a_at	NM_146149	2010309H15	cDNA sequence BC026682
87	4.0	gnf1m30608_x_at	NM_001007552		intelectin b	69	4.2	gnf1m15871_a_at	NM_027450	G430030C05	GLI pathogenesis-related 2
No. 12, blastocysts specific genes						70	4.2	gnf1m28768_a_at	XM_917740	A530057A03	similar to predicted similar to mitochondrial glycerol 3-phosphate acyltransferase
#1	#2	#3	#4	#5	#6						
1	7.4	gnf1m32207_at			preferentially expressed antigen in melanoma like 7	71	4.2	gnf1m07439_s_at	NM_008602	4930503N10	protein inhibitor of activated STAT 2
2	7.2	gnf1m10140_at	NM_178249		preferentially expressed antigen in melanoma like 6	72	4.2	gnf1m04103_a_at	NM_021463	I730048G12	phosphoribosyl pyrophosphate synthetase 1
3	6.9	gnf1m32993_x_at		I1C0037K09	unclassifiable	73	4.2	gnf1m04639_a_at	NM_025663	I920080F14	G patch domain containing 4
4	6.7	gnf1m09737_at	NM_178247	I1C0025M01	developmental pluripotency associated 1	74	4.1	gnf1m30194_a_at	NM_001033310	F830006B07	cDNA sequence BC038311
5	6.7	gnf1m30349_at	NM_001034897	I1C0031F10	similar to protease	75	4.1	gnf1m12990_a_at	XM_906312	E430002N06	phosphatidylserine synthase 1
6	6.5	gnf1m05155_at	NM_027344	I0C0030P07	RIKEN cDNA 2310051M13 gene	76	4.1	gnf1m19147_a_at	NM_194344	I420001D24	SH3 domain and tetratricopeptide repeats 1
7	6.5	gnf1m05279_a_at	NM_028218	2210409E12	RIKEN cDNA 2210409E12 gene	77	4.1	gnf1m28148_at		E130203M01	weakly similar to KIAA0042 PROTEIN [Homo sapiens]
8	6.4	gnf1m29226_a_at	XM_915636	I1C0037D04	nuclear domain 10 protein 52	78	4.1	gnf1m09348_a_at	NM_153548	E430025E21	RIKEN cDNA E430025E21 gene
9	6.2	gnf1m32956_x_at	NM_001033638	I1C0031F22	Crx opposite strand transcript 1 inferred: ref NP_034375.1 (NM_010245) Friend virus susceptibility 4 [Mus musculus]	79	4.1	gnf1m22820_a_at	NM_001025156	I420019J23	RIKEN cDNA 4633402D15 gene
10	6.2	gnf1m33449_x_at			mCG124469	80	4.1	gnf1m25585_at		A430033H03	inferred: RIKEN cDNA 4932432N11 gene
11	5.8	gnf1m31026_s_at		G630020J15	hypothetical LOC434126	81	4.1	gnf1m28582_a_at		1500003O18	makorin, ring finger protein, 1
12	5.8	gnf1m33860_at	NM_001025435	I1C0015P14	cDNA sequence BC053393	82	4.1	gnf1m12854_a_at	NM_080452	G730023G11	mitochondrial ribosomal protein S2
13	5.7	gnf1m22399_at		D630033B11	transient receptor potential cation channel, subfamily V, member 5	83	4.1	gnf1m00844_a_at	NM_007515	G730021I22	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3
14	5.6	gnf1m13158_at	NM_011790	I1C0031E08	ariadne homolog 2 (Drosophila)	84	4.0	gnf1m01735_a_at	XM_911233	I1C0050J07	stromal cell derived factor receptor 2
15	5.4	gnf1m35498_x_at			obsolete Celera prediction mCT146197	85	4.0	gnf1m29874_a_at	XM_908144	9430066F19	glutamyl-prolyl-tRNA synthetase
16	5.3	gnf1m33306_x_at			uncharacterized Celera prediction mCG126957						
17	5.3	gnf1m08675_a_at	NM_177731	C130073F10	RIKEN cDNA C130073F10 gene	No. 13, placenta specific genes					
18	5.2	gnf1m00385_a_at	NM_133792	F630115J08	lysophospholipase 3	#1	#2	#3	#4	#5	#6
19	5.2	gnf1m07231_at	NM_148942		serine (or cysteine) peptidase inhibitor, clade B, member 6c	1	7.2	gnf1m30798_at	NM_001033372	I920038K03	gene model 648, (NCBI)
20	5.2	gnf1m03790_a_at	NM_019727	I920049H08	sorting nexin 1	2	7.1	gnf1m16016_a_at		1600012P17	RIKEN cDNA 1600012P17 gene
21	5.1	gnf1m21099_at		C230095C13	unclassifiable	3	7.0	gnf1m03049_x_at	NM_011963		pregnancy specific glycoprotein 18
22	5.1	gnf1m18865_a_at	NM_013827	E330027A01	metal response element binding transcription factor 2	4	6.9	gnf1m32962_at	NM_001029987	G630014J02	diamine oxidase-like protein 2
23	5.0	gnf1m16204_a_at	NM_028615	I1C0040O20	developmental pluripotency associated 2	5	6.7	gnf1m09648_a_at	NM_020261	1620401C02	pregnancy-specific glycoprotein 23
24	5.0	gnf1m03897_at	NM_020018		melanoma antigen, family A, 5	6	6.7	gnf1m04749_a_at	NM_025896	1600032A24	prolactin like protein I
25	4.9	gnf1m02130_a_at	NM_009903		claudin 4	7	6.7	gnf1m16800_at	NM_029355	1600014J19	prolactin-like protein N
26	4.9	gnf1m09355_s_at	NM_025274	I1C0038J20	developmental pluripotency associated 5	8	6.6	gnf1m29570_at			inferred: ref XP_065416.1 (XM_065416) similar to fibulin 1 isoform C precursor (H. sapiens) [Homo sapiens] mCG21007
27	4.9	gnf1m16230_a_at	NM_015798	I1C0048I09	F-box protein 15	9	6.5	gnf1m04964_a_at	NM_026429	I530008A16	trophoblast specific protein beta
28	4.9	gnf1m30904_at	XM_918785		Unknown (protein for IMAGE:3003377)	10	6.5	gnf1m30794_at	XM_904271	I530030E10	pregnancy-specific glycoprotein 30
29	4.8	gnf1m13938_a_at	NM_025890	I1C0007M13	RIKEN cDNA 2410004A20 gene	11	6.5	gnf1m05493_a_at	NM_029636	1600010J02	cathepsin Q
30	4.8	gnf1m29385_s_at	NM_010136	C130084G11	eomesodermin homolog (Xenopus laevis)	12	6.5	gnf1m33489_at	XM_916868		papalysin 2
31	4.7	gnf1m08808_a_at	NM_172822	F630022B06	phosphatidylinositol glycan, class Z	13	6.4	gnf1m32390_at			inferred: ref XP_067564.1 (XM_067564) hypothetical protein XP_067564 [Homo sapiens] mCG21029
32	4.7	gnf1m06235_a_at	NM_134248	5031400I12	hepatitis A virus cellular receptor 1	14	6.4	gnf1m33745_at	NM_054060		pregnancy-specific glycoprotein 25
33	4.7	gnf1m19280_at	NM_001033321	4932417I16	RIKEN cDNA 4932417I16 gene	15	6.3	gnf1m15571_a_at	XM_921301	1600014K23	RIKEN cDNA 1600014K23 gene
34	4.7	gnf1m09637_a_at	NM_152810	I920070H23	cell division cycle 5-like (S. pombe)	16	6.3	gnf1m02675_a_at	NM_011168	1600027O19	prolactin-like protein F
35	4.6	gnf1m12684_a_at	NM_007673	C430044A20	caudal type homeo box 2	17	6.3	gnf1m05085_a_at	XM_895640	1600000I23	cathepsin 3
36	4.6	gnf1m31183_a_at	XM_485202	C130020L13	zinc finger and BTB domain containing 10	18	6.2	gnf1m04302_a_at	NM_023289	I530005M18	CEA-related cell adhesion molecule 11
37	4.6	gnf1m07339_at	NM_153417		transient receptor potential cation channel, subfamily M, member 6	19	6.2	gnf1m05868_x_at	NM_054063		pregnancy-specific glycoprotein 28
38	4.6	gnf1m02280_a_at	NM_010269	I1C0017N07	ganglioside-induced differentiation-associated-protein 2	20	6.2	gnf1m11080_a_at	NM_012007	1600023H08	cathepsin J
39	4.6	gnf1m12533_a_at	NM_029094	G430147P21	phosphatidylinositol 3-kinase, catalytic, beta polypeptide	21	6.2	gnf1m03882_a_at	NM_019991	1600012E17	prolactin-like protein M
40	4.6	gnf1m05056_a_at	NM_026728	I1C0025L16	enoyl Coenzyme A hydratase domain containing 2	22	6.1	gnf1m03922_a_at	NM_020284	3830409D04	cathepsin R
41	4.6	gnf1m10775_a_at	NM_008624	C820001L23	muscle and microspikes RAS	23	6.0	gnf1m04578_a_at	NM_025532	2310047B08	prolactin-like protein K
42	4.6	gnf1m00324_a_at	NM_146093	4930455J02	DNA segment, Chr 19, ERATO Doi 721, expressed	24	6.0	gnf1m18606_a_at	XM_904257	I530030E10	pregnancy-specific glycoprotein 30
43	4.6	gnf1m08503_a_at	NM_172758	D430050E18	cDNA sequence BC031853	25	5.9	gnf1m05311_at	NM_028477	1600017L04	prolactin like protein C delta
44	4.6	gnf1m29738_at		I830072P10	RAB20, member RAS oncogene family	26	5.9	gnf1m17882_at		8030442B19	pregnancy specific glycoprotein 16
45	4.5	gnf1m16279_at	NM_134249	I1C0024G10	T-cell immunoglobulin and mucin domain containing 2	27	5.8	gnf1m07686_a_at	NM_023741	I530009E04	prolactin-like protein C 3
46	4.5	gnf1m12675_a_at	XM_922775	I1C0015J23	leucyl-tRNA synthetase	28	5.7	gnf1m04093_a_at	NM_021445	1600022N02	cathepsin 6
47	4.5	gnf1m09876_a_at	NM_145950	C230027H09	cDNA sequence BC010311	29	5.7	gnf1m11084_a_at	NM_009411	2610015G13	trophoblast specific protein alpha
48	4.5	gnf1m10749_a_at	NM_180678	I730038J10	glycyl-tRNA synthetase	30	5.7	gnf1m11083_a_at	XM_895696	1600027J17	cathepsin M
49	4.5	gnf1m03440_a_at	NM_181329	I730062F04	coilin	31	5.7	gnf1m08759_at	NM_173420	D930020E02	RIKEN cDNA D930020E02 gene
50	4.5	gnf1m17293_at		4833426J09	RIKEN cDNA 4833426J09 gene	32	5.6	gnf1m05138_a_at	NM_028171	I530025P09	CEA-related cell adhesion molecule 13
51	4.5	gnf1m22649_at		E530001F21	RIKEN cDNA E530001F21 gene	33	5.5	gnf1m06261_a_at	NM_138648		oxidized low density lipoprotein (lectin-like) receptor 1
52	4.4	gnf1m05466_a_at	NM_029456	E430019I11	SAPS domain family, member 3	34	5.5	gnf1m11081_a_at	NM_008865	I530016N24	chorionic somatomammotropin hormone 2
53	4.4	gnf1m30025_s_at	XM_904497	6330513H14	Wilms' tumour 1-associating protein	35	5.5	gnf1m09346_s_at	NM_181852	I530023D16	proliferin
54	4.4	gnf1m06099_a_at	NM_133937	1700020E14	RIKEN cDNA 6720456B07 gene	36	5.4	gnf1m04824_a_at	NM_026087	I530016C18	CEA-related cell adhesion molecule 12
55	4.4	gnf1m10821_at	NM_011396	B930066D05	solute carrier family 22 (organic cation transporter), member 5	37	5.3	gnf1m11077_a_at	NM_011167	1600017E04	prolactin-like protein C 1
56	4.4	gnf1m31134_at	XM_903021	F630103C07	oxysterol binding protein-like 7	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						(XM_060406) similar to
45	5.0	gnf1m19297_a_at	NM_001033424	I530025D16	RIKEN cDNA 5031408O05 gene						diaphanous homologue (H.
46	4.9	gnf1m30812_at	XM_907647		gene model 719, (NCBI)						sapiens) [Homo sapiens]
47	4.9	gnf1m11543_a_at	NM_028958	4933438I11	TAF7-like RNA polymerase II, associated factor		28	4.7	gnf1m34324_at	XM_905672	mCG1036717
					TATA box binding protein (TBP)-associated factor		29	4.6	gnf1m18462_a_at	NM_027551	gene model 1075, (NCBI)
48	4.8	gnf1m00926_a_at	NM_007677		pregnancy specific glycoprotein 17		30	4.6	gnf1m32122_at	NM_001033042	RIKEN cDNA 4631423F02 gene
49	4.8	gnf1m15536_at		4930486L24	RIKEN cDNA 4930486L24 gene		31	4.6	gnf1m03360_a_at	XM_924012	expressed sequence A1595366
50	4.6	gnf1m16953_a_at	NM_027512	C430021A01	RIKEN cDNA 3830417A13 gene						calcium channel, voltage-
51	4.6	gnf1m05252_at	NM_028045	1600014E20	RIKEN cDNA 1600014E20 gene		32	4.6	gnf1m19063_at		dependent, L type, alpha 1S subunit
52	4.6	gnf1m19995_at		A130029G22	hypothetical protein					A230005G17	ankyrin repeat and SOCS box-
53	4.6	gnf1m11323_a_at	NM_011453	5031401I15	serine (or cysteine) peptidase inhibitor, clade B, member 9c		33	4.6	gnf1m33481_at		containing 16
					inferred: ref NP_058704.1						(NM_017008) glyceraldehyde-3-
54	4.5	gnf1m17335_at	XM_919174	4933402E13	RIKEN cDNA 4933402E13 gene						phosphate dehydrogenase [Rattus
55	4.5	AFFX-TransRecMur/X57349_5_at		0	alpha fetoprotein		34	4.6	gnf1m31103_at	XM_358900	norvegicus] mCG123870
56	4.5	gnf1m00788_a_at	NM_007423	I920085C12	RIKEN cDNA 5031408O05 gene						rabphilin 3A-like (without C2
57	4.5	gnf1m29081_s_at	XM_908287	I530025D16	0		35	4.6	gnf1m14303_at		domains)
58	4.4	AFFX-TransRecMur/X57349_3_at		I530026J03	decidual/trophoblast prolactin-related protein		36	4.6	gnf1m23260_at		2310074I15
59	4.4	gnf1m02205_at	NM_010088		prolactin like protein O					2310058C22	myosin, heavy polypeptide 1,
60	4.4	gnf1m09276_s_at	XM_895253	3830412A07	tumor necrosis factor receptor superfamily, member 11b		37	4.5	gnf1m21860_a_at	XM_919342	skeletal muscle, adult
61	4.4	gnf1m00108_at	NM_008764	I530030F10	(osteoprotegerin)						myosin, light polypeptide kinase 2,
					serine (or cysteine) peptidase inhibitor, clade B, member 9e		38	4.5	gnf1m32807_at	NM_011652	skeletal muscle
62	4.3	gnf1m02812_a_at	NM_011456	C430007E01	RIKEN cDNA 1600015I10 gene		39	4.5	gnf1m32799_at	XM_912786	titin
					reproductive homeobox 9						similar to tripartite motif-
63	4.3	gnf1m05136_a_at	XM_904843	1600015I10	triggering receptor expressed on myeloid cells 2		40	4.4	gnf1m17057_at	XM_907184	containing 63
64	4.3	gnf1m04385_a_at	NM_023894	1600026O01	mitochondrial tumor suppressor 1		41	4.4	gnf1m33513_at	XM_905086	RIKEN cDNA 2310015B20 gene
65	4.3	gnf1m05649_a_at	NM_031254	F730040N08	0						similar to Triosephosphate
					coagulation factor XI		42	4.4	gnf1m08139_a_at	NM_177707	isomerase (TIM) (Triose-phosphate
66	4.3	gnf1m20286_s_at	NM_001005863	F430107K21	0		43	4.4	gnf1m11347_a_at	NM_080444	isomerase)
67	4.2	AFFX-TransRecMur/X57349_M_at		1600027G01	RIKEN cDNA 4933402E13 gene						SH3 and cysteine rich domain 3
68	4.2	gnf1m05257_a_at	NM_028066	G630096J22	protocadherin 12		44	4.4	gnf1m25405_s_at	NM_172381	ankyrin repeat and SOCS box-
69	4.2	gnf1m17336_a_at	XM_919174	4933402E13	hypothetical protein 9530076L18		45	4.4	gnf1m11169_a_at	NM_023784	containing protein 10
70	4.2	gnf1m03557_s_at	NM_017378	G630096J22	pregnancy-specific glycoprotein 29		46	4.4	gnf1m22171_at		expressed sequence A1314180
71	4.2	gnf1m19802_at		9530076L18	RIKEN cDNA 3110043J09 gene		47	4.3	gnf1m31602_x_at		2310016N21
72	4.1	gnf1m33493_at	NM_054064	C430030O18	zinc finger protein 36, C3H type-like 3						Yip1 domain family, member 7
73	4.1	gnf1m09438_s_at	NM_028455	E430007O20	serine (or cysteine) peptidase inhibitor, clade B, member 9e						hypothetical protein
74	4.1	gnf1m34547_at	NM_001009549		gene model 719, (NCBI)						inferred: gb AAK91790.1
					VH coding region		48	4.3	gnf1m01879_a_at	NM_009416	(AY042194) MrgA4 RF-amide G
					lipase, endothelial		49	4.3	gnf1m12991_a_at	NM_080856	protein-coupled receptor [Mus
					solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12						musculus] mCG62041
					proline-rich acidic protein 1						tropomyosin 2, beta
											ankyrin repeat and SOCS box-
							50	4.3	gnf1m19330_a_at	XM_916258	containing protein 14
							51	4.3	gnf1m30611_s_at	NM_009109	leiomodlin 3 (fetal)
											ryanodine receptor 1, skeletal
							52	4.3	gnf1m03459_a_at	NM_016749	muscle
							53	4.3	gnf1m18333_s_at	XM_905765	myosin binding protein H
							54	4.3	gnf1m34867_at		myopalladin
											inferred: gb AAL61273.1
											(AY073610) olfactory receptor
											MOR256-19 [Mus musculus]
											mCG56478
No. 14, skeletal muscle specific genes							55	4.3	gnf1m13416_a_at		ankyrin repeat domain 23
#1	#2	#3	#4	#5	#6		56	4.3	gnf1m32724_at	NM_001013013	dehydrogenase/reductase (SDR
1	6.7	gnf1m03905_at	NM_020033	4833407M17	ankyrin repeat domain 2 (stretch responsive muscle)						family) member 7C
2	6.4	gnf1m01571_a_at	NM_173021	B230365M07	phosphorylase kinase alpha 1		57	4.2	gnf1m22074_at		16 days embryo head cDNA,
3	6.2	gnf1m07402_a_at	NM_153786	D930008K19	vestigial like 2 homolog (Drosophila)					C130073O12	RIKEN full-length enriched library,
4	5.9	gnf1m34804_x_at	NM_206870		alpha-interferon						clone: C130073O12
5	5.8	gnf1m31922_at			ENSMUST00000087566 transcript (in rel.37.34e)						product: hypothetical protein, full
6	5.6	gnf1m30823_a_at		2310033H20	calcium channel, voltage-dependent, gamma subunit 6		58	4.2	gnf1m09174_a_at		insert sequence
7	5.6	gnf1m20338_a_at	NM_001013799	A530098C11	RIKEN cDNA A530098C11 gene		59	4.2	gnf1m01743_a_at	NM_009161	aldolase 1, A isoform, pseudogene
8	5.5	gnf1m05628_a_at	NM_031173	F630207K13	calcium channel, voltage-dependent, beta 1 subunit						2
9	5.4	gnf1m05245_a_at	NM_028001	2310032K21	RIKEN cDNA 2300003C06 gene		60	4.2	gnf1m10776_a_at	NM_021508	sarcoglycan, alpha (dystrophin-
10	5.4	gnf1m11854_at	NM_026056	7630403A08	CAP, adenylate cyclase-associated protein, 2 (yeast)		61	4.2	gnf1m16196_s_at	NM_011743	associated glycoprotein)
11	5.3	gnf1m27133_at		C630012A10	DUAL-SPECIFICITY PHOSPHATASE TS-DSP1 homolog [Mus musculus]		62	4.2	gnf1m31378_x_at		myozenin 1
12	5.2	gnf1m05911_a_at	NM_080466	A030001A14	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3						zinc finger protein 106
13	5.1	gnf1m30505_a_at		6030430B11	hypothetical Zinc finger, C2H2 type containing protein						inferred: ref NP_032110.1
14	5.1	gnf1m02082_a_at	NM_009813		calsequestrin 1						(NM_008084) glyceraldehyde-3-
15	5.1	gnf1m31732_at			ENSMUST00000058085 transcript (in rel.37.34e)						phosphate dehydrogenase [Mus
16	5.0	gnf1m32501_at			inferred: ref NP_031464.1 (NM_007438) aldolase 1, A isoform [Mus musculus]						musculus] mCG8986
17	4.9	gnf1m00652_a_at	NM_177776	D830039B09	RIKEN cDNA D130058I21 gene		63	4.2	gnf1m30588_a_at	XM_905765	myopalladin
18	4.9	gnf1m05478_a_at	NM_029569	1110018D09	ankyrin repeat and SOCs box-containing protein 5		64	4.2	gnf1m26247_at		hypothetical protein
19	4.9	gnf1m09475_a_at	NM_133723	2310005F16	aspartate-beta-hydroxylase		65	4.2	gnf1m10184_a_at	NM_139297	UDP-glucose pyrophosphorylase 2
20	4.8	gnf1m32144_x_at			ENSMUST00000071116 transcript (in rel.37.34e)		66	4.2	gnf1m30069_at		inferred: ref NP_059127.1
21	4.8	gnf1m03409_a_at	NM_015825		SH3-binding domain glutamic acid-rich protein						(NM_017431) protein kinase,
22	4.8	gnf1m35257_at	XM_911774		similar to Fructose-bisphosphate aldolase A (Muscle-type aldolase) (Aldolase 1)						AMP-activated, gamma 3 non-
23	4.8	gnf1m31500_at	NM_011652		titin						catalytic subunit [Homo sapiens]
24	4.7	gnf1m23094_at		1110018A23	asparagine-linked glycosylation 2 homolog (yeast, alpha-1,3-mannosyltransferase)		67	4.2	gnf1m02316_a_at	NM_010351	mCG133883
25	4.7	gnf1m03011_a_at	NM_011892	4833420L09	sarcoglycan, gamma (dystrophin-associated glycoprotein)		68	4.2	gnf1m12411_a_at	NM_175456	goosecoid
26	4.7	gnf1m31979_at			similar to interferon inducible GTPase similar to interferon-inducible GTPase mCG6032		69	4.1	gnf1m28960_at	NM_001033303	actin-binding Rho activating
27	4.7	gnf1m35934_x_at			inferred: ref XP_060406.1		70	4.1	gnf1m32530_at		protein
											adenosine monophosphate
											deaminase 1 (isoform M)
											inferred: ref NP_032110.1
											(NM_008084) glyceraldehyde-3-
											phosphate dehydrogenase [Mus
											musculus] mCG13844
											5'-nucleotidase, cytosolic III
											similar to Dual specificity protein
											phosphatase 13 (Testis- and
											skeletal-muscle-specific DSP)
											phosphorylase kinase gamma 1
											inferred: ref NP_032110.1
											(NM_008084) glyceraldehyde-3-
											phosphate dehydrogenase [Mus
											musculus] mCG22107
											SARI gene homolog B (S.
											cerevisiae)
											hemochromatosis type 2 (juvenile)
											(human homolog)
											defensin related cryptidin, related
											sequence 12
											tropomodulin 4
											DNA segment, Chr 9, ERATO Doi
											402, expressed

80	4.0	gnf1m32522_at	XM_906658	9830113L01	similar to triadin 95	71	4.1	gnf1m23837_at		4932439N05	DIPEPTIDYL PEPTIDASE 8 homolog [Homo sapiens]
No. 15, thymus specific genes						72	4.0	gnf1m27907_at		D930002G07	unclassifiable
#1	#2	#3	#4	#5	#6	73	4.0	gnf1m05850_a_at	NM_181664	A630014I17	cysteine-rich protein 3 similar to T-cell receptor beta chain VNDNJ precursor
1	6.5	gnf1m22768_at		G630024G08	hypothetical protein	74	4.0	gnf1m34314_at			
2	5.9	gnf1m04258_s_at	NM_023064	4930403I07	RIKEN cDNA 1700021K02 gene	No. 16, snout epidermis specific genes					
3	5.8	gnf1m25105_a_at		9630050A10	unclassifiable	#1	#2	#3	#4	#5	#6
4	5.6	gnf1m13663_at		8230401J17	Stam binding protein like 1	1	6.8	gnf1m32364_at	XM_910151	7530403J15	similar to Serpinb6c protein
5	5.6	gnf1m22627_a_at		E430014B02	RIKEN cDNA E430014B02 gene	2	6.3	gnf1m05120_a_at	NM_027105	2310002B14	RIKEN cDNA 2310002B14 gene
6	5.6	gnf1m04257_a_at	NM_023064	E430019H22	RIKEN cDNA 1700021K02 gene	3	5.8	gnf1m03864_a_at	NM_019956	1110055M01	keratin complex 2, basic, gene 6g
7	5.4	gnf1m20000_a_at		A130034K24	RIKEN cDNA A130034K24 gene	4	5.7	gnf1m03246_a_at	NM_013707		keratin associated protein 14
8	5.4	gnf1m16764_at		2810043O03	RIKEN cDNA 2810043O03 gene	5	5.5	gnf1m03251_at	NM_013713		keratin associated protein 15
9	5.4	gnf1m22098_at		C130095N07	unclassifiable	6	5.4	gnf1m02466_a_at	NM_010666	5430409L11	keratin complex-1, acidic, gene C29
10	5.3	gnf1m13107_a_at	NM_009345	E430024C24	deoxynucleotidyltransferase, terminal	7	5.4	gnf1m07746_a_at	NM_130857	A030006N06	keratin associated protein 16-5
11	5.3	gnf1m01663_a_at	NM_009019	E430001F04	recombination activating gene 1 gb=X00439 Mouse thymocyte mRNA fragment for T-cell receptor pseudogene (86T3)	8	5.3	gnf1m31127_a_at		1920089L09	ADP-ribosylhydrolase like 2
12	5.2	gnf1m17589_at				9	5.3	gnf1m12125_a_at	NM_175424	A030004J04	RIKEN cDNA A030004J04 gene
13	5.1	gnf1m20254_a_at		A430093H23	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430093H23 product:unclassifiable, full insert sequence	10	5.2	gnf1m33887_at	XM_906239		diacylglycerol O-acyltransferase 2-like 3
14	4.9	gnf1m00613_at	NM_009913	4632401H02	chemokine (C-C motif) receptor 9	11	5.2	gnf1m03667_at	NM_019398		eosinophil-associated, ribonuclease A family, member 5
15	4.9	gnf1m25913_a_at		A630097D09	ankyrin repeat domain 10	12	5.2	gnf1m05531_a_at	XM_919025	A030005L19	RIKEN cDNA A030005L19 gene
16	4.8	gnf1m25851_at		A630050N17	epsilon-tubulin 1	13	5.1	gnf1m02617_a_at	NM_011060		peptidyl arginine deiminase, type III
17	4.8	gnf1m27467_a_at		D130059J10	nuclear factor of activated T-cells, cytoplasmic 3	14	5.0	gnf1m08678_at	NM_177661	C130079G13	RIKEN cDNA C130079G13 gene
18	4.8	gnf1m25325_at		C920018K02	T-cell receptor beta, variable 13	15	5.0	gnf1m31483_at			uncharacterized Celera prediction mCG2980
19	4.8	gnf1m25811_at		A630024J20	CD3 antigen, epsilon polypeptide	16	5.0	gnf1m02738_a_at	NM_011310	5430416K16	S100 calcium binding protein A3
20	4.8	gnf1m21369_at		D330030A04	unclassifiable	17	4.9	gnf1m05210_a_at	NM_027844	4833428E21	keratin associated protein 5-2
21	4.8	gnf1m21843_at		I830153K09	unclassifiable	18	4.9	gnf1m18889_at	XM_919033	A030014E15	RIKEN cDNA A030014E15 gene
22	4.7	gnf1m20488_at		A730051E03	unclassifiable	19	4.8	gnf1m13773_at	XM_917709	5530401F02	keratin associated protein 8-1
23	4.7	gnf1m11598_s_at	NM_133206	9630029E07	zinc and ring finger 1	20	4.8	gnf1m00244_a_at	NM_153108		defensin beta 8
24	4.7	gnf1m20046_at		A130077L17	transcription factor 7, T-cell specific	21	4.8	gnf1m16351_at	XR_000508	A030006P16	RIKEN cDNA A030006P16 gene
25	4.7	gnf1m08796_at	NM_178666	E430004N04	RIKEN cDNA E430004N04 gene	22	4.8	gnf1m31507_at	XM_916083		similar to arylacetamide deacetylase
26	4.7	gnf1m13686_at		C630040K21	RIKEN cDNA C630040K21 gene	23	4.7	gnf1m03509_a_at	NM_016880	4833411P03	keratin complex 1, acidic, gene 24
27	4.6	gnf1m20026_at		A130055N14	unclassifiable	24	4.7	gnf1m29350_a_at	XM_904709		keratin complex 1, acidic, gene 3
28	4.6	gnf1m25793_at		A630007H13	T-cell receptor alpha chain precursor V-J region (TA72) (fragment) homolog [Mus musculus]	25	4.7	gnf1m13744_a_at	NM_010668	4732448G14	keratin complex 2, basic, gene 17
29	4.6	gnf1m03450_a_at	NM_016720	C730047I07	neuraminidase 3	26	4.6	gnf1m05238_a_at	NM_027983	A030014I10	RIKEN cDNA 2310015J09 gene
30	4.6	gnf1m25650_at		A430104A14	special AT-rich sequence binding protein 1	27	4.6	gnf1m05741_at	NM_033478		lymphocyte antigen 6 complex, locus G6D
31	4.6	gnf1m28074_at		E130002N09	RIKEN cDNA A430106G13 gene	28	4.6	gnf1m04203_a_at	NM_022322	4833424O07	tenomodulin
32	4.6	gnf1m06569_at	NM_145566		HIV-1 Rev binding protein-like	29	4.6	gnf1m05207_a_at	NM_027819	9030405D14	gamma-glutamyltransferase 6
33	4.6	gnf1m20228_at		A430046P16	hypothetical protein	30	4.6	gnf1m13603_at		A030001H12	keratin associated protein 5-5
34	4.6	gnf1m27019_at		C430005I18	cDNA sequence BC023882	31	4.6	gnf1m05953_at	NM_130870		keratin associated protein 16-1
35	4.5	gnf1m12132_at	XM_909371	A130010M04	RIKEN cDNA 5830406J20 gene	32	4.6	gnf1m02471_a_at	NM_010676		keratin associated protein 8-2
36	4.5	gnf1m18858_a_at	NM_198297	A430035I04	T cell receptor associated transmembrane adaptor 1	33	4.5	gnf1m11033_s_at	NM_007703	1300004I20	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast) like 3
37	4.5	gnf1m28369_s_at		E430013N08	RIKEN cDNA 1110007A06 gene	34	4.5	gnf1m16438_at		2310040C09	RIKEN cDNA 2310040C09 gene
38	4.4	gnf1m02686_a_at	NM_011195		pre T-cell antigen receptor alpha	35	4.5	gnf1m05873_at	NM_054074		defensin beta 6
39	4.4	gnf1m21857_a_at		9630045H20	RIKEN cDNA 9630045H20 gene	36	4.5	gnf1m28699_a_at	NM_001033171	G830034I03	RIKEN cDNA 2310020F24 gene
40	4.4	gnf1m01333_a_at	NM_008418		potassium voltage-gated channel, shaker-related subfamily, member 3	37	4.5	gnf1m06689_a_at	NM_146063	4733401E22	cDNA sequence BC031593
41	4.4	gnf1m13655_s_at		E430032M10	T-cell receptor gamma, variable 4	38	4.4	gnf1m05849_a_at	NM_053249		keratin complex 2, basic, gene 20
42	4.4	gnf1m20342_at		A630005I04	RIKEN cDNA A630005I04 gene	39	4.4	gnf1m13354_a_at	XM_919110	5530401N06	RIKEN cDNA 5530401N06 gene
43	4.4	gnf1m14243_at		5530401D11	RIKEN cDNA 5530401D11 gene	40	4.4	gnf1m32206_at			gene model 247, (NCBI)
44	4.4	gnf1m21085_a_at		E430002K11	RIKEN cDNA C230085N15 gene	41	4.4	gnf1m06048_a_at	NM_133730	4631426H08	RIKEN cDNA 4631426H08 gene
45	4.4	gnf1m17830_at		C920008N22	RIKEN cDNA C920008N22 gene	42	4.3	gnf1m03967_at	NM_020576	A030012F01	psoriasis susceptibility 1 candidate 2 (human)
46	4.4	gnf1m25080_at		9630042D24	unclassifiable	43	4.3	gnf1m17405_a_at	NM_028973	5430427N11	leucine rich repeat containing 15
47	4.4	gnf1m19341_at		5830444F18	RIKEN cDNA 5830444F18 gene	44	4.3	gnf1m17069_a_at	XM_894986	4632435A09	G protein-coupled receptor 115
48	4.3	gnf1m04270_a_at	NM_023137	2010309G22	ubiquitin D	45	4.2	gnf1m15703_at			keratin associated protein 16-9
49	4.3	gnf1m25648_at		A430103G07	inferred: Mouse (clone RAD11) T-cell receptor rearranged delta-chain mRNA V-D-J-C region, 3' end	46	4.2	gnf1m05066_at	NM_026807	1110033F04	RIKEN cDNA 1110033F04 gene
50	4.3	gnf1m25146_at		9830125P17	myeloblastosis oncogene	47	4.2	gnf1m21863_at	XM_919372	9930021F22	diacylglycerol O-acyltransferase 2-like 6
51	4.3	gnf1m25878_at		A630074B15	nuclear receptor coactivator 6 interacting protein	48	4.2	gnf1m08176_a_at	NM_177723	A030011M19	hypothetical protein A030011M19
52	4.3	gnf1m13884_at			Mouse T cell receptor mRNA /cgs=UNKNOW /gb=M97158 /gi=200865 /len=1093 gnl[UG]/Mm#S121750	49	4.2	gnf1m02463_a_at	NM_010663		keratin complex 1, acidic, gene 17
53	4.3	gnf1m21072_at	NM_207265	C230071H18	RIKEN cDNA C230071H18 gene	50	4.2	gnf1m06678_a_at	NM_146030	F630041G20	pleckstrin homology domain containing, family H (with MyTH4 domain) member 3
54	4.3	gnf1m27741_a_at		D430042L22	Adult male thymus cDNA, RIKEN full-length enriched library, clone:5830431N23 product:unclassifiable, full insert sequence	51	4.2	gnf1m11415_a_at	NM_008127	4733401H10	gap junction membrane channel protein beta 4
55	4.3	gnf1m27277_at		D030017L14	RAB14, member RAS oncogene family	52	4.2	gnf1m29988_a_at	NM_010667	4732481L17	keratin complex 2, basic, gene 10
56	4.3	gnf1m13116_a_at	NM_177194	E430003K09	RIKEN cDNA A130023I24 gene	53	4.1	gnf1m30692_a_at		9130204L05	RIKEN cDNA 9130204L05 gene
57	4.2	gnf1m20047_at		A130077N19	unclassifiable	54	4.1	gnf1m02470_a_at	NM_010673		keratin associated protein 6-2
58	4.2	gnf1m07721_a_at		E430026B20	thyroid hormone receptor associated protein 2	55	4.1	gnf1m29164_a_at	XM_925719	2310051B22	X-ray repair complementing defective repair in Chinese hamster cells 1
59	4.2	gnf1m19347_at		5830468D02	unclassifiable	56	4.1	gnf1m21868_at		A030010G24	6 days neonate skin cDNA, RIKEN full-length enriched library, clone:A030010G24 product:hypothetical protein, full insert sequence
60	4.2	gnf1m25123_a_at		A130079G03	RIKEN cDNA A130001G05 gene	57	4.1	gnf1m05184_a_at	NM_027563	4733401E01	keratin complex 1, acidic, gene 4
61	4.2	gnf1m19996_at		A130029H20	unclassifiable	58	4.1	gnf1m21643_at	XM_905488	4833413O15	RIKEN cDNA 4833413O15 gene
62	4.2	gnf1m01729_a_at	NM_009138	4921533C11	chemokine (C-C motif) ligand 25	59	4.1	gnf1m29218_a_at	XM_130987	5430417P09	retinoic acid receptor responder (tazarotene induced) 1
63	4.2	gnf1m18624_a_at		9030625I09	RIKEN cDNA 1700069O15 gene	60	4.0	gnf1m06739_a_at	NM_146213	A030007M20	cDNA sequence BC026374
64	4.2	gnf1m02324_a_at	NM_010364	I530030O21	general transcription factor II H, polypeptide 4	61	4.0	gnf1m14590_a_at	XM_916112	4930449A18	RIKEN cDNA 4930449A18 gene
65	4.2	gnf1m24091_s_at		A130043E07	similar to T-cell receptor alpha chain V region CTL-F3 precursor [Mus musculus]	62	4.0	gnf1m15601_at	NM_183189		keratin associated protein 13-1
66	4.1	gnf1m20621_at	NM_001001497	A930013B10	RIKEN cDNA A930013B10 gene	63	4.0	gnf1m15672_at	NM_001013823		similar to keratin associated protein 4-10; keratin associated protein 4.10
67	4.1	gnf1m25293_at		A130022O15	protease, serine, 16 (thymus)	64	4.0	gnf1m09801_s_at	NM_016879	4732459O18	keratin complex 2, basic, gene 18
68	4.1	gnf1m29160_s_at		9230110J10	hypothetical protein	65	4.0	gnf1m15543_at	XM_924606	1110030O19	kallikrein 5
69	4.1	gnf1m20028_at		A130058I09	unclassifiable	66	4.0	gnf1m19951_at		A030004L08	gene model 312, (NCBI)
70	4.1	gnf1m18427_a_at		E430019C18	RIKEN cDNA 2600010L24 gene	67	4.0	gnf1m05296_a_at		2810039D03	angiopoietin-like 1
No. 17, mammary gland (lact) specific genes						68	4.0	gnf1m05946_a_at	NM_130856	1110002D05	keratin associated protein 16-8
#1	#2	#3	#4	#5	#6	No. 17, mammary gland (lact) specific genes					
1	7.4	gnf1m10696_a_at	NM_133892	D730001H10	L-amino acid oxidase 1	#1	#2	#3	#4	#5	#6

2	7.1	gnflm03113_a_at	NM_013483	D730003G03	butyrophilin, subfamily 1, member A1	No. 18, bone marrow specific genes					
3	7.1	gnflm12986_a_at	NM_009973	D730045O16	casein delta	#1	#2	#3	#4	#5	#6
4	7.0	gnflm02472_a_at	NM_010679		lactalbumin, alpha	1	5.6	gnflm28110_at		E130103H07	inferred: ADP-ribosylation factor-directed GTPase activating protein isoform b [Mus musculus]
5	6.7	gnflm10796_a_at	NM_011709	D730001D15	whey acidic protein						
6	6.7	gnflm00987_a_at	NM_007784	D730016P16	casein alpha	2	5.4	gnflm18248_a_at		E130213N17	unclassifiable
7	6.5	gnflm15416_a_at			casein kappa	3	5.1	gnflm14290_a_at	XR_000511	4930456L15	RIKEN cDNA 4930456L15 gene
8	6.5	gnflm32098_at			inferred: ref NP_055712.1 (NM_014897) KIAA0924 protein [Homo sapiens] mCG3800	4	5.1	gnflm32867_x_at	XM_917898		similar to zinc finger protein 658
						5	5.1	gnflm27552_at		D230014K09	ARF10 actin-related protein 10 homolog (S. cerevisiae)
9	6.3	gnflm00588_a_at	NM_009972	D730049P05	casein beta	6	5.0	gnflm33375_x_at			ENSMUST00000090609 transcript (in rel.37.34e)
10	6.3	gnflm33440_at	XM_904420		similar to Golgi autoantigen, golgin subfamily A member 2 (Golgi matrix protein GM130)	7	5.0	gnflm34742_at	NM_207621		olfactory receptor 553
11	5.9	gnflm27777_s_at	NM_199009	I420028O07	RIKEN cDNA 4632419K20 gene	8	4.8	gnflm19694_a_at		A730034A12	RIKEN cDNA 9330209N08 gene
12	5.9	gnflm00988_at	NM_007785	D730050N06	casein gamma	9	4.8	gnflm32725_at	XM_908293		similar to glucagon-like peptide 2 receptor
13	5.8	gnflm08137_at	NM_172732	9830005G06	C-type lectin domain family 9, member a	10	4.7	gnflm20333_at		A530095B06	hypothetical protein
14	5.8	gnflm30289_a_at		4732460E09	lysyl-tRNA synthetase, pseudogene 1	11	4.7	gnflm02136_at	NM_009921	7330411H24	cathelicidin antimicrobial peptide solute carrier family 6 (neurotransmitter transporter, serotonin), member 4
15	5.5	gnflm02199_a_at			dentin sialophosphoprotein	12	4.7	gnflm24540_at			RIKEN cDNA 9830134C10 gene
16	5.5	gnflm26737_at		C130045M15	expressed sequence AI197445	13	4.6	gnflm19887_a_at	NM_001002786	9830134C10	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]
17	5.4	gnflm05767_a_at	NM_033618		suppressor of Ty 16 homolog (S. cerevisiae)	14	4.6	gnflm15155_at		4833426L05	cDNA sequence BC027057
18	5.3	gnflm00179_at	NM_022317	G830037O11	solute carrier family 28 (sodium-coupled nucleoside transporter), member 3						unclassifiable
19	5.2	gnflm28323_at		E330031L19	RIKEN cDNA 4432405B04 gene						Transcribed locus
20	5.1	gnflm26667_at		C130015N15	unclassifiable						glycophorin A
21	5.1	gnflm15655_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	15	4.6	gnflm08144_a_at	NM_145976	C330008G01	tripartite motif protein 10
					inferred: gb AAC14131.1 (AF057564) putative retrovirus-related gag protein [Rattus norvegicus] mCG1032495	16	4.6	gnflm21943_at		A730098E24	RIKEN cDNA 2310033K02 gene
22	5.0	gnflm35992_at			Mouse clone IMAGE:3674789, mRNA, partial cds /cds=UNKNOWN /gb=BC019591 /gi=18044323 /len=1114 gnl UG Mm#S2534025	17	4.6	gnflm28319_at		E330031I18	RAB27b, member RAS oncogene family
23	5.0	gnflm13932_x_at			inferred: ref NP_035895.1 (NM_011765) zinc finger protein 97 [Mus musculus] mCG1029834	18	4.5	gnflm00065_at	NM_010369	I530023F06	Transcribed locus
					olfactory receptor 47	19	4.5	gnflm02725_a_at	NM_011280	2510041F02	unclassifiable
24	4.9	gnflm35483_at				20	4.5	gnflm32940_at		F930043F05	glycophorin A
25	4.9	gnflm06823_x_at	NM_146370			21	4.5	gnflm27124_at			tripartite motif protein 10
26	4.8	gnflm27835_at		D730002K16	casein alpha	22	4.5	gnflm28038_at		E030029M14	RIKEN cDNA 2310033K02 gene
27	4.8	gnflm18116_at		3732413O03	plasma membrane proteolipid cDNA sequence AJ543404	23	4.4	gnflm10282_a_at		C730049K16	RAB27b, member RAS oncogene family
28	4.8	gnflm28885_at	NM_175936			24	4.4	gnflm28018_at		E030019E14	Transcribed locus
29	4.7	gnflm24682_at		9230118I10	ceruloplasmin	25	4.4	gnflm23478_at		4631409B15	glycophorin A
30	4.7	gnflm21715_at		5031438A03	RIKEN cDNA 5031438A03 gene	26	4.4	gnflm10422_a_at	NM_027292	9830132N02	hypothetical protein
31	4.6	gnflm24385_at		6430528J02	hypothetical Ribosome recycling factor containing protein cofactor required for Sp1 transcriptional activation, subunit 2	27	4.4	gnflm05996_a_at	NM_133245	2510041L04	benzodiazepine receptor, peripheral-like 1
32	4.6	gnflm25197_at		9930001L01	milk fat globule-EGF factor 8 protein	28	4.4	gnflm11882_s_at	NM_178611	A730095M18	erythroid associated factor
33	4.5	gnflm01436_a_at	NM_008594	I830047G19	tetratricopeptide repeat domain 9	29	4.4	gnflm03319_a_at	NM_013848	9830164O15	leukocyte-associated Ig-like receptor 1
34	4.5	gnflm17416_a_at	XM_905179	4933439G10	2810455O05	30	4.4	gnflm25867_at		A630061O15	RNA guanylyltransferase and 5'-phosphatase
35	4.5	gnflm16416_a_at		2810455O05	RIKEN cDNA 2810455O05 gene	31	4.3	gnflm01494_a_at	NM_008694	F420005O16	neutrophilic granule protein
36	4.4	gnflm06955_at	NM_146779		olfactory receptor 196	32	4.3	gnflm20848_at		B830028K19	unclassifiable
37	4.4	gnflm28950_a_at	XR_000481		gene model 566, (NCBI) inferred: ref NP_058797.1 (NM_017101) peptidylprolyl isomerase A (cyclophilin A) [Rattus norvegicus] mCG8332	33	4.3	gnflm07499_at		I1C0028I03	ATP synthase 6, mitochondrial uncharacterized Celera prediction mCG56733
38	4.4	gnflm34258_x_at				34	4.3	gnflm34859_at			unclassifiable
39	4.3	gnflm10367_a_at	NM_133709	1810022C01	chordin-like 2	35	4.3	gnflm25815_at		A630025C14	unclassifiable
40	4.3	gnflm32837_at	XM_909329		OVO homolog-like 3 (Drosophila)	36	4.3	gnflm02787_a_at	NM_011403	K0C0005O03	solute carrier family 4 (anion exchanger), member 1
41	4.3	gnflm09034_at	NM_001011525		olfactory receptor 1415	37	4.3	gnflm01169_at	NM_008089	I920074C13	GATA binding protein 1
42	4.3	gnflm05718_a_at	NM_033072	K430314N15	methyl-CpG binding domain protein 6	38	4.3	gnflm28990_a_at	XM_917669	4930527A11	RIKEN cDNA 2410076I21 gene
43	4.3	gnflm27502_at	XM_925219	F830013L16	RIKEN cDNA 9430038I01 gene	39	4.3	gnflm32465_at	XM_914211		similar to heat shock protein 1, beta
44	4.3	gnflm21947_at		A830015M10	unclassifiable	40	4.3	gnflm13954_at		4933433G08	RIKEN cDNA 4933433G08 gene
45	4.3	gnflm14534_at		4933416A02	RIKEN cDNA 4933416A02 gene	41	4.2	gnflm07500_at		0610041B20	cytochrome b, mitochondrial
46	4.2	gnflm34962_at	XM_912363		similar to malate dehydrogenase, mitochondrial	42	4.2	gnflm26753_at		C130052O19	demethyl-Q 7
47	4.2	gnflm24652_s_at	XM_889153		hypothetical protein LOC624610	43	4.2	gnflm20788_at		B230350J17	unclassifiable
48	4.2	gnflm28597_a_at		D730042M18	butyrophilin, subfamily 1, member A1	44	4.2	gnflm20285_at		A530018P15	hypothetical protein
49	4.2	gnflm31701_at			uncharacterized Celera prediction mCG55760	45	4.2	gnflm02422_a_at	NM_010575	F930117J03	integrin alpha 2b
50	4.2	gnflm15778_a_at	NM_008134	D730050C14	glycosylation dependent cell adhesion molecule 1	46	4.2	gnflm28509_at		F830048D03	UVRAG (FRAGMENT) homolog [Mus musculus]
51	4.2	gnflm00454_a_at	NM_013912	6030430G11	apelin	47	4.1	gnflm09214_a_at	NM_146317		olfactory receptor 725
52	4.1	gnflm32208_at			inferred: ref NP_113808.1 (NM_031620) 3-phosphoglycerate dehydrogenase [Rattus norvegicus] mCG20679	48	4.1	gnflm00558_a_at	NM_026331	C730046J21	solute carrier family 25, member 37
53	4.1	gnflm22440_a_at	NM_177135	D830030K20	RIKEN cDNA D830030K20 gene	49	4.1	gnflm20379_at		A630042D17	hypothetical gene supported by AK040104
54	4.1	gnflm33450_at			uncharacterized Celera prediction mCG124428	50	4.1	gnflm33498_at			uncharacterized Celera prediction mCG123560
55	4.1	gnflm07399_a_at	NM_153782	E030006B12	cDNA sequence BC029169	51	4.1	gnflm23222_a_at		2010308F09	RIKEN cDNA 2010308F09 gene
56	4.1	gnflm19455_at		6430537K16	RIKEN cDNA 6430537K16 gene	52	4.1	gnflm12064_at	NM_021384	9830001A05	radical S-adenosyl methionine domain containing 2
57	4.1	gnflm11684_a_at	NM_007740	5930402D07	procollagen, type IX, alpha 1	53	4.1	gnflm15634_at			Mouse Similar to AD037 protein, clone MGC:27537
58	4.1	gnflm13007_at	NM_175280	D930025J04	RIKEN cDNA 4930529M08 gene	54	4.1	gnflm14798_at		IMAGE:4459337, mRNA, complete cds /cds=(98,748) /gb=BC023245 /gi=23270958 /len=2817 gnl UG Mm#S2779056	demethyl-Q 7
59	4.1	gnflm09929_a_at	NM_145921	E230009B14	thioesterase domain containing 1	55	4.1	gnflm15456_at		4930572C08	RIKEN cDNA 4930572C08 gene
60	4.1	gnflm20091_at		A230020D02	unclassifiable	56	4.1	gnflm35431_at		2610301H18	RIKEN cDNA 2610301H18 gene
61	4.0	gnflm34500_at			inferred: ref NP_080720.1 (NM_026444) citrate synthase [Mus musculus] mCG1049880						inferred: gb AAFA91328.1 AF246633_1 (AF246633) protease [Mus musculus] mCG1034501
62	4.0	gnflm21921_a_at		A630021E21	unclassifiable	57	4.1	gnflm02815_a_at	XM_904631	F430201D02	spectrin alpha 1
						58	4.0	gnflm05712_a_at	NM_032540	4432406O14	Kell blood group
						59	4.0	gnflm27280_at		6630019B03	kinesin-like 1
						60	4.0	gnflm31026_s_at		G630020I15	hypothetical LOC434126
						61	4.0	gnflm08210_s_at	NM_145486	E130018A02	membrane-associated ring finger (C3HC4) 2

No. 19, spleen specific genes						No. 20, tongue specific genes					
#1	#2	#3	#4	#5	#6	#1	#2	#3	#4	#5	#6
1	5.4	gnf1m20804_a_at	NM_183142	6030406L03	expressed sequence A1849156	1	6.6	gnf1m15482_a_at	NM_001033177	9930024P18	RIKEN cDNA 2310001L23 gene
2	5.3	gnf1m04279_a_at	NM_023182	2300003F21	chymotrypsin-like	2	6.4	gnf1m05889_a_at	NM_054100	2310034C09	RIKEN cDNA 2310034C09 gene
3	5.2	gnf1m32666_at	XM_901323	A830029C13	SH3/ankyrin domain gene 2	3	6.3	gnf1m16827_a_at	XM_911145	2300002O18	RIKEN cDNA 2300002O18 gene
4	5.1	gnf1m05089_a_at		1810007A24	pancreatic lipase	4	6.3	gnf1m05131_a_at	NM_027170	2310057N15	RIKEN cDNA 2310057N15 gene
5	5.0	gnf1m34728_at	XM_908024		similar to melanoma antigen, family B, 2	5	6.2	gnf1m25803_at		A630017J09	adenosine deaminase
6	4.9	gnf1m10963_s_at	NM_023182	2300003F21	chymotrypsin-like	6	6.2	gnf1m19077_a_at		1110013A16	serine (or cysteine) peptidase inhibitor, clade B, member 3C
7	4.9	gnf1m31687_at	NM_001033419	F930006J18	CEA-related cell adhesion molecule 16	7	5.9	gnf1m02469_a_at	NM_010671	1110029H15	keratin associated protein 13
8	4.8	gnf1m04959_a_at	NM_026419	2310074F01	elastase 3, pancreatic	8	5.6	gnf1m14009_at		2310079G19	RIKEN cDNA 2310079G19 gene
9	4.8	gnf1m04601_a_at	NM_025583	9030613K09	chymotrypsinogen B1	9	5.5	gnf1m17002_at	XM_917616	2310061N02	RIKEN cDNA 2310061N02 gene
10	4.8	gnf1m01890_at	NM_009430	0910001K11	protease, serine, 2	10	5.4	gnf1m01854_s_at	NM_009374	9930009I11	transglutaminase 3, E polypeptide
11	4.8	gnf1m32881_at	XM_906114		RIKEN cDNA 1700027L20 gene	11	5.3	gnf1m32664_at	XM_911927	2310014L03	similar to protein kinase Bsk146
12	4.7	gnf1m01435_a_at	NM_008593		forkhead box D2	12	5.2	gnf1m05243_a_at	NM_027997		serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiprotease, antitrypsin), member 9
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	13	5.2	gnf1m15568_at	XM_914283	2310008B01	kallikrein 12
18	4.7	gnf1m28804_at	NM_001024698		similar to Carboxypeptidase A2 precursor	14	5.2	gnf1m11157_a_at	NM_019728	2310011K19	defensin beta 4
19	4.7	gnf1m01676_a_at	NM_009043	2010012A06	regenerating islet-derived 2	15	4.9	gnf1m23262_a_at		4833442E01	keratin complex 1, acidic, gene 13
20	4.6	gnf1m23206_s_at	NM_029706	2210008M23	carboxypeptidase B1 (tissue)	16	4.8	gnf1m05116_a_at	NM_027087	2300006N05	RIKEN cDNA 2300006N05 gene
21	4.6	gnf1m12930_at	NM_010101	D430018B13	endothelial differentiation, sphingolipid G-protein-coupled receptor, 3	17	4.8	gnf1m04342_a_at	NM_023631	2310003G12	aldehyde oxidase 4
22	4.6	gnf1m01675_a_at	NM_009042	5033401N17	regenerating islet-derived 1	18	4.8	gnf1m00001_at	NM_009126		serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3A
23	4.6	gnf1m31774_at	XM_916785		disrupted in schizophrenia 1	19	4.8	gnf1m18383_at	XM_918929	2310001H18	hypothetical LOC545549
24	4.5	gnf1m28562_at		G630034I07	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)	20	4.8	gnf1m16119_at	NM_008474		keratin complex 2, basic, gene 16
25	4.5	gnf1m24434_at		6430627B09	RIKEN cDNA 0610037L13 gene	21	4.8	gnf1m32331_s_at	NM_198680	1110013A16	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3B
26	4.5	gnf1m23254_a_at		A430061F24	zinc finger protein 99	22	4.8	gnf1m05236_a_at	NM_027971	A530016D18	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 12
27	4.5	gnf1m07472_a_at		0910001K16	syncoilin	23	4.7	gnf1m13841_at		2310043M15	RIKEN cDNA 2310043M15 gene
28	4.5	gnf1m35851_at	NM_001012269		olfactory receptor 1513	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
29	4.4	gnf1m14425_at		1700069L16	RIKEN cDNA 1700069L16 gene	25	4.7	gnf1m16876_at	XM_918693	4732468B01	keratin complex 1, acidic, gene 5
30	4.4	gnf1m29398_a_at	NM_029706	0910001A18	carboxypeptidase B1 (tissue)	26	4.7	gnf1m03271_a_at	NM_013756		defensin beta 3
31	4.4	gnf1m24582_a_at		8030492B03	rad and gem related GTP binding protein 1	27	4.6	gnf1m02005_a_at	NM_009659	2310043I18	arachidonate 12-lipoxygenase, 12R type
32	4.4	gnf1m11108_a_at	NM_011271	1810011N10	ribonuclease, RNase A family, 1 (pancreatic)	28	4.6	gnf1m28862_a_at	XM_485520	8430427K15	myomesin family, member 3
33	4.4	gnf1m09672_s_at	NM_134252	0610030P10	transient receptor potential cation channel, subfamily M, member 8	29	4.6	gnf1m28723_a_at	XM_915395	2310002L13	RIKEN cDNA 2310002L13 gene
34	4.3	gnf1m04787_a_at	NM_025989	2310046E09	glycoprotein 2 (zymogen granule membrane)	30	4.6	gnf1m08163_a_at	NM_175148	9930102M17	RIKEN cDNA 2300002M23 gene
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	31	4.6	gnf1m01366_a_at	NM_008475		keratin complex 2, basic, gene 4
36	4.3	gnf1m07968_at		5330438O12	hypothetical protein	32	4.6	gnf1m02795_a_at	NM_011414	2310075E18	secretory leukocyte peptidase inhibitor
37	4.3	gnf1m23660_at		4833425M04	leucine rich repeat containing 17	33	4.5	gnf1m02825_a_at	NM_011478		small proline-rich protein 3
38	4.2	gnf1m25786_at		I730057O13	interleukin 2 receptor, alpha chain	34	4.5	gnf1m15481_at		2310046K23	RIKEN cDNA 2310046K23 gene
39	4.2	gnf1m07266_at	NM_153072	4930577G14	Hus1 homolog b (S. pombe)	35	4.5	gnf1m01363_a_at	NM_008470		keratin complex 1, acidic, gene 16
40	4.2	gnf1m34431_at			inferred: ref NP_001763.1 (NM_001772) CD33 antigen (gp67) [Homo sapiens] mCG49602	36	4.5	gnf1m04788_s_at	NM_025990	2310075A07	RIKEN cDNA 2310075A07 gene
41	4.2	gnf1m10178_at	NM_177635		histocompatibility 2, M region locus 11	37	4.5	gnf1m33717_at	NM_001013756		expressed sequence A1561912
42	4.2	gnf1m11106_a_at	NM_023707	1810009J06	RIKEN cDNA 1810009J06 gene	38	4.5	gnf1m10998_a_at	NM_014569	1110033G16	interleukin 1 family, member 6
43	4.2	gnf1m03655_a_at	NM_018874	1810032A23	pancreatic lipase related protein 1	39	4.5	gnf1m10266_a_at	NM_195369	2310042O12	WAP four-disulfide core domain 5
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	40	4.5	gnf1m02467_s_at	NM_010669	9930033J10	keratin complex 2, basic, gene 6a
45	4.1	gnf1m27587_at		D230033C05	similar to CDNA FLJ12949 FIS, CLONE NT2RP2005336, WEAKLY SIMILAR TO TRICHOHYALIN [Homo sapiens] inferred: ref NP_032645.1 (NM_008619) Moloney leukemia virus 10 [Mus musculus] mCG18552	41	4.4	gnf1m06043_a_at	NM_133712	2300002A13	kallikrein 10
46	4.1	gnf1m32704_at			inferred: ref NP_032645.1 (NM_008619) Moloney leukemia virus 10 [Mus musculus] mCG18552	42	4.4	gnf1m01721_a_at	NM_009126		serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3A
47	4.1	gnf1m24972_at		9530065C24	smoothelin	43	4.3	gnf1m32304_at	NM_199422		S100 calcium binding protein A15
48	4.1	gnf1m32018_at	XM_907327	G630062J21	dpy-19-like 4 (C. elegans)	44	4.3	gnf1m04564_a_at	NM_025501	2310007F04	RIKEN cDNA 2310007F04 gene
49	4.1	gnf1m11686_a_at	XM_915769	F430010A04	similar to E2F transcription factor 7	45	4.3	gnf1m08395_a_at	NM_181490	C130046K08	claudin 17
50	4.1	gnf1m22573_a_at	NM_207252	E130006D01	RIKEN cDNA E130006D01 gene	46	4.3	gnf1m13300_at		1810006M18	envoplakin
51	4.1	gnf1m21862_a_at	XM_911566	9830166G18	glycoprotein 6 (platelet)	47	4.3	gnf1m32847_at	NM_001039042		kallikrein 13
52	4.1	gnf1m25386_at		A130093M04	inferred: HYPOTHETICAL PROTEIN KIAA0310 (FRAGMENT). [Human] [Homo sapiens]	48	4.2	gnf1m01707_a_at	NM_009100	2310079L14	repetin
53	4.1	gnf1m21898_at		A430092C21	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430092C21 product:hypothetical protein, full insert sequence	49	4.1	gnf1m21550_at		E130203F07	unclassifiable
54	4.1	gnf1m27700_a_at	NM_024241	D430019P19	kinesin family member 24	50	4.1	gnf1m29163_a_at	XM_921005	2210418J09	cornifelin
55	4.1	gnf1m30562_x_at			trypsinogen 16 trypsinogen 16 mCG124046	51	4.1	gnf1m29248_a_at	XM_914186	2210412E05	RIKEN cDNA 2210412E05 gene
56	4.0	gnf1m31920_at	XM_910134		cerebellar degeneration-related protein 2-like	52	4.1	gnf1m31108_a_at	XM_911951	5430402E13	RIKEN cDNA 2310047D13 gene
57	4.0	gnf1m23200_at		1810012N22	similar to MITOCHONDRIAL 39S RIBOSOMAL PROTEIN L18 (MRP-L18) [Homo sapiens]	53	4.1	gnf1m12016_at	NM_181320	9530081F05	dual specificity phosphatase 16
58	4.0	gnf1m28805_a_at	NM_025350	1810004B15	carboxypeptidase A1	54	4.1	gnf1m19078_at	XM_902000	4831413C10	similar to keratin associated protein 9-1
59	4.0	gnf1m02010_a_at	XM_911199	9130414I10	amylase 2, pancreatic	55	4.1	gnf1m18385_at		2310002A05	RIKEN cDNA 2310002A05 gene
60	4.0	gnf1m08234_a_at		A530045M11	weakly similar to KIAA1751 PROTEIN (FRAGMENT) [Homo sapiens]	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	gnf1m02237_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	31	4.7	gnf1m04152_a_at	NM_021610			glycoprotein A33 (transmembrane)
15	4.6	gnf1m13807_at		F630206K19	tumor necrosis factor receptor superfamily, member 13b	32	4.7	gnf1m00241_s_at	NM_013921	2010015P21		transmembrane protease, serine 8 (intestinal)
16	4.6	gnf1m10519_a_at	NM_010386	I920078O06	histocompatibility 2, class II, locus DMa	33	4.7	gnf1m13512_a_at		C230008K20		cDNA sequence BC023744
17	4.5	gnf1m13615_a_at	NM_007758	1810013M23	complement receptor 2	34	4.6	gnf1m13126_a_at	NM_027988	E430007K11		NADPH oxidase organizer 1
18	4.5	gnf1m16327_a_at		A530066G20	hypothetical protein	35	4.5	gnf1m30976_a_at	NM_008100	C820020M20		glucagon
19	4.5	gnf1m28507_at		F830036K21	complement receptor 2	36	4.5	gnf1m04218_a_at	NM_022430	2010004L09		membrane-spanning 4-domains, subfamily A, member 8A
20	4.5	gnf1m17260_at	NM_019866		Spi-B transcription factor (Spi-1/PU.1 related)	37	4.4	gnf1m02627_a_at	NM_011076			ATP-binding cassette, sub-family B (MDR/TAP), member 1A
21	4.5	gnf1m16740_at	NM_181734	F830034J19	RIKEN cDNA 5830472M02 gene similar to Ig kappa chain V-V region MOPC 21 precursor	38	4.4	gnf1m04633_a_at	NM_025655	2310003K08		transmembrane and immunoglobulin domain containing
22	4.5	gnf1m13502_s_at	XM_912724			39	4.4	gnf1m02779_a_at	NM_011388			solute carrier family 10, member 2
23	4.5	gnf1m16986_at	NM_009302	I920052L14	SWA-70 protein	40	4.4	gnf1m30177_a_at	NM_001033364	G630055D06		cDNA sequence BC040758
24	4.5	gnf1m02841_a_at	NM_011518	F420003H05	spleen tyrosine kinase	41	4.4	gnf1m13288_a_at		F830007N10		cadherin 17
25	4.5	gnf1m05658_a_at	NM_031376	I830174K10	phosphoinositide-3-kinase adaptor protein 1	42	4.3	gnf1m15280_at		1190002B21		UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5
26	4.4	gnf1m03393_a_at	NM_015790	A630008D12	icos ligand	43	4.3	gnf1m02861_a_at	NM_011575	2010306I07		trefoil factor 3, intestinal
27	4.4	gnf1m29681_a_at	NM_030098	A230056F18	ribonuclease, RNase A family, 6	44	4.3	gnf1m30033_a_at		2210021I22		glucosaminyl (N-acetyl) transferase 3, mucin type
28	4.4	gnf1m02495_a_at	NM_010735	F830035M07	lymphotoxin A	45	4.2	gnf1m01164_a_at	NM_008081			beta-1,4-N-acetyl-galactosaminyl transferase 2
29	4.3	gnf1m03132_a_at	NM_013517		Fc receptor, IgE, low affinity II, alpha polypeptide	46	4.2	gnf1m10113_a_at	NM_145435	C820007C10		peptide YY
30	4.3	gnf1m12072_a_at	NM_178165	A230020G22	Fc receptor-like 1	47	4.2	gnf1m00826_a_at	NM_007474	1920039O06		aquaporin 8
31	4.3	gnf1m32629_a_at		6330574L03	beaded filament structural protein 2, phakinin	48	4.1	gnf1m19593_at		9030624O13		solute carrier family 9 (sodium/hydrogen exchanger), member 3
32	4.3	gnf1m01227_a_at	NM_008206	F630118D21	histocompatibility 2, O region alpha locus	49	4.1	gnf1m30770_a_at		9130020L07		chloride channel calcium activated 6
33	4.3	gnf1m12099_a_at	NM_172900	F830048K03	sialic acid binding Ig-like lectin G	50	4.1	gnf1m30769_s_at	NM_207208	9130020L07		chloride channel calcium activated 6
34	4.3	gnf1m10418_a_at	NM_145141	F830204N13	ubiquinol-cytochrome c reductase binding protein	51	4.1	gnf1m07377_a_at	NM_153568	D230014F07		cDNA sequence BC031901
35	4.2	gnf1m34612_at			inferred: gb AAC18780.1 (M23690) immunoglobulin light chain kappa [Mus musculus] mCG1036442	52	4.0	gnf1m30529_a_at	NM_201256	1110004O12		eukaryotic translation initiation factor 4E binding protein 3
36	4.2	gnf1m10984_a_at	NM_010745	1110007J13	lymphocyte antigen 86	53	4.0	gnf1m19071_a_at	XM_908069	A430096B05		Fc fragment of IgG binding protein
37	4.2	gnf1m09406_a_at	NM_010407	I830077E17	hemopoietic cell kinase	54	4.0	gnf1m03908_a_at	NM_020049	9030613J17		solute carrier family 6 (neurotransmitter transporter), member 14
38	4.2	gnf1m06625_a_at	NM_181318	G430095K03	RasGEF domain family, member 1B	55	4.0	gnf1m32627_a_at	XM_907141	2010010B23		myosin 1A
39	4.2	gnf1m34194_at	NM_207246		RAS, guanyl releasing protein 3	No. 23, stomach specific genes						
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	#1	#2	#3	#4	#5	#6	
42	4.2	gnf1m11147_a_at	NM_009514	2210401P05	pre-B lymphocyte gene 3	1	6.9	gnf1m11150_a_at	NM_009362	2310075I07		trefoil factor 1
43	4.2	gnf1m04438_a_at	NM_025444	1810054N16	cytochrome P450, family 4, subfamily f, polypeptide 18	2	6.8	gnf1m23236_a_at		9130006K20		annexin A10
44	4.2	gnf1m08243_at	NM_177584	A630002H24	B and T lymphocyte associated	3	6.5	gnf1m04780_a_at	NM_025973	2210416O16		prograstriscin (pepsinogen C)
45	4.2	gnf1m02660_a_at	NM_011136	E430020O13	POU domain, class 2, associating factor 1	4	6.4	gnf1m02036_a_at	NM_009724	2310065K03		ATPase, H+/K+ exchanging, beta polypeptide
46	4.1	gnf1m35384_s_at	XM_911979		immunoglobulin kappa chain variable 34 (V34)	5	6.4	gnf1m10234_a_at	NM_030181	4930405J24		V-set and immunoglobulin domain containing 1
47	4.1	gnf1m27099_at		C530043A01	B-cell CLL/lymphoma 11A (zinc finger protein)	6	6.4	gnf1m04549_a_at	NM_025467	2210419G06		RIKEN cDNA 1810036H07 gene
48	4.1	gnf1m00864_a_at	NM_007551	F830112L05	Burkitt lymphoma receptor 1	7	6.4	gnf1m28611_a_at		2310038I05		ATPase, H+/K+ exchanging, alpha polypeptide
49	4.1	gnf1m10735_a_at	NM_178087	F830014J16	promyelocytic leukemia	8	6.3	gnf1m11149_a_at	NM_021488	2210408M22		ghrelin
50	4.1	gnf1m04527_a_at	NM_025423	1110059E24	RIKEN cDNA 1110059E24 gene	9	6.3	gnf1m07731_a_at	NM_029727	2210006M16		RIKEN cDNA 2210006M16 gene
51	4.0	gnf1m00599_a_at	NM_025340	1110008I16	SHANK-associated RH domain interacting protein	10	6.2	gnf1m11904_a_at	NM_008118	9130204L19		gastric intrinsic factor
52	4.0	gnf1m28628_at	NM_011306	I420027M12	retinoid X receptor beta	11	5.9	gnf1m16988_at		2210005L13		mucin 5, subtypes A and C, tracheobronchial/gastric
53	4.0	gnf1m12251_a_at	NM_172842	E430019B13	lymphocyte transmembrane adaptor 1	12	5.8	gnf1m16746_a_at	XM_915229	1190003M12		RIKEN cDNA 1190003M12 gene
54	4.0	gnf1m03379_a_at	NM_015766	F730317H01	Epstein-Barr virus induced gene 3	13	5.7	gnf1m18350_a_at		1810010D01		RIKEN cDNA 1810010D01 gene
55	4.0	gnf1m23499_at		4632409G01	unclassifiable	14	5.6	gnf1m11146_a_at	NM_011922	1920046M24		annexin A10
56	4.0	gnf1m26221_a_at	NM_199198	E430029A03	histone deacetylase 10	15	5.4	gnf1m04548_a_at	NM_025466	2210420L15		gastrophilin
No. 22, large intestine specific genes						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
#1	#2	#3	#4	#5	#6	18	4.9	gnf1m10041_a_at	NM_026935	G630025A20		sulfolipase family, cytosolic, 1C, member 2
1	7.1	gnf1m05146_a_at	NM_027239	1810065E05	RIKEN cDNA 1810065E05 gene	19	4.9	gnf1m06355_a_at	NM_144544			RIKEN cDNA 2210407C18 gene
2	6.7	gnf1m05208_a_at	NM_027832	9130404C18	seminal vesicle antigen-like 1	20	4.9	gnf1m08742_at	NM_172737	D430041B17		RIKEN cDNA D430041B17 gene
3	6.4	gnf1m04551_s_at	XM_904677	1810073D07	RIKEN cDNA 1810030J14 gene	21	4.8	gnf1m13073_a_at	NM_021453	1920065H02		pepsinogen 5, group I
4	6.3	gnf1m01218_a_at	NM_008190	2010007F09	guanylate cyclase activator 2a (guanylin)	22	4.7	gnf1m27088_at	NM_178280	C530030G16		sal-like 3 (Drosophila)
5	6.0	gnf1m02976_a_at	NM_011831		insulin-like 5	23	4.5	gnf1m18901_at		4930572F24		RIKEN cDNA 2610528E23 gene
6	5.8	gnf1m04382_a_at		9030012B21	resistin like beta	24	4.5	gnf1m04280_a_at	NM_023186	2210020N23		chitinase, acidic
7	5.7	gnf1m09735_a_at	NM_145474		cDNA sequence BC018285	25	4.4	gnf1m10569_a_at	NM_007799	1530011F11		cathepsin E
8	5.7	gnf1m00809_at			angiogenin, ribonuclease A family, member 3	26	4.4	gnf1m11152_a_at	NM_025620	2210417D09		RIKEN cDNA 2210417D09 gene
9	5.6	gnf1m13814_at	NM_009880		caudal type homeo box 1	27	4.4	gnf1m04616_a_at	NM_025622	2200008F12		lectin, galactose-binding, soluble 2
10	5.6	gnf1m16178_at	NM_027220		protease, serine, 32	28	4.3	gnf1m05278_a_at	NM_028216	2210408B04		prostate stem cell antigen
11	5.4	gnf1m21823_a_at	NM_489685	9130004I05	hypothetical gene supported by AK078896	29	4.3	gnf1m01108_a_at	NM_007989			forkhead box H1
12	5.4	gnf1m05264_a_at	NM_028089	2010318C06	cytochrome P450, family 2, subfamily c, polypeptide 55	30	4.3	gnf1m32773_at	XM_914516			gene model 935, (NCBI)
13	5.3	gnf1m30028_a_at	XM_905190	9130012O13	RIKEN cDNA 9130012O13 gene	31	4.3	gnf1m02645_a_at	NM_011107	2310012E07		phospholipase A2, group IB, pancreas
14	5.2	gnf1m19589_at	NM_177744	9030421J09	RIKEN cDNA 9030421J09 gene	32	4.3	gnf1m21557_a_at	NM_001005477	E130309B19		RIKEN cDNA E130309B19 gene
15	5.1	gnf1m09020_at	NM_177544		angiogenin, ribonuclease A family, member 4	33	4.3	gnf1m33973_at				uncharacterized Celera prediction mCG115317
16	5.1	gnf1m04467_a_at	NM_025308	2010104G20	RIKEN cDNA 1810007E14 gene	34	4.3	gnf1m09755_at	NM_181729			mucin 6, gastric
17	5.1	gnf1m10609_a_at	NM_023154	0610025L15	ethylmalonic encephalopathy 1	35	4.2	gnf1m01766_a_at	NM_009207			solute carrier family 4 (anion exchanger), member 2
18	5.0	gnf1m16117_a_at	NM_011463		serine peptidase inhibitor, Kazal type 4	36	4.2	gnf1m11141_a_at	NM_023709	2200003B16		calpain 9 (mCL-4)
19	4.9	gnf1m28989_a_at	XM_916703	4930516G09	mucin 3, intestinal	37	4.2	gnf1m09966_a_at	NM_145209	I830016G04		2'-5' oligoadenylate synthetase-like 1
20	4.9	gnf1m29326_a_at	NM_027339	9130416C03	RIKEN cDNA 2210415F13 gene	38	4.2	gnf1m04545_a_at	NM_025458	1810057G13		transmembrane emp24 protein transport domain containing 6
21	4.9	gnf1m00681_a_at	NM_007500	C230040F02	atonal homolog 1 (Drosophila)	39	4.1	gnf1m32563_at				aldehyde dehydrogenase family 7 member A1 aldehyde
22	4.9	gnf1m24650_at		9130013M11	solute carrier family 26, member 3	40	4.1	gnf1m30502_a_at				dehydrogenase family 7, member A1
23	4.9	gnf1m04542_a_at	NM_025453	5033426G15	transmembrane 4 L six family member 20	41	4.1	gnf1m09844_a_at	NM_172469	5730466J16		mCG16296
24	4.8	gnf1m04112_a_at	NM_021475	F830031L06	ADAM-like, decysin 1	42	4.1	gnf1m33051_at				fer-1-like 4 (C. elegans)
25	4.8	gnf1m31167_a_at		4930403C10	RIKEN cDNA 4930403C10 gene							chloride intracellular channel 6
26	4.8	gnf1m34080_at			gene model 1123, (NCBI)							inferred: gb AAH12778.1 AAH12778 (BC012778) Unknown (protein for IMAGE:3939659) [Homo sapiens] mCG130493
27	4.8	gnf1m08067_a_at	NM_178899	C820005A15	expressed sequence A1987662							
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							

43	4.1	gnf1m00852_a_at	NM_007526		BarH-like homeobox 1 inferred: ref NP_036064.1 (NM_011934) estrogen related receptor, beta; estrogen receptor related 2 [Mus musculus] mCG50969		12	5.3	gnf1m33007_at	XM_913800		vomeronasal organ family 2, receptor, 14 [Mus musculus] mCG56771
44	4.1	gnf1m35002_at										similar to odorant binding protein 2B
45	4.0	gnf1m05364_a_at	NM_028775	A330069N14	cytochrome P450, family 2, subfamily s, polypeptide 1 claudin 18		13	5.3	gnf1m15428_a_at	XM_920036		vomeronasal 2, receptor, 13
46	4.0	gnf1m03816_a_at	NM_019815				14	5.2	gnf1m33575_at	XM_912883		S100 calcium binding protein, zeta
47	4.0	gnf1m10964_a_at	NM_009363	0910001O22	trefoil factor 2 (spasmolytic protein 1)		15	5.0	gnf1m13290_s_at	NM_019918		tissue-type vomeronasal neurons putative pheromone receptor V2R2
48	4.0	gnf1m34830_x_at	NM_146636		olfactory receptor 1487		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
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		20	4.9	gnf1m07372_a_at	NM_153558		lipocalin 13
4	6.5	gnf1m03575_a_at	NM_017471	9830120G21	probasin		21	4.9	gnf1m17488_at		A430105L04	transient receptor potential cation channel, subfamily C, member 2
5	6.2	gnf1m11992_a_at	NM_020264	9530004K16	seminal vesicle protein, secretion 7							phosphodiesterase 5A, cGMP- specific
6	6.1	gnf1m11564_a_at	NM_008267	5033401H24	homo box B13		22	4.8	gnf1m07344_at	NM_153422		
7	6.0	gnf1m27244_at		C920006B11	HISTONE H2A.F GENE (FRAGMENT) homolog [Gallus gallus]		23	4.7	gnf1m09872_a_at	NM_053184	C130005L05	UDP glucuronosyltransferase 2 family, polypeptide A1
8	6.0	gnf1m08117_at	NM_177911	9530008N10	transglutaminase 4 (prostate)		24	4.7	gnf1m02571_a_at	NM_010916		nescent helix loop helix 1
9	6.0	gnf1m11987_a_at	NM_017390	G630066O15	seminal vesicle protein, secretion 2		25	4.7	gnf1m01924_x_at	NM_009489		vomeronasal 2, receptor, 14
10	5.9	gnf1m15728_a_at		G430099L10	DnaJ (Hsp40) homolog, subfamily C, member 10		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
11	5.8	gnf1m02575_a_at	NM_010921	9530090D16	NK-3 transcription factor, locus 1 (Drosophila)							similar to olfactory receptor 365
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) similar to calmodulin 1		28	4.5	gnf1m34943_at	XM_915884	A430105L04	transient receptor potential cation channel, subfamily C, member 2
							29	4.3	gnf1m07446_a_at	NM_011644		hypothetical protein
							30	4.3	gnf1m25038_at		9630019I16	RIKEN cDNA 9430071P14 gene
							31	4.3	gnf1m21784_at		6720465N03	guanine nucleotide binding protein (G protein), gamma 8 subunit
							32	4.3	gnf1m09963_a_at	NM_010320	G730009J10	folliatin-like 5
13	5.6	gnf1m35116_at	XM_904194		cDNA sequence BC025076		33	4.2	gnf1m12520_a_at	NM_178673	B930093L07	RIKEN cDNA 2810405F17 gene
14	5.6	gnf1m29041_a_at	XM_906807	2610025P07	spermine binding protein		34	4.2	gnf1m16364_at		2810405F17	vomeronasal 2, receptor, 15
15	5.6	gnf1m02743_a_at	XM_914346	9530039G05	expressed sequence BB123696		35	4.2	gnf1m01925_x_at	NM_009490		RIKEN cDNA 9230116B18 gene
16	5.5	gnf1m02997_a_at	NM_011867		FGF receptor activating protein 1		36	4.2	gnf1m17463_a_at	XM_908788	9230116B18	histone 2, H2bb
17	5.2	gnf1m24987_a_at		9530079O21	RIKEN cDNA 9530002B09 gene		37	4.1	gnf1m11843_a_at	NM_178214	I920051L22	cDNA sequence U46068
18	5.2	gnf1m29298_at		I830091H05	RIKEN cDNA 4930408F14 gene		38	4.1	gnf1m07341_a_at	NM_153418	I920034C14	ENSMUST00000071760 transcript (in rel.37.34e)
19	5.1	gnf1m11988_a_at	NM_023865	4930408F14	transglutaminase 4 (prostate)		39	4.1	gnf1m33679_x_at			solute carrier organic anion transporter family, member 1a5
20	5.1	gnf1m14622_at	XM_356334	4930408F14	RIKEN cDNA 5430419D17 gene							calreticulin 4
21	5.1	gnf1m14007_at	NM_027128	2310011G06	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2		40	4.0	gnf1m05950_a_at	NM_130861	4930486M03	vomeronasal 2, receptor, 1
22	4.9	gnf1m09912_a_at	NM_025610	4933423N16	proacrosin binding protein		41	4.0	gnf1m30271_a_at		4933403L16	
23	4.8	gnf1m08118_a_at	NM_177911	9530008N10	FGF receptor activating protein 1		42	4.0	gnf1m17391_x_at	NM_009485		
24	4.8	gnf1m07623_at	NM_175166	9530082P11	olfactory receptor 76		No. 26, heart specific genes					
25	4.7	gnf1m07724_a_at	NM_172426	C630015N03	RIKEN cDNA 1300007B12 gene		#1	#2	#3	#4	#5	#6
					defensin beta 1		1	6.1	gnf1m31874_x_at			inferred: ref NP_113808.1 (NM_031620) 3-phosphoglycerate dehydrogenase [Rattus norvegicus] mCG50387
26	4.7	gnf1m03486_a_at	NM_016845	4921539N17	S-adenosylmethionine decarboxylase 1		2	6.0	gnf1m30834_at	NM_008725	I920194N08	natriuretic peptide precursor type A
27	4.7	gnf1m29297_a_at		I830091H05	membrane metallo endopeptidase		3	5.8	gnf1m08513_s_at	NM_175441	I920041I20	RIKEN cDNA D830007F02 gene
28	4.5	gnf1m31210_a_at	NM_146682		unclassifiable		4	5.7	gnf1m01466_a_at	NM_008653	I920180J22	myosin binding protein C, cardiac
29	4.4	gnf1m03975_a_at	NM_020588	I830087K14	similar to nuclear localized factor 1		5	5.5	gnf1m08732_a_at	NM_172750	D330008N11	ADP-ribosylhydrolase like 1
30	4.4	gnf1m10772_at	NM_007843		3'-phosphoadenosine 5'- phosphosulfate synthase 2		6	5.5	gnf1m24218_a_at		F420007B19	RIKEN cDNA D830007F02 gene
31	4.3	gnf1m02008_s_at	NM_009665	I920063F03	leukocyte receptor cluster (LRC) member 1		7	5.3	gnf1m00526_a_at	NM_023129	0610013B18	phospholamban
32	4.3	gnf1m11713_a_at	NM_008604	6030454K05	RIKEN cDNA D930028F11 gene		8	5.2	gnf1m10923_a_at	NM_009406	I920092G04	troponin I, cardiac
33	4.3	gnf1m22192_at		C530028E13	RIKEN cDNA A130010J15 gene		9	5.1	gnf1m17989_at		6030406G17	unclassifiable
34	4.2	gnf1m35415_x_at	XM_917952		mucin 10, submandibular gland salivary mucin		10	5.0	gnf1m02083_a_at	NM_009814	3110082J19	calsequestrin 2
35	4.2	gnf1m02996_a_at	NM_011864	9930024B13	RIKEN cDNA 5330420D20 gene		11	5.0	gnf1m10871_a_at	NM_013468	I920078A07	ankyrin repeat domain 1 (cardiac muscle)
36	4.1	gnf1m09372_s_at	NM_027203		acireductone dioxygenase 1		12	4.9	gnf1m23903_a_at		I420023L02	Ras-related associated with diabetes
37	4.1	gnf1m08394_at		C130036J11	inferred: HYPOTHETICAL PROTEIN KIAA0310 (FRAGMENT). [Human] {Homo sapiens}		13	4.9	gnf1m00672_s_at	XM_919974	D830041H11	triadin
38	4.1	gnf1m09797_a_at	NM_181048	C030010L06	SAM pointed domain containing ets transcription factor		14	4.9	gnf1m11169_a_at	NM_023784	2310016N21	Yip1 domain family, member 7
39	4.1	gnf1m01462_a_at	NM_008644		WAP four-disulfide core domain 3		15	4.8	gnf1m02252_a_at	NM_010212	I920089C03	four and a half LIM domains 2
40	4.1	gnf1m25386_at		A130093M04	melanophilin		16	4.8	gnf1m31518_at	NM_001033208	I920069H02	expressed sequence AA407270
41	4.0	gnf1m10631_a_at	NM_013891	9030406H20	RIKEN cDNA 5330420D20 gene		17	4.8	gnf1m27893_at		D830041H11	unclassifiable
42	4.0	gnf1m30009_a_at	XM_909954	1700127F16	acireductone dioxygenase 1		18	4.8	gnf1m33637_at	XM_925036		TNNI3 interacting kinase
43	4.0	gnf1m05777_at					19	4.6	gnf1m11516_at	NM_013868	4932416D13	heat shock protein family, member 7 (cardiovascular)
44	4.0	gnf1m23974_at		5730402C02			20	4.6	gnf1m01866_a_at	NM_009393		troponin C, cardiac/slow skeletal
45	4.0	gnf1m06134_a_at	NM_134052				21	4.5	gnf1m02884_a_at	NM_011619	I920078H23	troponin T2, cardiac
No. 25, vomeralnasal organ specific genes												
#1	#2	#3	#4	#5	#6							
1	6.5	gnf1m01928_s_at	XM_620407		vomeronasal 2, receptor, 4		22	4.5	gnf1m00171_a_at	NM_178869	I920085F07	tubulin tyrosine ligase-like 1
2	6.5	gnf1m32795_at	XM_912696	A430104B10	similar to Uromodulin precursor (Tamm-Horsfall urinary glycoprotein) (THP)		23	4.5	gnf1m17296_a_at		1110018J23	RIKEN cDNA 1110018J23 gene
							24	4.5	gnf1m27860_a_at		D830005K03	RIKEN cDNA A530058N18 gene
3	6.5	gnf1m01923_x_at	NM_009487		vomeronasal 2, receptor, 10		25	4.5	gnf1m10968_a_at	NM_013808	2610029O20	cysteine and glycine-rich protein 3
4	6.2	gnf1m06175_a_at	NM_134180		vomeronasal 1 receptor, C25		26	4.4	gnf1m16562_a_at	NM_028838	4933431K03	leucine rich repeat containing 2
5	5.9	gnf1m02475_a_at	NM_010694		lipocalin 3		27	4.4	gnf1m21353_at		D330008I21	13 days embryo heart cDNA, RIKEN full-length enriched library, clone:D330008I21
6	5.6	gnf1m02476_at	NM_010695		lipocalin 4							product:hypothetical protein, full insert sequence
7	5.6	gnf1m25839_a_at		A630091H24	lipocalin 4		28	4.4	gnf1m02546_s_at	NM_080728		myosin, heavy polypeptide 6, cardiac muscle, alpha
8	5.6	gnf1m12375_a_at	NM_009141	F830049O18	chemokine (C-X-C motif) ligand 5		29	4.2	gnf1m16193_a_at	NM_053098	I920184N14	leiomodulin 2 (cardiac)
9	5.5	gnf1m35337_at			inferred: gbl AAF72554.1 AF269232_1 (AF269232) butyrophilin-like protein BUTR-1 [Mus musculus] mCG1038007		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
10	5.4	gnf1m07884_at	NM_134170	4831417D05	vomeronasal 1 receptor, C15		33	4.1	gnf1m10927_a_at	NM_024179	2310016M19	RIKEN cDNA 0610009O20 gene
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;		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 nexin 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			gbj 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<S>-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	ficollin 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 immunoglobulin-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	7	4.9	gnf1m17824_at	NR_002862	C230040C07	poly(A)-binding protein,
2	6.3	gnf1m00790_a_at	NM_007425	1200016F14	advanced glycosylation end						cytoplasmic pseudogene
3	6.3	gnf1m02764_a_at	NM_011359		product-specific receptor	8	4.7	gnf1m05787_a_at	NM_053095		interleukin 24
4	5.6	gnf1m13985_at		1110050K14	surfactant associated protein C	9	4.7	gnf1m09080_at	NM_001011811		olfactory receptor 487
5	5.5	gnf1m02753_a_at	NM_011339	E030017H13	RIKEN cDNA 1110050K14 gene	10	4.7	gnf1m08880_at	NM_032006	C430029P05	matrix metalloproteinase 1a
					chemokine (C-X-C motif) ligand						(interstitial collagenase)
6	5.4	gnf1m03156_s_at	NM_013565	A930004K02	integrin alpha 3	11	4.6	gnf1m09471_a_at	NM_019539	5630400J12	cathepsin 7
7	5.2	gnf1m26239_at	NM_013565	B130039D23	pleckstrin homology domain	12	4.6	gnf1m02205_at	NM_010088	I530026J03	decidual/trophoblast prolactin-
					containing, family K member 1						related protein
8	5.1	gnf1m24301_at		6330501C04	ERG PROTEIN homolog [Mus	13	4.5	gnf1m15786_a_at	NM_008554	2410083I15	achaeete-scute complex homolog-
					musculus]						like 2 (Drosophila)
9	4.9	gnf1m09808_a_at	NM_028306		heat shock protein 12B	14	4.5	gnf1m09640_a_at		4631401O15	myosin 1H
10	4.9	gnf1m09513_a_at	NM_029928	M5C1105K07	protein tyrosine phosphatase,	15	4.4	gnf1m07087_at	NM_146961		olfactory receptor 539
					receptor type, B	16	4.3	gnf1m34478_x_at			inferred:
11	4.9	gnf1m06553_at	NM_145536		cDNA sequence BC020535						gb AAH12655.1 AAH12655
12	4.8	gnf1m13225_a_at	NM_025437	G430080G23	eukaryotic translation initiation						(BC012655) Unknown (protein for
					factor 1A, Y-linked						IMAGE:3669867) [Mus musculus]
13	4.8	gnf1m05862_a_at	NM_054038	8430440N01	secretoglobulin, family 3A, member	17	4.3	gnf1m11820_at	NM_010499	F630103C03	immediate early response 2
					2	18	4.3	gnf1m33507_at			inferred: ref NP_058593.1
14	4.8	gnf1m00353_a_at	NM_181444		G protein-coupled receptor, family						(NM_016897) translocase of inner
					C, group 5, member A						mitochondrial membrane 23
15	4.7	gnf1m02912_a_at	NM_011681	I530005I22	secretoglobulin, family 1A, member						homolog (yeast); translocase of
					1 (uteroglobulin)						inner mitochondrial membrane
16	4.7	gnf1m02745_a_at	NM_011326	F530014I17	sodium channel, nonvoltage-gated						[Mus musculus] mCG123348
					1 gamma						histocompatibility 2, class II
17	4.7	gnf1m34849_at	NM_001001807		olfactory receptor 234	19	4.2	gnf1m13268_a_at		F930102P07	antigen E alpha
18	4.7	gnf1m02786_a_at	NM_011402	I1C0020L19	solute carrier family 34 (sodium	20	4.2	gnf1m26254_at		B130047P03	Cdc42 GTPase-activating protein
					phosphate), member 2	21	4.2	gnf1m15908_at	NM_001013825		similar to hypothetical protein
19	4.6	gnf1m03236_a_at	NM_013690		endothelial-specific receptor						FLJ14345
					tyrosine kinase	22	4.2	gnf1m16840_at		5730442A01	tumor rejection antigen gp96
20	4.6	gnf1m11873_a_at	NM_177356	8430417I16	lysosomal-associated membrane	23	4.1	gnf1m02674_a_at	NM_011166		prolactin-like protein B
					protein 3	24	4.1	gnf1m30449_at			expressed sequence AI427833
21	4.5	gnf1m24246_a_at		6030475M24	unclassifiable						expressed sequence AI427833
22	4.4	gnf1m01742_a_at	NM_009160		surfactant associated protein D						mCG126575
23	4.3	gnf1m01885_a_at	NM_009425	A630004M21	tumor necrosis factor (ligand)	25	4.1	gnf1m21118_at	XM_914594	C430002N04	CEA-related cell adhesion
					superfamily, member 10						molecule 15
24	4.2	gnf1m03816_a_at	NM_019815		claudin 18	26	4.0	gnf1m01922_a_at	NM_009482	2410026A04	undifferentiated embryonic cell
25	4.2	gnf1m07350_a_at	NM_153513		cDNA sequence BC028528						transcription factor 1
26	4.2	gnf1m15595_a_at	NM_033525	K230315E09	nephroneurin	27	4.0	gnf1m01893_a_at	NM_009434	2400006G02	pleckstrin homology-like domain,
27	4.2	gnf1m28929_a_at	NM_007695	F630225K06	chitinase 3-like 1						family A, member 2
28	4.1	gnf1m00030_a_at	NM_018881	2310042I22	flavin containing monooxygenase 2	28	4.0	gnf1m26996_at		C330022A02	tripartite motif protein 27
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	No. 34, pituitary specific genes					
1	6.3	gnf1m01156_a_at	NM_008068	9630012C19	gamma-aminobutyric acid (GABA-	#1	#2	#3	#4	#5	#6
					A) receptor, subunit alpha 6	1	7.2	gnf1m16838_at	NM_008045	5730420N04	follicle stimulating hormone beta
2	5.6	gnf1m23531_at		4732433A03	aspartate-beta-hydroxylase	2	6.5	gnf1m01892_a_at	NM_009432		thyroid stimulating hormone, beta
3	5.6	gnf1m19471_a_at	NM_176952	C630040G20	RIKEN cDNA 6430573F11 gene						subunit
4	5.1	gnf1m02315_a_at	NM_010350	M5C1026K02	glutamate receptor, ionotropic,	3	6.3	gnf1m02124_a_at	NM_009889		glycoprotein hormones, alpha
					NMDA2C (epsilon 3)						subunit
5	5.1	gnf1m24456_at		6530411F08	glutamate receptor, ionotropic,	4	5.7	gnf1m01297_a_at	NM_008355	3110047H05	interleukin 13
					delta 2	5	5.6	gnf1m23424_a_at		A430027H14	hypothetical protein
6	5.0	gnf1m01379_s_at	NM_008498	C230045C03	LIM homeobox protein 1	6	5.6	gnf1m17959_at			potassium channel, subfamily K,
7	5.0	gnf1m25400_at		A230008P07	unclassifiable						member 2
8	4.8	gnf1m09707_a_at	XM_907237	I1C0004A05	protein phosphatase 1, regulatory	7	5.6	gnf1m18099_a_at		2810449D17	RIKEN cDNA 2810449D17 gene
					subunit 10	8	5.5	gnf1m30143_a_at		4732455E07	mitogen activated protein kinase
											kinase 7
9	4.7	gnf1m03541_s_at	NM_054079	1500012D04	interleukin 22	9	5.5	gnf1m11611_a_at	NM_008895	5730420K11	pro-opiomelanocortin-alpha
10	4.7	gnf1m02223_a_at	NM_010134		engrailed 2	10	5.3	gnf1m01378_a_at	NM_008497	A230101A12	luteinizing hormone beta
11	4.6	gnf1m08920_a_at	NM_026380	6530413N01	regulator of G-protein signaling 8	11	4.9	gnf1m23937_a_at	NM_001003685	5330422G23	growth hormone releasing hormone
12	4.6	gnf1m13918_a_at	NM_007592	1300004E06	carbonic anhydrase 8						receptor
13	4.6	gnf1m12517_a_at	NM_019820	B930083H17	cerebellin 3 precursor protein	12	4.8	gnf1m01580_a_at			ENSMUST00000075861 transcript
14	4.5	gnf1m18269_a_at		A630033B20	unclassifiable						(in rel.37.34e)
15	4.5	gnf1m08292_at	NM_177790	A930006D11	RIKEN cDNA A930006D11Rik	13	4.8	gnf1m18480_a_at	XM_922596	D030058A04	zinc finger, RAN-binding domain
					gene						containing 3
16	4.5	gnf1m13274_at		K230334G01	neurogenic differentiation 2	14	4.5	gnf1m03198_a_at	NM_013628		proprotein convertase
17	4.5	gnf1m01762_a_at	NM_009200	I420008D08	solute carrier family 1 (high	15	4.4	gnf1m19291_at	NM_001004168	4933413G10	subtilisin/kexin type 1
					affinity aspartate/glutamate						hypothetical gene supported by
					transporter), member 6	16	4.4	gnf1m26869_s_at			AK030184
						17	4.4	gnf1m02672_a_at	NM_011164	D430042D24	unclassifiable
						18	4.4	gnf1m10439_a_at	NM_183336	5730421F19	prolactin
										5530402E03	immunoglobulin superfamily,
											member 1
18	4.4	gnf1m18590_at		2900083I11	RIKEN cDNA 2900083I11 gene	19	4.3	gnf1m26987_at	XM_900840	C330007E15	RIKEN cDNA C330024D21 gene
19	4.4	gnf1m11812_a_at	NM_011153	6530401M09	G substrate	20	4.2	gnf1m21014_at		C130048C12	similar to L1
20	4.4	gnf1m03749_a_at	NM_019626	K430357H14	cerebellin 1 precursor protein						RETROTRANSPOSON, TF
21	4.4	gnf1m30730_at	XM_925385		Src homology 2 domain containing						SUBFAMILY L1MD-TF18,
					F						PARTIAL SEQUENCE [Mus
											musculus domesticus]
22	4.4	gnf1m14886_at		6330436F06	RIKEN cDNA 6330436F06 gene	21	4.2	gnf1m09621_a_at	NM_008117	5730422D01	growth hormone
23	4.4	gnf1m26901_at		C230053I05	Unc4.1 homeobox (C. elegans)	22	4.2	gnf1m12417_at		B130049A16	RAD23a homolog (S. cerevisiae)
24	4.3	gnf1m17757_at		B230312E22	B230312E22 unclassifiable clone	23	4.2	gnf1m03930_a_at	NM_020293		claudin 9
25	4.3	gnf1m03701_a_at	NM_019465	B930098P10	cytotoxic and regulatory T cell	24	4.1	gnf1m29363_a_at		1110011K07	RIKEN cDNA 1110014L17 gene
					molecule	25	4.1	gnf1m22826_at		4930519F09	RIKEN cDNA 4930519F09 gene
26	4.3	gnf1m26515_at		B930002F08	zinc finger protein of the	26	4.0	gnf1m32192_at	XM_924616		hypothetical protein LOC623757
					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	No. 35, brown fat specific genes					
1	5.5	gnf1m11382_a_at	NM_010203	4732467I02	fibroblast growth factor 5	#1	#2	#3	#4	#5	#6
2	5.4	gnf1m12921_at	NM_009004	D330036L06	kinesin family member 20A	1	5.6	gnf1m27192_at		C730025J11	adrenergic receptor, alpha 1a,
3	5.3	gnf1m03276_a_at	NM_013766	4921529H02	prolactin-like protein I						ALPHA 1A-ADRENOCEPTOR
4	5.3	gnf1m03727_a_at	NM_019540	C430005G24	pore forming protein-like	2	4.9	gnf1m23653_at		4833405B16	uncoupling protein 1,
5	5.2	gnf1m32200_at			inferred:						mitochondrial
					gb AAH18387.1 AAH18387	3	4.9	gnf1m15492_at	NM_178139	5430410E06	RIKEN cDNA 5430410E06 gene
					(BC018387) Similar to RIKEN	4	4.8	gnf1m08231_at	NM_029690	A530025J20	otopetrin 1
					cDNA 2700091N06 gene [Mus	5	4.6	gnf1m18802_at		B930042O03	actin related protein M1
					musculus] mCG20935	6	4.6	gnf1m20070_at		A130094L10	16 days neonate thymus cDNA,
											RIKEN full-length enriched library,
											clone:A130094L10
											product:unclassifiable, full insert
											sequence
6	5.1	gnf1m10359_a_at	NM_172156	C430027I15	chorionic somatomammotropin	7	4.6	gnf1m29715_at	NM_181857	4930565H06	DNA polymerase N
					hormone 1	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	gnflm35999_at				inferred: ref NP_032529.2 (NM_008503) ribosomal protein S2; repeat family 3 gene [Mus musculus] mCG1032252	16	4.2	gnflm11804_a_at	NM_080644	A930104B02	calcium channel, voltage-dependent, gamma subunit 5
11	4.4	gnflm26432_at				B430117C13 Fc receptor, IgG, low affinity IIb	17	4.2	gnflm32315_at	XM_905651		similar to transmembrane protein 46
12	4.3	gnflm00326_s_at	NM_134093			K230305F10 LETM1 domain containing 1	18	4.1	gnflm01135_a_at	NM_008036		FBJ osteosarcoma oncogene B
13	4.3	gnflm08622_at	XM_906543			6030441H18 RIKEN cDNA 6030441H18 gene	19	4.1	gnflm02246_a_at	NM_010195	4022446J01	leucine rich repeat containing G protein coupled receptor 5
14	4.3	gnflm07163_a_at	NM_147063			olfactory receptor 520	20	4.0	gnflm21985_at		B930068K11	RIKEN cDNA B930068K11 gene
15	4.2	gnflm20409_at				A630064P09 hypothetical protein	No. 39, trachea specific genes					
16	4.2	gnflm06879_at	NM_146590			olfactory receptor 1085	#1	#2	#3	#4	#5	#6
17	4.2	gnflm17413_at				2610042G18 tetraspanin 18	1	5.6	gnflm05861_a_at	NM_170727	1110030K16	secretoglobins, family 3A, member 1
18	4.2	gnflm26429_at				F630017G06 lipoprotein lipase	2	5.4	gnflm05862_a_at	NM_054038	8430440N01	secretoglobins, family 3A, member 2
19	4.1	gnflm18155_at				A130098A21 unclassifiable	3	5.1	gnflm02825_a_at	NM_011478		small proline-rich protein 3
20	4.1	gnflm34713_x_at	XM_888474			I1C0046E08 cDNA sequence BC052688	4	4.8	gnflm02912_a_at	NM_011681	I530005I22	secretoglobins, family 1A, member 1 (uteroglobins)
21	4.1	gnflm34388_x_at	XM_911502			similar to ribosomal protein L7-like 1	5	4.8	gnflm29223_a_at	XM_923104	4930443F05	cytokine like 1
22	4.1	gnflm19577_at				8430406N14 unclassifiable	6	4.7	gnflm23262_a_at		4833442E01	keratin complex 1, acidic, gene 13
23	4.0	gnflm18547_at				A630019I02 hypothetical LOC408254	7	4.6	gnflm27118_at	NM_001024478	C630001B07	RIKEN cDNA 1110049B09 gene
No. 36, bladder specific genes							8	4.5	gnflm11157_a_at	NM_019728	2310011K19	defensin beta 4
#1	#2	#3	#4	#5	#6		9	4.5	gnflm29986_a_at	NM_177369		myosin, heavy polypeptide 8, skeletal muscle, perinatal
1	6.6	gnflm01915_a_at	NM_009476			1110017C07 uroplakin 3A	10	4.4	gnflm01366_a_at	NM_008475		secretory leukocyte peptidase inhibitor
2	6.3	gnflm04323_a_at	NM_023478			E130303A22 GATA binding protein 3	11	4.3	gnflm02795_a_at	NM_011414	2310075E18	hypothetical LOC545549
3	5.6	gnflm28162_at				1110031P12 uroplakin 1A	12	4.3	gnflm18383_at	XM_918929		cDNA sequence BC038167
4	5.3	gnflm29262_a_at	NM_026815			9530013F18 purinergic receptor P2X, ligand-gated ion channel, 1	13	4.2	gnflm34138_at	XM_904952		aggrecaan 1
5	4.9	gnflm10663_a_at	NM_008771			9530014B21 N-acylsphingosine amidohydrolase 3-like	14	4.1	gnflm00789_a_at	NM_007424		RIKEN cDNA 2310002A05 gene
6	4.9	gnflm06333_a_at	NM_139306			5031404D23 neurotrophin Y receptor Y6	15	4.1	gnflm18385_at		2310002A05	
7	4.8	gnflm11546_at	NM_010935			D430024L03 sonic hedgehog	No. 40, CD4+T-cells specific genes					
8	4.8	gnflm27709_a_at	NM_009170			A530032A05 CD200 receptor 3	#1	#2	#3	#4	#5	#6
9	4.6	gnflm25707_a_at	NM_029018			9530006G20 synaptopodin 2	1	6.0	gnflm05717_a_at	NM_033042	A430110L22	tumor necrosis factor receptor superfamily, member 25
10	4.5	gnflm24933_at				E230008G13 leucine rich repeat containing 54	2	5.7	gnflm01869_a_at	NM_009400	C130084C11	tumor necrosis factor receptor superfamily, member 18
11	4.4	gnflm28221_a_at	NM_001024619			2310002D06 RIKEN cDNA 2310002D06 gene	3	4.7	gnflm04233_a_at	NM_022888	0910001L11	folate receptor 4 (delta)
12	4.4	gnflm18386_a_at				Mouse clone IMAGE:3989034, mRNA /cds=UNKNOWN	4	4.6	gnflm32609_at	XM_909582		immunoglobulin heavy chain variable region
13	4.2	gnflm13875_at				/gb=BC012717 /gi=15706467 /len=1655 gnl UG Mm#S2204884	5	4.5	gnflm00913_a_at	NM_007650	F430014J22	CD5 antigen
14	4.2	gnflm11144_a_at	NM_018802			2210012D01 synaptotagmin VIII	6	4.5	gnflm04349_a_at	NM_023684	F830221O09	Lck interacting transmembrane adaptor 1
15	4.2	gnflm12734_a_at	NM_178924			C630013E24 uroplakin 1B	7	4.5	gnflm31021_a_at	NM_175258	E330007P07	Rap guanine nucleotide exchange factor (GEF) 6
16	4.1	gnflm25748_a_at				A530078I09 inferred: actin, alpha 2, smooth muscle, aorta	8	4.4	gnflm34314_at			similar to T-cell receptor beta chain VDNJC precursor
17	4.1	gnflm02263_a_at	NM_010232			I920090I12 flavin containing monooxygenase 5	9	4.4	gnflm08477_a_at	NM_172293	D130052A12	cDNA sequence BC038822
18	4.1	gnflm08900_a_at	NM_025712			9530003D19 RIKEN cDNA 4631426E05 gene	10	4.3	gnflm22690_a_at	NM_177320	G530023B10	phosphoinositide-3-kinase, regulatory subunit 5, p101
19	4.1	gnflm01781_at	NM_009235			2410119O10 SRY-box containing gene 15	11	4.3	gnflm08249_a_at	NM_173766	E430020L17	RIKEN cDNA A630023P12 gene
20	4.0	gnflm01331_a_at	NM_008412			1110032A04 RIKEN cDNA 1110032A04 gene	12	4.1	gnflm24046_a_at	XM_915161	5830405F06	similar to T-cell receptor beta chain V region 86T1 precursor
21	4.0	gnflm06028_a_at	NM_133675				13	4.1	gnflm02904_a_at	NM_011659		tumor necrosis factor receptor superfamily, member 4
No. 37, dorsal root ganglia specific genes							14	4.0	gnflm10816_a_at	NM_009539	E430037O03	zeta-chain (TCR) associated protein kinase
#1	#2	#3	#4	#5	#6		No. 41, epidermis specific genes					
1	5.4	gnflm05878_at	NM_054084			4930555K19 calcitonin-related polypeptide, beta	#1	#2	#3	#4	#5	#6
2	5.3	gnflm13444_s_at	XM_912838			motif containing 1	1	5.0	gnflm21641_at		4832428G11	RIKEN cDNA 4832428G11 gene
3	5.1	gnflm09535_s_at	NM_009134			sodium channel, voltage-gated, type X, alpha	2	4.9	gnflm28593_at	NM_030601	5830469K03	chloride channel calcium activated 2
4	5.0	gnflm31984_at	NM_198860			expressed sequence AI646023	3	4.8	gnflm07746_a_at	NM_130857	A030006N06	keratin associated protein 16-5
5	4.9	gnflm03008_a_at	NM_011887			sodium channel, voltage-gated, type XI, alpha	4	4.7	gnflm20436_a_at	XM_912879	A630098G03	RIKEN cDNA A630098G03 gene
6	4.9	gnflm33299_at	XM_916337			gene model 765, (NCBI)	5	4.6	gnflm02471_a_at	NM_010676		keratin associated protein 8-2
7	4.8	gnflm03206_a_at	NM_013639			7120476M05 peripherin 1	6	4.4	gnflm05953_at	NM_130870		keratin associated protein 16-1
8	4.7	gnflm16713_at	NM_001033954			calcitonin/calcitonin-related polypeptide, alpha	7	4.3	gnflm04524_a_at	NM_025420	4833420N21	late cornified envelope 5A
9	4.6	gnflm04997_a_at	NM_026523			3110023K12 neuremedin B	8	4.2	gnflm11849_a_at	NM_024450	7530414A03	stearyl-coenzyme A desaturase 3
10	4.6	gnflm01989_a_at	NM_009635			F730316L09 advillin	9	4.2	gnflm15703_at			keratin associated protein 16-9
11	4.5	gnflm02805_a_at	NM_011430			C530045H03 synuclein, gamma	10	4.1	gnflm03251_at	NM_013713		keratin associated protein 15
12	4.5	gnflm00748_at	NM_021369			A930003O18 cholinergic receptor, nicotinic, alpha polypeptide 6	11	4.1	gnflm19913_at	NM_001013804	9930021H12	flaggrin 2
13	4.5	gnflm13492_a_at	NM_033217			A030014A01 nerve growth factor receptor (TNFR superfamily, member 16)	12	4.0	gnflm19028_at		4733401I12	RIKEN cDNA 4733401I12 gene
14	4.4	gnflm08103_a_at				C530048O08 RIKEN cDNA 9430031J16 gene	No. 42, preoptic specific genes					
15	4.4	gnflm01988_at	NM_009635			advillin	#1	#2	#3	#4	#5	#6
16	4.3	gnflm33690_at	XM_916777			diacylglycerol kinase, eta	1	5.4	gnflm10962_a_at	NM_011025	0710008H05	oxytocin
17	4.1	gnflm12600_at	NM_008309			C130095B09 5-hydroxytryptamine (serotonin) receptor 1D	2	5.3	gnflm02041_at	NM_009732	A230025O05	arginine vasopressin
18	4.1	gnflm16660_a_at				2700049H19 hypothetical LOC228584	3	5.3	gnflm12931_a_at	NM_177121	D430022H10	RIKEN cDNA B930095G15 gene
19	4.1	gnflm17918_a_at				4833429M11 Bcl-associated death promoter	4	4.9	gnflm13910_at		6330406O05	RIKEN cDNA 6330406O05 gene
20	4.1	gnflm16507_at				5830411H19 solute carrier family 36 (proton/amino acid symporter), member 1	5	4.8	gnflm30112_a_at	XM_619443		RIKEN cDNA 0610007P22 gene
No. 38, olfactory bulb specific genes							6	4.5	gnflm30314_a_at	NM_029971	A230109K23	pro-melanin-concentrating hormone
#1	#2	#3	#4	#5	#6		7	4.4	gnflm02349_a_at	NM_010410		hypocretin
1	6.1	gnflm28883_s_at	NM_001037750			6430524C05 gene model 1533, (NCBI)	8	4.3	gnflm10035_a_at	XM_918655	D630008O05	dynein, axonemal, heavy chain 1
2	5.5	gnflm04065_a_at	NM_021390			sal-like 1 (Drosophila)	9	4.1	gnflm01886_a_at	NM_009426	2410044F19	thyrotropin releasing hormone
3	5.1	gnflm02185_a_at	NM_010053			6430538C22 distal-less homeobox 1	10	4.1	gnflm00887_a_at	NM_007588	A230103M05	calcitonin receptor
4	4.8	gnflm19621_at				A530051K19 cytoplasmic polyadenylation element binding protein 3	No. 43, adipose tissue specific genes					
5	4.7	gnflm13651_a_at	NM_010025			2610028K20 doublecortin	#1	#2	#3	#4	#5	#6
6	4.7	gnflm26184_at				B130002G13 similar to somatostatin intron-related protein RDE.25 (fragment) [Rattus norvegicus]	1	6.3	gnflm11918_a_at	NM_008324	9230107E06	indoleamine-pyrrole 2,3 dioxygenase
7	4.7	gnflm14373_at				2900073C17 RIKEN cDNA 2900073C17 gene	2	5.4	gnflm04226_a_at	NM_022814	9430006B19	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1
8	4.6	gnflm33170_at	NM_001034898			E530011F12 gene model 1286, (NCBI)	3	5.0	gnflm10602_a_at	NM_009704	9130206K13	amphiregulin
9	4.6	gnflm09450_s_at	XM_922114			A830081I04 echinoderm microtubule associated protein like 5	4	4.9	gnflm16461_a_at		2310076O14	apolipoprotein L, 6
10	4.4	gnflm20130_at				A430077E20 unclassifiable	5	4.8	gnflm03098_at			ENSMUST00000038079 transcript (in rel.37.34e)
11	4.3	gnflm26452_at				B230106O20 5-hydroxytryptamine (serotonin) receptor 1F	6	4.3	gnflm11678_a_at	NM_008493	D730002G04	leptin
12	4.3	gnflm19658_at				9330169N05 RIKEN cDNA C230040D10 gene	7	4.2	gnflm26921_at	NM_011994	C230066M19	ATP-binding cassette, sub-family D (ALD), member 2
13	4.3	gnflm12430_at	NM_008310			B230106O20 5-hydroxytryptamine (serotonin) receptor type, O	8	4.1	gnflm23821_a_at	NM_010719	4932412K13	lipase, hormone sensitive
14	4.3	gnflm00656_a_at	NM_011216			4833442A19 unclassifiable						
15	4.2	gnflm19216_at										

9	4.1	gnf1m05871_a_at	NM_054071		fibroblast growth factor receptor-like 1	4	4.2	gnf1m25410_at		A230027G02	adenylate cyclase activating polypeptide 1
No. 44, embryo day 7.5 specific genes						5	4.1	gnf1m18631_at	XM_909450	1110017D07	PDZ domain containing RING finger 4
#1	#2	#3	#4	#5	#6	6	4.0	gnf1m02349_a_at	NM_010410		hypocretin
1	5.8	gnf1m02673_a_at	NM_011165	C430019L15	prolactin-like protein A	7	4.0	gnf1m00792_a_at	NM_007427	A430075H22	agouti related protein
2	5.0	gnf1m01983_at	NM_009627	G730018N16	adrenomedullin	No. 51, lymph node specific genes					
3	4.9	gnf1m03727_a_at	NM_019540	C430005G24	pore forming protein-like	#1	#2	#3	#4	#5	#6
4	4.8	gnf1m03030_a_at	NM_011927		CEA-related cell adhesion molecule 9	1	6.0	gnf1m00984_s_at	NM_007781	I830081A20	colony stimulating factor 2 receptor, beta 1, low-affinity (granulocyte-macrophage)
5	4.8	gnf1m10359_a_at	NM_172156	C430027I15	chorionic somatomammotropin hormone 1	2	4.4	gnf1m00985_a_at	NM_007781		colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage)
6	4.1	gnf1m09471_a_at	NM_019539	5630400J12	cathepsin 7	3	4.4	gnf1m02509_a_at	NM_010766	I920095G17	macrophage receptor with collagenous structure
7	4.1	gnf1m02264_a_at	NM_010235	G830028K10	fos-like antigen 1	4	4.2	gnf1m25017_at		9630004O19	unclassifiable
8	4.1	gnf1m02650_x_at	NM_011118		proliferin 2	5	4.2	gnf1m03009_at	NM_011888	G630025K01	chemokine (C-C motif) ligand 19
9	4.1	gnf1m08880_at	NM_032006	C430029P05	matrix metalloproteinase 1a (interstitial collagenase)	6	4.1	gnf1m02647_a_at	NM_011109		phospholipase A2, group IID
No. 45, CD8+T-cells specific genes						7	4.0	gnf1m30032_at	NM_026972	A530056D21	CD209b antigen
#1	#2	#3	#4	#5	#6	No. 52, ovary specific genes					
1	5.9	gnf1m32844_at		F830032L03	G protein-coupled receptor 114	#1	#2	#3	#4	#5	#6
2	5.2	gnf1m33464_at	XM_204856	5830463C22	similar to apolipoprotein L, 3 (predicted)	1	6.0	gnf1m16904_a_at	NM_007696		oviductal glycoprotein 1
3	4.8	gnf1m22690_a_at	NM_177320	G530023B10	phosphoinositide-3-kinase, regulatory subunit 5, p101	2	5.4	gnf1m13270_a_at	NM_010564		inhibin alpha
4	4.7	gnf1m02458_a_at	NM_010654	A430011E14	killer cell lectin-like receptor, subfamily D, member 1	3	4.9	gnf1m21820_at		9030017N01	unclassifiable
5	4.5	gnf1m31021_a_at	NM_175258	E330007P07	Rap guanine nucleotide exchange factor (GEF) 6	4	4.5	gnf1m00997_a_at	NM_007809	6030448H16	hypothetical cytochrome P450, family 17, subfamily a, polypeptide 1
6	4.3	gnf1m05592_a_at		E430004O20	chemokine (C-X-C motif) receptor 6	5	4.5	gnf1m19802_at		9530076L18	hypothetical protein 9530076L18
7	4.1	gnf1m11208_a_at	NM_024253	E430014G21	natural killer cell group 7 sequence	6	4.4	gnf1m05187_a_at	NM_027582	4921521F21	RIKEN cDNA 4921521F21 gene
8	4.1	gnf1m15860_a_at	XM_915243		T-cell receptor beta, variable 13	7	4.2	gnf1m28954_a_at	NM_001012434		potassium channel tetramerisation domain containing 14
No. 46, trigeminal specific genes						No. 53, dorsal striatum specific genes					
#1	#2	#3	#4	#5	#6	#1	#2	#3	#4	#5	#6
1	5.3	gnf1m07822_a_at	NM_153105	F530003O17	claudin 19	1	4.3	gnf1m29979_at	NM_197945	5730599K07	ProSAPiP1 protein
2	5.1	gnf1m06563_a_at	NM_145555	I530014I18	RIKEN cDNA A330049M08 gene	2	4.2	gnf1m02144_a_at	NM_009946		complexin 2
3	4.3	gnf1m01989_a_at	NM_009635	F730316L09	advillin	3	4.2	gnf1m04217_a_at	NM_022427		G-protein coupled receptor 88
4	4.3	gnf1m03206_a_at	NM_013639	7120476M05	peripherin 1	4	4.1	gnf1m34682_at		A830030P14	G protein-coupled receptor 6
5	4.3	gnf1m09535_s_at	NM_009134		sodium channel, voltage-gated, type X, alpha	5	4.1	gnf1m02722_a_at	NM_011268		regulator of G-protein signaling 9
6	4.1	gnf1m16713_at	NM_001033954		calcitonin/calcitonin-related polypeptide, alpha	No. 54, embryo day 8.5 specific genes					
7	4.1	gnf1m29643_a_at	NM_183000	3830432N09	amiloride-sensitive cation channel 3	#1	#2	#3	#4	#5	#6
8	4.0	gnf1m09621_a_at	NM_008117	5730422D01	growth hormone	1	4.6	gnf1m04647_a_at	NM_025684	5730557A08	RIKEN cDNA 5730521E12 gene
No. 47, uterus specific genes						2	4.3	gnf1m13899_a_at	NM_010405	G630096F14	carbonic anhydrase 7
#1	#2	#3	#4	#5	#6	3	4.2	gnf1m11633_a_at		5730460L13	hemoglobin X, alpha-like
1	6.0	gnf1m02820_at	NM_011472		small proline-rich protein 2F	4	4.0	gnf1m11262_a_at	NM_008219	2810007M22	embryonic chain in Hba complex
2	5.8	gnf1m11079_a_at	NM_019511	1600021K13	receptor (calcitonin) activity modifying protein 3	No. 55, embryo day 9.5 specific genes					
3	5.6	gnf1m02616_a_at	NM_011059	A030006O20	peptidyl arginine deiminase, type I	#1	#2	#3	#4	#5	#6
4	4.7	gnf1m05781_a_at	NM_053085	5031404B19	transcription factor 23	1	4.6	gnf1m22666_at	NM_198605	F630043A04	RIKEN cDNA F630043A04 gene
5	4.4	gnf1m01564_a_at	XM_915139	F630107K01	peptidyl arginine deiminase, type II	2	4.3	gnf1m28731_a_at		0610016J10	RIKEN cDNA 0610016J10 gene
6	4.2	gnf1m28608_a_at		F630204G22	hydroxysteroid 11-beta dehydrogenase 2	3	4.2	gnf1m11633_a_at	NM_010405	5730460L13	hemoglobin X, alpha-like
7	4.2	gnf1m32206_at			gene model 247, (NCBI)	4	4.1	gnf1m19351_at		5930402A21	embryonic chain in Hba complex
8	4.1	gnf1m29898_a_at	NM_008381	4022431B02	inhibin beta-B	No. 56, spinal cord lower specific genes					
No. 48, embryo day 10.5 specific genes						#1	#2	#3	#4	#5	#6
#1	#2	#3	#4	#5	#6	1	5.6	gnf1m03022_a_at	NM_011910		urotensin 2
1	4.4	gnf1m23332_at		2700008K06	unclassifiable	2	4.3	gnf1m24400_at		6430545K04	glycine receptor, alpha 1 subunit
2	4.4	gnf1m11633_a_at	NM_010405	5730460L13	hemoglobin X, alpha-like	3	4.1	gnf1m20806_a_at		B230397M16	glycine receptor, alpha 1 subunit
3	4.4	gnf1m16677_a_at	NM_009234	6230403H02	SRY-box containing gene 11	No. 57, substantia nigra specific genes					
4	4.3	gnf1m22972_at		1110038H03	SRY-box containing gene 11	#1	#2	#3	#4	#5	#6
5	4.1	gnf1m01653_a_at	NM_008988	D030056K15	putative neuronal cell adhesion molecule	1	5.2	gnf1m02174_a_at	NM_010020	9330165P06	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3
6	4.1	gnf1m12588_a_at	NM_172412	C530010J15	glypican 2 (cerebroglycan)	2	4.3	gnf1m23556_a_at		A130081F14	inferred: protein associating with small stress protein PASS1 (Rattus norvegicus)
7	4.0	gnf1m03436_a_at	NM_016701	1190008F12	nestin	3	4.1	gnf1m08549_at	NM_177057	E230015B07	RIKEN cDNA E230015B07 gene
No. 49, hippocampus specific genes						No. 58, amygdala specific genes					
#1	#2	#3	#4	#5	#6	#1	#2	#3	#4	#5	#6
1	6.4	gnf1m08348_at	NM_178887	B230372M18	fibrinogen C domain containing 1	1	4.8	gnf1m31999_at	XM_907532		cadherin 9
2	5.3	gnf1m08349_a_at	NM_178887	B230372M18	fibrinogen C domain containing 1	2	4.1	gnf1m16736_at			LIM domain only 3
3	5.1	gnf1m15269_at		8030496P19	glycoprotein m6b	No. 59, cerebral cortex specific genes					
4	5.0	gnf1m08380_a_at	NM_177193	B930052A04	immunoglobulin superfamily containing leucine-rich repeat 2	#1	#2	#3	#4	#5	#6
5	4.6	gnf1m07985_at	NM_177854	6030405A18	RIKEN cDNA 6030405A18 gene	1	4.3	gnf1m08380_a_at	NM_177193	B930052A04	immunoglobulin superfamily containing leucine-rich repeat 2
6	4.6	gnf1m24427_at		6430587E11	similar to COPINE VII [Homo sapiens]	No. 60, frontal cortex specific genes					
7	4.2	gnf1m26520_a_at		D930018L04	glutamate receptor, ionotropic, NMDA2A (epsilon 1)	#1	#2	#3	#4	#5	#6
No. 50, hypothalamus specific genes						1	4.3	gnf1m30549_at	NM_182839	C630015P20	RIKEN cDNA 2900041A09 gene
#1	#2	#3	#4	#5	#6	No. 61, spinal cord upper specific genes					
1	4.8	gnf1m30314_a_at	NM_029971	A230109K23	pro-melanin-concentrating hormone	#1	#2	#3	#4	#5	#6
2	4.6	gnf1m11894_a_at	NM_178896	9030622J04	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	1	4.1	gnf1m25497_a_at		A230103O17	glial fibrillary acidic protein
3	4.5	gnf1m02041_at	NM_009732	A230025O05	arginine vasopressin						

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	Molecular function	Gene Ontology Classification Biological process	Cellular component	Annotation
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	AAAAAATA	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	AAAAAATA	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	AAAAAAA	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 [Psammecinus 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)

79	gnf1m15372_a_at	C3	GGGCGGGG	1700006F03	6.37	enzyme regulator activity	process 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 comifed 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 (Hspa11)
87	gnf1m03870_a_at	A3	ATGTACACA	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 (Cyp13)
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	GGGCGGGG	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
108	gnf1m04975_a_at	A2	TCACAATG	1700129C05	6.14				Mus musculus
109	gnf1m13089_a_at	A1*	TGACATCA	4933432H20	6.13	catalytic activity	response to stimulus, regulation of biological process	organelle, cell part	hypothetical protein
110	gnf1m04681_a_at	B6	CAGCCAAT	1700027I20	6.12	catalytic activity	physiological process, cellular process	cell part, organelle	tubby-like protein 2
111	gnf1m29783_a_at	A2	TCACAATG	1700125D06	6.11				aldolase 1, A isoform, pseudogene 1
112	gnf1m05339_a_at	A15	GGTTGCTA	4930432H15	6.11				basic proline-rich protein [Sus scrofa]
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	AAAAAANA	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 similar to ankyrin repeat and SOCS box-containing protein 17
134	gnf1m13311_a_at	A1	TGATGTCA	4933436O18	6.00				H1 histone family, member N, testis-specific (H1fnt)
135	gnf1m05152_a_at	A4	GATGTCAC	NM_027304	5.99	binding			ATPase, H+ transporting, lysosomal V1 subunit E2
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	hypothetical protein
137	gnf1m15286_a_at	A13	CTCTGTGA	1700054J20	5.97				hypothetical protein
138	gnf1m17051_a_at	A5	ATGTCATA	1700034O15	5.97				ARM repeat structure containing protein
139	gnf1m17239_a_at	B34	GGCAGAGG	1700016M24	5.97				protein phosphatase 1, regulatory (inhibitor) subunit 14B (Ppp1r14b)
140	gnf1m04675_a_at	B28	GCAGCTGC	4933415F23	5.97	enzyme regulator activity, binding	physiological process, cellular process	cell part, organelle part, organelle	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 Cln 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 CCH 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	CTCCACAG	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	AAAAAATA	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 metalloproteinase 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	ATGCATA	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	ATGCATA	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	AAAAA	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	AAAAA	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	TTTAAAA	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	AAAAA	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 microorchidia 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	AAAAA	4921510J17	5.38	binding	regulation of biological process, physiological process, cellular process	cell part, organelle	hypothetical EF-hand containing protein

259	gnf1m05104_a_at	B15	AAAAA	170006D24	5.37	binding	process 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 Cyp15 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	CTCCAGA	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	CTCCAGA	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	AAAAA	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 norvegicus]

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	AAAAAATA	NM_029294	5.16	catalytic activity, binding			phosphoribosyl pyrophosphate synthetase 1-like 1 (Prps11)
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 (Efca5)
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		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	GGGCGGGG	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	AAAAAATA	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	AAAAAATA	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	AAAAA	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	AAAAA	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 membrane-spanning 4-domains, subfamily A, member 13 (Ms4a13), Mus musculus CatSper channel subunit beta mRNA
478	gnf1m17138_a_at	B23	AGAGGCAG	1700060E18	4.56				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]
479	gnf1m11494_a_at	B11	AGCAGCTG	4932415G16	4.55				hypothetical protein
480	gnf1m05314_a_at	B32	AAACAAAA	4933403P17	4.55	catalytic activity, binding	physiological process, cellular process	cell part	tubulin, alpha 3B (Tuba3b)
481	gnf1m28856_at	C3	GGGCGGGG	4932419B04	4.55				
482	gnf1m00002_f_at	B35	CTCTCTCT	NM_009449	4.54	structural molecule activity, binding, catalytic activity			
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	GGGCGGGG	1700007N08	4.49				weakly similar to testis specific gene A2 (MORN motif containing)
498	gnf1m09549_a_at	B19	GCCCAATCA	NM_029354	4.48				hypothetical protein
499	gnf1m05485_a_at	C3	GGGCGGGG	NM_029610	4.48				LYR motif containing 1 (Lyrn1)
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	AAAAA	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	AAAAA	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) (Sel112)
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	AAAAAAA	1700112I01	4.40				DYnein Light chain (Tctex type) family member (dytl-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 Butyrophilin-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:359771). [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	GGGCGGGG	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 (Cccl81) 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	TCCTGTGT	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				sialoporphin, 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	AAAAAATA	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	GGGGCGGG	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	GGGGCGGG	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	GGGGCGGG	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	AAAAAATA	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	AAAAAATA	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	GGGGCGGG	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	GGGGCGGG	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) (If74)
611	gnf1m29032_a_at	B6	CAGCCAAT	4931413D17	4.07			arylsulfatase A
612	gnf1m10239_a_at	A26	GAGCTCTG	4933403H06	4.06	binding	cellular process	leucine rich repeat containing 44
							cell part, protein complex, organelle part, organelle	
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	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	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	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	hypothetical a disintegrin and metalloproteinase 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	hypothetical Barrier to autointegration factor (BAF) containing protein
623	gnf1m13538_a_at	A1*	TGACATCA	4930557A04	4.03	binding	reproduction, physiological process, cellular process	hypothetical Histone-fold structure containing protein
624	gnf1m30249_s_at	A35	TCCAGGAG	4932419D11	4.03	binding	physiological process, cellular process, regulation of biological process	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	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	weakly similar to predicted EF-hand containing protein
634	gnf1m22843_a_at	A32*	CACAGAGA	4930544N01	4.01		organelle, cell part	weakly similar 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	Molecular function	Gene Ontology Classification Biological process	Cellular component	Annotation
1	gnflm21655_at	NM_199034	7.32	binding			weakly similar to predicted CD69 antigen (p60, early T-cell activation antigen)
2	gnflm31778_at	2410022A04	7.04	binding	physiological process, cellular process		glutamine rich 2 (Qrich2)
3	gnflm12377_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	gnflm04821_a_at	NM_026084	6.65				hypothetical protein
5	gnflm13831_a_at	4921511C04	6.59				Peptidase, eukaryotic cysteine peptidase active site containing protein
6	gnflm03322_a_at	E030006L06	6.50	binding			Janus kinase 3
7	gnflm18722_a_at	4930597B14	6.42	binding	reproduction, development, regulation of biological process, cellular process	cell part	leucine rich repeat containing 56
8	gnflm30191_s_at	I920062J18	6.13				hypothetical Proline-rich region profile containing protein
9	gnflm06267_a_at	MSC1099J02	6.11	binding	cellular process, regulation of biological process, physiological process	cell part	suppressor of cytokine signaling 7 (Socs7)
10	gnflm08368_a_at	D330025M16	6.08	binding		organelle, cell part	zinc finger, HIT domain containing 2
11	gnflm16052_a_at	1700081D17	6.00			organelle, cell part	similar to PEBP family protein precursor
12	gnflm10564_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	gnflm29416_a_at	F630225G14	5.88				testis specific protein kinase 1
14	gnflm07900_a_at	NM_177765	5.83	catalytic activity	physiological process, cellular process		tubulin tyrosine ligase-like family, member 13 (Ttl13)
15	gnflm30626_at	G630078G02	5.75			extracellular region	maelstrom homolog (Drosophila)
16	gnflm16137_a_at	I190002A17	5.75	catalytic activity, binding	physiological process, cellular process		hypothetical Adenylate kinase containing protein
17	gnflm16775_a_at	NM_011516	5.72	binding	physiological process, cellular process	cell part, organelle part, organelle	atonal homolog 8 (Drosophila)
18	gnflm22221_a_at	C920025L08	5.66	binding		cell part	sperm mitochondria-associated cysteine-rich protein
19	gnflm16828_a_at	2410015A16	5.59			extracellular region	ring finger protein 148
20	gnflm27335_a_at	D030060E19	5.58				hypothetical S-adenosyl-L-methionine-dependent methyltransferases structure containing protein
21	gnflm13456_at	4930432J16	5.55				coiled-coil domain containing 116
22	gnflm17690_at	A630039F22	5.49				spermatogenesis associated 21
23	gnflm13287_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	gnflm11136_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	gnflm08962_s_at	C130098D09	5.33				ATP/GTP binding protein-like 5 (Agbl5), transcript variant 3
26	gnflm31215_s_at	4933439H17	5.31	catalytic activity	physiological process, cellular process		hypothetical Peptidase, eukaryotic cysteine peptidase active site containing protein
27	gnflm18853_a_at	5930422B18	5.30				unclassifiable
28	gnflm30265_a_at	I920019O09	5.20	catalytic activity, binding	physiological process, cellular process	organelle, cell part	ribonuclease H2, large subunit
29	gnflm04978_s_at	1700062C23	5.19				zinc finger protein 217
30	gnflm28680_a_at	1810037J08	5.18				phosphoglycerate kinase 2
31	gnflm05239_a_at	G530145B18	5.16		regulation of biological process, physiological process, cellular process		MAD2 mitotic arrest deficient-like 2 (yeast) (Mad212)
32	gnflm00466_a_at	E430037N03	5.08	binding	regulation of biological process, physiological process, cellular process	organelle, cell part	WD repeat domain 62
33	gnflm09512_a_at	A630082B21	5.07	binding			regulatory factor X, 2 (influences HLA class II expression)
34	gnflm04905_at	4930465K10	5.03				asteroid homolog 1 (Drosophila)
35	gnflm09987_s_at	F630205N16	5.00	catalytic activity, binding	physiological process, cellular process		6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 4 (Pfkfb4)
36	gnflm11605_a_at	5430408G21	5.00	catalytic activity, binding			WW domain binding protein 11
37	gnflm07602_a_at	5730427C23	4.96	binding			melanoma associated antigen (mutated) 1
38	gnflm13975_a_at	4930432J01	4.96				unclassifiable
39	gnflm16773_a_at	I110017D15	4.96				diablo homolog (Drosophila)

40	gnflm05337_a_at	I110014P06	4.92		cellular process	organelle, cell part	solute carrier family 22 (organic cation transporter), member 21
41	gnflm13937_a_at	C920013G19	4.80			cell part	hypothetical protein
42	gnflm30004_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	gnflm30753_at	4922504L10	4.80			organelle, cell part	similar to Salivary glue protein Sgs-4 precursor
44	gnflm31291_a_at	2010109A12	4.79		physiological process, cellular process		fibrous sheath-interacting protein 1
45	gnflm29201_at	I0C0026C19	4.78				hypothetical protein
46	gnflm02430_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	gnflm15242_at	I920045P05	4.74	enzyme regulator activity	physiological process, cellular process, regulation of biological process		cyclin K
48	gnflm31664_at	F630047G17	4.71	binding		cell part, organelle	X-ray radiation resistance associated 1 protein
49	gnflm18101_at	9930109I05	4.67				kinesin family member 2B
50	gnflm30390_a_at	4930453N24	4.63	catalytic activity	physiological process, cellular process		hypothetical Peptidase, eukaryotic cysteine peptidase active site containing protein
51	gnflm32280_a_at	M5C1026A22	4.62	catalytic activity	physiological process, cellular process	cell part	glycosyltransferase 8 domain containing 3
52	gnflm18179_at	A430076A20	4.61				ring finger protein 126
53	gnflm22576_a_at	E130303B06	4.56				weakly similar to sodium channel and clathrin linker 1 (Sclt1)
54	gnflm23608_at	4733401H18	4.55			organelle, cell part	nuclear protein E3-3
55	gnflm29679_a_at	2900041A11	4.53				hypothetical protein
56	gnflm13335_a_at	5330430P22	4.51				cytochrome P450, family 17, subfamily a, polypeptide 1
57	gnflm04043_a_at	G830022G14	4.51	binding, catalytic activity	reproduction, development, cellular process	cell part, organelle	spermatogenesis associated 5
58	gnflm03205_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	gnflm24904_a_at	I830061M19	4.44	catalytic activity, enzyme regulator activity, binding	physiological process, cellular process		myotubularin related protein 9
60	gnflm16751_at	2610318N02	4.43				hypothetical Proline-rich region profile containing protein
61	gnflm04335_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	gnflm10285_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	gnflm09744_a_at	F630050M23	4.38	catalytic activity			Rsb-66 protein (Rsb66)
64	gnflm28413_a_at	E430036P15	4.37				X-ray radiation resistance associated 1
65	gnflm17370_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	gnflm16233_a_at	4732409C05	4.33				hypothetical protein
67	gnflm07312_a_at	A630069B14	4.32	catalytic activity, antioxidant activity	cellular process, physiological process	cell part	prion protein dublet
68	gnflm05029_a_at	A930018P22	4.31				coiled-coil domain containing 11
69	gnflm29259_a_at	F630110C03	4.31				MAD2 mitotic arrest deficient-like 2 (yeast)
70	gnflm20339_at	A630001I11	4.30				poly A binding protein, cytoplasmic 2
71	gnflm18488_a_at	3110023G01	4.30	binding			homologue katanin p60 subunit A-like 2 (Katnal2)
72	gnflm25228_s_at	E430035G08	4.30				elongation factor 1 homolog (ELF1, S. cerevisiae)
73	gnflm04244_a_at	A730048L21	4.23	binding	physiological process, cellular process	cell part	alanine and arginine rich domain containing protein
74	gnflm16560_a_at	2610020H08	4.23	catalytic activity			exonuclease NEF-sp
75	gnflm08351_a_at	B230381K07	4.20				cofactor required for Sp1 transcriptional activation, subunit 7
76	gnflm07300_s_at	I530023E14	4.18	binding, catalytic activity			nudix (nucleoside diphosphate linked moiety X)-type motif 18
77	gnflm04036_s_at	5430416M17	4.18	enzyme regulator activity, binding	physiological process, cellular process	cell part, organelle part, organelle	HLA-B-associated transcript 3
78	gnflm30720_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	gnflm09413_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	gnflm10515_a_at	I110020C03	4.09				kelch-like 10 (Drosophila)
81	gnflm29825_a_at	S033427P15	4.09			cell part	cystatin 8 (cystatin-related epididymal spermatogenic)
82	gnflm18605_a_at	E130217B17	4.06				coiled-coil domain containing 65
83	gnflm12974_a_at	D630044H03	4.04				hypothetical S-adenosyl-L-methionine-dependent methyltransferases structure containing protein
84	gnflm12431_a_at	G730044P08	4.02				hypothetical protein
85	gnflm02369_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 Molecular function	Gene Ontology Biological process	Cellular component	Annotation
1	gnflm31206_a_at	1700019B01	7.01				weakly similar to predicted coiled-coil domain containing 89 (Ccdc89)
2	gnflm29756_a_at	1700021F07	6.94				similar to low in lung cancer 1
3	gnflm16054_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	gnflm18742_a_at	1700022P22	6.87				hypothetical protein
5	gnflm17312_a_at	4933405J11	6.75				hypothetical protein
6	gnflm30572_a_at	4933413C15	6.72				weakly similar to coiled-coil domain containing 67 (Ccdc67)
7	gnflm05112_s_at	1700018F24	6.71				hypothetical Ras GEF structure containing protein
8	gnflm31877_at	4933439I02	6.56				hypothetical protein
9	gnflm08577_a_at	4922504H04	6.53	transporter activity, binding	physiological process, cellular process	cell part, protein complex	potassium channel tetramerisation domain containing 19
10	gnflm28686_a_at	1700095K08	6.53				TBC1 domain family, member 21
11	gnflm31096_a_at	1700003O08	6.51				unclassifiable
12	gnflm16159_a_at	1700025M08	6.48	catalytic activity	physiological process, cellular process	cell part, extracellular region, organelle	sperm acrosome associated 3
13	gnflm18375_a_at	1700016G14	6.47				unclassifiable
14	gnflm02714_a_at	4930569O14	6.46	binding		organelle, cell part	RNA binding motif protein, Y chromosome, family 1, member A1
15	gnflm18660_at	1700108N11	6.44				ovo-like 2 (Drosophila)
16	gnflm17095_a_at	4930579F01	6.43				similar to predicted stromal protein associated with thymii and lymph nodes isoform 2
17	gnflm23185_a_at	1700056E22	6.40				hypothetical protein
18	gnflm30605_a_at	4930467B22	6.32				ATP-binding cassette, sub-family C (CFTR/MRP), member 12
19	gnflm17234_a_at	1700049K14	6.30	catalytic activity	physiological process, cellular process	cell part	weakly similar to predicted Plasma kallikrein precursor (Plasma prekallikrein) (Kininogenin) (Kininogenin) (Fletcher factor)
20	gnflm17328_a_at	4933432N21	6.29	structural molecule activity	physiological process, cellular process	cell part, organelle	homologue testis specific 10 (Tsga10)
21	gnflm13976_a_at	4930570O04	6.24				unclassifiable
22	gnflm29757_a_at	1810013N20	6.24				testis specific 10 interacting protein (Tsga10ip)
23	gnflm17352_a_at	4921530D09	6.24				hypothetical protein
24	gnflm13790_a_at	1700056A17	6.19				melanoma antigen, family B, 5
25	gnflm05414_a_at	4930503E14	6.13				weakly similar to alpha12-takusan
26	gnflm23650_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	gnflm16285_at	4930571K23	6.10				unclassifiable
28	gnflm23176_x_at	1700029H17	6.02		reproduction		similar to predicted Sty2 protein isoform 1
29	gnflm25487_at	A230094D06	6.00	signal transducer activity, binding	cellular process	cell part, extracellular region part	G protein-coupled receptor 106
30	gnflm14468_at	4930405A07	5.99				unclassifiable
31	gnflm21682_at	4930551J12	5.99				unclassifiable
32	gnflm31099_a_at	1700027A15	5.99				hypothetical protein
33	gnflm30571_a_at	3300001K11	5.87				tektin 5 (Tek5)
34	gnflm14530_a_at	4933422M21	5.86	binding	physiological process, cellular process	cell part	ADP-ribosylation factor-like 13
35	gnflm22995_a_at	4933425D22	5.83				unclassifiable
36	gnflm21654_a_at	4922501K12	5.78				hypothetical protein
37	gnflm16440_at	4930442P07	5.77				unclassifiable
38	gnflm14460_a_at	4930415F15	5.74				hypothetical protein
39	gnflm30457_a_at	1700019G24	5.72				unclassifiable
40	gnflm07557_at	A930027N24	5.70				cDNA sequence BC049715
41	gnflm09162_s_at	1700023A18	5.70	binding, enzyme regulator activity		cell part	phosphatidylethanolamine binding protein 2
42	gnflm16079_a_at	6330543E12	5.64				IQ motif and WD repeats 1
43	gnflm31171_a_at	3526402J02	5.63	catalytic activity			ataxia telangiectasia and rad3 related
44	gnflm19128_at	1700042K15	5.62	catalytic activity, binding	physiological process, cellular process		ring finger protein 133
45	gnflm18415_a_at	1700030G11	5.62				weakly similar to novel protein containing an anlyrin domain
46	gnflm21667_at	4930427O07	5.56				hypothetical protein
47	gnflm19258_at	4931412E05	5.53				zinc finger protein 148, pseudogene 1
48	gnflm13500_a_at	1700113H08	5.53				hypothetical protein
49	gnflm30831_a_at	1700012C08	5.45				unclassifiable
50	gnflm18455_at	3830402K23	5.45				synaptonemal complex protein 2 (Sycp2)

51	gnflm23022_a_at	1700108A15	5.44				unclassifiable
52	gnflm23777_at	4930555L03	5.40				IBR domain containing 3
53	gnflm23355_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	gnflm16866_a_at	4930527E24	5.36				weakly similar to Xlr-like
55	gnflm13830_a_at	1700023A16	5.35				hypothetical protein
56	gnflm14298_a_at	4930535E05	5.35				weakly similar to predicted T-cell activation Rho GTPase-activating protein isoform b
57	gnflm13520_at	4930452G13	5.34				unclassifiable
58	gnflm17104_at	4933438K21	5.31				unclassifiable
59	gnflm28768_a_at	A530057A03	5.30	catalytic activity	physiological process, cellular process	cell part	similar to predicted similar to mitochondrial glycerol 3-phosphate acyltransferase
60	gnflm18414_at	1700030L20	5.27				developmentally regulated repeat element-containing transcript 1a
61	gnflm30921_s_at	4921509O09	5.27				weakly similar to predicted Sycp3 like Y-linked
62	gnflm23872_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	gnflm11101_a_at	6030488D03	5.23				hypothetical protein
64	gnflm13832_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	gnflm13833_at	4930449C09	5.18				unclassifiable
66	gnflm23167_a_at	1700018G05	5.17				unclassifiable
67	gnflm18868_a_at	4933440C21	5.14	binding		cell part	DC-STAMP domain containing 1
68	gnflm14147_at	4932703K07	5.12				heat shock protein 1, alpha
69	gnflm30771_a_at	4930578E11	5.11				unclassifiable
70	gnflm13328_a_at	4933422B16	5.11				hypothetical Tetratricopeptide repeat (TPR) structure containing protein
71	gnflm18620_a_at	1700048O14	5.10				unclassifiable
72	gnflm16843_s_at	4921511M17	5.09			cell part	hypothetical protein
73	gnflm16116_a_at	3110013H01	5.08	catalytic activity	physiological process	organelle, cell part	proline-rich polypeptide 6
74	gnflm18655_at	4931438A05	5.08				weakly similar to predicted vitamin A-deficient testicular protein 11-like
75	gnflm17085_a_at	4930435E18	5.08				unclassifiable
76	gnflm13998_a_at	1700017D01	5.07				hypothetical protein
77	gnflm28673_a_at	4930469G21	5.06				hypothetical protein
78	gnflm17273_a_at	1700063H04	5.06				hypothetical protein
79	gnflm11449_at	4921521M13	5.03	binding, catalytic activity	reproduction, development, cellular process	cell part, organelle	DNA segment, Chr 1, Pasteur Institute 1
80	gnflm29797_a_at	2900092C05	4.94				hypothetical protein
81	gnflm23957_a_at	5330437G15	4.93				serine/threonine kinase 33
82	gnflm30296_at	3632444A02	4.93				tetratricopeptide repeat domain 21B
83	gnflm13582_a_at	1700013H16	4.93				hypothetical protein
84	gnflm18132_a_at	1700003H21	4.92				EF hand calcium binding protein 1
85	gnflm19031_at	4933404M19	4.89				weakly similar to predicted proline-rich cyclin A1-interacting protein isoform 1
86	gnflm05196_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	gnflm14178_a_at	4933422A05	4.88				unclassifiable
88	gnflm09828_a_at	F830031M20	4.87				intraflagellar transport 140 homolog (Chlamydomonas)
89	gnflm05434_a_at	1700012P12	4.85	transporter activity, binding	physiological process, cellular process	cell part, organelle	profilin 3
90	gnflm16015_at	4933429H19	4.85	signal transducer activity, transporter activity	physiological process, cellular process	cell part	hypothetical TonB-dependent receptor protein containing protein
91	gnflm17688_at	4931436F15	4.82				hypothetical protein
92	gnflm14866_at	1700003F17	4.81				hypothetical protein
93	gnflm05419_a_at	4930542N07	4.81			cell part	hypothetical protein
94	gnflm16980_a_at	4933434G05	4.78				coiled-coil domain containing 57 (Ccde57)
95	gnflm13323_a_at	4930433I05	4.77			organelle part, cell part	cylicin, basic protein of sperm head cytoskeleton 1
96	gnflm03386_a_at	1700021G14	4.76	enzyme regulator activity, binding	physiological process, cellular process	cell part	immunoglobulin (CD79A) binding protein 1b
97	gnflm29246_s_at	9230104I23	4.75				tripartite motif-containing 36
98	gnflm33184_at	1700014P15	4.74	transporter activity, binding	physiological process, cellular process, reproduction, development	cell part, organelle	solute carrier family 9, member 10 (Slc9a10)
99	gnflm16929_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	gnflm23708_at	4930408P03	4.72	binding	physiological process, cellular process	cell part, organelle, protein complex, organelle part	HISTONE H2B (FRAGMENT) homolog [Mus musculus]
101	gnflm29612_a_at	1700020H17	4.71	catalytic activity			molybdenum cofactor synthesis 3
102	gnflm31156_a_at	C330017P09	4.67				hypothetical protein
103	gnflm14489_at	4933412L11	4.66				unclassifiable
104	gnflm14693_a_at	4930527J03	4.64				hypothetical Alanine-rich region containing protein

105	gnflm23738_s_at	4930476G21	4.62	binding			ring finger protein 17
106	gnflm14207_at	4933435G04	4.61				hypothetical protein
107	gnflm01848_a_at	1700030B16	4.59	catalytic activity	physiological process, cellular process		testicular serine protease 2
108	gnflm14175_a_at	4933413D07	4.58				unclassifiable
109	gnflm30081_a_at	4930572N15	4.58	binding, transcription regulator activity	regulation of biological process		ankyrin repeat domain 53 (Ankrd53)
110	gnflm15511_a_at	G430033H23	4.58				leucine rich repeat containing 27
111	gnflm14180_a_at	4933413N12	4.58				hypothetical protein
112	gnflm17307_a_at	1700016C15	4.56				hypothetical protein
113	gnflm11444_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	gnflm13353_a_at	5133400G04	4.53		reproduction, development, cellular process	cell part	homologue TATA-binding protein-like factor-interacting protein isoform 2
115	gnflm13926_a_at	1700051I12	4.51	structural molecule activity	cellular process		collagen, type XX, alpha 1
116	gnflm15539_a_at	4933401F05	4.50	catalytic activity	physiological process, cellular process	cell part	weakly similar to adrenal mitochondrial protease
117	gnflm29295_a_at	1700023D19	4.49				weakly similar to predicted SCRL protein variant 1
118	gnflm32673_at	C230012F14	4.45	binding			armadillo repeat containing 2
119	gnflm18823_at	4932416M14	4.40				hypothetical protein
120	gnflm32296_at	4922503N05	4.40				cancer antigen 1
121	gnflm15939_at	1700014B07	4.39				hypothetical protein
122	gnflm17231_a_at	4930444P10	4.39				hypothetical Arginine-rich region containing protein
123	gnflm16847_a_at	1700011E04	4.38			extracellular region part	predicted GLI pathogenesis-related 1 like 1 (Gliplr11)
124	gnflm14697_a_at	4930544O15	4.37			cell part	hypothetical protein
125	gnflm09652_a_at	1730086C16	4.35				IQ motif containing G
126	gnflm15124_a_at	4930570E03	4.34				hypothetical protein
127	gnflm07476_a_at	1810009N24	4.34	catalytic activity	physiological process, cellular process	extracellular region, extracellular region part	lysozyme-like 4
128	gnflm16596_at	1700062G21	4.33				neurexin 1
129	gnflm17179_a_at	1700067K01	4.33				hypothetical protein
130	gnflm13554_a_at	1700034F02	4.31				hypothetical ARM repeat structure containing protein
131	gnflm30342_a_at	1700026J12	4.31		cellular process	cell part	weakly similar to CD47 antigen
132	gnflm14608_a_at	4930511J24	4.30				unclassifiable
133	gnflm07915_a_at	4933417L03	4.29				hypothetical protein
134	gnflm17027_a_at	4933424N20	4.29				unclassifiable
135	gnflm10081_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	gnflm19228_at	4930526M03	4.26				weakly similar to predicted Ribosome-binding protein 1 (Ribosome receptor protein) (mRRp)
137	gnflm08204_a_at	A330015D16	4.25				weakly similar to predicted Myosin heavy chain, fast skeletal muscle, embryonic
138	gnflm29417_a_at	A130090N03	4.25				amyotrophic lateral sclerosis 4 homolog (human)
139	gnflm19278_at	4932416H13	4.25				hypothetical protein
140	gnflm21703_at	4933402M05	4.25				Adult male testis cDNA, RIKEN full-length enriched library, clone:4933402M05 product:serine/threonine kinase 33, full insert sequence
141	gnflm27322_at	D030054G02	4.25				hypothetical protein
142	gnflm19389_at	6030430N23	4.24				DEAD (Asp-Glu-Ala-Asp) box polypeptide 4
143	gnflm30176_a_at	1700023F06	4.23				hypothetical protein
144	gnflm14198_at	4933417D19	4.19				unclassifiable
145	gnflm29567_a_at	1700008J08	4.18				ankyrin repeat domain 48
146	gnflm28873_a_at	4930404K22	4.16	catalytic activity			spermidine/spermine N1-acetyl transferase-like 1
147	gnflm00055_a_at	C330007K24	4.13				serine threonine kinase 31
148	gnflm17834_at	4632417E12	4.13	binding, transcription regulator activity	regulation of biological process		unclassifiable
149	gnflm17325_s_at	4930412B11	4.13				hypothetical protein
150	gnflm21504_a_at	E130009J12	4.12				hypothetical protein
151	gnflm29010_at	4933400N17	4.10	binding	regulation of biological process		similar to predicted DNA-binding protein RFX2
152	gnflm14462_a_at	4930423M02	4.09				unclassifiable
153	gnflm14629_at	4930445B03	4.08				unclassifiable
154	gnflm31677_at	4931417M15	4.07				hypothetical Leucine-rich repeat/Leucine-rich repeat, typical subtype containing protein
155	gnflm14404_a_at	1700041E20	4.06	binding			homologue calcium and integrin binding family member 4
156	gnflm16968_at	4933436F18	4.05				unclassifiable
157	gnflm05321_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.

#1	Calibri	Clone ID	#2	Gene Ontology Classification			Annotation
				Molecular function	Biological process	Cellular component	
1	gnflm05228_s_at	1700001F09	6.26				hypothetical Cytochrome c family heme-binding site containing protein
2	gnflm30192_a_at	I920062J18	5.97				Proline-rich region profile containing protein
3	gnflm16354_at	1700110M21	5.59				gamma-aminobutyric acid (GABA-B) receptor binding protein
4	gnflm14433_s_at	4930551J12	5.30				unclassifiable
5	gnflm18537_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	gnflm13049_s_at	4930414P16	5.10	binding, enzyme regulator activity	physiological process, cellular process	cell part	proacrosin binding protein
7	gnflm08682_a_at	C130098D09	4.86				ATP/GTP binding protein-like 5 (Agbl5), transcript variant 3
8	gnflm17184_a_at	4921517J08	4.85	binding	physiological process, cellular process	cell part	weakly similar to predicted speedy homolog 1 (Drosophila)
9	gnflm16842_a_at	4921511M17	4.72			cell part	hypothetical protein
10	gnflm10539_at	NM_016915	4.57	catalytic activity, nutrient reservoir activity			phospholipase A2, group VI
11	gnflm05484_at	1700023A18	4.47	binding, enzyme regulator activity		cell part	phosphatidylethanolamine binding protein 2
12	gnflm02953_a_at	4932703D08	4.39	catalytic activity, binding	physiological process	organelle, cell part	a disintegrin and metalloproteinase domain 25 (testase 2)
13	gnflm33186_at	1700014P15	4.35	transporter activity, binding	physiological process, cellular process, reproduction, development	cell part, organelle	solute carrier family 9, member 10 (Slc9a10)
14	gnflm00675_s_at	NM_175240	4.29				transmembrane protein 162 (Tmem162)
15	gnflm25893_s_at	4932441M08	4.16				P-loop containing nucleotide triphosphate hydrolases structure containing protein Mus musculus
16	gnflm17230_at	4930444P10	4.07				hypothetical Arginine-rich region containing protein
17	gnflm23725_at	4930445I03	4.06				hypothetical protein
18	gnflm00044_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	gnflm01980_a_at	7.21
2	gnflm01166_at	7.07
3	gnflm07353_a_at	7.04
4	gnflm09241_a_at	7.00
5	gnflm01533_a_at	6.95
6	gnflm28688_at	6.87
7	gnflm01973_a_at	6.85
8	gnflm04179_a_at	6.85
9	gnflm31560_x_at	6.83
10	gnflm29198_at	6.78
11	gnflm02000_a_at	6.70
12	gnflm32513_at	6.69
13	gnflm02899_a_at	6.65
14	gnflm31337_at	6.64
15	gnflm31231_s_at	6.62
16	gnflm01847_a_at	6.61
17	gnflm32279_at	6.46
18	gnflm06613_at	6.39
19	gnflm31104_at	6.30
20	gnflm30747_at	6.25
21	gnflm32681_at	6.19
22	gnflm01883_a_at	6.18
23	gnflm35021_at	6.05
24	gnflm04122_a_at	6.02
25	gnflm31219_at	6.02
26	gnflm15984_a_at	5.99
27	gnflm33287_at	5.95
28	gnflm13524_at	5.94
29	gnflm35156_at	5.90
30	gnflm30644_at	5.85
31	gnflm03857_at	5.85
32	gnflm10353_at	5.79
33	gnflm30330_at	5.79
34	gnflm34052_at	5.78
35	gnflm31382_at	5.78
36	gnflm32047_at	5.74
37	gnflm01946_x_at	5.68
38	gnflm01894_a_at	5.65
39	gnflm31519_at	5.58
40	gnflm31638_at	5.58

#1	Microarray ID	#2
41	gnflm33591_at	5.55
42	gnflm31460_at	5.54
43	gnflm03383_a_at	5.53
44	gnflm32251_at	5.52
45	gnflm05913_a_at	5.50
46	gnflm34195_at	5.50
47	gnflm30329_at	5.50
48	gnflm17628_s_at	5.48
49	gnflm02371_a_at	5.42
50	gnflm34642_at	5.39
51	gnflm29752_a_at	5.39
52	gnflm35671_at	5.38
53	gnflm29143_at	5.36
54	gnflm31738_at	5.29
55	gnflm02318_a_at	5.28
56	gnflm09049_at	5.27
57	gnflm00344_s_at	5.27
58	gnflm15214_at	5.27
59	gnflm01899_x_at	5.26
60	gnflm32619_at	5.25
61	gnflm33789_x_at	5.21
62	gnflm34257_at	5.18
63	gnflm33886_at	5.12
64	gnflm01008_a_at	5.08
65	gnflm31643_at	5.05
66	gnflm31572_at	5.04
67	gnflm32037_at	5.00
68	gnflm33866_at	4.96
69	gnflm30625_at	4.94
70	gnflm31344_at	4.93
71	gnflm34001_at	4.93
72	gnflm15387_a_at	4.92
73	gnflm32998_at	4.88
74	gnflm31891_at	4.87
75	gnflm33005_at	4.87
76	gnflm31390_at	4.83
77	gnflm34576_at	4.83
78	gnflm34600_at	4.80
79	gnflm31889_at	4.77
80	gnflm33206_at	4.69

#1	Microarray ID	#2
81	gnflm07302_a_at	4.65
82	gnflm34875_at	4.61
83	gnflm04027_a_at	4.60
84	gnflm31239_at	4.57
85	gnflm03738_a_at	4.55
86	gnflm10388_a_at	4.52
87	gnflm19017_at	4.51
88	gnflm03884_a_at	4.50
89	gnflm06357_a_at	4.50
90	gnflm33946_at	4.50
91	gnflm31824_at	4.50
92	gnflm09736_at	4.49
93	gnflm33278_at	4.46
94	gnflm32514_at	4.46
95	gnflm16235_at	4.40
96	gnflm34313_at	4.39
97	gnflm06329_a_at	4.37
98	gnflm05722_a_at	4.35
99	gnflm03234_a_at	4.34
100	gnflm31792_at	4.32
101	gnflm31775_at	4.31
102	gnflm35588_at	4.23
103	gnflm30456_at	4.20
104	gnflm34794_at	4.20
105	gnflm30490_at	4.19
106	gnflm03665_a_at	4.18
107	gnflm16056_at	4.18
108	gnflm13294_a_at	4.15
109	gnflm34064_at	4.14
110	gnflm06747_a_at	4.12
111	gnflm01774_x_at	4.10
112	gnflm33369_at	4.09
113	gnflm29003_at	4.09
114	gnflm31545_at	4.07
115	gnflm33894_x_at	4.06
116	gnflm33931_at	4.02
117	gnflm31032_at	4.01
118	gnflm01590_a_at	4.00

PUBLICATIONS

Main paper:

Yamashita, A., Goto, N., Nishiguchi, S., Shimada, K., Yamanishi, H., Yasunaga, T., 2008. Computational search for over-represented 8-mers within the 5'-regulatory regions of 634 mouse testis-specific genes. *Gene* 427, 93-98.

Reference papers:

Nakamura, S., Yang, C-S., Sakon, N., Ueda, M., Tougan, T., Yamashita, A., Goto, N., Takahashi, K., Yasunaga, T., Ikuta, K., Mizutani, T., Okamoto, Y., Tagami, M., Morita, R., Maeda, N., Kawai, J., Hayashizaki, Y., Nagai, Y., Horii, T., Iida, T., Nakaya, T., 2009. Direct Metagenomic Detection of Viral Pathogens in Nasal and Fecal Specimens Using an Unbiased High-Throughput Sequencing Approach. *PLoS ONE* 4, e4219.

Yoshida, M., Yamashita, A., Idoji, Y., Nishiguchi, S., Shimada, K., Yasunaga, T., Yamanishi, H., 2008. *In silico* study of a novel gene evolved from an ancestral SVIP gene and highly expressed in the adult mouse testes. *Int. J. Mol. Med* 22, 143-148.

Idoji, Y., Watanabe, Y., Yamashita, A., Yamanishi, K., Nishiguchi, S., Shimada, K., Yasunaga, T., Yamanishi, H., 2008. *In silico* study of whey-acidic-protein domain containing oral protease inhibitors. *Int. J. Mol. Med.* 21, 461-468.

Kashiwada, R., Yamashita, A., Goto, N., Shota, N., Yasunaga, T., 2007. Analysis of HERV-K replication mechanism in the human genome. *The proceedings of the 2007 annual conference of the Japanese society for bioinformatics* P061.

Shibasaki, T., Yamashita, A., Goto, N., Shota, N., Yasunaga, T., 2007. Conservation of Nested genes in Eukaryote. *The proceedings of the 2007 annual conference of the Japanese society for bioinformatics* P062.

Yamashita, A., Kurokawa, K., Yasunaga, T., 2003. Mapping Database of cDNA and Genome Designed to Use for Various Applications. *Genome Informatics* 14, 418-419.