ORIGINAL ARTICLE

A genome-wide analysis of open chromatin in human tracheal epithelial cells reveals novel candidate regulatory elements for lung function

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ABSTRACT

Background Distal cell-type-specific regulatory elements may be located at very large distances from the genes that they control and are often hidden within intergenic regions or in introns of other genes. The development of methods that enable mapping of regions of open chromatin genome wide has greatly advanced the identification and characterisation of these elements.

Methods Here we use DNase I hypersensitivity mapping followed by deep sequencing (DNase-seq) to generate a map of open chromatin in primary human tracheal epithelial (HTE) cells and use bioinformatic approaches to characterise the distribution of these sites within the genome and with respect to gene promoters, intronic and intergenic regions.

Results Genes with HTE-selective open chromatin at their promoters were associated with multiple pathways of epithelial function and differentiation. The data predict novel cell-type-specific regulatory elements for genes involved in HTE cell function, such as structural proteins and ion channels, and the transcription factors that may interact with them to control gene expression. Moreover, the map of open chromatin can identify the location of potentially critical regulatory elements in genome-wide association studies (GWAS) in which the strongest association is with single nucleotide polymorphisms in non-coding regions of the genome. We demonstrate its relevance to a recent GWAS that identifies modifiers of cystic fibrosis lung disease severity.

Conclusion Since HTE cells have many functional similarities with bronchial epithelial cells and other differentiated cells in the respiratory epithelium, these data are of direct relevance to elucidating the molecular basis of normal lung function and lung disease.

INTRODUCTION

The epithelia that line the trachea and bronchi of the human airway have important functions in protecting the respiratory system from environmental insults and pathogenic organisms while maintaining the conduit for air to and from the alveoli. Furthermore, major lung diseases such as chronic obstructive pulmonary disease (COPD), asthma and cystic fibrosis are associated with malfunction of the airway epithelium. The epithelial layer interacts closely with other cells in the airway, such as endothelial and immune cells. This critical cell layer requires the establishment and maintenance of coordinate patterns of gene expression, which ensure structural differentiation of the epithelium, including apical/basolateral polarity, integration of the mucociliary escalator and appropriate regulation of ion transport. Though the regulatory mechanisms for many individual genes that are active in the airway epithelium were characterised by classical methods, other genes, particularly those which show tight cell-type-specific control involving *cis*-acting elements that lie outside the promoter or coding region, are less well understood. Until recently, the cellular machinery that achieves coordinated function of airway epithelium has been hard to evaluate since this requires global analysis of regulatory elements in relatively small numbers of differentiated primary airway epithelial cells. However, techniques developed in part by the ENCODE consortium,[1] including methods to identify regions of open chromatin genome wide, such as DNase I hypersensitivity mapping followed by deep sequencing (DNase-seq)[2] and formaldehyde-assisted identification of regulatory elements (FAIRE),[3] have enabled these analyses. Here we describe a genome-wide map of open chromatin in primary human tracheal epithelial (HTE) cells generated by DNase-seq analysis. We use bioinformatic tools to identify tracheal epithelial-cell-selective regions of

Key messages

What is the key question?
- What are the regulatory elements that control gene expression in the airway epithelium and where in the genome are they located?

What is the bottom line?
- We describe a resource that will enable rapid identification of functional genetic elements that control transcriptional networks in the airway epithelium.

Why read on?
- This has immediate relevance to determining the normal differentiation of the airway epithelium and what goes wrong in airway disease.

open chromatin and determine their distribution throughout the genome. We determine that the peaks of open chromatin are more evident at the promoters of genes that are highly expressed in HTE cells than at inactive gene promoters. Moreover, HTE-selective peaks of open chromatin are associated with genes involved in pathways of epithelial differentiation and function. Within these peaks, predicted binding sites for some epithelial-specific transcription factors are over-represented. Next, we illustrate the power of these data to facilitate the characterisation of regulatory elements for genes that are coordinately expressed in HTE cells, such as structural proteins and ion channels. Finally, we demonstrate the use of these data to identify the molecular basis of genome-wide association studies (GWAS) that identify non-coding regions of the genome as strong candidates for disease effectors or modifiers. These results will enhance the understanding of transcriptional networks that coordinate lung epithelial function in health and disease.

RESULTS

Identification of DNase hypersensitive sites genome-wide

HTE cells were evaluated for regions of open chromatin genome-wide by mapping DNase I hypersensitive sites using DNase-seq. The sequence reads were then analysed with the F-seq application, a feature density estimator for high-throughput sequence tags,[4] which identified 153 504 DNase hypersensitive sites (DHS) in the HTE cells. These sites represent elements in the genome where multiple sequence reads (peak signals) aligned to a common region. Since regulatory elements are often located within DHS, this map of open chromatin has the potential to identify regulatory elements for all genes that are expressed in the HTE cells. To distinguish between ubiquitous and cell-type-selective regulatory elements, we next subtracted DNase-seq data sets from five different cell types generated by the ENCODE consortium.[1] These included skin fibroblasts (FibroPark), a lymphoblastoid cell line (GM12878), a cervical carcinoma cell line (HeLa-S3), a liver carcinoma cell line (HepG2), and human umbilical vein endothelial cells (HUVEC). Though two of these lines are carcinomas, open chromatin data from relevant primary cells are not available for these epithelial cell types. The genomic overlap between HTE DHS and the other five cell types is shown in figure 1 and the numbers of DHS are shown in table 1. Of the 153 504 HTE sites, 39 656 (25.8%) were found to be cell type selective, in that they did not intersect with the hypersensitive sites present in any of the five other cell types, and 31 146 (20.3%) sites were ubiquitous, in that they overlapped (at least partially) with DHS from all five of the other cell types. Further analysis of the HTE DHS across different cell types revealed 974 National Center for Biotechnology Information (NCBI) Reference Sequence (RefSeq) genes with a greater representation of DHS within their promoters and coding regions than the five background cell types combined (see online supplementary table 1). Many of these genes code for proteins that have well characterised functions in the airway epithelium and some of these are discussed further below.

Distribution of DHS across the genome

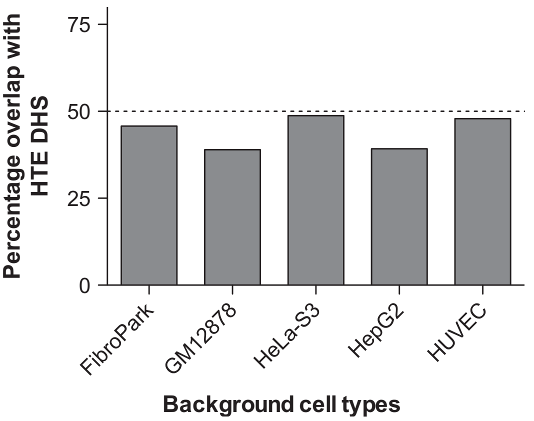

Figure 1 Cell-type specificity of DNase I hypersensitive sites (DHS) in human tracheal epithelial (HTE) cells. The genomic overlap between HTE DHS and the other five cell types measured as the percentage of HTE DHS that overlap with each of the individual background cell types. FibroPark, skin fibroblasts; GM12878, a lymphoblastoid cell line; HeLa-S3, a cervical carcinoma cell line; HepG2, a liver carcinoma cell line; HUVEC, human umbilical vein endothelial cell.

Next we analysed the distribution of DHS with respect to different genomic elements, according to the following categories: promoter (2 kb of sequence 5′ to the transcriptional start site), exon 1, intron 1, other genic, 2 kb of sequence 3′ to the transcriptional stop site, and intergenic (figure 2). DHS were subdivided according to whether they were HTE selective or ubiquitous (as defined above) and a third group (genome wide), which included all sites. We observed that the ubiquitous sites occur more frequently (25.6%) in promoter regions than HTE-selective sites (2.5%) and genome-wide sites (1.2%). A similar distribution of DHS is seen in the first exon of genes and to a lesser extent in the first introns and 2 kb downstream of genes. In contrast, the HTE-selective sites are most common in other genic sites and also more common than ubiquitous sites in intergenic regions.

Correlation of DNase-seq data with gene expression

Total RNA was extracted from the same cell cultures that were used for DNase-seq and evaluated on Nimblegen 72K HG18 60mer microarrays to characterise gene expression profiles. To look for a correlation between gene expression in HTE cells and the DNase-seq signal, gene expression values were divided into three groups: high expression (top 20%), middle expression (middle 20%) and low expression (bottom 20%). The remaining 40% of gene expression values were not included in the analysis. The DNase-seq base overlap signal, which is the number of reads that align to each base pair position of the genome, was averaged across the 1 kb before and after the transcription start site of the genes within each of these categories (figure 3). The data show that the most highly expressed genes correlate with an increased DNase-seq signal.

Table 1 Number of open chromatin sites in human tracheal epithelial cells and the six other cell types that were used for comparison

DNase-seq cell lines	Number of open chromatin sites
HTE (human tracheal epithelial cell)	153 504
FibroP (normal fibroblast from patients with Parkinson's)	139 663
GM12878 (lymphoblastoid)	124 321
HeLa-S3 (cervical carcinoma)	141 165
HepG2 (liver carcinoma)	115 765
HUVEC (human umbilical vein endothelial cell)	126 284
NHEK (normal human epidermal keratinocyte)	140 520

DNase-seq, DNase I hypersensitivity mapping followed by deep sequencing.

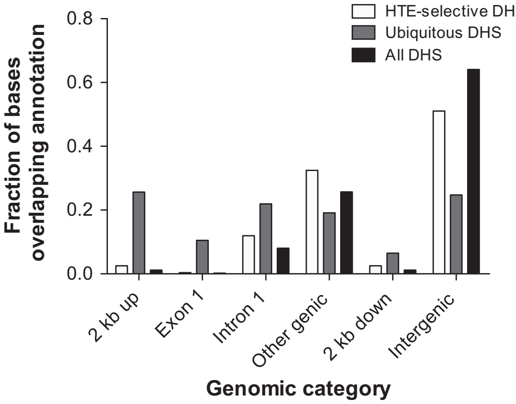

Figure 2 Human tracheal epithelial (HTE)-selective DNase I hypersensitive sites (DHS) are generally located in distal regions of genes or in intergenic sequences, rather than in promoters, where ubiquitous DHS predominate. Three categories of DHS (all DHS, HTE-selective DHS, and ubiquitous DHS) were overlapped with different genomic regions to determine their distribution with respect to genes. 2 kb up, including 2 kb 5′ to genes; other genic, all exons and introns of genes excluding the first; 2 kb down, including 2 kb 3′ to genes; intergenic, all genomic sequence more than 2 kb from genes.

Pathways of epithelial structure and function revealed by HTE-selective promoter DHS

The Entrez Gene IDs for the 1061 genes that exhibited one or more HTE-selective promoter DHS (representing 1118 DHS) were compiled into a text file and analysed with DAVID (Database for Annotation, Visualisation and Integrated Discovery)[5] to look for gene processes that might be over-represented compared with all human genes. The top 10 most statistically significant DAVID ontologies/pathways are shown in table 2 and the entire list ($p<0.1$) is presented in online supplementary table 2. Five of the top 10 DAVID results are directly related to epithelial function, including epithelial cell differentiation (GO:0030855), epithelium development (GO:0060429), ectoderm development (GO:0007398), epidermis development (GO:0008544), and epidermal cell differentiation (GO:0009913). Moreover, three additional pathways are relevant to the function of polarised cells in the epithelial sheet lining the airway, including cell junction (GO:0030054), apicolateral plasma membrane (GO:0016327) and apical junction complex (GO:0043296). This analysis thus validates the use of DNase-seq to identify cell-type-specific regulatory elements that are associated with open chromatin in HTE cells.

Table 2 Top 10 statistically over-represented processes from Database for Annotation, Visualisation and Integrated Discovery (DAVID) analysis when comparing a list of genes with human tracheal epithelial (HTE)-selective DNase I hypersensitive sites in their promoter to all human genes

Category	GO Biological process	p Value
GOTERM_BP_FAT	GO:0030855: Epithelial cell differentiation	1.46×10^{-6}
GOTERM_BP_FAT	GO:0060429: Epithelium development	2.64×10^{-6}
GOTERM_CC_FAT	GO:0044459: Plasma membrane part	6.19×10^{-6}
KEGG_PATHWAY	hsa04080: Neuroactive ligand–receptor interaction	7.97×10^{-6}
GOTERM_BP_FAT	GO:0007398: Ectoderm development	9.69×10^{-6}
GOTERM_BP_FAT	GO:0008544: Epidermis development	2.14×10^{-5}
GOTERM_CC_FAT	GO:0030054: Cell junction	5.38×10^{-5}
GOTERM_CC_FAT	GO:0016327: Apicolateral plasma membrane	6.02×10^{-5}
GOTERM_BP_FAT	GO:0009913: Epidermal cell differentiation	1.21×10^{-4}
GOTERM_CC_FAT	GO:0043296: Apical junction complex	1.43×10^{-4}

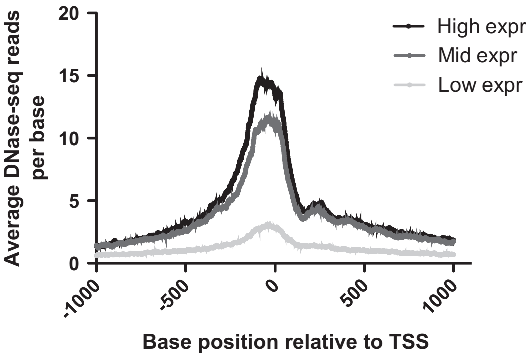

Figure 3 The intensity of DNase I hypersensitive sites (DHS) at gene promoters correlates with gene expression in human tracheal epithelial (HTE) cells. Genes for which microarray expression data were available were separated into three categories: high expression (top 20%), mid expression (middle 20%), and low expression (bottom 20%). Then, the average number of DNase-se reads was calculated at each base between 1 kb 5′ and 1 kb 3′ to the transcription start site (TSS) for each of these categories.

HTE-selective COREs overlapping promoter regions identify genes with multiple functions in airway epithelial cells

Next we took a global view of HTE-selective DHS and observed that these tended to be clustered, rather than being randomly distributed throughout the genome, as has previously been observed for islet-cell-selective regions of open chromatin, defined by FAIRE.[6] Following their definition of a CORE (cluster of open regulatory elements, a cluster of three or more discrete regions of open chromatin separated by <20 kb) we identified 3608 HTE-selective COREs. We next evaluated the 998 HTE-selective COREs that overlapped with the promoter regions (2 kb upstream of transcriptional start sites) of 1328 genes (see online supplementary table 3). An additional data set (of 1975 COREs) was generated for this analysis that subtracted the open chromatin map for normal human epidermal keratinocytes (NHEK) since these too are differentiated primary epithelial cells and we wanted to distinguish between genes involved in epithelial function generally and HTE cells specifically (the overlap between HTE and NHEK is greater than that of the other cell types examined in DHS; see online supplementary figure 1). Microarray data for RNA abundance derived from the same HTE samples that were used to map open chromatin were incorporated into this analysis and we evaluated in detail the top 500 expressed genes associated with HTE-selective COREs overlapping their promoters. This analysis is clearly biased towards identification of HTE-selective COREs that are associated with transcriptional activation and not repression. Multiple genes were identified that were relevant to airway epithelial function, including structural proteins, ion channel components and transcription factors. Among structural proteins, keratin 5 (*KRT5*) and 6A (*KRT6A*) in the keratin gene cluster on chromosome 12 (figure 4A), together with keratin 19 (*KRT19*), in the equivalent cluster on chromosome 17 are among the most highly expressed genes in the tracheal epithelial cells and all exhibit HTE-selective COREs overlapping their promoters. Moreover, though both *KRT5* and *KRT6A* are expressed in epidermal keratinocytes (NHEKs)[7] as well as tracheal epithelial cells, several DHS spanning the *KRT5* gene are unique to HTE cells

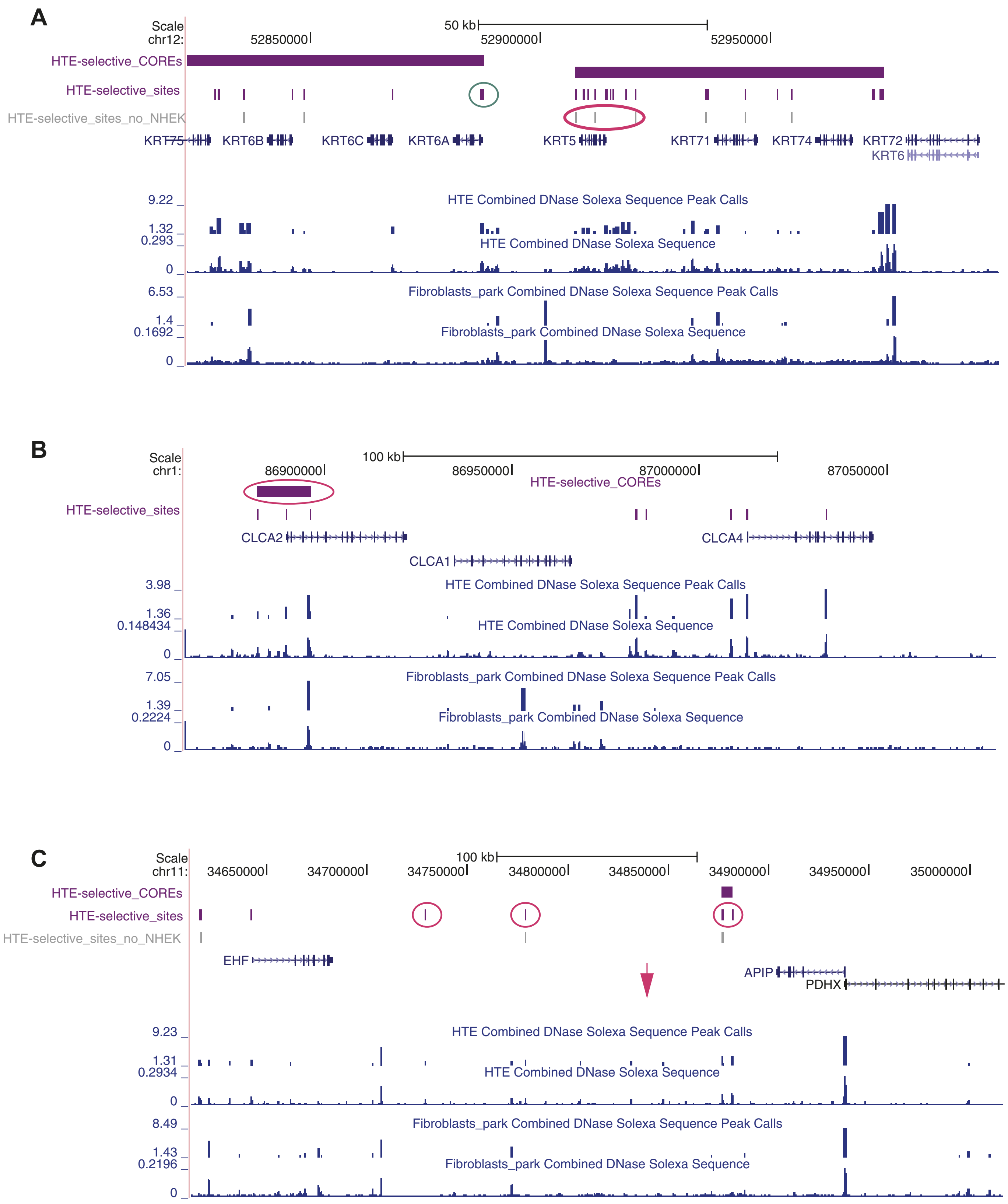

Figure 4 COREs of open chromatin are associated with critical genes in human tracheal epithelial cell function. Each panel (A—C) shows a region of the human genome on the University of California Santa Cruz (UCSC) genome browser (http://genome.ucsc.edu) with combined DNase Solexa (Illumina) sequence data and peak calls for two biological replicates of human tracheal epithelial (HTE) cells and skin fibroblasts (Fibroblasts_park). UCSC genes within the region are also shown. Above these tracks are HTE-selective COREs (horizontal purple bars), HTE-selective DNase I hypersensitive sites (DHS) (vertical purple bars) and (in A, C) HTE-selective sites that do not overlap with sites in normal human epidermal keratinocytes (NHEK) (vertical grey bars, HTE-selective_sites_no_NHEK). Pink and teal circles show HTE-selective COREs or DHS of particular interest (see text). (A) Part of the type II cytokeratin cluster on chromosome 12q12-q13 showing the regions of open chromatin around the keratin 5 (*KRT5*) and 6A (*KRT6A*) genes, which are both highly expressed in HTE cells. (B) The calcium-sensitive chloride channel accessory protein (CLCA) cluster on

(pink circle in figure 4A). In contrast, the *KRT6A* promoter exhibits a common DHS in HTE and NHEK cells which is thus lost when the NHEK sites are subtracted (teal circle in figure 4A). One of the critical functions of tracheal epithelial cells is to control the airway luminal environment, so it was probable that we would find some regulatory elements for ion channels. Chloride channel accessory 2 protein (CLCA2), which is known to show some tracheal specificity[8 9] and is highly expressed in the cultured HTE cells, is associated with a HTE-selective CORE at its gene promoter, in contrast to the neighbouring *CLCA1* gene on chromosome 1, which is expressed in intestinal epithelial cells and lacks an HTE-selective CORE (figure 4B). HTE-selective COREs are also associated with the promoter regions of multiple epithelial transcriptional regulator genes, including *ELF3* (epithelial-specific, Ets domain transcription factor, E74-like factor 3),[10] Kruppel-like factor 5 (*KLF5*)[11] (see online supplementary figure 2) and GATA-binding protein 6 (*GATA6*),[12] all of which are expressed in these cells and bronchial epithelial cells and/or lung. Several proteins implicated in airway disease also have HTE-selective COREs coincident with their promoters or within the gene itself, including S100 calcium-binding protein A9 (*S100A9*) which was linked with cystic fibrosis lung disease[13–16] and *IL2RB* which was identified as an asthma susceptibility locus.[17] The fact that this gene shows very low expression levels in the HTE cells suggests some of the *cis*-regulatory elements in the CORE may have an inhibitory effect on gene expression. When we extended this analysis to the list of 974 NCBI reference sequence genes with a greater representation of HTE-selective DHS within their promoters and coding regions than the five background cell types combined (see online supplementary table 1), many of the same loci were identified, including *KRT5*, *KRT6A*, *KLF5* and *S100A9*.

HTE-selective DHS are enriched for binding sites for epithelial transcription factors

The HTE-selective DHS within promoter and intergenic regions were analysed with the use of Clover[18] to search for over-represented sequence motifs that could identify transcription factor binding sites used in HTE cells. These sequence regions were each analysed in three different groups: all DHS, HTE-selective DHS and ubiquitous DHS. The results of the promoter analyses are given in online supplementary table 4, and the intergenic analyses are in online supplementary table 5. Of particular interest are the comparisons between the intergenic sites for which the representation of motifs is markedly different in the HTE-selective and ubiquitous sites. As expected, the ubiquitous sites contain a high frequency of CTCF-binding motifs, which are over-represented on 23/23 chromosomes but not in HTE-selective sites. CTCF (CCCTC binding factor) sites are often associated with enhancer blocking insulator function[19 20] and play a critical role in maintaining higher order chromatin structure.[21–23] In contrast, among HTE-selective sites, binding sites for the epithelial-specific Ets transcription factor ELF5 are over-represented on all chromosomes. ELF5 is known to regulate a number of epithelial-specific genes in tissues containing glandular epithelium.[24] Also over-represented in the HTE-selective intergenic sites on multiple chromosomes are binding sites for the Forkhead transcription factors FOXA1 (forkhead box A1, hepatocyte nuclear factor 3α, HNF3α, on 19/23 chromosomes) and FOXA2 (forkhead box A2, HNF3β, on 15/23 chromosomes). These factors are thought to be 'pioneer' factors that establish the nucleus of a regulatory complex by opening the chromatin to provide access to other proteins.[25] FOXA1/A2 are involved in the development of multiple endoderm-derived organ systems such as lung, pancreas and prostate (reviewed in Kaestner[26]). Motifs for Kruppel-like factor 4 (KLF4) binding are also over-represented in HTE-selective intergenic DHS on 19/23 chromosomes. KLF4 is known to play a role in epithelial differentiation and to function as both an activator and a repressor.

HTE-selective sites identify enhancer elements in multiple genes

To further validate our genome-wide data in HTE cells we looked for peaks of open chromatin that coincided with previously characterised regulatory elements. Multiple examples were found, including enhancers in the first introns of peptidylarginine deiminase type I[27] and aquaporin 5[28] and 5′ to the keratin 5 gene.[29] The location of peaks of open chromatin in HTE cells coinciding with these mapped enhancers are shown in online supplementary figure 3.

HTE-selective sites identify candidate regulatory regions in GWAS

Multiple GWAS have been undertaken to identify novel regions of the genome that contribute to the aetiology of complex lung diseases, such as COPD,[30] asthma[17 31–33] and sarcoidosis.[34] Some of these studies found the strongest associations with single nucleotide polymorphisms (SNPs) located in introns of genes or in intergenic regions, implicating regulatory elements in the mechanism underlying the association. Similarly, a recent GWAS for modifier loci influencing lung disease severity in cystic fibrosis identified several peaks of association with SNPs in non-coding regions.[35] Figure 4C illustrates one of these regions of significant association with CF lung severity on chromosome 11p13, between *EHF* (Ets homologous factor, epithelial specific) and *APIP* (APAF1-interacting protein, anti-apoptotic) and the location of the SNP, which shows the highest significance (pink arrow). In HTE cells, multiple regions of open chromatin are evident in this genomic region, some of which are HTE specific and others are ubiquitous. Further functional analysis is underway to determine whether these DHS contain regulatory elements such as enhancers, and moreover, which genes are associated with sites that are relevant to cystic fibrosis lung disease severity.

DISCUSSION

A greater understanding of the transcriptional networks that distinguish one differentiated cell type from another will be generated by detailed analysis of regulatory elements genome wide in primary cells. Here we present genome-wide open chromatin data on primary HTE cells generated by DNase-seq. These cells represent the most proximal part of a continuous epithelial sheet that lines the respiratory system from the trachea, through bronchi and bronchioles to the gas exchange surface in alveoli. Some differentiated functions are maintained

[Continued]

chromosome 1p22. CLCA2 is highly expressed in HTE cells, CLCA1 is not. (C) The *EHF–APIP* (Ets homologous factor, epithelial specific–APAF1-interacting protein, anti-apoptotic) interval which shows strong association with lung disease severity in a cystic fibrosis modifier genome-wide association study. The pink arrow shows the location of the single nucleotide polymorphism with the highest association. PDHX, pyruvate dehydrogenase complex, component X.

throughout the epithelium, while others are spatially restricted to different parts of the airway. The generation of additional maps of open chromatin from other primary airway epithelial cell types, such as bronchial cells, will enable bioinformatic comparisons to reveal differences in transcriptional networks and cell-specific regulatory elements in these cell types. This may have significant utility in the clinical management of complex lung disease.

In addition to addressing these more global questions of transcriptional regulation our data provide a valuable resource to search for novel regulatory elements for coordinately regulated gene families and individual genes. One such locus that encodes part of a multi-subunit protein complex and has novel HTE-selective DHS flanking the gene is *SCNN1B*, which encodes the β subunit of the non-voltage-gated, amiloride-sensitive, epithelial sodium channel. This protein, together with the α and γ subunits encoded by *SCNN1A* and *SCNN1G* respectively, is critical to normal fluid transport in the airway epithelium.[36–38]

Finally, our genome-wide open chromatin data on HTE cells may assist in advancing GWAS for lung diseases, from SNPs associated with a phenotype, to functional elements for mechanistic study. This will be particularly relevant in diseases associated with airway epithelial dysfunction in which critical SNPs are located within non-coding regions of the genome. However, due to the functional complexity of the genome, analysis of these regions should not be restricted to the peaks of open chromatin that coincide with SNPs.

METHODS

HTE cells

Human trachea were collected post mortem from healthy donors. HTE cells were isolated from these trachea and grown as described previously.[39]

DNase-seq

Two technical replicas of DNase-seq were carried out as described previously[2] on two independent cultures of primary HTE cells from different donors. Sequencing by Illumina GAIIx produced 39 642 133 and 40 694 564 reads respectively for HTE samples 1 and 2. To check for reproducibility between the samples the percentage of the top 50 000 peaks from sample 1 that overlapped with the top 100 000 peaks from sample 2 were compared, and vice versa. This standard has been accepted by the ENCODE consortium. The overlap was 80% in one direction and 85% in the other direction, which passes the threshold of acceptable reproducibility. The DNase-seq data on five ENCODE cell types (FibroP, GM12878, HeLa-S3, HepG2 and HUVEC) were generated by the ENCODE consortium.

DNase I hypersensitive sites

Full details of the bioinformatic analysis are provided in the online supplement.

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Competing interests None.

Contributors JMB and AH designed experiments and analysed data. JB, CJO, S-HL, NG, LS and DL performed experiments. TSF, CUC and GEC contributed reagents/analytical tools. JMB and AH wrote the paper.

Provenance and peer review Not commissioned; externally peer reviewed.

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Journal club

Azithromycin 250 mg daily reduces exacerbation frequency and improves quality of life in selected COPD patients

This multicentre study randomised 1142 subjects at risk of acute exacerbations of chronic obstructive pulmonary disease (COPD) to receive azithromycin 250 mg daily (n=570) or placebo (n=572) for 1 year, in addition to usual care. The enrolled subjects were allowed to continue on inhaled treatments and/or oxygen. None of the subjects were on oral theophylline. The primary outcome, time to the first exacerbation, was significantly increased to 266 days (95% CI 227 to 313) in the azithromycin group compared with 174 days (95% CI 143 to 215) in the placebo group. The HR for having an acute exacerbation of COPD per patient-year was 0.73 in the azithromycin group compared with the placebo group. The secondary outcomes included quality of life measures (St George's Respiratory Questionnaire (SGRQ) scores), which improved more in the azithromycin compared with the placebo group. There was no significant reduction in hospitalisation rates and emergency department or urgent care visits and no difference in mortality. Hearing loss was more common in the azithromycin group and increased colonisation with macrolide resistant pathogens was noted.

The authors concluded that the addition of azithromycin to usual care of COPD patients who have had an acute exacerbation in the last year or require oxygen supplementation is a valuable option but careful patient selection is required with the exclusion of patients with or at risk of QTc prolongation, resting tachycardia (>100 beats per minute) and hearing defect. Concern also remains about the long-term effects of daily azithromycin on bacterial resistance patterns in the community. Further studies with mortality, hospitalisations and bacterial resistance as primary end points are warranted.

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METHODS

Human tracheal epithelial cells (HTE)

Human trachea were collected post-mortem from healthy donors. HTE cells were isolated from these as described previously [1] and their differentiation was monitored by evaluating *CFTR* expression levels by qRT-PCR [2]. Loss of *CFTR* transcription coincides with de- differentiation of these cells.

DNase-seq

Two technical replicas of DNase-seq were carried out as described previously [3] on two independent cultures of primary HTE cells from different donors. Sequencing by Illumina GAIIx produced 39,642,133 and 40,694,564 reads respectively for HTE samples 1 and 2. To check for reproducibility between the samples the % of the top 50, 000 peaks from sample 1 that overlapped with the top 100,000 peaks sample 2 were compared, and vice versa. This standard has been accepted by the ENCODE consortium. The overlap was 80% in one direction and 85% in the other direction, which passes the threshold of acceptable reproducibility. The DNase-seq data on five ENCODE cell types (FibroP, GM12878, HeLa-S3, HepG2, and HUVEC) was generated by the ENCODE consortium.

DNase I hypersensitive sites

The peak calls for the DNase-seq data were made with the F-seq application to give a discrete number of DHS within the human tracheal epithelial cells [4]. These sites were determined by F-seq by fitting the data to a gamma distribution to calculate p-values. P-values below a 0.05/0.01 threshold in contiguous regions were considered significant. All DHS identified on chromosome Y were removed from the analysis to allow for comparison across both male and female cell types. After producing the number and location of DHS for these primary cells, the peaks for five non-related cell types were intersected with the HTE data for comparison. The five cell types included FibroP, GM12878 *Tier1*, HeLa-S3 *Tier2*, HepG2 *Tier2*, and HUVEC *Tier2*. Next, the genomic indices of the DHS from each of these five cell types were overlapped with the DHS from the HTE cells. Those sites from the HTE cells that were not overlapped by any other data sets made up the list of HTE-selective sites. The HTE sites that were overlapped by a DHS in all of the cell types composed the list of ubiquitous sites. The same analysis was also performed including the sixth background cell type, NHEK. The Galaxy platform was utilized to cluster HTE-selective DHS by genomic location [5]. The settings for clustering these sites were those previously used by Gaulton et al. 2010 to identify what they termed COREs (Cluster of Open Regulatory Elements) [6]. Each cluster consisted of at least three HTE-selective sites within less than or equal to 20kb of one another.

DHS overlapping gene annotation

The genomic indices of HTE-selective DHS, ubiquitous DHS, and all DHS were intersected with the genomic indices of all human genes, their promoters (2kb upstream of transcriptional start sites), exons, introns, and intergenic sequence. The human gene annotation was derived from a list of all human Entrez genes downloaded from NCBI. These Entrez genes were each linked to their representative RefSeq sequences, and the RefSeq indices were downloaded from UCSC's genome browser (http://www.ncbi.nlm.nih.gov, http://genome.ucsc.edu).

In a different approach to identify RefSeq genes that were associated with HTE-selective DHS, all DHS from HTE cells and all six background cell types were individually overlapped with RefSeq genes (including 2kb flanking each gene). The number of base pairs overlapping between each gene and the DHS of all cell types were tabulated. If a gene was found to overlap more HTE DHS regions than the DHS regions of all other cell types combined, that gene was identified as being associated with HTE-selective DHS.

Microarray analysis

RNA was isolated by Trizol extraction from the same primary cultures of HTE cells that were used for DNase-seq and at the same timepoint. Total RNA was purified by Millipore Microcon YM-100 filter centrifugation and shipped to Nimblegen, Iceland for gene expression analysis on 4 x 72K HG18 60mer arrays. Gene expression data will be available at GEO www.ncbi.nlm.nih.gov/geo/.

David analysis

The DAVID tool can be used to read in a gene list, and identify within that list any statistically significant enrichments of genes from a common GO (Gene Ontology) term or over 40 other annotation categories including protein-protein interactions and pathways [7, 8]. For this purpose, the human genes with an HTE-selective DHS present in their promoter region were analyzed with DAVID. The background gene list used for this analysis was the same human Entrez gene list used to identify overlap between DHS and gene annotation.

Clover analysis

The *Clover* application was used to search for motifs common to DHS within promoter and intergenic sequence near genes. *Clover* is an open-source application that performs random sampling to identify motifs (from an input set) that are statistically over- or under-represented with respect to random [9]. The promoter regions were defined as 2kb upstream of the transcription start site of all human genes. The intergenic regions that were searched included any genomic region more than 2kb but less then 10kb from the start or stop of gene transcription. The set of motifs we searched for included 1,422 transcription factor binding motifs from TRANSFAC and 1,316 from Jaspar [10], [11].

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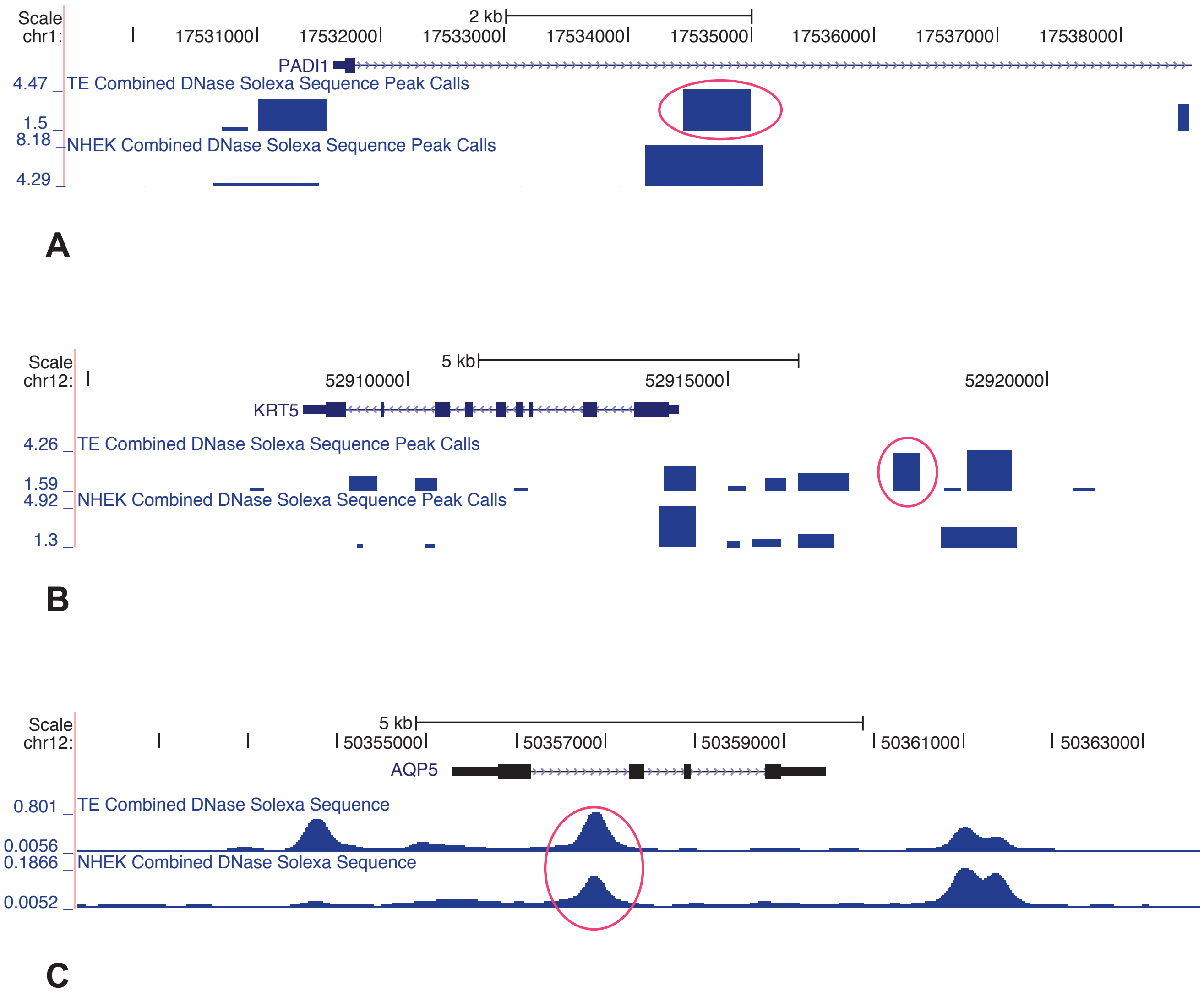
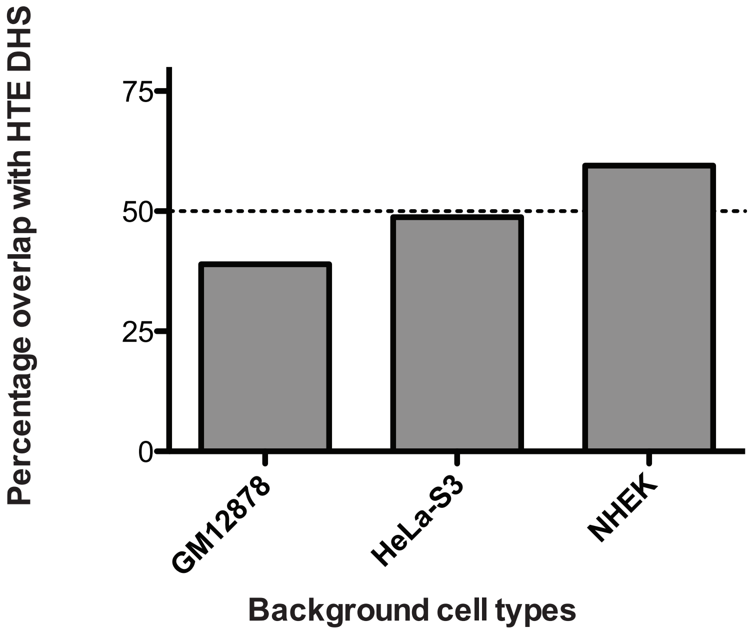
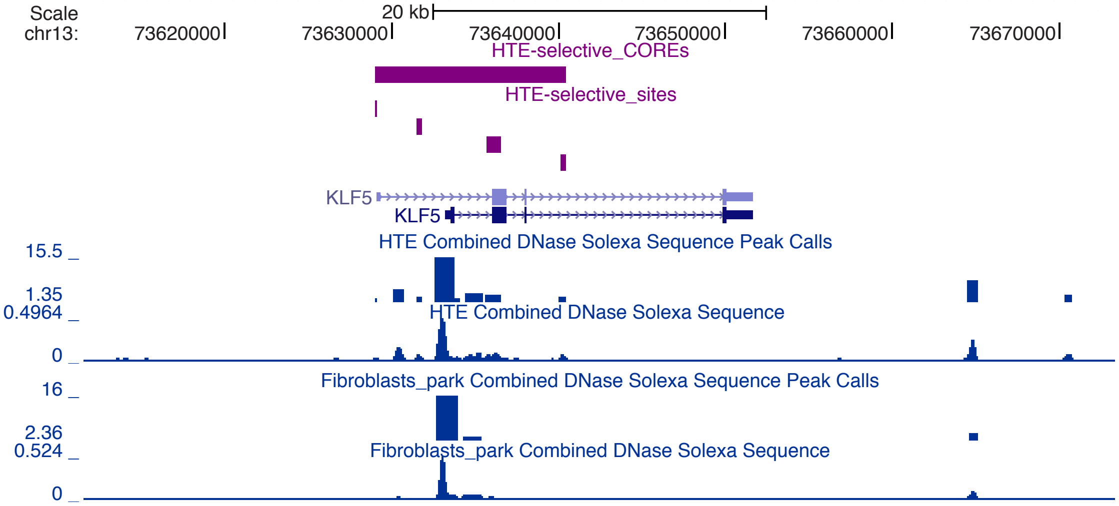


Supplementary Figure 3. Open chromatin sites in human tracheal epithelial cells that overlap known enhancer elements.
Each panel (A-C) shows a region of the human genome on the UCSC genome browser (http://genome.ucsc.edu) with combined DNase Solexa peaks calls (A, B) or sequence reads (C) for human tracheal epithelial cells (TE) and NHEK cells. UCSC genes within the region are also shown. A) Peptidylarginine deiminase type I (PADI1); B) Keratin 5 (KRT5); C) Aquaporin 5.
The pink circle in each panel shows the relevant peak of open chromatin.



Supplementary Figure 1. Cell-type specificity of DNase I hypersensitive sites (DHS) in HTE cells. The genomic overlap between DHS in HTE and NHEK cells measured as the percentage of HTE DHS that overlap with each of the individual background cell types. Also shown are GM12878 and Hela-S3 for comparison.



Supplementary Figure 2. A CORE of open chromatin associated with the KLF5 gene promoter in human tracheal epithelial cells.

A region of the human genome encompassing the KLF5 gene is shown on the UCSC genome browser (http://genome.ucsc.edu) with combined DNase Solexa sequence data and peak calls for 2 biological replicates of human tracheal epithelial cells (HTE) and skin fibroblasts (Fibroblasts_park). Above these tracks are HTE-selective COREs (horizontal purple bars, HTE-selective COREs), HTE-selective DHS (vertical purple bars, HTE-selective-sites).

Supplementary Table 1. List of genes (including 2kb 5' and 3' to the gene) with a greater amount (measured in base pairs) of HTE DHS than all five background cell types DHS combined.

Gene Name	Gene RefSeq	Gene Chrom	Gene Strand	Start Minus 2kbp	Stop Plus 2kbp	TE DHS coverage(bp)	Background DHS coverage(bp)	Expression Value
KRT5	NM_000424	chr12	-	52906357	52916244	2264	306	15.76723
KRT6A	NM_005554	chr12	-	52878956	52889182	816	156	15.748045
TMSL3	NM_183049	chr4	-	91757640	91762270	176	0	15.7353
KRT17	NM_000422	chr17	-	39773690	39782883	3011	2547	15.61449
KRT6C	NM_173086	chr12	-	52860298	52869570	365	0	15.37582
EDF1	NM_153200	chr9	-	139755231	139762739	1854	1698	15.2039775
ANXA8L2	NM_001630	chr10	+	47744918	47765041	474	273	15.16625
H2AFZ	NM_002106	chr4	-	100867242	100873513	3459	3376	15.116015
GJB2	NM_004004	chr13	-	20759602	20769115	2787	2738	15.024885
FGFBP1	NM_005130	chr4	-	15935191	15941972	878	492	15.02352
PTHLH	NM_198966	chr12	-	28109015	28124895	3201	2654	14.96137833
SPRR1A	NM_005987	chr1	+	152954555	152960291	336	0	14.586635
PRKAR1A	NM_212472	chr17	+	66506541	66530911	2093	2057	14.521455
SPRR1B	NM_003125	chr1	+	153001677	153007377	1104	398	14.50909
SLC25A1	NM_005984	chr22	-	19161092	19168302	4127	3759	14.37009
GABARAPL1	NM_031412	chr12	+	10363487	10377725	2980	2932	14.36447
KLK5	NM_012427	chr19	-	51444557	51458345	667	514	14.36122
SERPINB3	NM_006919	chr18	-	61320429	61331198	419	349	14.35049
NUPR1	NM_012385	chr16	-	28546660	28552496	891	792	14.322175
CEACAM6	NM_002483	chr19	+	42257396	42278114	1285	724	14.291405
MARCKS	NM_002356	chr6	+	114176525	114186653	5430	5111	14.242325

KRT6B	NM_005555	chr12	-	52838433	52847911	351	0	14.240575
S100A9	NM_002965	chr1	+	153328328	153335504	1044	678	14.167335
MRPS15	NM_031280	chr1	-	36919360	36932041	2067	2054	14.14857
AKR1C1	NM_001353	chr10	+	5003452	5022159	1028	775	14.114515
FAM60A	NM_021238	chr12	-	31431518	31481122	3115	3083	14.08635
SCEL	NM_144777	chr13	+	78107807	78221399	1532	1002	14.0761
NARS	NM_004539	chr18	-	55265892	55291178	1156	1133	14.042685
PRDX4	NM_006406	chrX	+	23683643	23706515	1121	1027	14.03884
TINF2	NM_012461	chr14	-	24706849	24713881	1594	1446	14.035445
UGT1A1	NM_000463	chr2	+	234666917	234683946	868	161	13.983455
RPL36	NM_033643	chr19	+	5688270	5693679	4098	3868	13.9024975
PDPN	NM_198389	chr1	+	13908250	13946453	4083	2626	13.89192
SSH3	NM_017857	chr11	+	67068917	67082079	4898	3960	13.8244075
TRIP10	NM_004240	chr19	+	6737705	6753530	7349	6898	13.82371
CALML3	NM_005185	chr10	+	5564922	5570226	1408	719	13.81053
PIP4K2C	NM_024779	chr12	+	57982940	57999212	2999	2957	13.782845
GPX4	NM_002085	chr19	+	1101934	1108788	6073	6071	13.73975667
KCTD11	NM_001002914	chr17	+	7253206	7260263	4565	4373	13.73162
ZFP36	NM_003407	chr19	+	39895485	39902046	4849	3811	13.72992
CIRBP	NM_001280	chr19	+	1267265	1275172	3804	2943	13.71607
HMGB3	NM_005342	chrX	+	150149761	150161249	3059	2748	13.66429
NCDN	NM_014284	chr1	+	36021391	36034381	4298	3582	13.6359
COQ5	NM_032314	chr12	-	120939080	120968965	1360	1325	13.634705
PRSS8	NM_002773	chr16	-	31140752	31149152	4595	3851	13.618025

PRNP	NM_183079	chr20	+	4664795	4684235	1933	1746	13.60486
PAICS	NM_006452	chr4	+	57299913	57329535	1952	1902	13.484505
NAE1	NM_003905	chr16	-	66834779	66866880	1498	1120	13.466805
C1QBP	NM_001212	chr17	-	5334097	5344472	1382	1330	13.45343
BTG1	NM_001731	chr12	-	92532052	92541674	2694	2692	13.41024
NUS1	NM_138459	chr6	+	117994615	118033887	1660	1282	13.40878
PPP4R1	NM_005134	chr18	-	9544790	9616601	3151	3023	13.39344
PREP	NM_002726	chr6	-	105723440	105853000	3862	3733	13.33848
YTHDC1	NM_133370	chr4	-	69174103	69217825	1095	1079	13.32953
ESRP1	NM_017697	chr8	+	95651362	95721695	5131	4095	13.3271975
DYNLT1	NM_006519	chr6	-	159055505	159067805	2167	2149	13.3114
C6orf72	NM_138785	chr6	+	149885526	149914068	2403	2004	13.25113
EIF2S1	NM_004094	chr14	+	67825032	67855234	2069	1797	13.249685
NANOS1	NM_199461	chr10	+	120787226	120795855	2385	2362	13.24876
TSPAN13	NM_014399	chr7	+	16791349	16826162	1888	1588	13.198795
RAB38	NM_022337	chr11	-	87844413	87910636	1001	917	13.197265
SOX4	NM_003107	chr6	+	21591970	21600850	4534	4367	13.17126
ACTR10	NM_018477	chr14	+	58664831	58704354	1466	1465	13.116875
TMPRSS11E	NM_014058	chr4	+	69311165	69365323	540	531	13.11672
UFM1	NM_016617	chr13	+	38921940	38939144	1200	1142	13.11457
DSC3	NM_024423	chr18	-	28568050	28624782	3107	1343	13.09876
CCNG2	NM_004354	chr4	+	78076355	78093214	2306	2153	13.09432
ARF5	NM_001662	chr7	+	127226515	127233753	2026	1995	13.09363
ZNF703	NM_025069	chr8	+	37551299	37558397	5567	4645	13.08573

CSNK2A1	NM_177560	chr20	-	461336	526483	2599	2519	13.072325
BNC1	NM_001717	chr15	-	83922653	83955469	3866	3765	13.064775
FEM1A	NM_018708	chr19	+	4789726	4797572	1723	1398	13.06051
PRRG4	NM_024081	chr11	+	32849487	32878106	2523	2434	13.05982
UMPS	NM_000373	chr3	+	124447211	124470120	1996	1773	13.036375
CAPNS2	NM_032330	chr16	+	55598582	55603593	332	0	13.03131
SERPINB7	NM_003784	chr18	+	61440610	61474605	880	627	13.010615
ATF5	NM_012068	chr19	+	50429957	50439194	2514	2422	13.00015
PDCD5	NM_004708	chr19	+	33070102	33080330	1574	1445	12.993845
HN1L	NM_144570	chr16	+	1726276	1754074	3320	2799	12.971635
RDX	NM_002906	chr11	-	110098164	110169438	3177	2598	12.963145
NKX2-1	NM_003317	chr14	-	36983602	36990904	6783	5668	12.95704
SERPINB4	NM_002974	chr18	-	61302491	61313503	626	422	12.94
FZD6	NM_003506	chr8	+	104309057	104347095	1798	1467	12.926045
KCNK6	NM_004823	chr19	+	38808482	38821650	2415	2088	12.916985
KLF5	NM_001730	chr13	+	73631140	73653677	3558	2801	12.886225
ATP6V1D	NM_015994	chr14	-	67802587	67828592	1951	1755	12.84845
SLC6A8	NM_005629	chrX	+	152951750	152964049	5099	4528	12.837425
GJA1	NM_000165	chr6	+	121754743	121772874	1133	855	12.821655
PTTG1	NM_004219	chr5	+	159846863	159857747	1102	766	12.80344
PAAF1	NM_025155	chr11	+	73586031	73640780	2345	2330	12.788555
TMPRSS11D	NM_004262	chr4	-	68684592	68751717	725	560	12.787165
PLEC	NM_201384	chr8	-	144987319	145015759	21187	20904	12.777195
CEACAM3	NM_001815	chr19	+	42298532	42317592	1213	831	12.69175

KLK11	NM_144947	chr19	-	51523485	51532886	2850	2346	12.673705
IL18	NM_001562	chr11	-	112011974	112036841	1408	1327	12.64669
CXCL14	NM_004887	chr5	-	134904369	134916970	1862	1343	12.63403
GNB2	NM_005273	chr7	+	100269361	100278793	6781	6754	12.63339
TMEM11	NM_003876	chr17	-	21099261	21119909	4156	4100	12.631775
HIATL1	NM_032558	chr9	+	97134831	97225203	3150	2808	12.6111
RUSC1	NM_014328	chr1	+	155292216	155302910	3165	3154	12.59723
ADRM1	NM_175573	chr20	+	60876025	60885919	8090	7388	12.5791175
SLC25A4	NM_001151	chr4	+	186062415	186073539	1810	1592	12.55696
SSFA2	NM_006751	chr2	+	182754470	182797465	1610	1510	12.520845
APOBEC3C	NM_014508	chr22	+	39408263	39416826	1807	1500	12.497715
CD46	NM_172361	chr1	+	207923381	207970862	1947	1886	12.49447
GJB3	NM_024009	chr1	+	35244788	35253966	5123	4559	12.491675
DSG3	NM_001944	chr18	+	29025730	29060666	813	415	12.48767
ENTPD3	NM_001248	chr3	+	40426671	40472111	1895	1016	12.46067
DDT	NM_001355	chr22	-	24311552	24324020	2775	2420	12.448625
NOP56	NM_006392	chr20	+	2631252	2641040	1952	1724	12.39722
CXCL1	NM_001511	chr4	+	74733107	74738956	1774	1685	12.388935
MFSD1	NM_022736	chr3	+	158517713	158549509	1494	1170	12.3856
TSTA3	NM_003313	chr8	-	144692786	144701733	3460	3324	12.36481
UCHL3	NM_006002	chr13	+	76121925	76182069	1929	1681	12.35968
CST3	NM_000099	chr20	-	23612292	23620575	2195	1482	12.34836
DSC2	NM_024422	chr18	-	28643940	28684389	2653	1907	12.3417
PRMT2	NM_206962	chr21	+	48053525	48086864	4344	3842	12.323005

PKP2	NM_004572	chr12	-	32941678	33051781	2941	2156	12.287155
PLBD1	NM_024829	chr12	-	14654595	14722792	2626	1302	12.27064
TMEM30B	NM_001017970	chr14	-	61742087	61750531	1906	1428	12.264215
NCCRP1	NM_001001414	chr19	+	39685602	39694523	2746	2559	12.2582
SERINC1	NM_020755	chr6	-	122762491	122794953	835	807	12.256545
TFCP2L1	NM_014553	chr2	-	121972162	122044779	4473	4160	12.22148
IDH3B	NM_174856	chr20	-	2637039	2646844	1183	1063	12.21752
SERPINB13	NM_012397	chr18	+	61252532	61268434	438	206	12.21259
MSMB	NM_138634	chr10	+	51547551	51564593	1362	1228	12.1906675
SMAD1	NM_005900	chr4	+	146400949	146482326	3596	3315	12.188885
C20orf4	NM_015511	chr20	+	34822445	34846854	1497	1144	12.140885
LMO4	NM_006769	chr1	+	87792149	87816608	5498	5470	12.138215
ZNF562	NM_017656	chr19	-	9757336	9787777	1276	1132	12.133065
DNM1L	NM_012063	chr12	+	32830135	32900585	1762	1484	12.11321667
C12orf54	NM_152319	chr12	+	48874284	48892298	1185	370	12.10712
DNASE2	NM_001375	chr19	-	12984023	12994336	2011	1908	12.104695
SAAL1	NM_138421	chr11	-	18099888	18129639	972	811	12.060585
FNBP1L	NM_017737	chr1	+	93911686	94022219	3834	2948	12.056625
TCEAL3	NM_032926	chrX	+	102860832	102866856	1355	1073	12.0566075
VSNL1	NM_003385	chr2	+	17719805	17839707	5240	4408	12.043515
CLCA4	NM_012128	chr1	+	87010757	87048433	796	0	12.036785
AGR2	NM_006408	chr7	-	16830262	16846739	1011	770	12.02685
TUSC1	NM_001004125	chr9	-	25674385	25680857	1626	1538	12.025205
INTS12	NM_020395	chr4	-	106601783	106631882	1274	1247	12.01615

DNAJB14	NM_001031723	chr4	-	100818708	100869880	1471	1242	11.9846925
PPIC	NM_000943	chr5	-	122357076	122374426	2166	2124	11.984645
UPK1B	NM_006952	chr3	+	118890423	118926001	2239	1970	11.978865
SESN3	NM_144665	chr11	-	94904131	94966247	1675	1274	11.97292
PIGG	NM_017733	chr4	+	490987	535321	3501	2552	11.9697
USO1	NM_003715	chr4	+	76647827	76737367	2079	1907	11.96663
STEAP1	NM_012449	chr7	+	89781687	89796142	1454	1208	11.906755
ZBED2	NM_024508	chr3	-	111309745	111316167	917	451	11.90485
WDR41	NM_018268	chr5	-	76726067	76790333	1193	1161	11.90359
MFSD2A	NM_032793	chr1	+	40418782	40437629	4321	3399	11.90122
DIABLO	NM_138929	chr12	-	122690207	122714069	2009	1810	11.88122667
ABCC10	NM_033450	chr6	+	43397487	43420164	2090	1711	11.870745
YEATS4	NM_006530	chr12	+	69751530	69786577	1329	1220	11.80925
PDCD2	NM_144781	chr6	-	170888833	170895749	1315	1217	11.79592
IVNS1ABP	NM_006469	chr1	-	185263520	185288462	2366	2181	11.79067
RNPC3	NM_017619	chr1	+	104066576	104099860	1288	1234	11.771865
NUDT16L1	NM_032349	chr16	+	4741692	4747861	5197	5125	11.76317
PAPD4	NM_173797	chr5	+	78906241	78984472	1054	993	11.759015
SMNDC1	NM_005871	chr10	-	112050796	112066708	1346	1309	11.74236
CLTB	NM_007097	chr5	-	175817454	175845541	5076	4458	11.73723
CDS1	NM_001263	chr4	+	85502055	85574494	3421	1627	11.728725
PUF60	NM_078480	chr8	-	144896545	144913538	11762	11581	11.7271625
BRMS1	NM_015399	chr11	-	66102802	66114583	4553	4206	11.722805
C16orf42	NM_001001410	chr16	-	1397239	1403874	2226	1945	11.711785

GPR109A	NM_177551	chr12	-	123183838	123189905	1157	996	11.703265
GJB5	NM_005268	chr1	+	35218719	35226113	2322	1884	11.68649
ARFGEF1	NM_006421	chr8	-	68107895	68257913	3290	3249	11.686335
ACP2	NM_001610	chr11	-	47258851	47272458	1647	1518	11.682445
GALE	NM_001127621	chr1	-	24120087	24128061	3696	3350	11.678335
TMPRSS4	NM_019894	chr11	+	117945725	117992557	3226	2294	11.6690425
CROT	NM_021151	chr7	+	86972949	87031113	1126	1082	11.664475
HMG20B	NM_006339	chr19	+	3570941	3581082	4941	4537	11.663005
TMEM68	NM_152417	chr8	-	56649318	56687886	1345	1202	11.60894
REPIN1	NM_014374	chr7	+	150066256	150073134	3212	2978	11.60765
RABEP1	NM_004703	chr17	+	5183556	5291133	2635	2465	11.60277
TFPI2	NM_006528	chr7	-	93513743	93522066	1121	1086	11.590905
GPR109B	NM_006018	chr12	-	123197301	123203440	1007	993	11.590215
RAB32	NM_006834	chr6	+	146862826	146878087	2285	2097	11.582055
CGGBP1	NM_003663	chr3	-	88099098	88110147	1661	1605	11.569585
BAP1	NM_004656	chr3	-	52433023	52446010	3894	3599	11.55741
TAB2	NM_015093	chr6	+	149637434	149734748	2425	2390	11.505655
NMU	NM_006681	chr4	-	56459396	56504466	1925	1485	11.497885
YIPF5	NM_030799	chr5	-	143535727	143552279	830	748	11.4961125
A2ML1	NM_144670	chr12	+	8973148	9031378	1192	1019	11.48883
GATAD1	NM_021167	chr7	+	92074763	92090743	1882	1665	11.47406
DVL2	NM_004422	chr17	-	7126659	7139864	2159	1789	11.471365
C14orf101	NM_017799	chr14	+	57044509	57118233	1352	1156	11.44763
PPAPDC2	NM_203453	chr9	+	4660296	4667259	2480	2190	11.445525

AK3	NM_016282	chr9	-	4709156	4743228	2249	1762	11.434975
HES2	NM_019089	chr1	-	6473292	6481980	5462	4937	11.42107
MYST1	NM_182958	chr16	+	31126983	31144715	5055	4605	11.418885
SLC35A5	NM_017945	chr3	+	112278893	112305004	1718	1649	11.39886
LGALS9C	NM_001040078	chr17	+	18378097	18400260	2113	1860	11.391385
STUB1	NM_005861	chr16	+	728113	734769	4986	4567	11.39031
MRPL23	NM_021134	chr11	+	1966500	1979840	6429	6422	11.372725
ATRN	NM_139322	chr20	+	3449663	3598551	2646	2443	11.372185
MMP10	NM_002425	chr11	-	102639231	102653360	691	436	11.37004
PLEKHJ1	NM_018049	chr19	-	2231153	2238329	4951	4921	11.3586
ENOPH1	NM_021204	chr4	+	83349724	83384245	3397	3227	11.35489
MLLT10	NM_004641	chr10	+	21821099	22034560	4035	3948	11.35025
ZNF498	NM_145115	chr7	+	99212569	99232031	2271	1541	11.344585
PPBP	NM_002704	chr4	-	74850154	74855908	163	0	11.335625
CPEB2	NM_182646	chr4	+	15002296	15073778	4187	4130	11.307885
PIGO	NM_152850	chr9	-	35086686	35098580	1024	988	11.2829875
ARL4C	NM_005737	chr2	-	235399684	235407694	3770	3179	11.280385
ARHGAP8	NM_181335	chr22	+	45146436	45260665	6472	5105	11.27462
FANCL	NM_018062	chr2	-	58384376	58470516	869	868	11.26252
NAPG	NM_003826	chr18	+	10523871	10554767	1382	1323	11.24886
SNX7	NM_152238	chr1	+	99125234	99228057	2528	2337	11.247565
NR4A2	NM_006186	chr2	-	157178942	157191288	2922	2852	11.23115
RNF146	NM_030963	chr6	+	127586018	127611505	1674	1525	11.22947
CSTA	NM_005213	chr3	+	122042009	122062816	594	0	11.220925

MINA	NM_153182	chr3	-	97658659	97693296	1420	1316	11.2177725
ARNTL2	NM_020183	chr12	+	27483986	27575467	4813	3994	11.21116
WDR43	NM_015131	chr2	+	29115531	29173081	2376	1767	11.20869
KLK13	NM_015596	chr19	-	51557461	51570368	572	537	11.204115
RRM2B	NM_015713	chr8	-	103214727	103253347	1844	1694	11.203575
GAS2L1	NM_152237	chr22	+	29700995	29710775	8465	8346	11.18762333
DALRD3	NM_018114	chr3	-	49050433	49060468	4721	4588	11.140315
PLS1	NM_002670	chr3	+	142340264	142434506	940	706	11.12484
PSG9	NM_002784	chr19	-	43755433	43775683	580	345	11.11606
SIX2	NM_016932	chr2	-	45230322	45238543	6909	6402	11.10281
C10orf57	NM_025125	chr10	+	81836424	81854308	1713	1245	11.099945
LDOC1L	NM_032287	chr22	-	44886448	44896006	1669	1616	11.08344
C20orf11	NM_017896	chr20	+	61567439	61581828	2218	2049	11.078215
MORC2	NM_014941	chr22	-	31320598	31366188	2924	2326	11.076065
SLC15A2	NM_021082	chr3	+	121611169	121665035	1090	259	11.0742
CCDC111	NM_152683	chr4	+	185568765	185618113	2535	2282	11.06678
FAM160B2	NM_022749	chr8	+	21944712	21963892	6591	5660	11.06086
MRPL27	NM_016504	chr17	-	48443226	48452563	979	972	11.00685833
SPINK5	NM_006846	chr5	+	147441533	147518926	248	107	10.97009
ZNF414	NM_032370	chr19	-	8574214	8581049	3352	3161	10.95982
MOBKL2C	NM_201403	chr1	-	47071385	47084564	3018	3015	10.953505
GJB6	NM_006783	chr13	-	20794099	20807373	2008	1530	10.946035
IRX2	NM_033267	chr5	-	2744277	2753770	6808	5987	10.9399
LNX2	NM_153371	chr13	-	28118048	28196721	4105	3986	10.93573

ZNF589	NM_016089	chr3	+	48280594	48314480	2880	2395	10.92373
YEATS2	NM_018023	chr3	+	183413604	183532414	3500	3339	10.894635
CECR5	NM_033070	chr22	-	17616408	17642170	2179	1925	10.89274
C19orf24	NM_017914	chr19	+	1273518	1281244	4908	3777	10.888385
VGLL1	NM_016267	chrX	+	135612309	135640967	271	0	10.86132
ZNF398	NM_170686	chr7	+	148842558	148882119	2467	2099	10.856575
CRCT1	NM_019060	chr1	+	152484976	152490482	1613	1057	10.83777
FAM35A	NM_019054	chr10	+	88852951	88953223	2292	2198	10.833905
ENSA	NM_207168	chr1	-	150597520	150604099	1123	1021	10.83251167
KCNJ5	NM_000890	chr11	+	128759311	128789952	6138	5891	10.83195
SNAPC2	NM_003083	chr19	+	7983192	7990137	3767	3335	10.79973
ENDOG	NM_004435	chr9	+	131578777	131586956	3057	3050	10.799005
C9orf85	NM_182505	chr9	+	74524421	74590372	2543	2484	10.798225
LCE3E	NM_178435	chr1	-	152536128	152541249	639	394	10.77159
FBXW5	NM_018998	chr9	-	139832885	139841174	4413	3740	10.74843333
DLK2	NM_206539	chr6	-	43416088	43425787	3562	2399	10.734435
THSD1	NM_199263	chr13	-	52949301	52982630	1185	1065	10.72583
EID2	NM_153232	chr19	-	40027445	40032839	1342	1263	10.71709
ZNF426	NM_024106	chr19	-	9636679	9651304	1392	933	10.71308
KRT24	NM_019016	chr17	-	38852241	38862003	812	0	10.709845
ANKRD9	NM_152326	chr14	-	102971196	102978129	6060	5671	10.70912
SPATA5L1	NM_024063	chr15	+	45692517	45715617	1946	1893	10.687095
RNF39	NM_170769	chr6	-	30036041	30045627	2732	2715	10.686155
FOXE1	NM_004473	chr9	+	100613535	100620998	3882	3579	10.67052

C3orf78	NM_001124767	chr3	+	52568619	52576587	2128	2043	10.660745
IRS2	NM_003749	chr13	-	110404182	110440915	7527	6111	10.65387
FOXD1	NM_004472	chr5	-	72740083	72746353	2357	2253	10.64131
JMJD8	NM_001005920	chr16	-	729665	736440	4911	4202	10.636545
PROS1	NM_000313	chr3	-	93589879	93694935	1914	1642	10.591775
C12orf41	NM_017822	chr12	-	49044993	49078036	1239	1207	10.58853
JOSD2	NM_138334	chr19	-	51007257	51016346	3671	3516	10.56813
APOBEC3B	NM_004900	chr22	+	39376403	39390784	3639	3451	10.560305
QPCT	NM_012413	chr2	+	37569751	37602466	2547	2502	10.55911
CNDP2	NM_018235	chr18	+	72161498	72192690	3758	3291	10.54087
C11orf93	NM_001136105	chr11	+	111167974	111181354	2078	1835	10.535725
SLC25A17	NM_006358	chr22	-	41163637	41217393	1213	1099	10.52902
NR2C1	NM_003297	chr12	-	95412056	95469405	1286	1241	10.511385
OSTM1	NM_014028	chr6	-	108360611	108397942	2225	2022	10.5068
LRRN1	NM_020873	chr3	+	3839119	3891388	2417	1313	10.49871
LCE1E	NM_178353	chr1	+	152756751	152762902	448	220	10.4987
DCLRE1A	NM_014881	chr10	-	115592482	115615860	1831	1676	10.487165
PRPF39	NM_017922	chr14	+	45551300	45586805	1526	1310	10.480015
PKIB	NM_181795	chr6	+	122929375	123049519	2592	1480	10.452605
CHMP4C	NM_152284	chr8	+	82642686	82673749	1498	1171	10.414445
GJD3	NM_152219	chr17	-	38514903	38522946	4149	3681	10.40955
RAB27B	NM_004163	chr18	+	52493838	52559212	1612	1382	10.400955
C9orf69	NM_152833	chr9	-	139004425	139012732	3906	2958	10.397455
NDUFA4L2	NM_020142	chr12	-	57626684	57636476	5769	5356	10.373

SERAC1	NM_032861	chr6	-	158528534	158591313	2444	2237	10.348165
LCE1C	NM_178351	chr1	-	152775309	152781108	489	0	10.34552
ABCC5	NM_005688	chr3	-	183635722	183737728	3681	3479	10.341125
PCSK5	NM_006200	chr9	+	78503558	78810347	5967	5287	10.31702
SPRY1	NM_199327	chr4	+	124315954	124326908	3195	2764	10.3036125
CTXN1	NM_206833	chr19	-	7987379	7993052	3689	2382	10.29321
C1orf59	NM_144584	chr1	-	109188908	109206149	1495	1426	10.280945
DMRT2	NM_181872	chr9	+	1048618	1059555	3407	2960	10.27857
HLA-G	NM_002127	chr6	+	29792754	29800900	322	199	10.273635
THAP1	NM_199003	chr8	-	42689815	42700475	1584	1512	10.271085
HPS6	NM_024747	chr10	+	103823145	103829794	2105	1772	10.268285
FAM83B	NM_001010872	chr6	+	54709567	54808820	3801	2982	10.261605
POGLUT1	NM_152305	chr3	+	119185783	119215555	1363	1191	10.257365
FAM84A	NM_145175	chr2	+	14770808	14782169	3726	2975	10.249965
SLC12A2	NM_001046	chr5	+	127417481	127527381	3015	2938	10.243415
ZNF135	NM_007134	chr19	+	58568605	58583111	1329	1172	10.2424
DENND2C	NM_198459	chr1	-	115125194	115214733	2848	1763	10.231145
VPS36	NM_016075	chr13	-	52984735	53026764	2605	2468	10.23045
SOX2	NM_003106	chr3	+	181427720	181434224	4426	2263	10.22905
SMARCAD1	NM_020159	chr4	+	95127014	95214444	1085	933	10.212175
ABCA12	NM_173076	chr2	-	215794264	216005152	2682	2524	10.18816
TBRG4	NM_199122	chr7	-	45137697	45153318	1816	1685	10.181765
SDR16C5	NM_138969	chr8	-	57210568	57235242	1845	1247	10.178005
IRX5	NM_005853	chr16	+	54963109	54970396	6373	5424	10.16918

AGAP9	NM_001190810	chr10	+	48213722	48239509	243	0	10.160345
TRIM68	NM_018073	chr11	-	4617900	4631438	1418	1081	10.154115
BARX2	NM_003658	chr11	+	129243879	129324175	4196	2205	10.142245
GINS3	NM_022770	chr16	+	58424296	58442049	1387	1348	10.09046
MSL2	NM_018133	chr3	-	135865758	135916689	3190	2919	10.089925
PTPRZ1	NM_002851	chr7	+	121511157	121704091	3047	2018	10.08715
C1orf190	NM_001013615	chr1	+	46667004	46688929	2836	2665	10.085325
LY6G6C	NM_025261	chr6	-	31684423	31691511	1402	643	10.068535
PLEKHN1	NM_032129	chr1	+	899875	912485	5408	5150	10.063765
KLF16	NM_031918	chr19	-	1850396	1865565	12282	12221	10.05217
LZTS2	NM_032429	chr10	+	102754963	102769588	7213	6707	10.024915
RNPEPL1	NM_018226	chr2	+	241506102	241520144	4901	4705	10.01952
CYP4X1	NM_178033	chr1	+	47487238	47518424	1194	937	10.003795
SOCS4	NM_199421	chr14	+	55491842	55518207	1271	1180	9.995595
TMEM80	NM_174940	chr11	+	693614	706130	4547	4353	9.98517
BMPR1B	NM_001203	chr4	+	95677126	96081602	5372	3368	9.983985
SLC16A9	NM_194298	chr10	-	61408520	61471650	2921	1968	9.98083
SAP30	NM_003864	chr4	+	174290091	174300684	2645	2608	9.965805
CKAP2	NM_018204	chr13	+	53027493	53052764	1658	1637	9.9657
UCK1	NM_031432	chr9	-	134397181	134408663	4157	3791	9.960145
CCDC3	NM_031455	chr10	-	12936623	13045705	3395	2456	9.942935
FAM110C	NM_001077710	chr2	-	36812	48589	3309	3037	9.94275
KRT31	NM_002277	chr17	-	39547975	39555845	992	240	9.941685
RFX7	NM_022841	chr15	-	56380729	56537484	2442	2313	9.94161

TYSND1	NM_173555	chr10	-	71895731	71908497	2902	2795	9.92802
ZNF654	NM_018293	chr3	+	88186260	88195815	235	220	9.923455
DACT2	NM_214462	chr6	-	168705582	168722403	2479	2356	9.91734
PRR21	NM_001080835	chr2	-	240979228	240984400	474	0	9.89413
SPSB3	NM_080861	chr16	-	1824711	1834582	7105	4184	9.87558
NUP62CL	NM_017681	chrX	-	106364655	106451671	1868	1589	9.87353
USP43	NM_153210	chr17	+	9546948	9635004	5730	5597	9.86906
SOX21	NM_007084	chr13	-	95359877	95366390	4749	4367	9.847125
DEPDC7	NM_139160	chr11	+	33035726	33057129	1166	1053	9.845615
SIPA1L2	NM_020808	chr1	-	232531710	232653244	1978	1568	9.838925
TREM2	NM_018965	chr6	-	41124244	41132923	271	176	9.83238
KLHL17	NM_198317	chr1	+	893965	903100	6692	6585	9.82833
NDUFB3	NM_002491	chr2	+	201934460	201952474	1198	1072	9.827385
CARD17	NM_001007232	chr11	-	104961194	104974159	138	0	9.817725
CEP57L1	NM_173830	chr6	+	109448505	109487116	350	329	9.81236
ASF1A	NM_014034	chr6	+	119213239	119232336	2296	2279	9.808815
CAPS	NM_080590	chr19	+	5912191	5918223	2189	2067	9.79182
SLC7A4	NM_004173	chr22	-	21381005	21388848	1326	1199	9.78683
MSGN1	NM_001105569	chr2	+	17995784	18000368	536	346	9.77404
BCL11B	NM_138576	chr14	-	99633623	99739823	17582	16688	9.765045
NEDD1	NM_152905	chr12	+	97298999	97349470	1675	1561	9.75054
TPSB2	NM_024164	chr16	-	1276334	1282186	2958	2748	9.714775
SIRPB2	NM_001134836	chr20	-	1453234	1474234	1821	1081	9.707925
SPCS3	NM_021928	chr4	+	177239088	177255397	1603	1317	9.688255

EXOSC5	NM_020158	chr19	-	41890274	41905257	1497	1213	9.652285
SPRR3	NM_005416	chr1	+	152972221	152978333	431	0	9.651565
CCNA1	NM_003914	chr13	+	37004407	37019020	1424	1292	9.648305
TP53AIP1	NM_022112	chr11	-	128803268	128815295	3641	1912	9.63656
CCDC138	NM_144978	chr2	+	109401217	109494848	1503	1213	9.62468
TREM1	NM_018643	chr6	-	41241710	41256458	756	737	9.612575
CHAC1	NM_024111	chr15	+	41243634	41250718	2914	2669	9.60963
TTBK2	NM_173500	chr15	-	43034540	43215008	2890	2793	9.59962
SMPD1	NM_001007593	chr11	+	6409642	6418229	1351	1275	9.584655
MED30	NM_080651	chr8	+	118530963	118554502	1005	906	9.579155
SMOC2	NM_022138	chr6	+	168839829	169070675	12648	11698	9.56561
NXT2	NM_018698	chrX	+	108777008	108789914	1499	1289	9.550125
C12orf29	NM_001009894	chr12	+	88427266	88445938	959	901	9.548995
SERTAD3	NM_203344	chr19	-	40944746	40952283	2633	2448	9.545135
CHL1	NM_006614	chr3	+	236648	453098	3559	2383	9.53591
KRTAP10-2	NM_198693	chr21	-	45968316	45973389	2276	1191	9.51689
WDR54	NM_032118	chr2	+	74646883	74654883	2739	1924	9.51029
C3orf63	NM_015224	chr3	-	56652158	56700075	266	253	9.49665
ZNF626	NM_145297	chr19	-	20825507	20846403	814	756	9.49131
ZMYM5	NM_001142684	chr13	-	20395622	20439777	3627	3487	9.490745
FBN2	NM_001999	chr5	-	127591599	127875736	3880	3066	9.449785
BBOX1	NM_003986	chr11	+	27060507	27151355	1143	1143	9.43296
RNF222	NM_001146684	chr17	-	8292021	8303145	1608	1367	9.428305
TMPRSS11F	NM_207407	chr4	-	68916914	68997588	1027	0	9.422205

SUSD4	NM_017982	chr1	-	223392159	223539545	5820	5685	9.419095
ACVR2A	NM_001616	chr2	+	148600568	148690394	2410	2233	9.401385
DRD2	NM_016574	chr11	-	113278315	113348002	4930	3928	9.39099
ZC3H8	NM_032494	chr2	-	112971437	113014665	1376	905	9.381055
ZNF606	NM_025027	chr19	-	58486439	58516715	1549	1431	9.36385
HTR7	NM_019860	chr10	-	92498574	92619672	4865	4210	9.355475
MPST	NM_021126	chr22	+	37413700	37427864	4202	4089	9.35158
SERF1A	NM_022968	chr5	+	69319070	69330526	939	799	9.34901
CCDC113	NM_014157	chr16	+	58281838	58319735	2495	1614	9.343995
STOX2	NM_020225	chr4	+	184824507	184940876	4655	4406	9.341645
MUC16	NM_024690	chr19	-	8957518	9094019	637	297	9.341315
C4orf19	NM_018302	chr4	+	37583853	37597133	243	138	9.335395
CCDC66	NM_001141947	chr3	+	56589182	56657849	1079	1019	9.330405
C20orf46	NM_018354	chr20	-	1159213	1167118	2644	2576	9.326765
UBL4B	NM_203412	chr1	+	110653060	110658570	464	259	9.324015
ADAM28	NM_021777	chr8	+	24149578	24195613	427	341	9.3238925
NLGN4X	NM_181332	chrX	-	5806081	6148707	5145	4359	9.301035
CAPN6	NM_014289	chrX	-	110486325	110515775	680	591	9.281865
ZFP42	NM_174900	chr4	+	188914923	188928200	840	756	9.27113
SATB1	NM_002971	chr3	-	18387132	18468830	1614	1607	9.26758
CYP2J2	NM_000775	chr1	-	60356978	60394424	710	590	9.265115
ZFP28	NM_020828	chr19	+	57048315	57070171	1693	1591	9.259765
NEK3	NM_001146099	chr13	-	52704777	52735997	1177	1150	9.25709
SREK1IP1	NM_173829	chr5	-	64011976	64066497	1003	989	9.245685

LPCAT2	NM_017839	chr16	+	55540911	55622583	1944	1264	9.245245
PSG5	NM_002781	chr19	-	43669893	43692689	691	591	9.241305
ZNF211	NM_198855	chr19	+	58142533	58156148	1003	946	9.23055
IL1RL1	NM_016232	chr2	+	102925960	102970498	1194	892	9.2186825
TSSC4	NM_005706	chr11	+	2421521	2427107	2398	1940	9.20646
MBOAT2	NM_138799	chr2	-	8994699	9145877	3881	3433	9.199095
DAPL1	NM_001017920	chr2	+	159649827	159674497	917	792	9.17009
PHPT1	NM_014172	chr9	+	139741254	139747491	4976	4320	9.167215
DYRK1B	NM_006484	chr19	-	40313988	40326842	4723	4507	9.16566
MAPK8	NM_139049	chr10	+	49607685	49645184	682	211	9.142105
BAZ2B	NM_013450	chr2	-	160173488	160475060	3414	3319	9.12264
PROL1	NM_021225	chr4	+	71261597	71277915	100	0	9.11901
RPUSD1	NM_058192	chr16	-	832972	840384	6226	5488	9.098555
ZNF22	NM_006963	chr10	+	45494271	45502778	1949	1762	9.09407
PELI1	NM_020651	chr2	-	64317784	64373606	1851	1786	9.087135
RNMTL1	NM_018146	chr17	+	683511	697742	4204	2915	9.08262
TTC36	NM_001080441	chr11	+	118396208	118403741	2340	2214	9.072245
HRASLS	NM_020386	chr3	+	192956916	192990645	1053	860	9.05415
NAP1L2	NM_021963	chrX	-	72430152	72436685	584	579	9.04906
LIG4	NM_206937	chr13	-	108857790	108869883	1454	1424	9.04767
CD274	NM_014143	chr9	+	5448501	5472568	1327	1239	9.04725
OSBPL6	NM_145739	chr2	+	179182969	179262876	655	357	9.04609
FAM183A	NM_001101376	chr1	+	43611592	43624068	1038	600	9.03901
ZNF551	NM_138347	chr19	+	58191355	58203170	1016	1002	9.032465

C2orf85	NM_173821	chr2	+	242809884	242817483	4552	4420	9.02815
RAD52	NM_134424	chr12	-	1019253	1060864	2222	1911	9.02462
KPRP	NM_001025231	chr1	+	152728504	152736530	1023	135	9.02005
ATOH1	NM_005172	chr4	+	94748076	94753143	1599	928	9.01169
CYP4B1	NM_001099772	chr1	+	47262668	47287022	507	82	8.98142
ZNF662	NM_207404	chr3	+	42945400	42962826	1080	913	8.97512
NKX6-1	NM_006168	chr4	-	85412434	85421388	4015	3898	8.97485
C22orf26	NM_018280	chr22	-	46444337	46452025	3994	3962	8.9692
ODF2L	NM_020729	chr1	-	86813775	86864026	1344	1227	8.956075
PATZ1	NM_032052	chr22	-	31719788	31744250	6391	6329	8.955265
FOXA2	NM_153675	chr20	-	22559640	22568102	4765	4675	8.95196
MRPS34	NM_023936	chr16	-	1819894	1825141	5188	4799	8.95044
EYA1	NM_172060	chr8	-	72107666	72270980	2118	1240	8.94867
CGB8	NM_033183	chr19	-	49548893	49554369	538	501	8.94105
MRGPRX3	NM_054031	chr11	+	18140500	18162028	396	0	8.940185
FAIM	NM_018147	chr3	+	138325917	138354214	1969	1810	8.936795
DGCR14	NM_022719	chr22	-	19115790	19134191	2900	2276	8.926185
FLG	NM_002016	chr1	-	152272649	152299680	186	0	8.923855
FUT4	NM_002033	chr11	+	94275015	94285065	2681	2075	8.9159
LY6K	NM_017527	chr8	+	143779527	143787585	2145	2056	8.91484
IRX3	NM_024336	chr16	-	54315210	54322379	5892	5590	8.904885
GLRB	NM_001166061	chr4	+	157995275	158095243	1727	1481	8.904145
CGB5	NM_033043	chr19	+	49545100	49550569	341	323	8.901765
ISL1	NM_002202	chr5	+	50676956	50692564	3648	2215	8.86956

A2M	NM_000014	chr12	-	9218302	9270559	252	0	8.855895
CCDC34	NM_080654	chr11	-	27368417	27386796	1058	935	8.855225
PRKCQ	NM_006257	chr10	-	6467103	6624239	3179	3037	8.85415
NOL12	NM_024313	chr22	+	38080342	38091486	2187	1534	8.840565
FAM150A	NM_207413	chr8	-	53444595	53480022	2102	1798	8.81972
LENG9	NM_198988	chr19	-	54970977	54976895	4398	4141	8.81879
LILRA4	NM_012276	chr19	-	54842690	54852422	182	161	8.815315
CCDC8	NM_032040	chr19	-	46911584	46918920	1446	1043	8.798635
APLNR	NM_005161	chr11	-	56999050	57006928	225	0	8.777
ZNF524	NM_153219	chr19	+	56109728	56116505	3375	3252	8.768765
FLRT2	NM_013231	chr14	+	85994486	86096271	5407	4832	8.764455
C20orf141	NM_080739	chr20	+	2793655	2798477	1283	1086	8.76127
POF1B	NM_024921	chrX	-	84530393	84636749	506	165	8.753825
ZNF789	NM_213603	chr7	+	99068513	99087218	1483	1432	8.74977
ACN9	NM_020186	chr7	+	96743903	96813076	1835	1438	8.727795
SLC2A12	NM_145176	chr6	-	134306717	134375790	1823	1686	8.72735
CBLN3	NM_001039771	chr14	-	24893738	24900732	3926	3829	8.7207
ZNF470	NM_001001668	chr19	+	57076888	57096263	1119	1112	8.71214
KLK9	NM_012315	chr19	-	51503767	51514891	2337	2192	8.706975
ASPDH	NM_001114598	chr19	-	51012855	51019143	5288	5229	8.6999
SLC6A15	NM_182767	chr12	-	85251265	85308607	1559	1457	8.691775
CYP4V2	NM_207352	chr4	+	187110672	187136618	2773	2638	8.68791
TCEAL2	NM_080390	chrX	+	101378658	101384685	1515	1457	8.682865
CHST9	NM_031422	chr18	-	24493593	24767290	3623	2887	8.67163

ZNF433	NM_001080411	chr19	-	12123530	12148526	1153	1036	8.671205
CHRM4	NM_000741	chr11	-	46404638	46410108	3468	3421	8.666975
MCART2	NM_001034172	chr18	-	29337657	29342844	114	0	8.653635
EFCAB7	NM_032437	chr1	+	63987011	64040365	949	885	8.646905
MXD4	NM_006454	chr4	-	2247158	2265740	5864	5505	8.644575
FOLH1	NM_004476	chr11	-	49166185	49232223	688	672	8.6199675
LRIT1	NM_015613	chr10	-	85989274	86003218	438	319	8.597085
NUDT10	NM_153183	chrX	+	51073081	51082378	2215	2137	8.596395
HRH2	NM_022304	chr5	+	175106462	175113559	303	200	8.577695
EME2	NM_001010865	chr16	+	1821227	1828240	6646	4157	8.54587
KIAA1328	NM_020776	chr18	+	34407078	34807289	2432	2212	8.54407
GSTT2	NM_000854	chr22	+	24320312	24328107	1997	1457	8.54297
KIAA1919	NM_153369	chr6	+	111578480	111592262	1438	1410	8.540285
GATM	NM_001482	chr15	-	45651320	45672981	1152	1008	8.536585
IFNK	NM_020124	chr9	+	27522310	27528497	434	205	8.532695
PLAC8L1	NM_001029869	chr5	-	145461874	145485947	602	335	8.53041
TWIST1	NM_000474	chr7	-	19153089	19159296	3277	2790	8.528955
OSCP1	NM_206837	chr1	-	36891899	36918087	2076	1851	8.5205325
TEX101	NM_031451	chr19	+	43890761	43924768	753	0	8.504125
FOXD2	NM_004474	chr1	+	47899687	47908364	5401	5237	8.500285
ACBD5	NM_145698	chr10	-	27482141	27531809	1910	1801	8.4988
RTP1	NM_153708	chr3	+	186913272	186921254	987	590	8.496085
C6	NM_001115131	chr5	-	41140334	41263541	409	280	8.48318
GLIPR1L1	NM_152779	chr12	+	75726461	75766170	704	647	8.48229

SCXB	NM_001080514	chr8	+	145488601	145494132	4847	4677	8.472695
SULT1E1	NM_005420	chr4	-	70704928	70727871	586	157	8.46898
HYI	NM_031207	chr1	-	43914822	43921661	2583	2386	8.46687
MYL5	NM_002477	chr4	+	669709	677818	7649	6966	8.43995
RIBC2	NM_015653	chr22	+	45807572	45830296	2183	1967	8.433865
ALX1	NM_006982	chr12	+	85672034	85697562	1723	1554	8.426795
S100A12	NM_005621	chr1	-	153344182	153350076	694	584	8.409455
ZNF177	NM_003451	chr19	+	9471694	9495294	142	0	8.4056
PCDH7	NM_032457	chr4	+	30720035	31150424	5730	5581	8.401675
DUS3L	NM_020175	chr19	-	5783151	5793250	3773	3287	8.394535
ZMYND17	NM_001024593	chr10	-	75181335	75195320	240	0	8.38612
TRIM45	NM_025188	chr1	-	117651675	117666412	1380	1247	8.38089
OSBPL7	NM_145798	chr17	-	45882731	45901148	3686	3660	8.3795475
ATP13A4	NM_032279	chr3	-	193117864	193274697	1331	409	8.3504
RNF175	NM_173662	chr4	-	154629310	154683388	2292	1897	8.343875
C13orf31	NM_153218	chr13	+	44451967	44470069	1490	1277	8.341395
ATHL1	NM_025092	chr11	+	287136	297689	6557	6233	8.33568
C3orf30	NM_152539	chr3	+	118862995	118872303	645	433	8.332445
KRT75	NM_004693	chr12	-	52815852	52830111	1276	714	8.32483
ESCO2	NM_001017420	chr8	+	27630056	27664425	1138	1086	8.306545
HMGB2	NM_002129	chr4	-	174250525	174257596	2131	2022	8.28392
FOXD4L1	NM_012184	chr2	+	114254659	114260728	559	227	8.281415
FZD10	NM_007197	chr12	+	130645030	130652286	2694	2534	8.260565
HPGD	NM_001145816	chr4	-	175409326	175445793	1502	1069	8.25736

NHLH2	NM_005599	chr1	-	116376997	116385748	2068	1708	8.251295
CXCL3	NM_002090	chr4	-	74900310	74906491	1284	939	8.24825
GJA5	NM_181703	chr1	-	147226330	147234715	774	472	8.24526
IL1RAP	NM_134470	chr3	+	190229838	190350074	4586	4352	8.244805
EDIL3	NM_005711	chr5	-	83236124	83682612	2702	2574	8.241255
TDRKH	NM_006862	chr1	-	151742039	151765011	2190	1990	8.23386
MGAM	NM_004668	chr7	+	141693677	141808548	1107	408	8.230015
RECQL4	NM_004260	chr8	-	145734665	145745211	5787	5721	8.209135
OR10S1	NM_001004474	chr11	-	123845401	123850399	371	0	8.2011
CRYBB2	NM_000496	chr22	+	25613610	25629837	1890	1325	8.192905
C9orf123	NM_033428	chr9	-	7794489	7801800	1078	1034	8.179175
KRTAP12-3	NM_198697	chr21	+	46075847	46080259	217	188	8.179055
SLAMF7	NM_021181	chr1	+	160707075	160726602	721	176	8.172315
C4orf48	NM_001168243	chr4	+	2041718	2047698	5080	4719	8.168295
FOXI2	NM_207426	chr10	+	129533536	129541451	2163	1824	8.16379
ZNF428	NM_182498	chr19	-	44109374	44126015	2091	1946	8.139205
MEP1A	NM_005588	chr6	+	46759092	46809520	1138	113	8.12878
TRMU	NM_018006	chr22	+	46729296	46755238	7746	6262	8.126024
GLI4	NM_138465	chr8	+	144347605	144361102	8081	7960	8.124615
C18orf62	NM_001037331	chr18	-	73119825	73141590	758	748	8.113605
NPPB	NM_002521	chr1	-	11915519	11920993	1092	782	8.111615
USP51	NM_201286	chrX	-	55509047	55517632	2015	1896	8.1052
SYDE2	NM_032184	chr1	-	85621354	85668729	2001	1993	8.085775
SLITRK6	NM_032229	chr13	-	86364920	86375484	314	273	8.08181

CNTN1	NM_175038	chr12	+	41084356	41466095	2645	1560	8.073015
IZUMO4	NM_001039846	chr19	+	2094866	2101584	4089	3416	8.061198333
WFDC6	NM_080827	chr20	-	44160834	44170135	324	0	8.061145
C16orf68	NM_024109	chr16	+	8713525	8742080	2434	2282	8.04464
ZNF571	NM_016536	chr19	-	38053153	38087674	1529	1517	8.03249
LILRA3	NM_006865	chr19	-	54797853	54806266	154	147	8.01969
ZFP57	NM_001109809	chr6	-	29638167	29646932	1401	521	8.006545
ABP1	NM_001091	chr7	+	150547571	150560380	683	683	8.001735
C5orf38	NM_178569	chr5	+	2750260	2757512	6130	6100	7.99812
ZNF429	NM_001001415	chr19	+	21686435	21723080	1137	1029	7.975385
FOXD4	NM_207305	chr9	-	114232	120418	646	380	7.966735
KRTAP19-1	NM_181607	chr21	-	31850362	31854637	85	0	7.949915
FZD8	NM_031866	chr10	-	35925175	35932363	4392	4117	7.94913
COX6A2	NM_005205	chr16	-	31437053	31441722	1225	1112	7.936395
ZNF430	NM_025189	chr19	+	21201424	21244853	1276	1156	7.934905
CDH9	NM_016279	chr5	-	26878707	27040690	160	0	7.92571
PAGE4	NM_007003	chrX	+	49591904	49600571	37	0	7.92158
ARID2	NM_152641	chr12	+	46121618	46303820	2958	2924	7.89893
WDR72	NM_182758	chr15	-	53803936	54053860	1235	905	7.898405
CLEC18B	NM_001011880	chr16	-	74440527	74457369	544	520	7.893225
CXorf57	NM_018015	chrX	+	105853158	105924674	855	855	7.88238
KRT33A	NM_004138	chr17	-	39500369	39509057	622	130	7.876315
C6orf138	NM_207499	chr6	-	47865343	48038426	755	69	7.875975
C8orf30A	NM_016458	chr8	+	145435878	145442829	3602	3011	7.86598

ENPP5	NM_021572	chr6	-	46125760	46140718	595	514	7.850805
TOX3	NM_001146188	chr16	-	52469916	52583715	2240	1830	7.84675
SLC5A1	NM_000343	chr22	+	32437017	32511012	2194	1944	7.84092
KEL	NM_000420	chr7	-	142636199	142661504	1874	1183	7.836565
FOLH1B	NM_153696	chr11	+	89390463	89433887	238	53	7.821425
LCE3D	NM_032563	chr1	-	152549858	152554981	520	437	7.81877
TRPC1	NM_003304	chr3	+	142441264	142528730	1719	1696	7.78144
C11orf65	NM_152587	chr11	-	108251725	108340259	1359	1178	7.77869
OR52M1	NM_001004137	chr11	+	4564419	4569375	245	135	7.77045
ACTR8	NM_022899	chr3	-	53899092	53918230	1411	1318	7.770265
PENK	NM_006211	chr8	-	57351511	57360594	1875	983	7.766385
CDK5R2	NM_003936	chr2	+	219822396	219828878	4898	4832	7.76284
IER5L	NM_203434	chr9	-	131935829	131942541	5318	5236	7.74995
EIF2C4	NM_017629	chr1	+	36271826	36323189	1823	1775	7.74161
FEZF2	NM_018008	chr3	-	62353345	62361191	3804	3486	7.73766
CYP2A13	NM_000766	chr19	+	41592366	41604100	372	325	7.73482
EFCAB1	NM_024593	chr8	-	49633951	49649871	638	564	7.707335
ST6GAL2	NM_032528	chr2	-	107416054	107505564	2334	2050	7.694645
CSAG1	NM_153478	chrX	+	151901226	151911519	187	117	7.69193
FAM117B	NM_173511	chr2	+	203497899	203636481	3475	2829	7.6758
SLC29A4	NM_153247	chr7	+	5320559	5345705	6681	6481	7.650645
GUCY1A2	NM_000855	chr11	-	106555908	106891172	3719	2969	7.64223
DEFB4A	NM_004942	chr8	+	7750197	7756238	247	189	7.63967
BMP2	NM_001200	chr20	+	6746743	6762911	3388	3149	7.632695

FBXO8	NM_012180	chr4	-	175155808	175207403	1582	1521	7.62431
GABRG3	NM_033223	chr15	+	27214427	27780374	5668	3955	7.616405
PTPRD	NM_130393	chr9	-	8312244	8735947	2766	1336	7.6164
PRMT8	NM_019854	chr12	+	3598423	3705139	4292	3934	7.60614
LEP	NM_000230	chr7	+	127879329	127899683	985	937	7.57826
STX19	NM_001001850	chr3	-	93731213	93749455	384	0	7.56018
NKX2-4	NM_033176	chr20	-	21374003	21380048	1849	1629	7.554645
GALNT12	NM_024642	chr9	+	101567979	101614360	4229	4146	7.549235
CCK	NM_001174138	chr3	-	42297316	42307440	1846	1818	7.54731
LASS3	NM_178842	chr15	-	100938598	101086926	1570	845	7.539645
POU3F4	NM_000307	chrX	+	82761267	82766776	957	740	7.527765
UCP1	NM_021833	chr4	-	141479048	141491960	1089	995	7.51818
CXCR2	NM_001557	chr2	+	218988734	219003977	339	126	7.495795
PTF1A	NM_178161	chr10	+	23479458	23485182	3413	2842	7.48868
CLDN8	NM_199328	chr21	-	31584322	31590470	219	0	7.48612
RAB19	NM_001008749	chr7	+	140101841	140128051	629	560	7.45721
ZFP2	NM_030613	chr5	+	178320914	178362211	1276	1004	7.45263
CCDC11	NM_145020	chr18	-	47751561	47794866	2070	1684	7.445045
PHKA1	NM_002637	chrX	-	71796662	71936030	4192	4038	7.441685
RBP2	NM_004164	chr3	-	139169724	139197353	484	331	7.43861
MESP1	NM_018670	chr15	-	90291096	90296541	2142	1994	7.425455
HSPB9	NM_033194	chr17	+	40272754	40277372	2176	1520	7.41326
LRFN2	NM_020737	chr6	-	40357371	40557127	7420	5947	7.38609
RNF2	NM_007212	chr1	+	185012549	185073741	1904	1718	7.38139

SNX18	NM_052870	chr5	+	53811591	53818835	1913	1880	7.380715
ANKK1	NM_178510	chr11	+	113256511	113273141	1302	829	7.37709
C5orf43	NM_001048249	chr5	-	60451534	60460303	1272	1226	7.36838
SH2D1A	NM_002351	chrX	+	123478130	123509011	340	0	7.364625
CHML	NM_001821	chr1	-	241790165	241801233	441	428	7.353325
CYSLTR1	NM_006639	chrX	-	77526128	77585088	902	336	7.35327
OR10A3	NM_001003745	chr11	-	7958121	7963068	116	0	7.34732
KRT37	NM_003770	chr17	-	39574807	39582823	899	358	7.340675
GYS2	NM_021957	chr12	-	21687121	21759782	432	177	7.33584
MBD2	NM_015832	chr18	-	51727045	51753159	1865	1809	7.3192375
PGLYRP1	NM_005091	chr19	-	46520410	46528557	1205	936	7.318175
MFSD6L	NM_152599	chr17	-	8698426	8704668	763	133	7.317695
ERP27	NM_152321	chr12	-	15064974	15093464	586	349	7.290685
STK32A	NM_145001	chr5	+	146612577	146730393	1801	1130	7.28586
ZNF319	NM_020807	chr16	-	58026571	58035763	5069	3770	7.280485
KLF14	NM_138693	chr7	-	130415394	130420889	1675	1660	7.28012
H2BFM	NM_001164416	chrX	+	103292514	103299022	119	0	7.2742
ZIK1	NM_001010879	chr19	+	58093626	58105759	818	791	7.2735
CLDN25	NM_001101389	chr11	+	113648516	113653208	915	489	7.26823
LYZL4	NM_144634	chr3	-	42436573	42454066	177	0	7.261845
RIN1	NM_004292	chr11	-	66097540	66106001	3621	3462	7.25799
TDRD6	NM_001168359	chr6	+	46653610	46674057	267	222	7.252165
ZC3HAV1L	NM_080660	chr7	-	138708450	138722776	2380	2216	7.251905
C2orf61	NM_173649	chr2	-	47353585	47384518	399	360	7.23381

ZNF347	NM_032584	chr19	-	53639955	53664323	1133	976	7.233375
PSG3	NM_021016	chr19	-	43223792	43246669	216	0	7.230035
IL1F10	NM_173161	chr2	+	113823545	113835428	1019	214	7.2233475
S100G	NM_004057	chrX	+	16666279	16674792	100	0	7.22068
OAZ3	NM_016178	chr1	+	151737129	151745807	622	0	7.216245
ATP13A5	NM_198505	chr3	-	192990829	193098515	861	531	7.21511
GDA	NM_004293	chr9	+	74762291	74869141	1666	1631	7.19519
SST	NM_001048	chr3	-	187384692	187390202	292	272	7.180285
TIGD5	NM_032862	chr8	+	144678072	144684486	5348	5022	7.17221
DDIT4L	NM_145244	chr4	-	101105025	101113656	1342	1200	7.164355
PARP15	NM_152615	chr3	+	122332523	122357537	495	349	7.15906
KCNS2	NM_020697	chr8	+	99437248	99445024	2207	1918	7.151235
MCM9	NM_153255	chr6	-	119229760	119258304	1303	1205	7.131725
ARHGDIG	NM_001176	chr16	+	328604	335004	6025	5984	7.1145
SOX14	NM_004189	chr3	+	137481577	137486397	1213	853	7.104185
UGT2B15	NM_001076	chr4	-	69510313	69538375	51	0	7.08356
PPP4R4	NM_058237	chr14	+	94638647	94748073	3540	3307	7.0661775
SDR9C7	NM_148897	chr12	-	57314936	57330190	329	227	7.060185
ZNF80	NM_007136	chr3	-	113951478	113958426	47	0	7.05912
LRRC66	NM_001024611	chr4	-	52857864	52885787	245	0	7.04454
C12orf39	NM_030572	chr12	+	21677254	21686211	1005	849	7.034685
RASGEF1B	NM_152545	chr4	-	82346217	82395062	3609	1691	7.01997
BHLHE41	NM_030762	chr12	-	26270957	26280004	4559	4531	7.00431
DUSP21	NM_022076	chrX	+	44701247	44706135	617	573	6.99094

RDH16	NM_003708	chr12	-	57343214	57353419	641	569	6.970065
IBSP	NM_004967	chr4	+	88718700	88735602	83	0	6.967165
SPOCK3	NM_016950	chr4	-	167652534	168157742	2719	1832	6.936455
MAGEL2	NM_019066	chr15	-	23886694	23894994	2348	1363	6.918345
IL1F5	NM_173170	chr2	+	113814213	113824321	444	0	6.91387
CXCL9	NM_002416	chr4	-	76920621	76930642	381	222	6.912545
COL21A1	NM_030820	chr6	-	55919386	56114379	2189	1666	6.88939
SNTG2	NM_018968	chr2	+	944552	1373385	7920	7428	6.87619
DSCAM	NM_001389	chr21	-	41382341	42221040	6839	2801	6.86484
IL1F9	NM_019618	chr2	+	113733604	113745228	71	0	6.861105
DMRT3	NM_021240	chr9	+	974962	993733	3006	2762	6.85526
UGT2B17	NM_001077	chr4	-	69400901	69436246	159	0	6.844095
ACTL7A	NM_006687	chr9	+	111622601	111628036	487	381	6.838355
SLN	NM_003063	chr11	-	107576099	107584788	142	98	6.8363
ACTBL2	NM_001017992	chr5	-	56773841	56780637	120	95	6.83282
AMPD1	NM_001172626	chr1	-	115213718	115240240	472	265	6.828385
SOSTDC1	NM_015464	chr7	-	16499104	16507475	213	0	6.827585
CCDC67	NM_181645	chr11	+	93061881	93173637	1038	457	6.81278
SPRR4	NM_173080	chr1	+	152941126	152947070	312	0	6.808745
MT1B	NM_005947	chr16	+	56683809	56689117	648	522	6.803505
HHLA2	NM_007072	chr3	+	108019330	108099127	562	535	6.7911
RBMXL3	NM_001145346	chrX	+	114421961	114429432	231	0	6.786725
SCN2B	NM_004588	chr11	-	118031517	118049338	3724	3360	6.78128
NOS1	NM_000620	chr12	-	117646775	117801608	6898	5956	6.761075

FREM2	NM_207361	chr13	+	39259171	39463268	1145	546	6.75432
RBFOX1	NM_145893	chr16	+	7380749	7765341	1811	1027	6.7518775
KRT1	NM_006121	chr12	-	53066518	53076192	478	212	6.74943
AMIGO3	NM_198722	chr3	-	49752265	49759239	2041	1760	6.749085
CNGA4	NM_001037329	chr11	+	6258328	6267708	190	0	6.74636
KIR2DL4	NM_002255	chr19	+	55313065	55327973	132	0	6.72467
KBTBD8	NM_032505	chr3	+	67046725	67063633	1436	1299	6.69751
C2orf71	NM_001029883	chr2	-	29282556	29299128	2793	1670	6.682395
KRT32	NM_002278	chr17	-	39613763	39625639	778	747	6.667765
CALCB	NM_000728	chr11	+	15093144	15102178	1214	1058	6.654455
TSSK2	NM_053006	chr22	+	19116319	19122137	1496	163	6.63054
DNASE2B	NM_058248	chr1	+	84872032	84882692	269	194	6.624435
TAS2R14	NM_023922	chr12	-	11088851	11093807	239	222	6.62417
H1FNT	NM_181788	chr12	+	48720761	48726063	490	0	6.609765
XAGE3	NM_133179	chrX	-	52889556	52899120	62	0	6.59945
C1QTNF7	NM_031911	chr4	+	15427627	15449792	377	121	6.59393
HS6ST3	NM_153456	chr13	+	96741091	97493813	3635	3563	6.59356
C1orf49	NM_032126	chr1	+	178480210	178493790	657	628	6.59318
DSEL	NM_032160	chr18	-	65171817	65185968	1691	1543	6.58966
IFT57	NM_018010	chr3	-	107877657	107943418	823	815	6.588315
OR1N2	NM_001004457	chr9	+	125313447	125318442	76	0	6.563205
IGSF11	NM_152538	chr3	-	118617477	118866899	2331	2237	6.56115
PIWIL1	NM_004764	chr12	+	130820431	130858878	2323	1504	6.560385
EFCAB6	NM_198856	chr22	-	43922622	44210218	6326	4595	6.55535

FGF9	NM_002010	chr13	+	22243213	22280641	7442	7340	6.54429
TSSK1B	NM_032028	chr5	-	112766249	112772729	388	59	6.529985
UNC45B	NM_173167	chr17	+	33472834	33518365	3793	3227	6.522525
PPP3R2	NM_147180	chr9	-	104351895	104359284	625	43	6.52028
DUXA	NM_001012729	chr19	-	57661092	57680857	115	0	6.510855
HTR1B	NM_000863	chr6	-	78169946	78175121	1020	391	6.499335
KCTD4	NM_198404	chr13	-	45764986	45777176	272	0	6.497035
REN	NM_000537	chr1	-	204121942	204137466	2025	1794	6.47526
MAGEE2	NM_138703	chrX	-	75000821	75007080	190	38	6.45914
SCGN	NM_006998	chr6	+	25650427	25704009	1368	1178	6.45038
OPRM1	NM_001145287	chr6	+	154405640	154442595	796	0	6.4375425
ZNF257	NM_033468	chr19	+	22233264	22275904	395	392	6.435435
ZAR1	NM_175619	chr4	+	48490307	48498423	2309	2027	6.43152
NECAB1	NM_022351	chr8	+	91801919	91973631	614	503	6.43013
CALCRL	NM_005795	chr2	-	188205847	188315022	778	723	6.41602
APLF	NM_173545	chr2	+	68692689	68809295	1579	1218	6.401225
ARSF	NM_004042	chrX	+	2982851	3032748	559	465	6.400815
SLITRK5	NM_015567	chr13	+	88322868	88333871	3011	2835	6.39942
IQCF1	NM_152397	chr3	-	51926890	51939387	549	0	6.38671
GRXCR1	NM_001080476	chr4	+	42893281	43034674	389	206	6.37243
OR7A10	NM_001005190	chr19	-	14949758	14954690	140	0	6.36118
IRAK1BP1	NM_001010844	chr6	+	79575187	79610321	1150	1104	6.357615
IL21	NM_021803	chr4	-	123531781	123544212	189	0	6.33611
LANCL3	NM_198511	chrX	+	37428820	37538751	3507	3363	6.334715

C2orf51	NM_152670	chr2	+	88822167	88831104	194	186	6.334415
LOC154872	NM_001024603	chr7	-	124415344	124432865	553	514	6.327125
ANKRD7	NM_019644	chr7	+	117862710	117884785	227	0	6.32234
CWH43	NM_025087	chr4	+	48986263	49066096	1020	581	6.313845
SORCS3	NM_014978	chr10	+	106398857	107026994	4582	3992	6.30426
C10orf96	NM_198515	chr10	+	118081938	118141542	275	0	6.304025
CHRNA9	NM_017581	chr4	+	40335467	40358974	1357	1302	6.2979
GPLD1	NM_177483	chr6	-	24471324	24491800	447	444	6.29129
CSMD1	NM_033225	chr8	-	2790873	4854329	6919	4156	6.28079
DEFB125	NM_153325	chr20	+	66349	79297	321	0	6.260385
AADAC	NM_001086	chr3	+	151529859	151548277	473	336	6.247835
ADAMTS20	NM_025003	chr12	-	43746010	43947725	965	869	6.244205
PCDHAC2	NM_031883	chr5	+	140344350	140351007	835	583	6.244135
CYP39A1	NM_016593	chr6	-	46515443	46622524	1770	1367	6.24118
CST8	NM_005492	chr20	+	23469764	23478656	136	0	6.21506
CRISPLD1	NM_031461	chr8	+	75894706	75948794	1280	757	6.207585
APOL5	NM_030642	chr22	+	36111917	36127530	706	125	6.1961
EGR3	NM_004430	chr8	-	22543172	22552816	5765	5608	6.168005
LRIT3	NM_198506	chr4	+	110770484	110795472	232	0	6.16
SLC22A14	NM_004803	chr3	+	38345443	38361860	321	96	6.127885
RASSF10	NM_001080521	chr11	+	13028968	13035654	3171	3141	6.118145
DYNLRB2	NM_130897	chr16	+	80572852	80586542	1180	953	6.110545
DPY19L2	NM_173812	chr12	-	63950691	64064355	162	0	6.107365
OR13F1	NM_001004485	chr9	+	107264542	107269504	413	0	6.101825

LYG2	NM_175735	chr2	-	99856709	99873571	339	0	6.099285
ABHD13	NM_032859	chr13	+	108868761	108888604	1243	1168	6.09743
C17orf77	NM_152460	chr17	+	72579055	72592349	160	118	6.07561
PCDHGA9	NM_032089	chr5	+	140780518	140787007	675	663	6.049475
ZP4	NM_021186	chr1	-	238039162	238056223	1046	241	6.037375
PAGE2	NM_207339	chrX	+	55113495	55121261	138	129	6.03717
C16orf82	NM_001145545	chr16	+	27076217	27082488	143	70	6.01739
GAB4	NM_001037814	chr22	-	17440825	17491113	112	0	6.0145225
RSAD2	NM_080657	chr2	+	7015794	7040364	528	476	6.004325
OR56A5	NM_001146033	chr11	-	5986781	5991725	322	0	6.00399
SERPINB12	NM_080474	chr18	+	61221391	61236245	93	0	5.97628
GPR111	NM_153839	chr6	+	47622324	47667534	1997	1297	5.9745
ZNF345	NM_003419	chr19	+	37339265	37372471	1765	1527	5.969525
CLDN17	NM_012131	chr21	-	31536239	31540972	473	0	5.954885
SMC1B	NM_148674	chr22	-	45737943	45811501	1969	1364	5.932555
RBM11	NM_144770	chr21	+	15586464	15602694	637	369	5.92598
KCNH8	NM_144633	chr3	+	19188015	19579136	2483	2330	5.92406
DSC1	NM_024421	chr18	-	28707212	28744820	842	0	5.92287
SEMG2	NM_003008	chr20	+	43848008	43855100	158	0	5.9145
SCGB2A1	NM_002407	chr11	+	61974138	61983412	243	125	5.913205
DYDC1	NM_138812	chr10	-	82093860	82118501	2132	325	5.902485
TRPM3	NM_206948	chr9	-	73396776	73485975	527	297	5.893175
STK31	NM_032944	chr7	+	23747995	23874128	1334	1231	5.88677
IGFL2	NM_001135113	chr19	+	46649498	46666562	90	0	5.883935

OR9A4	NM_001001656	chr7	+	141616674	141621621	257	0	5.88003
MOS	NM_005372	chr8	-	57023499	57028542	830	685	5.87645
PLA2G3	NM_015715	chr22	-	31528791	31538470	1131	1129	5.84243
ALB	NM_000477	chr4	+	74267970	74289130	85	34	5.837035
NPFFR2	NM_053036	chr4	+	72902847	73015919	374	335	5.82842
ARSH	NM_001011719	chrX	+	2922652	2953427	615	177	5.821465
KRT71	NM_033448	chr12	-	52935691	52948932	1294	886	5.817405
ZNF582	NM_144690	chr19	-	56892646	56906890	1356	902	5.78686
SERPINA9	NM_175739	chr14	-	94927056	94944671	742	685	5.778815
UGT2B7	NM_001074	chr4	+	69960191	69980706	455	0	5.777145
HEPHL1	NM_001098672	chr11	+	93752376	93849375	972	300	5.771325
CRYGD	NM_006891	chr2	-	208984329	208991314	258	118	5.75637
TET2	NM_017628	chr4	+	106065941	106165929	3522	3425	5.753995
HRG	NM_000412	chr3	+	186381796	186398024	307	161	5.74779
MAEL	NM_032858	chr1	+	166956517	166993448	144	0	5.741415
MUM1L1	NM_152423	chrX	+	105410296	105454950	555	0	5.728975
PIK3C2G	NM_004570	chr12	+	18412472	18803353	2459	2147	5.719945
ZPLD1	NM_175056	chr3	+	102151857	102200686	356	314	5.713835
AGBL1	NM_152336	chr15	+	86683240	87574284	5958	2841	5.703565
ELAVL2	NM_004432	chr9	-	23688101	23828064	2672	1916	5.700865
C10orf140	NM_207371	chr10	-	21800407	21816612	4461	4278	5.693865
NOX4	NM_016931	chr11	-	89055520	89226654	1411	1047	5.69181
LRAT	NM_004744	chr4	+	155663161	155676271	1262	701	5.67938
TFAP2B	NM_003221	chr6	+	50784437	50817327	2883	1597	5.67887

BTG4	NM_017589	chr11	-	111336254	111385065	1579	1250	5.665735
HS3ST2	NM_006043	chr16	+	22823858	22929660	2561	2279	5.66503
SCN9A	NM_002977	chr2	-	167049695	167234498	2222	1821	5.659625
CST5	NM_001900	chr20	-	23854570	23862381	832	677	5.657185
OR2C3	NM_198074	chr1	-	247691432	247699142	664	68	5.6545
CDH12	NM_004061	chr5	-	21748971	22855732	3118	2776	5.65222
CST11	NM_130794	chr20	-	23429039	23435483	205	73	5.651845
ASCL4	NM_203436	chr12	+	108166160	108172422	698	350	5.648305
KCNC2	NM_153748	chr12	-	75431894	75605512	1271	836	5.637091667
OR1D5	NM_014566	chr17	-	2963961	2968902	183	0	5.616735
PON3	NM_000940	chr7	-	94987182	95027688	1087	1087	5.61358
AVPR1B	NM_000707	chr1	+	206222281	206233483	1693	1594	5.603695
TMEM207	NM_207316	chr3	-	190144442	190169666	386	223	5.591435
FAM184A	NM_024581	chr6	-	119278994	119401813	1738	1611	5.58763
BTBD8	NM_183242	chr1	+	92543860	92615402	1246	1110	5.57481
PTH	NM_000315	chr11	-	13511599	13519568	140	0	5.573965
RFX6	NM_173560	chr6	+	117196374	117255327	1204	1053	5.551085
C4orf39	NM_153027	chr4	+	165876098	165882274	1131	821	5.541275
RNF17	NM_031277	chr13	+	25336299	25456059	698	234	5.53185
LMO3	NM_018640	chr12	-	16699305	16761432	1067	936	5.522015
PHYHIPL	NM_032439	chr10	+	60934346	61009535	2075	2027	5.503185
CD3D	NM_001040651	chr11	-	118207787	118215460	452	379	5.502795
KRT27	NM_181537	chr17	-	38931058	38940787	336	267	5.489855
SLC7A3	NM_032803	chrX	-	70143428	70152976	593	120	5.488075

CDH18	NM_004934	chr5	-	19471153	19990354	1307	617	5.482075
POM121L2	NM_033482	chr6	-	27274840	27282012	1113	1007	5.480885
SYCP2	NM_014258	chr20	-	58436616	58509210	820	776	5.469715
KCNMB2	NM_181361	chr3	+	178252222	178564218	2549	2212	5.449785
IL3	NM_000588	chr5	+	131394345	131400897	1434	1149	5.4478
SRD5A2	NM_000348	chr2	-	31747654	31808041	1567	659	5.44109
RGPD4	NM_182588	chr2	+	108441386	108511001	102	0	5.435795
TMPRSS11A	NM_182606	chr4	-	68774017	68831233	540	408	5.43044
ABRA	NM_139166	chr8	-	107769709	107784473	685	681	5.42522
MPPED2	NM_001584	chr11	-	30429616	30604041	486	403	5.406955
KHDRBS2	NM_152688	chr6	-	62387863	62998101	870	837	5.40383
C2orf40	NM_032411	chr2	+	106680111	106696610	63	0	5.403615
TEDDM1	NM_172000	chr1	-	182365250	182371752	714	406	5.401435
KRTAP4-11	NM_033059	chr17	-	39271432	39276607	176	0	5.39603
GPR101	NM_054021	chrX	-	136110305	136115834	1357	1038	5.385405
ZNF486	NM_052852	chr19	+	20276081	20310985	1509	1227	5.384355
DAOA	NM_172370	chr13	+	106116362	106145384	265	0	5.37897
LINGO2	NM_152570	chr9	-	27946526	28721304	1643	1261	5.36444
AQP4	NM_004028	chr18	-	24430006	24444576	652	480	5.35759
NMUR2	NM_020167	chr5	-	151769100	151786841	245	159	5.35315
LPHN3	NM_015236	chr4	+	62360837	62940169	1666	1264	5.347195
HIST1H2BJ	NM_021058	chr6	-	27098093	27102576	1116	1078	5.340975
KLRC1	NM_213658	chr12	-	10596636	10609216	258	0	5.336833333
TMPRSS12	NM_182559	chr12	+	51234699	51283664	933	568	5.33561

RP1	NM_006269	chr8	+	55526625	55545395	915	706	5.325195
GPR12	NM_005288	chr13	-	27327337	27336923	1634	1578	5.306065
NAT2	NM_000015	chr8	+	18246753	18260724	394	122	5.289635
OR7A5	NM_017506	chr19	-	14935137	14941277	95	0	5.282815
ADAM7	NM_003817	chr8	+	24296507	24368276	497	449	5.278945
GUCA1C	NM_005459	chr3	-	108624640	108674678	688	457	5.27306
GABRA5	NM_001165037	chr15	+	27110271	27196358	4279	3410	5.265305
KLRC3	NM_007333	chr12	-	10566181	10575195	423	192	5.26202
TTC29	NM_031956	chr4	-	147626177	147869035	808	533	5.2574
CA3	NM_005181	chr8	+	86349054	86363268	72	0	5.254765
LCE1B	NM_178349	chr1	+	152782445	152787586	367	0	5.246285
NPHP3	NM_153240	chr3	-	132397452	132443277	1742	1728	5.22285
MC2R	NM_000529	chr18	-	13880041	13917536	1455	1239	5.203155
KLB	NM_175737	chr4	+	39406471	39455154	1202	1182	5.179405
EPHA3	NM_182644	chr3	+	89154672	89451496	2418	1609	5.1720975
SPINK6	NM_205841	chr5	+	147580355	147596701	301	0	5.16761
NT5C1B	NM_033253	chr2	-	18742135	18772839	448	244	5.138775
XK	NM_021083	chrX	+	37543131	37593384	1598	1298	5.124365
C7	NM_000587	chr5	+	40907597	40985043	263	0	5.12205
LPL	NM_000237	chr8	+	19794580	19826771	1106	1016	5.120795
SLC26A7	NM_134266	chr8	+	92259514	92408947	1450	1178	5.117265
TEX15	NM_031271	chr8	-	30687058	30708534	110	0	5.111785
DYDC2	NM_032372	chr10	+	82114556	82129830	1664	325	5.103495
EPHA7	NM_004440	chr6	-	93947738	94131301	3320	2591	5.10189

C10orf113	NM_001177483	chr10	-	21412690	21437489	273	0	5.08054
BAI3	NM_001704	chr6	+	69343630	70101404	2907	2621	5.075795
HIST1H2AG	NM_021064	chr6	+	27098815	27103315	1116	1078	5.07573
RPE65	NM_000329	chr1	-	68892505	68917643	435	337	5.0523
TLL1	NM_012464	chr4	+	166792408	167026994	4508	3824	5.040215
KRTAP2-4	NM_033184	chr17	-	39219366	39224132	500	285	5.036965
WIF1	NM_007191	chr12	-	65442402	65517347	452	324	5.033465
KLRK1	NM_007360	chr12	-	10522950	10544641	217	45	5.032745
ADAMTS19	NM_133638	chr5	+	128794101	129076377	2950	2490	5.032245
OR2H1	NM_030883	chr6	+	29424228	29434100	207	0	5.0322
KCNV1	NM_014379	chr8	-	110977231	110988960	924	318	5.02032
ART3	NM_001179	chr4	+	76993861	77035956	1215	879	5.018255
SPAM1	NM_153189	chr7	+	123563284	123602101	315	0	5.0166325
PRSS54	NM_001080492	chr16	-	58311899	58330952	1265	117	5.008025
FGL1	NM_201553	chr8	-	17719898	17754914	466	336	4.9983375
SCN3A	NM_006922	chr2	-	165942028	166062578	227	0	4.997805
SLC5A7	NM_021815	chr2	+	108600993	108632444	186	0	4.990015
CALCR	NM_001742	chr7	-	93051797	93206043	1435	1197	4.984715
ST8SIA4	NM_175052	chr5	-	100219013	100240971	762	674	4.9830375
POTEC	NM_001137671	chr18	-	14509735	14545600	44	0	4.98231
CENPC1	NM_001812	chr4	-	68335987	68413257	1022	890	4.969985
LHX8	NM_001001933	chr1	+	75592117	75629219	692	578	4.96153
CA1	NM_001738	chr8	-	86238456	86292343	412	238	4.93995
SLC17A6	NM_020346	chr11	+	22357665	22403047	292	161	4.922945

MAGEA4	NM_002362	chrX	+	151082707	151095643	605	378	4.91411
SOST	NM_025237	chr17	-	41829097	41838157	3186	2541	4.906105
PLCZ1	NM_033123	chr12	-	18834114	18892919	1018	906	4.90241
DEFB110	NM_001037728	chr6	-	49974849	49991695	97	0	4.90197
GPR149	NM_001038705	chr3	-	154053459	154149505	344	185	4.88907
HHIP	NM_022475	chr4	+	145565171	145661882	2111	1102	4.88151
SYNPR	NM_144642	chr3	+	63426751	63604598	628	451	4.851435
POU3F2	NM_005604	chr6	+	99280578	99288667	3929	3923	4.818575
LRRC3B	NM_052953	chr3	+	26662298	26754266	1648	1162	4.808025
AMIGO2	NM_181847	chr12	-	47467488	47475735	2531	2438	4.80576
CLGN	NM_004362	chr4	-	141307605	141350816	1470	1437	4.803665
SMCP	NM_030663	chr1	+	152848796	152859524	1130	777	4.803345
GZMB	NM_004131	chr14	-	25098159	25105433	487	0	4.77329
C14orf39	NM_174978	chr14	-	60900672	60954765	816	0	4.770665
CLEC5A	NM_013252	chr7	-	141625155	141648784	339	0	4.764725
SLC10A2	NM_000452	chr13	-	103694346	103721197	449	140	4.76383
SCN2A	NM_021007	chr2	+	166148339	166250821	924	692	4.74905
HRNR	NM_001009931	chr1	-	152182556	152198670	575	0	4.739165
ICOS	NM_012092	chr2	+	204799469	204828299	541	85	4.73868
CXorf22	NM_152632	chrX	+	35935849	36010270	653	0	4.700705
MAGEC2	NM_016249	chrX	-	141288126	141295077	261	182	4.67852
PGR	NM_000926	chr11	-	100898353	101002545	2457	1971	4.63997
OXGR1	NM_080818	chr13	-	97635971	97648605	760	441	4.63972
DIRAS2	NM_017594	chr9	-	93370112	93407109	561	421	4.553535

HMGCLL1	NM_019036	chr6	-	55297169	55446013	680	642	4.50821
SYT10	NM_198992	chr12	-	33526346	33594755	1199	1069	4.455865
UNC13C	NM_001080534	chr15	+	54303099	54922807	1064	781	4.35839
FGF20	NM_019851	chr8	-	16848332	16861675	1245	1111	4.305195
C1orf68	NM_001024679	chr1	+	152689996	152694906	389	0	
TSTD1	NM_001113207	chr1	-	161005420	161010775	1126	937	
LOC642587	NM_001104548	chr1	+	209600166	209607893	1964	475	
RGPD2	NM_001078170	chr2	-	88054716	88127287	320	42	
RGPD6	NM_001123363	chr2	-	111269377	111338310	462	376	
PSAPL1	NM_001085382	chr4	-	7430019	7438701	3141	2332	
SERF1B	NM_022978	chr5	+	69319076	69340935	939	799	
FAM169A	NM_015566	chr5	-	74071397	74164616	2409	2369	
FAM153C	NM_001079527	chr5	+	177433687	177476657	306	0	
ZNF879	NM_001136116	chr5	+	178448774	178463389	828	806	
C6orf58	NM_001010905	chr6	+	127896317	127914961	364	194	
LOC389493	NM_001145712	chr7	-	56180372	56186091	625	259	
ZNF727	NM_001159522	chr7	+	63503819	63540928	438	383	
WEE2	NM_001105558	chr7	+	141406151	141433072	334	0	
LOC100127983	NM_001190972	chr8	-	91968704	91999486	1194	1157	
LRRC69	NM_001129890	chr8	+	92112845	92233465	857	789	
SCXA	NM_001008271	chr8	+	145488601	145494132	4847	4677	
ANKRD20A4	NM_001098805	chr9	+	69379979	69427110	131	67	
KRTAP5-5	NM_001001480	chr11	+	1649031	1654160	731	698	

LOC283299	NM_001190788	chr11	-	7870296	7929503	1999	1959	
KLRF2	NM_001190765	chr12	+	10032086	10050433	229	0	
SLC15A5	NM_001170798	chr12	-	16339417	16432620	502	64	
C12orf71	NM_001080406	chr12	-	27231988	27237456	856	626	
SFTA3	NM_001101341	chr14	-	36940492	36984991	5891	4350	
CT62	NM_001102658	chr15	-	71400581	71409840	2780	2221	
GOLGA6C	NM_001164404	chr15	+	75548897	75567797	412	381	
LGALS9B	NM_001042685	chr17	-	20351174	20372849	2786	2017	
LOC730755	NM_001165252	chr17	-	39213491	39218345	1206	1040	
KRTAP4-7	NM_033061	chr17	+	39238457	39243397	723	516	
KRTAP4-8	NM_031960	chr17	-	39251232	39256376	529	68	
KRTAP4-9	NM_001146041	chr17	+	39259639	39264741	471	431	
LOC643008	NM_001162995	chr17	+	73627512	73639487	4925	4230	
FLJ22184	NM_001190467	chr19	-	7931603	7941327	5793	5734	
ZNF878	NM_001080404	chr19	-	12152618	12169128	1173	1029	
SRRM5	NM_001145641	chr19	+	44114251	44120651	151	65	
F8A3	NM_001007524	chrX	-	154685144	154690262	207	71	
H2AFB3	NM_080720	chrX	-	154687078	154691597	207	71	

Supplementary Table 2. Statistically over-represented ($p < 0.1$) processes from DAVID analysis when comparing a list of genes with HTE-selective DHS in their promoter to all human genes.

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0030855~epithelial cell differentiation	24	2.274881517	1.46E-06	727	136	13114	3.183267255	0.004005499	0.004005499	0.002603367
GOTERM_BP_FAT	GO:0060429~epithelium development	32	3.033175355	2.64E-06	727	226	13114	2.554125939	0.00722096	0.003617022	0.004700787
GOTERM_CC_FAT	GO:0044459~plasma membrane part	171	16.20853081	6.19E-06	713	2163	12337	1.367916619	0.002696242	0.002696242	0.008745068
KEGG_PATHWAY	hsa04080:Neuroactive ligand-receptor interaction	33	3.127962085	7.97E-06	280	255	5042	2.330336134	0.001354196	0.001354196	0.009724331
GOTERM_BP_FAT	GO:0007398~ectoderm development	28	2.654028436	9.69E-06	727	195	13114	2.590145664	0.026285225	0.008839651	0.017276612
GOTERM_BP_FAT	GO:0008544~epidermis development	26	2.464454976	2.14E-05	727	181	13114	2.591167821	0.057224832	0.014623879	0.03821622
GOTERM_CC_FAT	GO:0030054~cell junction	53	5.023696682	5.38E-05	713	515	12337	1.780691458	0.023169856	0.011652822	0.075906008
GOTERM_CC_FAT	GO:0016327~apicolateral plasma membrane	18	1.706161137	6.02E-05	713	101	12337	3.083693222	0.025891017	0.008705912	0.084934776
GOTERM_BP_FAT	GO:0009913~epidermal cell differentiation	14	1.327014218	1.21E-04	727	71	13114	3.556890172	0.28385072	0.064592793	0.216329602
GOTERM_CC_FAT	GO:0043296~apical junction complex	17	1.611374408	1.43E-04	713	98	12337	3.001531328	0.060337434	0.0154382	0.201386465
GOTERM_BP_FAT	GO:0030216~keratinocyte differentiation	13	1.232227488	2.03E-04	727	65	13114	3.607702889	0.427357777	0.088729675	0.360967749
GOTERM_CC_FAT	GO:0005911~cell-cell junction	25	2.369668246	2.08E-04	713	188	12337	2.300923577	0.086641139	0.017962009	0.293126235
SP_PIR_KEYWORDS	cell junction	41	3.886255924	3.19E-04	1037	398	18289	1.81682036	0.160161888	0.160161888	0.464234149
GOTERM_CC_FAT	GO:0005576~extracellular region	144	13.6492891	3.76E-04	713	1906	12337	1.30725295	0.151081616	0.026929463	0.529150101
UP_SEQ_FEATURE	site:Stutter	9	0.853080569	4.06E-04	1037	33	18267	4.804155343	0.658523769	0.658523769	0.717671921

GOTERM_CC_FAT	GO:0031226~intrinsic to plasma membrane	98	9.289099526	4.08E-04	713	1207	12337	1.40487874	0.162856376	0.025074511	0.574143656
SP_PIR_KEYWORDS	palmoplantar keratoderma	7	0.663507109	4.67E-04	1037	19	18289	6.497639953	0.225299988	0.119829555	0.67822803
SP_PIR_KEYWORDS	Secreted	125	11.84834123	5.23E-04	1037	1643	18289	1.341787226	0.24889175	0.090992407	0.760079664
SP_PIR_KEYWORDS	signal	219	20.75829384	6.87E-04	1037	3158	18289	1.22304713	0.31341799	0.089723974	0.997433532
UP_SEQ_FEATURE	signal peptide	219	20.75829384	7.52E-04	1037	3158	18267	1.221575915	0.863642101	0.630733296	1.326743814
SP_PIR_KEYWORDS	disease mutation	119	11.27962085	0.001051223	1037	1580	18289	1.328315003	0.437475853	0.108691119	1.522022576
SP_PIR_KEYWORDS	glycoprotein	281	26.63507109	0.001054227	1037	4209	18289	1.177439491	0.438400461	0.091682272	1.52634115
GOTERM_CC_FAT	GO:0001533~cornified envelope	7	0.663507109	0.001216105	713	22	12337	5.505482596	0.411715488	0.064166846	1.703855019
SP_PIR_KEYWORDS	developmental protein	65	6.161137441	0.001380506	1037	771	18289	1.486860356	0.530298904	0.102328643	1.994323298
PIR_SUPERFAMILY	PIRSF002282:cytoskeletal keratin	11	1.042654028	0.001442185	397	60	7196	3.32308984	0.449812067	0.449812067	2.002767843
GOTERM_CC_FAT	GO:0005887~integral to plasma membrane	93	8.815165877	0.001572016	713	1180	12337	1.363706706	0.496382557	0.073383382	2.197386278
SP_PIR_KEYWORDS	nitration	7	0.663507109	0.001814657	1037	24	18289	5.143964963	0.629728686	0.116787904	2.613813232
GOTERM_BP_FAT	GO:0051896~regulation of protein kinase B signaling cascade	6	0.568720379	0.001816546	727	17	13114	6.366534509	0.993250093	0.510334297	3.190126329
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	267	25.30805687	0.002209801	1037	4021	18267	1.16967622	0.997149444	0.858210779	3.852165983
GOTERM_BP_FAT	GO:0051897~positive regulation of protein kinase B signaling cascade	5	0.473933649	0.002247701	727	11	13114	8.199324747	0.99794172	0.538482619	3.933063974
UP_SEQ_FEATURE	region of interest:Head	12	1.137440758	0.002323703	1037	72	18267	2.93587271	0.997893344	0.785761057	4.046877047

UP_SEQ_FEATURE	region of interest:Coil 2	11	1.042654028	0.002713556	1037	63	18267	3.075676172	0.999251905	0.762976553	4.710501877
UP_SEQ_FEATURE	region of interest:Linker 12	11	1.042654028	0.002713556	1037	63	18267	3.075676172	0.999251905	0.762976553	4.710501877
GOTERM_MF_FAT	GO:0005200~structural constituent of cytoskeleton	12	1.137440758	0.002787479	710	74	12549	2.866159117	0.913052424	0.913052424	4.242568408
UP_SEQ_FEATURE	region of interest:Tail	12	1.137440758	0.002899686	1037	74	18267	2.856524799	0.99954373	0.72253792	5.02581011
SP_PIR_KEYWORDS	gamma-carboxyglutamic acid	6	0.568720379	0.003447649	1037	19	18289	5.569405674	0.848795551	0.189336709	4.911419817
INTERPRO	IPR013090:Phospholipase A2, active site	6	0.568720379	0.003793547	933	19	16090	5.445929937	0.993742753	0.993742753	6.036205713
INTERPRO	IPR002383:Coagulation factor, Gla region	5	0.473933649	0.003805587	933	12	16090	7.185602001	0.993842902	0.921532825	6.054806937
UP_SEQ_FEATURE	sequence variant	710	67.2985782	0.004123719	1037	11801	18267	1.059809994	0.999982377	0.79065246	7.074954672
GOTERM_CC_FAT	GO:0044463~cell projection part	25	2.369668246	0.004212465	713	233	12337	1.856539195	0.841264163	0.168106945	5.787549548
SP_PIR_KEYWORDS	polymorphism	684	64.83412322	0.004401192	1037	11351	18289	1.06275506	0.91043274	0.214375663	6.229594075
GOTERM_CC_FAT	GO:0030057~desmosome	6	0.568720379	0.004735836	713	20	12337	5.19088359	0.873780085	0.171515566	6.484462468
SP_PIR_KEYWORDS	rna editing	5	0.473933649	0.004847041	1037	13	18289	6.783250501	0.929896165	0.21464243	6.840076393
GOTERM_BP_FAT	GO:0051967~negative regulation of synaptic transmission, glutamatergic	4	0.379146919	0.00499941	727	7	13114	10.30772254	0.999998962	0.783653053	8.54933666
UP_SEQ_FEATURE	DNA-binding region:Homeobox	21	1.990521327	0.005085239	1037	188	18267	1.967659369	0.999998636	0.815138022	8.655292755
GOTERM_BP_FAT	GO:0007409~axonogenesis	21	1.990521327	0.005138489	727	193	13114	1.962739913	0.999999293	0.757368726	8.777004991
UP_SEQ_FEATURE	region of interest:Coil 1B	11	1.042654028	0.005318978	1037	69	18267	2.80822607	0.999999268	0.791898841	9.035611542

UP_SEQ_FEATURE	region of interest:Linker 1	11	1.042654028	0.005318978	1037	69	18267	2.80822607	0.999999268	0.791898841	9.035611542
UP_SEQ_FEATURE	region of interest:Coil 1A	11	1.042654028	0.005318978	1037	69	18267	2.80822607	0.999999268	0.791898841	9.035611542
SP_PIR_KEYWORDS	keratinization	8	0.758293839	0.005734595	1037	39	18289	3.6177336	0.956969754	0.230607729	8.044362213
UP_SEQ_FEATURE	region of interest:Rod	11	1.042654028	0.005898132	1037	70	18267	2.768108555	0.999999844	0.79133829	9.971529305
GOTERM_BP_FAT	GO:0048667~cell morphogenesis involved in neuron differentiation	22	2.085308057	0.005986791	727	209	13114	1.898790994	0.999999932	0.777014823	10.15410736
UP_SEQ_FEATURE	domain:Gla	5	0.473933649	0.006512656	1037	14	18267	6.291155807	0.99999997	0.792680765	10.95466674
GOTERM_BP_FAT	GO:0030182~neuron differentiation	38	3.601895735	0.006519489	727	437	13114	1.568566473	0.999999984	0.776511658	11.00881525
GOTERM_MF_FAT	GO:0008376~acetylgalactosaminyltransferase activity	7	0.663507109	0.006966675	710	31	12549	3.991049523	0.997795322	0.953046	10.28892686
INTERPRO	IPR000294:Gamma-carboxyglutamic acid-rich (GLA) domain	5	0.473933649	0.00701357	933	14	16090	6.159087429	0.999916953	0.956371082	10.8896597
GOTERM_BP_FAT	GO:0006811~ion transport	59	5.592417062	0.007214591	727	757	13114	1.405907995	0.999999998	0.783710729	12.11256067
GOTERM_CC_FAT	GO:0045095~keratin filament	12	1.137440758	0.00725275	713	82	12337	2.532138337	0.958152451	0.232392572	9.769534682
GOTERM_CC_FAT	GO:0031012~extracellular matrix	32	3.033175355	0.007343316	713	339	12337	1.633316371	0.959784359	0.219009468	9.885718341
GOTERM_BP_FAT	GO:0048812~neuron projection morphogenesis	22	2.085308057	0.00740054	727	213	13114	1.863132947	0.999999999	0.767427334	12.40562768
GOTERM_BP_FAT	GO:0031424~keratinization	8	0.758293839	0.007664321	727	42	13114	3.435907513	0.999999999	0.75586281	12.81978292
GOTERM_BP_FAT	GO:0001655~urogenital system development	14	1.327014218	0.007678747	727	110	13114	2.295810929	0.999999999	0.734036458	12.84237858
SMART	SM00069:GLA	5	0.473933649	0.007877233	530	14	8828	5.948787062	0.880849238	0.880849238	9.870368755

SP_PIR_KEYWORDS	cysteine proteinase inhibitor	4	0.379146919	0.008185894	1037	8	18289	8.818225651	0.98884772	0.292384716	11.29553046
GOTERM_CC_FAT	GO:0044421~extracellular region part	73	6.91943128	0.008709984	713	946	12337	1.335216709	0.977944384	0.238482405	11.62216719
INTERPRO	IPR003267:Small proline-rich	6	0.568720379	0.009058354	933	23	16090	4.498811687	0.999994701	0.952021462	13.84842768
GOTERM_BP_FAT	GO:0048858~cell projection morphogenesis	24	2.274881517	0.009254661	727	245	13114	1.76703815	1	0.777649686	15.27782783
SP_PIR_KEYWORDS	Intermediate filament	11	1.042654028	0.009489283	1037	75	18289	2.586679524	0.994567863	0.311011147	12.98030563
INTERPRO	IPR019412:Outer membrane protein, IML2, mitochondrial/Tetratricopeptide repeat protein 39	3	0.28436019	0.009667938	933	3	16090	17.2454448	0.99999767	0.925271862	14.71247737
UP_SEQ_FEATURE	compositionally biased region:Gly-rich	23	2.180094787	0.010052238	1037	227	18267	1.784803674	1	0.89249951	16.42305863
GOTERM_MF_FAT	GO:0001653~peptide receptor activity	14	1.327014218	0.010432536	710	112	12549	2.209330986	0.99989655	0.953056311	15.03031682
GOTERM_MF_FAT	GO:0008528~peptide receptor activity, G-protein coupled	14	1.327014218	0.010432536	710	112	12549	2.209330986	0.99989655	0.953056311	15.03031682
SP_PIR_KEYWORDS	ion transport	47	4.454976303	0.011249556	1037	574	18289	1.444099671	0.997946852	0.338045686	15.20837449
GOTERM_BP_FAT	GO:0006812~cation transport	44	4.170616114	0.012009923	727	545	13114	1.456320432	1	0.842019764	19.38224769
INTERPRO	IPR003117:cAMP-dependent protein kinase, regulatory subunit, type I/II alpha/beta	4	0.379146919	0.012504079	933	9	16090	7.664642134	0.999999949	0.939171579	18.62661972
SMART	SM00394:RIIa	4	0.379146919	0.01369332	530	9	8828	7.40293501	0.975496894	0.843465321	16.5716003
GOTERM_MF_FAT	GO:0004623~phospholipase A2 activity	6	0.568720379	0.013868552	710	26	12549	4.078764897	0.999995069	0.952876292	19.49861604
SP_PIR_KEYWORDS	G protein-coupled receptor	14	1.327014218	0.014177445	1037	116	18289	2.128537226	0.99959457	0.386245381	18.79703379
GOTERM_CC_FAT	GO:0005886~plasma	239	22.65402844	0.0145350	713	3663	12337	1.128966401	0.998311314	0.346613847	18.6804648

	membrane			84							
SP_PIR_KEYWORDS	heterotetramer	7	0.663507109	0.014736988	1037	36	18289	3.429309975	0.999702805	0.37979982	19.46654383
UP_SEQ_FEATURE	metal ion-binding site:Calcium; via carbonyl oxygen	7	0.663507109	0.014817581	1037	36	18267	3.425184828	1	0.952258793	23.28609384
PIR_SUPERFAMILY	PIRSF005670:polypeptide N-acetylgalactosaminyltransferase	4	0.379146919	0.014851306	397	10	7196	7.250377834	0.997959487	0.954827962	18.9209102
SP_PIR_KEYWORDS	calcium	61	5.781990521	0.014975299	1037	798	18289	1.348149786	0.999739639	0.367784275	19.75012684
GOTERM_BP_FAT	GO:0032990~cell part morphogenesis	24	2.274881517	0.015096869	727	256	13114	1.691110729	1	0.889300317	23.75760545
GOTERM_BP_FAT	GO:0031175~neuron projection development	24	2.274881517	0.015096869	727	256	13114	1.691110729	1	0.889300317	23.75760545
GOTERM_CC_FAT	GO:0031526~brush border membrane	6	0.568720379	0.015097171	713	26	12337	3.992987377	0.998683212	0.339352595	19.33307865
GOTERM_BP_FAT	GO:0007411~axon guidance	13	1.232227488	0.015107878	727	107	13114	2.191595213	1	0.87661232	23.7728007
INTERPRO	IPR012287:Homeodomain-related	23	2.180094787	0.015117071	933	231	16090	1.71707892	0.999999999	0.945254227	22.08292971
INTERPRO	IPR000832:GPCR, family 2, secretin-like	8	0.758293839	0.015847098	933	46	16090	2.999207792	0.999999999	0.930446718	23.02364005
GOTERM_MF_FAT	GO:0004653~polypeptide N-acetylgalactosaminyltransferase activity	5	0.473933649	0.016382764	710	18	12549	4.909624413	0.999999472	0.94446423	22.62782727
PIR_SUPERFAMILY	PIRSF000548:PK_regulatory	3	0.28436019	0.016830249	397	4	7196	13.59445844	0.999112431	0.903897627	21.17438518
PIR_SUPERFAMILY	PIRSF000548:cAMP-dependent protein kinase, regulatory subunit	3	0.28436019	0.016830249	397	4	7196	13.59445844	0.999112431	0.903897627	21.17438518
UP_SEQ_FEATURE	binding site:cAMP 1	3	0.28436019	0.017856969	1037	4	18267	13.21142719	1	0.966936496	27.38179624
UP_SEQ_FEATURE	region of interest:Dimerization and phosphorylation	3	0.28436019	0.017856969	1037	4	18267	13.21142719	1	0.966936496	27.38179624

UP_SEQ_FEATURE	binding site:cAMP 2	3	0.28436019	0.017856969	1037	4	18267	13.21142719	1	0.966936496	27.38179624
INTERPRO	IPR003302:Cornifin (SPRR)	3	0.28436019	0.018594409	933	4	16090	12.9340836	1	0.938217572	26.46909712
INTERPRO	IPR012198:cAMP-dependent protein kinase regulatory subunit	3	0.28436019	0.018594409	933	4	16090	12.9340836	1	0.938217572	26.46909712
UP_SEQ_FEATURE	domain:PDZ 3	6	0.568720379	0.019211701	1037	28	18267	3.774693484	1	0.967476766	29.14006853
UP_SEQ_FEATURE	topological domain:Cytoplasmic	213	20.18957346	0.019314786	1037	3287	18267	1.141480171	1	0.960406495	29.27220125
INTERPRO	IPR017970:Homeobox, conserved site	22	2.085308057	0.019404049	933	223	16090	1.70134433	1	0.926898255	27.45652086
SP_PIR_KEYWORDS	keratin	15	1.421800948	0.019710456	1037	134	18289	1.974229623	0.999981343	0.436236612	25.1955628
INTERPRO	IPR017983:GPCR, family 2, secretin-like, conserved site	8	0.758293839	0.019739257	933	48	16090	2.8742408	1	0.911041716	27.86167784
UP_SEQ_FEATURE	region of interest:Catalytic subdomain A	5	0.473933649	0.02012676	1037	19	18267	4.635588489	1	0.957921308	30.30488318
UP_SEQ_FEATURE	region of interest:Catalytic subdomain B	5	0.473933649	0.02012676	1037	19	18267	4.635588489	1	0.957921308	30.30488318
GOTERM_MF_FAT	GO:0030414~peptidase inhibitor activity	16	1.516587678	0.020134035	710	148	12549	1.910772745	0.999999981	0.948500087	27.085775
INTERPRO	IPR001356:Homeobox	22	2.085308057	0.020288726	933	224	16090	1.693749043	1	0.897749774	28.52121555
UP_SEQ_FEATURE	compositionally biased region:Ala-rich	16	1.516587678	0.020967497	1037	148	18267	1.904349866	1	0.955777694	31.35914154
GOTERM_BP_FAT	GO:0030001~metal ion transport	37	3.507109005	0.021775955	727	459	13114	1.454085042	1	0.943981391	32.46931445
GOTERM_CC_FAT	GO:0005923~tight junction	10	0.947867299	0.022169051	713	72	12337	2.403186847	0.999943114	0.437277126	27.13878682
GOTERM_CC_FAT	GO:0070160~occluding junction	10	0.947867299	0.022169051	713	72	12337	2.403186847	0.999943114	0.437277126	27.13878682

SP_PIR_KEYWORDS	Homeobox	22	2.085308057	0.022218899	1037	231	18289	1.679662029	0.999995406	0.459110157	27.93884032
GOTERM_BP_FAT	GO:0044259~multicellular organismal macromolecule metabolic process	6	0.568720379	0.023101122	727	30	13114	3.607702889	1	0.946090819	34.08210175
GOTERM_CC_FAT	GO:0042734~presynaptic membrane	6	0.568720379	0.023651947	713	29	12337	3.579919718	0.999970648	0.439982141	28.68386541
INTERPRO	IPR001478:PDZ/DHR/GLGF	16	1.516587678	0.024694696	933	148	16090	1.864372411	1	0.923295342	33.60875275
PIR_SUPERFAMILY	PIRSF005503:G protein-coupled receptor, peptide hormone receptor type	4	0.379146919	0.025087146	397	12	7196	6.041981528	0.99997297	0.927895907	29.96357956
GOTERM_BP_FAT	GO:0030198~extracellular matrix organization	12	1.137440758	0.025328544	727	102	13114	2.12217817	1	0.953407248	36.71134635
GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	46	4.360189573	0.025424625	710	592	12549	1.37336791	1	0.960012042	32.96588572
GOTERM_CC_FAT	GO:0005578~proteinaceous extracellular matrix	28	2.654028436	0.025782633	713	315	12337	1.538039582	0.999988677	0.450861349	30.85066051
PIR_SUPERFAMILY	PIRSF800007:secretin receptor-like G protein-coupled receptors	7	0.663507109	0.026120708	397	42	7196	3.020990764	0.999982577	0.888255827	30.99724981
INTERPRO	IPR000372:Leucine-rich repeat, cysteine-rich flanking region, N-terminal	12	1.137440758	0.026149021	933	98	16090	2.111687119	1	0.920075825	35.21200434
GOTERM_BP_FAT	GO:0015672~monovalent inorganic cation transport	27	2.559241706	0.026171529	727	314	13114	1.551082452	1	0.952052871	37.68033162
GOTERM_BP_FAT	GO:0015909~long-chain fatty acid transport	5	0.473933649	0.026250106	727	21	13114	4.294884391	1	0.94633654	37.76993595
GOTERM_MF_FAT	GO:0004866~endopeptidase inhibitor activity	15	1.421800948	0.026824589	710	140	12549	1.893712274	1	0.948901928	34.44588563
SP_PIR_KEYWORDS	epidermolysis bullosa	4	0.379146919	0.027138564	1037	12	18289	5.878817101	0.999999709	0.511621319	33.04906342
SMART	SM00389:HOX	22	2.085308057	0.027351229	530	224	8828	1.635916442	0.999424328	0.916812422	30.53988515
GOTERM_BP_FAT	GO:0042574~retinal metabolic	3	0.28436019	0.0273657	727	5	13114	10.82310867	1	0.946801772	39.02911395

	process			58							
GOTERM_BP_FAT	GO:0007598~blood coagulation, extrinsic pathway	3	0.28436019	0.027365758	727	5	13114	10.82310867	1	0.946801772	39.02911395
GOTERM_BP_FAT	GO:0043288~apocarotenoid metabolic process	3	0.28436019	0.027365758	727	5	13114	10.82310867	1	0.946801772	39.02911395
KEGG_PATHWAY	hsa04530:Tight junction	14	1.327014218	0.028242921	280	131	5042	1.924427481	0.992329721	0.912419869	29.49723129
GOTERM_MF_FAT	GO:0005509~calcium ion binding	66	6.255924171	0.028256754	710	910	12549	1.281897539	1	0.938378518	35.92825151
GOTERM_BP_FAT	GO:0042471~ear morphogenesis	9	0.853080569	0.0286161	727	66	13114	2.459797424	1	0.947975619	40.41171711
UP_SEQ_FEATURE	nucleotide phosphate-binding region:cAMP 2	3	0.28436019	0.028649357	1037	5	18267	10.56914176	1	0.982623869	40.31928304
UP_SEQ_FEATURE	nucleotide phosphate-binding region:cAMP 1	3	0.28436019	0.028649357	1037	5	18267	10.56914176	1	0.982623869	40.31928304
GOTERM_MF_FAT	GO:0042165~neurotransmitter binding	12	1.137440758	0.028818865	710	102	12549	2.07937034	1	0.922594684	36.50144833
GOTERM_BP_FAT	GO:0048568~embryonic organ development	17	1.611374408	0.029082378	727	172	13114	1.782876427	1	0.944845022	40.91970022
GOTERM_BP_FAT	GO:0007423~sensory organ development	21	1.990521327	0.029273114	727	229	13114	1.654186914	1	0.940173977	41.12631504
GOTERM_BP_FAT	GO:0000904~cell morphogenesis involved in differentiation	22	2.085308057	0.030080142	727	244	13114	1.626423433	1	0.939107778	41.99300746
INTERPRO	IPR000483:Cysteine-rich flanking region, C-terminal	11	1.042654028	0.030653081	933	88	16090	2.1556806	1	0.937388826	39.94973231
GOTERM_BP_FAT	GO:0051046~regulation of secretion	19	1.800947867	0.031427274	727	202	13114	1.696691953	1	0.941082756	43.41295999
SMART	SM00228:PDZ	16	1.516587678	0.031515278	530	148	8828	1.800713921	0.999818467	0.883924905	34.34752843
SMART	SM00013:LRRNT	12	1.137440758	0.03204817	530	98	8828	2.039584136	0.999843448	0.82664695	34.82063813
SP_PIR_KEYWOR	cleavage on pair of basic	24	2.274881517	0.032395	1037	269	18289	1.573512384	0.999999985	0.559036285	38.13481275

DS	residues										
GOTERM_MF_FAT	GO:0031420~alkali metal ion binding	21	1.990521327	0.032420239	710	227	12549	1.635099584	1	0.927314451	40.06153293
GOTERM_BP_FAT	GO:0048562~embryonic organ morphogenesis	14	1.327014218	0.032773934	727	133	13114	1.898790994	1	0.942883176	44.79957656
UP_SEQ_FEATURE	disulfide bond	176	16.68246445	0.033679725	1037	2715	18267	1.141908501	1	0.989302344	45.57572205
SP_PIR_KEYWORDS	synapse	20	1.895734597	0.033807238	1037	213	18289	1.656004817	0.999999993	0.558655501	39.43852201
GOTERM_BP_FAT	GO:0042472~inner ear morphogenesis	8	0.758293839	0.033972465	727	56	13114	2.576930635	1	0.943820182	46.00663527
GOTERM_MF_FAT	GO:0015267~channel activity	33	3.127962085	0.034249129	710	405	12549	1.440156495	1	0.921220332	41.79710835
GOTERM_BP_FAT	GO:0048598~embryonic morphogenesis	26	2.464454976	0.034283501	727	307	13114	1.527691777	1	0.940426962	46.31578824
GOTERM_BP_FAT	GO:0060341~regulation of cellular localization	22	2.085308057	0.03463656	727	248	13114	1.600190797	1	0.937255537	46.66468468
GOTERM_BP_FAT	GO:0030030~cell projection organization	30	2.843601896	0.034920432	727	368	13114	1.470531069	1	0.933744372	46.94365628
UP_SEQ_FEATURE	region of interest:Calmodulin-binding	8	0.758293839	0.034967653	1037	55	18267	2.562216183	1	0.988778074	46.84950112
GOTERM_MF_FAT	GO:0022803~passive transmembrane transporter activity	33	3.127962085	0.035326186	710	406	12549	1.436609311	1	0.911143987	42.79709302
GOTERM_BP_FAT	GO:0019932~second-messenger-mediated signaling	21	1.990521327	0.035612877	727	234	13114	1.61884104	1	0.932403878	47.61838184
GOTERM_BP_FAT	GO:0035270~endocrine system development	9	0.853080569	0.036111659	727	69	13114	2.35284971	1	0.930102793	48.09937212
GOTERM_BP_FAT	GO:0010518~positive regulation of phospholipase activity	9	0.853080569	0.036111659	727	69	13114	2.35284971	1	0.930102793	48.09937212
UP_SEQ_FEATURE	site:Reactive bond	7	0.663507109	0.036715758	1037	44	18267	2.80242395	1	0.988936595	48.53344632

UP_SEQ_FEATURE	topological domain:Extracellular	171	16.20853081	0.036989424	1037	2639	18267	1.14141925	1	0.986976589	48.79246601
SMART	SM00082:LRRCT	11	1.042654028	0.037035661	530	88	8828	2.082075472	0.999960993	0.815841895	39.09840092
UP_SEQ_FEATURE	short sequence motif:Selectivity filter	8	0.758293839	0.038084899	1037	56	18267	2.516462323	1	0.986236845	49.81704291
GOTERM_MF_FAT	GO:0004857~enzyme inhibitor activity	23	2.180094787	0.038088444	710	260	12549	1.563526544	1	0.911702913	45.28870726
GOTERM_CC_FAT	GO:0005882~intermediate filament	17	1.611374408	0.038390683	713	171	12337	1.720175849	0.999999961	0.574038009	42.47032225
GOTERM_BP_FAT	GO:0051047~positive regulation of secretion	12	1.137440758	0.038702167	727	109	13114	1.985891498	1	0.938097788	50.53115208
INTERPRO	IPR003091:Voltage-dependent potassium channel	6	0.568720379	0.039752946	933	33	16090	3.135535418	1	0.966109328	48.54662781
INTERPRO	IPR002190:MAGE protein	6	0.568720379	0.039752946	933	33	16090	3.135535418	1	0.966109328	48.54662781
GOTERM_BP_FAT	GO:0016331~morphogenesis of embryonic epithelium	8	0.758293839	0.040103655	727	58	13114	2.488070958	1	0.939970098	51.80152328
GOTERM_CC_FAT	GO:0005615~extracellular space	51	4.834123223	0.040397146	713	675	12337	1.307333645	0.999999984	0.57519847	44.14261286
SP_PIR_KEYWORDS	disulfide bond	181	17.1563981	0.040877281	1037	2819	18289	1.13238655	1	0.613737705	45.58922179
GOTERM_BP_FAT	GO:0030802~regulation of cyclic nucleotide biosynthetic process	12	1.137440758	0.040950301	727	110	13114	1.967837939	1	0.939400534	52.55397415
GOTERM_BP_FAT	GO:0030808~regulation of nucleotide biosynthetic process	12	1.137440758	0.040950301	727	110	13114	1.967837939	1	0.939400534	52.55397415
GOTERM_MF_FAT	GO:0019206~nucleoside kinase activity	4	0.379146919	0.040981923	710	14	12549	5.049899396	1	0.912924439	47.7895533
SP_PIR_KEYWORDS	neurotransmitter receptor	8	0.758293839	0.04115347	1037	57	18289	2.475291411	1	0.601277886	45.81725248
SP_PIR_KEYWORDS	voltage-gated ion channel	3	0.28436019	0.041284193	1037	6	18289	8.818225651	1	0.588107948	45.92487034

UP_SEQ_FEATURE	domain:P-type	3	0.28436019	0.041376007	1037	6	18267	8.807618129	1	0.988638039	52.78003967
GOTERM_BP_FAT	GO:0007610~behavior	36	3.412322275	0.041778455	727	467	13114	1.390549293	1	0.938778906	53.27925217
GOTERM_BP_FAT	GO:0010517~regulation of phospholipase activity	9	0.853080569	0.041783647	727	71	13114	2.286572253	1	0.93469262	53.2837657
INTERPRO	IPR002373:cAMP/cGMP-dependent protein kinase	3	0.28436019	0.043015138	933	6	16090	8.622722401	1	0.9683418	51.33643093
GOTERM_CC_FAT	GO:0005903~brush border	7	0.663507109	0.043310807	713	45	12337	2.691569269	0.999999996	0.584172154	46.49072859
GOTERM_MF_FAT	GO:0004620~phospholipase activity	10	0.947867299	0.044058166	710	83	12549	2.129475649	1	0.914916397	50.33081632
INTERPRO	IPR016044:Filament	9	0.853080569	0.045307366	933	69	16090	2.249405844	1	0.967896807	53.21107132
GOTERM_CC_FAT	GO:0045111~intermediate filament cytoskeleton	17	1.611374408	0.045849461	713	175	12337	1.680857544	0.999999999	0.589221861	48.46151238
GOTERM_MF_FAT	GO:0005254~chloride channel activity	9	0.853080569	0.046158353	710	71	12549	2.240448324	1	0.91217218	51.9987765
GOTERM_BP_FAT	GO:0044243~multicellular organismal catabolic process	5	0.473933649	0.046654138	727	25	13114	3.607702889	1	0.949460966	57.34155031
GOTERM_BP_FAT	GO:0007215~glutamate signaling pathway	5	0.473933649	0.046654138	727	25	13114	3.607702889	1	0.949460966	57.34155031
GOTERM_BP_FAT	GO:0044236~multicellular organismal metabolic process	6	0.568720379	0.046669208	727	36	13114	3.006419074	1	0.946046968	57.35357238
GOTERM_BP_FAT	GO:0060042~retina morphogenesis in camera-type eye	4	0.379146919	0.046707716	727	15	13114	4.810270518	1	0.942650143	57.38427937
SP_PIR_KEYWORDS	hydroxylation	9	0.853080569	0.046903738	1037	71	18289	2.235606503	1	0.622143983	50.36736403
GOTERM_CC_FAT	GO:0044456~synapse part	22	2.085308057	0.046986225	713	246	12337	1.547417872	0.999999999	0.582840887	49.32194503
GOTERM_BP_FAT	GO:0007267~cell-cell signaling	44	4.170616114	0.047407093	727	599	13114	1.32503278	1	0.941614638	57.93834805

GOTERM_BP_FAT	GO:0030799~regulation of cyclic nucleotide metabolic process	12	1.137440758	0.048232941	727	113	13114	1.915594454	1	0.941056822	58.58385563
SP_PIR_KEYWORDS	Cardiomyopathy	7	0.663507109	0.048250479	1037	47	18289	2.626705513	1	0.619438403	51.38028618
INTERPRO	IPR018039:Intermediate filament protein, conserved site	9	0.853080569	0.048673455	933	70	16090	2.217271475	1	0.96998279	55.84140969
INTERPRO	IPR001664:Intermediate filament protein	9	0.853080569	0.048673455	933	70	16090	2.217271475	1	0.96998279	55.84140969
GOTERM_MF_FAT	GO:0005230~extracellular ligand-gated ion channel activity	9	0.853080569	0.049477087	710	72	12549	2.209330986	1	0.915133355	54.5280438
UP_SEQ_FEATURE	domain:PDZ 4	4	0.379146919	0.049638738	1037	15	18267	4.697396336	1	0.994412708	59.5082722
GOTERM_MF_FAT	GO:0005520~insulin-like growth factor binding	5	0.473933649	0.049651111	710	25	12549	3.534929577	1	0.904179764	54.65716691
UP_SEQ_FEATURE	domain:Ricin B-type lectin	5	0.473933649	0.050288438	1037	25	18267	3.523047252	1	0.993668607	59.99701354
UP_SEQ_FEATURE	domain:Collagen-like	6	0.568720379	0.050941799	1037	36	18267	2.93587271	1	0.992892104	60.48289034
GOTERM_BP_FAT	GO:0060191~regulation of lipase activity	10	0.947867299	0.050943898	727	87	13114	2.073392465	1	0.946785688	60.63771528
GOTERM_BP_FAT	GO:0006928~cell motion	36	3.412322275	0.050960157	727	475	13114	1.367129516	1	0.943623408	60.64973802
GOTERM_MF_FAT	GO:0022834~ligand-gated channel activity	13	1.232227488	0.05260076	710	126	12549	1.823574782	1	0.905958369	56.79424502
GOTERM_MF_FAT	GO:0015276~ligand-gated ion channel activity	13	1.232227488	0.05260076	710	126	12549	1.823574782	1	0.905958369	56.79424502
GOTERM_BP_FAT	GO:0030817~regulation of cAMP biosynthetic process	11	1.042654028	0.052677971	727	101	13114	1.964590682	1	0.945902583	61.90064327
GOTERM_BP_FAT	GO:0018149~peptide cross-linking	5	0.473933649	0.052812397	727	26	13114	3.468945085	1	0.943208891	61.99693162
INTERPRO	IPR017981:GPCR, family 2-like	8	0.758293839	0.053217943	933	59	16090	2.338365397	1	0.974017032	59.17284474

KEGG_PATHWAY	hsa00232:Caffeine metabolism	3	0.28436019	0.053267033	280	7	5042	7.717346939	0.999909077	0.95503323	48.71628578
GOTERM_BP_FAT	GO:0051491~positive regulation of filopodium assembly	3	0.28436019	0.053383057	727	7	13114	7.730791904	1	0.941895601	62.4031383
GOTERM_BP_FAT	GO:0051489~regulation of filopodium assembly	3	0.28436019	0.053383057	727	7	13114	7.730791904	1	0.941895601	62.4031383
GOTERM_BP_FAT	GO:0046033~AMP metabolic process	3	0.28436019	0.053383057	727	7	13114	7.730791904	1	0.941895601	62.4031383
GOTERM_BP_FAT	GO:0007216~metabotropic glutamate receptor signaling pathway	3	0.28436019	0.053383057	727	7	13114	7.730791904	1	0.941895601	62.4031383
GOTERM_BP_FAT	GO:0001503~ossification	12	1.137440758	0.053548773	727	115	13114	1.882279768	1	0.939295163	62.5203282
GOTERM_MF_FAT	GO:0042277~peptide binding	18	1.706161137	0.05396748	710	197	12549	1.614942447	1	0.900897168	57.75217342
BIOCARTA	h_no1Pathway:Actions of Nitric Oxide in the Heart	4	0.379146919	0.054377151	70	18	1406	4.463492063	0.999262747	0.999262747	47.80695691
GOTERM_BP_FAT	GO:0001932~regulation of protein amino acid phosphorylation	16	1.516587678	0.054380921	727	172	13114	1.678001344	1	0.938870222	63.10360621
GOTERM_BP_FAT	GO:0060193~positive regulation of lipase activity	9	0.853080569	0.054825537	727	75	13114	2.164621733	1	0.937208543	63.41172793
BIOCARTA	h_nos1Pathway:Nitric Oxide Signaling Pathway	3	0.28436019	0.054876228	70	8	1406	7.532142857	0.999311283	0.973756589	48.12640792
UP_SEQ_FEATURE	DNA-binding region:H-T-H motif winged-type	3	0.28436019	0.055783235	1037	7	18267	7.549386968	1	0.994716406	63.91356104
SP_PIR_KEYWORDS	tumor antigen	6	0.568720379	0.056030277	1037	37	18289	2.859965076	1	0.662978742	56.86473027
GOTERM_BP_FAT	GO:0006140~regulation of nucleotide metabolic process	12	1.137440758	0.056348166	727	116	13114	1.866053218	1	0.939015263	64.44862172
SP_PIR_KEYWORDS	extracellular matrix	21	1.990521327	0.056404313	1037	241	18289	1.536786213	1	0.653052492	57.11329741
GOTERM_BP_FAT	GO:0019935~cyclic-nucleotide-	13	1.232227488	0.0564242	727	130	13114	1.803851444	1	0.936246211	64.4996969

	mediated signaling			46							
GOTERM_BP_FAT	GO:0015718~monocarboxylic acid transport	7	0.663507109	0.056603465	727	50	13114	2.525392022	1	0.933789805	64.61973858
GOTERM_CC_FAT	GO:0045202~synapse	29	2.748815166	0.057768554	713	355	12337	1.413480039	1	0.645751156	56.8450638
GOTERM_MF_FAT	GO:0008603~cAMP-dependent protein kinase regulator activity	4	0.379146919	0.058017055	710	16	12549	4.418661972	1	0.907184418	60.47514585
GOTERM_BP_FAT	GO:0008016~regulation of heart contraction	9	0.853080569	0.05844942	727	76	13114	2.136139868	1	0.936670878	65.83407536
GOTERM_BP_FAT	GO:0030814~regulation of cAMP metabolic process	11	1.042654028	0.058731775	727	103	13114	1.92644329	1	0.934629892	66.01631269
SP_PIR_KEYWORDS	cell membrane	138	13.08056872	0.059067988	1037	2131	18289	1.142107123	1	0.658468352	58.8452473
GOTERM_MF_FAT	GO:0005198~structural molecule activity	44	4.170616114	0.059350327	710	597	12549	1.302654116	1	0.90247741	61.33510232
GOTERM_BP_FAT	GO:0032963~collagen metabolic process	5	0.473933649	0.059389875	727	27	13114	3.340465638	1	0.933775581	66.4375079
INTERPRO	IPR003054:Type II keratin	5	0.473933649	0.060563969	933	26	16090	3.316431693	1	0.981157871	64.06356146
INTERPRO	IPR000772:Ricin B lectin	5	0.473933649	0.060563969	933	26	16090	3.316431693	1	0.981157871	64.06356146
SP_PIR_KEYWORDS	differentiation	35	3.317535545	0.060584407	1037	455	18289	1.3566501	1	0.656412454	59.8019084
GOTERM_BP_FAT	GO:0021510~spinal cord development	6	0.568720379	0.062355598	727	39	13114	2.775156068	1	0.939759639	68.27522223
GOTERM_BP_FAT	GO:0033555~multicellular organismal response to stress	6	0.568720379	0.062355598	727	39	13114	2.775156068	1	0.939759639	68.27522223
GOTERM_MF_FAT	GO:0022836~gated channel activity	25	2.369668246	0.062864471	710	305	12549	1.44874163	1	0.906251869	63.51858887
GOTERM_BP_FAT	GO:0009719~response to endogenous stimulus	31	2.938388626	0.063262585	727	405	13114	1.380725797	1	0.939619222	68.81799443
GOTERM_MF_FAT	GO:0005253~anion channel activity	9	0.853080569	0.064274456	710	76	12549	2.093050408	1	0.902231944	64.36179478

KEGG_PATHWAY	hsa00591:Linoleic acid metabolism	5	0.473933649	0.06596416	280	28	5042	3.215561224	0.999990842	0.944988879	56.50491886
GOTERM_BP_FAT	GO:0045017~glycerolipid biosynthetic process	9	0.853080569	0.066141519	727	78	13114	2.081367051	1	0.944649983	70.48336121
GOTERM_BP_FAT	GO:0007200~activation of phospholipase C activity by G-protein coupled receptor protein signaling pathway coupled to IP3 second messenger	7	0.663507109	0.066198297	727	52	13114	2.42826156	1	0.942315174	70.51534529
GOTERM_BP_FAT	GO:0006081~cellular aldehyde metabolic process	5	0.473933649	0.066381304	727	28	13114	3.221163293	1	0.94028813	70.61821361
GOTERM_BP_FAT	GO:0015908~fatty acid transport	5	0.473933649	0.066381304	727	28	13114	3.221163293	1	0.94028813	70.61821361
INTERPRO	IPR000215:Protease inhibitor I4, serpin	6	0.568720379	0.066542246	933	38	16090	2.722964969	1	0.984678896	67.63186492
SMART	SM00458:RICIN	5	0.473933649	0.066861324	530	26	8828	3.203193033	0.999999992	0.930003712	59.72127516
GOTERM_MF_FAT	GO:0008188~neuropeptide receptor activity	6	0.568720379	0.066866716	710	39	12549	2.719176598	1	0.902615634	65.86464964
GOTERM_BP_FAT	GO:0051270~regulation of cell motion	17	1.611374408	0.06698752	727	192	13114	1.597160133	1	0.939374407	70.95655282
GOTERM_MF_FAT	GO:0004867~serine-type endopeptidase inhibitor activity	10	0.947867299	0.067267749	710	90	12549	1.963849765	1	0.895310632	66.09178005
PIR_SUPERFAMILY	PIRSF001638:cystatin	3	0.28436019	0.067851919	397	8	7196	6.797229219	1	0.992157423	62.65406302
INTERPRO	IPR001879:GPCR, family 2, extracellular region	5	0.473933649	0.067973915	933	27	16090	3.193600889	1	0.983192672	68.43556433
SP_PIR_KEYWORDS	collagen degradation	4	0.379146919	0.068059614	1037	17	18289	4.149753247	1	0.689125498	64.22246396
BIOCARTA	h_dreampathway:Repression of Pain Sensation by the Transcriptional Regulator DREAM	3	0.28436019	0.068359953	70	9	1406	6.695238095	0.999892103	0.952393047	56.10933641
GOTERM_BP_FAT	GO:0051050~positive	19	1.800947867	0.0696740	727	223	13114	1.536913787	1	0.943713385	72.41218853

	regulation of transport			75							
SP_PIR_KEYWORDS	protease inhibitor	11	1.042654028	0.070186468	1037	104	18289	1.865393888	1	0.689868986	65.39483594
GOTERM_BP_FAT	GO:0048839~inner ear development	9	0.853080569	0.070211206	727	79	13114	2.055020633	1	0.942666745	72.69483329
GOTERM_MF_FAT	GO:0016494~C-X-C chemokine receptor activity	3	0.28436019	0.071140847	710	8	12549	6.627992958	1	0.900360102	68.21377041
GOTERM_MF_FAT	GO:0004372~glycine hydroxymethyltransferase activity	3	0.28436019	0.071140847	710	8	12549	6.627992958	1	0.900360102	68.21377041
SP_PIR_KEYWORDS	cAMP binding	3	0.28436019	0.071487328	1037	8	18289	6.613669238	1	0.68626001	66.09415981
UP_SEQ_FEATURE	domain:HP	3	0.28436019	0.071639865	1037	8	18267	6.605713597	1	0.998589525	73.28617673
INTERPRO	IPR000998:MAM	4	0.379146919	0.071793372	933	17	16090	4.057751718	1	0.984142508	70.48899887
GOTERM_MF_FAT	GO:0042923~neuropeptide binding	6	0.568720379	0.073037712	710	40	12549	2.651197183	1	0.898566125	69.20707974
KEGG_PATHWAY	hsa00340:Histidine metabolism	5	0.473933649	0.073335554	280	29	5042	3.104679803	0.999997619	0.924947525	60.51246489
UP_SEQ_FEATURE	domain:PDZ 1	6	0.568720379	0.074083778	1037	40	18267	2.642285439	1	0.998608455	74.50777061
UP_SEQ_FEATURE	domain:PDZ 2	6	0.568720379	0.074083778	1037	40	18267	2.642285439	1	0.998608455	74.50777061
GOTERM_BP_FAT	GO:0060491~regulation of cell projection assembly	4	0.379146919	0.074167582	727	18	13114	4.008558765	1	0.949395347	74.69407311
GOTERM_BP_FAT	GO:0046717~acid secretion	4	0.379146919	0.074167582	727	18	13114	4.008558765	1	0.949395347	74.69407311
INTERPRO	IPR003128:Villin headpiece	3	0.28436019	0.074360196	933	8	16090	6.467041801	1	0.983856267	71.79777904
SMART	SM00093:SERPIN	6	0.568720379	0.074493889	530	38	8828	2.62999007	0.999999999	0.925953651	63.84198234
GOTERM_CC_FAT	GO:0031253~cell projection	8	0.758293839	0.0746925	713	64	12337	2.162868163	1	0.727953486	66.59114026

	membrane			47							
SMART	SM00008:HormR	5	0.473933649	0.074937434	530	27	8828	3.084556254	0.999999999	0.902525285	64.06902853
GOTERM_BP_FAT	GO:0009260~ribonucleotide biosynthetic process	12	1.137440758	0.075177869	727	122	13114	1.774280109	1	0.949407778	75.18198192
INTERPRO	IPR001173:Glycosyl transferase, family 2	5	0.473933649	0.075828503	933	28	16090	3.079543715	1	0.982560815	72.52173325
INTERPRO	IPR016160:Aldehyde dehydrogenase, conserved site	5	0.473933649	0.075828503	933	28	16090	3.079543715	1	0.982560815	72.52173325
SP_PIR_KEYWORDS	membrane	367	34.78672986	0.075977221	1037	6079	18289	1.064743811	1	0.698999408	68.40803784
SMART	SM00137:MAM	4	0.379146919	0.077759658	530	17	8828	3.919200888	1	0.886679961	65.48311973
GOTERM_MF_FAT	GO:0016646~oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor	4	0.379146919	0.077836024	710	18	12549	3.927699531	1	0.905904008	71.5916483
GOTERM_MF_FAT	GO:0016702~oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	8	0.758293839	0.077900499	710	66	12549	2.142381562	1	0.898649795	71.62248036
GOTERM_BP_FAT	GO:0060348~bone development	12	1.137440758	0.078660794	727	123	13114	1.759855068	1	0.9542777	76.79683103
SMART	SM00153:VHP	3	0.28436019	0.078907106	530	8	8828	6.246226415	1	0.866014855	66.04320923
GOTERM_BP_FAT	GO:0043583~ear development	10	0.947867299	0.079697094	727	95	13114	1.898790994	1	0.954283	77.2578248
GOTERM_BP_FAT	GO:0003002~regionalization	17	1.611374408	0.080117683	727	197	13114	1.556623074	1	0.953154615	77.44244455
GOTERM_BP_FAT	GO:0048663~neuron fate commitment	6	0.568720379	0.080662579	727	42	13114	2.576930635	1	0.952263556	77.67952588
KEGG_PATHWAY	hsa00512:O-Glycan biosynthesis	5	0.473933649	0.08110646	280	30	5042	3.001190476	0.999999431	0.908970821	64.36788905

GOTERM_MF_FAT	GO:0022838~substrate specific channel activity	30	2.843601896	0.081306407	710	391	12549	1.356111091	1	0.90161056	73.20738794
GOTERM_BP_FAT	GO:0034614~cellular response to reactive oxygen species	5	0.473933649	0.081576375	727	30	13114	3.006419074	1	0.952072058	78.07184219
GOTERM_MF_FAT	GO:0016701~oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	8	0.758293839	0.082980914	710	67	12549	2.110405718	1	0.899432672	73.95586801
GOTERM_MF_FAT	GO:0030594~neurotransmitter receptor activity	10	0.947867299	0.083434258	710	94	12549	1.88028169	1	0.893764505	74.15511508
PIR_SUPERFAMILY	PIRSF005569:ultra-high-sulfur keratin	3	0.28436019	0.084143235	397	9	7196	6.041981528	1	0.994474486	70.83220664
GOTERM_BP_FAT	GO:0051966~regulation of synaptic transmission, glutamatergic	4	0.379146919	0.084595854	727	19	13114	3.797581988	1	0.955628928	79.32240404
GOTERM_BP_FAT	GO:0042220~response to cocaine	4	0.379146919	0.084595854	727	19	13114	3.797581988	1	0.955628928	79.32240404
GOTERM_BP_FAT	GO:0014073~response to tropane	4	0.379146919	0.084595854	727	19	13114	3.797581988	1	0.955628928	79.32240404
GOTERM_BP_FAT	GO:0030574~collagen catabolic process	4	0.379146919	0.084595854	727	19	13114	3.797581988	1	0.955628928	79.32240404
GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	25	2.369668246	0.08464752	727	322	13114	1.40050578	1	0.953934875	79.34320475
GOTERM_BP_FAT	GO:0001976~neurological system process involved in regulation of systemic arterial blood pressure	3	0.28436019	0.085071838	727	9	13114	6.012838148	1	0.952884843	79.51328743
GOTERM_BP_FAT	GO:0045176~apical protein localization	3	0.28436019	0.085071838	727	9	13114	6.012838148	1	0.952884843	79.51328743
GOTERM_BP_FAT	GO:0032781~positive regulation of ATPase activity	3	0.28436019	0.085071838	727	9	13114	6.012838148	1	0.952884843	79.51328743
UP_SEQ_FEATURE	transmembrane region	290	27.48815166	0.085155396	1037	4755	18267	1.07432566	1	0.99936863	79.41087353
GOTERM_MF_FAT	GO:0030246~carbohydrate binding	27	2.559241706	0.086005195	710	347	12549	1.375260787	1	0.894417197	75.25834134

KEGG_PATHWAY	hsa00983:Drug metabolism	6	0.568720379	0.086668837	280	43	5042	2.512624585	0.999999797	0.889381044	66.91192244
GOTERM_BP_FAT	GO:0034599~cellular response to oxidative stress	6	0.568720379	0.087335783	727	43	13114	2.517002015	1	0.955019453	80.39864578
UP_SEQ_FEATURE	domain:MAGE	5	0.473933649	0.087468437	1037	30	18267	2.93587271	1	0.999355845	80.3159234
GOTERM_BP_FAT	GO:0044057~regulation of system process	24	2.274881517	0.088120991	727	308	13114	1.405598528	1	0.954614233	80.69718818
GOTERM_MF_FAT	GO:0019958~C-X-C chemokine binding	3	0.28436019	0.088132087	710	9	12549	5.891549296	1	0.893800275	76.13755446
GOTERM_MF_FAT	GO:0016861~intramolecular oxidoreductase activity, interconverting aldoses and ketoses	3	0.28436019	0.088132087	710	9	12549	5.891549296	1	0.893800275	76.13755446
GOTERM_MF_FAT	GO:0004890~GABA-A receptor activity	4	0.379146919	0.08870933	710	19	12549	3.720978503	1	0.888841988	76.37108093
GOTERM_MF_FAT	GO:0002020~protease binding	4	0.379146919	0.08870933	710	19	12549	3.720978503	1	0.888841988	76.37108093
UP_SEQ_FEATURE	site:Reactive site	3	0.28436019	0.088735494	1037	9	18267	5.871745419	1	0.99928249	80.79564798
UP_SEQ_FEATURE	domain:EGF-like 1; calcium-binding	4	0.379146919	0.089545423	1037	19	18267	3.708470791	1	0.999175038	81.0964944
GOTERM_CC_FAT	GO:0045211~postsynaptic membrane	13	1.232227488	0.089927692	713	135	12337	1.666209548	1	0.781650821	73.57388456
GOTERM_MF_FAT	GO:0005216~ion channel activity	29	2.748815166	0.090320599	710	380	12549	1.348854707	1	0.886929216	77.01166465
UP_SEQ_FEATURE	lipid moiety-binding region:S-palmitoyl cysteine	16	1.516587678	0.090666261	1037	181	18267	1.557147957	1	0.999082252	81.50549778
INTERPRO	IPR003150:DNA-binding RFX	3	0.28436019	0.092033373	933	9	16090	5.748481601	1	0.991551321	79.43453651
INTERPRO	IPR017857:Coagulation factor, subset, Gla region	3	0.28436019	0.092033373	933	9	16090	5.748481601	1	0.991551321	79.43453651
INTERPRO	IPR019794:Peroxidase, active site	3	0.28436019	0.092033373	933	9	16090	5.748481601	1	0.991551321	79.43453651

GOTERM_MF_FAT	GO:0019205~nucleobase, nucleoside, nucleotide kinase activity	6	0.568720379	0.093333274	710	43	12549	2.466229938	1	0.889005755	78.16602963
SP_PIR_KEYWORDS	postsynaptic cell membrane	11	1.042654028	0.093888742	1037	110	18289	1.76364513	1	0.767201091	76.25288918
INTERPRO	IPR004182:GRAM	4	0.379146919	0.094025982	933	19	16090	3.630619958	1	0.99097723	80.16151138
GOTERM_BP_FAT	GO:0006813~potassium ion transport	14	1.327014218	0.095506844	727	157	13114	1.60852995	1	0.964014956	83.3029053
GOTERM_BP_FAT	GO:0009126~purine nucleoside monophosphate metabolic process	4	0.379146919	0.095607479	727	20	13114	3.607702889	1	0.962698213	83.33600061
GOTERM_BP_FAT	GO:0009167~purine ribonucleoside monophosphate metabolic process	4	0.379146919	0.095607479	727	20	13114	3.607702889	1	0.962698213	83.33600061
PIR_SUPERFAMILY	PIRSF001630:serpin	5	0.473933649	0.096494189	397	32	7196	2.832178841	1	0.994758849	75.88730868
GOTERM_MF_FAT	GO:0008289~lipid binding	33	3.127962085	0.097024911	710	446	12549	1.307765427	1	0.892747492	79.50661293
GOTERM_BP_FAT	GO:0032956~regulation of actin cytoskeleton organization	9	0.853080569	0.097771471	727	85	13114	1.909960353	1	0.964117323	84.03285652
BIOCARTA	h_extrinsicPathway:Extrinsic Prothrombin Activation Pathway	3	0.28436019	0.098077808	70	11	1406	5.477922078	0.999998353	0.964173647	69.89491176

Supplementary Table 3. List of genes with an HTE-selective CORE overlapping their promoter (within 2kb upstream of the transcription start site).

CORE Chrom	CORE Start	CORE Stop	Gene Name	Gene RefSeq	Gene Chrom	Gene Strand	Promoter Start	Promoter Stop	Overlap(bp)	Expression Value
chr12	52907538	52974591	KRT5	NM_000424	chr12	-	52914244	52916244	2001	15.76723
chr12	52820870	52887480	KRT6A	NM_005554	chr12	-	52887182	52889182	299	15.748045
chr19	17959789	17983888	RPL18A	NM_000980	chr19	+	17968729	17970729	2001	15.74742
chr17	39743108	39820235	KRT17	NM_000422	chr17	-	39780883	39782883	2001	15.61449
chr12	6297232	6338827	CD9	NM_001769	chr12	+	6307553	6309553	2001	15.59768
chr8	146015609	146031861	RPL8	NM_033301	chr8	-	146017730	146019730	2001	15.4463
chrX	118589289	118635962	SLC25A5	NM_001152	chrX	+	118600361	118602361	2001	15.43477
chr9	136179690	136232109	RPL7A	NM_000972	chr9	+	136213067	136215067	2001	15.426485
chr17	39743108	39820235	KRT16	NM_005557	chr17	-	39769080	39771080	2001	15.386095
chr12	52820870	52887480	KRT6C	NM_173086	chr12	-	52867570	52869570	2001	15.37582
chr17	39743108	39820235	KRT14	NM_000526	chr17	-	39743148	39745148	2001	15.33091
chr18	21263752	21290396	LAMA3	NM_198129	chr18	+	21267560	21269560	2001	15.293675
chr8	82184423	82197862	FABP5	NM_001444	chr8	+	82190783	82192783	2001	15.275335
chr16	2560914	2578176	ATP6V0C	NM_001694	chr16	+	2561951	2563951	2001	15.23641
chr16	56709889	56718813	MT1X	NM_005952	chr16	+	56714380	56716380	2001	15.192305
chr17	74561487	74583300	ST6GALNAC2	NM_006456	chr17	-	74582146	74584146	1155	15.04813
chr22	36769390	36792473	MYH9	NM_002473	chr22	-	36784064	36786064	2001	15.03295
chr19	54937804	54971008	LENG8	NM_052925	chr19	+	54958063	54960063	2001	15.00143
chr4	187620452	187648566	FAT1	NM_005245	chr4	-	187644988	187646988	2001	14.990905
chr7	128468762	128561570	ATP6V1F	NM_004231	chr7	+	128500896	128502896	2001	14.97625
chr5	135363078	135370653	TGFBI	NM_000358	chr5	+	135362582	135364582	1505	14.97352

chr2	219132248	219163140	TMBIM1	NM_022152	chr2	-	219157281	219159281	2001	14.96145
chr1	95008733	95019204	F3	NM_001993	chr1	-	95007414	95009414	682	14.94626
chr1	86882170	86896383	CLCA2	NM_006536	chr1	+	86887767	86889767	2001	14.896205
chr15	101417568	101446363	ALDH1A3	NM_000693	chr15	+	101418007	101420007	2001	14.87284
chr3	52003452	52021750	ABHD14B	NM_032750	chr3	-	52008647	52010647	2001	14.769545
chr1	86020483	86048926	CYR61	NM_001554	chr1	+	86044442	86046442	2001	14.73906
chr5	175385631	175413026	THOC3	NM_032361	chr5	-	175395546	175397546	2001	14.73083
chr1	152890432	152976512	SPRR1A	NM_005987	chr1	+	152954555	152956555	2001	14.586635
chr6	7532572	7560215	DSP	NM_004415	chr6	+	7539868	7541868	2001	14.495115
chr11	2396519	2482161	CD81	NM_004356	chr11	+	2396545	2398545	2001	14.46802
chr4	75463923	75485725	AREG	NM_001657	chr4	+	75478627	75480627	2001	14.42852
chr4	83806760	83820089	SEC31A	NM_016211	chr4	-	83812413	83814413	2001	14.42491
chr17	39680188	39697532	KRT19	NM_002276	chr17	-	39684642	39686642	2001	14.39085
chr22	19163979	19187060	SLC25A1	NM_005984	chr22	-	19166302	19168302	2001	14.37009
chrX	153655472	153675381	GDI1	NM_001493	chrX	+	153663257	153665257	2001	14.369065
chr11	64070818	64089422	TRMT112	NM_016404	chr11	-	64085034	64087034	2001	14.366525
chr18	61306314	61329312	SERPINB3	NM_006919	chr18	-	61329198	61331198	115	14.35049
chr11	61093540	61117118	DDB1	NM_001923	chr11	-	61100667	61102667	2001	14.338065
chr1	31862911	31908214	SERINC2	NM_178865	chr1	+	31883961	31885961	2001	14.33186
chr19	42238436	42306526	CEACAM6	NM_002483	chr19	+	42257396	42259396	2001	14.291405
chr22	20076835	20131975	RANBP1	NM_002882	chr22	+	20103022	20105022	2001	14.27383
chr12	52820870	52887480	KRT6B	NM_005555	chr12	-	52845911	52847911	2001	14.240575
chr16	2306105	2327686	RNPS1	NM_080594	chr16	-	2318115	2320115	2001	14.196765
chrX	153655472	153675381	ATP6AP1	NM_001183	chrX	+	153654976	153656976	1505	14.19439

chr2	95939604	95974537	PROM2	NM_144707	chr2	+	95938199	95940199	596	14.170585
chr11	102324592	102327412	TMEM123	NM_052932	chr11	-	102323776	102325776	1185	14.16833
chr1	153315567	153359389	S100A9	NM_002965	chr1	+	153328328	153330328	2001	14.167335
chr1	201956097	201984314	ELF3	NM_004433	chr1	+	201977688	201979688	2001	14.164525
chr1	159883546	159929591	TAGLN2	NM_003564	chr1	-	159895285	159897285	2001	14.15357
chr1	36891604	36942685	MRPS15	NM_031280	chr1	-	36930041	36932041	2001	14.14857
chr7	99058290	99082974	ATP5J2	NM_004889	chr7	-	99063809	99065809	2001	14.10345
chr13	78090508	78128367	SCEL	NM_144777	chr13	+	78107807	78109807	2001	14.0761
chr1	11973491	12003749	PLOD1	NM_000302	chr1	+	11992744	11994744	2001	14.01929
chr1	153924325	153940770	SLC39A1	NM_014437	chr1	-	153940189	153942189	582	14.00591
chrX	152068908	152114784	ZNF185	NM_007150	chrX	+	152080984	152082984	2001	13.99977
chr2	234651310	234670477	UGT1A1	NM_000463	chr2	+	234666917	234668917	2001	13.983455
chr21	44843387	44872288	SIK1	NM_173354	chr21	-	44847003	44849003	2001	13.96396
chr17	76973826	77000147	LGALS3BP	NM_005567	chr17	-	76976062	76978062	2001	13.905685
chr19	5666968	5715071	RPL36	NM_033643	chr19	+	5688270	5690270	2001	13.9024975
chr19	2080611	2101935	MOBKL2A	NM_130807	chr19	-	2096270	2098270	2001	13.882415
chr6	33654522	33702457	C6orf125	NM_032340	chr6	-	33679505	33681505	2001	13.824095
chr19	6733015	6750491	TRIP10	NM_004240	chr19	+	6737705	6739705	2001	13.82371
chr10	5522208	5572766	CALML3	NM_005185	chr10	+	5564922	5566922	2001	13.81053
chr12	57966563	58022490	PIP4K2C	NM_024779	chr12	+	57982940	57984940	2001	13.782845
chrX	47069468	47081477	CDK16	NM_033018	chrX	+	47075526	47077526	2001	13.778395
chr12	2880551	2909700	FKBP4	NM_002014	chr12	+	2902106	2904106	2001	13.762515
chr3	190036497	190044028	CLDN1	NM_021101	chr3	-	190040236	190042236	2001	13.74576
chr17	7251199	7265679	KCTD11	NM_001002914	chr17	+	7253206	7255206	2001	13.73162

chr19	1257485	1279145	CIRBP	NM_001280	chr19	+	1267265	1269265	2001	13.71607
chr19	46008540	46025703	VASP	NM_003370	chr19	+	46008686	46010686	2001	13.7095275
chr4	83295961	83316539	HNRNPD	NM_031370	chr4	-	83295150	83297150	1190	13.6839575
chr17	3561568	3600311	TAX1BP3	NM_014604	chr17	-	3571974	3573974	2001	13.65731
chr15	66652140	66693965	MAP2K1	NM_002755	chr15	+	66677209	66679209	2001	13.64964
chr14	100836534	100864172	WARS	NM_213646	chr14	-	100841928	100843928	2001	13.588505
chr19	6733015	6750491	GPR108	NM_020171	chr19	-	6737305	6739305	2001	13.54836
chr4	87507237	87517191	PTPN13	NM_080685	chr4	+	87513466	87515466	2001	13.542245
chr19	13098598	13128062	NFIX	NM_002501	chr19	+	13104582	13106582	2001	13.541425
chr1	3518344	3571185	TPRG1L	NM_182752	chr1	+	3539554	3541554	2001	13.53598
chr10	104384642	104416923	TRIM8	NM_030912	chr10	+	104402250	104404250	2001	13.5339
chr6	116686952	116697622	DSE	NM_013352	chr6	+	116690108	116692108	2001	13.527205
chr16	66866681	66881347	NAE1	NM_003905	chr16	-	66864880	66866880	200	13.466805
chr9	132928800	132974058	NCS1	NM_014286	chr9	+	132932855	132934855	2001	13.4584
chr1	32028468	32057799	TINAGL1	NM_022164	chr1	+	32040084	32042084	2001	13.45525
chr9	112257365	112300855	PTPN3	NM_002829	chr9	-	112260594	112262594	2001	13.45286
chr9	131636749	131653228	LRRC8A	NM_019594	chr9	+	131642389	131644389	2001	13.44815
chr16	28850366	28885949	TUFM	NM_003321	chr16	-	28857730	28859730	2001	13.41595
chr19	51476183	51644831	KLK10	NM_145888	chr19	-	51522955	51524955	2001	13.412875
chr18	9616035	9648737	PPP4R1	NM_005134	chr18	-	9614601	9616601	567	13.39344
chr5	180196937	180239180	MGAT1	NM_002406	chr5	-	180230049	180232049	2001	13.373685
chr14	60628033	60646543	DHRS7	NM_016029	chr14	-	60632212	60634212	2001	13.327185
chr15	90733914	90747445	SEMA4B	NM_198925	chr15	+	90742560	90744560	2001	13.325465
chrX	13706702	13739822	RAB9A	NM_004251	chrX	+	13705238	13707238	537	13.31957

chr6	159067484	159107731	DYNLT1	NM_006519	chr6	-	159065805	159067805	322	13.3114
chr6	128812533	128854266	PTPRK	NM_002844	chr6	-	128841820	128843820	2001	13.303555
chr2	110351878	110373216	SEPT10	NM_178584	chr2	-	110371784	110373784	1433	13.29222
chr10	72544248	72590304	SGPL1	NM_003901	chr10	+	72573702	72575702	2001	13.26699
chrX	68043694	68067101	EFNB1	NM_004429	chrX	+	68046838	68048838	2001	13.258645
chr1	24611808	24650075	GRHL3	NM_198174	chr1	+	24643810	24645810	2001	13.220595
chr7	128071310	128097763	C7orf68	NM_013332	chr7	+	128093882	128095882	2001	13.214875
chr10	105540305	105616840	SH3PXD2A	NM_014631	chr10	-	105615165	105617165	1676	13.199605
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chr22	43251824	43281343	ARFGAP3	NM_014570	chr22	-	43253409	43255409	2001	12.920085
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chr3	46720057	46744132	ALS2CL	NM_182775	chr3	-	46718900	46720900	844	12.318315
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chr9	124463964	124587585	DAB2IP	NM_138709	chr9	+	124503062	124505062	2001	11.5993425
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chr12	8972156	8981968	A2ML1	NM_144670	chr12	+	8973148	8975148	2001	11.48883
chr3	38025556	38048442	VILL	NM_015873	chr3	+	38033076	38035076	2001	11.4816
chr20	61896072	61915408	ARFGAP1	NM_175609	chr20	+	61902163	61904163	2001	11.478545
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chr6	99786160	99798811	C6orf168	NM_032511	chr6	-	99797532	99799532	1280	10.59168
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chr9	139292909	139320166	SNAPC4	NM_003086	chr9	-	139292890	139294890	1982	10.521835
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chr6	168417468	168535217	FRMD1	NM_024919	chr6	-	168479840	168481840	2001	10.35431
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chr10	73150212	73158394	CDH23	NM_052836	chr10	+	73154689	73156689	2001	9.000025
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chr9	132375202	132384211	C9orf50	NM_199350	chr9	-	132383056	132385056	1156	8.93427
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chr22	19086492	19139196	DGCR14	NM_022719	chr22	-	19132191	19134191	2001	8.926185
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chr19	4175654	4195619	SIRT6	NM_016539	chr19	-	4182597	4184597	2001	8.919395
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chr15	40627378	40652635	C15orf52	NM_207380	chr15	-	40633169	40635169	2001	8.91493
chr3	52839344	52879051	MUSTN1	NM_205853	chr3	-	52869221	52871221	2001	8.9019
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chr19	11030431	11063744	C19orf52	NM_138358	chr19	+	11037422	11039422	2001	8.81344
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chr17	48158991	48190452	PDK2	NM_002611	chr17	+	48170694	48172694	2001	8.800255
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chr19	43841994	43865209	CD177	NM_020406	chr19	+	43855823	43857823	2001	8.78392
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chr11	57005134	57011182	APLNR	NM_005161	chr11	-	57004928	57006928	1795	8.777
chr1	209982970	209999482	C1orf107	NM_014388	chr1	+	209999310	210001310	173	8.773765
chr8	144876537	144921747	SCRIB	NM_182706	chr8	-	144897550	144899550	2001	8.7638525

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chr3	125880351	125900436	ALDH1L1	NM_012190	chr3	-	125899486	125901486	951	8.74926
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chr1	1381962	1396389	ATAD3C	NM_001039211	chr1	+	1383067	1385067	2001	8.729205
chr3	129220001	129304339	H1FOO	NM_153833	chr3	+	129260055	129262055	2001	8.716365
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chr22	24114075	24122591	MMP11	NM_005940	chr22	+	24113034	24115034	960	8.7051
chr22	38438792	38481490	SLC16A8	NM_013356	chr22	-	38479171	38481171	2001	8.70483
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chr2	220092676	220117258	GLB1L	NM_024506	chr2	-	220110132	220112132	2001	8.644075
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chr19	33549226	33563071	RHPN2	NM_033103	chr19	-	33555825	33557825	2001	8.590285
chr6	159067484	159107731	SYTL3	NM_001009991	chr6	+	159069044	159071044	2001	8.58582
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chr1	3518344	3571185	MEGF6	NM_001409	chr1	-	3528060	3530060	2001	8.574635
chr22	23481158	23501967	RAB36	NM_004914	chr22	+	23485511	23487511	2001	8.572045
chr11	61490076	61526210	C11orf9	NM_013279	chr11	+	61520859	61522859	2001	8.56913
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chr21	47555426	47577670	FTCD	NM_206965	chr21	-	47575482	47577482	2001	8.450505
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chr1	151690417	151712803	CELF3	NM_007185	chr1	-	151689291	151691291	875	8.374095
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chr8	133686621	133716108	LRRC6	NM_012472	chr8	-	133687814	133689814	2001	8.30471
chr12	130385791	130390171	TMEM132D	NM_133448	chr12	-	130388213	130390213	1959	8.29868
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chr9	139956910	139979454	C9orf140	NM_178448	chr9	-	139965029	139967029	2001	8.281635
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chr4	7029327	7049691	CCDC96	NM_153376	chr4	-	7044729	7046729	2001	8.256625
chr3	190213667	190261768	IL1RAP	NM_134470	chr3	+	190229838	190231838	2001	8.244805
chr3	24513813	24539132	THRB	NM_001128177	chr3	-	24536314	24538314	2001	8.23743
chr21	46345336	46398926	ITGB2	NM_001127491	chr21	-	46348754	46350754	2001	8.232095
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chr12	115109611	115139187	TBX3	NM_016569	chr12	-	115121970	115123970	2001	8.21399
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chr22	38829711	38866797	KCNJ4	NM_152868	chr22	-	38851204	38853204	2001	8.18948
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chr2	172965785	172993475	DLX2	NM_004405	chr2	-	172967479	172969479	2001	8.16643
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chr20	32238904	32272116	C20orf144	NM_080825	chr20	+	32248118	32250118	2001	8.14937
chr5	168725303	168728897	SLIT3	NM_003062	chr5	-	168728134	168730134	764	8.148505
chr3	46720057	46744132	TMIE	NM_147196	chr3	+	46740821	46742821	2001	8.146535
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chr13	113736009	113820307	F10	NM_000504	chr13	+	113775111	113777111	2001	8.04868
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chr22	50644124	50705002	TUBGCP6	NM_020461	chr22	-	50683401	50685401	2001	7.9674
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chr17	34066013	34095416	GAS2L2	NM_139285	chr17	-	34079898	34081898	2001	7.94571
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chr19	451428	466666	SHC2	NM_012435	chr19	-	460997	462997	2001	7.92482
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chr8	143859675	143883023	LYNX1	NM_177477	chr8	-	143858745	143860745	1071	7.91934
chr19	46384392	46423983	IRF2BP1	NM_015649	chr19	-	46389377	46391377	2001	7.91711
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chr16	67956715	67978912	CTRL	NM_001907	chr16	-	67965779	67967779	2001	7.89307
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chr9	139808714	139847309	LCN12	NM_178536	chr9	+	139844766	139846766	2001	7.864875

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chr1	11086267	11117160	MASP2	NM_139208	chr1	-	11107286	11109286	2001	7.854955
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chr3	50559403	50608885	C3orf18	NM_016210	chr3	-	50605224	50607224	2001	7.84443
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chr17	33457083	33487283	NLE1	NM_018096	chr17	-	33469323	33471323	2001	7.832325
chr15	79089873	79107462	ADAMTS7	NM_014272	chr15	-	79103774	79105774	2001	7.83171
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chr1	152538994	152555552	LCE3D	NM_032563	chr1	-	152552981	152554981	2001	7.81877
chr20	25040795	25066437	ACSS1	NM_032501	chr20	-	25039617	25041617	823	7.81728
chr17	17375960	17418738	RASD1	NM_016084	chr17	-	17399708	17401708	2001	7.816995
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chr22	30939215	30980664	GAL3ST1	NM_004861	chr22	-	30960877	30962877	2001	7.783685
chr17	5021528	5030702	ZNF232	NM_014519	chr17	-	5026398	5028398	2001	7.78283
chr20	32238904	32272116	C20orf134	NM_001024675	chr20	+	32252302	32254302	2001	7.77939

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chr7	128468762	128561570	FLNC	NM_001458	chr7	+	128468481	128470481	1720	7.76409
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chr13	114263532	114324165	GRK1	NM_002929	chr13	+	114319595	114321595	2001	7.734705
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chr19	8209308	8216939	FBN3	NM_032447	chr19	-	8212386	8214386	2001	7.727395
chr10	5522208	5572766	CALML5	NM_017422	chr10	-	5541534	5543534	2001	7.72422
chr10	134881052	134953434	GPR123	NM_001083909	chr10	+	134899407	134901407	2001	7.722235
chr22	19835827	19861467	GNB1L	NM_053004	chr22	-	19842463	19844463	2001	7.7215
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chr21	46016366	46036924	KRTAP10-8	NM_198695	chr21	+	46029994	46031994	2001	7.695405
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chr11	26341550	26355813	ANO3	NM_031418	chr11	+	26351676	26353676	2001	7.681045
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chr5	131394814	131425363	CSF2	NM_000758	chr5	+	131407483	131409483	2001	7.676825
chr4	8579768	8620296	GPR78	NM_080819	chr4	+	8580289	8582289	2001	7.674655
chr8	144575780	144645387	ZC3H3	NM_015117	chr8	-	144623621	144625621	2001	7.67242
chr2	121512775	121655675	GLI2	NM_005270	chr2	+	121552865	121554865	2001	7.666026667

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chr19	3477186	3496977	C19orf77	NM_001136503	chr19	-	3480541	3482541	2001	7.662245
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chr16	57559357	57575670	CCDC102A	NM_033212	chr16	-	57570478	57572478	2001	7.632665
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chr19	49916371	49942762	PTH2	NM_178449	chr19	-	49926699	49928699	2001	7.632195
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chr17	34066013	34095416	C17orf50	NM_145272	chr17	+	34085914	34087914	2001	7.61647
chr10	118973891	118999427	SLC18A2	NM_003054	chr10	+	118998582	119000582	846	7.61642
chr17	79602642	79631371	TSPAN10	NM_031945	chr17	+	79607347	79609347	2001	7.6079
chr11	295817	317285	IFITM5	NM_001025295	chr11	-	299527	301527	2001	7.598475
chr13	20724392	20763536	GJA3	NM_021954	chr13	-	20735184	20737184	2001	7.587835
chr8	145067338	145096214	SPATC1	NM_198572	chr8	+	145084580	145086580	2001	7.584095
chr11	61093540	61117118	DAK	NM_015533	chr11	+	61098652	61100652	2001	7.58133
chr1	228332351	228347110	GJC2	NM_020435	chr1	+	228335551	228337551	2001	7.57552
chr9	132408535	132450097	PRRX2	NM_016307	chr9	+	132425918	132427918	2001	7.572175
chr3	8766083	8785886	CAV3	NM_033337	chr3	+	8773484	8775484	2001	7.564715
chr1	4683354	4729331	AJAP1	NM_018836	chr1	+	4713103	4715103	2001	7.56133
chr15	67517247	67546189	IQCH	NM_022784	chr15	+	67545136	67547136	1054	7.553705
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chr14	101345976	101356331	RTL1	NM_001134888	chr14	-	101351185	101353185	2001	7.50318
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chr17	43906614	43921217	IMP5	NM_175882	chr17	+	43920254	43922254	964	7.324605
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chr1	37497429	37518066	GRIK3	NM_000831	chr1	-	37499845	37501845	2001	7.315125
chr1	40100149	40160008	NT5C1A	NM_032526	chr1	-	40137711	40139711	2001	7.312725
chr16	28512622	28522028	IL27	NM_145659	chr16	-	28518156	28520156	2001	7.31263
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chr1	21026101	21062620	KIF17	NM_020816	chr1	-	21044318	21046318	2001	7.30465
chr7	127990720	128006807	PRRT4	NM_001174164	chr7	-	128001740	128003740	2001	7.304555
chr7	150868480	150895240	ASB10	NM_080871	chr7	-	150884920	150886920	2001	7.29176
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chr17	43507639	43560969	SH3D20	NM_174919	chr17	-	43510283	43512283	2001	7.262325
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chr19	39970203	39995166	DLL3	NM_203486	chr19	+	39987555	39989555	2001	7.2577825
chr10	43568906	43597126	RET	NM_020975	chr10	+	43570515	43572515	2001	7.2576525
chr22	30654795	30698906	OSM	NM_020530	chr22	-	30662841	30664841	2001	7.23887
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chr1	36024866	36054992	TFAP2E	NM_178548	chr1	+	36036969	36038969	2001	7.234635
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chr17	77433863	77536248	RBFOX3	NM_001082575	chr17	-	77478564	77480564	2001	7.19464
chr17	6674411	6700763	FBXO39	NM_153230	chr17	+	6677550	6679550	2001	7.19089
chr18	13612800	13654373	C18orf1	NM_181483	chr18	+	13618865	13620865	2001	7.157455
chr16	1552999	1604870	TMEM204	NM_024600	chr16	+	1582229	1584229	2001	7.155285
chr9	138378175	138433705	LCN1	NM_002297	chr9	+	138411284	138413284	2001	7.14515
chr14	94229277	94264171	PRIMA1	NM_178013	chr14	-	94254767	94256767	2001	7.142495
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chr1	19140881	19195259	TAS1R2	NM_152232	chr1	-	19186156	19188156	2001	7.138445
chr19	17959789	17983888	SLC5A5	NM_000453	chr19	+	17980780	17982780	2001	7.137925
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chr17	72442902	72479408	CD300A	NM_007261	chr17	+	72460520	72462520	2001	7.127875
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chr14	50548411	50566329	C14orf183	NM_001014830	chr14	-	50559362	50561362	2001	7.0182
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chr17	48635028	48672894	CACNA1G	NM_198397	chr17	+	48636447	48638447	2001	6.982736
chr7	44260200	44369316	CAMK2B	NM_172084	chr7	-	44365231	44367231	2001	6.981700714
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chr1	40231729	40266485	OXCT2	NM_022120	chr1	-	40237021	40239021	2001	6.974025
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chr20	31577719	31603314	SUN5	NM_080675	chr20	-	31592240	31594240	2001	6.89093
chr7	149461797	149478695	SSPO	NM_198455	chr7	+	149471129	149473129	2001	6.88909
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chr21	42209631	42223377	DSCAM	NM_001389	chr21	-	42219040	42221040	2001	6.86484
chr17	46807258	46827126	HOXB13	NM_006361	chr17	-	46806112	46808112	855	6.856275
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chr5	122401850	122432687	PRDM6	NM_001136239	chr5	+	122422839	122424839	2001	6.848665
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chr19	51334063	51342686	KLK15	NM_138564	chr19	-	51334780	51336780	2001	6.775555
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chr17	61558897	61570530	ACE	NM_152830	chr17	+	61560176	61562176	2001	6.7463625
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chr2	29287871	29299606	C2orf71	NM_001029883	chr2	-	29297128	29299128	2001	6.682395
chr11	20568430	20632666	SLC6A5	NM_004211	chr11	+	20618944	20620944	2001	6.680825
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chr10	50316869	50328148	C10orf72	NM_144984	chr10	-	50323560	50325560	2001	6.659495
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chr1	16539138	16574847	C1orf89	NM_030907	chr1	-	16563660	16565660	2001	6.632455
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chr12	108981887	109004693	TMEM119	NM_181724	chr12	-	108991895	108993895	2001	6.61524
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chr19	47973805	48015833	SLC8A2	NM_015063	chr19	-	47975308	47977308	2001	6.611605

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chr12	52748164	52771054	KRT85	NM_002283	chr12	-	52761310	52763310	2001	6.59239
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chrX	102347492	102381623	NXF3	NM_022052	chrX	-	102348023	102350023	2001	6.585655
chr13	53405163	53423169	PCDH8	NM_032949	chr13	-	53422775	53424775	395	6.5835775
chr22	37421494	37554170	IL2RB	NM_000878	chr22	-	37545963	37547963	2001	6.578395
chr6	36195209	36214598	PNPLA1	NM_173676	chr6	+	36208943	36210943	2001	6.566455
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chr2	11809553	11817635	NTSR2	NM_012344	chr2	-	11810330	11812330	2001	6.556015
chr13	22237422	22308364	FGF9	NM_002010	chr13	+	22243213	22245213	2001	6.54429
chr16	50708773	50785700	SNX20	NM_182854	chr16	-	50715265	50717265	2001	6.5353925
chr4	8246447	8299335	HTRA3	NM_053044	chr4	+	8269487	8271487	2001	6.532195
chr14	77577508	77613122	ZDHHC22	NM_174976	chr14	-	77608135	77610135	2001	6.53128
chr3	126223107	126240196	UROC1	NM_144639	chr3	-	126236617	126238617	2001	6.52921
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chr19	58853367	58881362	A1BG	NM_130786	chr19	-	58864866	58866866	2001	6.52554
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chr20	39973951	40028489	EMILIN3	NM_052846	chr20	-	39995499	39997499	2001	6.46822
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chr17	27331689	27348401	SEZ6	NM_178860	chr17	-	27333082	27335082	2001	6.352635
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chr9	38420842	38443830	IGFBPL1	NM_001007563	chr9	-	38424445	38426445	2001	6.34138
chr17	15235762	15285312	TEKT3	NM_031898	chr17	-	15244959	15246959	2001	6.332575
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chr5	74530120	74539292	ANKRD31	NM_001164443	chr5	-	74532704	74534704	2001	6.3040725
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chr11	2396519	2482161	TRPM5	NM_014555	chr11	-	2444276	2446276	2001	6.293555
chr12	124770914	124802833	FAM101A	NM_181709	chr12	+	124771708	124773708	2001	6.29213
chr19	58853367	58881362	ZNF497	NM_198458	chr19	-	58874121	58876121	2001	6.29161
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chr5	139166140	139206641	PSD2	NM_032289	chr5	+	139173404	139175404	2001	6.2026
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chr11	118763955	118774534	CXCR5	NM_032966	chr11	+	118762099	118764099	145	6.17618
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chr12	54352252	54384109	HOXC11	NM_014212	chr12	+	54364908	54366908	2001	6.1176
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chr12	109725023	109748739	FOXN4	NM_213596	chr12	-	109747026	109749026	1714	6.109735
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chr15	88793207	88847021	NTRK3	NM_002530	chr15	-	88799662	88801662	2001	6.100378333
chr13	108846248	108872802	ABHD13	NM_032859	chr13	+	108868761	108870761	2001	6.09743
chr19	46384392	46423983	NANOS2	NM_001029861	chr19	-	46418037	46420037	2001	6.09378
chr20	3665176	3693230	SIGLEC1	NM_023068	chr20	-	3687776	3689776	2001	6.080875
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chr7	155591921	155655070	SHH	NM_000193	chr7	-	155604968	155606968	2001	6.04352
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chr3	126070049	126093771	KLF15	NM_014079	chr3	-	126076237	126078237	2001	6.015965
chr1	46989391	47023375	KNCN	NM_001097611	chr1	-	47016888	47018888	2001	6.011965
chr13	28539465	28566296	CDX2	NM_001265	chr13	-	28543318	28545318	2001	5.99592
chr8	6720222	6800413	DEFB1	NM_005218	chr8	-	6735530	6737530	2001	5.98687
chr1	208077186	208087557	CD34	NM_001773	chr1	-	208084684	208086684	2001	5.981175
chr4	174438219	174459368	HAND2	NM_021973	chr4	-	174451379	174453379	2001	5.96595
chr2	233346399	233399944	ECEL1	NM_004826	chr2	-	233352533	233354533	2001	5.94473
chr4	55080097	55104857	PDGFRA	NM_006206	chr4	+	55093262	55095262	2001	5.944045
chr1	152446398	152493428	LCE5A	NM_178438	chr1	+	152481318	152483318	2001	5.935845

chr22	45796009	45838121	SMC1B	NM_148674	chr22	-	45809501	45811501	2001	5.932555
chr17	16332173	16411584	C17orf76	NM_207387	chr17	-	16395481	16397481	2001	5.904725
chr6	39003550	39015168	GLP1R	NM_002062	chr6	+	39014555	39016555	614	5.89024
chrX	136631350	136657897	ZIC3	NM_003413	chrX	+	136646344	136648344	2001	5.87719
chr2	68693500	68702463	FBXO48	NM_001024680	chr2	-	68694391	68696391	2001	5.857935
chr2	102005606	102027430	CREG2	NM_153836	chr2	-	102003966	102005966	361	5.85595
chr22	31530354	31538977	PLA2G3	NM_015715	chr22	-	31536470	31538470	2001	5.84243
chr1	40100149	40160008	HEYL	NM_014571	chr1	-	40105349	40107349	2001	5.83871
chr12	52907538	52974591	KRT71	NM_033448	chr12	-	52946932	52948932	2001	5.817405
chr1	1848818	1879275	TMEM52	NM_178545	chr1	-	1850741	1852741	2001	5.805995
chr22	43805352	43843581	MPPED1	NM_001044370	chr22	+	43806018	43808018	2001	5.803615
chr6	39199740	39293404	KCNK17	NM_031460	chr6	-	39282237	39284237	2001	5.7975
chr3	10507870	10590953	ATP2B2	NM_001683	chr3	-	10547269	10549269	2001	5.793485
chr8	41512338	41556914	ANK1	NM_020480	chr8	-	41522805	41524805	2001	5.782025
chr10	88411676	88433186	LDB3	NM_007078	chr10	+	88426424	88428424	2001	5.773125
chr11	93744743	93793826	HEPHL1	NM_001098672	chr11	+	93752376	93754376	2001	5.771325
chrX	150341728	150348838	GPR50	NM_004224	chrX	+	150343054	150345054	2001	5.765145
chr8	1415501	1462295	DLGAP2	NM_004745	chr8	+	1447567	1449567	2001	5.76495
chr6	160758253	160799579	SLC22A3	NM_021977	chr6	+	160767423	160769423	2001	5.75182
chr4	96469896	96506715	UNC5C	NM_003728	chr4	-	96470362	96472362	2001	5.73257
chr10	44876742	44891010	CXCL12	NM_199168	chr10	-	44880546	44882546	2001	5.70763
chr17	40017935	40026143	KLHL11	NM_018143	chr17	-	40021630	40023630	2001	5.704905
chr9	87279361	87292326	NTRK2	NM_006180	chr9	+	87281464	87283464	2001	5.697045
chr7	28994383	28999961	TRIL	NM_014817	chr7	-	28998030	29000030	1932	5.685335

chr1	22962874	23008392	C1QA	NM_015991	chr1	+	22961116	22963116	243	5.680225
chr6	50785106	50790263	TFAP2B	NM_003221	chr6	+	50784437	50786437	1332	5.67887
chr2	223161745	223176909	PAX3	NM_181461	chr2	-	223163716	223165716	2001	5.667712
chr13	114263532	114324165	ATP4B	NM_000705	chr13	-	114312514	114314514	2001	5.665945
chr11	111371287	111409893	BTG4	NM_017589	chr11	-	111383065	111385065	2001	5.665735
chr17	5956462	5984291	WSCD1	NM_015253	chr17	+	5971932	5973932	2001	5.652945
chr2	223907554	223924375	KCNE4	NM_080671	chr2	+	223914860	223916860	2001	5.63657
chr2	80530153	80538747	LRRTM1	NM_178839	chr2	-	80531488	80533488	2001	5.63573
chr10	102500186	102511516	PAX2	NM_003990	chr10	+	102503466	102505466	2001	5.63484
chr10	134757917	134806685	C10orf93	NM_173572	chr10	-	134756090	134758090	174	5.624185
chr17	2929535	2968750	OR1D5	NM_014566	chr17	-	2966902	2968902	1849	5.616735
chr6	4066789	4104646	C6orf146	NM_173563	chr6	-	4079392	4081392	2001	5.61095
chr12	121080694	121097181	CABP1	NM_031205	chr12	+	121086369	121088369	2001	5.585696667
chr11	64383640	64415926	NRXN2	NM_138734	chr11	-	64410788	64412788	2001	5.52052
chr1	40100149	40160008	HPCAL4	NM_016257	chr1	-	40157090	40159090	2001	5.50512
chr13	113274011	113307105	C13orf35	NM_207440	chr13	+	113299356	113301356	2001	5.50397
chr5	75377712	75381525	SV2C	NM_014979	chr5	+	75377303	75379303	1592	5.49167
chr4	4856593	4874746	MSX1	NM_002448	chr4	+	4859390	4861390	2001	5.46924
chr8	6720222	6800413	DEFA6	NM_001926	chr8	-	6783599	6785599	2001	5.468255
chr1	157060676	157115194	ETV3L	NM_001004341	chr1	-	157069601	157071601	2001	5.46757
chr1	47656816	47703553	TAL1	NM_003189	chr1	-	47695444	47697444	2001	5.466995
chr5	131394814	131425363	IL3	NM_000588	chr5	+	131394345	131396345	1532	5.4478
chr15	78617973	78637706	CRABP1	NM_004378	chr15	+	78630664	78632664	2001	5.44005
chr10	91292353	91309554	SLC16A12	NM_213606	chr10	-	91295314	91297314	2001	5.43882

chr2	108425136	108450294	RGPD4	NM_182588	chr2	+	108441386	108443386	2001	5.435795
chr22	19086492	19139196	GSC2	NM_005315	chr22	-	19137797	19139797	1400	5.421855
chr22	45310559	45410969	PHF21B	NM_138415	chr22	-	45405582	45407582	2001	5.415915
chr8	25897353	25908446	EBF2	NM_022659	chr8	-	25902393	25904393	2001	5.41012
chr2	106669618	106681819	C2orf40	NM_032411	chr2	+	106680111	106682111	1709	5.403615
chr17	39238880	39276311	KRTAP4-11	NM_033059	chr17	-	39274607	39276607	1705	5.39603
chr11	134225440	134287387	B3GAT1	NM_054025	chr11	-	134281813	134283813	2001	5.391445
chr11	18802036	18826408	PTPN5	NM_032781	chr11	-	18813390	18815390	2001	5.383125
chr4	83806760	83820089	THAP9	NM_024672	chr4	+	83819835	83821835	255	5.35611
chr7	98453862	98479514	TMEM130	NM_152913	chr7	-	98467674	98469674	2001	5.348575
chr1	157801879	157832610	CD5L	NM_005894	chr1	-	157811635	157813635	2001	5.312705
chr12	10573074	10606119	KLRC2	NM_002260	chr12	-	10588593	10590593	2001	5.310925
chr22	37581743	37623287	SSTR3	NM_001051	chr22	-	37608354	37610354	2001	5.2883
chr3	129220001	129304339	RHO	NM_000539	chr3	+	129245480	129247480	2001	5.267165
chr12	10573074	10606119	KLRC3	NM_007333	chr12	-	10573195	10575195	2001	5.26202
chr8	86348011	86365516	CA3	NM_005181	chr8	+	86349054	86351054	2001	5.254765
chr1	152766774	152797737	LCE1B	NM_178349	chr1	+	152782445	152784445	2001	5.246285
chr17	39457481	39481820	KRTAP17-1	NM_031964	chr17	-	39471948	39473948	2001	5.22867
chr18	13868627	13916366	MC2R	NM_000529	chr18	-	13915536	13917536	831	5.203155
chr8	101641821	101691337	SNX31	NM_152628	chr8	-	101661894	101663894	2001	5.19872
chr20	23062114	23081593	CD93	NM_012072	chr20	-	23066978	23068978	2001	5.197935
chr2	228243296	228262568	TM4SF20	NM_024795	chr2	-	228244023	228246023	2001	5.18563
chr1	13829581	13867729	LRRC38	NM_001010847	chr1	-	13840243	13842243	2001	5.183045
chr17	50206214	50238432	CA10	NM_020178	chr17	-	50236133	50238133	2001	5.167585

chr12	106958918	107001268	RFX4	NM_213594	chr12	+	106975031	106977031	2001	5.14333
chr10	72544248	72590304	C10orf27	NM_152710	chr10	-	72545158	72547158	2001	5.132575
chrX	148760982	148798501	MAGEA11	NM_005366	chrX	+	148791736	148793736	2001	5.130985
chr10	50869360	50896424	C10orf53	NM_182554	chr10	+	50885682	50887682	2001	5.105245
chr5	178394603	178423704	GRM6	NM_000843	chr5	-	178422125	178424125	1580	5.07826
chr22	48881976	48983192	FAM19A5	NM_015381	chr22	+	48970116	48972116	2001	5.058295
chr6	29415534	29433356	OR2H1	NM_030883	chr6	+	29424228	29426228	2001	5.0322
chr4	186453438	186473737	PDLIM3	NM_014476	chr4	-	186456713	186458713	2001	5.015455
chr17	41834718	41836665	SOST	NM_025237	chr17	-	41836157	41838157	509	4.906105
chr14	57263234	57275732	OTX2	NM_172337	chr14	-	57272346	57274346	2001	4.875925
chr3	194091699	194107132	LRRC15	NM_130830	chr3	-	194090473	194092473	775	4.795475
chrX	113814461	113819142	HTR2C	NM_000868	chrX	+	113816549	113818549	2001	4.77444
chrX	141288180	141302158	MAGEC2	NM_016249	chrX	-	141293077	141295077	2001	4.67852
chr15	32979820	33012117	GREM1	NM_013372	chr15	+	33008203	33010203	2001	4.615305
chr8	65490721	65499284	BHLHE22	NM_152414	chr8	+	65490812	65492812	2001	4.547665
chr2	241927711	241943588	SNED1	NM_001080437	chr2	+	241936253	241938253	2001	4.540935
chr2	223161745	223176909	CCDC140	NM_153038	chr2	+	223160864	223162864	1120	4.523425
chr15	65691334	65718771	IGDCC4	NM_020962	chr15	-	65715411	65717411	2001	4.353905
chr1	13740143	13777051	PRAMEF21	NM_001100114	chr1	+	13740800	13742800	2001	
chr1	21026101	21062620	SH2D5	NM_001103161	chr1	-	21059134	21061134	2001	
chr1	151690417	151712803	C1orf230	NM_001144956	chr1	+	151692011	151694011	2001	
chr1	152690732	152743156	C1orf68	NM_001024679	chr1	+	152689996	152691996	1265	
chr1	209589280	209604570	LOC642587	NM_001104548	chr1	+	209600166	209602166	2001	
chr2	191400421	191437272	TMEM194B	NM_001142645	chr2	-	191399469	191401469	1049	

chr2	242662946	242703825	D2HGDH	NM_152783	chr2	+	242672028	242674028	2001	
chr4	7029327	7049691	TADA2B	NM_152293	chr4	+	7043154	7045154	2001	
chr4	7367751	7492963	PSAPL1	NM_001085382	chr4	-	7436701	7438701	2001	
chr7	128468762	128561570	KCP	NM_199349	chr7	-	128550774	128552774	2001	
chr7	141397049	141406598	KIAA1147	NM_001080392	chr7	-	141401954	141403954	2001	
chr7	141397049	141406598	WEE2	NM_001105558	chr7	+	141406151	141408151	448	
chr7	144096246	144113851	NOBOX	NM_001080413	chr7	-	144100787	144102787	2001	
chr8	142231113	142248073	SLC45A4	NM_001080431	chr8	-	142238674	142240674	2001	
chr9	34715639	34741924	C9orf144B	NM_001141917	chr9	-	34729536	34731536	2001	
chr11	1218575	1242443	MUC5B	NM_002458	chr11	+	1242293	1244293	151	
chr11	1650819	1712142	KRTAP5-5	NM_001001480	chr11	+	1649031	1651031	213	
chr11	2182173	2237853	INS-IGF2	NM_001042376	chr11	-	2182440	2184440	2001	
chr11	2277729	2350869	C11orf21	NM_001142946	chr11	-	2323144	2325144	2001	
chr12	10025223	10050371	KLRF2	NM_001190765	chr12	+	10032086	10034086	2001	
chr12	27229324	27249590	C12orf71	NM_001080406	chr12	-	27235456	27237456	2001	
chr13	28539465	28566296	PRHOXNB	NM_001105577	chr13	-	28562775	28564775	2001	
chr14	36976566	36986367	SFTA3	NM_001101341	chr14	-	36982991	36984991	2001	
chr14	93640204	93659637	C14orf109	NM_015676	chr14	+	93649294	93651294	2001	
chr14	94914389	94941468	SERPINA11	NM_001080451	chr14	-	94919123	94921123	2001	
chr15	42094340	42157010	JMJD7	NM_001114632	chr15	+	42118281	42120281	2001	
chr15	42094340	42157010	PLA2G4B	NM_001114633	chr15	+	42129009	42131009	2001	
chr16	66972097	66997078	CES3	NM_024922	chr16	+	66993130	66995130	2001	
chr17	6545800	6585564	C17orf100	NM_001105520	chr17	+	6553057	6555057	2001	

chr17	20349098	20379052	LGALS9B	NM_001042685	chr17	-	20370849	20372849	2001	
chr17	39238880	39276311	KRTAP4-7	NM_033061	chr17	+	39238457	39240457	1578	
chr17	39238880	39276311	KRTAP4-8	NM_031960	chr17	-	39254376	39256376	2001	
chr17	39238880	39276311	KRTAP4-9	NM_001146041	chr17	+	39259639	39261639	2001	
chr17	72536469	72596081	CD300LD	NM_001115152	chr17	-	72588371	72590371	2001	
chr19	7675216	7711628	LOC100131801	NM_001171155	chr19	+	7692669	7694669	2001	
chr19	53544918	53561272	HERV-V2	NM_001191055	chr19	+	53545989	53547989	2001	
chr22	24296477	24320634	GSTT2B	NM_001080843	chr22	-	24303369	24305369	2001	
chr22	24296477	24320634	DDTL	NM_001084393	chr22	+	24307024	24309024	2001	
chr22	30939215	30980664	LOC730005	NM_001193336	chr22	-	30942670	30944670	2001	
chrX	70980284	70993016	CXorf49B	NM_001145139	chrX	+	70981138	70983138	2001	
chrX	151910466	151933518	CSAG2	NM_004909	chrX	+	151925732	151927732	2001	

Supplementary Table 4. Clover results indicate the number of chromosomes that returned transcription factor binding motifs as statistically over- or under-represented in HTE DHS overlapping promoters. Analysis was divided into three groups (all DHS, HTE-selective DHS, and ubiquitous DHS). Motifs with more than one entry in the databases were edited to include only the first occurrence of the motif .

All DHS x 2kbUp				TE-selective DHS x 2kbUp				Ubiquitous DHS x 2kbUp			
ID	**Name**	**$p < 0.01$**	**$p > 0.99$**	**ID**	**Name**	**$p < 0.01$**	**$p > 0.99$**	**ID**	**Name**	**$p < 0.01$**	**$p > 0.99$**
MA0028.1	ELK1	23	0	V$FRA1_Q5	FRA1	16	0	MA0027.1	En1	23	0
MA0039.2	Klf4	23	0	V$AP1_Q4_01	AP-1	15	0	MA0028.1	ELK1	23	0
MA0060.1	NFYA	23	0	V$AP1FJ_Q2	activator protein 1	10	0	MA0039.2	Klf4	23	0
MA0062.2	GABPA	23	0	V$BACH1_01	BTB and CNC homolog 1	9	0	MA0060.1	NFYA	23	0
MA0068.1	Pax4	23	0	V$MAFB_01	MAFB	9	0	MA0062.2	GABPA	23	0
MA0076.1	ELK4	23	0	V$NFE2_01	NF-E2 p45	9	0	MA0063.1	Nkx2-5	23	0
MA0079.2	SP1	23	0	V$CMAF_02	C-MAF	8	0	MA0068.1	Pax4	23	0
MA0080.2	SPI1	23	0	V$BACH2_01	BTB and CNC homolog 2	7	0	MA0076.1	ELK4	23	0
MA0081.1	SPIB	23	0	V$HEB_Q6	HEB	7	0	MA0079.2	SP1	23	0
MA0098.1	ETS1	23	0	V$P53_05	p53	7	0	MA0080.2	SPI1	23	0
MA0108.2	TBP	23	0	V$P63_01	p63	7	0	MA0081.1	SPIB	23	0
MA0113.1	NR3C1	23	0	V$MAF_Q6_01	MAF	6	0	MA0084.1	SRY	23	0
MA0136.1	ELF5	23	0	V$AP4_Q6	activator protein 4	5	0	MA0098.1	ETS1	23	0
V$ALX3_01	ALX-3	23	0	V$ELF1_Q5	ELF1	5	0	MA0108.2	TBP	23	0
V$ALX4_02	Alx-4	23	0	V$ETS_Q4	Ets	5	0	MA0113.1	NR3C1	23	0
V$AMEF2_Q6	myocyte enhancer factor	23	0	V$GABPALPHA_Q4	GABP-alpha	5	0	MA0151.1	ARID3A	23	0
V$ARX_01	Arx	23	0	V$MYOGENIN_Q6	myogenin	5	0	V$ALX3_01	ALX-3	23	0
V$BARHL1_01	Barhl-1	23	0	V$NRF2_Q4	heterodimer	5	0	V$ALX4_02	Alx-4	23	0

					containing Nrf2						
V$BARHL2_01	Barhl2	23	0	MA0080.2	SPI1	4	0	V$AMEF2_Q6	myocyte enhancer factor	23	0
V$BARX1_01	Barx1	23	0	MA0089.1	NFE2L1::MafG	4	0	V$AP2_Q6	activator protein 2	23	0
V$BARX2_01	Barx-2	23	0	MA0106.1	TP53	4	0	V$ARX_01	Arx	23	0
V$BCL6_01	BCL6	23	0	V$CACBINDINGPROTEIN_Q6	CAC-binding protein	4	0	V$BARHL1_01	Barhl-1	23	0
V$BRN2_01	POU factor Brn-2	23	0	V$ETS1_B	c-ETS-1 binding site	4	0	V$BARHL2_01	Barhl2	23	0
V$BRN3C_01	Brn-3c	23	0	V$ETS2_Q6	ETS2	4	0	V$BARX1_01	Barx1	23	0
V$BRN4_01	Brn-4	23	0	V$GR_Q6_01	half-site matrix	4	0	V$BARX2_01	Barx-2	23	0
V$BSX_01	Bsx	23	0	V$MATH1_Q2	E47:MATH1	4	0	V$BCL6_01	BCL6	23	0
V$CART1_02	CART1	23	0	V$MYOD_Q6	myoblast determining factor	4	0	V$BRN2_01	POU factor Brn-2	23	0
V$CDC5_01	cell division control protein 5	23	0	V$NEUROD_01	Neuro D	4	0	V$BRN3C_01	Brn-3c	23	0
V$CDP_03	CDP	23	0	V$PEA3_Q6	PEA3	4	0	V$BRN4_01	Brn-4	23	0
V$CDX1_01	Cdx-1	23	0	MA0039.2	Klf4	3	0	V$BSX_01	Bsx	23	0
V$CDX2_01	Cdx-2	23	0	MA0081.1	SPIB	3	0	V$CART1_02	CART1	23	0
V$CDX_Q5	Cdx	23	0	V$AR_Q6	half-site matrix	3	0	V$CDC5_01	cell division control protein 5	23	0
V$CEBP_01	CCAAT/enhancer binding protein	23	0	V$CKROX_Q2	CKROX	3	0	V$CDP_03	CDP	23	0
V$CEBPA_01	CCAAT/enhancer binding protein alpha	23	0	V$E2A_Q2	E2A	3	0	V$CDX1_01	Cdx-1	23	0
V$CETS1P54_02	c-Ets-1(p54)	23	0	V$ESE1_Q3	ESE1	3	0	V$CDX2_01	Cdx-2	23	0

V$CKROX_Q2	CKROX	23	0	V$HMX1_01	H6 homeobox 3	3	0	V$CDX_Q5	Cdx	23	0
V$CNOT3_01	CNOT3	23	0	V$NFY_C	NF-Y binding site	3	0	V$CEBP_01	CCAAT/enhancer binding protein	23	0
V$CPHX_01	Cphx	23	0	V$PU1_Q6	PU.1	3	0	V$CEBPA_01	CCAAT/enhancer binding protein alpha	23	0
V$CRX_02	Crx	23	0	V$PUR1_Q4	PUR1	3	0	V$CEBPGAMMA_Q6	C/EBPgamma	23	0
V$DBX1_01	Dbx-1	23	0	V$SMAD4_Q6	SMAD4	3	0	V$CETS1P54_01	c-Ets-1(p54)	23	0
V$DBX2_01	Dbx-2	23	0	V$STAT5A_04	signal transducer and activator of transcription 5a	3	0	V$CKROX_Q2	CKROX	23	0
V$DLX1_01	Dlx-1	23	0	V$TBX5_02	TBX5	3	0	V$CNOT3_01	CNOT3	23	0
V$DLX2_01	Dlx-2	23	0	V$TCF11_01	TCF11/KCR-F1/Nrf1 homodimers	3	0	V$CPHX_01	Cphx	23	0
V$DLX3_01	dlx3	23	0	MA0003.1	TFAP2A	2	0	V$CREBP1CJUN_01	CRE-binding protein 1:c-Jun heterodimer	23	0
V$DLX5_01	dlx5	23	0	MA0056.1	MZF1_1-4	2	0	V$CRX_02	Crx	23	0
V$DLX7_01	Dlx7	23	0	MA0136.1	ELF5	2	0	V$DBX1_01	Dbx-1	23	0
V$DOBOX4_01	Dobox4	23	0	MA0145.1	Tcfcp2l1	2	0	V$DBX2_01	Dbx-2	23	0
V$DOBOX5_01	Dobox5	23	0	MA0152.1	NFATC2	2	0	V$DLX1_01	Dlx-1	23	0
V$DUXL_01	Duxl	23	0	MA0156.1	FEV	2	0	V$DLX2_01	Dlx-2	23	0
V$E2F1_01	E2F1	23	0	V$AP2ALPHA_01	AP-2alpha	2	0	V$DLX3_01	dlx3	23	0
V$E2F6_01	E2F6	23	0	V$AP2GAMMA_01	AP-2gamma	2	0	V$DLX5_01	dlx5	23	0
V$ELF1_Q5	ELF1	23	0	V$AP2REP_01	AP-2 repressor	2	0	V$DLX7_01	Dlx7	23	0

V$EMX2_01	EMX2	23	0	V$ATF3_Q6	activating transcription factor 3	2	0	V$DOBOX4_01	Dobox4	23	0
V$EN1_02	En-1	23	0	V$CACCCBINDINGFACTOR_Q6	CACCC-binding factor	2	0	V$DOBOX5_01	Dobox5	23	0
V$EN2_01	En-2	23	0	V$CREB_02	cAMP-responsive element binding protein	2	0	V$DRI1_01	DRI1 b.s.	23	0
V$ERG_01	ERG	23	0	V$E12_Q6	E12	2	0	V$DUXL_01	Duxl	23	0
V$ESX1_01	Esx1	23	0	V$EBOX_Q6_01	Ebox	2	0	V$E2F1_01	E2F1	23	0
V$ETF_Q6	ETF	23	0	V$GKLF_02	GKLF (KLF4)	2	0	V$E2F1DP1_01	E2F-1:DP-1 heterodimer	23	0
V$ETS2_Q6	ETS2	23	0	V$GLI3_Q5_01	GLI3	2	0	V$E2F6_01	E2F6	23	0
V$ETS_Q6	Ets	23	0	V$IK1_01	Ikaros 1	2	0	V$E2F_Q2	E2F	23	0
V$EVI1_04	ectopic viral integration site 1 encoded factor	23	0	V$LBP1_Q6	LBP-1	2	0	V$EHF_01	EHF	23	0
V$EVX1_01	Evx-1	23	0	V$LMAF_Q2	LMAF	2	0	V$ELF1_Q5	ELF1	23	0
V$EVX2_01	Evx2	23	0	V$MAFA_Q4_01	MAFA	2	0	V$ELF5_01	ELF5	23	0
V$FLI1_Q6	FLI1	23	0	V$MAZ_Q6	MAZ	2	0	V$EMX2_01	EMX2	23	0
V$FOXP3_01	forkhead box P3	23	0	V$MZF1_Q5	MZF1	2	0	V$EN2_01	En-2	23	0
V$FREAC7_01	Fork head RElated ACtivator-7	23	0	V$NERF_Q2	new ets-related factor 1a	2	0	V$ERG_01	ERG	23	0
V$GABPALPHA_Q4	GABP-alpha	23	0	V$NFAT_Q4_01	NF-AT	2	0	V$ESX1_01	Esx1	23	0
V$GADP_01	Growth-associated binding protein	23	0	V$SMAD3_Q6	SMAD3	2	0	V$ETF_Q6	ETF	23	0
V$GBX1_01	Gbx1	23	0	V$SP1_Q2_01	Sp1	2	0	V$EVI1_04	ectopic viral	23	0

									integration site 1 encoded factor		
V$GBX2_01	Gbx2	23	0	V$SRF_Q5_01	SRF	2	0	V$EVX1_01	Evx-1	23	0
V$GSC_01	Gsc	23	0	V$STAT3_02	signal transducer and activator of transcription 3	2	0	V$EVX2_01	Evx2	23	0
V$GSH2_01	GSH2	23	0	V$STAT6_02	signal transducer and activator of transcription 6	2	0	V$FOXO3_01	fork head box O3	23	0
V$HB24_01	HB24	23	0	V$TAL1_01	Tal-1 (Scl)	2	0	V$FOXO3A_Q1	FOXO3A	23	0
V$HB9_01	HB9	23	0	V$TAL1BETAITF2_01	Tal-1beta:ITF-2 heterodimer	2	0	V$FOXO4_01	fork head box O4	23	0
V$HDX_01	Hdx	23	0	V$TBR2_01	TBR2	2	0	V$FOXP3_01	forkhead box P3	23	0
V$HMBOX1_01	Hmbox1	23	0	V$TEL2_Q6	Tel-2	2	0	V$FREAC7_01	Fork head RElated ACtivator-7	23	0
V$HMGIY_01	HMGIY	23	0	V$USF_Q6	upstream stimulating factor	2	0	V$GABPALPHA_Q4	GABP-alpha	23	0
V$HMX1_02	HMX1	23	0	V$AP2_Q3	AP-2	2	1	V$GADP_01	Growth-associated binding protein	23	0
V$HMX3_02	Nkx5-1	23	0	V$CACD_01	CACD	2	1	V$GBX1_01	Gbx1	23	0
V$HNF1_02	HNF-1alpha	23	0	V$PR_Q2	half-site matrix	2	1	V$GBX2_01	Gbx2	23	0
V$HNF1B_01	HNF-1beta	23	0	MA0002.2	RUNX1	1	0	V$GKLF_02	GKLF (KLF4)	23	0
V$HNF3_Q6_01	HNF3	23	0	MA0004.1	Arnt	1	0	V$GSC_01	Gsc	23	0
V$HOMEZ_01	Homez	23	0	MA0031.1	FOXD1	1	0	V$GSH2_01	GSH2	23	0
V$HOX13_02	HOXA5	23	0	MA0047.2	Foxa2	1	0	V$HB24_01	HB24	23	0
V$HOXA10_01	HOXA10	23	0	MA0058.1	MAX	1	0	V$HB9_01	HB9	23	0

V$HOXA11_01	HOXA11	23	0	MA0059.1	MYC::MAX	1	0	V$HBP1_Q2	hbp1	23	0
V$HOXA13_02	HOXA13	23	0	MA0060.1	NFYA	1	0	V$HDX_01	Hdx	23	0
V$HOXA1_01	HOXA1	23	0	MA0061.1	NF-kappaB	1	0	V$HMBOX1_01	Hmbox1	23	0
V$HOXA2_01	HoxA2	23	0	MA0067.1	Pax2	1	0	V$HMGIY_01	HMGIY	23	0
V$HOXA3_02	HOXA3	23	0	MA0090.1	TEAD1	1	0	V$HMX1_02	HMX1	23	0
V$HOXA4_01	HOXA4	23	0	MA0091.1	TAL1::TCF3	1	0	V$HMX3_02	Nkx5-1	23	0
V$HOXA6_01	HOXA6	23	0	MA0092.1	Hand1::Tcfe2a	1	0	V$HNF1_02	HNF-1alpha	23	0
V$HOXA7_02	HOXA7	23	0	MA0093.1	USF1	1	0	V$HNF1B_01	HNF-1beta	23	0
V$HOXA9_01	hoxa9	23	0	MA0100.1	Myb	1	0	V$HNF3_Q6_01	HNF3	23	0
V$HOXB13_01	HOXB13	23	0	MA0104.2	Mycn	1	0	V$HNF3B_01	Hepatocyte Nuclear Factor 3beta	23	0
V$HOXB3_01	HOXB3	23	0	MA0107.1	RELA	1	0	V$HNF6_Q6	HNF6	23	0
V$HOXB4_01	HOXB4	23	0	MA0108.2	TBP	1	0	V$HOMEZ_01	Homez	23	0
V$HOXB5_01	HoxB5	23	0	MA0117.1	Mafb	1	0	V$HOX13_02	HOXA5	23	0
V$HOXB6_01	HOXB6	23	0	MA0130.1	ZNF354C	1	0	V$HOXA10_01	HOXA10	23	0
V$HOXB7_01	HOXB7	23	0	MA0146.1	Zfx	1	0	V$HOXA11_01	HOXA11	23	0
V$HOXB8_01	HOXB8	23	0	MA0147.1	Myc	1	0	V$HOXA13_02	HOXA13	23	0
V$HOXB9_01	HOXB9	23	0	MA0150.1	NFE2L2	1	0	V$HOXA1_01	HOXA1	23	0
V$HOXC10_01	HOXC10	23	0	MA0154.1	EBF1	1	0	V$HOXA2_01	HoxA2	23	0
V$HOXC11_01	HOXC11	23	0	MA0157.1	FOXO3	1	0	V$HOXA3_02	HOXA3	23	0
V$HOXC12_01	HOXC12	23	0	MA0161.1	NFIC	1	0	V$HOXA4_01	HOXA4	23	0
V$HOXC13_01	HOXC13	23	0	MA0162.1	Egr1	1	0	V$HOXA6_01	HOXA6	23	0
V$HOXC4_01	HOXC4	23	0	MA0164.1	Nr2e3	1	0	V$HOXA7_02	HOXA7	23	0

V$HOXC5_01	HOXC5	23	0	V$ALX4_01	Alx-4	1	0	V$HOXA9_01	hoxa9	23	0
V$HOXC6_01	HOXC6	23	0	V$AREB6_01	AREB6 (Atp1a1 regulatory element binding factor 6)	1	0	V$HOXB13_01	HOXB13	23	0
V$HOXC8_01	HOXC-8	23	0	V$ATF5_01	ATF5 binding site	1	0	V$HOXB3_01	HOXB3	23	0
V$HOXC9_01	HOXC9	23	0	V$BEN_01	BEN	1	0	V$HOXB4_01	HOXB4	23	0
V$HOXD10_01	HOXD10	23	0	V$CEBP_01	CCAAT/enhancer binding protein	1	0	V$HOXB5_01	HoxB5	23	0
V$HOXD11_01	HOXD11	23	0	V$CEBPE_01	cebpe	1	0	V$HOXB6_01	HOXB6	23	0
V$HOXD12_01	HOXD12	23	0	V$CETS1P54_01	c-Ets-1(p54)	1	0	V$HOXB7_01	HOXB7	23	0
V$HOXD13_01	HOXD13	23	0	V$CHCH_01	Churchill	1	0	V$HOXB8_01	HOXB8	23	0
V$HOXD1_01	HOXD1	23	0	V$CP2_01	CP2	1	0	V$HOXB9_01	HOXB9	23	0
V$HOXD3_01	HOXD3	23	0	V$CTCF_02	CCCTC-binding factor	1	0	V$HOXC10_01	HOXC10	23	0
V$HOXD8_01	HOXD8	23	0	V$DEC_Q1	DEC	1	0	V$HOXC11_01	HOXC11	23	0
V$HP1SITEFACTOR_Q6	HP1 site factor	23	0	V$DELTAEF1_01	deltaEF1	1	0	V$HOXC12_01	HOXC12	23	0
V$IPF1_05	homeobox transcription factor Pdx-1	23	0	V$DMRT5_01	DMRT5	1	0	V$HOXC13_01	HOXC13	23	0
V$IRF3_Q3	IRF3	23	0	V$E47_02	E47	1	0	V$HOXC4_01	HOXC4	23	0
V$IRF_Q6	IRF	23	0	V$EBF_Q6	EBF	1	0	V$HOXC5_01	HOXC5	23	0
V$IRX2_01	Irx2	23	0	V$ER_Q6_02	half-site matrix, half-ERE	1	0	V$HOXC6_01	HOXC6	23	0
V$IRX3_01	Irx-3	23	0	V$FLI1_Q6	FLI1	1	0	V$HOXC8_01	HOXC-8	23	0
V$IRX4_01	IRX4	23	0	V$FOXO4_02	fork head box O4	1	0	V$HOXC9_01	HOXC9	23	0
V$IRX5_01	Irx5	23	0	V$FXR_Q2	half-site	1	0	V$HOXD10_01	HOXD10	23	0
V$IRXB3_01	IRXB3	23	0	V$GLI1_01	GLI1	1	0	V$HOXD11_01	HOXD11	23	0
V$ISL2_01	Isl2	23	0	V$GLI2_01	GLI2	1	0	V$HOXD12_01	HOXD12	23	0

V$ISX_01	isx	23	0	V$GZF1_01	plays a role in renal branching morphogenesis	1	0	V$HOXD13_01	HOXD13	23	0
V$K2B_01	K-2b	23	0	V$HELIOSA_01	Helios A	1	0	V$HOXD1_01	HOXD1	23	0
V$KROX_Q6	KROX	23	0	V$HEN1_01	HEN1	1	0	V$HOXD3_01	HOXD3	23	0
V$LBX2_01	Lbx2	23	0	V$HFH8_01	HNF-3/Fkh Homolog-8	1	0	V$HOXD8_01	HOXD8	23	0
V$LH2_01	LH-2	23	0	V$HNF3A_01	FOXA1	1	0	V$HP1SITEFACTOR_Q6	HP1 site factor	23	0
V$LHX3_02	Lhx3	23	0	V$HNF4_Q6_01	HNF4	1	0	V$IPF1_05	homeobox transcription factor Pdx-1	23	0
V$LHX4_01	Lhx4	23	0	V$HSF1_Q6	HSF1	1	0	V$IRF3_Q3	IRF3	23	0
V$LHX5_01	Lhx5	23	0	V$HSF2_02	Heat shock transcription factor 2	1	0	V$IRF7_01	interferon regulatory factor 7	23	0
V$LHX61_01	lhx6.1	23	0	V$IPF1_Q6	IPF1	1	0	V$IRF_Q6	IRF	23	0
V$LHX8_01	Lhx8	23	0	V$KID3_01	Kid3	1	0	V$IRX2_01	Irx2	23	0
V$LHX9_01	Lhx9	23	0	V$LBP9_01	LBP9 (Tcfcp211)	1	0	V$IRX3_01	Irx-3	23	0
V$LIM1_01	Lim-1	23	0	V$LFA1_Q6	LF-A1	1	0	V$IRX4_01	IRX4	23	0
V$LMX1_01	Lmx-1	23	0	V$LMO2COM_01	complex of Lmo2 bound to Tal-1, E2A proteins, and GATA-1, half-site 1	1	0	V$IRX5_01	Irx5	23	0
V$LMX1B_01	lmx1b	23	0	V$LRF_Q2	LRF	1	0	V$IRXB3_01	IRXB3	23	0
V$MAZ_Q6	MAZ	23	0	V$LTF_Q6	LTF	1	0	V$ISL2_01	Isl2	23	0
V$MEF2_Q6_01	MEF-2	23	0	V$MEIS1_01	Meis-1 (myeloid ecotropic viral integration site 1)	1	0	V$ISX_01	isx	23	0
V$MEIS1_02	Meis1	23	0	V$MEIS2_02	MEIS2	1	0	V$K2B_01	K-2b	23	0
V$MEIS2_01	Meis2	23	0	V$MTF1_01	MTF1	1	0	V$KROX_Q6	KROX	23	0

V$MMEF2_Q6	myocyte enhancer factor	23	0	V$MYCMAX_03	c-Myc:Max heterodimer	1	0	V$LBX2_01	Lbx2	23	0
V$MOX1_01	Mox1	23	0	V$NF1_Q6	nuclear factor 1	1	0	V$LH2_01	LH-2	23	0
V$MRG2_01	MRG2	23	0	V$NFAT2_Q5	NF-AT2	1	0	V$LHX3_02	Lhx3	23	0
V$MSX1_01	msh-like (muscle segment homeobox) homeobox protein 1	23	0	V$NFAT3_Q3	NFAT3	1	0	V$LHX4_01	Lhx4	23	0
V$MSX2_01	Msx-2	23	0	V$NFKAPPAB_01	NF-kappaB	1	0	V$LHX5_01	Lhx5	23	0
V$MSX3_01	Msx-3	23	0	V$NFKB_Q6	NF-kappaB	1	0	V$LHX61_01	lhx6.1	23	0
V$NCX_02	Ncx	23	0	V$NMYC_01	N-Myc	1	0	V$LHX8_01	Lhx8	23	0
V$NFAT1_Q6	NFAT1	23	0	V$NRSF_Q4	NRSF	1	0	V$LHX9_01	Lhx9	23	0
V$NFAT_Q6	Nuclear factor of activated T-cells	23	0	V$OCT1_07	octamer factor 1	1	0	V$LIM1_01	Lim-1	23	0
V$NFY_01	nuclear factor Y (Y-box binding factor)	23	0	V$P50RELAP65_Q5_01	P50:RELA-P65	1	0	V$LMX1_01	Lmx-1	23	0
V$NKX11_01	Nkx1-1	23	0	V$PAX_Q6	Pax	1	0	V$LMX1B_01	lmx1b	23	0
V$NKX12_01	Nkx1-2	23	0	V$POU1F1_Q6	POU1F1	1	0	V$MAZ_Q6	MAZ	23	0
V$NKX21_01	Nkx2-1	23	0	V$PPARA_01	PPAR:RXR heterodimers	1	0	V$MEF2_Q6_01	MEF-2	23	0
V$NKX22_02	NKX22	23	0	V$PPARG_Q6	half-site	1	0	V$MEIS1_02	Meis1	23	0
V$NKX23_01	Nkx2-3	23	0	V$RBPJK_01	RBP-Jkappa	1	0	V$MEIS2_01	Meis2	23	0
V$NKX24_01	Nkx2-4	23	0	V$REX1_03	REX1	1	0	V$MMEF2_Q6	myocyte enhancer factor	23	0
V$NKX25_03	NKX25	23	0	V$SEF1_C	SEF1 binding site	1	0	V$MOX1_01	Mox1	23	0
V$NKX26_01	Nkx2-6	23	0	V$SIX1_01	Six-1	1	0	V$MRG2_01	MRG2	23	0
V$NKX29_01	Nkx2-9	23	0	V$SIX2_01	Six-2	1	0	V$MSX1_01	msh-like (muscle	23	0

									segment homeobox) homeobox protein 1		
V$NKX32_02	Nkx3-2	23	0	V$SMAD1_01	SMAD1	1	0	V$MSX2_01	Msx-2	23	0
V$NKX3A_02	Nkx3A	23	0	V$SMAD_Q6	SMAD	1	0	V$MSX3_01	Msx-3	23	0
V$NKX52_01	Nkx5-2	23	0	V$SOX_01	SOX	1	0	V$NANOG_02	Nanog	23	0
V$NKX61_01	NKX6-1	23	0	V$T3R_Q6	half-site matrix	1	0	V$NCX_01	Ncx	23	0
V$NKX62_Q2	NK related homeobox factor 6-2	23	0	V$TATA_01	cellular and viral TATA box elements	1	0	V$NFAT3_Q3	NFAT3	23	0
V$NKX63_01	Nkx6-3	23	0	V$TEF_01	TEF b.s.	1	0	V$NFAT_Q6	Nuclear factor of activated T-cells	23	0
V$NRF2_01	nuclear respiratory factor 2	23	0	V$TGIF_01	TGIF (5'TG3' interacting factor)	1	0	V$NFY_01	nuclear factor Y (Y-box binding factor)	23	0
V$OBOX1_01	Obox1	23	0	V$TITF1_Q3	TTF-1, TITF1 (thyroid transcription factor 1)	1	0	V$NKX11_01	Nkx1-1	23	0
V$OBOX2_01	Obox2	23	0	V$TR4_01	TR4	1	0	V$NKX12_01	Nkx1-2	23	0
V$OBOX3_01	Obox3	23	0	V$UF1H3BETA_Q6	UF1H3BETA	1	0	V$NKX21_01	Nkx2-1	23	0
V$OBOX5_01	Obox5	23	0	V$ZBED6_01	ZBED6	1	0	V$NKX22_02	NKX22	23	0
V$OBOX6_01	Obox6	23	0	V$ZIC3_01	zinc finger protein of the cerebellum 3	1	0	V$NKX23_01	Nkx2-3	23	0
V$OCT1_03	octamer factor 1	23	0	V$ZNF515_01	Glis binding sites	1	0	V$NKX24_01	Nkx2-4	23	0
V$OCT2_01	2-Oct	23	0	MA0124.1	NKX3-1	1	1	V$NKX25_02	homeo domain factor Nkx-2.5/Csx,	23	0

									tinman homolog		
V$OCTAMER_01	Octamer	23	0	MA0138.2	REST	1	1	V$NKX26_01	Nkx2-6	23	0
V$OG2_02	OG-2	23	0	MA0153.1	HNF1B	1	1	V$NKX29_01	Nkx2-9	23	0
V$OTP_01	OTP	23	0	V$CEBPDELTA_Q6	C/EBPdelta	1	1	V$NKX32_02	Nkx3-2	23	0
V$OTX1_01	Otx1	23	0	V$EVI1_06	ectopic viral integration site 1 encoded factor	1	1	V$NKX3A_02	Nkx3A	23	0
V$OTX2_01	Otx2	23	0	V$GCNF_01	GCNF (germ cell nuclear factor)	1	1	V$NKX52_01	Nkx5-2	23	0
V$OTX3_01	Otx3	23	0	V$HIF2A_01	HIF-2alpha	1	1	V$NKX61_01	NKX6-1	23	0
V$P53_03	tumor suppressor p53	23	0	V$IK3_01	Ikaros 3	1	1	V$NKX62_Q2	NK related homeobox factor 6-2	23	0
V$PARP_Q3	PARP	23	0	V$MECP2_01	MECP2 b.s.	1	1	V$NKX63_01	Nkx6-3	23	0
V$PAX2_01	Pax-2	23	0	V$MEIS1BHOXA9_02	Meis-1b:HOXA9 heterodimeric binding	1	1	V$NRF1_Q6	nuclear respiratory factor 1	23	0
V$PAX6_02	pax6	23	0	V$NKX22_01	NK2 class homeobox factor 2	1	1	V$NRF2_01	nuclear respiratory factor 2	23	0
V$PAX7_01	Pax-7	23	0	V$RFX1_02	X-box binding protein RFX1	1	1	V$OBOX1_01	Obox1	23	0
V$PAX8_01	Pax-8 binding sites	23	0	V$SIX3_01	Six-3	1	1	V$OBOX2_01	Obox2	23	0
V$PBX1_01	Pbx-1	23	0	V$VDR_Q3	vitamin D receptor; mediates vitamin D3-signaling, often dimerizes with RXR-alpha	1	1	V$OBOX3_01	Obox3	23	0
V$PEA3_Q6	PEA3	23	0	V$ZABC1_01	ZABC1 b.s.	1	1	V$OBOX5_01	Obox5	23	0
V$PIT1_01	Pit-1	23	0	V$FOXP1_01	FOXP1	1	2	V$OBOX6_01	Obox6	23	0

V$PITX1_01	Pitx1	23	0	V$PARP_Q3	PARP	1	2	V$OCT1_03	octamer factor 1	23	0
V$PITX2_01	PITX2	23	0	MA0019.1	Ddit3::Cebpa	1	3	V$OCT2_01	2-Oct	23	0
V$PITX3_01	Pitx3	23	0	MA0006.1	Arnt::Ahr	0	1	V$OCT_Q6	Octamer	23	0
V$PKNOX2_01	PKNOX2	23	0	MA0017.1	NR2F1	0	1	V$OCTAMER_01	Octamer	23	0
V$PMX2A_01	PMX2A	23	0	MA0029.1	Evi1	0	1	V$OG2_02	OG-2	23	0
V$PMX2B_01	PMX2B	23	0	MA0032.1	FOXC1	0	1	V$OTP_01	OTP	23	0
V$POU2F3_01	POU2F3	23	0	MA0042.1	FOXI1	0	1	V$OTX1_01	Otx1	23	0
V$POU6F1_02	POU6F1	23	0	MA0051.1	IRF2	0	1	V$OTX2_01	Otx2	23	0
V$PREP1_01	PREP1	23	0	MA0062.2	GABPA	0	1	V$OTX3_01	Otx3	23	0
V$PROP1_02	Prop-1	23	0	MA0063.1	Nkx2-5	0	1	V$OTX_Q1	OTX	23	0
V$PSX1_01	PSX1	23	0	MA0074.1	RXRA::VDR	0	1	V$P53_03	tumor suppressor p53	23	0
V$PU1_Q4	PU.1	23	0	MA0076.1	ELK4	0	1	V$PARP_Q3	PARP	23	0
V$RAX_01	rax	23	0	MA0077.1	SOX9	0	1	V$PAX2_01	Pax-2	23	0
V$RHOX11_01	Rhox11	23	0	MA0084.1	SRY	0	1	V$PAX6_02	pax6	23	0
V$S8_02	S8	23	0	MA0087.1	Sox5	0	1	V$PAX7_01	Pax-7	23	0
V$SATB1_01	Consensus SATB1 Binding Sequence	23	0	MA0101.1	REL	0	1	V$PAX8_01	Pax-8 binding sites	23	0
V$SHOX2_01	Shox2	23	0	MA0115.1	NR1H2::RXRA	0	1	V$PBX1_01	Pbx-1	23	0
V$SIX1_01	Six-1	23	0	MA0131.1	MIZF	0	1	V$PEA3_Q6	PEA3	23	0
V$SIX2_01	Six-2	23	0	MA0132.1	Pdx1	0	1	V$PIT1_01	Pit-1	23	0
V$SIX3_01	Six-3	23	0	MA0158.1	HOXA5	0	1	V$PITX1_01	Pitx1	23	0
V$SIX4_01	six4	23	0	MA0160.1	NR4A2	0	1	V$PITX2_01	PITX2	23	0
V$SIX6_01	Six-6	23	0	MA0163.1	PLAG1	0	1	V$PITX3_01	Pitx3	23	0

V$SOX2_Q6	SOX2	23	0	MA0258.1	ESR2	0	1	V$PKNOX2_01	PKNOX2	23	0
V$SOX4_01	SOX4	23	0	MA0259.1	HIF1A::ARNT	0	1	V$PMX2A_01	PMX2A	23	0
V$SP1SP3_Q4	SP1:SP3	23	0	V$AHR_Q5	aryl hydrocarbon / dioxin receptor	0	1	V$PMX2B_01	PMX2B	23	0
V$SP2_01	SP2	23	0	V$AHRARNT_02	aryl hydrocarbon receptor:Arnt heterodimers, fixed core	0	1	V$POU1F1_Q6	POU1F1	23	0
V$SP4_Q5	SP4	23	0	V$ARX_01	Arx	0	1	V$POU2F3_01	POU2F3	23	0
V$SRY_01	sex-determining region Y gene product	23	0	V$ATF4_Q2	activating transcription factor 4	0	1	V$POU6F1_02	POU6F1	23	0
V$STAT1_02	signal transducer and activator of transcription 1	23	0	V$BCL6_01	BCL6	0	1	V$PREP1_01	PREP1	23	0
V$STAT1STAT1_Q3	STAT1:STAT1	23	0	V$BRACH_01	Brachyury	0	1	V$PROP1_02	Prop-1	23	0
V$STAT3_02	signal transducer and activator of transcription 3	23	0	V$BRF1_01	BRF-1	0	1	V$PSX1_01	PSX1	23	0
V$STAT4_01	signal transducer and activator of transcription 4	23	0	V$BSX_01	Bsx	0	1	V$PU1_Q4	PU.1	23	0
V$STAT5A_03	signal transducer and activator of transcription 5a	23	0	V$CART1_01	Cart-1 (cartilage homeoprotein 1)	0	1	V$PXRRXR_01	RXR half-site	23	0
V$STAT6_01	signal transducer and activator of transcription 6	23	0	V$CDP_02	transcriptional repressor CDP	0	1	V$RAX_01	rax	23	0
V$TATA_01	cellular and viral TATA box elements	23	0	V$CEBPB_01	CCAAT/enhancer binding protein beta	0	1	V$RHOX11_01	Rhox11	23	0

V$TCF4_01	TCF-4	23	0	V$COUP_01	COUP-TF, HNF-4	0	1	V$S8_02	S8	23	0
V$TEF_Q6	TEF	23	0	V$CPHX_01	Cphx	0	1	V$SAP1A_01	SAP-1a	23	0
V$TGIF2_01	TGIF2	23	0	V$CREBP1_01	cAMP-responsive element binding protein 1	0	1	V$SATB1_01	Consensus SATB1 Binding Sequence	23	0
V$TGIF_02	TGIF1	23	0	V$CREL_01	c-Rel	0	1	V$SHOX2_01	Shox2	23	0
V$TST1_01	POU-factor Tst-1/Oct-6	23	0	V$CRX_02	Crx	0	1	V$SIX1_01	Six-1	23	0
V$UNCX4.1_01	Uncx-4.1	23	0	V$DBP_Q6	DBP	0	1	V$SIX2_01	Six-2	23	0
V$VAX1_01	Vax-1	23	0	V$DLX2_01	Dlx-2	0	1	V$SIX3_01	Six-3	23	0
V$VAX2_01	Vax-2	23	0	V$DLX5_01	dlx5	0	1	V$SIX4_01	six4	23	0
V$VSX1_01	Vsx1	23	0	V$DOBOX4_01	Dobox4	0	1	V$SIX6_01	Six-6	23	0
V$ZFP206_01	Zfp206	23	0	V$DOBOX5_01	Dobox5	0	1	V$SOX2_Q6	SOX2	23	0
MA0143.1	Sox2	22	0	V$DUXL_01	Duxl	0	1	V$SOX4_01	SOX4	23	0
MA0151.1	ARID3A	22	0	V$E2F1_Q4_01	E2F-1	0	1	V$SOX_Q6	SOX	23	0
V$AP2_Q6	activator protein 2	22	0	V$E2F1DP1_01	E2F-1:DP-1 heterodimer	0	1	V$SP1SP3_Q4	SP1:SP3	23	0
V$BEN_01	BEN	22	0	V$E2F1DP2_01	E2F-1:DP-2 heterodimer	0	1	V$SP2_01	SP2	23	0
V$CEBPB_01	CCAAT/enhancer binding protein beta	22	0	V$E2F4DP1_01	E2F-4:DP-1 heterodimer	0	1	V$SP4_Q5	SP4	23	0
V$CEBPGAMMA_Q6	C/EBPgamma	22	0	V$E2F4DP2_01	E2F-4:DP-2 heterodimer	0	1	V$STAT1_02	signal transducer and activator of transcription 1	23	0
V$CHCH_01	Churchill	22	0	V$E2F6_01	E2F6	0	1	V$STAT1STAT1_Q3	STAT1:STAT1	23	0
V$DRI1_01	DRI1 b.s.	22	0	V$E2F_Q4	E2F	0	1	V$STAT3_02	signal transducer and	23	0

		22	0			0	1		activator of transcription 3	23	
V$EHF_01	EHF	22	0	V$EGR3_01	early growth response gene 3 product	0	1	V$STAT4_01	signal transducer and activator of transcription 4	23	0
V$FOXJ2_02	fork head box J 2	22	0	V$EMX2_01	EMX2	0	1	V$STAT5A_03	signal transducer and activator of transcription 5a	23	0
V$FOXO3A_Q1	FOXO3A	22	0	V$EN1_02	En-1	0	1	V$STAT6_01	signal transducer and activator of transcription 6	23	0
V$FOXO4_01	fork head box O4	22	0	V$EN2_01	En-2	0	1	V$TATA_01	cellular and viral TATA box elements	23	0
V$GABP_B	GA binding protein	22	0	V$EVX1_01	Evx-1	0	1	V$TCF4_01	TCF-4	23	0
V$HNF3B_01	Hepatocyte Nuclear Factor 3beta	22	0	V$EVX2_01	Evx2	0	1	V$TEF_Q6	TEF	23	0
V$IRF7_01	interferon regulatory factor 7	22	0	V$GATA1_01	GATA-binding factor 1	0	1	V$TGIF2_01	TGIF2	23	0
V$NFAT2_Q5	NF-AT2	22	0	V$GATA2_01	GATA-binding factor 2	0	1	V$TGIF_02	TGIF1	23	0
V$NFAT3_Q3	NFAT3	22	0	V$GATA3_02	GATA-binding factor 3	0	1	V$TST1_01	POU-factor Tst-1/Oct-6	23	0

V$NRF1_Q6	nuclear respiratory factor 1	22	0	V$GATA4_Q3	GATA-4	0	1	V$UNCX4.1_01	Uncx-4.1	23	0
V$OCT_Q6	Octamer	22	0	V$GATA_C	GATA binding site	0	1	V$VAX1_01	Vax-1	23	0
V$SOX_Q6	SOX	22	0	V$GBX1_01	Gbx1	0	1	V$VAX2_01	Vax-2	23	0
V$TR4_01	TR4	22	0	V$GBX2_01	Gbx2	0	1	V$VSX1_01	Vsx1	23	0
MA0040.1	Foxq1	21	0	V$GFI1_Q6	Gfi1	0	1	V$ZFP206_01	Zfp206	23	0
MA0050.1	IRF1	21	0	V$GSC_01	Gsc	0	1	MA0033.1	FOXL1	22	0
MA0063.1	Nkx2-5	21	0	V$GSH2_01	GSH2	0	1	MA0040.1	Foxq1	22	0
MA0139.1	CTCF	21	0	V$HB9_01	HB9	0	1	MA0050.1	IRF1	22	0
MA0152.1	NFATC2	21	0	V$HDX_01	Hdx	0	1	MA0143.1	Sox2	22	0
MA0156.1	FEV	21	0	V$HFH4_01	HFH4 (FOXJ1)	0	1	MA0158.1	HOXA5	22	0
V$BLIMP1_Q6	BLIMP1	21	0	V$HMBOX1_01	Hmbox1	0	1	V$BEN_01	BEN	22	0
V$COMP1_01	COMP1	21	0	V$HMEF2_Q6	myocyte enhancer factor	0	1	V$BRCA_01	BRCA1 containing protein complex with USF2	22	0
V$DMRT7_01	DMRT7	21	0	V$HMGIY_Q6	HMG IY	0	1	V$CEBPB_01	CCAAT/enhancer binding protein beta	22	0
V$EGR_Q6	Egr	21	0	V$HNF1_Q6	HNF1	0	1	V$COMP1_01	COMP1	22	0
V$FOXO3_01	fork head box O3	21	0	V$HNF4ALPHA_Q6	HNF4alpha	0	1	V$CREB_01	cAMP-responsive element binding protein	22	0
V$GKLF_02	GKLF (KLF4)	21	0	V$HOXA13_01	HOXA13 binding site	0	1	V$CREBATF_Q6	CREB, ATF	22	0
V$HELIOSA_02	Helios A	21	0	V$HOXA3_01	HOXA3 (homeobox cluster protein)	0	1	V$DMRT7_01	DMRT7	22	0

V$HFH1_01	HNF-3/Fkh Homolog 1	21	0	V$HOXA7_03	HOXA7	0	1	V$E2F1DP2_01	E2F-1:DP-2 heterodimer	22	0
V$HNF6_Q6	HNF6	21	0	V$HOXB3_01	HOXB3	0	1	V$E2F4DP2_01	E2F-4:DP-2 heterodimer	22	0
V$ICSBP_Q6	ICSBP	21	0	V$HOXB7_01	HOXB7	0	1	V$ETS_Q4	Ets	22	0
V$ISRE_01	interferon-stimulated response element	21	0	V$HP1SITEFACTOR_Q6	HP1 site factor	0	1	V$FAC1_01	fetal Alz-50 clone 1	22	0
V$NANOG_02	Nanog	21	0	V$IK2_01	Ikaros 2	0	1	V$FLI1_Q6	FLI1	22	0
V$OCT4_01	Sox2-Oct4 joint motif, in silico predicted	21	0	V$ING4_01	ING4	0	1	V$FOXJ2_02	fork head box J 2	22	0
V$POU1F1_Q6	POU1F1	21	0	V$IRF1_Q6	IRF-1	0	1	V$FOXO1_02	fork head box O1	22	0
V$PXRRXR_01	RXR half-site	21	0	V$IRF3_Q3	IRF3	0	1	V$GABP_B	GA binding protein	22	0
V$SIRT6_01	SIRT6	21	0	V$IRF7_01	interferon regulatory factor 7	0	1	V$GATA4_Q3	GATA-4	22	0
V$ZFP281_01	Zfp281	21	0	V$IRF_Q6_01	IRF	0	1	V$HELIOSA_02	Helios A	22	0
V$ALPHACP1_01	alpha-CP1	20	0	V$IRX2_01	Irx2	0	1	V$HFH1_01	HNF-3/Fkh Homolog 1	22	0
V$AP1_Q6	activator protein 1	20	0	V$IRX3_02	Irx-3	0	1	V$ICSBP_Q6	ICSBP	22	0
V$CREB_01	cAMP-responsive element binding protein	20	0	V$IRX4_01	IRX4	0	1	V$NFAT1_Q6	NFAT1	22	0
V$CREBP1CJUN_0	CRE-binding protein 1:c-Jun	20	0	V$IRX5_01	Irx5	0	1	V$NFAT2_Q5	NF-AT2	22	0

1	heterodimer										
V$E2F1DP1_01	E2F-1:DP-1 heterodimer	20	0	V$IRXB3_01	IRXB3	0	1	V$OCT4_01	Sox2-Oct4 joint motif, in silico predicted	22	0
V$E2F_Q2	E2F	20	0	V$ISL1_Q6	ISL1	0	1	V$RNF96_01	RNF96	22	0
V$FAC1_01	fetal Alz-50 clone 1	20	0	V$K2B_01	K-2b	0	1	V$STAT3STAT3_Q3	STAT3:STAT3	22	0
V$FOXO1_01	fork head box O1	20	0	V$KROX_Q6	KROX	0	1	V$YY1_01	Yin and Yang 1	22	0
V$FPM315_01	Zinc finger protein FPM315 with KRAB and SCAN domains	20	0	V$LH2_01	LH-2	0	1	MA0152.1	NFATC2	21	0
V$GAF_Q6	GAF	20	0	V$LHX3_01	LIM homeobox transcription factor 3	0	1	MA0156.1	FEV	21	0
V$GATA4_Q3	GATA-4	20	0	V$LHX4_01	Lhx4	0	1	I$ANTP_Q6_01	Antp	21	0
V$GFI1_01	growth factor independence 1	20	0	V$LHX61_01	lhx6.1	0	1	V$AFP1_Q6	AFP1	21	0
V$HBP1_Q2	hbp1	20	0	V$LHX9_01	Lhx9	0	1	V$ALPHACP1_01	alpha-CP1	21	0
V$HNF3ALPHA_Q6	HNF3alpha	20	0	V$LXR_Q3	LXR	0	1	V$AREB6_04	AREB6 (Atp1a1 regulatory element binding factor 6)	21	0
V$RNF96_01	RNF96	20	0	V$MEF2_01	myogenic enhancer factor 2	0	1	V$CHCH_01	Churchill	21	0
V$UF1H3BETA_Q6	UF1H3BETA	20	0	V$MRF2_01	modulator recognition factor 2	0	1	V$EGR_Q6	Egr	21	0
MA0046.1	HNF1A	19	0	V$NFKAPPAB50_01	NF-kappaB (p50)	0	1	V$ETS2_Q6	ETS2	21	0

MA0158.1	HOXA5	19	0	V$NKX12_01	Nkx1-2	0	1	V$FREAC2_01	Fork head RElated ACtivator -2	21	0
I$ANTP_Q6_01	Antp	19	0	V$NKX21_01	Nkx2-1	0	1	V$GAF_Q6	GAF	21	0
V$AFP1_Q6	AFP1	19	0	V$NKX26_01	Nkx2-6	0	1	V$GATA3_03	GATA-binding factor 3	21	0
V$CREBATF_Q6	CREB, ATF	19	0	V$NKX32_02	Nkx3-2	0	1	V$ISRE_01	interferon-stimulated response element	21	0
V$OTX_Q1	OTX	19	0	V$NKX3A_01	NK class homeobox factor 3A	0	1	V$POU3F2_02	POU3F2	21	0
V$SAP1A_01	SAP-1a	19	0	V$NKX52_01	Nkx5-2	0	1	V$SIRT6_01	SIRT6	21	0
V$TAL1_01	Tal-1 (Scl)	19	0	V$NRSE_B	neural-restrictive-silencer-element	0	1	MA0018.2	CREB1	20	0
V$TEL2_Q6	Tel-2	19	0	V$OBOX3_01	Obox3	0	1	MA0046.1	HNF1A	20	0
V$TFIIA_Q6	TFIIA	19	0	V$OBOX5_01	Obox5	0	1	MA0139.1	CTCF	20	0
MA0038.1	Gfi	18	0	V$OBOX6_01	Obox6	0	1	V$ATF_B	ATF binding site	20	0
MA0135.1	Lhx3	18	0	V$OCT2_01	2-Oct	0	1	V$BLIMP1_Q6	BLIMP1	20	0
V$ATF_B	ATF binding site	18	0	V$OCT_Q6	Octamer	0	1	V$CREBP1_Q2	CRE-binding protein 1	20	0
V$FRA1_Q5	FRA1	18	0	V$OG2_02	OG-2	0	1	V$E2F1DP1RB_01	Rb:E2F-1:DP-1 trimeric complex	20	0
V$FREAC2_01	Fork head RElated ACtivator-2	18	0	V$OTX1_01	Otx1	0	1	V$E2F4DP1_01	E2F-4:DP-1 heterodimer	20	0

V$PTF1BETA_Q6	PTF1-beta	18	0	V$OTX2_01	Otx2	0	1	V$GFI1_01	growth factor independence 1	20	0
V$STAT3STAT3_Q3	STAT3:STAT3	18	0	V$PAX1_B	Pax-1 binding sites	0	1	V$STAT_01	signal transducers and activators of transcription	20	0
V$STAT_01	signal transducers and activators of transcription	18	0	V$PAX5_02	B-cell-specific activating protein	0	1	V$TFIIA_Q6	TFIIA	20	0
V$YY1_01	Yin and Yang 1	18	0	V$PBX1_01	Pbx-1	0	1	V$UF1H3BETA_Q6	UF1H3BETA	20	0
MA0027.1	En1	17	0	V$PITX1_01	Pitx1	0	1	V$ZF5_01	ZF5	20	0
MA0030.1	FOXF2	17	0	V$PITX3_01	Pitx3	0	1	MA0030.1	FOXF2	19	0
MA0033.1	FOXL1	17	0	V$PMX2A_01	PMX2A	0	1	MA0038.1	Gfi	19	0
MA0142.1	Pou5f1	17	0	V$PNR_01	PNR	0	1	MA0075.1	Prrx2	19	0
V$E2F1DP2_01	E2F-1:DP-2 heterodimer	17	0	V$POU2F3_01	POU2F3	0	1	MA0135.1	Lhx3	19	0
V$E2F4DP2_01	E2F-4:DP-2 heterodimer	17	0	V$POU3F2_01	POU3F2	0	1	V$ATF1_Q6	ATF1	19	0
V$ESE1_Q3	ESE1	17	0	V$POU6F1_02	POU6F1	0	1	V$ATF3_Q6	activating transcription factor 3	19	0
V$GATA3_03	GATA-binding factor 3	17	0	V$PSX1_01	PSX1	0	1	V$FOX_Q2	FOX factors	19	0
V$SMAD1_01	SMAD1	17	0	V$PXRRXR_01	RXR half-site	0	1	V$HNF3ALPHA_Q6	HNF3alpha	19	0
V$TFEB_01	TFEB	17	1	V$RAX_01	rax	0	1	V$IRF8_Q6	IRF8	19	0
MA0051.1	IRF2	16	0	V$RSRFC4_01	related to serum response factor, C4	0	1	V$POU5F1_01	POU5F1 b.s.	19	0

MA0056.1	MZF1_1-4	16	0	V$S8_02	S8	0	1	V$SMAD1_01	SMAD1	19	0
V$AREB6_04	AREB6 (Atp1a1 regulatory element binding factor 6)	16	0	V$SAP1A_01	SAP-1a	0	1	V$TR4_01	TR4	19	0
V$ATF3_Q6	activating transcription factor 3	16	0	V$SF1_Q6	SF1	0	1	MA0051.1	IRF2	18	0
V$BRCA_01	BRCA1 containing protein complex with USF2	16	0	V$SREBP1_01	sterol regulatory element-binding protein 1	0	1	V$AIRE_01	AIRE	18	0
V$CIZ_01	CIZ (Cas-associated zinc finger protein)	16	0	V$STAT1_01	signal transducer and activator of transcription 1	0	1	V$CIZ_01	CIZ (Cas-associated zinc finger protein)	18	0
V$FREAC3_01	Fork head RElated ACtivator-3	16	0	V$TAXCREB_01	Tax/CREB complex	0	1	V$FOXD3_01	fork head box D3	18	0
V$IRF8_Q6	IRF8	16	0	V$TCF3_01	TCF-3	0	1	V$HSF2_01	heat shock factor 2	18	0
V$NERF_Q2	new ets-related factor 1a	16	0	V$TCF4_01	TCF-4	0	1	V$PTF1BETA_Q6	PTF1-beta	18	0
V$POU3F2_02	POU3F2	16	0	V$TTF1_Q6	TTF-1 (Nkx2-1)	0	1	V$SOX5_01	Sox-5	18	0
MA0031.1	FOXD1	15	0	V$VAX1_01	Vax-1	0	1	V$SOX9_B1	SOX (SRY-related HMG box)	18	0
MA0144.1	Stat3	15	0	V$VAX2_01	Vax-2	0	1	V$TEL2_Q6	Tel-2	18	0
V$AIRE_01	AIRE	15	0	V$VDRRXR_01	VDR:RXR	0	1	V$TFEB_01	TFEB	18	0
V$CEBPE_01	cebpe	15	0	V$YY2	YY2	0	1	V$ZFP281_01	Zfp281	18	0

V$FOXD3_01	fork head box D3	15	0	V$ZF5_B	ZF5 binding sites	0	1	V$ZNF333_01	ZNF333	18	0
V$SOX9_B1	SOX (SRY-related HMG box)	15	0	V$ZNF219_01	ZNF219	0	1	V$FREAC3_01	Fork head RElated ACtivator-3	17	0
V$AR_Q6	half-site matrix	14	0	V$ZNF333_01	ZNF333	0	1	V$VBP_01	PAR-type chicken vitellogenin promoter-binding protein	17	0
V$ATF1_Q6	ATF1	14	0	VS$HMGA2_01	HMGA2 binding site	0	1	MA0031.1	FOXD1	16	0
V$CREBP1_Q2	CRE-binding protein 1	14	0	MA0040.1	Foxq1	0	2	MA0125.1	Nobox	16	0
V$DMRT4_01	DMRT4	14	0	MA0046.1	HNF1A	0	2	V$ISL1_Q6	ISL1	16	0
V$HFH8_01	HNF-3/Fkh Homolog-8	14	0	MA0135.1	Lhx3	0	2	V$MRF2_01	modulator recognition factor 2	16	0
V$HMEF2_Q6	myocyte enhancer factor	14	0	MA0151.1	ARID3A	0	2	V$RSRFC4_Q2	RSRFC4	16	0
V$HSF_Q6	HSF	14	0	V$AIRE_02	AIRE	0	2	V$STAF_01	Se-Cys tRNA gene transcription activating factor	16	0
V$PLZF_02	PLZF	14	0	V$ALX3_01	ALX-3	0	2	V$STRA13_01	Stra13	16	0
V$RSRFC4_Q2	RSRFC4	14	0	V$BARHL2_01	Barhl2	0	2	MA0041.1	Foxd3	15	0
V$SOX5_01	Sox-5	14	0	V$BARX2_01	Barx-2	0	2	V$AR_Q2	androgen receptor	15	0
V$STAF_01	Se-Cys tRNA gene transcription	14	0	V$BRN3C_01	Brn-3c	0	2	V$CEBPE_01	cebpe	15	0

	activating factor										
MA0018.2	CREB1	13	0	V$BRN4_01	Brn-4	0	2	V$GATA_C	GATA binding site	15	0
V$FOX_Q2	FOX factors	13	0	V$CDX2_01	Cdx-2	0	2	V$GR_Q6	glucocorticoid receptor	15	0
V$HNF3A_01	FOXA1	13	0	V$CDX_Q5	Cdx	0	2	V$HFH8_01	HNF-3/Fkh Homolog-8	15	0
V$IK1_01	Ikaros 1	13	0	V$DBX2_01	Dbx-2	0	2	V$HMEF2_Q6	myocyte enhancer factor	15	0
V$STRA13_01	Stra13	13	0	V$DLX1_01	Dlx-1	0	2	V$HSF1_01	heat shock factor 1	15	0
V$WT1_Q6	WT1	13	0	V$DLX3_01	dlx3	0	2	V$HSF_Q6	HSF	15	0
V$AP1FJ_Q2	activator protein 1	12	0	V$DLX7_01	Dlx7	0	2	V$PLZF_02	PLZF	15	0
V$ATF5_01	ATF5 binding site	12	0	V$ESX1_01	Esx1	0	2	MA0025.1	NFIL3	14	0
V$E2F1DP1RB_01	Rb:E2F-1:DP-1 trimeric complex	12	0	V$ETF_Q6	ETF	0	2	MA0093.1	USF1	14	0
V$FOXJ3_01	foxj3	12	0	V$FAC1_01	fetal Alz-50 clone 1	0	2	MA0101.1	REL	14	0
V$GATA_C	GATA binding site	12	0	V$FOXD3_01	fork head box D3	0	2	MA0142.1	Pou5f1	14	0
V$GR_Q6	glucocorticoid receptor	12	0	V$FOXO3A_Q1	FOXO3A	0	2	V$AP2GAMMA_01	AP-2gamma	14	0
V$HSF2_01	heat shock factor 2	12	0	V$GADP_01	Growth-associated binding protein	0	2	V$CREL_01	c-Rel	14	0
V$MZF1_01	MZF1	12	0	V$HMX3_02	Nkx5-1	0	2	V$DMRT4_01	DMRT4	14	0
V$NFKB_Q6_01	NF-kappaB	12	0	V$HNF3_Q6	HNF3	0	2	V$EFC_Q6	RFX1 (EF-C)	14	0

V$RFX1_02	X-box binding protein RFX1	12	0	V$HNF6_Q6	HNF6	0	2	V$FPM315_01	Zinc finger protein FPM315 with KRAB and SCAN domains	14	0
MA0041.1	Foxd3	11	0	V$HOMEZ_01	Homez	0	2	MA0004.1	Arnt	13	0
V$AP2GAMMA_01	AP-2gamma	11	0	V$HOX13_02	HOXA5	0	2	MA0109.1	Hltf	13	0
V$E2F4DP1_01	E2F-4:DP-1 heterodimer	11	0	V$HOXA11_01	HOXA11	0	2	V$ESE1_Q3	ESE1	13	0
V$EFC_Q6	RFX1 (EF-C)	11	0	V$HOXA1_01	HOXA1	0	2	V$RFX1_02	X-box binding protein RFX1	13	0
V$ISL1_Q6	ISL1	11	0	V$HOXA2_01	HoxA2	0	2	V$RUSH1A_02	RUSH-1alpha	13	0
V$KLF15_Q2	KLF15	11	0	V$HOXA4_01	HOXA4	0	2	V$USF_01	upstream stimulating factor	13	0
V$LBP1_Q6	LBP-1	11	0	V$HOXA6_01	HOXA6	0	2	V$TCF3_01	TCF-3	13	1
V$MRF2_01	modulator recognition factor 2	11	0	V$HOXA9_01	hoxa9	0	2	V$FOXJ3_01	foxj3	12	0
V$NEUROD_02	NeuroD	11	0	V$HOXB4_01	HOXB4	0	2	V$HNF4_01	hepatic nuclear factor 4	12	0
V$NFE2_01	NF-E2 p45	11	0	V$HOXB5_01	HoxB5	0	2	V$STAT5B_01	signal transducer and activator of transcription 5b	12	0
V$TCF3_01	TCF-3	11	2	V$HOXB6_01	HOXB6	0	2	V$WHN_B	winged-helix factor nude	12	0

MA0101.1	REL	10	0	V$HOXB9_01	HOXB9	0	2	MA0003.1	TFAP2A	11	0
V$EAR2_Q2	EAR2	10	0	V$HOXC10_01	HOXC10	0	2	MA0087.1	Sox5	11	0
V$NFKAPPAB65_01	NF-kappaB (p65)	10	0	V$HOXC11_01	HOXC11	0	2	V$AP2ALPHA_01	AP-2alpha	11	0
V$RFX3_01	RFX3 dimer	10	0	V$HOXC12_01	HOXC12	0	2	V$E4BP4_01	E4BP4	11	0
V$STAT5B_01	signal transducer and activator of transcription 5b	10	0	V$HOXC13_01	HOXC13	0	2	V$EAR2_Q2	EAR2	11	0
MA0047.2	Foxa2	9	0	V$HOXC5_01	HOXC5	0	2	V$GATA1_05	GATA-binding factor 1	11	0
MA0107.1	RELA	9	0	V$HOXC6_01	HOXC6	0	2	V$HLF_01	hepatic leukemia factor	11	0
MA0125.1	Nobox	9	0	V$HOXC8_01	HOXC-8	0	2	V$IK1_01	Ikaros 1	11	0
V$HNF4_01	hepatic nuclear factor 4	9	0	V$HOXC9_01	HOXC9	0	2	V$MECP2_02	MECP2 b.s.	11	0
V$LEF1_Q2_01	LEF1	9	0	V$HOXD12_01	HOXD12	0	2	V$RFX3_01	RFX3 dimer	11	0
V$NF1_Q6_01	NF-1	9	0	V$HOXD1_01	HOXD1	0	2	MA0014.1	Pax5	10	0
V$USF_01	upstream stimulating factor	9	0	V$HOXD3_01	HOXD3	0	2	MA0042.1	FOXI1	10	0
V$ZABC1_01	ZABC1 b.s.	9	0	V$HOXD8_01	HOXD8	0	2	MA0052.1	MEF2A	10	0
MA0003.1	TFAP2A	8	0	V$ISL2_01	Isl2	0	2	MA0058.1	MAX	10	0
MA0042.1	FOXI1	8	0	V$MMEF2_Q6	myocyte enhancer factor	0	2	MA0124.1	NKX3-1	10	0
MA0052.1	MEF2A	8	0	V$MOX1_01	Mox1	0	2	V$CEBPDELTA_Q6	C/EBPdelta	10	0
MA0087.1	Sox5	8	0	V$MSX1_02	Msx-1	0	2	V$DMRT5_01	DMRT5	10	0
MA0109.1	Hltf	8	0	V$MSX3_01	Msx-3	0	2	V$FOXM1_01	FOXM1	10	0

MA0148.1	FOXA1	8	0	V$NCX_02	Ncx	0	2	V$FREAC4_01	Fork head RElated ACtivator-4	10	0
V$AP2ALPHA_01	AP-2alpha	8	0	V$NKX24_01	Nkx2-4	0	2	V$KLF15_Q2	KLF15	10	0
V$CEBPDELTA_Q6	C/EBPdelta	8	0	V$NKX25_03	NKX25	0	2	V$NERF_Q2	new ets-related factor 1a	10	0
V$EBF_Q6	EBF	8	0	V$NKX61_01	NKX6-1	0	2	V$ZFX_01	Zfx	10	0
V$GATA1_06	GATA-binding factor 1	8	0	V$NKX63_01	Nkx6-3	0	2	MA0006.1	Arnt::Ahr	9	0
V$HNF4ALPHA_Q6	HNF4alpha	8	0	V$OBOX1_01	Obox1	0	2	MA0107.1	RELA	9	0
V$HSF1_01	heat shock factor 1	8	0	V$OBOX2_01	Obox2	0	2	MA0144.1	Stat3	9	0
V$MAZR_01	MAZ related factor	8	0	V$OCT4_01	Sox2-Oct4 joint motif, in silico predicted	0	2	MA0162.1	Egr1	9	0
V$RUSH1A_02	RUSH-1alpha	8	0	V$OCTAMER_01	Octamer	0	2	V$ATF5_01	ATF5 binding site	9	0
V$SRF_Q5_02	SRF	8	0	V$OTP_01	OTP	0	2	V$HNF3A_01	FOXA1	9	0
V$ZNF333_01	ZNF333	8	0	V$PAX4_05	Pax-4	0	2	V$HNF4ALPHA_Q6	HNF4alpha	9	0
MA0004.1	Arnt	7	0	V$PAX6_02	pax6	0	2	V$HTF_01	HTF	9	0
MA0025.1	NFIL3	7	0	V$PIT1_01	Pit-1	0	2	V$NFKB_Q6_01	NF-kappaB	9	0
MA0055.1	Myf	7	0	V$PMX2B_01	PMX2B	0	2	V$RBPJK_01	RBP-Jkappa	9	0
MA0093.1	USF1	7	0	V$PROP1_02	Prop-1	0	2	V$REX1_03	REX1	9	0
V$E4BP4_01	E4BP4	7	0	V$RNF96_01	RNF96	0	2	V$WT1_Q6	WT1	9	0
V$HFH3_01	HFH-3 (HNF3/fork head homolog	7	0	V$SHOX2_01	Shox2	0	2	V$ZABC1_01	ZABC1 b.s.	9	0

	3)										
V$RBPJK_Q4	RBP-Jkappa	7	0	V$TRF1_01	TRF1	0	2	MA0047.2	Foxa2	8	0
V$REX1_03	REX1	7	0	V$TST1_02	6-Oct	0	2	V$CHX10_01	CHX10	8	0
V$TCF11_01	TCF11/KCR-F1/Nrf1 homodimers	7	0	V$UNCX4.1_01	Uncx-4.1	0	2	V$DMRT3_01	DMRT3	8	0
V$VBP_01	PAR-type chicken vitellogenin promoter-binding protein	7	0	V$VSX1_01	Vsx1	0	2	V$E4F1_Q6	E4F1	8	0
MA0075.1	Prrx2	7	1	MA0033.1	FOXL1	0	3	V$LEF1_Q2_01	LEF1	8	0
MA0014.1	Pax5	6	0	MA0041.1	Foxd3	0	3	V$TAL1_01	Tal-1 (Scl)	8	0
V$BACH2_01	BTB and CNC homolog 2	6	0	V$CDX1_01	Cdx-1	0	3	MA0088.1	znf143	7	0
V$CHX10_01	CHX10	6	0	V$CEBPGAMMA_Q6	C/EBPgamma	0	3	MA0148.1	FOXA1	7	0
V$CREL_01	c-Rel	6	0	V$CNOT3_01	CNOT3	0	3	V$HFH3_01	HFH-3 (HNF3/fork head homolog 3)	7	0
V$DMRT2_01	DMRT2	6	0	V$DRI1_01	DRI1 b.s.	0	3	V$NFKAPPAB65_01	NF-kappaB (p65)	7	0
V$DMRT3_01	DMRT3	6	0	V$FOX_Q2	FOX factors	0	3	V$NFMUE1_Q6	NF-muE1	7	0
V$DMRT5_01	DMRT5	6	0	V$HB24_01	HB24	0	3	V$PAX3_B	Pax-3 binding sites	7	0
V$MECP2_02	MECP2 b.s.	6	0	V$HFH1_01	HNF-3/Fkh Homolog 1	0	3	MA0132.1	Pdx1	7	1
V$TCF11MAFG_01	TCF11:MafG heterodimers	6	0	V$HOXB13_01	HOXB13	0	3	MA0029.1	Evi1	6	0
V$FOXM1_01	FOXM1	6	1	V$HOXB8_01	HOXB8	0	3	V$CLOCKBMA	CLOCK:B	6	0

								L_Q6	MAL		
MA0162.1	Egr1	5	0	V$HOXC4_01	HOXC4	0	3	V$DMRT2_01	DMRT2	6	0
MA0164.1	Nr2e3	5	0	V$HOXD11_01	HOXD11	0	3	V$GATA2_02	GATA-binding factor 2	6	0
V$BACH1_01	BTB and CNC homolog 1	5	0	V$LBX2_01	Lbx2	0	3	V$TCF11_01	TCF11/KCR-F1/Nrf1 homodimers	6	0
V$GATA2_03	GATA-binding factor 2	5	0	V$LHX5_01	Lhx5	0	3	MA0067.1	Pax2	5	0
V$LEF1TCF1_Q4	LEF1, TCF1	5	0	V$NKX29_01	Nkx2-9	0	3	MA0140.1	Tal1::Gata1	5	0
V$MAX_01	Max	5	0	V$NKX62_Q2	NK related homeobox factor 6-2	0	3	V$GATA6_01	GATA-6	5	0
V$MEIS1BHOXA9_02	Meis-1b:HOXA9 heterodimeric binding	5	0	V$PAX7_01	Pax-7	0	3	V$MEIS1BHOXA9_02	Meis-1b:HOXA9 heterodimeric binding	5	0
V$MIF1_01	MIBP-1 / RFX1 complex	5	0	MA0052.1	MEF2A	0	4	V$MYB_Q5_01	MYB	5	0
V$P50RELAP65_Q5_01	P50:RELA-P65	5	0	V$AMEF2_Q6	myocyte enhancer factor	0	4	V$NF1_Q6_01	NF-1	5	0
V$WHN_B	winged-helix factor nude	5	0	V$DBX1_01	Dbx-1	0	4	V$PR_01	high affinity binding sites for progesterone receptor	5	0
V$ZF5_01	ZF5	5	0	V$HOXA10_01	HOXA10	0	4	V$SRF_Q4	SRF	5	0
MA0029.1	Evi1	4	0	V$HOXD10_01	HOXD10	0	4	V$TCF11MAFG_01	TCF11:MafG heterodimers	5	0

MA0043.1	HLF	4	0
MA0088.1	znf143	4	0
MA0140.1	Tal1::Gata1	4	0
V$FREAC4_01	Fork head RElated ACtivator-4	4	0
V$GATA6_01	GATA-6	4	0
V$HTF_01	HTF	4	0
V$MAF_Q6	MAF	4	0
V$MYCMAX_03	c-Myc:Max heterodimer	4	0
V$NFMUE1_Q6	NF-muE1	4	0
V$NRSF_01	neuron-restrictive silencer factor	4	0
V$OLF1_01	olfactory neuron-specific factor	4	0
V$PR_02	progesterone receptor	4	0
V$SP3_Q3	Sp3	4	0
V$CACBINDINGPROTEIN_Q6	CAC-binding protein	4	3
MA0006.1	Arnt::Ahr	3	0
V$HOXD13_01	HOXD13	0	4
V$LIM1_01	Lim-1	0	4
V$LMX1_01	Lmx-1	0	4
V$LMX1B_01	lmx1b	0	4
V$SATB1_01	Consensus SATB1 Binding Sequence	0	4
MA0075.1	Prrx2	0	5
I$ANTP_Q6_01	Antp	0	5
V$GTF2IRD1_01	GTF2IRD1-isoform2	0	5
V$LUN1_01	LUN-1	0	5
V$BDP1_01	BDP1	0	6
V$MEF2C_01	MEF-2C	0	6
V$ERALPHA_01	2 ERE half-sites with a 3bp spacer within	0	7
V$RPC155_01	RPC155	0	7
V$PITX2_Q2	pituitary homeobox factor 2	0	9
MA0056.1	MZF1_1-4	4	0
V$AP1_Q2	activator protein 1	4	0
V$LEF1TCF1_Q4	LEF1, TCF1	4	0
V$MAZR_01	MAZ related factor	4	0
V$MIF1_01	MIBP-1 / RFX1 complex	4	0
V$MYCMAX_03	c-Myc:Max heterodimer	4	0
V$MZF1_01	MZF1	4	0
V$NRSE_B	neural-restrictive-silencer-element	4	0
V$RELBP52_01	kappaB site	4	0
MA0017.1	NR2F1	3	0
MA0061.1	NF-kappaB	3	0
MA0115.1	NR1H2::RXRA	3	0
MA0164.1	Nr2e3	3	0
V$AP1FJ_Q2	activator protein 1	3	0
V$ATF4_Q2	activating transcription factor	3	0

MA0061.1	NF-kappaB	3	0
MA0114.1	HNF4A	3	0
MA0138.2	REST	3	0
F$AMT1_Q2	AMT1	3	0
V$DR1_Q3	Direct repeat 1	3	0
V$LTF_Q6	LTF	3	0
V$MYB_Q6	c-Myb	3	0
V$NFKAPPAB_01	NF-kappaB	3	0
V$P50P50_Q3	P50:P50	3	0
V$ZFX_01	Zfx	3	0
MA0017.1	NR2F1	2	0
MA0035.2	Gata1	2	0
MA0057.1	MZF1_5-13	2	0

	4		
V$ATF6_01	activating transcription factor 6	3	0
V$CDPCR3_01	cut-like homeodomain protein	3	0
V$COUP_01	COUP-TF, HNF-4	3	0
V$DEAF1_02	DEAF1	3	0
V$EGR2_01	Egr-2/Krox-20 early growth response gene product	3	0
V$GFI1B_01	Gfi1b	3	0
V$MEIS1AHOXA9_01	Meis-1a:HOXA9 heterodimeric binding	3	0
V$MIZF_01	MIZF	3	0
V$NFKAPPAB_01	NF-kappaB	3	0
V$NGFIC_01	nerve growth factor-induced protein C	3	0
V$PBX_Q3	Pbx	3	0
V$RXRLXRB_01	RXR:LXR-beta	3	0
V$SOX17_01	half-site	3	0

MA0124.1	NKX3-1	2	0
V$COUP_01	COUP-TF, HNF-4	2	0
V$E4F1_Q6	E4F1	2	0
V$EGR3_01	early growth response gene 3 product	2	0
V$FOXP1_01	FOXP1	2	0
V$GFI1B_01	Gfi1b	2	0
V$HFH4_01	HFH4 (FOXJ1)	2	0
V$MEIS1AHOXA9_01	Meis-1a:HOXA9 heterodimeric binding	2	0
V$MYOGNF1_01	myogenin / nuclear factor 1 or related factors	2	0
V$NGFIC_01	nerve growth factor-induced protein C	2	0
V$NRSE_B	neural-restrictive-silencer-element	2	0
V$P63_01	p63	2	0
V$PAX3_B	Pax-3 binding sites	2	0

V$TITF1_Q3	TTF-1, TITF1 (thyroid transcription factor 1)	3	0
V$XBP1_01	X-box-binding protein 1	3	0
VS$HMGA2_01	HMGA2 binding site	3	0
V$LBP1_Q6	LBP-1	3	1
MA0035.2	Gata1	2	0
MA0059.1	MYC::MAX	2	0
MA0114.1	HNF4A	2	0
MA0138.2	REST	2	0
V$AP3_Q6	AP-3	2	0
V$DAX1_01	Dax1	2	0
V$EGR3_01	early growth response gene 3 product	2	0
V$FOXP1_01	FOXP1	2	0
V$HFH4_01	HFH4 (FOXJ1)	2	0

V$PBX_Q3	Pbx	2	0
V$PPARG_01	PPAR-gamma (peroxisome proliferator-activated receptor gamma)	2	0
V$RELBP52_01	kappaB site	2	0
V$TITF1_Q3	TTF-1, TITF1 (thyroid transcription factor 1)	2	0
V$XBP1_01	X-box-binding protein 1	2	0
V$ZNF219_01	ZNF219	2	0
MA0132.1	Pdx1	2	1
V$HAND1E47_01	Hand1:E47 heterodimer	2	1
V$SMAD3_Q6	SMAD3	2	1
V$TFIII_Q6	TFII-I	2	2
V$RPC155_01	RPC155	2	18
V$IK_Q5	Ikaros	2	20
MA0007.1	Ar	1	0
MA0048.1	NHLH1	1	0
MA0059.1	MYC::MAX	1	0

V$LTF_Q6	LTF	2	0
V$NRSF_01	neuron-restrictive silencer factor	2	0
V$OLF1_01	olfactory neuron-specific factor	2	0
V$P50RELAP65_Q5_01	P50:RELA-P65	2	0
V$PNR_01	PNR	2	0
V$FXR_IR1_Q6	FXR inverted repeat 1	2	1
V$PPARA_01	PPAR:RXR heterodimers	2	1
MA0007.1	Ar	1	0
MA0048.1	NHLH1	1	0
MA0057.1	MZF1_5-13	1	0
MA0069.1	Pax6	1	0
MA0104.2	Mycn	1	0
MA0147.1	Myc	1	0
V$BRACH_01	Brachyury	1	0
V$CDPCR1_01	cut-like homeodomain	1	0

MA0067.1	Pax2	1	0
MA0069.1	Pax6	1	0
MA0072.1	RORA_2	1	0
MA0090.1	TEAD1	1	0
MA0104.2	Mycn	1	0
MA0115.1	NR1H2::RXRA	1	0
MA0154.1	EBF1	1	0
V$AP3_Q6	AP-3	1	0
V$AP4_01	activator protein 4	1	0
V$CDPCR3_01	cut-like homeodomain protein	1	0
V$CLOCKBMAL_Q6	CLOCK:BMAL	1	0
V$CMAF_02	C-MAF	1	0
V$DAX1_01	Dax1	1	0
	protein		
V$CMYC_02	c-Myc heterodimer (with a 26-29 kDa factor)	1	0
V$EBF_Q6	EBF	1	0
V$FRA1_Q5	FRA1	1	0
V$GZF1_01	plays a role in renal branching morphogenesis	1	0
V$HAND1E47_01	Hand1:E47 heterodimer	1	0
V$HIF2A_01	HIF-2alpha	1	0
V$MAF_Q6	MAF	1	0
V$MTF1_01	MTF1	1	0
V$NFKAPPAB50_01	NF-kappaB (p50)	1	0
V$NUR77_Q5	NUR77	1	0
V$P50P50_Q3	P50:P50	1	0
V$PAX1_B	Pax-1 binding sites	1	0
V$PPARG_01	PPAR-gamma (peroxiso	1	0

V$DEAF1_02	DEAF1	1	0
V$EGR2_01	Egr-2/Krox-20 early growth response gene product	1	0
V$FXR_IR1_Q6	FXR inverted repeat 1	1	0
V$GZF1_01	plays a role in renal branching morphogenesis	1	0
V$HEN1_02	HEN1	1	0
V$IK3_01	Ikaros 3	1	0
V$MIZF_01	MIZF	1	0
V$NFKAPPAB50_01	NF-kappaB (p50)	1	0
V$NMYC_01	N-Myc	1	0
V$PAX1_B	Pax-1 binding sites	1	0
V$PNR_01	PNR	1	0
V$PPARA_01	PPAR:RXR heterodimers	1	0
V$RORA2_01	RAR-related orphan receptor	1	0

	me proliferator-activated receptor gamma)		
V$PXR_Q2	half-site matrix	1	0
V$RXRG_01	RXRG dimer	1	0
V$TAXCREB_02	Tax/CREB complex	1	0
V$ZNF219_01	ZNF219	1	0
MA0150.1	NFE2L2	1	1
MA0442.1	SOX10	1	1
F$AMT1_Q2	AMT1	1	1
V$RORA1_01	RAR-related orphan receptor alpha1	1	1
V$TBX18_01	T-box 18	1	1
MA0090.1	TEAD1	1	2
V$AHRHIF_Q6	AhR, Arnt, HIF-1	1	2
V$P300_01	p300	1	6
V$RPC155_01	RPC155	1	21

	alpha2		
V$RXRG_01	RXRG dimer	1	0
V$RXRLXRB_01	RXR:LXR-beta	1	0
V$SOX17_01	half-site	1	0
V$TAL1BETAITF2_01	Tal-1beta:ITF-2 heterodimer	1	0
V$TAXCREB_02	Tax/CREB complex	1	0
V$TBX15_02	T-box 15	1	0
V$TBX18_01	T-box 18	1	0
V$ZBED6_01	ZBED6	1	0
MA0065.2	PPARG::RXRA	1	1
MA0150.1	NFE2L2	1	1
V$TAL1BETAE47_01	Tal-1beta:E47 heterodimer	1	1
V$ZBRK1_01	ZBRK1	1	1
V$P300_01	p300	1	3
V$SOX10_Q6	SOX10	1	5

V$IK_Q5	Ikaros	1	22
MA0072.1	RORA_2	0	1
MA0074.1	RXRA::VDR	0	1
MA0091.1	TAL1::TCF3	0	1
MA0141.1	Esrrb	0	1
MA0149.1	EWSR1-FLI1	0	1
V$AHR_Q5	aryl hydrocarbon / dioxin receptor	0	1
V$AHRARNT_01	aryl hydrocarbon receptor: Arnt heterodimers	0	1
V$AP4_01	activator protein 4	0	1
V$CACCCBINDINGFACTOR_Q6	CACCC-binding factor	0	1
V$DBP_Q6	DBP	0	1
V$GCNF_01	GCNF (germ cell nuclear factor)	0	1
V$LXR_Q3	LXR	0	1
V$NEUROD_02	NeuroD	0	1

V$LYF1_01	LyF-1	1	21
MA0002.2	RUNX1	0	1
MA0074.1	RXRA::VDR	0	1
MA0149.1	EWSR1-FLI1	0	1
V$AML2_01	AML2	0	1
V$ATF4_Q2	activating transcription factor 4	0	1
V$BRACH_01	Brachyury	0	1
V$CACD_01	CACD	0	1
V$COREBINDINGFACTOR_Q6	core-binding factor	0	1
V$DBP_Q6	DBP	0	1
V$ERR2_01	ERR2 (ESRRB)	0	1
V$HEB_Q6	HEB	0	1
V$LMAF_Q2	LMAF	0	1

V$PAX_Q6	Pax	0	1
V$RFX_Q6	RFX	0	1
V$RORA2_01	RAR-related orphan receptor alpha2	0	1
V$TAL1BETAE47_01	Tal-1beta:E47 heterodimer	0	1
V$VDRRXR_01	VDR:RXR	0	1
V$ZBED6_01	ZBED6	0	1
V$ZEC_01	zinc finger protein expressed in embryonal cells and certain adult organs	0	1
MA0133.1	BRCA1	0	2
MA0155.1	INSM1	0	2
V$AML_Q6	AML	0	2
V$BACH1_01	BTB and CNC homolog 1	0	2
V$CACD_01	CACD	0	2
V$COREBINDINGFACTOR_Q6	core-binding factor	0	2

V$LMO2COM_02	complex of Lmo2 bound to Tal-1, E2A proteins, and GATA-1, half-site 2	0	1
V$MOVOB_01	MOVO-B	0	1
V$MTERF_01	mTERF binding site	0	1
V$MTF1_Q4	MTF-1	0	1
V$MYOD_01	myoblast determination gene product	0	1
V$RORA1_01	RAR-related orphan receptor alpha1	0	1
V$TEF1_Q6	TEF-1	0	1
V$VDRRXR_01	VDR:RXR	0	1
V$ZEC_01	zinc finger protein expressed in embryonal cells and certain adult organs	0	1
V$ZID_01	zinc finger with interaction domain	0	1
V$AHR_01	aryl hydrocarbon / dioxin receptor	0	2

V$MOVOB_01	MOVO-B	0	2
MA0002.2	RUNX1	0	3
MA0154.1	EBF1	0	3
V$ERR1_Q2	estrogen-related receptor alpha	0	3
V$RP58_01	58 KDA repressor protein	0	3
V$SZF11_01	SZF1-1	0	3
V$ZID_01	zinc finger with interaction domain	0	3
V$SMAD4_Q6	SMAD4	0	4
V$SREBP1_01	sterol regulatory element-binding protein 1	0	4
V$RREB1_01	Ras-responsive element binding protein 1	0	5
V$SMAD3_Q6	SMAD3	0	5

V$CP2_01	CP2	0	2
V$E12_Q6	E12	0	2
V$ER_Q6_02	half-site matrix, half-ERE	0	2
V$ERR1_Q2	estrogen-related receptor alpha	0	2
V$GCNF_01	GCNF (germ cell nuclear factor)	0	2
V$RREB1_01	Ras-responsive element binding protein 1	0	2
V$SZF11_01	SZF1-1	0	2
V$T3R_Q6	half-site matrix	0	2
V$VDR_Q3	vitamin D receptor; mediates vitamin D3-signaling, often dimerizes with RXR-alpha	0	2
MA0071.1	RORA_1	0	3
MA0119.1	TLX1::NFIC	0	3
MA0133.1	BRCA1	0	3
MA0141.1	Esrrb	0	3
V$AHRARNT_01	aryl hydrocarbon receptor:Arnt	0	3

V$TBX5_01	TBX5	0	5
V$TEF1_Q6	TEF-1	0	5
V$SF1_Q6_01	SF1	0	6
MA0163.1	PLAG1	0	7
V$COUPTF_Q6	COUPTF	0	7
V$E47_01	E47	0	7
V$GCM_Q2	GCM	0	7
V$IK2_01	Ikaros 2	0	7
V$MYOD_01	myoblast determination gene product	0	7
V$CHOP_01	heterodimers of CHOP and C/EBPalpha	0	8
V$TFIII_Q6	TFII-I	0	8
V$YY2	YY2	0	8
MA0119.1	TLX1::NFIC	0	9
MA0258.1	ESR2	0	9

	heterodimers		
V$CTF1_01	selection of the binding sites for CTCF by HOX11 cooperative DNA binding [2]	0	3
V$HIC1_02	HIC1	0	3
V$LXR_Q3	LXR	0	3
V$MATH1_Q2	E47:MATH1	0	3
V$SF1_Q6_01	SF1	0	3
V$TBX5_01	TBX5	0	3
V$GCM_Q2	GCM	0	4
V$SPZ1_01	spermatogenic Zip	0	4
MA0089.1	NFE2L1::MafG	0	5
MA0092.1	Hand1::Tcfe2a	0	5
V$AHRHIF_Q6	AhR, Arnt, HIF-	0	5

V$CACBINDINGPROTEIN_Q6	CAC-binding protein	0	9
V$CTF1_01	selection of the binding sites for CTCF by HOX11 cooperative DNA binding [2]	0	9
V$HIC1_02	HIC1	0	9
V$LRF_Q2	LRF	0	9
V$MEF2C_01	MEF-2C	0	9
V$VDR_Q3	vitamin D receptor; mediates vitamin D3-signaling, often dimerizes with RXR-alpha	0	9
V$CMAF_02	C-MAF	0	10
V$CP2_01	CP2	0	10
V$ER_Q6_02	half-site matrix, half-ERE	0	10
V$SPZ1_01	spermatogenic Zip	0	10
V$TBR2_01	TBR2	0	10

	1		
V$CHOP_01	heterodimers of CHOP and C/EBPalpha	0	5
V$EBOX_Q6_01	Ebox	0	5
V$LRF_Q2	LRF	0	5
V$MYOGENIN_Q6	myogenin	0	5
MA0032.1	FOXC1	0	6
MA0163.1	PLAG1	0	6
MA0258.1	ESR2	0	6
V$RORBETA_Q2	RORBETA	0	6
V$GLI3_01	GLI3	0	7
V$IK2_01	Ikaros 2	0	7
V$LRH1_Q5	LRH1	0	7
V$TBR2_01	TBR2	0	7
V$COUPTF_Q6	COUPTF	0	8
V$SREBP1_01	sterol regulatory element-binding protein 1	0	8
MA0112.2	ESR1	0	9
V$PUR1_Q4	PUR1	0	9
MA0161.1	NFIC	0	10
V$YY2	YY2	0	10
MA0111.1	Spz1	0	11

MA0089.1	NFE2L1::MafG	0	11
V$E12_Q6	E12	0	11
V$LRH1_Q5	LRH1	0	11
V$RORBETA_Q2	RORBETA	0	11
V$TFE_Q6	TFE	0	12
MA0146.1	Zfx	0	13
V$GLI3_01	GLI3	0	13
V$HEB_Q6	HEB	0	13
V$MATH1_Q2	E47:MATH1	0	13
V$T3R_Q6	half-site matrix	0	13
MA0112.2	ESR1	0	14
V$HES1_Q2	HES1	0	14
V$NURR1_Q3	NURR1	0	14
MA0092.1	Hand1::Tcfe2a	0	15
MA0111.1	Spz1	0	15
V$DEC_Q1	DEC	0	15
V$EBOX_Q6_01	Ebox	0	15
V$LMAF_Q2	LMAF	0	15
V$ZNF515_01	Glis binding sites	0	15

V$E2A_Q6	E2A	0	11
V$SMAD_Q6	SMAD	0	11
V$MEF2C_01	MEF-2C	0	12
V$TFE_Q6	TFE	0	13
V$ZNF515_01	Glis binding sites	0	13
V$HES1_Q2	HES1	0	14
V$SREBP_Q3	SREBP	0	14
V$DEC_Q1	DEC	0	15
V$MAFA_Q4_01	MAFA	0	15
V$NURR1_Q3	NURR1	0	15
V$USF2_Q6	USF2	0	15
MA0160.1	NR4A2	0	16
V$E47_02	E47	0	16
V$GLI1_01	GLI1	0	16
V$OSF2_Q6	Osf2	0	16
V$TTF1_Q6	TTF-1 (Nkx2-1)	0	17
MA0103.1	ZEB1	0	18
V$DELTAEF1_01	deltaEF1	0	18
V$GLI2_01	GLI2	0	18

MA0122.1	Nkx3-2	0	16
V$GLI1_01	GLI1	0	16
V$OSF2_Q6	Osf2	0	16
V$SMAD_Q6	SMAD	0	16
V$LMO2COM_01	complex of Lmo2 bound to Tal-1, E2A proteins, and GATA-1, half-site 1	0	17
V$USF2_Q6	USF2	0	17
V$GLI2_01	GLI2	0	18
MA0160.1	NR4A2	0	19
V$DELTAEF1_01	deltaEF1	0	19
V$TTF1_Q6	TTF-1 (Nkx2-1)	0	19
V$GLI_Q2	GLI	0	20
V$LUN1_01	LUN-1	0	20
V$SREBP_Q3	SREBP	0	20
MA0019.1	Ddit3::Cebpa	0	21
MA0103.1	ZEB1	0	21
MA0161.1	NFIC	0	21
V$LYF1_01	LyF-1	0	21
V$MYOGENIN_Q6	myogenin	0	21
V$AML1_01	runt-factor	0	22

V$LFA1_Q6	LF-A1	0	18
MA0122.1	Nkx3-2	0	19
MA0146.1	Zfx	0	19
V$GLI_Q2	GLI	0	19
V$AML1_Q4	AML1	0	20
V$MAFB_01	MAFB	0	20
V$AP2REP_01	AP-2 repressor	0	21
V$ZIC1_01	zinc finger protein of the cerebellum 1	0	21
V$ZIC2_01	zinc finger protein of the cerebellum 2	0	21
V$ZIC3_01	zinc finger protein of the cerebellum 3	0	21
MA0019.1	Ddit3::Cebpa	0	22
V$ERALPHA_01	2 ERE half-sites with a 3bp spacer within	0	22
V$ING4_01	ING4	0	22
V$KID3_01	Kid3	0	22
V$LUN1_01	LUN-1	0	22

	AML-1		
V$E2A_Q2	E2A	0	22
V$ERALPHA_01	2 ERE half-sites with a 3bp spacer within	0	22
V$TERALPHA_Q6	TERALPHA	0	22
MA0130.1	ZNF354C	0	23
V$AP2REP_01	AP-2 repressor	0	23
V$ARP1_01	apolipoprotein AI regulatory protein 1	0	23
V$BDP1_01	BDP1	0	23
V$GTF2IRD1_01	GTF2IRD1-isoform2	0	23
V$ING4_01	ING4	0	23
V$KID3_01	Kid3	0	23
V$LFA1_Q6	LF-A1	0	23
V$MAFA_Q4_01	MAFA	0	23
V$MAFB_01	MAFB	0	23
V$PUR1_Q4	PUR1	0	23
V$SREBP2_Q6	SREBP2	0	23

V$SREBP2_Q6	SREBP2	0	22
MA0130.1	ZNF354C	0	23
V$ARP1_01	apolipoprotein AI regulatory protein 1	0	23
V$BDP1_01	BDP1	0	23
V$GTF2IRD1_01	GTF2IRD1-isoform2	0	23
V$TERALPHA_Q6	TERALPHA	0	23
V$ZIC1_01	zinc finger protein of the cerebellum 1	0	23
V$ZIC2_01	zinc finger protein of the cerebellum 2	0	23
V$ZIC3_01	zinc finger protein of the cerebellum 3	0	23

Supplementary Table 5. Clover results indicate the number of chromosomes with transcription factor binding motifs statistically over- or under-represented in HTE DHS within intergenic sequence (more than 2kb outside of any gene). Analysis was divided into three groups (all DHS, HTE-selective DHS, and ubiquitous DHS). Motifs with more than one entry in the databases utilized were edited to retain only the first occurrence of the motif.

All DHS x Intergenic				TE-selective DHS x Intergenic				Ubiquitous DHS x Intergenic			
ID	**Name**	**p < 0.01**	**p > 0.99**	**ID**	**Name**	**p < 0.01**	**p > 0.99**	**ID**	**Name**	**p < 0.01**	**p > 0.99**
MA0002.2	RUNX1	23	0	MA0080.2	SPI1	23	0	MA0055.1	Myf	23	0
MA0003.1	TFAP2A	23	0	MA0089.1	NFE2L1::MafG	23	0	MA0068.1	Pax4	23	0
MA0039.2	Klf4	23	0	MA0098.1	ETS1	23	0	MA0080.2	SPI1	23	0
MA0055.1	Myf	23	0	MA0099.2	AP1	23	0	MA0098.1	ETS1	23	0
MA0056.1	MZF1_1-4	23	0	MA0136.1	ELF5	23	0	MA0139.1	CTCF	23	0
MA0079.2	SP1	23	0	MA0145.1	Tcfcp2l1	23	0	V$ALX3_01	ALX-3	23	0
MA0080.2	SPI1	23	0	MA0150.1	NFE2L2	23	0	V$ALX4_02	Alx-4	23	0
MA0081.1	SPIB	23	0	MA0156.1	FEV	23	0	V$AMEF2_Q6	myocyte enhancer factor	23	0
MA0089.1	NFE2L1::MafG	23	0	V$AP1FJ_Q2	activator protein 1	23	0	V$AP1_01	AP-1	23	0
MA0090.1	TEAD1	23	0	V$AP4_Q5	activator protein 4	23	0	V$AP2_Q6_01	AP-2	23	0
MA0098.1	ETS1	23	0	V$AR_Q6	half-site matrix	23	0	V$ARX_01	Arx	23	0
MA0099.2	AP1	23	0	V$BACH1_01	BTB and CNC homolog 1	23	0	V$BARHL1_01	Barhl-1	23	0
MA0136.1	ELF5	23	0	V$BACH2_01	BTB and CNC homolog 2	23	0	V$BARHL2_01	Barhl2	23	0
MA0139.1	CTCF	23	0	V$CMAF_02	C-MAF	23	0	V$BARX1_01	Barx1	23	0
MA0144.1	Stat3	23	0	V$E12_Q6	E12	23	0	V$BARX2_01	Barx-2	23	0
MA0145.1	Tcfcp2l1	23	0	V$E2A_Q2	E2A	23	0	V$BCL6_01	BCL6	23	0
MA0148.1	FOXA1	23	0	V$ELF1_Q5	ELF1	23	0	V$BEN_01	BEN	23	0
MA0150.1	NFE2L2	23	0	V$ETS2_Q6	ETS2	23	0	V$BRN3C_01	Brn-3c	23	0
MA0154.1	EBF1	23	0	V$ETS_Q4	Ets	23	0	V$BRN4_01	Brn-4	23	0
MA0156.1	FEV	23	0	V$FRA1_Q5	FRA1	23	0	V$BSX_01	Bsx	23	0

MA0161.1	NFIC	23	0	V$GABPALPHA_Q4	GABP-alpha	23	0	V$CART1_02	CART1	23	0
V$AP1FJ_Q2	activator protein 1	23	0	V$HEB_Q6	HEB	23	0	V$CDP_03	CDP	23	0
V$AP2_Q6_01	AP-2	23	0	V$LBP1_Q6	LBP-1	23	0	V$CDX1_01	Cdx-1	23	0
V$AP2ALPHA_01	AP-2alpha	23	0	V$MAF_Q6_01	MAF	23	0	V$CDX2_01	Cdx-2	23	0
V$AP2GAMMA_01	AP-2gamma	23	0	V$MAFB_01	MAFB	23	0	V$CETS1P54_02	c-Ets-1(p54)	23	0
V$AP4_01	activator protein 4	23	0	V$MATH1_Q2	E47:MATH1	23	0	V$DBX1_01	Dbx-1	23	0
V$AR_Q6	half-site matrix	23	0	V$MYOD_Q6	myoblast determining factor	23	0	V$DBX2_01	Dbx-2	23	0
V$BACH1_01	BTB and CNC homolog 1	23	0	V$MYOGENIN_Q6	myogenin	23	0	V$DLX1_01	Dlx-1	23	0
V$BACH2_01	BTB and CNC homolog 2	23	0	V$NEUROD_01	Neuro D	23	0	V$DLX3_01	dlx3	23	0
V$BLIMP1_Q6	BLIMP1	23	0	V$NFE2_01	NF-E2 p45	23	0	V$DLX7_01	Dlx7	23	0
V$CETS1P54_01	c-Ets-1(p54)	23	0	V$NRF2_Q4	heterodimer containing Nrf2	23	0	V$E12_Q6	E12	23	0
V$CKROX_Q2	CKROX	23	0	V$P53_02	tumor suppressor p53	23	0	V$E2F1_01	E2F1	23	0
V$CMAF_02	C-MAF	23	0	V$P63_01	p63	23	0	V$E2F6_01	E2F6	23	0
V$CP2_01	CP2	23	0	V$PEA3_Q6	PEA3	23	0	V$ELF1_Q5	ELF1	23	0
V$E12_Q6	E12	23	0	V$PU1_Q6	PU.1	23	0	V$EN1_02	En-1	23	0
V$E2A_Q6	E2A	23	0	V$PUR1_Q4	PUR1	23	0	V$EN2_01	En-2	23	0
V$E2F1_01	E2F1	23	0	V$STAT6_02	signal transducer and activator of transcription 6	23	0	V$ESX1_01	Esx1	23	0
V$E2F6_01	E2F6	23	0	V$TCF11_01	TCF11/KCR-F1/Nrf1 homodimers	23	0	V$ETS2_Q6	ETS2	23	0
V$E47_01	E47	23	0	V$TR4_01	TR4	23	0	V$ETS_Q4	Ets	23	0
V$EBF_Q6	EBF	23	0	MA0055.1	Myf	22	0	V$EVI1_04	ectopic viral integration site 1 encoded factor	23	0
V$ELF1_Q5	ELF1	23	0	MA0103.1	ZEB1	22	0	V$FPM315_01	Zinc finger protein FPM315 with KRAB	23	0

									and SCAN domains		
V$ER_Q6_02	half-site matrix, half-ERE	23	0	MA0106.1	TP53	22	0	V$GABPALPHA_Q4	GABP-alpha	23	0
V$ESE1_Q3	ESE1	23	0	V$AREB6_01	AREB6 (Atp1a1 regulatory element binding factor 6)	22	0	V$HB24_01	HB24	23	0
V$ETS2_B	c-Ets-2 binding sites	23	0	V$EBOX_Q6_01	Ebox	22	0	V$HDX_01	Hdx	23	0
V$ETS_Q4	Ets	23	0	V$FLI1_Q6	FLI1	22	0	V$HEB_Q6	HEB	23	0
V$FLI1_Q6	FLI1	23	0	V$LMAF_Q2	LMAF	22	0	V$HMBOX1_01	Hmbox1	23	0
V$FPM315_01	Zinc finger protein FPM315 with KRAB and SCAN domains	23	0	V$LMO2COM_01	complex of Lmo2 bound to Tal-1, E2A proteins, and GATA-1, half-site 1	22	0	V$HMGIY_Q3	HMGIY	23	0
V$FRA1_Q5	FRA1	23	0	V$MAFA_Q4_01	MAFA	22	0	V$HMX1_02	HMX1	23	0
V$GABPALPHA_Q4	GABP-alpha	23	0	V$NERF_Q2	new ets-related factor 1a	22	0	V$HMX3_02	Nkx5-1	23	0
V$GR_Q6_01	half-site matrix	23	0	V$SMAD3_Q6	SMAD3	22	0	V$HNF1_Q6	HNF1	23	0
V$HEB_Q6	HEB	23	0	V$T3R_Q6	half-site matrix	22	0	V$HNF1B_01	HNF-1beta	23	0
V$IRF_Q6	IRF	23	0	V$TAL1_Q6	TAL1	22	0	V$HOMEZ_01	Homez	23	0
V$KAISO_01	KAISO	23	0	V$TEL2_Q6	Tel-2	22	0	V$HOX13_02	HOXA5	23	0
V$LBP1_Q6	LBP-1	23	0	MA0081.1	SPIB	21	0	V$HOXA10_01	HOXA10	23	0
V$LMAF_Q2	LMAF	23	0	V$AP2GAMMA_01	AP-2gamma	21	0	V$HOXA13_03	HOXA13	23	0
V$LTF_Q6	LTF	23	0	V$ESE1_Q3	ESE1	21	0	V$HOXA1_01	HOXA1	23	0
V$MAFA_Q4_01	MAFA	23	0	V$NF1_Q6	nuclear factor 1	21	0	V$HOXA2_01	HoxA2	23	0
V$MAFB_01	MAFB	23	0	V$STAT3_02	signal transducer and activator of transcription 3	21	0	V$HOXA4_01	HOXA4	23	0
V$MATH1_Q2	E47:MATH1	23	0	MA0003.1	TFAP2A	20	0	V$HOXA6_01	HOXA6	23	0
V$MAZ_Q6	MAZ	23	0	V$AP2ALPHA_01	AP-2alpha	20	0	V$HOXA7_02	HOXA7	23	0
V$MEIS2_02	MEIS2	23	0	V$CETS1P54_01	c-Ets-1(p54)	20	0	V$HOXA9_01	hoxa9	23	0

V$MYOD_01	myoblast determination gene product	23	0	V$CP2_01	CP2	20	0	V$HOXB13_01	HOXB13	23	0
V$MYOGENIN_Q6	myogenin	23	0	V$DELTAEF1_01	deltaEF1	20	0	V$HOXB4_01	HOXB4	23	0
V$MZF1_Q5	MZF1	23	0	V$E47_01	E47	20	0	V$HOXB5_01	HoxB5	23	0
V$NERF_Q2	new ets-related factor 1a	23	0	V$FPM315_01	Zinc finger protein FPM315 with KRAB and SCAN domains	20	0	V$HOXB6_01	HOXB6	23	0
V$NEUROD_01	Neuro D	23	0	V$GR_Q6_01	half-site matrix	20	0	V$HOXB7_01	HOXB7	23	0
V$NF1_Q6	nuclear factor 1	23	0	V$MEIS2_02	MEIS2	20	0	V$HOXB8_01	HOXB8	23	0
V$NFAT1_Q6	NFAT1	23	0	V$SMAD4_Q6	SMAD4	20	0	V$HOXB9_01	HOXB9	23	0
V$NFAT2_Q5	NF-AT2	23	0	V$TCF4_03	Tcf-4 dimer	20	0	V$HOXC13_01	HOXC13	23	0
V$NFE2_01	NF-E2 p45	23	0	MA0002.2	RUNX1	19	0	V$HOXC4_01	HOXC4	23	0
V$NRF2_Q4	heterodimer containing Nrf2	23	0	MA0039.2	Klf4	19	0	V$HOXC5_01	HOXC5	23	0
V$PAX4_03	Pax-4 binding sites	23	0	MA0067.1	Pax2	19	0	V$HOXC6_01	HOXC6	23	0
V$PEA3_Q6	PEA3	23	0	MA0117.1	Mafb	19	0	V$HOXC8_01	HOXC-8	23	0
V$PU1_Q4	PU.1	23	0	MA0148.1	FOXA1	19	0	V$HOXC9_01	HOXC9	23	0
V$SMAD3_Q6	SMAD3	23	0	MA0161.1	NFIC	19	0	V$HOXD10_01	HOXD10	23	0
V$SMAD4_Q6	SMAD4	23	0	V$HNF4_Q6_03	half-site 2	19	0	V$HOXD13_01	HOXD13	23	0
V$SOX9_Q4	SOX9	23	0	V$LTF_Q6	LTF	19	0	V$HOXD1_01	HOXD1	23	0
V$SP4_Q5	SP4	23	0	V$MEIS1_01	Meis-1 (myeloid ecotropic viral integration site 1)	19	0	V$HOXD3_01	HOXD3	23	0
V$STAT1_03	signal transducer and activator of transcription 1	23	0	V$TCF11MAFG_01	TCF11:MafG heterodimers	19	0	V$HOXD8_01	HOXD8	23	0
V$STAT4_01	signal transducer and activator of transcription 4	23	0	V$USF_Q6_01	USF	19	0	V$IPF1_06	ipf1	23	0
V$T3R_Q6	half-site matrix	23	0	MA0144.1	Stat3	18	0	V$IRF3_Q3	IRF3	23	0
V$TAL1_01	Tal-1 (Scl)	23	0	V$USF2_Q6	USF2	18	0	V$ISL2_01	Isl2	23	0

V$TEF_01	TEF b.s.	23	0	MA0092.1	Hand1::Tcfe2a	17	0	V$K2B_01	K-2b	23	0
V$TEL2_Q6	Tel-2	23	0	F$AMT1_Q2	AMT1	17	0	V$LBP1_Q6	LBP-1	23	0
V$TR4_01	TR4	23	0	MA0090.1	TEAD1	16	0	V$LBX2_01	Lbx2	23	0
V$USF_Q6_01	USF	23	0	V$HNF3A_01	FOXA1	16	0	V$LH2_01	LH-2	23	0
V$WT1_Q6	WT1	23	0	V$MAZ_Q6	MAZ	16	0	V$LHX3_02	Lhx3	23	0
V$ZBED6_01	ZBED6	23	0	V$SOX9_Q4	SOX9	16	0	V$LHX5_01	Lhx5	23	0
MA0047.2	Foxa2	22	0	V$TEF1_Q6	TEF-1	16	0	V$LHX61_01	lhx6.1	23	0
MA0048.1	NHLH1	22	0	V$TEF_01	TEF b.s.	16	0	V$LHX9_01	Lhx9	23	0
MA0092.1	Hand1::Tcfe2a	22	0	V$TGIF_01	TGIF (5'TG3' interacting factor)	16	0	V$LIM1_01	Lim-1	23	0
MA0138.2	REST	22	0	MA0047.2	Foxa2	15	0	V$LMX1_01	Lmx-1	23	0
V$AREB6_04	AREB6 (Atp1a1 regulatory element binding factor 6)	22	0	V$AP2REP_01	AP-2 repressor	15	0	V$LMX1B_01	lmx1b	23	0
V$BEN_01	BEN	22	0	V$CACBINDINGPROTEIN_Q6	CAC-binding protein	15	0	V$MATH1_Q2	E47:MATH1	23	0
V$CACCCBINDINGFACTOR_Q6	CACCC-binding factor	22	0	V$CEBPB_01	CCAAT/enhancer binding protein beta	15	0	V$MMEF2_Q6	myocyte enhancer factor	23	0
V$DR1_Q3	Direct repeat 1	22	0	V$LBP9_01	LBP9 (Tcfcp211)	15	0	V$MSX1_02	Msx-1	23	0
V$EAR2_Q2	EAR2	22	0	V$SMAD_Q6_01	SMAD	15	0	V$MSX2_01	Msx-2	23	0
V$EBOX_Q6_01	Ebox	22	0	V$TTF1_Q6	TTF-1 (Nkx2-1)	15	1	V$MSX3_01	Msx-3	23	0
V$ELK1_01	Elk-1	22	0	V$CACCCBINDINGFACTOR_Q6	CACCC-binding factor	13	0	V$NANOG_02	Nanog	23	0
V$HNF1_Q6_01	HNF1	22	0	V$CEBP_Q2_01	C/EBP	13	0	V$NCX_02	Ncx	23	0
V$HNF3_Q6_01	HNF3	22	0	V$SP1_Q4_01	Sp1	13	0	V$NEUROD_02	NeuroD	23	0
V$HNF4_Q6_03	half-site 2	22	0	V$TBX5_02	TBX5	13	0	V$NFAT1_Q6	NFAT1	23	0
V$IRF3_Q3	IRF3	22	0	V$TFIII_Q6	TFII-I	13	0	V$NFE2_01	NF-E2 p45	23	0
V$LFA1_Q6	LF-A1	22	0	MA0154.1	EBF1	12	0	V$NKX12_01	Nkx1-2	23	0

V$LMO2COM_01	complex of Lmo2 bound to Tal-1, E2A proteins, and GATA-1, half-site 1	22	0	V$CKROX_Q2	CKROX	12	0	V$NKX22_02	NKX22	23	0
V$MAF_Q6_01	MAF	22	0	V$EBF_Q6	EBF	12	0	V$NKX52_01	Nkx5-2	23	0
V$MEIS1_01	Meis-1 (myeloid ecotropic viral integration site 1)	22	0	V$GKLF_02	GKLF (KLF4)	12	0	V$NKX61_02	NKX6.1	23	0
V$NFAT_Q4_01	NF-AT	22	0	V$KAISO_01	KAISO	12	0	V$NKX62_Q2	NK related homeobox factor 6-2	23	0
V$NRSF_01	neuron-restrictive silencer factor	22	0	V$PAX4_03	Pax-4 binding sites	12	0	V$NKX63_01	Nkx6-3	23	0
V$P53_02	tumor suppressor p53	22	0	V$PPARG_Q6	half-site	12	0	V$OBOX5_01	Obox5	23	0
V$PPARG_Q6	half-site	22	0	MA0048.1	NHLH1	11	0	V$OCT1_08	1-Oct	23	0
V$STAT5A_04	signal transducer and activator of transcription 5a	22	0	V$COREBINDINGFACTOR_Q6	core-binding factor	11	0	V$OCTAMER_01	Octamer	23	0
V$STAT6_01	signal transducer and activator of transcription 6	22	0	V$ER_Q6_02	half-site matrix, half-ERE	11	0	V$OTP_01	OTP	23	0
V$TFIII_Q6	TFII-I	22	0	V$SREBP2_Q6	SREBP2	11	0	V$OTX1_01	Otx1	23	0
MA0117.1	Mafb	21	0	V$TFE_Q6	TFE	11	0	V$OTX2_01	Otx2	23	0
F$AMT1_Q2	AMT1	21	0	V$ATF4_Q2	activating transcription factor 4	10	0	V$OTX3_01	Otx3	23	0
V$BRN4_01	Brn-4	21	0	V$CACD_01	CACD	10	0	V$PAX6_02	pax6	23	0
V$CACD_01	CACD	21	0	V$EHF_01	EHF	10	0	V$PAX7_01	Pax-7	23	0
V$FOXO4_01	fork head box O4	21	0	V$MZF1_Q5	MZF1	10	0	V$PEA3_Q6	PEA3	23	0
V$HNF3A_01	FOXA1	21	0	V$PKNOX2_01	PKNOX2	10	0	V$PIT1_01	Pit-1	23	0
V$HNF3B_01	Hepatocyte Nuclear Factor 3beta	21	0	V$ZBED6_01	ZBED6	10	0	V$PITX1_01	Pitx1	23	0
V$LHX3_02	Lhx3	21	0	MA0137.2	STAT1	9	0	V$PITX2_01	PITX2	23	0
V$LMX1B_01	lmx1b	21	0	V$MRG2_01	MRG2	9	0	V$PMX2A_01	PMX2A	23	0
V$NANOG_02	Nanog	21	0	V$PREP1_01	PREP1	9	0	V$PMX2B_01	PMX2B	23	0

V$NCX_02	Ncx	21	0
V$NFAT3_Q3	NFAT3	21	0
V$P63_01	p63	21	0
V$PIT1_01	Pit-1	21	0
V$PKNOX2_01	PKNOX2	21	0
V$PTF1BETA_Q6	PTF1-beta	21	0
V$TGIF_01	TGIF (5'TG3' interacting factor)	21	0
V$TST1_02	6-Oct	21	0
V$UF1H3BETA_Q6	UF1H3BETA	21	0
V$ZFP281_01	Zfp281	21	0
V$AP2REP_01	AP-2 repressor	20	0
V$CEBPB_01	CCAAT/enhancer binding protein beta	20	0
V$DBX1_01	Dbx-1	20	0
V$FOXO1_01	fork head box O1	20	0
V$GKLF_02	GKLF (KLF4)	20	0
V$HOXD8_01	HOXD8	20	0
V$LHX5_01	Lhx5	20	0
V$LIM1_01	Lim-1	20	0
V$RORBETA_Q2	RORBETA	9	0
V$AML_Q6	AML	8	0
V$NKX25_Q5	Nkx2-5	8	0
V$TITF1_Q3	TTF-1, TITF1 (thyroid transcription factor 1)	8	0
MA0060.1	NFYA	7	0
MA0119.1	TLX1::NFIC	7	0
MA0442.1	SOX10	7	0
V$ALPHACP1_01	alpha-CP1	7	0
V$BLIMP1_Q6	BLIMP1	7	0
V$CREB_Q3	CREB	7	0
V$CTF1_01	selection of the binding sites for CTCF by HOX11 cooperative DNA binding [2]	7	0
V$ELK1_01	Elk-1	7	0
V$HNF3ALPHA_Q6	HNF3alpha	7	0
V$MYC_Q2	Myc	7	0
V$NFY_01	nuclear factor Y (Y-box binding factor)	7	0
V$SMAD1_01	SMAD1	7	0
V$STAT5A_04	signal transducer and activator of transcription 5a	7	0
V$TGIF2_01	TGIF2	7	0
V$PROP1_02	Prop-1	23	0
V$PSX1_01	PSX1	23	0
V$PU1_Q6	PU.1	23	0
V$RHOX11_01	Rhox11	23	0
V$S8_02	S8	23	0
V$SHOX2_01	Shox2	23	0
V$STAT1_03	signal transducer and activator of transcription 1	23	0
V$STAT3_02	signal transducer and activator of transcription 3	23	0
V$STAT5A_04	signal transducer and activator of transcription 5a	23	0
V$STAT6_01	signal transducer and activator of transcription 6	23	0
V$TGIF_02	TGIF1	23	0
V$TR4_01	TR4	23	0
V$TST1_02	6-Oct	23	0
V$UNCX4.1_01	Uncx-4.1	23	0
V$VAX1_01	Vax-1	23	0
V$VSX1_01	Vsx1	23	0
MA0003.1	TFAP2A	22	0
MA0056.1	MZF1_1-4	22	0

V$LMX1_01	Lmx-1	20	0	MA0093.1	USF1	6	0	MA0079.2	SP1	22	0
V$NFKB_Q6_01	NF-kappaB	20	0	MA0164.1	Nr2e3	6	0	MA0081.1	SPIB	22	0
V$STAT_Q6	STAT	20	0	V$HNF3_Q6_01	HNF3	6	0	MA0151.1	ARID3A	22	0
V$TCF11_01	TCF11/KCR-F1/Nrf1 homodimers	20	0	V$NFAT2_Q5	NF-AT2	6	0	MA0156.1	FEV	22	0
V$TCF11MAFG_01	TCF11:MafG heterodimers	20	0	V$P300_01	p300	6	0	V$AP2ALPHA_01	AP-2alpha	22	0
MA0065.2	PPARG::RXRA	19	0	V$CEBPE_01	cebpe	5	0	V$AP2GAMMA_01	AP-2gamma	22	0
MA0067.1	Pax2	19	0	V$CTCF_02	CCCTC-binding factor	5	0	V$AP4_01	activator protein 4	22	0
V$ALPHACP1_01	alpha-CP1	19	0	V$E2F1_01	E2F1	5	0	V$AR_Q6	half-site matrix	22	0
V$COREBINDINGFACTOR_Q6	core-binding factor	19	0	V$E2F6_01	E2F6	5	0	V$BACH2_01	BTB and CNC homolog 2	22	0
V$HMX3_02	Nkx5-1	19	0	V$PR_Q2	half-site matrix	5	0	V$CHCH_01	Churchill	22	0
V$ICSBP_Q6	ICSBP	19	0	V$SREBP1_Q5	SREBP1	5	0	V$CKROX_Q2	CKROX	22	0
V$NKX52_01	Nkx5-2	19	0	V$NKX32_01	Nkx3-2	5	1	V$DLX2_01	Dlx-2	22	0
V$NKX63_01	Nkx6-3	19	0	MA0031.1	FOXD1	4	0	V$DOBOX4_01	Dobox4	22	0
V$OCT1_08	1-Oct	19	0	MA0056.1	MZF1_1-4	4	0	V$DOBOX5_01	Dobox5	22	0
V$P50RELAP65_Q5_01	P50:RELA-P65	19	0	MA0112.2	ESR1	4	0	V$E47_01	E47	22	0
V$PAX6_02	pax6	19	0	V$CEBPA_01	CCAAT/enhancer binding protein alpha	4	0	V$EGR_Q6	Egr	22	0
V$PREP1_01	PREP1	19	0	V$DR1_Q3	Direct repeat 1	4	0	V$ELK1_01	Elk-1	22	0
V$TEF1_Q6	TEF-1	19	0	V$EAR2_Q2	EAR2	4	0	V$EMX2_01	EMX2	22	0
MA0103.1	ZEB1	19	1	V$GADP_01	Growth-associated binding protein	4	0	V$ESE1_Q3	ESE1	22	0
V$SREBP2_Q6	SREBP2	19	1	V$NANOG_02	Nanog	4	0	V$EVX1_01	Evx-1	22	0
V$TCF4_03	Tcf-4 dimer	19	1	V$TFEB_01	TFEB	4	0	V$FAC1_01	fetal Alz-50 clone 1	22	0
MA0119.1	TLX1::NFIC	18	0	MA0004.1	Arnt	3	0	V$FLI1_Q6	FLI1	22	0
V$BRN3C_01	Brn-3c	18	0	MA0157.1	FOXO3	3	0	V$FRA1_Q5	FRA1	22	0

V$CEBP_Q2_01	C/EBP	18	0
V$CTF1_01	selection of the binding sites for CTCF by HOX11 cooperative DNA binding [2]	18	0
V$DBX2_01	Dbx-2	18	0
V$EHF_01	EHF	18	0
V$FOXP3_Q4	FOXP3	18	0
V$GADP_01	Growth-associated binding protein	18	0
V$HDX_01	Hdx	18	0
V$HNF3ALPHA_Q6	HNF3alpha	18	0
V$NKX61_03	NKX6.1	18	0
V$NRSE_B	neural-restrictive-silencer-element	18	0
V$SMAD_Q6	SMAD	18	0
V$SP3_Q3	Sp3	18	0
V$TGIF2_01	TGIF2	18	0
V$USF2_Q6	USF2	18	1
MA0060.1	NFYA	17	0
V$BARHL2_01	Barhl2	17	0
V$CEBPA_01	CCAAT/enhancer binding protein alpha	17	0
V$EVI1_04	ectopic viral integration site 1 encoded factor	17	0
V$GAF_Q6	GAF	17	0
MA0258.1	ESR2	3	0
V$AP2_Q6_01	AP-2	3	0
V$ATF3_Q6	activating transcription factor 3	3	0
V$ATF5_01	ATF5 binding site	3	0
V$CLOCKBMAL_Q6	CLOCK:BMAL	3	0
V$CMYC_02	c-Myc heterodimer (with a 26-29 kDa factor)	3	0
V$FOXP3_Q4	FOXP3	3	0
V$NGFIC_01	nerve growth factor-induced protein C	3	0
V$NRSF_01	neuron-restrictive silencer factor	3	0
V$PAX8_B	Pax-8 binding sites	3	0
V$PAX_Q6	Pax	3	0
V$PEBP_Q6	PEBP	3	0
V$SP3_Q3	Sp3	3	0
V$SP4_Q5	SP4	3	0
V$SREBP_Q6	SREBP	3	0
V$STAT4_01	signal transducer and activator of transcription 4	3	0
V$STAT_01	signal transducers and activators of transcription	3	0
V$ZFP281_01	Zfp281	3	0
V$CEBPDELTA_Q6	C/EBPdelta	3	1
V$GBX1_01	Gbx1	22	0
V$GBX2_01	Gbx2	22	0
V$GSC_01	Gsc	22	0
V$GSH2_01	GSH2	22	0
V$HOXA11_01	HOXA11	22	0
V$HOXA3_02	HOXA3	22	0
V$HOXB3_01	HOXB3	22	0
V$HOXC10_01	HOXC10	22	0
V$HOXC11_01	HOXC11	22	0
V$HOXC12_01	HOXC12	22	0
V$HOXD11_01	HOXD11	22	0
V$HOXD12_01	HOXD12	22	0
V$IRF_Q6	IRF	22	0
V$IRX2_01	Irx2	22	0
V$IRX3_01	Irx-3	22	0
V$IRX4_01	IRX4	22	0
V$IRX5_01	Irx5	22	0
V$IRXB3_01	IRXB3	22	0
V$LHX4_01	Lhx4	22	0

V$HOXC6_01	HOXC6	17	0	MA0058.1	MAX	2	0	V$LMAF_Q2	LMAF	22	0
V$RBPJK_Q4	RBP-Jkappa	17	0	MA0062.2	GABPA	2	0	V$MAZ_Q6	MAZ	22	0
V$SMAD1_01	SMAD1	17	0	V$AML1_Q4	AML1	2	0	V$MEF2_Q6_01	MEF-2	22	0
V$VDR_Q3	vitamin D receptor; mediates vitamin D3-signaling, often dimerizes with RXR-alpha	17	0	V$BEN_01	BEN	2	0	V$MOX1_01	Mox1	22	0
V$MRG2_01	MRG2	17	1	V$CREBP1_01	cAMP-responsive element binding protein 1	2	0	V$MYOGENIN_Q6	myogenin	22	0
V$CACBINDINGPROTEIN_Q6	CAC-binding protein	17	2	V$DBP_Q6	DBP	2	0	V$NFAT2_Q5	NF-AT2	22	0
MA0106.1	TP53	16	0	V$EGR2_01	Egr-2/Krox-20 early growth response gene product	2	0	V$NFAT3_Q3	NFAT3	22	0
V$AMEF2_Q6	myocyte enhancer factor	16	0	V$EGR3_01	early growth response gene 3 product	2	0	V$NFAT_Q4_01	NF-AT	22	0
V$ATF5_01	ATF5 binding site	16	0	V$FOXJ3_01	foxj3	2	0	V$NKX23_01	Nkx2-3	22	0
V$NFY_01	nuclear factor Y (Y-box binding factor)	16	0	V$FREAC4_01	Fork head RElated ACtivator-4	2	0	V$NKX29_01	Nkx2-9	22	0
V$SIX4_01	six4	16	0	V$GFI1B_01	Gfi1b	2	0	V$NKX32_02	Nkx3-2	22	0
V$STAT1STAT1_Q3	STAT1:STAT1	16	0	V$GLI3_01	GLI3	2	0	V$NKX3A_02	Nkx3A	22	0
V$TTF1_Q6	TTF-1 (Nkx2-1)	16	1	V$HEN1_02	HEN1	2	0	V$OBOX2_01	Obox2	22	0
MA0068.1	Pax4	15	0	V$HLF_01	hepatic leukemia factor	2	0	V$OBOX3_01	Obox3	22	0
MA0107.1	RELA	15	0	V$KLF15_Q2	KLF15	2	0	V$OCT2_01	2-Oct	22	0
V$AML_Q6	AML	15	0	V$LEF1TCF1_Q4	LEF1, TCF1	2	0	V$OG2_02	OG-2	22	0
V$HOXA10_01	HOXA10	15	0	V$LFA1_Q6	LF-A1	2	0	V$PARP_Q3	PARP	22	0
V$HOXD10_01	HOXD10	15	0	V$MYCMAX_01	c-Myc:Max heterodimer	2	0	V$PBX1_01	Pbx-1	22	0
V$LBP9_01	LBP9 (Tcfcp211)	15	0	V$NFAT1_Q6	NFAT1	2	0	V$POU2F3_01	POU2F3	22	0
V$MMEF2_Q6	myocyte enhancer	15	0	V$OLF1_01	olfactory neuron-	2	0	V$POU6F1_03	POU6F1	22	0

	factor				specific factor						
V$MSX3_01	Msx-3	15	0	V$REX1_03	REX1	2	0	V$RAX_01	rax	22	0
V$PARP_Q3	PARP	15	0	V$SF1_Q6	SF1	2	0	V$SATB1_Q3	SATB1	22	0
V$PUR1_Q4	PUR1	15	6	V$SOX_01	SOX	2	0	V$SP4_Q5	SP4	22	0
MA0152.1	NFATC2	14	0	V$TAXCREB_02	Tax/CREB complex	2	0	V$STAT4_01	signal transducer and activator of transcription 4	22	0
V$ALX3_01	ALX-3	14	0	V$TBR2_01	TBR2	2	0	V$TAL1_01	Tal-1 (Scl)	22	0
V$ATF3_Q6	activating transcription factor 3	14	0	V$WT1_Q6	WT1	2	0	V$TGIF2_01	TGIF2	22	0
V$ATF4_Q2	activating transcription factor 4	14	0	MA0025.1	NFIL3	1	0	V$VAX2_01	Vax-2	22	0
V$BARX1_01	Barx1	14	0	MA0035.2	Gata1	1	0	V$WT1_Q6	WT1	22	0
V$BARX2_01	Barx-2	14	0	MA0059.1	MYC::MAX	1	0	MA0084.1	SRY	21	0
V$FOXO3_01	fork head box O3	14	0	MA0065.2	PPARG::RXRA	1	0	MA0136.1	ELF5	21	0
V$FOXO3A_Q1	FOXO3A	14	0	MA0074.1	RXRA::VDR	1	0	MA0154.1	EBF1	21	0
V$GABP_B	GA binding protein	14	0	MA0083.1	SRF	1	0	V$AP1FJ_Q2	activator protein 1	21	0
V$HEN1_02	HEN1	14	0	MA0104.2	Mycn	1	0	V$AREB6_04	AREB6 (Atp1a1 regulatory element binding factor 6)	21	0
V$KLF15_Q2	KLF15	14	0	MA0113.1	NR3C1	1	0	V$BACH1_01	BTB and CNC homolog 1	21	0
V$NFKAPPAB65_01	NF-kappaB (p65)	14	0	MA0133.1	BRCA1	1	0	V$CEBPA_01	CCAAT/enhancer binding protein alpha	21	0
V$OCTAMER_02	Octamer	14	0	MA0138.2	REST	1	0	V$DLX5_01	dlx5	21	0
V$PAX8_B	Pax-8 binding sites	14	0	MA0147.1	Myc	1	0	V$DRI1_01	DRI1 b.s.	21	0
V$PEBP_Q6	PEBP	14	0	MA0152.1	NFATC2	1	0	V$DUXL_01	Duxl	21	0
V$P300_01	p300	14	1	V$AML2_01	AML2	1	0	V$ETF_Q6	ETF	21	0
MA0112.2	ESR1	13	0	V$ATF6_01	activating transcription factor 6	1	0	V$FOXO3A_Q1	FOXO3A	21	0

V$HAND1E47_01	Hand1:E47 heterodimer	13	0	V$BCL6_02	BCL6	1	0	V$HNF3_Q6_01	HNF3	21	0
V$HOXB3_01	HOXB3	13	0	V$CREBATF_Q6	CREB, ATF	1	0	V$ICSBP_Q6	ICSBP	21	0
V$HOXB4_01	HOXB4	13	0	V$CREBP1CJUN_01	CRE-binding protein 1:c-Jun heterodimer	1	0	V$ISX_01	isx	21	0
V$HOXB9_01	HOXB9	13	0	V$EGR1_01	Egr-1/Krox-24/NGFI-A immediate-early gene product	1	0	V$LMO2COM_01	complex of Lmo2 bound to Tal-1, E2A proteins, and GATA-1, half-site 1	21	0
V$HOXC4_01	HOXC4	13	0	V$ERG_01	ERG	1	0	V$LRF_Q2	LRF	21	0
V$HOXC5_01	HOXC5	13	0	V$EVI1_02	ectopic viral integration site 1 encoded factor	1	0	V$MEIS1_02	Meis1	21	0
V$HOXD3_01	HOXD3	13	0	V$FOXO4_01	fork head box O4	1	0	V$MEIS2_01	Meis2	21	0
V$ISL2_01	Isl2	13	0	V$FREAC2_01	Fork head RElated ACtivator-2	1	0	V$MRG2_01	MRG2	21	0
V$ISRE_01	interferon-stimulated response element	13	0	V$FREAC3_01	Fork head RElated ACtivator-3	1	0	V$MYOD_01	myoblast determination gene product	21	0
V$OLF1_01	olfactory neuron-specific factor	13	0	V$FXR_IR1_Q6	FXR inverted repeat 1	1	0	V$MZF1_Q5	MZF1	21	0
V$PAX_Q6	Pax	13	0	V$GABP_B	GA binding protein	1	0	V$NKX24_01	Nkx2-4	21	0
V$PROP1_02	Prop-1	13	0	V$GRE_C	Glucocorticoid response element	1	0	V$NKX25_03	NKX25	21	0
V$RORBETA_Q2	RORBETA	13	0	V$HAND1E47_01	Hand1:E47 heterodimer	1	0	V$NKX26_01	Nkx2-6	21	0
V$VSX1_01	Vsx1	13	0	V$IK3_01	Ikaros 3	1	0	V$NRSF_01	neuron-restrictive silencer factor	21	0
MA0062.2	GABPA	12	0	V$IPF1_02	A1	1	0	V$OBOX1_01	Obox1	21	0
MA0084.1	SRY	12	0	V$ISRE_01	interferon-stimulated response element	1	0	V$OBOX6_01	Obox6	21	0
MA0093.1	USF1	12	0	V$LRH1_Q5	LRH1	1	0	V$SIX4_01	six4	21	0
V$BARHL1_01	Barhl-1	12	0	V$MEIS1AHOXA9_01	Meis-1a:HOXA9 heterodimeric binding	1	0	V$SIX6_01	Six-6	21	0
V$CEBPE_01	cebpe	12	0	V$MYB_Q6	c-Myb	1	0	V$T3R_Q6	half-site matrix	21	0
V$CREBP1CJU	CRE-binding protein 1:c-Jun	12	0	V$MYOGNF1_01	myogenin / nuclear factor 1 or related	1	0	V$BLIMP1_Q6	BLIMP1	20	0

N_01	heterodimer				factors						
V$GLI3_Q5_01	GLI3	12	0	V$NFAT_Q4_01	NF-AT	1	0	V$BRN2_01	POU factor Brn-2	20	0
V$HOXA4_01	HOXA4	12	0	V$NFMUE1_Q6	NF-muE1	1	0	V$CACBINDINGPROTEIN_Q6	CAC-binding protein	20	0
V$HOXA9_01	hoxa9	12	0	V$NURR1_Q3	NURR1	1	0	V$CDX_Q5	Cdx	20	0
V$HOXB8_01	HOXB8	12	0	V$P50RELAP65_Q5_01	P50:RELA-P65	1	0	V$CEBP_Q2	CCAAT/enhancer binding factor	20	0
V$NKX25_Q5	Nkx2-5	12	0	V$PTF1BETA_Q6	PTF1-beta	1	0	V$EAR2_Q2	EAR2	20	0
V$NKX3A_02	Nkx3A	12	0	V$RBPJK_Q4	RBP-Jkappa	1	0	V$EBF_Q6	EBF	20	0
V$PAX7_01	Pax-7	12	0	V$RFX3_01	RFX3 dimer	1	0	V$FOXO4_01	fork head box O4	20	0
V$PITX2_01	PITX2	12	0	V$TAL1ALPHAE47_01	Tal-1alpha:E47 heterodimer	1	0	V$HB9_01	HB9	20	0
V$PMX2B_01	PMX2B	12	0	V$UF1H3BETA_Q6	UF1H3BETA	1	0	V$HNF3B_01	Hepatocyte Nuclear Factor 3beta	20	0
V$TFEB_01	TFEB	12	0	V$VBP_01	PAR-type chicken vitellogenin promoter-binding protein	1	0	V$NERF_Q2	new ets-related factor 1a	20	0
V$SOX_01	SOX	12	1	V$VDR_Q3	vitamin D receptor; mediates vitamin D3-signaling, often dimerizes with RXR-alpha	1	0	V$NKX11_01	Nkx1-1	20	0
MA0101.1	REL	11	0	V$VDRRXR_01	VDR:RXR	1	0	V$NKX21_01	Nkx2-1	20	0
V$BSX_01	Bsx	11	0	V$ZFP206_01	Zfp206	1	0	V$NRF2_01	nuclear respiratory factor 2	20	0
V$CREL_01	c-Rel	11	0	V$AIRE_02	AIRE	1	1	V$PAX2_02	paired box factor 2	20	0
V$ESX1_01	Esx1	11	0	V$DEC_Q1	DEC	1	1	V$PKNOX2_01	PKNOX2	20	0
V$HB24_01	HB24	11	0	V$PARP_Q3	PARP	1	1	V$PUR1_Q4	PUR1	20	0
V$HOXC9_01	HOXC9	11	0	V$PXRRXR_01	RXR half-site	1	1	V$SIRT6_01	SIRT6	20	0
V$HSF_Q6	HSF	11	0	V$SOX17_01	half-site	1	1	V$SOX4_01	SOX4	20	0
V$LHX9_01	Lhx9	11	0	V$ZID_01	zinc finger with interaction domain	1	1	V$SP1SP3_Q4	SP1:SP3	20	0
V$MSX1_02	Msx-1	11	0	V$BRF1_01	BRF-1	1	8	V$STAT1STAT1_Q3	STAT1:STAT1	20	0

V$OTP_01	OTP	11	0	V$CDPCR1_01	cut-like homeodomain protein	1	10	V$STAT_Q6	STAT	20	0
MA0050.1	IRF1	10	0	MA0046.1	HNF1A	0	1	V$TFIII_Q6	TFII-I	20	0
MA0061.1	NF-kappaB	10	0	MA0070.1	PBX1	0	1	V$UF1H3BETA_Q6	UF1H3BETA	20	0
MA0143.1	Sox2	10	0	MA0073.1	RREB1	0	1	MA0138.2	REST	19	0
V$CDX_Q5	Cdx	10	0	MA0078.1	Sox17	0	1	MA0144.1	Stat3	19	0
V$DOBOX5_01	Dobox5	10	0	MA0084.1	SRY	0	1	MA0152.1	NFATC2	19	0
V$GFI1_01	growth factor independence 1	10	0	MA0088.1	znf143	0	1	V$KROX_Q6	KROX	19	0
V$HFH8_01	HNF-3/Fkh Homolog-8	10	0	MA0130.1	ZNF354C	0	1	V$PREP1_01	PREP1	19	0
V$HOXD1_01	HOXD1	10	0	MA0140.1	Tal1::Gata1	0	1	V$SOX9_Q4	SOX9	19	0
V$IPF1_06	ipf1	10	0	MA0141.1	Esrrb	0	1	V$TBP_Q6	TBP	19	0
V$K2B_01	K-2b	10	0	V$AFP1_Q6	AFP1	0	1	V$ZFP281_01	Zfp281	19	0
V$MYC_Q2	Myc	10	0	V$ARX_01	Arx	0	1	I$ANTP_Q6_01	Antp	18	0
V$NFKAPPAB_01	NF-kappaB	10	0	V$CART1_01	Cart-1 (cartilage homeoprotein 1)	0	1	V$E2A_Q6	E2A	18	0
V$NKX12_01	Nkx1-2	10	0	V$CDC5_01	cell division control protein 5	0	1	V$FOXO1_01	fork head box O1	18	0
V$POU6F1_03	POU6F1	10	0	V$CEBPGAMMA_Q6	C/EBPgamma	0	1	V$IRF7_01	interferon regulatory factor 7	18	0
V$SATB1_Q3	SATB1	10	0	V$CNOT3_01	CNOT3	0	1	V$LHX8_01	Lhx8	18	0
V$TAL1ALPHAE47_01	Tal-1alpha:E47 heterodimer	10	0	V$CPHX_01	Cphx	0	1	V$NRSE_B	neural-restrictive-silencer-element	18	0
V$UNCX4.1_01	Uncx-4.1	10	0	V$DBX2_01	Dbx-2	0	1	V$TATA_C	Retroviral TATA box	18	0
V$SIRT6_01	SIRT6	10	1	V$DLX1_01	Dlx-1	0	1	V$TEL2_Q6	Tel-2	18	0
MA0031.1	FOXD1	9	0	V$DMRT1_01	DMRT1	0	1	MA0039.2	Klf4	17	0
MA0038.1	Gfi	9	0	V$DOBOX5_01	Dobox5	0	1	MA0050.1	IRF1	17	0
MA0155.1	INSM1	9	0	V$DR4_Q2	direct repeat 4	0	1	V$CEBPGAMMA_Q6	C/EBPgamma	17	0
MA0442.1	SOX10	9	0	V$E2F_03	E2F	0	1	V$CPHX_01	Cphx	17	0
V$CDP_03	CDP	9	0	V$ERR1_Q2	estrogen-related	0	1	V$FOXO3_01	fork head box O3	17	0

					receptor alpha						
V$CDX1_01	Cdx-1	9	0	V$ETF_Q6	ETF	0	1	V$FREAC7_01	Fork head RElated ACtivator-7	17	0
V$CDX2_01	Cdx-2	9	0	V$EVX2_01	Evx2	0	1	V$ISRE_01	interferon-stimulated response element	17	0
V$CREB_Q3	CREB	9	0	V$FOXJ2_01	fork head box J 2	0	1	V$LFA1_Q6	LF-A1	17	0
V$FAC1_01	fetal Alz-50 clone 1	9	0	V$FOXO1_Q5	FOXO1	0	1	V$TEF_Q6	TEF	17	0
V$FOXJ3_01	foxj3	9	0	V$GCM_Q2	GCM	0	1	V$USF_Q6_01	USF	17	0
V$FREAC7_01	Fork head RElated ACtivator-7	9	0	V$GSC_01	Gsc	0	1	MA0046.1	HNF1A	16	0
V$HMX1_02	HMX1	9	0	V$GSH2_01	GSH2	0	1	V$E2F_Q2	E2F	16	0
V$HOX13_02	HOXA5	9	0	V$GZF1_01	plays a role in renal branching morphogenesis	0	1	V$EVX2_01	Evx2	16	0
V$HOXA6_01	HOXA6	9	0	V$HBP1_Q2	hbp1	0	1	V$GADP_01	Growth-associated binding protein	16	0
V$HSF1_Q6	HSF1	9	0	V$HFH1_01	HNF-3/Fkh Homolog 1	0	1	V$GAF_Q6	GAF	16	0
V$MEF2_02	myogenic MADS factor MEF-2	9	0	V$HIC1_03	HIC1	0	1	V$HSF_Q6	HSF	16	0
V$NKX23_01	Nkx2-3	9	0	V$HMX1_02	HMX1	0	1	V$PTF1BETA_Q6	PTF1-beta	16	0
V$NURR1_Q3	NURR1	9	0	V$HNF1_01	hepatic nuclear factor 1	0	1	V$SMAD1_01	SMAD1	16	0
V$OTX1_01	Otx1	9	0	V$HOXD3_01	HOXD3	0	1	V$ZFP206_01	Zfp206	16	0
V$PITX1_01	Pitx1	9	0	V$HSF1_01	heat shock factor 1	0	1	MA0062.2	GABPA	15	0
V$PPAR_DR1_Q2	PPAR direct repeat 1	9	0	V$IRF1_01	interferon regulatory factor 1	0	1	V$ERG_01	ERG	15	0
V$ZFP206_01	Zfp206	9	0	V$IRF7_01	interferon regulatory factor 7	0	1	V$FOXD3_01	fork head box D3	15	0
V$PXRRXR_02	PXR half-site	9	3	V$IRF_Q6_01	IRF	0	1	V$HNF3ALPHA_Q6	HNF3alpha	15	0
V$CART1_03	CART1	8	0	V$LBX2_01	Lbx2	0	1	V$NFMUE1_Q6	NF-muE1	15	0
V$CREBP1_01	cAMP-responsive element binding protein 1	8	0	V$LEF1_Q2	LEF1	0	1	V$P53_03	tumor suppressor p53	15	0

V$EN2_01	En-2	8	0	V$LHX3_01	LIM homeobox transcription factor 3	0	1	V$SIX1_01	Six-1	15	0
V$HFH1_01	HNF-3/Fkh Homolog 1	8	0	V$LHX4_01	Lhx4	0	1	V$SOX2_Q6	SOX2	15	0
V$HOXA7_02	HOXA7	8	0	V$LHX5_01	Lhx5	0	1	V$TCF4_01	TCF-4	15	0
V$HOXB7_01	HOXB7	8	0	V$LHX61_01	lhx6.1	0	1	V$CRX_02	Crx	14	0
V$HOXC8_01	HOXC-8	8	0	V$LHX8_01	Lhx8	0	1	V$DMRT7_01	DMRT7	14	0
V$HOXD13_01	HOXD13	8	0	V$MMEF2_Q6	myocyte enhancer factor	0	1	V$FOX_Q2	FOX factors	14	0
V$HSF2_03	HSF2	8	0	V$MOVOB_01	MOVO-B	0	1	V$GATA4_Q3	GATA-4	14	0
V$KROX_Q6	KROX	8	0	V$MSX1_02	Msx-1	0	1	V$GFI1_01	growth factor independence 1	14	0
V$LBX2_01	Lbx2	8	0	V$MTF1_Q4	MTF-1	0	1	V$HFH1_01	HNF-3/Fkh Homolog 1	14	0
V$LRH1_Q5	LRH1	8	0	V$NKX22_01	NK2 class homeobox factor 2	0	1	V$KLF15_Q2	KLF15	14	0
V$MAZR_01	MAZ related factor	8	0	V$NKX23_01	Nkx2-3	0	1	V$MOVOB_01	MOVO-B	14	0
V$NUR77_Q5	NUR77	8	0	V$NUR77_Q5	NUR77	0	1	V$RNF96_01	RNF96	14	0
V$PBX1_04	Pbx1	8	0	V$OCT1_B	Octamer binding factor 1	0	1	V$RSRFC4_Q2	RSRFC4	14	0
V$PR_Q2	half-site matrix	8	0	V$OCT2_02	2-Oct	0	1	V$SMAD3_Q6	SMAD3	14	0
V$PSX1_01	PSX1	8	0	V$OCTAMER_01	Octamer	0	1	V$SP3_Q3	Sp3	14	0
V$REX1_03	REX1	8	0	V$PIT1_Q6	Pit-1	0	1	V$ATF5_01	ATF5 binding site	13	0
V$LRF_Q2	LRF	8	5	V$PITX2_01	PITX2	0	1	V$GABP_B	GA binding protein	13	0
MA0164.1	Nr2e3	7	0	V$PLZF_02	PLZF	0	1	V$HELIOSA_02	Helios A	13	0
MA0258.1	ESR2	7	0	V$POU3F2_01	POU3F2	0	1	V$MAFA_Q4_01	MAFA	13	0
V$ARX_01	Arx	7	0	V$RAX_01	rax	0	1	V$PITX3_01	Pitx3	13	0
V$DAX1_01	Dax1	7	0	V$RNF96_01	RNF96	0	1	V$PXRRXR_02	PXR half-site	13	0
V$EGR_Q6	Egr	7	0	V$RORA1_01	RAR-related orphan receptor alpha1	0	1	V$SOX_Q6	SOX	13	0
V$HFH4_01	HFH4 (FOXJ1)	7	0	V$RXRG_01	RXRG dimer	0	1	MA0101.1	REL	12	0
V$HOXB5_01	HoxB5	7	0	V$VAX2_01	Vax-2	0	1	MA0107.1	RELA	12	0

V$HOXB6_01	HOXB6	7	0
V$LH2_01	LH-2	7	0
V$MAX_01	Max	7	0
V$MOVOB_01	MOVO-B	7	0
V$OBOX5_01	Obox5	7	0
V$OTX2_01	Otx2	7	0
V$RELBP52_01	kappaB site	7	0
V$SHOX2_01	Shox2	7	0
V$SP1SP3_Q4	SP1:SP3	7	0
V$STAT5B_01	signal transducer and activator of transcription 5b	7	0
V$VAX1_01	Vax-1	7	0
V$TBX5_02	TBX5	7	1
V$SREBP1_Q5	SREBP1	7	3
V$RPC155_01	RPC155	7	10
MA0004.1	Arnt	6	0
V$BCL6_02	BCL6	6	0
V$CMYC_02	c-Myc heterodimer (with a 26-29 kDa factor)	6	0
V$FOX_Q2	FOX factors	6	0
V$FOXJ2_01	fork head box J 2	6	0
V$FREAC2_01	Fork head RElated ACtivator-2	6	0
V$FREAC3_01	Fork head RElated ACtivator-3	6	0
V$FREAC4_01	Fork head RElated ACtivator-4	6	0

V$ZF5_01	ZF5	0	1
V$ZFX_01	Zfx	0	1
V$ZNF515_01	Glis binding sites	0	1
MA0042.1	FOXI1	0	2
MA0068.1	Pax4	0	2
MA0087.1	Sox5	0	2
MA0114.1	HNF4A	0	2
MA0135.1	Lhx3	0	2
MA0160.1	NR4A2	0	2
V$AHR_01	aryl hydrocarbon / dioxin receptor	0	2
V$BARHL1_01	Barhl-1	0	2
V$CRX_02	Crx	0	2
V$DLX5_01	dlx5	0	2
V$FOXP1_01	FOXP1	0	2
V$FREAC7_01	Fork head RElated ACtivator-7	0	2
V$GATA2_02	GATA-binding factor 2	0	2
V$GLI_Q2	GLI	0	2
V$HNF4ALPHA_Q6	HNF4alpha	0	2
V$HOXB8_01	HOXB8	0	2
V$HOXC8_01	HOXC-8	0	2
V$IRX5_01	Irx5	0	2
V$ISL2_01	Isl2	0	2

MA0135.1	Lhx3	12	0
V$CREL_01	c-Rel	12	0
V$FOXJ2_02	fork head box J 2	12	0
V$KID3_01	Kid3	12	0
V$NFKAPPAB65_01	NF-kappaB (p65)	12	0
V$NFKB_Q6_01	NF-kappaB	12	0
V$P50RELAP65_Q5_01	P50:RELA-P65	12	0
V$SIX2_01	Six-2	12	0
V$SIX3_01	Six-3	12	0
V$TAL1ALPHAE47_01	Tal-1alpha:E47 heterodimer	12	0
V$ZBED6_01	ZBED6	12	0
MA0041.1	Foxd3	11	0
MA0113.1	NR3C1	11	0
V$CDC5_01	cell division control protein 5	11	0
V$E2F4DP2_01	E2F-4:DP-2 heterodimer	11	0
V$GR_Q6_01	half-site matrix	11	0
V$HMEF2_Q6	myocyte enhancer factor	11	0
MA0040.1	Foxq1	10	0
MA0060.1	NFYA	10	0
MA0143.1	Sox2	10	0
MA0145.1	Tcfcp2l1	10	0
V$CEBPB_01	CCAAT/enhancer binding protein beta	10	0

V$HFH3_01	HFH-3 (HNF3/fork head homolog 3)	6	0	V$LMX1B_01	lmx1b	0	2	V$E2F1DP1RB_01	Rb:E2F-1:DP-1 trimeric complex	10	0
V$HOMEZ_01	Homez	6	0	V$MIZF_01	MIZF	0	2	V$FOXP3_01	forkhead box P3	10	0
V$HOXA2_01	HoxA2	6	0	V$MSX3_01	Msx-3	0	2	V$FREAC3_01	Fork head RElated ACtivator-3	10	0
V$MYCMAX_01	c-Myc:Max heterodimer	6	0	V$NCX_02	Ncx	0	2	V$HNF6_Q6	HNF6	10	0
V$NKX62_Q2	NK related homeobox factor 6-2	6	0	V$OTX1_01	Otx1	0	2	V$MAF_Q6	MAF	10	0
V$OCT4_01	Sox2-Oct4 joint motif, in silico predicted	6	0	V$OTX2_01	Otx2	0	2	V$NFY_01	nuclear factor Y (Y-box binding factor)	10	0
V$P50P50_Q3	P50:P50	6	0	V$POU5F1_01	POU5F1 b.s.	0	2	V$OCT4_01	Sox2-Oct4 joint motif, in silico predicted	10	0
V$TITF1_Q3	TTF-1, TITF1 (thyroid transcription factor 1)	6	0	V$RHOX11_01	Rhox11	0	2	MA0048.1	NHLH1	9	0
V$NKX22_02	NKX22	6	1	V$S8_01	S8	0	2	MA0052.1	MEF2A	9	0
V$PPARA_Q6	half-site	6	1	V$TRF1_01	TRF1	0	2	MA0061.1	NF-kappaB	9	0
V$CPHX_01	Cphx	6	2	V$ZIC1_01	zinc finger protein of the cerebellum 1	0	2	MA0150.1	NFE2L2	9	0
MA0151.1	ARID3A	6	3	MA0040.1	Foxq1	0	3	V$CACCCBINDINGFACTOR_Q6	CACCC-binding factor	9	0
V$LYF1_01	LyF-1	6	13	MA0057.1	MZF1_5-13	0	3	V$CACD_01	CACD	9	0
MA0030.1	FOXF2	5	0	MA0111.1	Spz1	0	3	V$DR1_Q3	Direct repeat 1	9	0
MA0114.1	HNF4A	5	0	V$AHRHIF_Q6	AhR, Arnt, HIF-1	0	3	V$E2F4DP1_01	E2F-4:DP-1 heterodimer	9	0
MA0135.1	Lhx3	5	0	V$BARHL2_01	Barhl2	0	3	V$FREAC2_01	Fork head RElated ACtivator-2	9	0
MA0142.1	Pou5f1	5	0	V$BRACH_01	Brachyury	0	3	V$HFH8_01	HNF-3/Fkh Homolog-8	9	0
V$BRN2_01	POU factor Brn-2	5	0	V$CDPCR3HD_01	cut-like homeodomain protein	0	3	V$HIC1_02	HIC1	9	0
V$COUP_DR1_Q6	COUP direct repeat 1	5	0	V$CHCH_01	Churchill	0	3	V$HP1SITEFACTOR_Q6	HP1 site factor	9	0

V$EN1_02	En-1	5	0	V$DMRT5_01	DMRT5	0	3	V$MAZR_01	MAZ related factor	9	0
V$HOXB13_01	HOXB13	5	0	V$DMRT7_01	DMRT7	0	3	V$TCF3_01	TCF-3	9	0
V$IK1_01	Ikaros 1	5	0	V$FAC1_01	fetal Alz-50 clone 1	0	3	V$TTF1_Q6	TTF-1 (Nkx2-1)	9	1
V$IRF7_01	interferon regulatory factor 7	5	0	V$FOXO3A_Q1	FOXO3A	0	3	MA0051.1	IRF2	8	0
V$LHX61_01	lhx6.1	5	0	V$HOXA7_01	HOXA7	0	3	V$COMP1_01	COMP1	8	0
V$NKX29_01	Nkx2-9	5	0	V$HOXC10_01	HOXC10	0	3	V$CREB_01	cAMP-responsive element binding protein	8	0
V$NKX32_02	Nkx3-2	5	0	V$IRX2_01	Irx2	0	3	V$CREBP1CJUN_01	CRE-binding protein 1:c-Jun heterodimer	8	0
V$RFX3_01	RFX3 dimer	5	0	V$IRX4_01	IRX4	0	3	V$E2F1DP1_01	E2F-1:DP-1 heterodimer	8	0
V$RSRFC4_01	related to serum response factor, C4	5	0	V$ISL1_Q6	ISL1	0	3	V$EBOX_Q6_01	Ebox	8	0
V$S8_02	S8	5	0	V$LMX1_01	Lmx-1	0	3	V$EHF_01	EHF	8	0
V$DRI1_01	DRI1 b.s.	5	1	V$MEF2_01	myogenic enhancer factor 2	0	3	V$ER_Q6_02	half-site matrix, half-ERE	8	0
V$DELTAEF1_01	deltaEF1	5	4	V$NKX11_01	Nkx1-1	0	3	V$HSF2_01	heat shock factor 2	8	0
MA0052.1	MEF2A	4	0	V$NKX21_01	Nkx2-1	0	3	V$IRF8_Q6	IRF8	8	0
MA0059.1	MYC::MAX	4	0	V$NKX26_01	Nkx2-6	0	3	V$KAISO_01	KAISO	8	0
MA0104.2	Mycn	4	0	V$NKX3A_02	Nkx3A	0	3	V$LTF_Q6	LTF	8	0
MA0113.1	NR3C1	4	0	V$OBOX3_01	Obox3	0	3	V$NFKAPPAB_01	NF-kappaB	8	0
V$CHCH_01	Churchill	4	0	V$PNR_01	PNR	0	3	V$P50P50_Q3	P50:P50	8	0
V$ERG_01	ERG	4	0	V$PPARA_Q6	half-site	0	3	MA0075.1	Prrx2	8	1
V$EVX1_01	Evx-1	4	0	V$SATB1_01	Consensus SATB1 Binding Sequence	0	3	MA0065.2	PPARG::RXRA	7	0
V$GFI1B_01	Gfi1b	4	0	V$ZNF219_01	ZNF219	0	3	MA0148.1	FOXA1	7	0
V$HOXA1_01	HOXA1	4	0	MA0041.1	Foxd3	0	4	MA0158.1	HOXA5	7	0
V$HOXC13_01	HOXC13	4	0	MA0124.1	NKX3-1	0	4	V$FOXP1_01	FOXP1	7	0
V$IRX4_01	IRX4	4	0	MA0125.1	Nobox	0	4	V$HEN1_02	HEN1	7	0

V$OCT2_01	2-Oct	4	0	V$CDX_Q5	Cdx	0	4	V$HSF1_Q6	HSF1	7	0
V$OCT_C	Octamer binding site	4	0	V$COUPTF_Q6	COUPTF	0	4	V$PLZF_02	PLZF	7	0
V$OTX3_01	Otx3	4	0	V$DBX1_01	Dbx-1	0	4	V$PPARG_Q6	half-site	7	0
V$PMX2A_01	PMX2A	4	0	V$DLX7_01	Dlx7	0	4	V$RBPJK_Q4	RBP-Jkappa	7	0
V$POU2F3_01	POU2F3	4	0	V$DMRT2_01	DMRT2	0	4	V$SP2_01	SP2	7	0
V$CEBPDELTA_Q6	C/EBPdelta	4	1	V$HB24_01	HB24	0	4	V$VDR_Q3	vitamin D receptor; mediates vitamin D3-signaling, often dimerizes with RXR-alpha	7	0
V$IK_Q5	Ikaros	4	9	V$HOXA11_01	HOXA11	0	4	V$GKLF_02	GKLF (KLF4)	7	1
MA0046.1	HNF1A	3	0	V$HOXC12_01	HOXC12	0	4	V$MTF1_02	MTF1	7	1
V$ALX4_02	Alx-4	3	0	V$HOXD11_01	HOXD11	0	4	V$SREBP2_Q6	SREBP2	7	3
V$DLX1_01	Dlx-1	3	0	V$HOXD12_01	HOXD12	0	4	MA0076.1	ELK4	6	0
V$DLX2_01	Dlx-2	3	0	V$ISX_01	isx	0	4	MA0142.1	Pou5f1	6	0
V$GSH2_01	GSH2	3	0	V$LXR_Q3	LXR	0	4	V$E2F1DP2_01	E2F-1:DP-2 heterodimer	6	0
V$HMBOX1_01	Hmbox1	3	0	V$OBOX6_01	Obox6	0	4	V$MAX_01	Max	6	0
V$HMEF2_Q6	myocyte enhancer factor	3	0	V$PITX1_01	Pitx1	0	4	V$NFKAPPAB50_01	NF-kappaB (p50)	6	0
V$HNF1B_01	HNF-1beta	3	0	V$PITX3_01	Pitx3	0	4	V$OLF1_01	olfactory neuron-specific factor	6	0
V$IRF2_01	interferon regulatory factor 2	3	0	V$PLAG1_01	PLAG1 binding site	0	4	V$RELBP52_01	kappaB site	6	0
V$IRX5_01	Irx5	3	0	V$RSRFC4_01	related to serum response factor, C4	0	4	V$STAT5B_01	signal transducer and activator of transcription 5b	6	0
V$MOX1_01	Mox1	3	0	V$CHOP_01	heterodimers of CHOP and C/EBPalpha	0	5	MA0103.1	ZEB1	6	1
V$MSX2_01	Msx-2	3	0	V$DLX2_01	Dlx-2	0	5	MA0030.1	FOXF2	5	0
V$POU1F1_Q6	POU1F1	3	0	V$DMRT4_01	DMRT4	0	5	MA0031.1	FOXD1	5	0
V$RREB1_01	Ras-responsive element binding	3	0	V$GLI1_Q2	GLI1	0	5	MA0038.1	Gfi	5	0

	protein 1										
V$SF1_Q6	SF1	3	0	V$HELIOSA_02	Helios A	0	5	MA0057.1	MZF1_5-13	5	0
V$STAF_01	Se-Cys tRNA gene transcription activating factor	3	0	V$HMEF2_Q6	myocyte enhancer factor	0	5	V$AFP1_Q6	AFP1	5	0
V$STAT3STAT3_Q3	STAT3:STAT3	3	0	V$HOXC11_01	HOXC11	0	5	V$ATF3_Q6	activating transcription factor 3	5	0
V$KID3_01	Kid3	3	1	V$IRX3_01	Irx-3	0	5	V$CEBPE_01	cebpe	5	0
V$AML1_Q4	AML1	3	3	V$IRXB3_01	IRXB3	0	5	V$CIZ_01	CIZ (Cas-associated zinc finger protein)	5	0
V$NKX21_01	Nkx2-1	3	3	V$MRF2_01	modulator recognition factor 2	0	5	V$CNOT3_01	CNOT3	5	0
V$SREBP_Q6	SREBP	3	4	V$OBOX2_01	Obox2	0	5	V$CREBATF_Q6	CREB, ATF	5	0
MA0006.1	Arnt::Ahr	2	0	V$OCT_Q6	Octamer	0	5	V$CREBP1_01	cAMP-responsive element binding protein 1	5	0
MA0040.1	Foxq1	2	0	V$OTX_Q1	OTX	0	5	V$DR4_Q2	direct repeat 4	5	0
MA0057.1	MZF1_5-13	2	0	V$SIX1_01	Six-1	0	5	V$FOXJ3_01	foxj3	5	0
MA0159.1	RXR::RAR_DR5	2	0	V$SOX4_01	SOX4	0	5	V$HFH3_01	HFH-3 (HNF3/fork head homolog 3)	5	0
V$ATF6_01	activating transcription factor 6	2	0	V$ZIC3_01	zinc finger protein of the cerebellum 3	0	5	V$NRF1_Q6	nuclear respiratory factor 1	5	0
V$CLOCKBMAL_Q6	CLOCK:BMAL	2	0	V$GATA4_Q3	GATA-4	0	6	V$POU1F1_Q6	POU1F1	5	0
V$DLX7_01	Dlx7	2	0	V$GBX1_01	Gbx1	0	6	V$POU3F2_02	POU3F2	5	0
V$DOBOX4_01	Dobox4	2	0	V$HOXA13_03	HOXA13	0	6	V$SAP1A_01	SAP-1a	5	0
V$DUXL_01	Duxl	2	0	V$HP1SITEFACTOR_Q6	HP1 site factor	0	6	V$SOX5_01	Sox-5	5	0
V$E2F1DP1RB_01	Rb:E2F-1:DP-1 trimeric complex	2	0	V$NKX24_01	Nkx2-4	0	6	V$STAT3STAT3_Q3	STAT3:STAT3	5	0
V$E2F4DP1_01	E2F-4:DP-1 heterodimer	2	0	V$NKX29_01	Nkx2-9	0	6	V$TFEB_01	TFEB	5	0
V$E2F4DP2_01	E2F-4:DP-2 heterodimer	2	0	V$NKX61_01	NKX6-1	0	6	MA0125.1	Nobox	5	1

V$EGR3_01	early growth response gene 3 product	2	0	V$OBOX1_01	Obox1	0	6	V$BRF1_01	BRF-1	5	1
V$ERR2_01	ERR2 (ESRRB)	2	0	V$TERALPHA_Q6	TERALPHA	0	6	V$USF2_Q6	USF2	5	1
V$ETF_Q6	ETF	2	0	V$ZIC2_01	zinc finger protein of the cerebellum 2	0	6	MA0002.2	RUNX1	4	0
V$HOXA11_01	HOXA11	2	0	VS$HMGA2_01	HMGA2 binding site	0	6	MA0006.1	Arnt::Ahr	4	0
V$HOXA3_02	HOXA3	2	0	V$AMEF2_Q6	myocyte enhancer factor	0	7	MA0025.1	NFIL3	4	0
V$IK3_01	Ikaros 3	2	0	V$CDP_02	transcriptional repressor CDP	0	7	MA0092.1	Hand1::Tcfe2a	4	0
V$IRX2_01	Irx2	2	0	V$DLX3_01	dlx3	0	7	MA0105.1	NFKB1	4	0
V$IRXB3_01	IRXB3	2	0	V$DMRT3_01	DMRT3	0	7	MA0114.1	HNF4A	4	0
V$LHX4_01	Lhx4	2	0	V$GATA3_02	GATA-binding factor 3	0	7	MA0117.1	Mafb	4	0
V$NFKAPPAB50_01	NF-kappaB (p50)	2	0	V$HNF6_Q6	HNF6	0	7	V$CMAF_02	C-MAF	4	0
V$NGFIC_01	nerve growth factor-induced protein C	2	0	V$HOMEZ_01	Homez	0	7	V$CP2_01	CP2	4	0
V$OG2_02	OG-2	2	0	V$NKX62_Q2	NK related homeobox factor 6-2	0	7	V$DAX1_01	Dax1	4	0
V$PLZF_02	PLZF	2	0	V$OBOX5_01	Obox5	0	7	V$E4BP4_01	E4BP4	4	0
V$RFX1_02	X-box binding protein RFX1	2	0	V$POU2F3_01	POU2F3	0	7	V$HFH4_01	HFH4 (FOXJ1)	4	0
V$RHOX11_01	Rhox11	2	0	V$TST1_01	POU-factor Tst-1/Oct-6	0	7	V$HNF4_DR1_Q3	HNF4 direct repeat 1	4	0
V$TAL1BETAE47_01	Tal-1beta:E47 heterodimer	2	0	MA0108.2	TBP	0	8	V$IK1_01	Ikaros 1	4	0
V$VAX2_01	Vax-2	2	0	MA0122.1	Nkx3-2	0	8	V$OTX_Q1	OTX	4	0
V$CEBPGAMMA_Q6	C/EBPgamma	2	1	V$CDX1_01	Cdx-1	0	8	V$PR_Q2	half-site matrix	4	0
V$HNF6_Q6	HNF6	2	1	V$GATA6_01	GATA-6	0	8	V$REX1_03	REX1	4	0
V$LEF1TCF1_Q4	LEF1, TCF1	2	1	V$HOXC13_01	HOXC13	0	8	V$TAL1BETAE47_01	Tal-1beta:E47 heterodimer	4	0

V$NKX26_01	Nkx2-6	2	1	V$SIX2_01	Six-2	0	8	V$TAL1BETAITF2_01	Tal-1beta:ITF-2 heterodimer	4	0
V$TBP_01	TATA binding protein	2	1	V$TATA_01	cellular and viral TATA box elements	0	8	V$ZFX_01	Zfx	4	0
V$HELIOSA_02	Helios A	2	2	V$TCF3_01	TCF-3	0	8	MA0087.1	Sox5	4	1
V$HMGIY_Q3	HMGIY	2	2	V$CDX2_01	Cdx-2	0	9	V$DMRT2_01	DMRT2	4	1
V$TCF3_01	TCF-3	2	5	V$FOXM1_01	FOXM1	0	9	V$DMRT4_01	DMRT4	4	1
V$BRF1_01	BRF-1	2	6	V$HMGIY_Q6	HMG IY	0	9	V$NURR1_Q3	NURR1	4	1
V$ZIC3_01	zinc finger protein of the cerebellum 3	2	6	V$HOXA10_01	HOXA10	0	9	V$OCT_C	Octamer binding site	4	1
MA0017.1	NR2F1	1	0	V$HOXA9_01	hoxa9	0	9	V$SMAD_Q6	SMAD	4	1
MA0087.1	Sox5	1	0	V$IRF8_Q6	IRF8	0	9	MA0035.2	Gata1	3	0
MA0147.1	Myc	1	0	V$SIX6_02	Six-6	0	9	MA0042.1	FOXI1	3	0
V$ATF_01	activating transcription factor	1	0	MA0032.1	FOXC1	0	10	MA0047.2	Foxa2	3	0
V$CREBATF_Q6	CREB, ATF	1	0	MA0052.1	MEF2A	0	10	MA0073.1	RREB1	3	0
V$DLX3_01	dlx3	1	0	MA0158.1	HOXA5	0	10	MA0093.1	USF1	3	0
V$DLX5_01	dlx5	1	0	V$GFI1_Q6	Gfi1	0	10	MA0104.2	Mycn	3	0
V$DMRT7_01	DMRT7	1	0	V$HOXB9_01	HOXB9	0	10	F$AMT1_Q2	AMT1	3	0
V$DR3_Q4	direct repeat 3	1	0	V$POU6F1_01	POU6F1	0	10	V$ALPHACP1_01	alpha-CP1	3	0
V$DR4_Q2	direct repeat 4	1	0	V$YY1_01	Yin and Yang 1	0	10	V$ATF_B	ATF binding site	3	0
V$E4F1_Q6	E4F1	1	0	V$DOBOX4_01	Dobox4	0	11	V$BRCA_01	BRCA1 containing protein complex with USF2	3	0
V$EGR1_01	Egr-1/Krox-24/NGFI-A immediate-early gene product	1	0	V$HOXB13_01	HOXB13	0	11	V$CHX10_01	CHX10	3	0
V$EGR2_01	Egr-2/Krox-20 early growth response gene product	1	0	V$HOXD10_01	HOXD10	0	11	V$GATA3_03	GATA-binding factor 3	3	0

V$EMX2_01	EMX2	1	0
V$FXR_Q2	half-site	1	0
V$GBX1_01	Gbx1	1	0
V$GBX2_01	Gbx2	1	0
V$GSC_01	Gsc	1	0
V$HB9_01	HB9	1	0
V$HIC1_02	HIC1	1	0
V$HIF1_Q3	hypoxia induced factor	1	0
V$HOXA13_03	HOXA13	1	0
V$HOXC10_01	HOXC10	1	0
V$HOXC11_01	HOXC11	1	0
V$HOXC12_01	HOXC12	1	0
V$HOXD11_01	HOXD11	1	0
V$HOXD12_01	HOXD12	1	0
V$IRX3_02	Irx-3	1	0
V$ISX_01	isx	1	0
V$MYOGNF1_01	myogenin / nuclear factor 1 or related factors	1	0
V$NFMUE1_Q6	NF-muE1	1	0
V$NKX11_01	Nkx1-1	1	0
V$OBOX2_01	Obox2	1	0
V$OBOX3_01	Obox3	1	0
V$LRF_Q2	LRF	0	11
V$OG2_01	OG-2	0	11
MA0151.1	ARID3A	0	12
V$GATA_Q6	GATA	0	12
V$HOXD13_01	HOXD13	0	12
V$IK_Q5	Ikaros	0	13
MA0027.1	En1	0	14
V$SIX3_01	Six-3	0	14
V$DRI1_01	DRI1 b.s.	0	15
V$IK2_01	Ikaros 2	0	15
I$ANTP_Q6_01	Antp	0	16
V$LUN1_01	LUN-1	0	16
MA0063.1	Nkx2-5	0	17
V$AP3_Q6	AP-3	0	17
MA0019.1	Ddit3::Cebpa	0	18
MA0132.1	Pdx1	0	18
V$ARP1_01	apolipoprotein AI regulatory protein 1	0	18
V$ERALPHA_01	2 ERE half-sites with a 3bp spacer within	0	18
V$MEF2C_01	MEF-2C	0	19
MA0033.1	FOXL1	0	20
MA0109.1	Hltf	0	20
V$GFI1B_01	Gfi1b	3	0
V$HAND1E47_01	Hand1:E47 heterodimer	3	0
V$HNF3A_01	FOXA1	3	0
V$MIZF_01	MIZF	3	0
V$PAX8_B	Pax-8 binding sites	3	0
V$RFX1_02	X-box binding protein RFX1	3	0
V$SMAD4_Q6	SMAD4	3	0
V$STAF_01	Se-Cys tRNA gene transcription activating factor	3	0
V$TCF11MAFG_01	TCF11:MafG heterodimers	3	0
V$VBP_01	PAR-type chicken vitellogenin promoter-binding protein	3	0
MA0018.2	CREB1	3	1
V$DMRT3_01	DMRT3	3	1
MA0132.1	Pdx1	3	5
MA0059.1	MYC::MAX	2	0
MA0140.1	Tal1::Gata1	2	0
MA0155.1	INSM1	2	0
MA0164.1	Nr2e3	2	0
V$ARNT_02	AhR nuclear translocator homodimers	2	0
V$ATF1_Q6	ATF1	2	0
V$CEBPDELTA_Q6	C/EBPdelta	2	0
V$CMYC_02	c-Myc heterodimer (with a 26-29 kDa factor)	2	0

V$OBOX6_01	Obox6	1	0
V$PAX3_01	Pax-3 binding sites	1	0
V$PXR_Q2	half-site matrix	1	0
V$RAX_01	rax	1	0
V$ROAZ_01	rat Olf-1/EBF-associated zinc finger protein	1	0
V$RP58_01	58 KDA repressor protein	1	0
V$RXRG_01	RXRG dimer	1	0
V$RXRLXRB_01	RXR:LXR-beta	1	0
V$SP2_01	SP2	1	0
V$SRF_02	serum response factor	1	0
V$STRA13_01	Stra13	1	0
V$TAL1BETAITF2_01	Tal-1beta:ITF-2 heterodimer	1	0
V$TFIIA_Q6	TFIIA	1	0
V$ZABC1_01	ZABC1 b.s.	1	0
V$ZEC_01	zinc finger protein expressed in embryonal cells and certain adult organs	1	0
V$ZFX_01	Zfx	1	0
V$E4BP4_01	E4BP4	1	1
V$FOXP1_01	FOXP1	1	1
V$GCNF_01	GCNF (germ cell nuclear factor)	1	1
V$POU3F2_02	POU3F2	1	1
V$TRF1_01	TRF1	1	1
V$CIZ_01	CIZ (Cas-associated zinc finger protein)	0	20
V$ING4_01	ING4	0	20
V$RUSH1A_02	RUSH-1alpha	0	20
V$ZNF333_01	ZNF333	0	20
MA0075.1	Prrx2	0	21
V$HOXA3_01	HOXA3 (homeobox cluster protein)	0	21
V$LYF1_01	LyF-1	0	21
V$YY2	YY2	0	21
V$GTF2IRD1_01	GTF2IRD1-isoform2	0	22
V$BDP1_01	BDP1	0	23
V$HOXA4_Q2	HOXA4	0	23
V$RPC155_01	RPC155	0	23
V$ERR2_01	ERR2 (ESRRB)	2	0
V$LBP9_01	LBP9 (Tcfcp211)	2	0
V$MYC_Q2	Myc	2	0
V$MYCMAX_01	c-Myc:Max heterodimer	2	0
V$NUR77_Q5	NUR77	2	0
V$PPAR_DR1_Q2	PPAR direct repeat 1	2	0
V$RFX3_01	RFX3 dimer	2	0
V$STRA13_01	Stra13	2	0
V$TFIIA_Q6	TFIIA	2	0
V$WHN_B	winged-helix factor nude	2	0
V$XBP1_02	XBP1	2	0
V$ZNF219_01	ZNF219	2	0
VS$HMGA2_01	HMGA2 binding site	2	0
V$AP2REP_01	AP-2 repressor	2	1
V$P300_01	p300	2	1
V$HES1_Q2	HES1	2	3
MA0017.1	NR2F1	1	0
MA0063.1	Nkx2-5	1	0
MA0090.1	TEAD1	1	0
MA0091.1	TAL1::TCF3	1	0
MA0106.1	TP53	1	0

MA0041.1	Foxd3	1	2
V$LEF1_Q2	LEF1	1	2
V$ZNF219_01	ZNF219	1	2
V$NKX24_01	Nkx2-4	1	3
I$ANTP_Q6_01	Antp	1	4
V$TBR2_01	TBR2	1	5
V$SOX4_01	SOX4	1	6
V$CDPCR1_01	cut-like homeodomain protein	1	13
MA0009.1	T	0	1
MA0018.2	CREB1	0	1
MA0072.1	RORA_2	0	1
MA0130.1	ZNF354C	0	1
MA0131.1	MIZF	0	1
MA0133.1	BRCA1	0	1
MA0163.1	PLAG1	0	1
V$AIRE_02	AIRE	0	1
V$DMRT1_01	DMRT1	0	1
V$E2F_Q2	E2F	0	1
V$GATA2_03	GATA-binding factor 2	0	1
V$GRE_C	Glucocorticoid response element	0	1
V$LXR_Q3	LXR	0	1
V$MEIS1AHOXA9_01	Meis-1a:HOXA9 heterodimeric binding	0	1
V$MTF1_02	MTF1	0	1

MA0141.1	Esrrb	1	0
MA0147.1	Myc	1	0
MA0258.1	ESR2	1	0
MA0442.1	SOX10	1	0
V$AIRE_02	AIRE	1	0
V$COUP_01	COUP-TF, HNF-4	1	0
V$EGR3_01	early growth response gene 3 product	1	0
V$GATA2_02	GATA-binding factor 2	1	0
V$GATA6_01	GATA-6	1	0
V$GATA_C	GATA binding site	1	0
V$HBP1_Q2	hbp1	1	0
V$HNF4ALPHA_Q6	HNF4alpha	1	0
V$HTF_01	HTF	1	0
V$LEF1TCF1_Q4	LEF1, TCF1	1	0
V$LXR_Q3	LXR	1	0
V$MECP2_01	MECP2 b.s.	1	0
V$MYOGNF1_01	myogenin / nuclear factor 1 or related factors	1	0
V$NF1_Q6	nuclear factor 1	1	0
V$P63_01	p63	1	0
V$PAX5_01	B-cell-specific activating protein	1	0
V$PAX_Q6	Pax	1	0
V$RFX_Q6	RFX	1	0
V$ROAZ_01	rat Olf-1/EBF-associated zinc finger	1	0

V$PAX5_02	B-cell-specific activating protein	0	1
V$PNR_01	PNR	0	1
V$RORA2_01	RAR-related orphan receptor alpha2	0	1
V$RORA_Q4	RORalpha	0	1
V$SIX6_01	Six-6	0	1
V$SZF11_01	SZF1-1	0	1
V$TATA_01	cellular and viral TATA box elements	0	1
V$TBX15_02	T-box 15	0	1
V$TFE_Q6	TFE	0	1
V$ZID_01	zinc finger with interaction domain	0	1
MA0115.1	NR1H2::RXRA	0	2
MA0160.1	NR4A2	0	2
V$DMRT3_01	DMRT3	0	2
V$GATA4_Q3	GATA-4	0	2
V$HES1_Q2	HES1	0	2
V$HP1SITEFACTOR_Q6	HP1 site factor	0	2
V$OSF2_Q6	Osf2	0	2
V$OTX_Q1	OTX	0	2
V$PITX3_01	Pitx3	0	2
MA0071.1	RORA_1	0	3
MA0125.1	Nobox	0	3

	protein		
V$SF1_Q6_01	SF1	1	0
V$SRF_02	serum response factor	1	0
V$YY1_02	Yin and Yang 1	1	0
V$ZBRK1_01	ZBRK1	1	0
MA0112.2	ESR1	1	1
V$COUPTF_Q6	COUPTF	1	1
V$DMRT1_01	DMRT1	1	1
V$GCNF_01	GCNF (germ cell nuclear factor)	1	1
V$GLI3_Q5_01	GLI3	1	1
V$ZNF515_01	Glis binding sites	1	1
MA0119.1	TLX1::NFIC	1	2
MA0160.1	NR4A2	1	2
V$CTF1_01	selection of the binding sites for CTCF by HOX11 cooperative DNA binding [2]	1	2
V$PLAG1_01	PLAG1 binding site	1	2
V$TBX18_01	T-box 18	1	2
V$ZIC3_01	zinc finger protein of the cerebellum 3	1	2
MA0043.1	HLF	0	1
MA0069.1	Pax6	0	1
MA0072.1	RORA_2	0	1
MA0115.1	NR1H2::RXRA	0	1
V$AHR_Q5	aryl hydrocarbon /	0	1

MA0146.1	Zfx	0	3
V$AHRHIF_Q6	AhR, Arnt, HIF-1	0	3
V$COUPTF_Q6	COUPTF	0	3
V$DMRT5_01	DMRT5	0	3
V$ERR1_Q2	estrogen-related receptor alpha	0	3
V$GATA1_04	GATA-binding factor 1	0	3
V$IRF8_Q6	IRF8	0	3
V$MRF2_01	modulator recognition factor 2	0	3
V$SIX1_01	Six-1	0	3
V$AHR_Q5	aryl hydrocarbon / dioxin receptor	0	4
V$CDPCR3_01	cut-like homeodomain protein	0	4
V$DEC_Q1	DEC	0	4
V$PBX_Q3	Pbx	0	4
V$RORA1_01	RAR-related orphan receptor alpha1	0	4
MA0088.1	znf143	0	5
V$GATA3_02	GATA-binding	0	5

	dioxin receptor		
V$AHRARNT_01	aryl hydrocarbon receptor:Arnt heterodimers	0	1
V$BRACH_01	Brachyury	0	1
V$CDPCR1_01	cut-like homeodomain protein	0	1
V$CDPCR3HD_01	cut-like homeodomain protein	0	1
V$FXR_IR1_Q6	FXR inverted repeat 1	0	1
V$PBX_Q3	Pbx	0	1
V$PPARA_02	PPAR-alpha:RXR-alpha heterodimer (peroxisome proliferator activated factor alpha:retinoid X receptor alpha)	0	1
V$PXR_Q2	half-site matrix	0	1
V$RORA2_01	RAR-related orphan receptor alpha2	0	1
V$RP58_01	58 KDA repressor protein	0	1
V$RXRG_01	RXRG dimer	0	1
V$TCF11_01	TCF11/KCR-F1/Nrf1 homodimers	0	1
V$ZABC1_01	ZABC1 b.s.	0	1
V$ZEC_01	zinc finger protein expressed in embryonal cells and certain adult organs	0	1
V$ZID_01	zinc finger with interaction domain	0	1
MA0071.1	RORA_1	0	2

	factor 3		
V$ZNF515_01	Glis binding sites	0	5
VS$HMGA2_01	HMGA2 binding site	0	5
MA0149.1	EWSR1-FLI1	0	6
MA0158.1	HOXA5	0	6
V$BRACH_01	Brachyury	0	6
V$DBP_Q6	DBP	0	6
V$GZF1_01	plays a role in renal branching morphogenesis	0	6
V$SIX2_01	Six-2	0	6
MA0078.1	Sox17	0	7
V$SIX3_01	Six-3	0	7
V$CDPCR3HD_01	cut-like homeodomain protein	0	8
V$GLI_Q2	GLI	0	9
V$GCM_Q2	GCM	0	10
V$GLI1_01	GLI1	0	10
V$CHOP_01	heterodimers of CHOP and C/EBPalpha	0	11
V$ISL1_Q6	ISL1	0	11
V$SPZ1_01	spermatogenic Zip	0	11
V$GLI2_01	GLI2	0	12
MA0124.1	NKX3-1	0	13
V$GATA6_01	GATA-6	0	13

MA0146.1	Zfx	0	2
V$AHRHIF_Q6	AhR, Arnt, HIF-1	0	2
V$ATF4_Q2	activating transcription factor 4	0	2
V$ERR1_Q2	estrogen-related receptor alpha	0	2
V$RORA_Q4	RORalpha	0	2
V$RORBETA_Q2	RORBETA	0	2
V$TBX5_01	TBX5	0	2
V$TEF1_Q6	TEF-1	0	2
MA0130.1	ZNF354C	0	3
V$ING4_01	ING4	0	3
V$RORA1_01	RAR-related orphan receptor alpha1	0	3
V$CDPCR3_01	cut-like homeodomain protein	0	4
V$GLI1_01	GLI1	0	4
MA0088.1	znf143	0	5
MA0111.1	Spz1	0	5
V$AML1_Q4	AML1	0	5
V$CHOP_01	heterodimers of CHOP and C/EBPalpha	0	5
V$TBR2_01	TBR2	0	5
V$ZIC1_01	zinc finger protein of the cerebellum 1	0	5
MA0033.1	FOXL1	0	6

V$FOXM1_01	FOXM1	0	14
V$MEF2C_01	MEF-2C	0	14
V$TERALPHA_Q6	TERALPHA	0	14
V$ZIC1_01	zinc finger protein of the cerebellum 1	0	14
MA0111.1	Spz1	0	16
MA0063.1	Nkx2-5	0	17
V$CRX_Q4_01	CRX	0	17
V$GATA_Q6	GATA	0	17
MA0122.1	Nkx3-2	0	18
V$ZIC2_01	zinc finger protein of the cerebellum 2	0	18
V$CIZ_01	CIZ (Cas-associated zinc finger protein)	0	19
V$YY1_01	Yin and Yang 1	0	19
MA0027.1	En1	0	21
MA0033.1	FOXL1	0	21
MA0132.1	Pdx1	0	21
V$IK2_01	Ikaros 2	0	21
V$LUN1_01	LUN-1	0	21
MA0032.1	FOXC1	0	22
MA0075.1	Prrx2	0	22
V$AP3_Q6	AP-3	0	22
V$ARP1_01	apolipoprotein AI regulatory protein 1	0	22
V$ERALPHA_01	2 ERE half-sites with a 3bp spacer	0	22

MA0124.1	NKX3-1	0	6
V$DEC_Q1	DEC	0	6
V$GLI2_01	GLI2	0	6
V$GLI_Q2	GLI	0	6
V$OSF2_Q6	Osf2	0	6
V$SOX17_01	half-site	0	6
V$SREBP1_Q6	SREBP-1	0	6
V$SREBP_Q3	SREBP	0	6
V$ZNF333_01	ZNF333	0	6
V$FOXM1_01	FOXM1	0	7
V$IK2_01	Ikaros 2	0	7
V$DBP_Q6	DBP	0	9
V$GCM_Q2	GCM	0	9
V$MEF2C_01	MEF-2C	0	9
MA0078.1	Sox17	0	10
V$IK_Q5	Ikaros	0	10
V$AP3_Q6	AP-3	0	11
V$DELTAEF1_01	deltaEF1	0	11
V$ZIC2_01	zinc finger protein of the cerebellum 2	0	11
V$TERALPHA_Q6	TERALPHA	0	13
V$LYF1_01	LyF-1	0	15
MA0089.1	NFE2L1::MafG	0	16

	within		
V$ING4_01	ING4	0	22
MA0019.1	Ddit3::Cebpa	0	23
MA0109.1	Hltf	0	23
V$BDP1_01	BDP1	0	23
V$GTF2IRD1_01	GTF2IRD1-isoform2	0	23
V$RUSH1A_02	RUSH-1alpha	0	23
V$YY2	YY2	0	23
V$ZNF333_01	ZNF333	0	23

MA0109.1	Hltf	0	18
MA0122.1	Nkx3-2	0	18
V$RUSH1A_02	RUSH-1alpha	0	18
V$TFE_Q6	TFE	0	18
V$ERALPHA_01	2 ERE half-sites with a 3bp spacer within	0	19
V$LUN1_01	LUN-1	0	19
MA0019.1	Ddit3::Cebpa	0	20
V$ARP1_01	apolipoprotein AI regulatory protein 1	0	20
V$BDP1_01	BDP1	0	20
V$YY2	YY2	0	21
MA0032.1	FOXC1	0	22
V$GTF2IRD1_01	GTF2IRD1-isoform2	0	23
V$RPC155_01	RPC155	0	23