SUPPLEMENTAL INFORMATION

Identification of Genes Expressed in Hyperpigmented Skin using Meta-Analysis of Microarray Datasets

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SUPPLEMENTAL MATERIALS AND METHODS

Microarray Studies Included in the Meta-Analysis and Selection of Subsets used

Dataset 1: Repetitive UV (UV) dataset [GSE21429]
Six subjects with type II–III skin were irradiated 5 times a week for 2 weeks with UVA, UVB or UVA & UVB (termed SSR) at suberythemal doses (0.4 MED in week 1 and 0.5 MED in week 2) that produce comparable levels of visible skin tanning (Miyamura *et al.*, 2007). Skin biopsy specimens were taken from each subject on the treated and untreated areas. Microarray data are stored in the GEO database (GSE21429) (Choi *et al.*, 2010). For the meta-analysis, we used the paired comparison of SSR vs. CTL.

Dataset 2: Long-Lasting Pigmentation (LLP) dataset [GSE56754]
Seven subjects with type II–III skin were treated with SSR, UVA or UVB repeatedly for 2 weeks, as noted for the repetitive UV study noted above. Biopsies from each of the subjects of the UV-exposed areas and the corresponding control area were taken in the 3rd week, 7 days after irradiation (t1). One week later, a 1.5 MED SSR challenge was applied to the UV-exposed areas and the control area, and biopsy samples were taken immediately after the UV challenge (t2) and 4 days after the UV challenge (t3). In addition, in order to study the LLP effect, biopsy specimens of the UV-exposed, the UV-challenged (cha) and the corresponding control (CTL) areas were evaluated 4 months (t4) after the UV exposure regimen. Microarray data are stored in the GEO database (GSE56754) and are being reported separately (Coelho *et al.*, 2015a; Coelho *et al.*, 2015b). Common differentially expressed genes in response to SSR at all 4 time points identified by raw p value were loaded into the Mfuzz package. Twelve clusters were obtained by that analysis, and the time course pattern represented by cluster 7 was particularly interesting. Many genes important to pigmentation, such as SILV, TYR, DCT and KITLG (Figure S1), were found in cluster 7 and were up-regulated at the first time point (t1=day14) and then gradually returned towards the baseline (t2=day21). But 4 days after the UV challenge (t3=day25), their expression levels increased dramatically, and then returned to the baseline level at the last time

point (t4=4months). The peak expression level of those genes in cluster 7 was located at time point 3 (day25). Therefore, for the meta-analysis, we used the paired samples of SSR vs. CTL from the 7 subjects at the third time point (t3).

Dataset 3: Post-Inflammatory Hyperpigmentation (PIH) dataset [GSE56803]
A suction blister model was developed to study the gene expression pattern during the process of PIH. Fourteen subjects with type II–III skin were treated by the creation of suction blisters (SB), and samples from the treated areas and the corresponding control areas (from the same subjects) were taken 1 week (t1), 2 weeks (t2), 4 weeks (t3), 6 weeks (t4) and 16 weeks (t5) after treatment. For the meta-analysis we used paired samples from 14 subjects at the selected time point. Microarray data are stored in the GEO database (GSE56803) and will be reported separately (Ebsen et al., in preparation). There were mixed effects of inflammation and hyperpigmentation immediately after creation of the suction blister. The inflammation gradually reduced but the hyperpigmentation persisted. In order to identify the appropriate time point to investigate the hyperpigmentation with the lowest inflammation effect, IPA pathway analyses were applied to the dataset. Figure S2A shows the expression alteration of genes related to inflammation of the skin component. Seven out of those 8 genes were significantly altered ($p<0.05$ & fold change >1.2) at the first time point (t1=1week), which indicated that the inflammation effect was quite strong at that time (green = significantly down-regulated and red = significantly up-regulated). In contrast, at time point 4 (t4=6weeks), 7 of the 8 inflammation genes tested had returned to their normal baseline expression level, which indicated that only a minor inflammation impact remained at that time. Figure S2B shows the expression changes of genes related to melanocyte development and the pigmentation signaling pathways. Quite a few genes in this pathway had a significant change in their expression level at time point 1 (=1week), while the most important genes involved in pigmentation, such as TYR, TYRP1, SCF and PI3K, were still up-regulated at time point 4 (=6weeks). This suggested that there was still a moderate pigment effect at time point 4 but little or no inflammatory component. Therefore, for the meta-analysis, we used the paired samples of SB vs. CTL from the 14 subjects at the 4th time point (=6weeks).

Dataset 4: Age Spot (AS) dataset [GSE57103]
Subjects of phototypes I or II (all female, age = 53-70) with various sizes and colors of age spots were recruited for the study. Four mm whole skin punch biopsies were taken from age spots on the forearm of each subject and from a perilesional control area in the vicinity of each age spot. Microarray data are stored in the GEO database (GSE57103) and will be reported separately (Choi et al., in preparation). For the meta-analysis, we used the paired samples of age spot vs. the perilesional control area from 9 subjects.

Dataset 5: Ethnic Skin (ES) dataset [GSE54638]
Subjects in each of 3 racial/ethnic groups (Africans, Asians and Caucasians) were recruited. Four mm skin biopsies were taken from the forearm of each subject for microarray analysis. Microarray data are stored in the GEO database (GSE54638) and have been reported separately (Yin *et al.*, 2014). For the meta-analysis, we used 9 African samples vs. 9 Caucasian samples.

Microarray Data Preprocessing

All raw microarray data files contain the processed signal intensities from Agilent image processing software: Feature Extraction. Before preprocessing, the data distribution of 5 individual datasets and the chip quality of each individual study were explored by PCA analyses, density plots, box plots and MA plots. After log base 2 transformation of the intensities, quantile-normalization was performed on the dataset using the Bioconductor R-Project package LinearModels for Microarray Data (LIMMA) (Smyth *et al.*, 2005), which enabled comparison of samples. The R package of SVA was used to adjust the microarray data from several batches (different processing dates) to remove unwanted non-biological variations. To condense a microarray data object, values for within-array replicate probes were replaced with their averages. The preprocessed intensities of 41,000 probes were finally loaded into a statistical analysis program. In order to reduce the false positive rate, a gene filtering step was incorporated into the analysis program. Probes with intensities higher than 64 (higher than 5 after log2 scaled) in at least one experimental group in any of the individual studies were selected. Probes with small variations (IQR<0.2) across all samples in all 5 datasets were excluded from the meta-analysis. Finally, 27,761 probes were selected for further study.

Statistical Analysis

In this meta-analysis, we were interested in the alteration of gene expression levels before and after treatment or between two biological conditions. The effect size of each gene was represented by log fold change between control samples and hyperpigmented samples. First, we computed the effect size and the standard error of the effect size for each gene in each individual study, and then assessed the consistency of the effect across all 5 studies by calculating I^2, and a summary effect and its level of significance.

A paired t test was applied to the UV, LLP, PIH and AS datasets to compare expression levels of hyperpigmented samples and control samples for each gene. The resulting mean of difference between the paired samples was used as the treatment effect for the meta-analysis. An unpaired t test was employed to test differences between African skin specimens and Caucasian skin specimens. The resulting difference between means of the two groups was used as the treatment effect for the meta-analysis. After the test on individual studies, a random-effect model was employed to calculate the corresponding summary effect (weighted mean of individual effect M*), the variance of the summary effect (within study variance plus between study variance) and the standard error of the summary effect (square root of variance SE_{M*}) (Borenstein *et al.*, 2009). The statistical significance of a change in gene expression was tested by computing the p value corresponding to z statistics, where the z score=$M*/ SE_{M*}$. All meta-analysis was performed in R using the meta package (Schwarzer, 2012). False discovery rate adjustment was performed by the Benjamini&Hochberg method (Hochberg and Benjamini, 1990). To balance the false positive rate and the false negative rate, we applied the following criteria for the selection of differential genes (meta-genes) for further bioinformatics analysis.

1) meta-analysis p <0.05
2) summarized effect (absolute value of fold change) >1.2
3) Intensity filtering, which has been done before statistical analysis
    - log2(intensity)>5 in at least one biological group in 5 datasets
    - the inter quartile range (IQR) > 0.2

Bioinformatics Analysis

The curated website of color genes (http://www.espcr.org/micemut/) provides information on pigment genes that have been described in mice and in their human and zebrafish homologues. We compared the meta-genes with the 171 currently cloned color genes. Also, we compared the meta-gene list with proteins known to occur in human melanosomes (pigment granules) at various stages of maturation, identified by tandem mass spectrometry (Chi *et al.*, 2006) (http://pir.georgetown.edu/cgi-bin/textsearch_iprox.pl?data=mnt).

To identify functional relationships in differentially expressed genes, the R package GOstats (Falcon and Gentleman, 2007) based on the Gene Ontology database was used. To identify key regulators of hyperpigmentation, meta-genes were loaded into IPA (Ingenuity pathway analysis), which can identify the cascade of upstream transcriptional regulators and enzymes, and thereby explain the observed gene expression changes in our meta dataset.

Additionally, we did cluster analysis using the R package Mfuzz package (Futschik, 2012), which enabled us to group genes by alteration patterns, that is, group genes which increase or decrease consistently in the 5 different datasets. Before clustering, standardization of the expression values of each gene is performed, so that the average expression value for each gene is zero and the standard deviation is one. We were interested in identifying genes that share the same alteration pattern among different biological processes.

Furthermore, we tested the classification ability of our top 50 meta-genes by clustering analysis and PCA analysis. GEO microarray database was searched for testing dataset. All meta-genes were ranked by absolute values of fold change. The Top 50 genes were selected for classification test. Sample distances were calculated by the Euclidean method and sample clustering was performed by the Ward.D method.

Immunohistochemistry

Specimens from 6 subjects of 2 different racial/ethnic groups (Caucasian – S29, S30, S31; African Americans – S32, S36, S38) were used to validate expression patterns using immunohistochemistry. Those 6 subjects were part of a larger cohort approved by the Research Involving Human Subjects Committee of the US Food and Drug Administration which adhered to the Helsinki Guidelines and were previously characterized (Tadokoro *et al.*, 2003; Tadokoro *et al.*, 2005).

Paraffin-embedded skin biopsies were examined for expression of various target proteins using indirect immunofluorescence. Primary antibodies used were: TRIM63 antibody PA5-22112 from Pierce (Rockford, IL) and QPCT antibody HPA008406 from Sigma (St. Louis, MO). After incubation with each primary antibody in the presence of 5% goat serum overnight at 4°C, sections were incubated with an appropriate secondary antibody, Alexa Fluor® 594 goat anti-rabbit IgG (H+L), (1:500 dilution; Molecular Probes, Inc., Eugene, OR) in 5% serum for 1 hr at room temperature. Nuclei were counterstained with DAPI (Vector, Burlingame, CA). Fluorescence was observed and photographed using a Leica DMRB/DMLD microscope with a 3CCD 3-chip color video camera (Dage-MTI, Michigan City, IN), and images were processed using AxioVision software (Carl Zeiss MicroImaging GmbH, Frederick, MD).

Statistical Language and Packages

The statistical analysis was carried out in the R language version 3.1.1 (www.r-project.org), and packages were from the Bioconductor project (www.bioconductor.org).

SUPPLEMENTARY REFERENCES

Borenstein M, Hedges LV, Higgins JPT, Rothstein HR: Introduction to Meta-Analysis 1 ed. (Wiley, 2009).

Chi A, Valencia JC, Hu ZZ et al. (2006) Proteomic and bioinformatic characterization of the biogenesis and function of melanosomes. *J Proteome Res* 5:3135-44

Choi W, Miyamura Y, Wolber R et al. (2010) Regulation of human skin pigmentation in situ by repetitive UV exposure - Molecular characterization of responses to UVA and/or UVB. *J Invest Dermatol* 130:1685-96

Coelho SG, Yin L, Ebsen D et al. (2015a) Photobiological implications of melanin photoprotection after UVB-induced tanning of human skin but not UVA-induced tanning. *Pigment Cell Melanoma Res* 28:210-6

Coelho SG, Yin L, Valencia JC et al. (2015b) UV exposure modulates hemidesmosome plasticity contributing to long-term pigmentation in human skin. *J Pathol* 236:17-29

Falcon S, Gentleman R (2007) Using GOstats to test gene lists for GO term association. *Bioinformatics* 23:257-8

Futschik M: Mfuzz: Soft clustering of time series gene expression data. 2012).

Miyamura Y, Coelho SG, Wolber R et al. (2007) Regulation of human skin pigmentation and responses to ultraviolet radiation. *Pigment Cell Res* 20:2-13

Schwarzer G: Meta-Analysis with R 2012).

Smyth GK, Michaud J, Scott HS (2005) Use of within-array replicate spots for assessing differential expression in microarray experiments. *Bioinformatics* 21:2067-75

Tadokoro T, Kobayashi N, Zmudzka BZ et al. (2003) UV-induced DNA damage and melanin content in human skin differing in racial/ethnic origin and photosensitivity. *FASEB J* 17:1177-9

Tadokoro T, Yamaguchi Y, Batzer J et al. (2005) Mechanisms of skin tanning in different racial/ethnic groups in response to ultraviolet radiation. *J Invest Dermatol* 124:1326-32

Yin L, Coelho SG, Ebsen D et al. (2014) Epidermal gene expression and ethnic pigmentation variations among individuals of Asian, European and African ancestry. *Exp Dermatol* 23:731-5

SUPPLEMENTAL FIGURES

Figure S1. Time course plots of TYR, SILV, KITLG and DCT in the LLP dataset.

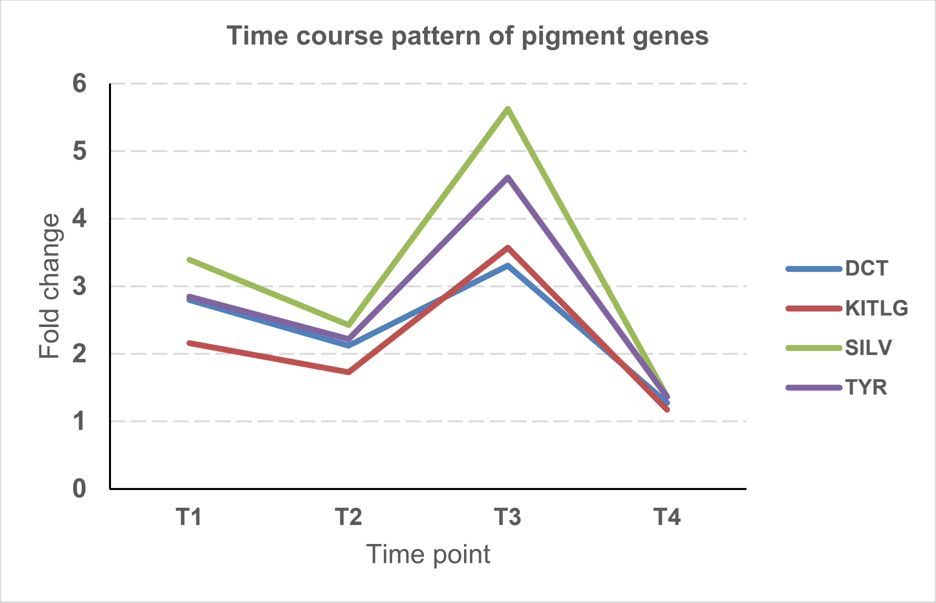
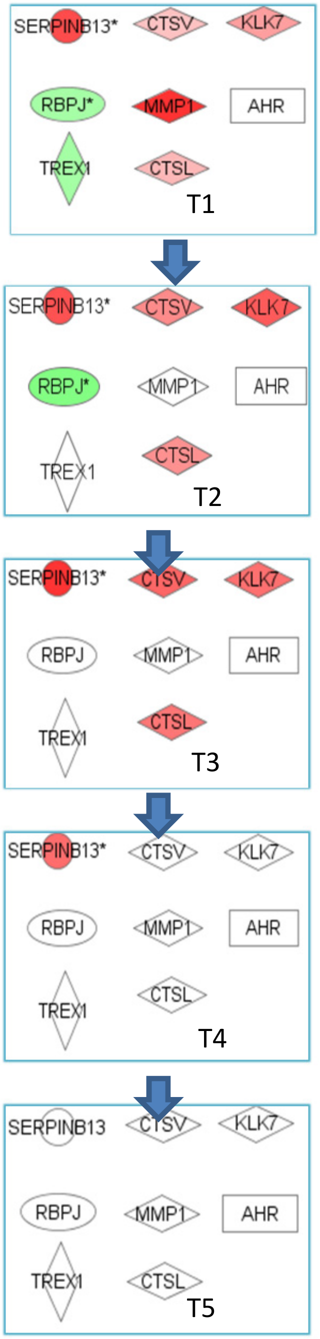


Figure S2. Expression changes of genes in the PIH dataset. Up-regulated and down-regulated genes were displayed in red and green. White genes were not significantly changed. **A)** genes related to inflammation of the skin; **B)** genes related to melanocyte development and pigmentation signaling.

A)



B)

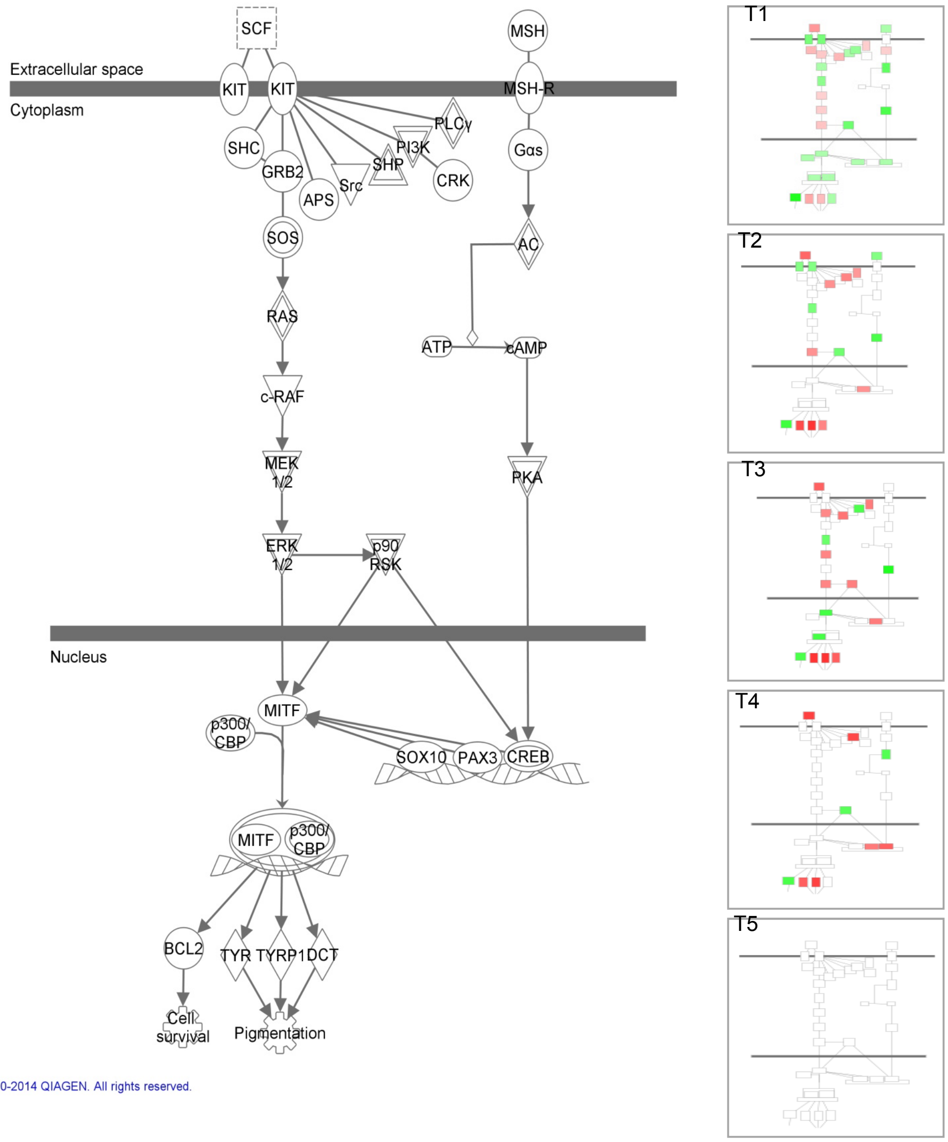

SCF
MSH
Extracellular space
Cytoplasm
KIT
KIT
MSH-R
PLCγ
PI3K
SHC
SHP
CRK
GRB2
Src
APS
Gαs
SOS
AC
RAS
ATP
cAMP
c-RAF
MEK 1/2
PKA
ERK 1/2
p90 RSK
Nucleus
MITF
p300/ CBP
SOX10
PAX3
CREB
MITF
p300/ CBP
BCL2
TYR
TYRP1
DCT
Cell survival
Pigmentation
T1
T2
T3
T4
T5

Figure S3. Distribution of I^2 statistics computed for all probes selected (27,761 probes). Among the 27,761 probes, 5,427 probes had no inconsistency (I^2=0), while 6,200 probes have high heterogeneity (I^2>0.75). Among probes with some heterogeneity, the distribution of I^2 is roughly flat. A similar distribution was observed in meta-gene probes. The diversity of I^2 values is to be expected since heterogeneity is likely to arise through different hyperpigmentation models.

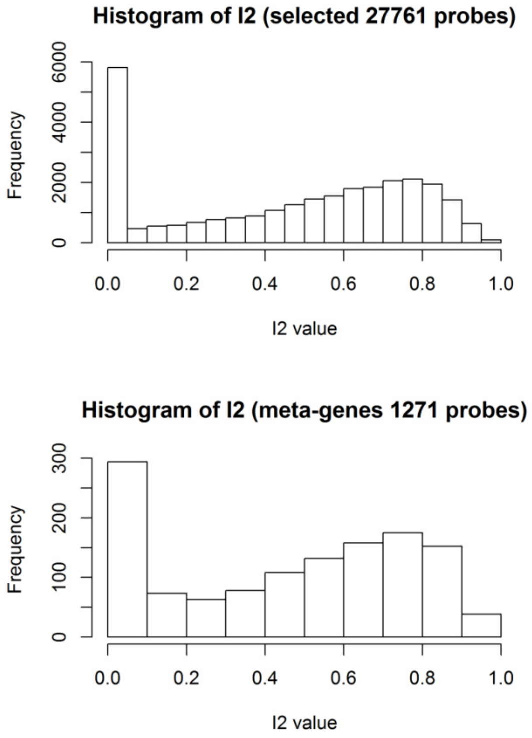


Figure S4. Forest plots of SOX2 and MYB, which were not identified as significant in any individual study but were significant in the meta-analysis.

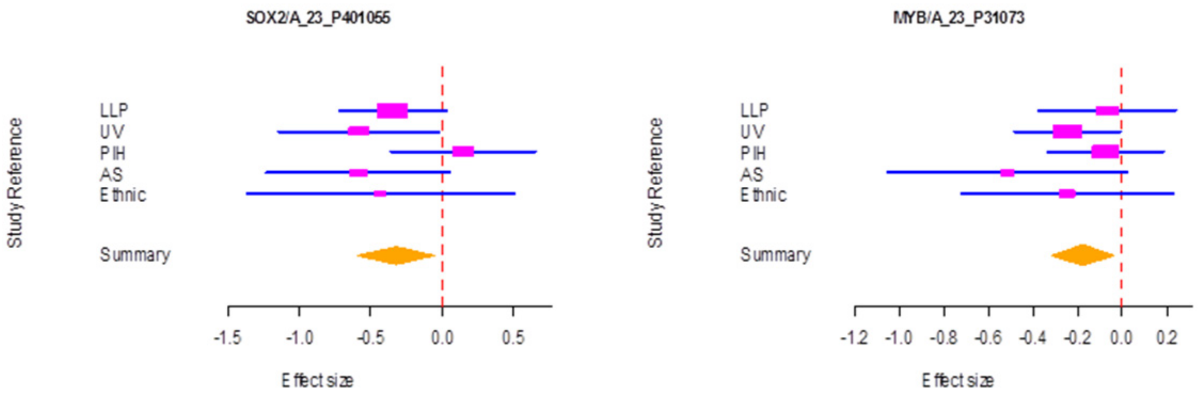


Figure S5. A) 40 gene alteration pattern clustered by the Mfuzz package. **B)** standardized (left) and unstandardized (right) gene alteration patterns of cluster 26; expression changes were measured by log fold change**.**

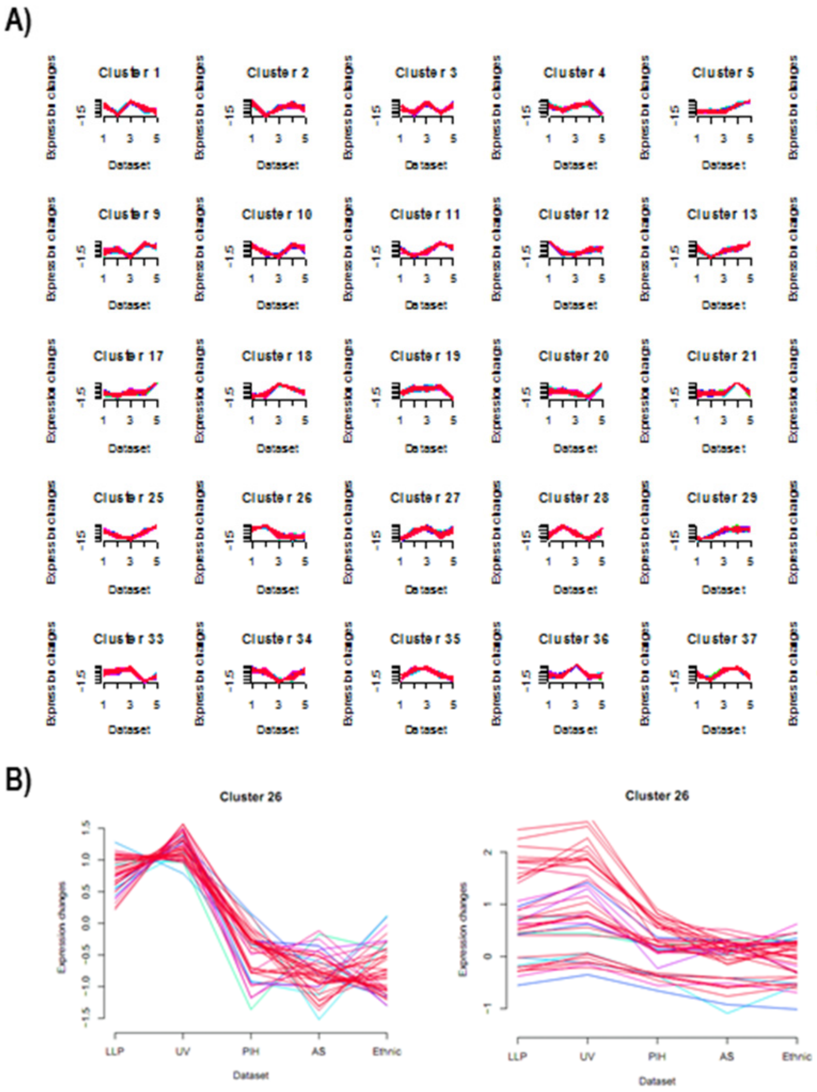
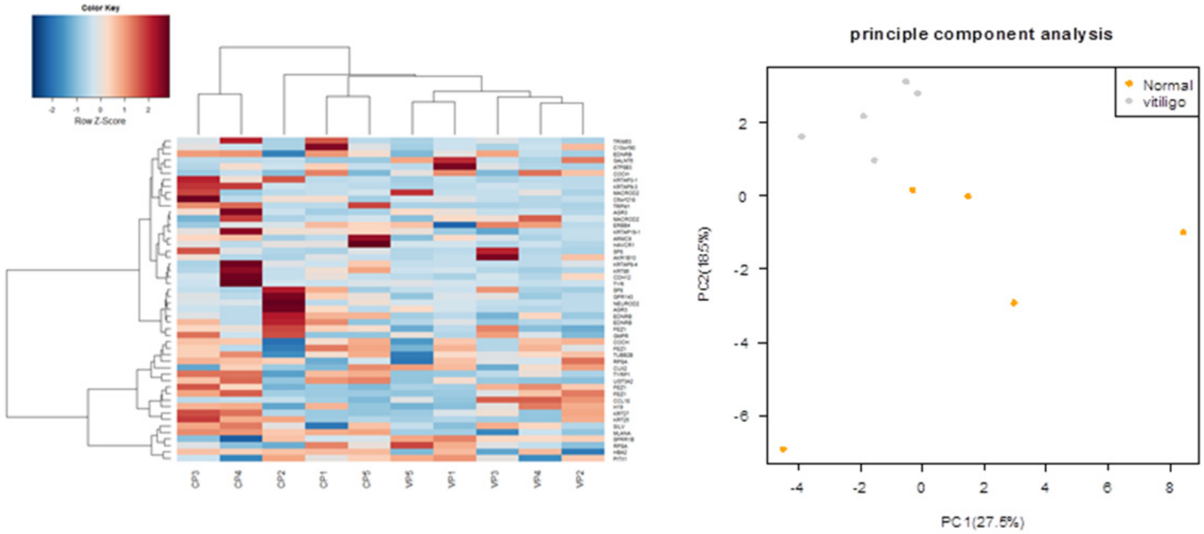


Figure S6. Clustering (left) and PCA analysis (right) results of 10 vitiligo and normal skin samples using the top 50 meta-genes.



SUPPLEMENTAL TABLES

Table S1. Summary of datasets used for the meta-analysis.

Study	GEO accession number	experimental model	Comparison	Sample size	Notes
Choi et al.	GSE21429	repetitive UV (UV)	SSR vs. CTL	6 pairs	
Choi et al.	GSE57103	Age spot (AS)	AS vs. CTL	9 pairs	
Ebsen et al.	GSE56803	Post-inflammatory hyperpigmentation (PIH)	SB vs. CTL	14 pairs	4th time point
Coelho et al.	GSE56754	Long lasting pigmentation (LLP)	SSR vs. CTL	7 pairs	3rd time point
Yin et al.	GSE54638	Ethnic skin (ES)	AF vs. CA	9 vs. 9	

Table S2. Data file information

DataSet	FileName	Condition	Status	Batch	SubjectID
Agespot	US91803681_251485050054_S01_GE1_105_Dec08_1_1.txt	control	Control	05.01.2010	199
Agespot	US91803681_251485053419_S01_GE1_105_Dec08_1_3.txt	control	Control	05.01.2010	371
Agespot	US91803681_251485053421_S01_GE1_105_Dec08_1_2.txt	control	Control	05.01.2010	1735
Agespot	US91803681_251485053418_S01_GE1_105_Dec08_1_3.txt	control	Control	05.01.2010	3296
Agespot	US91803681_251485053418_S01_GE1_105_Dec08_1_1.txt	control	Control	05.01.2010	4236
Agespot	US91803681_251485050054_S01_GE1_105_Dec08_1_3.txt	control	Control	05.01.2010	5112
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Agespot	US91803681_251485053419_S01_GE1_105_Dec08_1_2.txt	control	Control	05.01.2010	8188
Agespot	US91803681_251485054379_S01_GE1_105_Dec08_1_4.txt	control	Control	26.01.2010	12166
Agespot	US91803681_251485053420_S01_GE1_105_Dec08_1_2.txt	agespot	Hyperpigment	05.01.2010	199
Agespot	US91803681_251485053419_S01_GE1_105_Dec08_1_1.txt	agespot	Hyperpigment	05.01.2010	371
Agespot	US91803681_251485053419_S01_GE1_105_Dec08_1_4.txt	agespot	Hyperpigment	05.01.2010	1735
Agespot	US91803681_251485053420_S01_GE1_105_Dec08_1_1.txt	agespot	Hyperpigment	05.01.2010	3296
Agespot	US91803681_251485053420_S01_GE1_105_Dec08_1_4.txt	agespot	Hyperpigment	05.01.2010	4236
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Agespot	US91803681_251485053421_S01_GE1_105_Dec08_1_1.txt	agespot	Hyperpigment	05.01.2010	5711
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Ethnic	US91803681_251485074081_S01_GE1_105_Dec08_1_3.txt	control	Control	04.07.2012	2
Ethnic	US91803681_251485074080_S01_GE1_105_Dec08_1_3.txt	control	Control	04.07.2012	3
Ethnic	US91803681_251485074076_S01_GE1_105_Dec08_1_1.txt	control	Control	04.07.2012	4
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Ethnic	US91803681_251485074077_S01_GE1_105_Dec08_1_2.txt	control	Control	04.07.2012	6
Ethnic	US91803681_251485074078_S01_GE1_105_Dec08_1_2.txt	control	Control	04.07.2012	8
Ethnic	US91803681_251485074079_S01_GE1_105_Dec08_1_3.txt	control	Control	04.07.2012	9
Ethnic	US91803681_251485074049_S01_GE1_105_Dec08_1_4.txt	control	Control	04.07.2012	10
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Ethnic	US91803681_251485074049_S01_GE1_105_Dec08_1_3.txt	African	Hyperpigment	04.07.2012	5
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LLP	US91803681_251485070989_S01_GE1_105_Dec08_1_1.txt	control	Control	09.01.2012	19181

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PIH	US91803681_251485064934_S01_GE1_105_Dec08_1_4.txt	control	Control	16.11.2010	P29
PIH	US91803681_251485064934_S01_GE1_105_Dec08_1_2.txt	control	Control	16.11.2010	P30
PIH	US91803681_251485064845_S01_GE1_105_Dec08_1_3.txt	control	Control	16.11.2010	P31
PIH	US91803681_251485059476_S01_GE1_105_Dec08_1_2.txt	PIH	Hyperpigment	23.08.2010	4436
PIH	US91803681_251485059473_S01_GE1_105_Dec08_1_1.txt	PIH	Hyperpigment	19.08.2010	6665
PIH	US91803681_251485060998_S01_GE1_105_Dec08_1_4.txt	PIH	Hyperpigment	24.08.2010	7614
PIH	US91803681_251485062172_S01_GE1_105_Dec08_1_1.txt	PIH	Hyperpigment	23.08.2010	12565
PIH	US91803681_251485062172_S01_GE1_105_Dec08_1_4.txt	PIH	Hyperpigment	23.08.2010	13466
PIH	US91803681_251485060185_S01_GE1_105_Dec08_1_1.txt	PIH	Hyperpigment	19.08.2010	17061
PIH	US91803681_251485061019_S01_GE1_105_Dec08_1_2.txt	PIH	Hyperpigment	24.08.2010	18740
PIH	US91803681_251485064933_S01_GE1_105_Dec08_1_2.txt	PIH	Hyperpigment	16.11.2010	P25
PIH	US91803681_251485064932_S01_GE1_105_Dec08_1_2.txt	PIH	Hyperpigment	16.11.2010	P26
PIH	US91803681_251485064934_S01_GE1_105_Dec08_1_1.txt	PIH	Hyperpigment	16.11.2010	P27
PIH	US91803681_251485064845_S01_GE1_105_Dec08_1_4.txt	PIH	Hyperpigment	16.11.2010	P28
PIH	US91803681_251485064932_S01_GE1_105_Dec08_1_3.txt	PIH	Hyperpigment	16.11.2010	P29
PIH	US91803681_251485064932_S01_GE1_105_Dec08_1_1.txt	PIH	Hyperpigment	16.11.2010	P30
PIH	US91803681_251485064934_S01_GE1_105_Dec08_1_3.txt	PIH	Hyperpigment	16.11.2010	P31
UV	GSM535685.txt	control	Control	GEO data	P2
UV	GSM535687.txt	control	Control	GEO data	P20
UV	GSM535688.txt	control	Control	GEO data	P21
UV	GSM535689.txt	control	Control	GEO data	P22
UV	GSM535690.txt	control	Control	GEO data	P23
UV	GSM535686.txt	control	Control	GEO data	P3
UV	GSM535691.txt	UV	Hyperpigment	GEO data	P2
UV	GSM535693.txt	UV	Hyperpigment	GEO data	P20
UV	GSM535694.txt	UV	Hyperpigment	GEO data	P21
UV	GSM535695.txt	UV	Hyperpigment	GEO data	P22
UV	GSM535696.txt	UV	Hyperpigment	GEO data	P23
UV	GSM535692.txt	UV	Hyperpigment	GEO data	P3

Table S3. Complete list of 1,271 differentially expressed genes identified by meta analysis.

Please see the separate Excel file provided as Suppl Info for these data.

Table S4. Meta-genes that were not significantly different in any of the individual datasets.

118 probes showing a significant p value in the meta-analysis but not in any individual study, include:

* Enriched GO terms (see Tables S7a, S7b and S7c) for further information

ProbeID	**Fold change**	**P value**	**Primary Accession**	**UniGeneID**	**Gene Symbol**	**GeneName**	**Note***
A_24_P351283	1.28	6.28E-04	NM_018000	Hs.709755	MREG	melanoregulin	color gene; GO: 0008544 GO: 0021700 GO: 0030154 GO: 0030318 GO: 0032501 GO: 0048066 GO: 0048731; GO: 0016020 GO: 0044459 GO: 0071944
A_23_P401055	-1.25	1.72E-02	NM_003106	Hs.518438	SOX2	SRY (sex determining region Y)-box 2	color gene; GO: 0050678 GO:2000026
A_23_P2674	1.22	4.55E-02	NM_002272	Hs.654610	KRT4	keratin 4	color gene; GO: 0050678; GO: 0045095 GO: 0045111
A_24_P925505	1.47	1.19E-04	S67044		CD36	CD36 molecule (thrombospondin receptor)	melanosomal protein; GO: 0000302 GO: 0001952 GO: 0002684 GO: 0006952 GO: 0006955 GO: 0007166 GO: 0007599 GO: 0010033 GO: 0010646 GO: 0023052 GO: 0030154 GO: 0030155 GO: 0030168 GO: 0031589 GO: 0032101 GO: 0032655 GO: 0042060 GO: 0048584 GO: 0050817 GO: 0051094 GO: 0051240 GO: 0051707 GO: 0070887; GO: 0038023 GO0060086; GO: 0005887 GO: 0016020 GO: 0031224 GO: 0044459 GO: 0071944;
A_23_P206920	-1.28	5.79E-03	NM_001040114	Hs.460109	MYH11	myosin, heavy chain 11, smooth muscle	melanosomal protein; GO: 0006935 GO: 0007399 GO: 0009605 GO: 0040011 GO: 0072358
A_23_P203558	-1.62	1.42E-02	NM_000518	Hs.523443	HBB	hemoglobin, beta	GO: 0000302 GO: 0006952 GO: 0007167 GO: 0007599 GO: 0009605 GO: 0010033 GO: 0010646 GO: 0030154 GO: 0032502 GO: 0042060 GO: 0048731 GO: 0050817 GO: 0051240 GO: 0070887; GO: 0005576 GO: 0005833
A_23_P151915	1.27	3.49E-02	ENST00000267857	Hs.194710	GCNT3	glucosaminyl (N-acetyl) transferase 3, mucin type	GO: 0002250
A_24_P911788	-1.23	7.72E-03	BC020226		HLA-DOB	major histocompatibility complex, class II, DO beta	GO: 0002253 GO: 0002429 GO: 0002504 GO: 0002684 GO: 0002694 GO: 0002764 GO: 0006952 GO: 0006955 GO: 0031295 GO: 0034341 GO: 0050852 GO: 0050863 GO: 0050867 GO: 0051251 GO: 0060333 GO: 0071345; GO0032395 GO: 0038023; GO: 0000323 GO: 0005765 GO: 0010008 GO: 0042613 GO: 0044437
A_24_P393740	-1.23	3.35E-02	NM_001465	Hs.370503	FYB	FYN binding protein (FYB-120/130)	GO: 0002253 GO: 0002429 GO: 0002684 GO: 0002764 GO: 0006955 GO: 0007154 GO: 0007166 GO: 0023052 GO: 0048584 GO: 0050852
A_24_P416489	-1.34	5.82E-03	U39657	Hs.463978	MAP2K6	mitogen-activated protein kinase kinase 6	GO: 0002253 GO: 0002684 GO: 0002764 GO: 0006952 GO: 0006955 GO: 0007166 GO: 0048584 GO: 0051094
A_23_P152620	-1.23	2.65E-04	NM_172088	Hs.54673	TNFSF13	tumor necrosis factor (ligand) superfamily, member 13	GO: 0005576 GO: 0005615
A_23_P218442	-1.25	1.99E-02	NM_002483	Hs.466814	CEACAM6	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	GO: 0005887
A_23_P434809	1.32	3.38E-02	NM_002964	Hs.416073	S100A8	S100 calcium binding protein A8	GO: 0006935 GO: 0006954 GO: 0042060 GO: 0051707
A_23_P208167	-1.29	1.89E-04	NM_002030	Hs.445466	FPR3	formyl peptide receptor 3	GO: 0006935 GO: 0009605 GO: 0040011
A_32_P70158	-1.28	2.30E-02	NM_006864	Hs.631592	LILRB3	leukocyte immunoglobulin-like receptor, subfamily B	GO: 0006952

						(with TM and ITIM domains), member 3	
A_24_P304071	-1.21	1.16E-02	NM_001547	Hs.437609	IFIT2	interferon-induced protein with tetratricopeptide repeats 2	GO: 0006952 GO: 0006955 GO: 0007166 GO: 0051707 GO: 0070887
A_23_P153958	-1.21	1.37E-02	NM_002193	Hs.1735	INHBB	inhibin, beta B	GO: 0006952 GO: 0007167 GO: 0009605 GO: 0010033 GO: 0010646 GO: 0030154 GO: 0032502 GO: 0048731 GO: 0051240 GO: 0070887
A_23_P153964	-1.25	1.20E-03	NM_002193	Hs.1735	INHBB	inhibin, beta B	GO: 0006952 GO: 0007167 GO: 0009605 GO: 0010033 GO: 0010646 GO: 0030154 GO: 0032502 GO: 0048731 GO: 0051240 GO: 0070887; GO: 0005576
A_23_P36397	1.27	1.26E-02	NM_000785	Hs.524528	CYP27B1	cytochrome P450, family 27, subfamily B, polypeptide 1	GO: 0006952 GO: 0008544 GO: 0030216 GO: 0032101 GO: 0034341 GO: 0042592 GO: 0050801 GO: 0051094 GO: 0051707 GO:2000026
A_24_P229936	-1.21	4.71E-02	U18288	Hs.701991	CIITA	class II, major histocompatibility complex, transactivator	GO: 0006952 GO: 0034341 GO: 0060333 GO: 0071345
A_24_P367752	1.22	1.57E-03	BC012888	Hs.222055	NDST1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	GO: 0006954 GO: 0007167
A_23_P435394	-1.21	3.55E-03	NM_000958	Hs.199248	PTGER4	prostaglandin E receptor 4 (subtype EP4)	GO: 0006955 GO: 0007154 GO: 0007166 GO: 0032501; GO: 0038023 GO0060086;
A_23_P121665	1.36	2.05E-02	NM_020777	Hs.479099	SORCS2	sortilin-related VPS10 domain containing receptor 2	GO: 0007154 GO: 0007166 GO: 0023052; GO: 0038023 GO0060086; GO: 0016020 GO: 0031224
A_23_P11874	1.22	1.70E-03	NM_003953	Hs.493919	MPZL1	myelin protein zero-like 1	GO: 0007154 GO: 0007167 GO: 0023052
A_23_P139912	-1.27	8.71E-03	NM_002178	Hs.274313	IGFBP6	insulin-like growth factor binding protein 6	GO: 0007154; GO: 0005576 GO: 0005615
A_23_P344694	1.23	2.25E-02	BC014505	Hs.709178	MLLT4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4	GO: 0007155
A_24_P943180	1.21	3.00E-03	AK074160	Hs.656032	CDH23	cadherin-like 23	GO: 0007155 GO: 0042592 GO: 0050801
A_24_P62169	-1.21	8.18E-03	NM_130436	Hs.368240	DYRK1A	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	GO: 0007399
A_23_P214681	1.26	3.56E-04	NM_006238	Hs.696032	PPARD	peroxisome proliferator-activated receptor delta	GO: 0007399 GO: 0008284 GO: 0008544 GO: 0010646 GO: 0021700 GO: 0031589 GO: 0040011 GO: 0042060 GO: 0042592 GO: 0048584 GO: 0050678 GO: 0050801 GO: 0051094 GO: 0070887; GO: 0038023 GO0060086;
A_23_P29096	-1.25	3.32E-02	NM_002606	Hs.473927	PDE9A	phosphodiesterase 9A	GO: 0007599 GO: 0030168 GO: 0042060 GO: 0050817
A_24_P75190	-1.59	9.83E-03	NM_000519	Hs.699280	HBD	hemoglobin, delta	GO: 0007599 GO: 0050817; GO: 0005833
A_23_P20022	1.24	4.40E-03	NM_013332	Hs.710088	HIG2	hypoxia-inducible protein 2	GO: 0008284; GO: 0005615
A_23_P38537	1.22	1.83E-02	NM_005557	Hs.655160	KRT16	keratin 16 (focal non-epidermolytic palmoplantar keratoderma)	GO: 0008544; GO: 0045111
A_24_P247820	1.20	3.40E-04	AK074633		ELF5	E74-like factor 5 (ets domain transcription factor)	GO: 0030154 GO: 0032501 GO: 0032502 GO: 0048731
A_23_P64828	1.35	6.28E-04	NM_002534	Hs.524760	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	GO: 0034341 GO: 0051707 GO: 0060333
A_23_P302568	1.32	2.07E-03	NM_003459	Hs.467981	SLC30A3	solute carrier family 30 (zinc transporter), member 3	GO: 0042592 GO: 0050801

A_23_P77980	1.25	8.70E-04	NM_000342	Hs.443948	SLC4A1	solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group)	GO: 0042592 GO: 0050801
A_24_P230570	-1.23	2.91E-02	NM_004118	Hs.516971	FOXS1	forkhead box S1	GO: 0043069 GO: 0051240
A_23_P89665	1.55	7.22E-03	NM_002279	Hs.32950	KRT33B	keratin 33B	GO: 0045111
A_24_P302506	-1.22	3.88E-04	AB032989	Hs.709892	AMIGO1	adhesion molecule with Ig-like domain 1	GO: 0050801 GO: 0051094
A_23_P209116	1.31	1.26E-04	AB002454	Hs.106242	CYP4F3	cytochrome P450, family 4, subfamily F, polypeptide 3	GO: 0070887
A_23_P104073	1.28	1.57E-02	NM_002960	Hs.557609	S100A3	S100 calcium binding protein A3	
A_23_P117302	1.21	4.47E-02	AF354444	Hs.650087			
A_23_P118894	-1.31	1.18E-02	NM_024320	Hs.368260	ATAD4	ATPase family, AAA domain containing 4	
A_23_P133438	-1.21	4.44E-04	NM_019018	Hs.591751	FAM105A	family with sequence similarity 105, member A	
A_23_P139166	-1.31	2.87E-02	CB959193	Hs.97644			
A_23_P142756	-1.22	6.34E-03	NM_017759	Hs.445036	FLJ20309	hypothetical protein FLJ20309	
A_23_P150343	-1.35	1.31E-02	NM_003063	Hs.334629	SLN	sarcolipin	
A_23_P15798	1.27	3.84E-03	NM_031854	Hs.572443	KRTAP4-12	keratin associated protein 4-12	
A_23_P163475	1.24	1.78E-03	NM_207380	Hs.32433	C15orf52	chromosome 15 open reading frame 52	
A_23_P170608	-1.20	4.73E-04	NM_022117	Hs.136164	TSPYL2	TSPY-like 2	
A_23_P207939	-1.23	5.92E-03	NM_181482	Hs.149363	C18orf1	chromosome 18 open reading frame 1	
A_23_P216199	-1.21	7.14E-03	NM_024607	Hs.458513	PPP1R3B	protein phosphatase 1, regulatory (inhibitor) subunit 3B	
A_23_P26367	1.23	2.51E-02	AK022393	Hs.661121	FLJ12331	ribosomal protein S2 pseudogene	
A_23_P2904	1.24	1.14E-02	AK000041	Hs.675410	C14orf113	chromosome 14 open reading frame 113	
A_23_P302550	-1.26	2.98E-02	NM_130782	Hs.440890	RGS18	regulator of G-protein signaling 18	
A_23_P319050	1.21	4.19E-02	BC006408	Hs.656558	ZNF493	zinc finger protein 493	
A_23_P340148	-1.23	1.30E-02	NM_021998	Hs.326801	ZNF711	zinc finger protein 711	
A_23_P343826	1.20	1.61E-03	NM_033449	Hs.591257	FCHSD1	FCH and double SH3 domains 1	
A_23_P347027	1.22	2.56E-03	NM_018667	Hs.368421	SMPD3	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)	
A_23_P352484	-1.27	3.03E-02	NM_152721	Hs.569915	DOK6	docking protein 6	
A_23_P37505	-1.25	1.26E-02	NM_130810	Hs.126403	DYX1C1	dyslexia susceptibility 1 candidate 1	
A_23_P396934	1.47	3.50E-04	ENST00000309447	Hs.4280	KIAA1239	KIAA1239	
A_23_P402765	1.27	1.52E-02	NM_198060	Hs.268788	NRAP	nebulin-related anchoring	

						protein	
A_23_P43979	1.25	2.95E-02	M87790	Hs.449585			
A_23_P717	1.22	1.71E-04	NM_018252	Hs.445386	TMEM206	transmembrane protein 206	
A_23_P77697	1.22	2.33E-02	AK131087		POL3S	polyserase 3	
A_23_P87727	-1.26	4.13E-03	NM_033328	Hs.131288	CAPZA3	capping protein (actin filament) muscle Z-line, alpha 3	
A_24_P126246	1.21	1.73E-02					
A_24_P128741	-1.21	2.85E-03	THC2558699				
A_24_P165205	-1.29	8.10E-03	NM_024848	Hs.709528	MORN1	MORN repeat containing 1	
A_24_P168398	-1.29	4.18E-04	NM_003451	Hs.172979	ZNF177	zinc finger protein 177	
A_24_P169092	-1.23	6.76E-04	NM_032427	Hs.428214	MAML2	mastermind-like 2 (Drosophila)	
A_24_P178723	1.23	1.05E-02					
A_24_P194755	-1.25	2.83E-02	NM_032853	Hs.515016	MUM1	melanoma associated antigen (mutated) 1	
A_24_P247303	-1.31	2.55E-02					
A_24_P273360	1.26	4.34E-03	AF234262				
A_24_P282083	1.22	7.71E-03	AK097085	Hs.660415			
A_24_P320727	-1.35	8.33E-03	NM_152748	Hs.208093	KIAA1324L	KIAA1324-like	
A_24_P331918	-1.24	5.22E-03	NM_001848	Hs.474053	COL6A1	collagen, type VI, alpha 1	
A_24_P381029	1.28	3.68E-02	NM_006541	Hs.42644	GLRX3	glutaredoxin 3	
A_24_P411561	-1.23	3.46E-02	NM_032782	Hs.710500	HAVCR2	hepatitis A virus cellular receptor 2	
A_24_P535380	1.22	2.41E-03	AK025323	Hs.671557			
A_24_P569791	1.22	3.08E-02	AI682237	Hs.439122			
A_24_P601511	1.28	1.15E-02	AK090762	Hs.531632			
A_24_P60680	1.26	5.50E-04	NM_013941	Hs.631997	OR10C1	olfactory receptor, family 10, subfamily C, member 1	
A_24_P686965	1.25	3.20E-02	NM_001103161	Hs.591522	SH2D5	SH2 domain containing 5	
A_24_P705167	1.23	3.50E-02					
A_24_P77904	-1.20	1.25E-02	NM_018951	Hs.592166	HOXA10	homeobox A10	
A_24_P79529	-1.20	4.99E-02	NM_001080848	Hs.522810	CSAG2	CSAG family, member 2	
A_24_P822704	1.22	1.34E-02	NM_001005209	Hs.446664	TMEM198	transmembrane protein 198	
A_24_P867702	1.24	3.26E-02					
A_24_P892612	-1.31	4.85E-03	AL833309	Hs.622596			
A_24_P896765	-1.23	2.20E-02	THC2667205				
A_24_P928765	1.20	4.54E-03	BC032716	Hs.698373			
A_24_P932981	1.27	4.37E-02	BC015987	Hs.709396			
A_24_P934832	-1.31	2.39E-02	N34499	Hs.655670			
A_32_P12504	1.20	1.03E-03	BC024745				
A_32_P129810	1.21	1.95E-03	AK098511	Hs.633049			
A_32_P14762	-1.45	8.02E-03	NM_0010805	Hs.671212	OOEP	oocyte expressed protein	

			07			homolog (dog)	
A_32_P164477	-1.21	4.23E-03	AI379175	Hs.493819			
A_32_P176902	-1.27	3.39E-02					
A_32_P178724	1.24	8.63E-04					
A_32_P191120	1.22	1.42E-03	THC2744687				
A_32_P213661	-1.24	9.58E-03	NM_144974	Hs.170849	CCDC122	coiled-coil domain containing 122	
A_32_P220591	1.36	1.69E-02	THC2732746				
A_32_P22654	-1.55	9.14E-03	NM_000032	Hs.522666	ALAS2	aminolevulinate, delta-, synthase 2	
A_32_P233735	1.32	6.79E-03	NM_020704	Hs.489988	FAM40B	family with sequence similarity 40, member B	
A_32_P24382	1.21	4.90E-02	BC063625	Hs.406714	KRTAP2-4	keratin associated protein 2-4	
A_32_P25065	1.30	1.88E-02					
A_32_P25243	1.26	1.07E-02	THC2656826				
A_32_P30238	-1.28	7.35E-03	THC2719486				
A_32_P32116	1.27	2.31E-02	ENST00000357816	Hs.528335	FAM123A	family with sequence similarity 123A	
A_32_P3572	-1.21	3.71E-02	XM_001130623	Hs.116176	LOC645733	similar to hCG1812929	
A_32_P49764	-1.23	2.75E-04	CX788817	Hs.120377			
A_32_P53212	-1.24	3.05E-02	AA045093	Hs.130438			
A_32_P60709	1.21	4.20E-03	THC2663783				
A_32_P94631	1.26	7.44E-03	THC2659561				

Table S5. Common genes in the meta-gene list and the cloned color gene list

ID	**Symbol**	**Entrez Gene Name**	**Location**	**Type(s)**
Hs.150749	BCL2	B-cell CLL/lymphoma 2	Cytoplasm	transporter
Hs.82002	EDNRB	endothelin receptor type B	Plasma Membrane	G-protein coupled receptor
Hs.101915	ELOVL4	ELOVL fatty acid elongase 4	Cytoplasm	enzyme
Hs.533683	FGFR2	fibroblast growth factor receptor 2	Plasma Membrane	kinase
Hs.524134	GATA3	GATA binding protein 3	Nucleus	transcription regulator
Hs.269782	GNAQ	guanine nucleotide binding protein (G protein), q polypeptide	Plasma Membrane	enzyme
Hs.74124	GPR143	G protein-coupled receptor 143	Plasma Membrane	G-protein coupled receptor
Hs.404568	HPS1	Hermansky-Pudlak syndrome 1	Cytoplasm	other
Hs.654610	KRT4	keratin 4	Cytoplasm	other
Hs.513829	MC1R	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)	Plasma Membrane	G-protein coupled receptor
Hs.709755	MREG	melanoregulin	Cytoplasm	other
Hs.21213	MYO5A	myosin VA (heavy chain 12, myoxin)	Cytoplasm	enzyme
Hs.226780	OSTM1	osteopetrosis associated transmembrane protein 1	Cytoplasm	other
Hs.42146	PAX3	paired box 3	Nucleus	transcription regulator
Hs.570855	PDGFC	platelet derived growth factor C	Extracellular Space	growth factor
Hs.278962	SLC45A2	solute carrier family 45, member 2	Plasma Membrane	other
Hs.518438	SOX2	SRY (sex determining region Y)-box 2	Nucleus	transcription regulator
Hs.146196	TBX15	T-box 15	Nucleus	transcription regulator
Hs.701968	TIMP3	TIMP metallopeptidase inhibitor 3	Extracellular Space	other
Hs.503555	TYR	tyrosinase	Cytoplasm	enzyme
Hs.270279	TYRP1	tyrosinase-related protein 1	Cytoplasm	enzyme
Hs.370422	VLDLR	very low density lipoprotein receptor	Plasma Membrane	transporter

Table S6. Meta-genes that occur in the human melanosome proteomics database

Protein AC	**Gene Symbol**	**Group**	**Protein.Name**
P16671	CD36	Platelet	Platelet glycoprotein 4 (Platelet glycoprotein IV) (GPIV) (Glycoprotein IIIb) (GPIIIB) (Leukocyte differentiation antigen CD36) (CD36 antigen) (PAS IV) (PAS-4 protein) (Platelet collagen receptor) (Fatty acid translocase) (FAT) (Thrombospondin receptor)
P51795	CLCN5	Skmel28_stage1	Chloride channel protein 5 (ClC-5)
Q9ULM6	CNOT6	MNT1_stage4; unique_latestage	CCR4-NOT transcription complex subunit 6 (EC 3.1.-.-) (Cytoplasmic deadenylase) (Carbon catabolite repressor protein 4 homolog) (CCR4 carbon catabolite repression 4-like)
P50416	CPT1A	MNT1_stage2; Platelet	Carnitine O-palmitoyltransferase I, liver isoform (EC 2.3.1.21) (CPT I) (CPTI-L) (Carnitine palmitoyltransferase 1A)
Q9H3G5	CPVL	MNT1_stage1; MNT1_stage2; MNT1_stage4; commonMNT1; unqiueMNT1	Probable serine carboxypeptidase CPVL precursor (EC 3.4.16.-) (Carboxypeptidase, vitellogenic-like) (Vitellogenic carboxypeptidase- like protein) (VCP-like protein) (HVLP)
P04080	CYTB	MNT1_stage4; unique_latestage	Cystatin B (Liver thiol proteinase inhibitor) (CPI-B) (Stefin B)
P24530	EDNRB	MNT1_stage1; MNT1_stage2; Skmel28_stage1; commonB	Endothelin B receptor precursor (ET-B) (Endothelin receptor Non- selective type)
Q13642	FHL1	MNT1_stage1	Four and a half LIM domains protein 1 (FHL-1) (Skeletal muscle LIM- protein 1) (SLIM 1) (SLIM)
P50148	GNAQ	MNT1_stage2; Skmel28_stage2; commonA	Guanine nucleotide-binding protein G(q) subunit alpha (Guanine nucleotide-binding protein alpha-q)
O14964	HGS	MNT1_stage2	Hepatocyte growth factor-regulated tyrosine kinase substrate (Protein pp110) (Hrs)
P05362	ICAM1	Skmel28_stage1; Skmel28_stage2; commonSkmel28; uniqueSkmel28	Intercellular adhesion molecule 1 precursor (ICAM-1) (Major group rhinovirus receptor) (CD54 antigen)
O95373	IPO7	MNT1_stage4; Skmel28_stage2	Importin-7 (Imp7) (Ran-binding protein 7) (RanBP7)
P35749	MYH11	MNT1_stage1; MNT1_stage2; MNT1_stage4; Skmel28_stage1;	Myosin-11 (Myosin heavy chain, smooth muscle isoform) (SMMHC)

		Skmel28_stage2; commonA; commonB; commonMNT1; commonSkmel28; common_all_stage; common_early_stage	
Q9Y4I1	MYO5A	MNT1_stage2; MNT1_stage4	Myosin-5A (Myosin Va) (Dilute myosin heavy chain, non-muscle) (Myosin heavy chain 12) (Myoxin)
Q86WC4	OSTM1	MNT1_stage1; MNT1_stage2; Skmel28_stage1; commonB	Osteopetrosis-associated transmembrane protein 1 precursor
P11217	PYGM	Skmel28_stage1; Skmel28_stage2; commonSkmel28; uniqueSkmel28	Glycogen phosphorylase, muscle form (EC 2.4.1.1) (Myophosphorylase)
Q16769	QPCT	Skmel28_stage1	Glutaminyl-peptide cyclotransferase precursor (EC 2.3.2.5) (QC) (Glutaminyl-tRNA cyclotransferase) (Glutaminyl cyclase)
Q13637	RAB32	GTPase; MNT1_stage1; MNT1_stage2; Skmel28_stage2; commonA	Ras-related protein Rab-32
Q96D15	RCN3	Skmel28_stage1	Reticulocalbin-3 precursor (EF-hand calcium-binding protein RLP49)
O94804	STK10	MNT1_stage4; unique_latestage	Serine/threonine-protein kinase 10 (EC 2.7.11.1) (Lymphocyte-oriented kinase)
P35625	TIMP3	Skmel28_stage1; Skmel28_stage2; commonSkmel28; uniqueSkmel28	Metalloproteinase inhibitor 3 precursor (TIMP-3) (Tissue inhibitor of metalloproteinases 3) (Protein MIG-5)
O14773	TPP1	MNT1_stage1; MNT1_stage2; MNT1_stage4; NG; Skmel28_stage1; Skmel28_stage2; commonA; commonB; commonMNT1; commonSkmel28; common_all_stage; common_early_stage	Tripeptidyl-peptidase 1 precursor (EC 3.4.14.9) (Tripeptidyl-peptidase I) (TPP-I) (Tripeptidyl aminopeptidase) (Lysosomal pepstatin insensitive protease) (LPIC) (Growth-inhibiting gene 1 protein)
P17643	TYRP1	MNT1_stage1; MNT1_stage2; MNT1_stage4; commonMNT1; unqiueMNT1	5,6-dihydroxyindole-2-carboxylic acid oxidase precursor (EC 1.14.18.-) (DHICA oxidase) (Tyrosinase-related protein 1) (TRP-1) (TRP1) (TRP) (Catalase B) (Glycoprotein 75) (Melanoma antigen gp75)

Table S7a. Enriched Biological processes identified by the meta-gene analysis

GOBPID	Pvalue	Odds Ratio	Term	Involved_Gene
GO: 0002504	6.77E-18	76.43	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	HLA-DQB1,HLA-DRB3,THBS1,HLA-DPB1,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DPA1,HLA-DRB5,HLA-DQA2,HLA-DMA,CD74,HLA-DRB1,HLA-DRB4,HLA-DMB,HLA-DRA
GO: 0002604	3.94E-04	18.77	regulation of dendritic cell antigen processing and presentation	THBS1,CCR7,NOD2,CD74
GO: 0042438	6.81E-04	15.01	melanin biosynthetic process	SILV,SLC45A2,TYR,TYRP1
GO: 0018149	2.15E-05	8.88	peptide cross-linking	SPRR1B,CSTA,THBS1,SPRR1A,SPRR3,TGM1,ANXA1,F13A1
GO:2000107	9.16E-04	8.54	negative regulation of leukocyte apoptosis	CCL5,CXCL12,CCR7,NOD2,CD74
GO: 0048066	3.45E-06	8.22	developmental pigmentation	MREG,BCL2L11,HPS1,SLC45A2,EDNRB,TYR,GPR143,TYRP1,FOXD1,GNAQ
GO: 0060333	4.48E-11	7.75	interferon-gamma-mediated signaling pathway	HLA-DQB1,HSP90AB1,HLA-DRB3,ICAM1,HLA-DPB1,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-

				DPA1,HLA-DRB5,CIITA,HLA-A,IRF1,HLA-DQA2,HLA-DMA,PTAFR,OAS1,HLA-DRB1,HLA-DRB4,HLA-DMB,HLA-DRA
GO: 0031295	3.72E-09	7.02	T cell costimulation	CD86,HLA-DQB1,PIK3R1,HLA-DRB3,HLA-DPB1,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DPA1,HLA-DRB5,CCR7,VAV1,HLA-DQA2,HLA-DMA,HLA-DRB1,HLA-DRB4,HLA-DMB,HLA-DRA
GO: 0030318	8.12E-04	6.64	melanocyte differentiation	MREG,HPS1,EDNRB,TYRP1,FOXD1,GNAQ
GO: 0034341	9.83E-11	6.15	response to interferon-gamma	HLA-DQB1,HSP90AB1,HLA-DRB3,CCL5,ICAM1,HLA-DPB1,TLR3,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DPA1,HLA-DRB5,CIITA,CYP27B1,HLA-A,IRF1,HLA-DQA2,HLA-DMA,PTAFR,OAS1,HLA-DRB1,HLA-DRB4,HLA-DMB,HLA-DRA
GO: 0032655	7.69E-04	5.49	regulation of interleukin-12 production	CD36,THBS1,TLR3,CCR7,IRF1,NOD2,CD40
GO: 0050852	8.12E-08	5.18	T cell receptor signaling pathway	SKAP1,FYB,PTPRC,HLA-DQB1,PIK3R1,HLA-DRB3,HLA-DPB1,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DPA1,HLA-DRB5,HLA-DQA2,HLA-DMA,GATA3,HLA-DRB1,HLA-DRB4,HLA-DMB,HLA-DRA
GO: 0001952	6.50E-04	4.86	regulation of cell-matrix adhesion	CD36,ROCK1,EFNA5,CDK6,THBS1,PLAU,CCR7,ACVRL1
GO: 0002429	6.35E-08	4.53	immune response-activating cell surface receptor signaling pathway	SKAP1,FYB,PTPRC,HLA-DQB1,PIK3R1,HLA-DRB3,VAV3,PRKCB1,BCL2,HLA-DPB1,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DPA1,HLA-DRB5,HLA-DQA2,HLA-DMA,GATA3,HLA-DRB1,HLA-DRB4,HLA-DMB,HLA-DRA
GO: 0002685	2.21E-04	4.16	regulation of leukocyte migration	HMOX1,BDKRB1,CCL5,ICAM1,CXCL12,THBS1,CCR7,NOD2,CD74,VEGFA,STK10
GO: 0051251	5.03E-08	3.60	positive regulation of lymphocyte activation	CD86,PTPRC,HLA-DQB1,PIK3R1,HLA-DRB3,TNFSF13,CCL5,VAV3,HPS1,BCL2,HLA-DPB1,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DPA1,HLA-DRB5,CCR7,VAV1,NOD2,HLA-DQA2,HLA-DMA,IL6ST,CD40,CD74,GATA3,HLA-DRB1,HLA-DRB4,HLA-DMB,HLA-DRA
GO: 0071345	3.34E-10	3.60	cellular response to cytokine stimulus	KLF2,PTPRC,LIFR,HLA-DQB1,CHI3L1,HSP90AB1,HLA-DRB3,CCL5,ICAM1,LRP8,CXCL12,EGR1,HLA-DPB1,TLR3,HLA-DOA,STAT4,HLA-DOB,HLA-DQA1,HLA-DPA1,HLA-DRB5,CIITA,TNFRSF11A,HLA-A,IRF1,HLA-DQA2,HLA-DMA,VLDLR,IFI27,IL6ST,PTAFR,DUOX1,SLIT3,KLF6,CD74,IL2RB,HLA-DRB1,HLA-DRB4,
GO: 0050867	4.67E-08	3.44	positive regulation of cell activation	CD86,PTPRC,HLA-DQB1,PIK3R1,HLA-DRB3,TNFSF13,CCL5,VAV3,HPS1,THBS1,BCL2,PLEK,HLA-DPB1,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DPA1,HLA-DRB5,CCR7,VAV1,NOD2,HLA-DQA2,HLA-DMA,IL6ST,CD40,CD74,GATA3,HLA-DRB1,HLA-DRB4,HLA-DMB,HLA-DRA
GO: 0030216	9.64E-04	3.40	keratinocyte differentiation	WNT16,SPRR1B,CSTA,SPRR1A,CYP27B1,LCE3C,SPRR3,TGM1,ANXA1,RP1-21O18.1,FLG
GO: 0002764	3.17E-07	3.26	immune response-regulating signaling pathway	SKAP1,CD86,FYB,PTPRC,HLA-DQB1,PIK3R1,HLA-DRB3,VAV3,PRKCB1,MAP2K6,BCL2,HLA-DPB1,TLR3,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DPA1,HLA-DRB5,RPS6KA2,NOD2,HLA-DQA2,HLA-DMA,CD40,GATA3,TNFAIP3,HLA-DRB1,HLA-DRB4,HLA-DMB,HLA-DRA
GO: 0050863	4.29E-06	3.02	regulation of T cell activation	CD86,PTPRC,HLA-DQB1,PIK3R1,HLA-DRB3,CCL5,HLA-DPB1,HLA-DOA,HLA-DOB, HLA-DQA1,HLA-DPA1,HLA-DRB5,CCR7,FOXJ1,VAV1,NOD2,HLA-DQA2,HLA-DMA,LAX1,IL6ST,CD74,GATA3,HLA-DRB1,HLA-DRB4,HLA-DMB,HLA-DRA
GO: 0021700	1.76E-04	3.02	developmental maturation	MREG,KLF2,BARX2,BTK,PCSK4,SCLT1,PPARD,EDNRB,CCR7,ERBB4,NEUROD2,CNTN2,VEGFA,FARP2,MAP1B,ACVRL1,GNAQ
GO: 0000302	7.72E-04	2.94	response to reactive oxygen species	CD36,KLF2,HMOX1,FBLN5,BMP7,SDC1,HBB,HBA2,ERBB4,UCP2,RHOB,DUOX1,ANXA1,SLC8A1

GO: 0002694	3.52E-07	2.86	regulation of leukocyte activation	CD86,HMOX1,PTPRC,HLA-DQB1,PTPRE, PIK3R1, HLA-DRB3, TNFSF13,CCL5, VAV3,HPS1,THBS1,BCL2,HLA-DPB1,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DPA1,HLA-DRB5, CCR7,FOXJ1,VAV1,NOD2,HLA-DQA2, HLA-DMA , LAX1, IL6ST,CD40, CD74,GATA3,TNFAIP3, HLA-DRB1,HLA-DRB4, HLA-DMB,HLA-DRA
GO: 0050678	6.68E-05	2.86	regulation of epithelial cell proliferation	SERPINF1,NR4A1,FOXP2,ECM1,CDK6,FGFR2,CDKN1B,THBS1,PPARD,NFIB,CDKN2B,KRT4,KGFLP1,TGFA, SOX2,NOD2,ERBB4,VEGFA,OSR2,GATA3,ACVRL1
GO: 0002253	7.96E-07	2.85	activation of immune response	SKAP1,CD86,FYB,PTPRC,C1R,C2,HLA-DQB1,SERPING1,PIK3R1,HSP90AB1,HLA-DRB3,VAV3,PRKCB1,MAP2K6,BCL2,CLU,HLA-DPB1,TLR3,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DPA1,HLA-DRB5,RPS6KA2,NOD2,HLA-DQA2,HLA-DMA,GATA3,TNFAIP3,HLA-DRB1,HLA-DRB4,HLA-DMB,HLA-DRA
GO: 0008544	1.67E-05	2.71	epidermis development	MREG,CALML5,KRTAP5-9,BARX2,SNAI1,WNT16,KRT9,KRT25,SPRR1B,CSTA,FGFR2,PPARD,HPSE,SPRR1A,CYP27B1,KGFLP1,KRT16,KLK7,LCE3C,FABP5,SPRR3,TGM1,LAMA3,ANXA1,KRT71,RP1-21O18.1,FLG
GO: 0002250	5.80E-04	2.69	adaptive immune response	PTPRC,C1R,C2,SERPING1,GCNT3,TNFSF13,ICAM1,CLU,FOXJ1,TNFRSF11A,NOD2,IL6ST,CD40,CD74,VEGFA,TNFAIP3,CD8A
GO: 0030155	3.07E-04	2.46	regulation of cell adhesion	CD36,PDE3B,ROCK1,NRG1,CCL5,ICAM1,VWC2,EFNA5,CDK6,VAV3,THBS1,PLAU,PRSS2,CCR7,NUAK1,VAV1,CYR61,VEGFA,TESC,LAMA3,PSCDBP,ACVRL1
GO: 0031589	9.04E-04	2.42	cell-substrate adhesion	CD36,ITGBL1,ITGB8,ROCK1,FBLN5,BCL2L11,VWC2, EFNA5,CDK6,THBS1,AXL,PPARD,PLAU,HPSE,CCR7, FREM1,CYR61,CNTN2,ACVRL1
GO: 0042060	3.17E-08	2.34	wound healing	CD36,FMOD,PDE3B,HMOX1,APBB1IP,NRG1,SERPING1,PIK3R1,ADRB2,DOCK11,SDC1,TFPI,KIF3B,LRP8,VAV3,HPS1,HBB,SCARB1,SLC7A8,THBS1,PRKCB1,AXL,PLEK,TMPRSS6,F2R,PPARD,CLU,PLAU,ENTPD1,HPSE,GP6,PDE9A,PTGIR,INA,CD84,TSPAN8,KGFLP1,TGFA,P2RY1,VAV1,TIMP3,IRF1,PRKAR2B,S100A8,
GO: 0032101	1.19E-04	2.34	regulation of response to external stimulus	SERPINF1,CD36,SERPING1,ADRB2,CCL5,CXCL12,THBS1,PLEK,TMPRSS6,F2R,PLAU,HPSE,TLR3,PLA2G2A, PLXNA4,CCR7,CYP27B1,TSPAN8,KLK8,TNFRSF11A, CALCRL,NOD2,IL6ST,CD74,VEGFA,GATA3,ANXA1,TNFAIP3
GO: 0002684	6.66E-07	2.33	positive regulation of immune system process	SKAP1,CD86,CD36,HMOX1,FYB,PTPRC,C1R,BDKRB1,C2,HLA-DQB1,SERPING1,PIK3R1,HSP90AB1,HLA-DRB3,TNFSF13,CCL5,ICAM1,VAV3,HPS1,CXCL12,THBS1,PRKCB1,MAP2K6,BCL2,CLU,HLA-DPB1, TLR3,HLA-DOA,HLA-DOB,HLA-DQA1, HLA-DPA1,HLA-DRB5, RPS6KA2,CCR7,FOXJ1,VAV1,NOD2,HLA-DQA2,HLA-DM
GO: 0006952	3.42E-07	2.28	defense response	CD86,CD36,SPON2,PTPRC,C1R,TBKBP1,C2,HLA-DQB1,HSP90AB1,HLA-DRB3,ICAM1,INHBB,CD8B,CREBBP,MAP2K6,SOCS6, BCL2,SP140,EGR1,CLU,IFIT2,HLA-DPB1,TYROBP,RNASE6,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DPA1,HLA-DRB5, CIITA,RPS6KA2,CD84,CYP27B1,LILRB3,CD207,CX3CR1,HLA-A,IRF1,HLA-D
GO: 0006955	1.65E-08	2.19	immune response	SKAP1,IGSF6,CD86,CD36,CD70,HMOX1,SPON2,FYB,TBKBP1,HLA-DQB1,PIK3R1,HSP90AB1,HLA-DRB3,PTGER4,CCL5,CD8B,PRG4,CREBBP,ICAM3,VAV3,MR1,ZEB1,CXCL12,LCP1,THBS1,PRKCB1,MAP2K6,BCL2,EGR1,IFIT2,HLA-DPB1,CCL13,TYROBP,TLR3,HLA-DOA,BDKRB2,HLA-DOB,HLA-DQA1,HLA-DPA1,HLA-DR
GO: 0030168	9.04E-04	2.16	platelet activation	CD36,PDE3B,SERPING1,PIK3R1,LRP8,VAV3,THBS1,PRKCB1,AXL,PLEK,F2R,CLU,GP6,PDE9A,PTGIR,P2RY1,VAV1,RHOB,CD40,KCNMB4,VEGFA,SLC8A1,GNAQ,F13A1

GO: 0006954	9.14E-05	2.10	inflammatory response	SERPINF1,HMOX1,BDKRB1,SERPING1,ADRB2,CCL5,XCR1,THBS1,AXL,F2R,AIF1,CYSLTR1,CCL13,ALOX5AP,TLR3,NDST1,BDKRB2,CXCL2,PLA2G2A,LY75,CCR7,CCL3,TNFRSF11A,CALCRL,NOD2,S100A8,IL6ST,PTAFR,CCL18,CD40,LY86,GATA3,ANXA1,TNFAIP3,CXCL3,LTC4S,BLNK
GO: 0070887	1.19E-09	2.08	cellular response to chemical stimulus	SMOX,PAPSS2,CD36,CYP4B1,PDE3B,KLF2,HMOX1,PTPRC,NR4A1,LIFR,WNT16,HLA-DQB1,CHI3L1,PTPRE,PIK3R1,HSP90AB1,HLA-DRB3,LTK,FBLN5,CCL5,ICAM1,INHBB,BMP7,REST,EFNA5,LRP8,ZEB1,FGFR2,CXCL12,HBB,CDKN1B,CAB39L,THBS1,CYP4F3,CYP26B1,EGR1,AIF1,PPARD,CLU,CDKN2B,IFIT2,HLA-DP
GO: 0007155	2.59E-05	2.00	cell adhesion	ANXA9,PGM5,CRNN,SPON2,TMEM49,BARX2,DSG2,CDH12,MPZL2,TNXB,DLG5,MFAP4,ICAM3,CXCL12,SCARB1,SSPN,SIGLEC10,PLEK,PCDHB2,COL4A6,CDH23,FBLIM1,ENTPD1,CNTN3,RPSA,MLLT4,BOC,COL21A1,CD33,LAMB4,ADAM23,CD84,CLCA2,CX3CR1,ALCAM,CLDN8,TTYH1,RHOB,TPBG,PCDHB4,HNT,CELSR3,AMI
GO: 0051240	4.06E-04	1.97	positive regulation of multicellular organismal process	ZBTB16,ACVR2B,CD36,RGS2,HMOX1,NRG1,ADRB2,CCL5,ICAM1,INHBB,BMP7,GDNF,FGFR2,THBS1,F2R,NIPBL,AIF1,CYSLTR1,HPSE,TLR3,CCR7,P2RY1,TNFRSF11A,NOD2,ERBB4,IL6ST,CD40,CD74,VEGFA,OSR2,GATA3,LIPG,FOXD1,FOXS1,TBXAS1
GO: 0007599	8.95E-05	1.96	hemostasis	CD36,PDE3B,APBB1IP,SERPING1,PIK3R1,DOCK11,TFPI,KIF3B,LRP8,VAV3,HPS1,HBB,SLC7A8,THBS1,PRKCB1,AXL,PLEK,TMPRSS6,F2R,CLU,PLAU,ENTPD1,HPSE,GP6,PDE9A,PTGIR,CD84,TSPAN8,P2RY1,VAV1,IRF1,PRKAR2B,RHOB,HBG1,CD40,KCNMB4,VEGFA,GATA3,PRKAR1B,HBD,SLC8A1,FLI1,GNAQ,F13A1
GO: 0006935	8.22E-05	1.91	chemotaxis	SPON2,PTPRC,NR4A1,ROCK1,HSP90AB1,CSNK2A2,CCL5,BMP7,EFNA5,GDNF,XCR1,CXCL12,THBS1,MYH11,FPR3,NFIB,CYSLTR1,PLAU,BOC,CCL13,TYROBP,EDNRB,CXCL2,RPS6KA2,PLXNA4,CCR7,CCL3,TNFRSF11A,CX3CR1,ALCAM,SEMA6D,NOD2,S100A8,CYR61,RHOB,PTAFR,CCL18,SLIT3,CNTN2,CD74,VEGFA,TUBB
GO: 0050817	1.79E-04	1.91	coagulation	CD36,PDE3B,APBB1IP,SERPING1,PIK3R1,DOCK11,TFPI,KIF3B,LRP8,VAV3,HPS1,HBB,SLC7A8,THBS1,PRKCB1,AXL,PLEK,TMPRSS6,F2R,CLU,PLAU,ENTPD1,HPSE,GP6,PDE9A,PTGIR,CD84,TSPAN8,P2RY1,VAV1,IRF1,PRKAR2B,RHOB,HBG1,CD40,KCNMB4,VEGFA,GATA3,PRKAR1B,HBD,SLC8A1,GNAQ,F13A1
GO: 0048584	2.19E-06	1.90	positive regulation of response to stimulus	SKAP1,ACVR2B,CD86,MSX1,CD36,SEMA4C,HMOX1,FYB,PTPRC,C1R,TCF7L2,C2,WNT16,HLA-DQB1,SERPING1,PIK3R1,ADRB2,HSP90AB1,HLA-DRB3,TNFSF13,CCL5,BMP7,ECM1,TNFRSF10B,HIPK2,VAV3,FGFR2,CXCL12,THBS1,PRKCB1,MAP2K6,BCL2,F2R,PPARD,CLU,CDKN2B,RSPO1,ITSN1,HPSE,HLA-DPB1,TLR3,H
GO: 0043069	1.59E-04	1.89	negative regulation of programmed cell death	MSX1,TERT,HMOX1,TCF7L2,ROCK1,SNAI1,LIFR,NRG1,CCL5,BMP7,TSC22D1,GDNF,HIPK2,SORT1,FGFR2,CXCL12,CDKN1B,THBS1,BCL2,AXL,F2R,AIF1,CLU,ITSN1,CLN8,TAF9B,CCR7,PIM1,TGFA,CX3CR1,NOD2,ERBB4,CYR61,MAPK8IP2,IL6ST,HTATIP2,CD74,VEGFA,GATA3,ARNT2,ANXA1,TNFAIP3,IL2RB,FOXS1
GO: 0007166	2.58E-07	1.87	cell surface receptor linked signaling pathway	SKAP1,APC2,IGSF6,CD36,ITGBL1,RGS2,RGS11,RASD1,SORCS2,FYB,ITGB8,PTPRC,TCF7L2,BDKRB1,WNT16,HLA-DQB1,STK4,HSP90AB1,HLA-DRB3,PFTK1,PTGER4,CSNK2A2,CCL5,ICAM1,LEPR,TNFRSF10B,SDC1,SOX7,XCR1,LRP8,PARD3,CXCL12,SCARB1,PRKCB1,MAP2K6,BCL2,PLEK,TBL1XR1,F2R,RSPO1,IFIT2
GO: 0010033	5.03E-08	1.85	response to organic substance	SERPINF1,CPT1A,ACVR2B,CD36,PDE3B,KLF2,HMOX1,PTPRC,TCF7L2,NR4A1,BDKRB1,LIFR,HLA-DQB1,CHI3L1,PTPRE,PIK3R1,HSP90AB1,HLA-DRB3,CCL5,ICAM1,INHBB,BMP7,REST,EFNA5,SDC1,XCR1,LRP8,PFKFB2,SORT1,ZEB1,FGFR2,CXCL12,CC

				ND1,SCARB1,CDKN1B,CAB39L,THBS1,BCL2,BCHE,F2R,EGR1,AI
GO: 0008284	3.20E-04	1.83	positive regulation of cell proliferation	CD86,CRIP2,HMOX1,PTPRC,NR4A1,LIFR,FOXP2,NRG1,ADRB2,TNFSF13,CCL5,ECM1,TSC22D1,CDK6,HIPK2,HIG2,VAV3,FGFR2,CCND1,CDKN1B,BCL2,F2R,EGR1,AIF1,PPARD,CLU,HPSE,ATF3,HOXC10,KGFLP1,TGFA,E2F3,TNFRSF11A,CALCRL,NOD2,ERBB4,CYR61,IL6ST,CD40,PDGFC,CD74,VEGFA,OSR2,PGF,ARNT
GO: 0051707	9.43E-04	1.80	response to other organism	CD86,CD36,PTPRC,BDKRB1,CCL5,ICAM1,BCL2L11,CD8B,CDK6,CXCL12,SCARB1,BCL2,F2R,CLU,IFIT2,TLR3,CXCL2,PLA2G2A,CYP27B1,TNFRSF11A,CD207,CX3CR1,HLA-A,IL28A,NOD2,VLDLR,S100A8,PTAFR,CD40,OAS1,DCN,WFDC12,GATA3,DEFA6,MAOB,TNFAIP3,HCK,LTC4S,CD8A
GO: 0009605	3.99E-05	1.76	response to external stimulus	HMOX1,SPON2,PTPRC,NR4A1,ROCK1,FOXP2,NEURL,WIPI1,HSP90AB1,LTK,CSNK2A2,ICAM1,INHBB,BMP7,EFNA5,GDNF,TNFRSF10B,XCR1,ZEB1,CCND1,MYH11,BCL2,FPR3,AXL,BCHE,AIF1,CTSB,NFIB,CDKN2B,CYSLTR1,PSPH,BOC,CCL13,TYROBP,EDNRB,CXCL2,RPS6KA2,CCL3,P2RY1,TIMP3,CX3CR1,ALCAM,IRF1,
GO: 0051094	9.89E-04	1.75	positive regulation of developmental process	SERPINF1,ZBTB16,ACVR2B,CD86,CD36,HMOX1,TCF7L2,SNAI1,NRG1,ADRB2,CCL5,BMP7,VWC2,ECM1,GDNF,ZEB1,FGFR2,THBS1,MAP2K6,PPARD,CLU,CDKN2B,USP2,BOC,PLA2G2A,CYP27B1,CX3CR1,HEYL,CYR61,NEUROD2,IL6ST,RHOB,CD74,VEGFA,OSR2,GATA3,TESC,SOX5,AMIGO1,CDON,FOXD1,MAP1B
GO: 0050801	9.74E-04	1.74	ion homeostasis	SLC9A7,HMOX1,PTPRC,BDKRB1,SLC4A11,ADRB2,MTL5,MAL,XCR1,CXCL12,SLC7A8,BCL2,F2R,PPARD,CDH23,CYSLTR1,CCL13,EDNRB,SLC30A3,BDKRB2,CCR7,CYP27B1,KLK8,CCL3,TGFA,P2RY1,PYGM,STEAP2,MAPK8IP2,IL6ST,GJC3,CNTN2,KCNMB4,SLC4A1,CD52,ANPEP,AMIGO1,SLC8A1,CNIH2,TBXAS1,NFASC,G
GO: 0007167	2.36E-04	1.71	enzyme linked receptor protein signaling pathway	ACVR2B,MSX1,CSF1R,FMOD,PDE3B,MPZL1,NR4A1,KIDINS220,LIFR,NRG1,AKAP13,PTPRE,PIK3R1,ADRB2,LTK,CILP,INHBB,BCL2L11,BMP7,VWC2,ROR2,CD8B,EFNA5,HIPK2,VAV3,SORT1,FGFR2,CDKN1B,CAB39L,THBS1,AXL,EGR1,CDKN2B,ID1,ITSN1,GP6,NDST1,BDKRB2,GREM2,RPS6KA2,TGFA,VAV1,ERBB4,PRK
GO: 0048731	3.97E-05	1.70	system development	PAPSS2,ANKRD2,MREG,CD86,CRIP2,FMOD,SPI1,PDE3B,RPL3L,KLF2,CALML5,KRTAP5-9,BARX2,SNAI1,ELF5,ADRB2,TNFSF13,ICAM1,INHBB,BCL2L11,KRT9,KRT25,SPRR1B,SDC1,CSTA,SORT1,HPS1,CCND1,CDKN1B,LCP1,GJB2,FANCA,PAX3,PLEK,L3MBTL,LPCAT1,F2R,CTSB,CDKN2B,FHL1,USP2,NPR3,RPSA,HPS
GO: 0072358	9.81E-04	1.69	cardiovascular system development	SERPINF1,ACVR2B,MSX1,CHM,HMOX1,ITGB8,TCF7L2,NR4A1,WNT16,NRG1,MRE11A,CCL5,BMP7,BCOR,ECM1,REST,VAV3,FGFR2,THBS1,MYH11,TMPRSS6,NIPBL,EGR1,CSPG4,PLAU,ID1,BBS5,TNNT2,FOXJ1,TGFA,PLXDC1,CALCRL,CX3CR1,TNFAIP2,ERBB4,HEYL,VLDLR,CYR61,RHOB,HTATIP2,VEGFA,GATA3,PGF,AN
GO:2000026	3.54E-04	1.65	regulation of multicellular organismal development	SERPINF1,ZBTB16,ACVR2B,CD86,SPI1,HMOX1,TCF7L2,SNAI1,FOXP2,NRG1,ADRB2,LTK,TNFSF13,CCL5,BMP7,VWC2,BCOR,ECM1,REST,GDNF,CDK6,ZEB1,FGFR2,CDKN1B,THBS1,L3MBTL,NIPBL,EGR1,NFIB,CDKN2B,USP2,ID1,HPSE,BOC,EDNRB,TLR3,PLXNA4,FOXJ1,CYP27B1,KLK8,KGFLP1,SOX2,CX3CR1,SSH1,H
GO: 0042592	1.48E-04	1.64	homeostatic process	SLC9A7,TERT,SPI1,PDE3B,KLF2,HMOX1,PTPRC,TCF7L2,BDKRB1,SLC4A11,ADRB2,MRE11A,CCL5,ICAM1,BCL2L11,MTL5,CREBBP,TXNDC13,EFNA5,CDK6,MAL,XCR1,CXCL12,SCARB1,SLC7A8,BCL2,AXL,F2R,PPARD,CDH23,CYSLTR1,CCL13,EDNRB,SLC30A3,BDKRB2,MYLIP,PIF1,CCR7,CYP27B1,KLK8,KGFLP1,CCL3
GO: 0040011	9.83E-05	1.64	locomotion	HMOX1,SPON2,PTPRC,NR4A1,BDKRB1,SYNE2,ROCK1,SNAI1,NEURL,PIK3R1,HSP90AB1,CSNK2A2,CCL5,ICAM1,BMP7,ROR2,EFNA5,GDNF,XCR1,LRP8,VAV3,CXCL12,SCARB1,SLC7A8,THBS1,MYH11,FPR3,AXL,F2R,AIF1,PPARD,NFIB,CYSLTR1,PLAU,ID1,BOC,CCL13,

				GP6,TYROBP,EDNRB,CXCL2,RPS6KA2,PLXNA4,CC
GO: 0010646	8.01E-04	1.51	regulation of cell communication	APC2,CPT1A,ACVR2B,MSX1,CD36,SEMA4C,RGS2,PDE3B,CPLX3,RGS11,HMOX1,PTPRC,TCF7L2,SNAI1,WNT16,PTPRE,STK4,ADRB2,CILP,CCL5,INHBB,BMP7,VWC2,ECM1,REST,EFNA5,GDNF,TNFRSF10B,HIPK2,PFKFB2,FGFR2,THBS1,PRKCB1,SOCS6,PLEK,CYP26B1,BCHE,F2R,EGR1,PPARD,CDKN2B,RSPO1,ITSN1,HP
GO: 0023052	4.89E-07	1.50	signaling	SKAP1,APC2,CPT1A,PGDS,IGSF6,ACVR2B,CD86,MSX1,CSF1R,CD36,FIBCD1,ITGBL1,SEMA4C,RHOU,FMOD,RGS2,TRIM63,PDE3B,CPLX3,CRABP1,RGS11,RASD1,MPZL1,CD70,HMOX1,SORCS2,FYB,CENTB5,ITGB8,PTPRC,CALML5,APBB1IP,TCF7L2,NR4A1,BDKRB1,ROCK1,KIDINS220,SNAI1,LIFR,WNT16,NRG1,HLA-D
GO: 0030154	6.08E-05	1.47	cell differentiation	SERPINF1,ZBTB16,MREG,ACVR2B,CD86,MSX1,CD36,SEMA4C,RGS2,SPI1,KLF2,UPK1A,SPON2,PTPRC,HLX,TCF7L2,SEMA4G,ROCK1,BARX2,SNAI1,LIFR,WNT16,ELF5,NRG1,BTK,NEURL,NDRG4,HSP90AB1,LTK,CSNK2A2,CCL5,INHBB,BMP7,VWC2,SPRR1B,MTL5,PCSK4,REST,EFNA5,GDNF,CDK6,SDC1,HIPK2,CSTA,MA
GO: 0007154	2.46E-05	1.46	cell communication	SKAP1,PGDS,IGSF6,CD86,CSF1R,FIBCD1,ITGBL1,RHOU,FMOD,TRIM63,CRABP1,RASD1,MPZL1,CD70,SORCS2,FYB,CENTB5,ITGB8,CALML5,APBB1IP,NR4A1,BDKRB1,ROCK1,KIDINS220,FRAS1,LIFR,NRG1,HLA-DQB1,BTK,AKAP13,IGFBP6,WIPI1,PIK3R1,HSP90AB1,HLA-DRB3,PFTK1,PTGER4,LTK,CSNK2A2,TENC1
GO: 0007399	8.52E-04	1.45	nervous system development	SERPINF1,ZBTB16,MSX1,SEMA4C,SPON2,PTPRC,TCF7L2,SEMA4G,ROCK1,LIFR,FOXP2,WNT16,NRG1,NEURL,HSP90AB1,LTK,CSNK2A2,CCL5,BMP7,VWC2,REST,EFNA5,GDNF,CDK6,HIPK2,MAL,SCLT1,LRP8,TSPAN2,PARD3,ZEB1,FGFR2,MYH11,BCL2,AXL,DYRK1A,PCDHB2,NIPBL,PPARD,CLU,NFIB,CNTN3,GJB1,CLN8
GO: 0032502	3.22E-05	1.44	developmental process	PAPSS2,ANKRD2,MSX1,CSF1R,TERT,CHM,CRIP2,SEMA4C,RHOU,FMOD,RGS2,SPI1,PDE3B,CRABP1,RPL3L,UPK1A,SPON2,ITGB8,PTPRC,CALML5,NEK1,HLX,SEMA4G,NR4A1,ROCK1,KRTAP5-9,LIFR,FOXP2,WNT16,ELF5,NEURL,NDRG4,STK4,HSP90AB1,LTK,CSNK2A2,MRE11A,MPZL2,TNFSF13,ICAM1,INHBB,SHROOM1,
GO: 0032501	3.40E-04	1.35	multicellular organismal process	SERPINF1,PAPSS2,ANKRD2,BEST1,MREG,CD86,MSX1,CSF1R,CHM,CRIP2,SEMA4C,FMOD,SPI1,CPLX3,CRABP1,RPL3L,KLF2,SPON2,ITGB8,PTPRC,CALML5,HLX,TCF7L2,SEMA4G,NR4A1,SLC15A1,BDKRB1,TRPM1,ROCK1,KRTAP5-9,BARX2,SNAI1,LIFR,FOXP2,WNT16,ELF5,NEURL,NDRG4,HSP90AB1,PTGER4,LTK,CSN

Table S7b. Enriched cellular components identified by the meta-gene analysis

GOCCID	Pvalue	Odds Ratio	Term	Involved_Gene
GO: 0042613	2.39E-20	Inf	MHC class II protein complex	HLA-DQB1,HLA-DRB3,HLA-DPB1,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DPA1,HLA-DRB5,HLA-DQA2,HLA-DMA,CD74,HLA-DRB1,HLA-DRB4,HLA-DMB,HLA-DRA
GO: 0033162	0.000359	19.24	melanosome membrane	SLC45A2,TYR,GPR143,TYRP1
GO: 0005833	0.000107	16.06	hemoglobin complex	HBB,HBA2,CYB5R3,HBG1,HBD
GO: 0001533	0.000163	9.64	cornified envelope	SPRR1B,CSTA,SPRR1A,TGM1,ANXA1,RP1-21O18.1
GO: 0045095	0.000443	4.12	keratin filament	KRTAP5-9,KRTAP1-1,KRTAP2-4,KRT9,KRTAP4-12,KRT4,KRT74,KRTAP4-4,KRT71,KRT77
GO: 0005765	1.23E-05	3.65	lysosomal membrane	HLA-DQB1,HLA-DRB3,SORT1,HPSE,HLA-DPB1,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DPA1,HLA-DRB5,HLA-DQA2,HLA-DMA,GPR143,LAPTM5,HLA-DRB1,HLA-DRB4,HLA-DMB,HLA-DRA
GO: 0044437	2.05E-05	3.03	vacuolar part	TMEM49,HLA-DQB1,WIPI1,HLA-DRB3,SORT1,HPSE,HLA-DPB1,HLA-DOA,HLA-

				DOB,HLA-DQA1,HLA-DPA1,HLA-DRB5,HLA-DQA2,HLA-DMA,GPR143,LAPTM5,HLA-DRB1,HLA-DRB4,TPP1,HLA-DMB,ATG9B,HLA-DRA
GO: 0045111	9.17E-05	2.87	intermediate filament cytoskeleton	KRTAP5-9,PTPRE,KRTAP1-1,KRTAP19-1,KRTAP2-4,KRT9,KRT25,KRTAP4-12,KRT4,INA,KRT74,KRT16,KRTAP4-4,TACC1,PCDHB4,KRT33B,KRT71,FLG,KRT77,KRT28
GO: 0010008	9.16E-05	2.37	endosome membrane	SLC9A7,HLA-DQB1,WIPI1,HLA-DRB3,SORT1,SILV,HLA-DPB1,TLR3,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DPA1,HLA-DRB5,CLCN5,CD1A,HLA-A,HLA-DQA2,HLA-DMA,STEAP2,RHOB,CD1C,HGS,SNX10,TYRP1,HLA-DRB1,HLA-DRB4,HLA-DMB,HLA-DRA
GO: 0000323	8.29E-05	2.35	lytic vacuole	HLA-DQB1,ADRB2,HLA-DRB3,SORT1,HPS1,USP6,CTSB,HPSE,HLA-DPB1,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DPA1,HLA-DRB5,TYR,ANXA11,TSPAN8,PPT2,HLA-DQA2,HLA-DMA,GPR143,CTSS,CD74,LAPTM5,HLA-DRB1,HLA-DRB4,TPP1,HLA-DMB,HLA-DRA
GO: 0044459	2.19E-11	1.93	plasma membrane part	PTPRH,APC2,FCER1A,BEST1,IGSF6,MREG,SLC5A3,PGM5,ACVR2B,CD86,CSF1R,CD36,PARD3B,ITGBL1,RHOU,RGS2,TM7SF2,RGS11,MPZL1,CD70,UPK1A,HMOX1,ITGB8,PTPRC,APBB1IP,SLC15A1,BDKRB1,SYNE2,TRPM1,LIFR,CSF2RA,NRG1,HLA-DQB1,PLA2R1,SLC4A11,ADRB2,HSP90AB1,HLA-DRB3,LTK,CGN,TSPAN
GO: 0005887	1.32E-07	1.87	integral to plasma membrane	PTPRH,FCER1A,IGSF6,SLC5A3,ACVR2B,CSF1R,CD36,ITGBL1,TM7SF2,MPZL1,CD70,ITGB8,PTPRC,SLC15A1,BDKRB1,TRPM1,LIFR,CSF2RA,PLA2R1,ADRB2,HLA-DRB3,LTK,TSPAN9,SLC16A6,ICAM1,ROR2,ABCC2,CD8B,ICAM3,SDC1,MAL,XCR1,HPS1,SCARB1,SSPN,SLC7A8,AXL,PCDHB2,F2R,CEACAM6,CSPG4,CYSLT
GO: 0005615	3.97E-05	1.80	extracellular space	SERPINF1,FIBCD1,FMOD,CD70,HMOX1,C2,WNT16,NRG1,CHI3L1,SERPING1,IGFBP6,PLA2R1,FBLN5,CILP,TNFSF13,CCL5,ICAM1,BMP7,TNXB,VWC2,SMPDL3B,FAM3B,IL1F9,TFPI,HIG2,CXCL12,THBS1,BCHE,CLU,CTSB,RSPO1,PLAU,OVOS2,CCL13,PRSS2,CXCL2,PLA2G2A,GREM2,KLK8,KGFLP1,CCL3,TGFA,PRSS1,
GO: 0071944	8.67E-12	1.73	cell periphery	SKAP1,PTPRH,APC2,FCER1A,BEST1,IGSF6,MREG,SLC5A3,PGM5,ACVR2B,CD86,SC4MOL,CSF1R,CD36,LYNX1,PARD3B,ITGBL1,SEMA4C,RHOU,RGS2,TM7SF2,CPLX3,RGS11,RASD1,MPZL1,CD70,UPK1A,HMOX1,ITGB8,PTPRC,APBB1IP,SLC15A1,BDKRB1,SYNE2,TRPM1,PRSS21,TMEM49,FRAS1,LIFR,WNT16,CSF2RA,NR
GO: 0005576	1.12E-05	1.56	extracellular region	SERPINF1,SCUBE2,HTRA3,METRNL,PRSS27,LYNX1,FIBCD1,CRIP2,ITGBL1,FMOD,CD70,HMOX1,SPON2,C1R,LIFR,C2,WNT16,CSF2RA,NRG1,CHI3L1,SERPING1,IGFBP6,KRTAP1-1,PLA2R1,PRSS23,FBLN5,CILP,TNFSF13,CCL5,ICAM1,INHBB,BMP7,TNXB,GPLD1,VWC2,CD8B,PRG4,ECM1,SMPDL3B,LEPR,MFAP4,FAM3
GO: 0031224	8.8E-07	1.46	intrinsic to membrane	PTPRH,FCER1A,CPT1A,BEST1,IGSF6,SLC5A3,PIK3IP1,ACVR2B,CD86,SC4MOL,SLC9A7,CSF1R,CD36,LYNX1,FIBCD1,ITGBL1,SEMA4C,TM7SF2,PDE3B,MPZL1,CD70,UPK1A,SORCS2,ITGB8,PTPRC,SEMA4G,MPEG1,SLC15A1,BDKRB1,SYNE2,TRPM1,PRSS21,TMEM49,CD302,KIDINS220,FRAS1,LIFR,ARV1,CSF2RA,NRG
GO: 0016020	4.51E-07	1.45	membrane	SKAP1,PTPRH,APC2,FCER1A,CPT1A,BEST1,IGSF6,MREG,SLC5A3,PIK3IP1,PGM5,ACVR2B,CD86,SC4MOL,SLC9A7,CSF1R,FKBP5,CD36,LYNX1,FIBCD1,PARD3B,ITGBL1,SEMA4C,CYP4B1,RHOU,RGS2,CRNN,TM7SF2,PDE3B,CPLX3,RGS11,RASD1,MPZL1,CD70,UPK1A,HMOX1,SORCS2,ITGB8,PTPRC,APBB1IP,SEMA4G,M

Table S7c. Enriched molecular functions identified by the meta-gene analysis

GOMFID	Pvalue	Odds Ratio	Term	Involved_Gene
GO: 0032395	7.54E-14	Inf	MHC class II receptor activity	HLA-DQB1,HLA-DRB3,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DPA1,HLA-DQA2,HLA-DRB1,HLA-DRB4,HLA-DRA
GO: 0038023	1.84E-05	1.76	signaling receptor activity	PTPRH,ANXA9,IGSF6,ACVR2B,CD86,CSF1R,CD36,SORCS2,PTPRC,NR4A1,BDKRB1,LIFR,CSF2RA,HLA-DQB1,PTPRE,ADRB2,HLA-DRB3,PTGER4,LTK,ICAM1,ROR2,CD8B,LEPR,XCR1,LRP8,SORT1,MR1,FGFR2,SCARB1,FPR3,AXL,F2R,PPARD,CYSLTR1,NPR3,GP6,EDNRB,TLR3,HLA-DOA,BDKRB2,HLA-DOB,HLA-DQA1,HL
GO: 0060089	1.33E-06	1.75	molecular transducer activity	PTPRH,ANXA9,IGSF6,ACVR2B,CD86,CSF1R,CD36,RGS2,TRIM63,RGS11,HMOX1,SORCS2,PTPRC,NR4A1,BDKRB1,LIFR,CSF2RA,HLA-DQB1,AKAP13,PTPRE,ADRB2,HLA-DRB3,PTGER4,LTK,ICAM1,ROR2,CD8B,ECM1,LEPR,CREBBP,XCR1,LRP8,SORT1,MR1,FGFR2,CXCL12,SCARB1,CDKN1B,FPR3,AXL,F2R,PPARD,CSPG4

Table S8a. Top 10 activated upstream regulators identified by the meta-gene analysis

Upstream Regulator	Fold Change	Molecule Type	Predicted Activation State	Activation z-score	p-value of overlap
MITF	1.214	transcription regulator	Activated	2.660	5.47E-09
EGFR	-1.034	kinase	Activated	2.220	1.55E-08
SMAD7	-1.051	transcription regulator	Activated	2.417	1.07E-04
ERBB2	-1.019	kinase	Activated	2.037	1.24E-04
ERBB3	-1.027	kinase	Activated	2.094	4.19E-04
FAS	-1.063	transmembrane receptor	Activated	2.123	6.35E-04
SCD	1.416	enzyme	Activated	2.784	2.84E-03
Sod		group	Activated	2.000	3.14E-03
SREBF1	1.112	transcription regulator	Activated	2.228	5.29E-03
SOX11		transcription regulator	Activated	2.219	8.48E-03

Table S8b. Top 10 inhibited upstream regulators identified by the meta-gene analysis

Upstream Regulator	Fold Change	Molecule Type	Predicted Activation State	Activation z-score	p-value of overlap
TNF	-1.178	cytokine	Inhibited	-2.764	3.10E-11
IFNG		cytokine	Inhibited	-2.439	3.19E-10
AGT	-1.220	growth factor	Inhibited	-2.157	5.51E-10
IL27	-1.104	cytokine	Inhibited	-2.938	3.73E-08
IL1B	-1.197	cytokine	Inhibited	-3.910	6.20E-08
IL13		cytokine	Inhibited	-2.112	9.57E-08
CIITA	-1.514	transcription regulator	Inhibited	-2.452	2.10E-07
EBI3		cytokine	Inhibited	-2.744	3.63E-07
TLR4	-1.364	transmembrane receptor	Inhibited	-3.002	4.66E-07
F2R	-1.242	G-protein coupled receptor	Inhibited	-2.676	9.72E-07

Table S9. Gene Probes included in cluster 26

ID	**Symbol**	**Entrez Gene Name**	**Location**	**Type(s)**	**Drug(s)**
A_23_P209731	ARMC9	armadillo repeat containing 9	Other	other	
A_23_P209735	ARMC9	armadillo repeat containing 9	Other	other	
A_23_P83579	ARNT2	aryl-hydrocarbon receptor nuclear translocator 2	Nucleus	transcription regulator	
A_23_P104996	BEST1	bestrophin 1	Plasma Membrane	ion channel	
A_24_P100277	CYB5R3	cytochrome b5 reductase 3	Cytoplasm	enzyme	
A_23_P2831	EDNRB	endothelin receptor type B	Plasma Membrane	G-protein coupled receptor	bosentan, sitaxsentan, atrasentan
A_23_P348636	FOXJ1	forkhead box J1	Nucleus	transcription regulator	
A_32_P19294	GLT1D1	glycosyltransferase 1 domain containing 1	Extracellular Space	enzyme	
A_24_P277657	GMPR	guanosine monophosphate reductase	Cytoplasm	enzyme	
A_23_P45560	GPR143	G protein-coupled receptor 143	Plasma Membrane	G-protein coupled receptor	
A_23_P217704	GYG2	glycogenin 2	Cytoplasm	enzyme	
A_23_P388200	KDELC2	KDEL (Lys-Asp-Glu-Leu) containing 2	Other	other	
A_23_P302595	LINC00518	long intergenic non-protein coding RNA 518	Other	other	
A_32_P219581	LOC440934	uncharacterized LOC440934	Other	other	
A_23_P14853	LTK	leukocyte receptor tyrosine kinase	Plasma Membrane	kinase	pazopanib
A_23_P334173	LY75	lymphocyte antigen 75	Plasma Membrane	transmembrane receptor	
A_23_P329271	MC1R	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)	Plasma Membrane	G-protein coupled receptor	
A_24_P165205	MORN1	MORN repeat containing 1	Other	other	
A_23_P502706	PAX3	paired box 3	Nucleus	transcription regulator	
A_23_P76992	PGF	placental growth factor	Extracellular Space	growth factor	aflibercept
A_23_P2233	PMEL	premelanosome protein	Plasma Membrane	enzyme	
A_23_P312851	PMEL	premelanosome protein	Plasma Membrane	enzyme	
A_24_P347411	POSTN	periostin, osteoblast specific factor	Extracellular Space	other	
A_23_P335920	RPS6KA2	ribosomal protein S6 kinase, 90kDa, polypeptide 2	Nucleus	kinase	
A_24_P232158	SCARA3	scavenger receptor class A, member 3	Plasma Membrane	transmembrane receptor	
A_23_P203900	SCARB1	scavenger receptor class B, member 1	Plasma Membrane	transporter	
A_24_P925186	SOX5	SRY (sex determining region Y)-box 5	Nucleus	transcription regulator	
A_24_P25354	TACC1	transforming, acidic coiled-coil containing protein 1	Nucleus	other	
A_23_P428326	TBC1D16	TBC1 domain family, member 16	Extracellular Space	other	
A_23_P114983	TRIM63	tripartite motif containing 63, E3 ubiquitin protein ligase	Nucleus	enzyme	
A_23_P129225	TRPM1	transient receptor potential cation channel, subfamily M, member 1	Plasma Membrane	ion channel	
A_24_P314477	TUBB2B	tubulin, beta 2B class IIb	Cytoplasm	other	brentuximab vedotin, cabazitaxel
A_32_P194062	TYR	tyrosinase	Cytoplasm	enzyme	hydroquinone, azelaic acid
A_23_P94403	TYRP1	tyrosinase-related protein 1	Cytoplasm	enzyme	

ProbeID	Fold change					P value		
	LLP	UV	PIH	AS	Ethnic	LLP	UV	PIH
A_23_P55270	22.32	6.39	1.01	-1.10	9.98	3.57E-04	4.04E-04	9.58E-01
A_23_P15786	2.28	1.03	7.77	9.84	4.85	4.36E-01	9.48E-01	2.12E-02
A_24_P23546	-7.56	-1.19	-2.42	-3.68	-2.16	2.87E-04	3.64E-01	1.02E-03
A_23_P94403	6.42	6.69	1.77	1.06	1.20	7.94E-05	6.14E-05	2.81E-04
A_23_P312851	5.38	5.97	1.87	1.16	-1.02	1.56E-04	1.80E-04	2.99E-05
A_32_P25295	-3.58	-1.03	-2.74	-2.38	-3.11	4.62E-02	8.90E-01	1.14E-04
A_23_P2233	4.76	5.63	1.76	1.23	-1.04	7.06E-05	2.28E-04	1.14E-05
A_23_P42811	-1.62	-1.58	-3.85	-3.26	-1.36	1.86E-01	8.57E-02	2.45E-05
A_24_P271696	-3.68	-2.33	-2.81	1.28	-2.20	8.66E-03	2.42E-03	2.28E-05
A_32_P156237	1.92	-1.17	3.16	1.99	4.36	7.82E-02	2.45E-01	1.85E-04
A_24_P184803	-2.35	-2.60	-1.24	-4.21	-1.11	2.06E-01	6.43E-03	4.62E-01
A_32_P183765	-2.48	-1.73	-2.55	-1.48	-2.55	7.43E-02	1.25E-02	7.58E-04
A_23_P302595	3.49	3.26	1.68	1.35	1.07	4.81E-03	1.36E-03	2.25E-02
A_24_P151005	3.08	1.01	5.40	1.43	1.45	1.50E-01	9.80E-01	3.08E-03
A_23_P22398	-4.17	-3.69	-1.10	-1.21	-1.41	1.51E-04	1.12E-03	2.03E-01
A_23_P45560	3.00	3.63	1.66	1.15	1.20	5.79E-04	1.00E-03	4.17E-04
A_32_P31144	7.23	2.47	1.39	1.47	-1.05	3.02E-03	6.35E-02	1.42E-01
A_24_P142305	-1.08	-1.27	-1.96	-2.53	-1.78	8.75E-01	6.14E-01	9.19E-02
A_23_P79108	1.78	-1.27	1.41	4.01	3.39	1.62E-01	3.88E-01	8.56E-02
A_32_P165047	3.73	3.64	1.59	1.09	1.01	1.42E-04	9.54E-05	4.54E-04
A_23_P26457	1.04	-1.60	-1.78	-2.72	-1.76	9.37E-01	3.12E-01	1.38E-01
A_32_P194062	4.32	4.04	1.53	1.03	-1.23	1.96E-04	2.12E-04	1.04E-03
A_24_P367247	2.80	1.31	1.45	2.88	1.41	2.71E-02	4.18E-01	2.21E-01
A_23_P2831	3.51	3.59	1.57	-1.12	1.15	8.65E-05	1.03E-04	3.22E-04
A_32_P191441	2.25	3.56	-1.09	1.42	2.14	1.51E-02	7.22E-04	6.25E-01
A_23_P129225	3.57	3.69	1.55	1.08	-1.10	4.40E-04	6.15E-04	2.27E-02
A_24_P196878	1.33	1.36	1.52	2.57	3.13	3.34E-01	1.08E-01	1.01E-01
A_24_P184799	-2.28	-2.51	1.13	-3.32	-1.10	2.46E-01	1.48E-02	7.56E-01
A_23_P93641	2.57	1.20	2.04	2.15	1.67	4.77E-02	4.90E-01	2.93E-03
A_23_P209735	2.80	4.82	1.20	1.12	1.37	3.50E-03	2.94E-03	1.60E-02
A_23_P159406	1.73	1.05	1.38	3.58	1.78	2.33E-01	8.14E-01	1.09E-01
A_23_P347610	2.14	1.26	1.04	3.05	2.07	5.31E-02	3.14E-01	8.54E-01
A_24_P129341	2.63	1.22	1.92	2.16	1.83	4.89E-02	3.96E-01	1.28E-02
A_32_P10936	1.04	1.02	-1.79	-2.02	-5.16	8.83E-01	9.41E-01	2.46E-02
A_23_P114983	2.66	4.33	1.46	1.25	-1.25	4.99E-03	5.21E-04	4.61E-04
A_24_P277657	2.85	3.91	1.48	-1.04	1.03	1.29E-03	6.29E-04	5.18E-03
A_24_P363711	-1.64	-1.91	-3.93	-1.03	-1.21	2.43E-01	8.84E-02	4.57E-04
A_32_P61298	-2.32	-1.29	-1.30	-1.59	-2.97	2.66E-02	2.49E-01	2.86E-02
A_23_P84063	-2.06	-3.47	-1.72	1.14	-1.35	3.76E-03	8.19E-04	1.10E-02
A_24_P251950	-3.13	-1.92	-1.87	-1.11	-1.55	2.91E-02	1.29E-02	2.96E-03
A_23_P37856	1.04	-1.59	-1.75	-2.54	1.08	9.44E-01	3.57E-01	1.76E-01
A_24_P314477	1.84	2.77	1.46	1.43	1.18	1.61E-02	8.50E-04	6.88E-02
A_32_P189781	4.51	1.58	1.57	1.45	1.19	9.82E-03	1.16E-01	4.38E-02
A_24_P367242	2.12	1.35	-1.02	2.76	1.71	2.81E-02	4.00E-01	9.22E-01
A_23_P204133	1.11	1.39	2.08	2.01	1.87	5.43E-01	4.42E-02	1.89E-05
A_23_P51767	-2.12	-1.96	-1.59	-1.31	-1.28	2.48E-02	3.11E-03	3.03E-03

A_24_P565390	1.41	1.64	1.60	2.08	1.68	2.37E-01	2.18E-02	1.89E-02
A_24_P307964	-1.97	-2.18	-1.63	-1.64	-1.06	1.07E-01	4.29E-02	3.67E-02
A_23_P52499	-3.14	-2.16	-1.43	1.07	-1.76	1.97E-02	9.20E-03	4.27E-02
A_23_P259049	4.27	1.72	1.66	1.16	1.10	4.97E-03	5.23E-02	1.97E-02
A_23_P373017	2.25	1.91	1.00	2.02	1.48	7.22E-03	3.76E-03	9.90E-01
A_23_P115202	1.40	1.15	1.37	2.86	1.76	2.14E-01	6.23E-01	4.20E-02
A_23_P38603	2.77	1.24	3.02	1.44	1.26	1.67E-01	6.05E-01	1.79E-02
A_23_P379147	2.13	1.00	1.03	2.45	2.15	3.15E-02	9.80E-01	9.12E-01
A_23_P36531	-2.46	-1.27	-1.26	-1.89	-2.49	6.65E-02	3.18E-01	1.88E-01
A_23_P209731	3.26	2.91	1.24	1.19	-1.22	1.32E-03	1.77E-04	4.15E-02
A_23_P22422	1.39	2.80	1.21	2.36	-1.03	1.83E-02	2.19E-04	1.62E-01
A_23_P64161	-2.49	-1.00	-1.50	-3.40	-1.05	1.63E-02	9.66E-01	8.98E-03
A_23_P115478	1.57	1.06	2.08	2.21	1.36	2.07E-02	8.03E-01	2.40E-03
A_32_P219279	2.04	1.55	1.21	1.06	3.63	7.37E-03	1.11E-02	3.87E-01
A_32_P71858	2.12	1.17	1.16	2.49	1.70	8.53E-04	1.69E-01	3.56E-01
A_23_P74012	1.43	1.33	1.41	2.47	1.37	4.75E-01	4.72E-01	9.37E-02
A_23_P412577	2.13	1.56	1.98	-1.11	2.03	1.85E-02	8.28E-02	8.55E-05
A_23_P203558	1.04	-1.56	-1.66	-2.11	-1.46	9.49E-01	2.81E-01	2.36E-01
A_23_P134347	-2.29	-1.89	-1.08	-1.63	-1.68	7.77E-03	1.66E-02	3.71E-01
A_23_P114883	-1.16	-2.29	-1.17	-1.47	-2.64	5.61E-01	3.90E-03	2.36E-01
A_23_P258769	-2.16	-1.93	1.04	-1.10	-2.77	3.56E-03	5.12E-03	4.80E-01
A_23_P417100	1.65	1.85	2.43	1.75	-1.28	3.25E-01	6.87E-02	3.48E-02
A_24_P732106	1.20	1.43	1.10	2.32	2.87	4.89E-01	3.53E-01	4.64E-01
A_23_P503010	1.57	1.69	-1.24	2.51	2.08	2.17E-01	6.49E-02	2.99E-01
A_24_P7642	2.27	1.02	1.39	2.11	1.78	1.87E-02	9.21E-01	3.36E-03
A_24_P272515	2.01	1.08	1.63	2.06	1.62	2.00E-02	6.08E-01	5.91E-04
A_24_P246626	-1.81	-1.71	1.14	-1.55	-2.81	2.21E-03	3.41E-02	1.51E-01
A_24_P916853	1.75	1.62	1.99	1.05	1.79	3.95E-02	1.10E-01	3.67E-05
A_24_P75190	-1.06	-1.61	-1.79	-1.78	-1.43	9.14E-01	2.94E-01	1.47E-01
A_23_P117882	-1.88	1.37	-2.33	-1.61	-1.90	1.44E-02	8.88E-02	5.92E-08
A_23_P405295	2.07	1.16	-1.13	1.60	3.82	3.63E-02	2.92E-01	3.58E-01
A_24_P281497	1.97	-1.14	-1.02	1.71	4.10	1.04E-02	7.69E-01	9.07E-01
A_23_P8108	-2.63	-1.88	-1.04	-1.30	-1.66	5.34E-03	2.30E-03	5.32E-01
A_23_P31006	-2.19	-1.85	-1.10	-1.36	-1.76	4.43E-03	3.29E-03	1.73E-01
A_23_P109988	-2.13	-2.09	-1.24	-1.30	-1.35	4.88E-03	2.27E-03	8.18E-02
A_24_P826858	-1.57	-1.15	-1.26	-1.77	-2.90	1.54E-01	3.66E-01	1.41E-01
A_23_P62709	2.09	-1.08	1.04	1.75	3.38	2.99E-02	7.17E-01	6.96E-01
A_32_P215100	3.08	1.11	1.14	1.17	2.15	4.79E-04	4.74E-01	4.06E-01
A_23_P63032	-1.85	-1.53	-1.38	-1.38	-2.05	2.79E-02	5.31E-02	1.76E-02
A_23_P99044	1.92	1.15	3.82	3.73	1.32	3.70E-01	7.24E-02	8.32E-03
A_23_P360605	1.91	1.29	1.50	1.33	2.11	5.77E-03	7.33E-02	1.62E-02
A_32_P22654	-1.08	-1.43	-2.10	-1.66	-1.46	8.69E-01	5.64E-01	1.20E-01
A_23_P104996	2.09	2.57	1.06	1.04	1.54	3.83E-03	5.03E-04	4.64E-01
A_23_P160214	1.67	1.40	1.21	2.50	1.23	1.13E-01	9.94E-02	2.34E-01
A_23_P89665	1.88	1.00	2.13	1.68	1.92	2.48E-01	9.89E-01	7.30E-02
A_32_P50973	-1.69	-1.46	-1.58	-1.54	-1.32	2.95E-03	1.46E-02	1.12E-02
A_23_P82886	-1.30	-1.63	-2.78	-1.21	1.14	5.12E-01	1.24E-01	3.46E-04

A_24_P124879	1.48	1.31	1.54	1.73	1.34	1.73E-01	3.11E-01	2.96E-02
A_23_P61637	1.61	1.02	1.50	2.20	2.07	2.30E-01	8.95E-01	7.72E-03
A_23_P250444	1.45	2.04	1.53	1.41	1.10	7.44E-02	2.65E-03	1.10E-03
A_32_P128586	1.92	1.90	1.11	1.57	1.30	2.22E-03	1.07E-03	2.90E-01
A_32_P158786	1.55	1.23	1.31	1.70	1.68	1.52E-01	2.94E-01	8.29E-02
A_23_P77493	2.24	1.48	1.41	1.38	1.30	1.79E-04	4.40E-03	2.01E-04
A_24_P799048	3.36	1.06	1.54	1.36	1.13	2.64E-04	4.94E-01	1.04E-02
A_32_P89352	-2.62	-2.31	-1.14	-1.04	-1.15	4.55E-04	3.85E-03	4.93E-01
A_24_P166443	-2.24	-1.81	1.02	-1.34	-1.71	4.80E-03	9.13E-03	7.10E-01
A_23_P68436	1.83	-1.10	1.59	1.69	2.45	1.99E-01	7.14E-01	1.39E-02
A_32_P27657	2.15	1.32	-1.10	2.18	1.67	3.26E-02	2.61E-01	5.39E-01
A_32_P19294	-1.47	-1.27	-1.57	-1.89	-2.02	4.09E-02	6.58E-02	2.52E-02
A_23_P42302	-2.70	-1.83	-1.05	-1.24	-1.59	9.79E-03	2.74E-02	6.88E-01
A_32_P84369	-1.73	-1.07	-1.75	-1.04	-3.38	1.19E-01	8.44E-01	2.95E-03
A_24_P402222	-1.99	-1.85	1.03	-1.45	-1.67	8.47E-03	2.38E-03	7.32E-01
A_23_P125451	-1.62	-2.50	-1.10	-1.37	-1.29	2.65E-02	2.86E-04	3.65E-01
A_23_P33384	-1.89	-2.22	1.05	1.01	-2.42	4.92E-02	6.00E-03	5.49E-01
A_23_P63167	-2.76	-1.70	-1.16	-1.23	-1.49	5.14E-03	4.52E-03	4.56E-02
A_23_P16915	2.67	1.83	1.33	-1.20	1.53	8.21E-04	1.26E-04	1.79E-03
A_24_P231104	-1.09	-1.21	-1.68	-2.33	-1.01	7.21E-01	7.26E-01	8.21E-02
A_23_P42969	-1.73	-1.33	-1.04	-2.42	-1.42	4.00E-02	2.10E-03	6.58E-01
A_23_P252388	-1.66	-1.10	-1.42	1.01	-3.51	1.51E-01	4.24E-01	6.88E-02
A_32_P58215	-2.09	-2.18	-1.20	-1.15	-1.24	1.91E-02	9.44E-04	2.22E-01
A_32_P379379	1.38	1.57	1.12	1.93	1.77	1.82E-01	2.24E-02	2.65E-01
A_24_P257416	-1.15	-2.04	-1.57	-1.13	-1.31	6.86E-01	1.82E-02	2.87E-02
A_23_P361940	-1.77	-1.39	-1.26	-1.22	-1.95	3.56E-02	3.75E-01	4.84E-01
A_24_P239676	-2.09	-1.36	-1.30	-1.65	-2.36	4.32E-02	5.07E-02	1.62E-01
A_23_P126266	-3.18	-1.25	-1.21	-1.68	-1.32	2.23E-02	3.97E-01	3.46E-01
A_23_P158976	2.49	1.85	1.18	1.32	1.23	6.76E-03	8.12E-03	2.35E-01
A_32_P111394	1.42	2.11	1.79	1.27	-1.17	2.69E-01	9.41E-04	3.98E-03
A_24_P219474	3.69	1.87	1.09	1.28	-1.09	5.16E-03	1.03E-02	6.61E-01
A_23_P44569	3.17	1.69	1.17	1.23	1.09	1.22E-03	1.20E-02	2.18E-01
A_23_P398947	1.93	1.65	1.03	1.87	1.23	2.25E-02	2.35E-02	8.62E-01
A_24_P238499	2.46	1.50	1.16	1.55	1.55	1.77E-02	2.01E-02	2.73E-01
A_23_P34644	-1.71	-1.99	1.14	-1.36	-1.87	8.60E-03	3.06E-03	1.28E-01
A_32_P84373	-1.78	-1.21	-1.74	-1.05	-2.03	6.14E-02	5.31E-01	6.11E-04
A_23_P54770	-2.28	-1.67	-1.11	1.11	-2.38	1.14E-02	4.02E-03	2.70E-01
A_23_P217277	1.68	1.81	-1.01	1.29	1.97	9.00E-02	7.49E-03	9.37E-01
A_24_P746314	1.87	2.23	1.04	1.25	1.36	1.23E-03	1.08E-03	7.34E-01
A_24_P71468	2.53	1.82	1.30	-1.19	1.57	9.79E-04	3.23E-05	1.02E-04
A_24_P370472	-1.93	-1.81	-1.01	-1.23	-1.82	9.06E-03	3.64E-03	8.90E-01
A_24_P132383	-1.20	-1.45	-1.48	-1.71	-1.13	3.51E-01	6.11E-04	4.21E-02
A_23_P427014	-1.51	-1.58	-1.27	1.01	-3.41	1.66E-01	1.09E-02	3.93E-02
A_32_P427222	-1.64	-1.32	-1.57	-1.17	-1.73	6.52E-03	8.74E-02	9.84E-02
A_23_P59877	1.44	1.01	1.37	1.90	1.79	1.64E-01	9.67E-01	1.13E-02
A_32_P121549	2.51	1.65	1.51	1.04	1.02	1.50E-03	9.76E-02	6.76E-02
A_24_P418998	-1.13	1.67	1.14	1.35	3.74	4.71E-01	3.93E-02	2.99E-01

A_24_P852756	-2.51	-1.97	1.04	-1.05	-1.67	1.25E-02	1.72E-03	6.58E-01
A_23_P311901	1.63	1.04	1.27	2.11	1.46	2.95E-02	8.53E-01	1.32E-01
A_23_P125717	-1.52	-1.10	-1.19	-1.62	-2.62	9.70E-02	3.29E-01	3.53E-01
A_24_P114124	-1.63	-1.48	-1.28	-1.27	-1.62	4.56E-02	1.01E-01	2.71E-01
A_24_P343233	-2.05	-1.82	-1.05	-1.29	-1.51	3.94E-03	1.82E-03	3.70E-01
A_23_P78092	-1.62	-2.32	-1.01	-1.39	-1.35	2.74E-02	9.82E-04	9.11E-01
A_32_P741851	1.44	1.09	1.19	1.42	3.28	1.95E-01	4.44E-01	2.54E-01
A_24_P332647	1.64	1.30	1.56	1.51	1.42	6.40E-02	2.44E-01	1.35E-02
A_24_P52168	-2.14	-1.89	-1.24	-1.19	-1.22	1.21E-02	5.92E-03	1.10E-01
A_23_P396934	2.50	1.23	1.30	1.54	1.53	5.36E-02	4.91E-01	2.03E-01
A_24_P231546	1.27	1.30	1.05	3.22	1.32	2.28E-02	1.54E-02	4.72E-01
A_23_P111583	1.71	1.21	1.08	1.59	2.56	9.51E-02	1.30E-01	6.39E-01
A_23_P402670	-2.37	-1.68	-1.03	-1.62	-1.26	1.41E-02	1.94E-02	8.06E-01
A_23_P258151	-1.24	-2.09	-1.07	-1.25	-2.19	2.97E-01	2.13E-03	5.72E-01
A_24_P925505	1.83	1.31	1.42	1.45	1.81	9.25E-02	1.62E-01	2.01E-01
A_23_P166269	-2.24	-1.20	-2.00	-1.10	-1.58	6.09E-02	6.81E-02	4.52E-03
A_23_P14853	1.94	2.67	1.29	1.24	-1.25	4.78E-03	4.93E-04	6.30E-02
A_32_P34167	-1.19	1.36	1.15	1.95	2.65	5.84E-01	3.36E-01	4.63E-01
A_23_P74547	-1.38	-2.01	-1.04	-1.29	-1.79	2.87E-01	2.87E-04	6.39E-01
A_23_P103765	-1.92	-1.53	1.00	-1.59	-1.63	2.01E-02	5.08E-03	9.50E-01
A_24_P673063	1.50	1.04	1.39	1.94	1.51	1.13E-01	8.00E-01	3.13E-03
A_24_P243528	-1.63	-1.76	1.05	-1.61	-1.61	8.15E-03	1.70E-02	5.77E-01
A_32_P114914	1.37	1.49	-1.08	1.36	2.74	8.66E-02	7.63E-03	5.57E-01
A_23_P145336	-2.03	-1.78	1.03	-1.42	-1.43	1.01E-02	5.30E-03	7.60E-01
A_23_P73097	1.79	1.02	1.16	1.74	2.25	1.19E-01	9.09E-01	3.62E-01
A_24_P576191	-1.32	-2.21	-1.10	-1.67	-1.07	1.88E-01	9.74E-03	6.70E-01
A_23_P4400	1.22	1.34	1.89	1.20	1.77	5.36E-01	1.45E-01	2.16E-02
A_32_P204676	1.53	1.06	1.49	1.82	1.42	9.54E-02	7.07E-01	1.34E-03
A_24_P871940	1.64	1.95	1.59	1.32	-1.15	1.78E-02	3.10E-02	3.03E-02
A_24_P927756	-1.36	-1.35	-1.25	-1.24	-3.41	1.47E-01	1.57E-01	5.31E-02
A_23_P343398	-2.12	-1.70	-1.43	1.44	-1.45	1.23E-02	7.13E-02	1.02E-01
A_24_P152845	1.38	1.15	1.04	2.24	1.88	4.76E-01	5.73E-01	8.61E-01
A_23_P90626	-1.95	-1.57	-1.09	-1.33	-1.69	1.67E-02	4.88E-03	4.16E-01
A_32_P106615	-1.43	-2.82	-1.02	-1.56	1.25	1.26E-01	9.39E-04	8.99E-01
A_23_P67339	-1.49	-1.60	-1.12	-1.54	-1.69	2.92E-02	8.42E-03	9.33E-02
A_23_P90470	1.43	1.14	1.24	1.45	2.35	1.69E-01	6.13E-01	1.68E-01
A_32_P212471	3.21	1.40	1.37	1.20	-1.10	9.83E-04	9.70E-02	1.47E-02
A_24_P935986	-1.39	-2.28	-1.20	-1.35	-1.18	1.73E-01	6.24E-04	1.06E-01
A_32_P14762	-1.47	-1.73	-1.23	-1.04	-1.42	2.76E-01	6.02E-02	5.28E-01
A_23_P252175	1.07	1.14	1.23	2.00	2.85	6.95E-01	4.38E-01	2.83E-01
A_23_P12549	-1.43	-2.15	-1.13	-1.30	-1.31	4.81E-02	2.86E-03	3.90E-01
A_24_P84340	1.52	1.10	1.57	1.66	1.71	5.71E-02	3.78E-01	2.21E-02
A_32_P158181	-1.83	-2.07	-1.32	-1.34	1.22	3.48E-02	1.90E-03	9.75E-02
A_23_P42784	-1.88	-1.01	-1.72	-1.47	1.13	2.73E-02	9.81E-01	3.29E-02
A_23_P215913	-1.33	-1.21	-1.02	-2.18	-1.71	2.16E-01	1.28E-01	8.46E-01
A_23_P404785	1.97	1.15	1.47	1.15	1.76	1.26E-03	1.01E-01	3.33E-04
A_23_P77908	2.59	1.22	1.96	1.03	-1.09	4.24E-03	9.23E-02	4.94E-04

A_32_P212886	2.14	-1.06	1.45	1.68	1.46	2.81E-02	7.41E-01	8.40E-03
A_23_P102731	1.55	1.24	1.13	1.56	2.09	1.17E-01	5.95E-02	1.65E-01
A_23_P217326	1.07	-1.14	-1.39	-1.99	-2.30	6.22E-01	7.78E-02	1.59E-02
A_24_P288836	-1.98	-1.72	-1.08	-1.23	-1.59	2.41E-02	3.28E-03	2.27E-01
A_23_P259901	1.08	1.28	1.82	1.86	1.27	7.59E-01	5.82E-02	2.14E-03
A_24_P270424	-1.61	-1.55	-2.34	1.27	-1.32	2.44E-02	7.87E-02	4.11E-04
A_32_P29083	-1.33	-1.20	-2.20	1.07	-2.07	2.21E-01	1.64E-01	2.66E-04
A_23_P39790	-2.48	-1.72	1.00	-1.16	-1.61	2.40E-02	1.06E-02	9.92E-01
A_24_P642758	-1.04	1.43	1.21	1.55	2.87	7.57E-01	1.13E-01	2.68E-01
A_23_P70095	-1.95	-1.82	-1.06	-1.36	-1.26	8.03E-03	2.69E-02	4.66E-01
A_23_P166087	-1.67	-1.79	-1.07	-1.42	-1.40	2.06E-02	2.20E-03	3.83E-01
A_23_P160286	-1.37	1.00	-1.56	-2.19	-1.40	3.55E-01	9.92E-01	3.32E-02
A_23_P104493	-1.62	-2.17	-1.45	1.04	-1.37	1.14E-01	1.39E-02	3.14E-03
A_24_P216654	1.33	1.30	2.55	-1.59	1.61	4.08E-01	1.34E-01	8.89E-03
A_24_P935330	-1.81	-1.92	-1.26	-1.12	-1.25	2.84E-02	2.85E-03	3.95E-02
A_23_P35444	1.27	1.00	2.11	1.88	1.10	4.40E-01	9.76E-01	3.45E-04
A_24_P919283	1.16	2.09	1.03	1.73	1.48	1.64E-01	2.52E-03	6.12E-01
A_32_P49552	-1.65	-1.08	-1.51	-1.11	-2.87	1.40E-01	7.18E-01	1.03E-01
A_23_P135164	1.05	1.64	2.02	1.06	1.52	7.48E-01	2.90E-03	1.19E-04
A_23_P3681	1.15	1.01	2.06	1.63	1.47	6.45E-01	8.79E-01	4.10E-04
A_24_P822692	-1.28	-1.49	-1.39	-1.20	-2.07	5.84E-01	3.85E-02	3.17E-02
A_24_P91991	2.20	1.60	1.15	1.65	-1.01	2.53E-02	1.58E-01	5.00E-01
A_24_P206343	-1.99	-1.51	-1.12	1.04	-1.90	3.93E-02	6.86E-03	6.30E-01
A_23_P351667	2.13	1.46	1.20	2.35	-1.28	4.15E-02	2.35E-02	1.78E-01
A_23_P159986	1.25	1.47	1.47	1.76	1.39	1.61E-01	3.08E-02	9.83E-02
A_24_P92267	2.29	-1.05	1.11	1.46	2.12	5.37E-02	8.51E-01	6.74E-01
A_24_P365526	-1.83	-1.46	1.00	-1.30	-1.72	1.58E-03	2.06E-04	9.95E-01
A_23_P10506	-2.73	-1.43	-1.13	-1.36	-1.20	2.89E-03	1.18E-03	1.23E-01
A_32_P163858	1.69	1.75	1.10	1.15	1.60	1.19E-02	2.67E-02	5.09E-01
A_23_P29953	-1.38	-1.51	-1.18	-1.40	-1.07	2.44E-01	5.22E-03	4.12E-01
A_24_P354800	-1.66	-1.86	-1.01	-1.36	-1.38	1.43E-02	1.91E-03	8.79E-01
A_23_P85800	-1.82	-1.71	-1.12	1.02	-1.75	3.25E-02	5.06E-03	2.45E-01
A_23_P311346	2.08	-1.06	1.03	1.54	1.90	4.46E-02	7.85E-01	9.00E-01
A_23_P380754	2.08	1.37	-1.14	1.43	1.95	4.40E-02	2.57E-01	5.39E-01
A_23_P39871	1.68	-1.00	1.15	1.40	2.57	9.81E-02	9.93E-01	2.96E-01
A_23_P42306	-1.91	-1.67	-1.02	-1.10	-1.62	1.60E-04	4.41E-03	7.44E-01
A_23_P21907	-2.42	-1.52	-1.19	-1.33	-1.08	5.13E-03	7.35E-04	1.39E-01
A_23_P144980	-1.64	-1.45	-1.14	-1.72	-1.53	5.63E-02	1.46E-01	3.48E-01
A_23_P302654	2.17	1.37	1.37	-1.07	1.64	2.75E-03	3.05E-02	1.04E-02
A_24_P40626	-1.71	-1.10	-1.63	-1.71	1.25	2.41E-02	6.48E-01	3.38E-02
A_23_P352950	1.58	1.46	1.21	1.71	1.18	4.80E-03	2.56E-03	2.24E-02
A_23_P24260	-1.32	-1.67	1.11	-1.63	-1.75	2.36E-01	5.02E-03	4.41E-01
A_32_P34920	-1.31	-1.44	-1.53	-1.34	-1.29	3.50E-01	3.66E-02	3.24E-02
A_23_P377957	-1.58	-1.28	1.00	-1.55	-1.73	3.99E-03	9.27E-02	9.78E-01
A_23_P30913	-1.75	-1.91	1.09	-1.23	-1.50	8.38E-04	3.90E-03	1.08E-01
A_32_P223173	1.99	-1.02	1.05	1.73	1.55	2.72E-02	9.47E-01	7.16E-01
A_23_P45099	-2.04	-1.91	1.01	-1.21	-1.27	6.04E-03	9.74E-03	9.06E-01

A_23_P26976	-2.15	-1.63	-1.13	-1.10	-1.39	5.01E-03	1.22E-03	2.46E-01
A_23_P110791	-2.45	-1.47	1.00	-1.16	-1.53	3.32E-03	2.67E-03	9.94E-01
A_23_P112798	-1.32	-1.17	-1.17	-1.80	-1.81	1.14E-01	5.10E-02	1.54E-01
A_23_P502706	1.59	2.47	-1.17	1.16	1.23	1.21E-02	3.48E-03	5.45E-01
A_32_P107876	1.04	1.23	1.42	2.21	1.37	6.70E-01	5.50E-02	2.34E-04
A_24_P303480	2.50	1.58	1.18	1.02	1.27	1.56E-03	6.28E-03	3.12E-02
A_24_P666035	-1.44	-1.30	-1.19	-1.24	-2.22	3.66E-02	1.44E-01	1.90E-02
A_23_P3014	-1.75	-1.77	-1.17	-1.22	-1.21	3.39E-02	9.03E-03	2.96E-01
A_24_P381499	-1.36	-1.47	-1.08	-1.70	-1.61	1.40E-01	1.47E-01	5.90E-01
A_24_P350786	1.51	1.20	1.11	1.38	2.07	1.30E-01	4.34E-01	5.45E-01
A_32_P181443	-1.84	-1.32	-1.16	-1.14	-2.12	1.42E-01	2.23E-01	3.70E-01
A_23_P131834	1.20	1.48	-1.04	1.62	2.30	4.34E-01	5.39E-02	8.74E-01
A_23_P27994	-1.87	-1.64	-1.12	-1.02	-1.60	1.08E-02	4.05E-03	1.42E-01
A_32_P87697	-1.76	-2.00	1.01	-1.23	-1.39	2.05E-02	8.02E-03	8.91E-01
A_23_P127727	-1.49	-1.40	-1.56	-1.05	-1.39	5.94E-02	1.56E-01	1.25E-02
A_24_P170454	1.82	1.15	1.06	1.62	1.57	8.83E-03	3.62E-01	3.67E-01
A_23_P160881	-1.79	-1.98	-1.10	-1.12	-1.23	4.22E-02	1.21E-02	6.01E-01
A_32_P214665	1.16	1.23	2.32	1.27	1.21	5.15E-01	2.96E-01	9.44E-04
A_23_P53137	-1.28	-1.56	-2.31	-1.03	-1.64	5.83E-01	3.79E-01	3.63E-02
A_23_P217704	1.68	1.71	1.08	1.03	1.38	6.15E-02	1.27E-02	7.72E-01
A_23_P42975	-1.14	-1.81	-1.06	-1.45	-1.83	6.24E-01	5.27E-02	7.55E-01
A_23_P17955	1.38	1.21	1.62	-1.10	2.38	3.98E-02	5.17E-01	1.12E-02
A_24_P75994	-1.20	-1.54	-1.08	1.05	-3.05	4.13E-01	1.25E-03	6.29E-01
A_23_P151895	-1.24	-1.32	-1.31	-1.88	-1.09	3.58E-01	3.16E-01	5.42E-02
A_24_P175707	1.39	1.24	1.46	1.30	1.76	2.58E-01	2.99E-01	1.58E-02
A_23_P254212	1.09	1.63	-1.13	1.89	1.08	7.79E-01	8.16E-03	7.01E-01
A_23_P324706	-1.59	-1.13	-1.64	-1.05	-1.87	1.06E-01	4.85E-01	1.44E-04
A_23_P164057	-1.41	-1.12	-1.08	-1.94	-1.45	2.53E-01	7.09E-01	5.19E-01
A_23_P161352	2.40	1.82	1.22	-1.06	1.10	2.68E-03	4.17E-04	4.41E-02
A_23_P58557	-1.02	-1.57	-1.30	-1.73	-1.06	9.55E-01	1.17E-01	3.00E-01
A_24_P339126	1.71	1.10	1.22	2.76	-1.00	1.52E-01	6.41E-01	3.79E-01
A_32_P220463	1.77	1.79	1.84	1.17	-1.73	5.91E-03	1.87E-02	4.81E-03
A_23_P21495	-2.86	-1.85	1.02	-1.03	-1.38	8.93E-03	1.17E-02	8.03E-01
A_24_P879740	-1.76	-1.56	-1.03	-1.51	-1.30	3.70E-02	1.45E-02	7.88E-01
A_24_P380628	-1.14	-1.36	-1.19	-1.58	-1.73	3.31E-01	7.18E-03	1.04E-01
A_24_P16337	-1.39	-1.11	-1.75	-1.25	-1.60	4.45E-01	6.98E-01	3.88E-02
A_23_P117851	1.72	-1.25	1.27	1.34	2.18	1.16E-01	4.49E-01	1.84E-01
A_23_P388168	-1.30	-1.44	-1.33	-1.60	1.01	3.57E-01	1.77E-02	8.35E-02
A_23_P416468	1.81	-1.23	1.27	1.56	1.42	1.48E-01	6.16E-01	1.93E-01
A_23_P202361	1.44	1.14	1.20	1.61	1.63	1.29E-01	2.79E-01	3.70E-01
A_24_P33895	-1.36	-1.73	-1.02	1.08	-2.65	6.15E-02	4.11E-03	8.76E-01
A_24_P546043	1.21	-1.11	1.30	1.82	1.78	5.46E-01	6.41E-01	7.25E-02
A_24_P345866	1.30	1.06	1.46	1.49	1.47	3.39E-01	7.72E-01	4.07E-02
A_24_P63290	1.42	-1.10	1.37	1.71	1.76	3.65E-02	5.14E-01	1.35E-01
A_24_P845223	-2.06	-1.74	-1.09	-1.28	1.17	2.14E-02	1.89E-03	2.46E-01
A_23_P103617	1.68	-1.13	1.13	1.79	1.78	1.16E-01	5.30E-01	3.59E-01
A_23_P210158	2.15	1.18	-1.12	2.00	1.20	1.05E-02	1.32E-01	4.29E-01

A_23_P46356	-1.62	-2.15	-1.24	1.05	-1.17	4.37E-02	5.59E-04	5.04E-02
A_32_P188193	-1.01	1.18	1.03	1.91	2.53	9.15E-01	3.09E-01	8.18E-01
A_23_P257542	-1.88	-1.38	-1.36	-1.03	-1.45	4.83E-02	9.53E-03	1.18E-01
A_23_P119634	1.25	1.06	1.34	2.46	1.42	4.71E-01	4.40E-01	1.47E-01
A_23_P143334	-1.64	-1.58	-1.24	-1.16	-1.44	2.13E-02	1.27E-02	4.88E-02
A_24_P50245	-1.78	-1.68	1.07	-1.20	-1.54	1.47E-03	1.02E-02	4.19E-01
A_24_P930796	-1.65	-1.35	-1.26	-1.50	-1.07	9.59E-02	3.14E-02	2.79E-01
A_23_P105144	1.18	1.54	1.21	1.51	1.43	2.13E-01	1.23E-03	5.60E-02
A_23_P106629	-1.48	-1.54	-1.42	-1.37	-1.06	1.29E-01	2.69E-02	8.14E-02
A_24_P924752	2.06	-1.11	-1.01	1.42	1.82	3.58E-02	7.62E-01	9.58E-01
A_23_P118122	1.31	1.27	1.11	1.79	1.92	1.61E-01	9.85E-02	3.61E-01
A_24_P85243	-1.51	-1.36	-1.29	-1.02	-2.44	2.45E-02	1.61E-02	1.52E-01
A_32_P31832	1.15	1.63	1.22	1.33	1.48	4.29E-01	4.00E-03	9.14E-02
A_23_P109488	-1.31	-1.18	-1.21	-1.20	-2.59	8.81E-02	1.71E-01	6.71E-02
A_23_P51136	-1.21	-1.56	-1.12	-1.11	-2.38	5.40E-02	3.04E-04	2.90E-01
A_23_P86283	-1.61	-1.55	1.03	-1.35	-1.62	2.75E-02	5.59E-02	6.70E-01
A_24_P367454	1.54	1.57	1.11	1.32	-1.05	2.49E-02	3.48E-02	5.82E-01
A_23_P202013	-1.32	-1.24	-1.16	-2.19	-1.11	4.45E-01	2.66E-01	2.83E-01
A_32_P231415	1.27	1.88	1.17	1.13	1.49	4.12E-01	1.19E-02	3.33E-01
A_23_P148584	1.07	-1.38	-1.31	-1.88	-1.31	8.05E-01	2.44E-01	3.68E-01
A_23_P159335	-1.42	-1.44	-1.28	1.14	-2.02	5.68E-03	4.93E-02	4.38E-02
A_23_P401700	-1.25	-1.98	-1.17	-1.17	-1.26	2.14E-01	1.56E-05	3.27E-01
A_23_P208182	-1.45	-1.78	1.00	-1.37	-1.38	7.85E-02	6.49E-03	9.93E-01
A_23_P96556	1.70	1.03	1.86	1.27	1.26	2.81E-02	7.87E-01	2.00E-03
A_32_P187320	1.39	1.10	1.31	1.38	2.10	2.12E-01	7.80E-01	7.06E-02
A_23_P329271	1.63	1.82	1.15	1.19	1.16	1.83E-03	1.12E-03	7.99E-02
A_23_P151805	-1.39	-1.13	-1.24	-1.65	-1.50	1.95E-01	3.73E-01	2.33E-02
A_24_P232158	-1.30	-1.11	-1.47	-1.42	-1.61	1.52E-01	4.91E-01	1.01E-02
A_23_P501232	2.16	1.36	1.32	1.16	1.05	8.52E-05	2.77E-02	3.87E-04
A_23_P416711	2.51	1.77	1.12	1.11	1.04	4.97E-03	1.02E-01	4.03E-01
A_24_P322474	-1.64	-1.58	-1.09	-1.10	-1.61	1.89E-03	1.01E-03	2.14E-01
A_23_P22013	-1.63	-1.11	-1.34	-1.40	-1.37	6.03E-02	5.98E-01	1.30E-01
A_23_P113777	-1.63	1.03	-1.28	-1.73	-1.17	7.96E-02	8.97E-01	9.37E-02
A_32_P113322	-1.69	-1.21	-1.23	-1.38	-1.71	5.74E-02	2.21E-01	1.85E-01
A_32_P159176	1.01	1.49	-1.05	1.59	2.12	9.04E-01	4.72E-03	4.87E-01
A_23_P372946	1.41	1.58	-1.06	1.43	1.62	1.19E-01	2.42E-02	7.34E-01
A_23_P1682	1.11	1.40	1.04	1.85	1.57	6.28E-01	6.22E-02	6.44E-01
A_24_P307395	-1.26	-1.25	-1.11	-2.29	-1.30	5.98E-01	6.42E-02	6.53E-01
A_23_P400041	-1.06	1.82	1.29	1.31	2.23	6.09E-01	8.38E-02	1.60E-01
A_23_P348524	1.61	1.20	-1.23	1.61	1.98	5.65E-02	1.67E-01	2.15E-01
A_23_P360209	-1.35	-1.70	-1.05	-1.25	-1.67	1.66E-01	3.89E-03	5.53E-01
A_23_P67042	1.33	1.12	1.18	1.82	1.45	1.25E-01	2.76E-01	1.86E-01
A_23_P60146	-1.60	-1.42	-1.24	-1.84	1.03	1.60E-01	1.33E-01	1.16E-01
A_23_P200138	-2.22	-1.50	-1.18	1.07	-1.47	1.01E-02	5.59E-03	1.11E-01
A_24_P29733	-1.39	-1.81	1.03	-1.58	-1.20	4.64E-02	1.93E-02	8.41E-01
A_32_P139367	-1.02	-1.89	-1.21	-1.07	-2.04	9.53E-01	3.24E-02	3.38E-01
A_23_P421423	-1.79	-1.90	-1.14	-1.01	-1.17	8.35E-03	1.31E-03	1.41E-01

A_24_P119665	-1.38	-1.56	-1.18	-1.13	-1.84	1.84E-01	4.71E-02	2.26E-01
A_23_P121665	1.60	1.00	1.09	1.45	2.14	1.16E-01	9.94E-01	7.43E-01
A_24_P348006	-1.24	-1.45	1.04	-1.69	-1.52	3.91E-01	1.53E-02	8.11E-01
A_32_P220591	1.33	1.43	1.46	1.31	1.20	3.48E-01	1.62E-01	2.53E-01
A_24_P59387	-1.03	1.30	1.12	1.99	1.75	7.70E-01	9.97E-03	3.78E-01
A_24_P153568	-1.48	-1.89	-1.16	-1.30	-1.07	4.84E-02	5.16E-03	1.91E-01
A_23_P303286	1.01	-1.26	-1.92	-1.13	-1.67	9.76E-01	3.51E-01	7.72E-03
A_23_P66095	1.63	1.58	1.38	1.13	-1.30	2.32E-02	9.93E-04	2.25E-01
A_24_P253100	-1.16	-1.43	-1.60	-1.24	-1.37	5.71E-01	5.54E-02	4.24E-03
A_23_P158318	-1.30	-1.09	-1.44	-1.98	-1.14	1.09E-01	3.39E-01	1.42E-03
A_23_P140748	1.07	1.19	1.96	1.38	1.35	4.23E-01	6.52E-02	4.91E-06
A_24_P326084	-2.06	-1.57	-1.13	-1.15	-3.17	1.62E-01	3.97E-03	4.47E-01
A_32_P203749	1.29	1.65	1.10	-1.12	2.32	7.22E-02	1.84E-03	2.64E-01
A_23_P101908	1.41	1.14	1.69	1.37	1.25	3.53E-02	4.99E-01	1.63E-02
A_24_P390668	-1.64	-1.64	-1.00	-1.09	-1.61	1.87E-02	5.61E-03	9.68E-01
A_24_P637651	-2.06	-1.72	-1.04	1.01	-1.29	7.47E-03	2.21E-04	6.10E-01
A_24_P51115	-1.87	-1.63	-1.35	-1.04	-1.21	5.67E-02	3.71E-02	1.54E-01
A_32_P42253	-1.08	1.32	1.18	1.24	2.98	6.69E-01	4.86E-02	1.20E-01
A_23_P169460	1.66	1.05	1.47	1.41	1.74	1.21E-01	7.42E-01	2.95E-02
A_23_P408323	1.12	1.42	1.25	1.20	2.31	6.34E-01	2.51E-02	2.40E-01
A_23_P141394	1.47	1.53	1.11	1.05	2.16	1.51E-02	6.64E-03	9.81E-02
A_23_P119202	-1.79	-1.93	-1.19	-1.29	1.15	1.01E-01	3.47E-02	3.13E-01
A_24_P328504	-1.99	-1.72	-1.18	1.04	-1.20	7.67E-03	6.36E-03	8.75E-02
A_24_P320727	-1.12	-1.48	-1.06	-1.40	-1.84	7.33E-01	3.40E-01	8.09E-01
A_32_P88555	1.25	1.29	1.32	1.74	1.15	1.81E-01	3.15E-01	4.83E-02
A_23_P366726	1.23	-1.06	1.50	1.65	1.85	2.43E-01	6.26E-01	2.61E-02
A_24_P229884	-1.41	-1.25	-1.38	1.27	-2.40	6.83E-02	1.14E-01	7.58E-02
A_23_P55682	-1.14	-1.27	-1.49	-1.47	-1.25	3.66E-01	3.05E-02	1.03E-04
A_24_P548966	-1.48	-1.24	-1.08	-2.01	-1.24	1.90E-01	3.46E-02	4.84E-01
A_23_P370782	1.95	1.64	1.19	1.06	-1.13	2.91E-03	3.67E-03	1.73E-01
A_23_P131846	-1.10	-1.66	-1.06	-1.26	-1.57	6.54E-01	1.00E-02	8.17E-01
A_23_P83579	1.71	1.71	1.07	1.13	1.22	5.40E-04	6.48E-04	2.28E-01
A_23_P150343	-1.50	-1.78	-1.34	-1.06	-1.50	3.53E-01	8.38E-02	2.47E-01
A_23_P64828	1.54	1.13	1.38	1.35	1.42	8.11E-02	5.50E-01	1.07E-01
A_23_P66694	-2.10	-1.81	-1.11	1.01	-1.16	1.53E-02	2.43E-02	3.88E-01
A_24_P671875	-1.19	-2.01	-1.33	-1.14	-1.27	5.05E-01	1.54E-02	1.13E-01
A_23_P150379	1.16	1.29	1.20	1.53	2.00	4.65E-01	2.67E-01	9.32E-02
A_23_P71570	-1.50	-1.07	-1.30	-1.51	-1.17	7.95E-02	7.85E-01	3.25E-02
A_32_P377880	1.59	1.04	1.86	-1.03	1.36	5.63E-02	8.96E-01	6.39E-03
A_23_P204847	-1.58	-1.69	-1.10	-1.09	-1.36	2.65E-02	2.42E-04	8.33E-02
A_32_P156851	-1.23	-1.02	-1.41	-1.39	-1.93	4.42E-01	9.22E-01	1.97E-03
A_23_P209678	-1.74	-1.85	1.06	-1.05	-1.36	8.90E-02	2.60E-02	7.89E-01
A_23_P115998	-1.60	-1.65	-1.34	1.13	-1.26	1.78E-01	8.00E-03	9.30E-02
A_23_P84910	-1.54	-1.37	-1.21	-1.21	-1.65	1.07E-01	1.06E-01	2.10E-01
A_24_P166527	-1.50	-1.48	-1.57	1.15	-1.57	1.80E-01	1.74E-02	2.76E-02
A_23_P206585	-1.82	-1.42	-1.27	-1.05	-1.37	3.58E-03	1.27E-02	1.33E-04
A_23_P116195	-1.43	-1.38	-1.21	-1.26	-1.41	2.72E-01	1.08E-02	3.24E-01

A_23_P42695	1.64	1.27	1.32	1.26	2.09	1.24E-01	5.61E-02	7.53E-04
A_23_P306987	1.18	1.17	1.82	1.15	1.37	3.95E-01	2.94E-01	8.08E-05
A_24_P416489	-1.20	-1.92	-1.44	-1.07	-1.63	4.94E-01	1.40E-01	8.12E-02
A_23_P201587	1.86	1.18	-1.00	1.31	1.99	1.29E-02	1.09E-01	9.70E-01
A_24_P551842	-1.45	-2.06	-1.05	-1.29	-1.08	1.39E-02	1.35E-04	4.25E-01
A_24_P203315	-1.15	1.24	1.12	1.57	2.70	6.22E-01	8.20E-02	3.33E-01
A_23_P43476	1.57	1.32	1.01	1.53	1.53	2.73E-02	7.57E-02	9.34E-01
A_23_P116114	1.57	1.17	1.09	1.24	1.54	4.60E-02	6.05E-01	7.62E-01
A_32_P351968	-2.08	-1.52	1.04	-1.10	-1.49	5.33E-03	1.23E-02	4.39E-01
A_24_P128442	-1.06	-1.34	-1.17	-1.56	-1.41	8.09E-01	2.22E-01	1.72E-01
A_23_P22660	-1.59	-1.15	-1.83	-1.09	-1.20	1.44E-02	6.86E-02	4.71E-05
A_32_P489662	1.57	-1.04	1.91	1.63	1.43	4.46E-01	8.45E-01	4.20E-02
A_23_P405815	-1.57	-1.13	-1.22	-1.87	-1.14	2.87E-02	4.36E-01	2.89E-01
A_24_P114142	-1.38	-1.18	-1.47	-1.34	-1.35	1.15E-01	4.00E-01	4.15E-02
A_32_P154053	1.27	1.35	1.41	1.25	1.38	2.10E-01	8.89E-02	1.98E-02
A_23_P327451	1.49	1.23	1.07	1.25	2.17	6.17E-02	1.04E-01	5.61E-01
A_23_P46426	-1.17	-1.68	-1.04	-1.22	-1.73	4.23E-01	1.39E-03	8.07E-01
A_23_P348636	-1.13	1.05	-1.29	-2.13	-1.47	5.05E-01	7.74E-01	2.37E-02
A_23_P501985	-1.25	-1.86	-1.08	-1.23	-1.19	4.81E-01	5.64E-03	6.29E-01
A_24_P585770	-1.08	-1.50	-1.90	-1.18	-1.14	6.39E-01	6.63E-02	2.96E-03
A_23_P348208	1.49	1.03	1.27	1.73	1.28	3.09E-01	8.70E-01	1.05E-01
A_32_P119949	-1.00	1.47	1.02	1.76	1.71	9.88E-01	1.51E-02	8.69E-01
A_23_P76136	-1.42	1.20	-1.24	-1.46	-2.15	1.34E-01	4.76E-01	7.61E-02
A_23_P17914	1.16	-1.04	1.24	1.42	2.59	4.98E-01	7.85E-01	8.80E-02
A_23_P253536	1.35	1.32	1.03	1.48	1.89	1.47E-01	7.37E-02	8.66E-01
A_23_P17053	1.65	1.09	-1.19	1.69	2.28	1.89E-01	2.09E-03	1.94E-01
A_23_P6535	1.79	1.09	1.01	1.41	2.58	1.21E-01	3.94E-01	9.20E-01
A_23_P16632	-1.29	-1.18	-1.52	1.05	-1.53	3.15E-01	4.12E-01	4.69E-03
A_23_P169738	1.06	1.11	1.87	1.45	1.27	6.84E-01	3.52E-01	1.44E-05
A_23_P135079	1.93	1.07	-1.06	1.57	1.44	2.75E-03	5.08E-01	4.61E-01
A_24_P710024	-1.21	-1.43	-1.01	-1.15	-2.23	3.89E-01	7.53E-03	8.90E-01
A_23_P3911	-1.30	-1.09	-1.28	-1.41	-1.97	2.28E-02	3.56E-01	1.73E-02
A_23_P43337	-1.14	-1.68	-1.01	-1.52	-1.56	5.01E-01	2.58E-02	8.25E-01
A_24_P659836	1.59	-1.02	1.44	1.66	1.19	4.91E-02	8.84E-01	3.96E-02
A_24_P109524	1.36	1.63	1.05	1.66	-1.03	1.73E-01	4.53E-03	7.20E-01
A_24_P315306	-1.60	-1.24	1.01	-1.54	-1.45	2.11E-02	1.85E-01	8.47E-01
A_32_P171530	-1.30	-1.38	-1.63	-1.06	-1.51	2.22E-01	1.16E-01	5.25E-03
A_32_P117354	-1.55	-1.35	-1.19	-1.33	-1.19	2.64E-04	1.86E-02	9.35E-03
A_24_P413669	1.87	1.13	1.08	1.42	1.35	7.69E-03	3.78E-01	5.09E-01
A_23_P382081	-1.26	-1.43	-1.15	-1.34	-1.34	4.47E-02	4.37E-03	2.83E-01
A_23_P205489	1.45	1.45	1.20	1.43	1.41	4.66E-02	2.06E-02	2.25E-02
A_23_P52067	1.59	1.43	1.18	1.51	1.11	4.48E-02	1.59E-02	6.19E-02
A_23_P161507	-1.22	-1.65	-1.15	-1.37	-1.32	1.47E-01	2.20E-02	4.88E-01
A_23_P57829	-1.45	-1.12	-1.14	-1.49	-1.53	1.63E-01	4.58E-01	3.88E-01
A_24_P137713	1.55	1.03	1.21	1.33	2.06	3.08E-02	8.55E-01	4.31E-01
A_24_P370946	-1.10	-1.64	-1.05	-1.29	-1.81	5.34E-01	2.94E-03	7.50E-01
A_24_P925186	-1.15	-1.07	-1.30	-1.52	-1.31	5.68E-01	6.66E-01	5.27E-02

A_23_P26024	-1.24	-1.66	-1.08	1.15	-2.27	1.68E-01	3.32E-04	5.61E-01
A_23_P369210	1.39	1.13	1.13	1.71	1.60	1.20E-01	6.03E-01	3.25E-01
A_23_P128609	1.24	-1.02	1.45	1.50	1.17	2.36E-01	9.24E-01	4.51E-02
A_23_P424637	-1.28	-1.34	-1.03	-1.26	-1.91	1.29E-01	5.65E-02	7.27E-01
A_23_P81262	-1.89	-1.20	-1.08	-1.17	-1.57	6.43E-03	1.99E-01	6.86E-01
A_23_P34325	1.39	1.12	1.31	1.19	2.46	2.86E-01	3.75E-01	9.99E-02
A_23_P217972	1.51	1.18	-1.02	1.79	1.45	4.69E-02	2.14E-01	8.00E-01
A_32_P9753	1.30	1.31	1.23	1.69	1.12	3.07E-02	4.47E-02	2.73E-02
A_24_P404840	1.61	1.47	1.58	1.01	-1.04	5.08E-02	1.99E-02	2.00E-03
A_32_P233735	1.64	1.33	1.28	1.26	1.36	2.13E-01	3.08E-01	1.99E-01
A_23_P44264	-1.32	-1.15	-1.79	-1.53	1.08	1.40E-02	2.31E-01	2.43E-05
A_32_P235358	1.36	-1.09	1.16	1.59	1.88	1.34E-01	5.13E-01	1.74E-01
A_24_P784846	1.15	1.38	1.04	1.25	2.19	3.23E-01	1.49E-02	8.36E-01
A_23_P5903	1.52	1.40	1.07	1.30	1.52	2.09E-02	6.75E-03	2.14E-01
A_23_P145889	-1.94	-1.37	-1.06	-1.61	1.09	5.53E-02	1.99E-01	6.85E-01
A_24_P921546	-1.11	-1.25	-1.52	-1.08	-2.18	8.04E-01	3.89E-01	8.27E-02
A_23_P304897	1.32	1.31	1.06	1.34	1.91	9.46E-02	1.33E-02	3.87E-01
A_32_P228625	1.22	1.45	-1.02	1.57	1.62	2.43E-01	6.85E-02	8.74E-01
A_24_P358137	-1.41	-1.19	-1.09	-1.35	-1.64	1.37E-02	2.41E-01	4.33E-01
A_24_P323974	2.31	1.07	-1.02	1.32	1.45	9.16E-03	7.44E-01	8.94E-01
A_32_P8732	1.19	1.58	1.19	1.37	1.41	2.90E-01	8.85E-03	3.25E-02
A_23_P65618	1.32	1.04	1.06	1.64	1.58	2.25E-01	8.91E-01	4.33E-01
A_23_P29975	1.20	1.40	1.03	1.45	1.92	1.88E-01	2.79E-02	9.07E-01
A_24_P33667	-1.36	-1.01	-1.09	-1.36	-2.56	1.97E-01	9.38E-01	5.61E-01
A_23_P216340	-1.98	-1.80	-1.15	-1.08	1.07	6.43E-03	1.03E-03	9.30E-02
A_24_P203000	-1.35	-1.48	-1.50	-1.05	1.12	1.22E-01	1.22E-02	2.43E-03
A_23_P407206	1.29	1.05	1.34	1.44	1.59	1.66E-01	7.65E-01	8.70E-02
A_23_P88626	-1.34	-1.39	-1.10	-1.52	-1.32	3.89E-01	7.19E-02	4.70E-01
A_23_P402254	1.03	-1.02	1.60	1.43	2.18	8.92E-01	8.89E-01	9.22E-03
A_23_P256107	1.82	-1.03	1.11	1.70	1.50	2.13E-01	8.70E-01	5.95E-01
A_23_P302568	1.31	1.13	1.24	1.42	1.50	2.47E-01	6.56E-01	2.13E-01
A_32_P128209	1.13	1.52	1.45	1.21	1.61	3.95E-01	6.70E-02	2.53E-02
A_23_P434809	1.38	1.11	1.46	1.86	-1.06	5.94E-01	6.50E-01	1.34E-01
A_32_P140139	-1.15	-1.10	-1.22	-2.09	-1.29	5.20E-01	4.75E-01	1.59E-01
A_24_P124550	-1.60	-1.24	-1.24	-1.10	-1.74	5.29E-02	3.24E-02	4.96E-02
A_23_P168388	-1.14	-1.27	-1.32	-1.62	-1.08	2.63E-01	3.33E-03	1.10E-01
A_23_P420281	-1.58	-1.39	1.03	-1.14	-1.27	6.60E-03	2.24E-02	8.74E-01
A_23_P50946	-1.28	-1.49	-1.03	-1.05	-2.27	1.70E-01	8.79E-02	7.82E-01
A_32_P468743	-1.38	-1.02	-1.49	-1.11	-1.18	1.29E-01	9.49E-01	1.09E-02
A_24_P540560	-1.01	-1.20	-1.05	-1.75	-1.79	9.78E-01	2.73E-01	6.89E-01
A_32_P147063	1.35	1.48	1.24	-1.13	1.76	2.65E-03	2.69E-03	1.44E-02
A_23_P38959	-1.46	-1.70	-1.11	-1.06	-1.42	5.51E-02	1.16E-02	3.50E-01
A_24_P334529	-1.29	-1.16	-1.49	-1.10	-1.53	1.65E-01	4.04E-01	5.17E-03
A_23_P42375	2.17	1.57	1.12	-1.00	1.13	2.61E-03	2.47E-03	7.87E-02
A_23_P118894	-2.21	-1.38	-1.38	1.07	-1.27	7.42E-02	1.13E-01	1.51E-01
A_24_P922252	1.02	1.26	1.01	1.77	1.82	9.26E-01	1.82E-01	9.33E-01
A_32_P224751	1.26	1.29	1.28	1.15	2.04	2.55E-01	2.27E-01	1.33E-01

A_24_P332461	1.24	1.08	1.10	1.48	1.96	1.73E-01	7.48E-01	5.52E-01
A_23_P166297	1.33	1.37	1.17	1.18	1.64	1.40E-01	2.54E-02	1.57E-01
A_24_P578437	-1.56	-1.78	-1.05	-1.19	-1.32	6.86E-02	1.74E-02	5.09E-01
A_32_P94444	1.14	1.30	-1.03	1.71	1.69	4.81E-01	1.33E-01	7.24E-01
A_23_P139166	-2.22	-1.16	-1.52	1.03	-1.47	8.39E-02	5.55E-01	1.31E-01
A_23_P203900	1.43	1.72	1.15	1.10	1.21	1.18E-03	1.85E-04	1.97E-02
A_24_P350656	1.27	1.00	1.48	1.33	1.33	2.70E-01	9.82E-01	9.85E-03
A_23_P407565	-1.44	-1.52	1.05	-1.36	-1.46	9.18E-04	3.66E-02	5.56E-01
A_23_P209116	1.36	1.10	1.32	1.50	1.32	7.54E-02	5.87E-01	6.26E-02
A_23_P213288	-1.39	-1.07	-1.54	-1.19	-1.67	1.23E-01	5.11E-01	2.05E-02
A_23_P157766	1.28	-1.01	1.21	1.11	2.74	1.56E-01	9.75E-01	2.37E-01
A_23_P51339	1.06	-1.63	-1.21	-1.44	-1.51	6.30E-01	2.77E-03	6.96E-02
A_24_P934832	-1.38	-1.10	1.01	-1.44	-1.76	1.45E-01	7.72E-01	9.76E-01
A_23_P46141	-1.27	-1.42	-1.06	-1.40	-1.57	8.91E-02	2.99E-02	4.18E-01
A_24_P150160	1.16	1.29	2.23	-1.38	1.15	7.81E-01	1.93E-01	4.67E-02
A_23_P98477	-1.19	-1.20	-1.14	-1.41	-1.58	3.32E-01	1.77E-01	2.67E-01
A_32_P70875	-1.16	1.92	1.16	1.31	1.52	2.91E-01	1.15E-03	5.02E-02
A_24_P892612	1.43	-1.28	-1.43	-1.53	-1.35	3.37E-01	1.58E-01	7.93E-02
A_23_P500300	1.32	1.10	1.23	1.57	-1.07	5.14E-01	7.05E-01	4.82E-01
A_23_P85250	1.34	1.26	1.27	1.68	1.04	1.83E-01	6.00E-02	2.04E-02
A_23_P13048	1.89	1.18	1.16	1.35	1.11	9.40E-03	3.66E-01	4.02E-01
A_23_P169030	2.00	1.14	1.44	1.24	1.28	2.20E-02	1.91E-01	2.84E-02
A_23_P399078	-1.44	-1.14	1.00	-1.81	-1.34	1.11E-01	2.36E-01	9.98E-01
A_32_P172141	-1.35	-1.64	-1.16	-1.33	-1.01	2.52E-02	5.27E-03	1.04E-02
A_24_P194688	-1.62	-1.05	-1.44	-1.28	1.16	3.29E-02	8.77E-01	1.33E-02
A_23_P27784	1.30	1.14	1.77	-1.10	1.63	1.29E-01	4.60E-01	4.27E-03
A_32_P154473	-1.07	-1.81	-1.03	-1.42	-1.27	6.14E-01	2.57E-03	8.26E-01
A_24_P788878	1.32	1.19	1.57	1.16	1.10	5.05E-02	2.32E-01	8.04E-04
A_24_P832737	1.80	1.06	1.17	1.17	2.07	6.22E-02	7.79E-01	3.05E-01
A_24_P247303	-1.11	-1.38	-1.29	1.14	-1.74	8.00E-01	2.68E-01	2.90E-01
A_24_P393958	1.05	-1.60	-1.14	-1.47	-1.58	6.10E-01	1.61E-03	1.31E-01
A_23_P41227	-1.51	-1.28	-1.25	-1.08	-1.64	8.64E-02	9.82E-02	8.91E-02
A_23_P300867	-1.14	-1.31	-1.72	-1.41	-1.21	3.87E-01	1.66E-01	9.86E-03
A_23_P65386	1.48	1.27	1.15	1.08	2.33	1.32E-01	1.97E-02	2.97E-01
A_23_P212781	1.00	-1.12	-1.28	-1.72	-1.38	9.97E-01	4.23E-01	1.91E-01
A_23_P152838	-1.39	-1.16	-1.24	1.01	-1.97	8.84E-02	5.70E-01	3.74E-01
A_23_P201193	1.21	-1.41	-1.82	-1.41	1.36	4.94E-01	9.75E-02	1.17E-04
A_32_P154830	1.75	1.14	1.08	1.26	1.55	4.66E-03	1.94E-01	3.37E-01
A_32_P25065	1.43	1.14	1.53	1.25	2.00	3.54E-01	4.50E-01	1.27E-01
A_24_P160466	1.20	1.30	1.63	-1.01	1.14	4.77E-01	1.09E-02	2.54E-03
A_23_P408376	1.66	1.39	1.00	1.11	1.55	2.86E-03	4.91E-02	9.89E-01
A_24_P919920	1.19	1.27	1.04	1.60	2.04	3.92E-01	1.86E-01	6.00E-01
A_23_P162739	-1.15	-1.04	-1.24	-1.41	-2.18	2.82E-01	5.46E-01	6.63E-03
A_24_P307695	-1.07	-1.90	-1.04	-1.87	-1.12	4.65E-01	3.21E-03	5.91E-01
A_23_P45456	-1.14	-1.35	-1.57	-1.15	1.28	5.75E-01	2.46E-03	4.17E-02
A_32_P162797	-1.54	-1.21	-1.16	-1.44	-1.31	5.03E-03	3.04E-02	5.45E-02
A_23_P76145	1.19	1.10	1.22	1.61	1.13	3.18E-01	7.32E-01	5.46E-02

A_23_P73096	1.26	1.11	1.91	1.20	1.35	4.11E-01	5.83E-01	2.95E-02
A_32_P16931	1.33	1.19	1.33	1.27	1.42	4.07E-02	4.16E-01	5.67E-02
A_23_P46429	-1.13	-1.64	1.00	-1.23	-1.65	4.96E-01	1.43E-03	9.95E-01
A_23_P100660	-1.46	-1.29	-1.11	-1.83	1.06	7.57E-02	3.70E-02	3.14E-01
A_24_P913900	-1.08	-1.72	1.09	-1.48	-1.46	6.89E-01	1.42E-02	6.76E-01
A_23_P151297	-1.40	-1.18	-1.09	-1.18	-1.97	3.33E-02	8.22E-02	3.92E-01
A_24_P152325	2.02	1.05	1.10	1.18	1.64	2.06E-02	7.91E-01	4.43E-01
A_32_P218875	1.37	1.20	1.12	1.48	1.85	1.09E-01	1.10E-01	2.75E-01
A_32_P332320	1.33	1.26	-1.14	1.58	2.02	2.17E-03	1.26E-01	1.34E-01
A_23_P302404	-1.52	-1.26	-1.21	-1.26	-1.31	1.38E-02	1.47E-01	8.73E-02
A_23_P160559	1.53	1.28	1.23	-1.07	1.80	1.66E-02	5.01E-02	5.31E-02
A_32_P213831	1.44	1.33	1.13	1.01	2.13	2.41E-01	2.31E-01	3.38E-01
A_32_P153244	-1.73	-1.56	-1.07	-1.28	-1.03	3.77E-03	3.37E-02	4.36E-01
A_23_P104555	-1.07	1.01	1.37	1.51	2.08	7.02E-01	9.52E-01	1.51E-02
A_23_P203702	-1.42	-1.27	-1.09	-1.06	-1.88	2.28E-02	1.87E-02	1.60E-01
A_23_P200222	1.21	-1.00	1.23	1.28	2.27	4.19E-01	9.99E-01	7.08E-02
A_24_P347378	-1.13	-1.71	-1.24	-1.11	-1.14	5.57E-01	6.66E-03	1.19E-01
A_24_P295590	-1.56	-1.49	-1.42	1.20	-1.27	3.60E-02	2.57E-03	2.96E-02
A_23_P50646	1.49	1.43	1.30	1.18	-1.18	5.00E-03	2.11E-03	3.18E-02
A_32_P66035	1.45	1.29	1.04	1.40	1.73	9.57E-02	2.98E-02	6.88E-01
A_24_P76635	1.22	-1.02	1.36	1.72	1.17	4.42E-01	9.40E-01	1.26E-01
A_23_P145529	-1.11	-1.56	-1.30	-1.59	1.01	4.99E-01	9.28E-03	5.75E-02
A_23_P207981	1.93	1.01	1.16	1.23	1.34	2.60E-03	9.29E-01	4.44E-01
A_24_P347411	-1.15	-1.01	-1.37	-1.70	-1.48	4.75E-01	9.26E-01	9.70E-03
A_32_P234849	-1.44	-1.07	-1.19	-1.10	-1.93	5.94E-02	7.24E-01	6.25E-02
A_23_P406928	-1.56	-1.42	-1.06	-1.27	-1.40	2.47E-02	8.92E-03	4.54E-01
A_32_P419502	1.33	-1.06	1.36	1.62	1.02	3.56E-01	8.36E-01	9.54E-02
A_32_P108748	1.74	1.42	-1.00	1.18	1.45	4.96E-02	5.55E-03	9.95E-01
A_23_P76538	-1.89	-1.64	-1.12	1.00	-1.10	1.12E-01	4.13E-02	6.03E-01
A_24_P147849	1.05	-1.61	-1.83	-1.19	-1.28	8.96E-01	2.14E-01	4.33E-02
A_32_P104334	1.51	1.68	1.22	-1.09	1.11	2.37E-02	3.11E-04	1.51E-01
A_24_P407742	1.12	1.25	1.15	1.52	1.93	2.85E-01	1.90E-01	2.28E-01
A_23_P208167	-1.60	-1.21	-1.45	-1.14	-1.89	1.30E-01	7.26E-02	6.04E-02
A_23_P143461	1.61	1.33	2.81	1.27	1.03	3.20E-01	1.54E-01	3.86E-02
A_24_P168398	-1.51	-1.30	-1.33	-1.29	1.20	5.86E-02	1.59E-01	1.91E-01
A_32_P187571	-1.29	-1.16	-1.11	-1.36	-1.73	1.20E-01	3.99E-01	5.95E-01
A_24_P935400	-1.10	1.45	1.25	1.50	1.61	5.99E-01	1.88E-01	2.56E-01
A_24_P682285	-1.25	-1.21	-1.02	-1.41	-1.93	9.49E-02	1.44E-01	8.37E-01
A_32_P207802	-1.02	1.62	1.05	1.49	1.52	8.35E-01	8.59E-03	5.71E-01
A_23_P39056	1.28	-1.22	1.17	1.69	1.40	1.88E-01	4.44E-01	3.26E-02
A_24_P238143	-1.25	-1.05	-1.14	-1.08	-2.43	1.81E-01	7.86E-01	1.17E-01
A_23_P356330	1.57	1.03	1.17	1.39	1.37	2.86E-03	7.44E-01	4.16E-02
A_23_P95070	-1.04	1.12	1.28	1.53	1.93	8.36E-01	2.71E-01	9.36E-02
A_23_P370408	1.33	-1.01	-1.09	1.88	1.53	1.37E-01	9.62E-01	7.89E-01
A_23_P321949	1.08	-1.42	-1.25	-1.59	-1.01	8.17E-01	2.63E-01	3.94E-01
A_24_P560519	1.05	1.35	1.27	1.23	1.66	7.13E-01	1.17E-02	2.02E-02
A_32_P94	-1.31	1.04	-1.17	-1.61	-1.04	1.49E-02	8.72E-01	5.18E-01

A_23_P385105	1.15	1.34	1.66	1.22	-1.04	6.40E-01	8.61E-02	2.72E-03
A_23_P27107	1.43	1.22	1.30	1.68	1.01	1.72E-01	1.38E-01	3.41E-01
A_32_P57453	1.37	1.04	1.08	1.26	2.12	1.02E-01	5.89E-01	4.90E-01
A_32_P83049	1.14	1.25	1.50	1.11	1.37	4.50E-01	8.26E-02	4.10E-04
A_23_P109304	-1.29	1.11	-1.34	-1.76	-1.34	1.48E-01	4.55E-01	4.63E-02
A_23_P358857	-1.24	-1.29	-1.02	-2.19	-1.23	2.79E-01	3.36E-01	7.60E-01
A_32_P117185	1.08	1.07	1.57	1.29	2.03	7.90E-01	6.18E-01	2.44E-02
A_23_P137139	-1.20	-1.73	-1.17	-1.10	-1.24	3.13E-01	1.46E-03	2.27E-01
A_24_P358406	-1.45	-1.16	-1.27	-1.03	-1.96	3.25E-01	4.76E-01	3.75E-01
A_23_P315252	-1.42	-1.45	-1.07	-1.20	-1.48	3.65E-02	4.29E-03	2.96E-01
A_32_P219581	1.36	1.36	1.15	1.25	1.23	1.33E-01	2.51E-02	4.05E-01
A_24_P107317	1.22	1.08	1.30	1.38	1.82	4.08E-01	6.16E-01	1.85E-01
A_23_P19030	1.68	1.48	1.11	1.20	1.15	2.15E-02	5.07E-03	2.29E-01
A_23_P128230	-1.27	-1.37	-1.34	1.08	-1.30	2.70E-01	2.33E-02	2.89E-02
A_24_P24002	1.71	1.03	-1.05	1.54	1.56	8.18E-02	8.92E-01	7.43E-01
A_24_P165205	-1.21	-1.16	-1.30	-1.51	-1.43	5.36E-01	3.90E-01	2.54E-01
A_32_P13337	-1.21	1.78	1.27	1.22	1.33	3.77E-01	3.84E-03	4.57E-02
A_23_P21976	1.04	1.51	-1.06	1.68	1.57	7.59E-01	7.81E-03	5.88E-01
A_24_P340284	1.17	1.11	1.15	1.95	1.13	5.03E-01	6.40E-01	2.10E-01
A_32_P228570	1.19	1.10	1.59	1.35	1.17	7.41E-02	6.52E-01	2.12E-03
A_23_P68031	-1.39	-1.82	1.09	-1.22	-1.32	7.92E-02	9.98E-03	4.65E-01
A_32_P210572	1.44	-1.04	1.65	1.37	1.20	6.07E-02	3.28E-01	3.00E-03
A_24_P381029	1.30	2.29	1.05	1.62	1.46	1.33E-01	1.15E-01	2.76E-01
A_23_P127068	1.29	-1.02	1.26	1.34	1.83	1.21E-01	8.14E-01	1.12E-02
A_23_P397248	1.17	2.63	1.31	1.12	1.38	4.72E-01	9.21E-02	2.78E-02
A_23_P64792	-1.12	-1.46	-1.60	-1.14	1.03	3.01E-01	3.73E-04	3.32E-06
A_24_P351283	1.51	1.20	1.35	1.48	1.09	9.32E-02	2.22E-01	9.53E-02
A_23_P250173	-1.17	-1.17	1.05	-1.61	-1.65	6.53E-01	6.95E-01	8.14E-01
A_24_P923300	-1.79	1.16	-1.11	-1.40	-1.24	1.39E-02	5.81E-01	4.55E-01
A_24_P381505	-1.32	-1.27	-1.14	-1.41	-1.43	2.20E-01	1.88E-02	1.61E-01
A_23_P149938	-1.00	1.25	1.12	1.19	2.19	9.94E-01	1.46E-01	1.11E-01
A_32_P79515	-1.26	1.35	1.19	1.44	1.87	3.36E-01	7.48E-02	1.95E-01
A_24_P910325	1.44	1.19	1.20	1.26	1.49	8.88E-02	2.62E-01	2.32E-01
A_24_P383762	1.15	1.16	1.37	1.06	2.15	5.03E-01	1.03E-01	5.59E-02
A_24_P43723	1.19	1.16	1.06	1.67	1.94	6.98E-01	3.41E-01	8.06E-01
A_23_P206920	-1.81	-1.19	-1.11	-1.58	-1.16	5.71E-02	3.69E-01	5.27E-01
A_32_P191665	1.04	1.30	-1.05	1.54	1.78	8.42E-01	1.18E-01	5.80E-01
A_23_P117654	2.20	1.24	1.03	1.10	1.18	4.45E-04	4.48E-02	5.78E-01
A_24_P186030	1.24	1.16	1.41	1.20	1.41	1.37E-01	1.58E-01	2.87E-03
A_24_P254949	-1.21	1.08	-1.50	1.32	-1.35	4.71E-01	8.11E-01	3.23E-02
A_24_P56363	-1.14	-1.61	-1.08	-1.46	-1.12	1.58E-01	1.26E-03	4.42E-01
A_23_P169766	1.13	1.28	1.34	1.39	1.21	3.03E-01	2.43E-02	5.23E-03
A_24_P307665	-1.05	1.43	1.22	1.46	1.54	7.00E-01	1.96E-02	2.23E-02
A_23_P166797	1.56	1.27	1.28	1.27	-1.42	2.05E-02	7.95E-02	1.20E-01
A_24_P417751	1.53	1.11	1.11	1.08	1.60	1.45E-02	6.66E-01	5.72E-01
A_23_P57036	-1.27	-1.30	-1.17	-1.33	-1.44	1.60E-02	8.01E-02	5.20E-02
A_24_P601511	1.22	-1.03	1.33	1.32	1.27	4.93E-01	9.40E-01	1.48E-01

A_32_P103131	1.18	1.51	1.73	-1.26	1.19	4.77E-01	2.10E-02	2.29E-02
A_23_P145874	-1.54	-1.53	-1.12	-1.41	1.34	4.79E-03	3.66E-02	3.47E-01
A_24_P681011	1.15	1.10	1.21	1.25	1.79	4.23E-01	3.64E-01	7.82E-02
A_23_P320070	1.21	1.21	-1.02	1.81	1.38	3.81E-01	1.18E-01	8.13E-01
A_23_P98335	-1.28	-1.29	-1.26	-1.33	-1.18	1.78E-01	4.00E-02	1.36E-01
A_23_P58588	-1.33	1.01	-1.18	-1.53	-1.37	1.26E-01	9.41E-01	4.86E-02
A_32_P98574	-1.02	1.46	1.07	1.37	1.79	9.33E-01	3.34E-02	5.31E-01
A_32_P43717	-1.25	-1.06	-1.52	-1.50	-1.08	1.30E-01	6.36E-01	9.42E-04
A_23_P204947	1.41	1.02	1.63	1.05	1.63	2.82E-01	8.00E-01	5.83E-04
A_23_P161197	1.17	1.14	1.04	1.31	1.51	3.74E-01	5.89E-01	8.20E-01
A_23_P128744	1.54	1.06	1.03	1.49	1.43	3.34E-02	7.36E-01	8.12E-01
A_32_P30238	-1.48	-1.44	-1.31	-1.04	1.22	8.11E-02	6.14E-02	1.34E-01
A_24_P196024	1.91	1.04	-1.03	1.47	1.45	2.41E-02	7.83E-01	7.51E-01
A_32_P70158	-1.28	-1.31	-1.51	1.04	-1.83	4.54E-01	1.65E-01	5.79E-02
A_23_P15734	1.11	1.10	2.14	1.30	1.05	6.24E-01	4.76E-01	1.14E-03
A_23_P120883	1.32	-1.19	1.18	1.46	1.89	1.29E-01	3.05E-01	1.68E-02
A_23_P104073	1.28	1.05	1.36	1.40	1.88	4.09E-01	6.31E-01	1.21E-01
A_24_P835500	-1.42	-1.25	-1.16	-1.46	-1.22	2.54E-02	1.32E-02	1.13E-02
A_24_P339024	-1.07	1.37	1.23	1.28	1.69	7.23E-01	1.64E-02	4.63E-01
A_32_P116660	-1.29	-1.61	1.01	-1.24	-1.52	8.12E-02	2.59E-02	8.56E-01
A_23_P110184	1.44	1.12	1.60	1.16	1.21	9.58E-02	4.39E-01	2.25E-02
A_32_P179964	1.00	1.07	1.16	1.38	2.48	9.71E-01	6.89E-01	1.32E-01
A_23_P18903	-1.61	-1.61	-1.21	1.04	-1.29	2.25E-02	4.09E-02	4.46E-02
A_23_P421483	-1.60	-1.23	-1.66	-1.19	-1.12	2.21E-01	1.05E-01	4.45E-02
A_24_P355649	-1.08	-1.53	-1.01	-1.30	-1.57	6.95E-01	3.02E-03	9.51E-01
A_23_P70688	-1.83	-1.34	-1.07	1.07	-1.35	8.69E-04	2.78E-02	2.65E-01
A_23_P257763	-1.41	-1.33	-1.14	-1.28	-1.34	5.20E-02	9.40E-03	1.31E-01
A_23_P382302	-1.16	-1.39	-1.09	-1.73	-1.28	4.03E-01	1.58E-01	2.77E-01
A_23_P63557	-1.46	-1.21	-1.38	-1.13	-1.21	9.08E-02	2.87E-01	1.93E-03
A_23_P17134	-1.04	-1.06	-1.53	-1.05	-1.96	8.21E-01	6.51E-01	1.64E-04
A_23_P151915	-1.12	1.37	1.12	1.20	2.13	7.09E-01	9.23E-02	4.57E-01
A_23_P127557	-1.14	-1.34	-1.20	-1.26	-1.87	5.01E-01	2.43E-01	1.51E-01
A_32_P201107	-1.06	1.26	1.17	1.45	1.49	8.58E-01	1.65E-01	5.18E-01
A_23_P15798	1.84	1.20	1.44	1.19	1.29	1.23E-01	2.96E-01	2.31E-01
A_24_P7950	-1.26	-1.59	-1.00	-1.20	-1.45	3.24E-01	4.90E-03	9.84E-01
A_32_P78816	1.31	-1.02	1.11	1.18	6.50	5.46E-02	7.21E-01	1.18E-01
A_23_P203920	-1.25	-1.16	-1.20	-2.01	1.07	1.82E-01	9.27E-02	5.80E-02
A_23_P119196	-1.26	-1.29	-1.09	-1.20	-2.00	1.64E-01	3.22E-02	3.55E-01
A_32_P220671	-1.15	-1.14	-1.37	-1.13	-1.79	5.18E-01	5.21E-01	4.86E-02
A_24_P213715	1.22	1.04	1.06	2.13	1.26	2.11E-01	7.30E-01	6.93E-01
A_23_P68487	1.51	1.17	1.00	1.38	1.52	1.62E-02	3.63E-02	9.85E-01
A_32_P210106	-1.45	-1.19	-1.07	-1.31	-2.18	2.99E-02	8.53E-02	5.58E-01
A_23_P389426	1.74	1.04	1.06	1.13	1.54	4.78E-03	7.79E-01	6.72E-01
A_23_P389588	-1.23	-1.32	-1.16	-1.68	-1.04	4.37E-01	2.30E-01	4.78E-01
A_24_P914155	-1.32	-1.39	-1.26	-1.00	-1.55	2.31E-01	2.17E-01	1.30E-01
A_23_P139912	-1.19	-1.20	-1.44	-1.44	1.11	5.54E-01	3.80E-01	5.19E-02
A_23_P139123	-1.29	-1.13	-1.08	-1.97	-1.12	2.23E-01	2.62E-01	4.66E-01

A_24_P94419	-1.23	-1.07	-1.30	-1.25	-1.81	1.97E-02	7.08E-01	4.93E-02
A_24_P100387	1.46	1.03	1.48	-1.02	1.58	7.39E-02	7.40E-01	7.81E-03
A_24_P923757	-1.32	-1.08	-1.05	-1.15	-1.97	1.43E-01	6.70E-01	4.94E-01
A_24_P259819	1.14	1.28	1.12	1.34	1.46	5.19E-01	2.89E-03	5.34E-01
A_23_P111766	1.17	1.33	1.01	1.74	1.21	2.91E-01	7.89E-02	8.50E-01
A_23_P137665	1.26	1.03	1.66	1.08	1.37	3.55E-01	9.09E-01	3.63E-02
A_23_P65278	-2.23	-1.05	1.00	-1.63	-1.29	4.07E-02	4.57E-01	9.78E-01
A_32_P133526	-1.17	1.15	1.51	1.81	1.24	3.41E-01	4.18E-01	1.00E-02
A_32_P176902	-1.46	1.01	-1.69	-1.32	-1.38	3.43E-01	9.50E-01	6.34E-02
A_23_P76992	1.34	1.54	1.10	1.09	1.28	1.91E-01	1.75E-02	5.72E-01
A_24_P932981	2.03	-1.15	1.23	1.58	1.25	1.14E-01	6.30E-01	2.93E-01
A_23_P324011	1.42	1.79	1.04	1.22	-1.03	2.43E-03	2.19E-03	5.12E-01
A_32_P124245	-1.09	1.16	1.27	1.72	1.41	8.24E-01	3.40E-01	3.50E-01
A_32_P32116	1.79	1.07	1.26	1.18	1.53	1.18E-01	7.46E-01	3.01E-01
A_23_P352484	-1.77	-1.05	-1.22	-1.43	-1.18	1.85E-01	8.54E-01	3.50E-01
A_32_P186226	-1.15	-1.12	-1.05	-1.64	-1.70	4.32E-01	3.15E-01	6.76E-01
A_23_P417363	1.40	1.14	-1.04	1.48	1.88	2.28E-01	3.18E-01	7.59E-01
A_23_P428326	1.46	1.72	1.08	1.01	1.23	3.49E-03	8.76E-04	1.33E-01
A_32_P34552	1.25	1.09	1.02	1.17	2.21	7.53E-02	6.73E-02	7.88E-01
A_23_P8253	1.42	1.10	1.14	1.46	1.18	1.35E-01	6.08E-01	3.17E-01
A_32_P330000	-1.11	1.31	1.08	1.64	1.78	5.23E-01	4.63E-02	2.91E-01
A_24_P331882	1.56	1.40	1.04	1.05	1.04	4.30E-02	5.22E-02	8.64E-01
A_24_P111061	-1.19	-1.32	-1.23	-1.36	-1.31	4.67E-01	2.26E-01	9.68E-03
A_23_P402765	1.13	1.38	1.18	1.68	1.15	5.70E-01	1.24E-01	4.17E-01
A_24_P64344	1.37	1.22	1.13	1.39	1.33	9.03E-02	1.53E-01	1.65E-01
A_23_P379034	1.47	1.19	1.17	1.41	1.34	3.60E-02	1.60E-02	1.76E-02
A_24_P913666	1.08	1.21	1.16	1.33	1.74	6.74E-01	2.01E-01	2.11E-01
A_24_P397294	-1.54	-1.31	-1.12	1.08	-1.50	7.77E-04	1.48E-02	1.99E-01
A_32_P142586	1.19	-1.04	1.35	1.85	1.36	3.72E-01	7.50E-01	2.19E-02
A_24_P110601	-1.56	-1.32	-1.20	-1.11	-1.13	4.87E-02	1.99E-03	6.40E-02
A_24_P933319	-1.26	-1.35	-1.10	-1.97	1.15	2.90E-01	8.79E-02	4.74E-01
A_24_P281730	1.69	1.10	1.14	-1.00	1.69	1.18E-02	3.90E-01	3.56E-01
A_23_P369328	-1.53	-1.21	-1.09	1.06	-1.74	1.53E-03	3.92E-05	3.04E-01
A_32_P206899	-1.01	1.27	1.11	2.06	1.33	9.53E-01	7.31E-03	5.51E-01
A_23_P143676	-1.30	-1.36	-1.37	1.11	-1.53	3.55E-02	5.82E-03	1.98E-04
A_23_P128486	1.89	1.13	1.12	1.24	1.32	2.49E-03	1.66E-02	1.04E-01
A_23_P13083	1.20	1.29	1.63	1.09	1.01	3.84E-01	1.37E-01	2.41E-03
A_24_P804992	-1.29	-1.17	-1.07	-1.69	-1.28	2.01E-01	2.82E-01	5.06E-01
A_23_P36397	1.20	1.20	-1.13	1.41	1.61	4.75E-01	3.90E-01	6.31E-01
A_32_P94685	1.41	-1.12	-1.01	1.48	1.53	9.75E-02	6.53E-01	9.64E-01
A_24_P366566	1.24	1.43	-1.05	1.36	1.57	1.94E-01	4.90E-02	5.97E-01
A_23_P254790	-1.07	-1.29	-1.14	-1.21	-1.55	6.45E-01	9.33E-04	2.73E-01
A_23_P41824	1.13	1.39	1.11	1.68	1.15	2.03E-01	1.25E-03	4.44E-01
A_23_P354805	-1.32	-1.14	-1.42	-1.71	1.22	1.58E-02	1.50E-01	3.21E-04
A_32_P147696	-1.27	-1.69	-1.14	-1.04	-1.20	2.11E-02	4.15E-04	7.50E-02
A_24_P667838	-1.06	1.66	1.13	1.35	1.58	6.67E-01	4.04E-02	1.21E-01
A_23_P392470	-1.51	-1.23	-1.59	-1.25	1.24	5.84E-02	6.53E-02	1.56E-02

A_23_P25069	1.96	1.36	1.33	1.01	-1.15	2.95E-03	9.15E-02	9.91E-04
A_32_P211188	1.16	1.30	1.24	1.15	1.70	3.47E-01	5.73E-02	1.75E-01
A_24_P608007	1.53	1.29	-1.01	1.47	1.36	1.66E-01	3.00E-02	9.22E-01
A_23_P214627	-1.49	-1.55	1.01	-1.12	-1.38	5.06E-02	6.26E-03	8.65E-01
A_23_P502078	1.03	1.22	1.45	1.30	1.57	8.50E-01	6.33E-02	7.45E-02
A_32_P106944	-1.13	-1.16	-1.21	-1.37	-1.52	2.75E-01	3.41E-01	9.39E-02
A_24_P68311	-1.34	-1.11	-1.18	-1.22	-1.66	1.47E-01	5.10E-01	5.57E-02
A_24_P60680	1.25	1.19	1.29	1.31	1.29	2.06E-01	2.75E-01	9.85E-02
A_23_P2793	-1.22	-1.67	-1.22	-1.09	1.08	2.59E-01	8.52E-03	9.90E-02
A_23_P101642	-1.85	-1.04	-1.16	-1.22	-1.38	1.46E-02	7.54E-01	2.57E-01
A_23_P348227	-1.29	-1.12	-1.51	-1.22	-1.09	7.14E-02	3.25E-01	3.25E-04
A_24_P301655	-1.89	-1.35	1.03	-1.19	-1.07	3.59E-03	1.51E-03	7.94E-01
A_23_P128650	1.23	1.26	1.26	1.18	1.54	1.15E-01	1.52E-02	7.42E-03
A_24_P204334	-1.53	-1.44	-1.02	-1.25	-1.30	3.60E-02	7.12E-03	8.07E-01
A_23_P397208	-1.62	-1.06	-1.22	-1.31	-1.30	2.18E-02	6.25E-01	2.44E-02
A_24_P347065	-1.53	-1.07	-1.31	-1.12	-1.32	3.32E-03	5.54E-01	7.79E-02
A_23_P348257	-1.47	-1.32	1.16	-1.37	-1.54	5.24E-02	8.81E-03	7.67E-02
A_23_P359277	1.47	1.04	1.17	1.38	1.70	9.60E-02	1.92E-01	1.01E-01
A_23_P431268	-1.33	-1.10	-1.20	-1.14	-1.99	1.38E-01	2.80E-01	7.68E-02
A_23_P157338	1.43	-1.24	1.25	1.15	1.81	7.04E-02	3.75E-01	1.39E-01
A_23_P369343	1.38	1.13	1.04	1.58	1.28	1.01E-01	1.91E-01	5.25E-01
A_32_P163247	-1.46	-1.89	-1.09	-1.03	1.03	2.52E-02	2.49E-02	5.52E-01
A_24_P915300	-1.36	-1.23	-1.04	-1.42	-1.41	8.42E-02	3.83E-01	6.71E-01
A_24_P246717	-1.21	-1.30	-1.05	-1.81	-1.10	4.81E-02	1.66E-01	5.86E-01
A_32_P25243	1.46	1.22	1.17	1.07	2.12	1.72E-01	1.85E-01	4.76E-01
A_23_P40415	-1.42	1.11	-1.20	-1.35	-1.22	1.58E-01	6.62E-01	2.19E-01
A_23_P78053	-1.51	-1.41	-1.19	1.01	-1.40	3.03E-02	1.72E-03	8.27E-03
A_23_P369701	1.24	1.39	1.02	1.23	1.58	1.14E-01	1.15E-02	6.83E-01
A_23_P87727	-1.17	-1.50	-1.27	-1.15	-1.21	3.64E-01	6.02E-02	1.82E-01
A_24_P355267	1.31	1.20	1.03	1.43	1.45	3.34E-02	7.58E-02	7.48E-01
A_24_P165864	-1.87	-1.63	-1.07	-1.29	-1.10	4.96E-02	9.43E-02	5.04E-01
A_24_P123385	-1.49	-1.51	-1.08	-1.29	-1.10	4.59E-02	5.25E-02	4.79E-01
A_32_P136622	1.28	1.19	1.12	1.54	1.57	3.96E-01	2.40E-01	5.84E-01
A_23_P8513	-1.27	-1.43	1.00	-1.15	-1.23	1.81E-01	1.33E-02	9.96E-01
A_32_P180825	1.54	1.40	-1.11	1.04	1.71	4.75E-03	3.11E-02	2.23E-01
A_23_P258912	-1.35	-1.29	-1.26	-1.15	1.14	1.19E-02	1.35E-02	1.02E-01
A_32_P221641	-1.09	1.18	1.81	1.56	1.26	6.60E-01	1.67E-01	2.24E-02
A_23_P501634	1.60	1.09	1.31	1.23	1.42	3.41E-02	4.79E-01	1.12E-01
A_23_P318904	-1.19	-1.41	1.07	-1.45	-1.50	2.39E-01	3.31E-04	4.19E-01
A_23_P142830	-1.25	-1.18	-1.00	-1.37	-1.72	2.73E-01	1.15E-01	9.87E-01
A_23_P26824	1.44	1.39	1.19	1.57	-1.33	9.29E-03	2.92E-02	7.30E-02
A_32_P40288	-1.34	-1.26	1.01	-1.64	-1.12	2.22E-01	1.77E-02	9.49E-01
A_24_P316586	1.26	1.28	1.12	1.68	1.04	1.73E-01	2.17E-01	2.58E-01
A_23_P124095	1.37	1.01	1.18	1.50	1.12	2.75E-01	9.73E-01	2.12E-01
A_23_P390518	1.45	1.08	1.12	1.89	1.42	1.73E-01	5.90E-01	3.37E-01
A_32_P94631	1.32	1.32	1.25	1.21	1.19	1.93E-01	2.06E-01	3.62E-01
A_24_P173790	1.08	1.55	-1.10	1.50	1.37	6.62E-01	1.69E-02	4.03E-01

A_23_P420863	1.05	1.17	1.19	1.52	1.49	6.64E-01	1.55E-01	2.18E-02
A_24_P218805	-1.24	-1.46	-1.13	-1.00	-1.41	1.60E-01	3.16E-03	3.08E-01
A_23_P502470	-1.25	-1.09	-1.02	-1.74	-1.41	3.97E-02	3.88E-01	8.41E-01
A_24_P466102	1.01	1.22	1.87	1.07	1.15	9.79E-01	2.05E-01	1.55E-03
A_23_P106806	1.82	-1.04	1.32	1.53	-1.13	1.08E-01	8.16E-01	4.37E-03
A_24_P665185	-1.10	1.28	1.46	1.43	1.19	4.56E-01	5.99E-02	6.86E-04
A_23_P2293	-1.40	-1.10	-1.40	1.05	-1.89	2.23E-01	3.62E-01	2.55E-02
A_24_P218265	1.84	1.16	1.26	1.23	-1.24	2.29E-03	6.20E-02	2.53E-02
A_32_P88817	-1.21	1.21	1.24	1.41	1.79	4.29E-01	2.13E-01	2.70E-01
A_32_P126362	1.08	1.54	-1.18	1.26	1.82	5.64E-01	1.55E-02	3.72E-01
A_23_P87952	-1.29	-1.02	-1.24	-1.18	-1.70	2.71E-01	8.82E-01	1.67E-02
A_32_P168375	1.92	1.23	-1.07	1.21	1.17	1.36E-02	2.93E-01	7.11E-01
A_23_P104563	-1.38	-1.16	-1.36	-1.17	-1.29	4.84E-02	1.37E-01	8.40E-03
A_32_P77225	1.16	1.56	1.18	1.29	1.08	3.14E-01	1.40E-02	1.06E-01
A_24_P273360	1.19	1.42	1.02	1.51	1.46	3.78E-01	5.06E-02	8.66E-01
A_24_P76319	1.63	2.05	1.07	1.06	1.15	3.52E-02	1.09E-01	7.72E-01
A_23_P167497	-1.38	1.05	-1.26	-1.41	-1.59	1.08E-01	6.50E-01	1.53E-01
A_24_P218151	1.33	1.10	1.28	1.50	1.35	2.03E-01	1.56E-01	8.67E-02
A_24_P412486	1.02	1.71	1.17	1.31	1.44	8.77E-01	2.04E-02	5.34E-02
A_23_P214681	1.41	1.24	1.30	1.23	1.16	1.14E-01	8.05E-02	1.47E-01
A_24_P913620	1.81	1.13	1.02	1.46	1.32	4.73E-02	5.90E-01	8.79E-01
A_24_P62530	-1.07	-1.98	-1.38	-1.30	1.26	4.48E-01	8.22E-03	3.39E-02
A_23_P79572	1.69	1.17	1.09	1.22	1.36	1.40E-02	1.39E-01	6.71E-01
A_23_P61406	-1.38	-1.56	-1.02	-1.16	-1.38	5.04E-02	3.13E-02	9.06E-01
A_23_P24104	-1.11	1.18	1.26	1.59	1.62	2.98E-01	1.62E-01	1.40E-02
A_23_P302550	-1.08	-1.25	-1.64	-1.23	-1.03	8.48E-01	2.08E-01	9.10E-02
A_23_P134601	-1.11	-1.51	-1.10	-1.32	-1.47	5.30E-01	2.54E-02	2.88E-01
A_23_P328259	1.10	1.25	1.23	1.64	1.19	3.60E-01	1.39E-01	1.27E-01
A_23_P377291	1.37	1.02	1.07	1.49	1.73	1.55E-01	7.54E-01	4.94E-01
A_24_P108779	-1.23	-1.31	-1.30	-1.12	-1.23	1.14E-02	6.18E-03	1.92E-02
A_23_P39131	-1.45	1.10	-1.08	-1.43	-1.61	4.47E-02	1.54E-01	2.24E-01
A_24_P686965	1.39	1.09	1.13	1.64	1.42	3.50E-01	7.35E-01	4.69E-01
A_24_P273599	-1.32	-1.33	-1.02	-1.24	-1.36	1.21E-01	3.61E-02	8.74E-01
A_32_P186364	-1.36	1.10	-1.32	-1.58	-1.16	6.60E-02	3.63E-01	3.10E-04
A_32_P199244	1.29	1.58	1.08	1.32	1.14	4.93E-02	4.64E-02	5.61E-01
A_32_P125945	-1.00	1.45	-1.02	1.35	1.49	9.88E-01	1.38E-02	8.59E-01
A_24_P25354	-1.22	1.03	-1.28	-1.48	-1.45	1.65E-01	7.00E-01	5.74E-03
A_32_P98776	1.13	1.13	1.07	1.73	1.54	5.88E-01	3.69E-01	7.44E-01
A_23_P401055	-1.27	-1.50	1.11	-1.50	-1.35	1.19E-01	9.95E-02	5.88E-01
A_32_P110751	-1.24	-1.17	-1.17	-1.29	-1.45	1.85E-01	1.71E-01	8.20E-02
A_32_P4934	-1.56	-1.32	1.13	-1.37	-1.12	1.28E-01	3.05E-01	5.46E-01
A_23_P13683	1.25	1.17	1.05	1.33	1.46	1.10E-01	2.23E-01	7.03E-01
A_23_P31041	-1.02	-1.33	-1.06	-1.54	-1.50	8.48E-01	9.36E-03	3.63E-01
A_32_P218766	1.09	1.31	1.01	1.07	1.70	7.45E-01	1.42E-02	9.65E-01
A_23_P340722	1.38	1.12	1.09	1.47	1.60	1.19E-01	3.44E-01	5.01E-01
A_23_P69497	-1.36	-1.08	-1.29	-1.36	-1.15	1.64E-01	5.39E-01	3.84E-02
A_23_P37505	-1.67	-1.26	-1.07	-1.29	-1.21	1.90E-01	1.83E-01	7.68E-01

A_23_P111206	-1.36	-1.25	-1.16	-1.23	-1.53	7.53E-02	1.87E-02	2.56E-01
A_23_P14915	1.40	1.14	1.15	1.28	1.62	1.18E-01	5.89E-01	1.42E-01
A_23_P388200	-1.01	-1.09	-1.28	-1.33	-1.43	9.39E-01	5.51E-01	7.39E-02
A_24_P238402	-1.13	-1.35	1.02	-1.36	-1.67	4.16E-01	1.56E-01	8.32E-01
A_23_P360213	-1.24	-1.58	-1.12	-1.10	-1.37	1.27E-01	3.69E-03	8.60E-02
A_23_P17095	-1.03	-1.08	-1.05	-1.64	-1.62	8.42E-01	6.62E-01	7.52E-01
A_23_P75260	-1.48	-1.58	-1.18	1.30	-1.31	8.23E-02	1.17E-02	8.75E-02
A_32_P55987	1.11	1.27	1.16	1.51	1.43	2.01E-01	3.92E-02	1.17E-01
A_24_P291278	1.06	1.69	1.02	1.30	1.49	6.98E-01	3.34E-02	9.01E-01
A_23_P11144	-1.14	-1.43	-1.04	-1.29	-1.36	3.02E-01	1.65E-02	7.40E-01
A_24_P101248	-1.23	-1.37	-1.06	-1.37	-1.10	6.18E-02	3.14E-02	5.83E-01
A_24_P324084	1.74	1.09	-1.01	1.35	1.59	1.17E-01	6.41E-01	9.42E-01
A_23_P138495	1.29	1.20	1.24	1.21	1.36	1.52E-01	2.84E-01	4.36E-02
A_23_P201963	-1.45	-1.15	-1.05	-1.27	-1.77	1.53E-02	6.67E-02	5.80E-01
A_32_P139505	1.17	1.16	1.01	1.49	1.45	2.20E-01	9.43E-02	8.90E-01
A_23_P77980	1.67	1.17	1.70	1.25	1.40	1.28E-01	1.14E-01	7.26E-02
A_24_P194755	-1.47	-1.01	-1.10	-1.66	-1.02	1.04E-01	9.62E-01	6.64E-01
A_24_P246841	-1.25	-1.26	-1.16	-1.39	-1.36	2.63E-01	1.77E-01	8.46E-02
A_32_P201417	-1.43	-1.11	-1.39	-1.04	-1.32	1.64E-02	3.36E-01	5.09E-02
A_23_P50815	-1.59	1.07	-1.27	-1.03	-1.62	5.37E-02	6.56E-01	7.19E-02
A_23_P109950	-1.28	-1.03	-1.20	-1.11	-1.89	1.32E-01	8.95E-01	2.25E-01
A_24_P134850	1.37	1.06	1.17	1.04	1.87	2.03E-02	6.48E-01	3.39E-01
A_23_P169756	1.04	1.29	1.30	1.43	1.13	7.32E-01	1.66E-02	1.14E-02
A_23_P357207	1.04	-1.74	-1.10	-1.28	-1.20	8.18E-01	1.11E-02	5.95E-01
A_23_P29096	-1.99	1.06	-1.36	-1.32	-1.27	7.28E-02	7.49E-01	1.58E-01
A_23_P167081	-1.37	-1.27	-1.09	-1.20	-1.50	8.92E-02	5.92E-03	3.28E-01
A_24_P124875	1.47	1.15	1.22	1.15	1.77	2.04E-01	4.56E-01	1.83E-01
A_23_P337726	-1.39	-1.48	-1.04	-1.22	-1.20	4.36E-02	2.55E-03	6.64E-01
A_23_P43979	1.69	1.09	1.43	1.29	1.21	2.29E-01	6.38E-01	1.30E-01
A_23_P56369	1.47	1.21	1.12	1.24	1.61	9.75E-02	3.20E-01	1.54E-01
A_23_P218442	-1.52	-1.09	-1.73	-1.19	-1.47	2.78E-01	5.53E-01	5.68E-02
A_23_P38618	1.18	1.18	1.22	1.37	1.75	1.41E-01	8.20E-02	1.10E-01
A_32_P846696	-1.18	-1.16	-1.13	-1.06	-2.55	1.19E-01	2.26E-01	5.05E-01
A_24_P914669	-1.71	1.03	-1.11	-1.38	-1.09	1.76E-02	8.99E-01	3.04E-01
A_23_P96590	-1.64	-1.12	-1.32	-1.33	-1.01	1.47E-02	2.39E-01	2.08E-03
A_24_P731648	1.28	1.01	1.45	1.28	1.25	2.40E-01	9.11E-01	7.75E-04
A_32_P166480	-1.36	-1.42	-1.08	-1.47	-1.22	1.03E-01	1.65E-01	2.14E-01
A_23_P427023	-1.33	-1.78	-1.12	-1.24	1.33	4.37E-01	4.40E-02	5.34E-01
A_32_P59678	-1.13	-1.41	-1.18	-1.21	-1.23	2.51E-01	7.57E-03	1.04E-01
A_32_P71585	-1.02	1.63	1.06	1.47	1.41	7.69E-01	6.33E-02	6.28E-01
A_23_P431853	-1.48	-1.08	-1.07	-1.22	-1.67	7.28E-02	5.48E-01	2.89E-01
A_23_P24004	-1.35	-1.37	1.03	-1.33	-1.44	2.60E-02	4.90E-02	7.68E-01
A_23_P352266	-1.22	1.02	-1.36	-1.42	-1.26	1.82E-01	8.63E-01	4.80E-05
A_23_P258582	1.14	1.09	1.42	1.05	1.36	4.04E-01	6.85E-01	1.03E-02
A_23_P94501	-1.07	-1.23	-1.06	-1.82	-1.58	5.71E-01	2.29E-01	5.29E-01
A_23_P211493	-1.54	-1.13	-1.06	-1.45	-1.45	8.35E-02	1.10E-01	6.30E-01
A_32_P184330	1.36	1.64	1.16	1.46	-1.21	8.47E-02	7.41E-02	2.50E-01

A_23_P96483	-1.25	-1.12	-1.14	-1.12	-1.60	2.97E-01	4.51E-01	3.78E-01
A_23_P35148	-1.11	-1.21	-1.03	-1.20	-1.90	4.24E-01	1.87E-01	7.56E-01
A_23_P77389	1.28	1.19	1.16	1.59	1.13	2.44E-01	2.47E-01	2.94E-02
A_23_P153964	-1.52	-1.33	-1.12	-1.24	-1.27	1.21E-01	1.53E-01	3.82E-01
A_24_P221323	-1.22	-1.80	-1.04	-1.17	-1.10	2.20E-01	2.82E-03	6.97E-01
A_23_P389250	1.34	-1.28	1.11	1.40	1.79	1.37E-01	2.16E-01	2.50E-01
A_32_P92163	1.27	1.05	-1.01	1.44	1.64	1.81E-01	8.52E-01	9.51E-01
A_24_P384239	-1.40	-1.50	-1.09	-1.18	-1.45	1.16E-01	3.40E-02	2.40E-01
A_24_P336931	-1.42	-1.62	-1.01	-1.40	-1.02	3.93E-02	1.82E-02	8.51E-01
A_23_P361679	1.55	1.55	1.13	1.08	-1.14	1.63E-02	5.34E-03	2.85E-01
A_23_P92093	1.19	-1.09	1.21	1.38	1.64	4.21E-01	5.20E-01	7.76E-02
A_32_P73452	1.34	-1.13	1.10	1.49	1.64	1.01E-01	5.81E-01	3.28E-01
A_23_P430658	-1.44	-1.44	-1.10	1.17	-1.30	2.51E-02	3.75E-02	5.52E-01
A_24_P23527	-1.37	-1.35	1.03	-1.04	-1.54	1.07E-01	3.54E-02	8.23E-01
A_23_P125423	-1.46	-1.48	-1.15	-1.47	1.44	6.24E-02	1.68E-04	2.58E-02
A_23_P212025	-1.10	-1.65	-1.12	-1.29	-1.10	3.37E-01	1.74E-03	1.72E-01
A_24_P155761	-1.15	-1.06	-1.09	-1.48	-1.35	3.59E-01	7.46E-01	3.71E-01
A_32_P53212	1.33	-1.24	-1.21	-1.43	-1.67	3.66E-01	1.58E-01	3.69E-01
A_24_P325992	-1.36	-1.06	-1.08	-1.55	-1.36	1.92E-01	6.61E-01	2.66E-01
A_24_P218905	1.49	1.12	-1.07	1.47	1.31	1.51E-01	3.92E-01	6.75E-01
A_23_P47704	-1.47	-1.30	-1.05	-1.27	-1.52	9.48E-02	2.19E-02	6.16E-01
A_23_P309996	-1.12	1.18	1.35	1.24	1.80	3.16E-01	8.84E-02	2.38E-02
A_24_P203407	1.39	1.27	1.07	1.54	-1.10	2.73E-01	4.17E-02	7.72E-01
A_24_P205008	1.03	1.27	1.04	1.58	1.47	7.57E-01	6.09E-02	6.28E-01
A_23_P97365	1.24	1.06	1.23	1.17	1.57	5.42E-02	6.47E-01	1.52E-02
A_24_P208452	1.58	1.11	1.25	1.27	1.17	2.71E-02	3.17E-01	1.85E-02
A_23_P41765	-1.42	-1.26	-1.00	1.01	-2.16	5.63E-02	1.08E-01	9.79E-01
A_23_P64873	-1.41	-1.28	-1.12	-1.64	1.15	3.28E-02	5.72E-03	1.09E-01
A_23_P163475	1.35	1.14	1.21	1.32	1.13	1.01E-01	4.91E-01	1.83E-01
A_23_P213562	-1.15	-1.20	1.02	-1.66	-1.33	2.28E-01	1.35E-01	7.80E-01
A_23_P156708	-1.38	-1.08	-1.22	-1.27	-1.23	2.75E-02	5.49E-01	5.47E-02
A_23_P365412	-1.25	-1.40	-1.16	-1.04	-1.31	3.65E-01	3.98E-02	3.18E-01
A_23_P358531	1.30	1.19	1.21	1.34	1.30	7.34E-02	3.66E-02	6.02E-03
A_23_P354187	1.55	1.07	1.12	1.37	1.27	4.04E-02	5.23E-01	1.08E-01
A_24_P922367	1.10	1.94	1.13	1.28	1.10	7.08E-01	3.01E-02	3.62E-01
A_32_P213661	-1.22	-1.67	-1.04	-1.39	-1.30	1.91E-01	5.46E-02	5.73E-01
A_23_P108103	1.28	1.27	1.01	1.43	1.36	3.07E-01	1.37E-01	9.06E-01
A_32_P189034	-1.07	-1.27	-1.29	-1.17	-1.52	6.72E-01	7.28E-02	2.76E-02
A_32_P178724	-1.01	1.24	1.33	1.31	1.15	9.57E-01	1.13E-01	6.58E-02
A_24_P331918	-1.34	-1.05	-1.18	-1.42	-1.47	2.37E-01	7.84E-01	2.42E-01
A_23_P152992	1.06	1.28	1.01	1.66	1.21	7.62E-01	6.03E-02	8.72E-01
A_32_P228331	-1.14	-1.16	-1.11	-1.30	-1.37	3.58E-01	3.74E-01	4.83E-01
A_24_P393470	1.45	1.15	1.04	1.52	1.12	5.60E-02	1.26E-01	5.62E-01
A_23_P127426	1.42	1.07	1.07	1.39	1.47	8.69E-02	5.76E-01	3.02E-01
A_23_P337934	-1.21	1.21	1.49	1.54	1.16	2.48E-01	2.95E-02	4.62E-05
A_23_P333802	1.24	1.17	1.16	1.18	1.62	1.26E-01	1.49E-01	1.54E-01
A_23_P20022	1.01	1.26	1.37	1.17	1.33	9.54E-01	1.48E-01	6.82E-02

A_23_P125705	-1.29	-1.34	-1.14	-1.15	-1.33	9.25E-02	4.52E-03	1.81E-01
A_32_P51688	-1.04	1.44	1.09	1.37	1.30	8.47E-01	1.04E-02	3.71E-01
A_23_P164691	-1.46	-1.32	-1.05	-1.06	-1.46	4.08E-02	2.61E-02	5.14E-01
A_24_P12401	1.03	1.23	1.36	1.21	1.22	8.98E-01	9.34E-02	3.61E-02
A_32_P232523	1.21	1.20	1.31	1.16	1.25	1.26E-01	2.03E-01	1.34E-03
A_24_P193011	-1.54	-1.22	-1.27	-1.20	-1.23	5.22E-02	3.16E-03	3.69E-03
A_23_P422831	-1.34	-1.13	-1.45	-1.26	1.02	7.01E-02	1.40E-01	4.23E-04
A_24_P342226	1.17	1.08	1.19	1.61	1.03	5.45E-01	6.79E-01	3.22E-01
A_23_P85008	-1.08	-1.16	-1.13	-1.59	-1.11	6.31E-01	3.03E-01	5.08E-01
A_32_P26738	-1.34	-1.21	-1.06	-1.28	-1.45	1.14E-01	8.00E-02	5.17E-01
A_24_P867702	-1.15	1.38	1.09	1.26	1.52	6.60E-01	2.01E-01	6.58E-01
A_23_P26890	-1.34	-1.06	-1.47	-1.18	-1.22	4.21E-02	4.29E-01	4.35E-04
A_23_P416314	1.71	1.12	1.03	1.26	1.27	1.39E-02	4.86E-01	7.31E-01
A_32_P224302	-1.24	-1.19	-1.67	-1.31	-1.18	1.27E-01	2.28E-02	8.67E-03
A_23_P141730	-1.34	-1.35	1.01	-1.55	-1.11	1.04E-01	2.26E-01	9.45E-01
A_32_P221799	1.18	-1.24	-1.03	-1.54	-1.70	4.81E-01	1.02E-01	7.52E-01
A_24_P279489	1.24	1.08	1.10	1.21	1.86	6.02E-02	5.66E-01	4.71E-01
A_23_P247	-1.16	-1.36	-1.27	-1.01	1.24	6.99E-01	3.53E-02	1.63E-01
A_23_P2904	1.46	1.26	1.03	1.16	1.55	1.89E-01	1.70E-01	8.63E-01
A_23_P322562	-1.48	-1.05	-1.27	-1.10	-1.31	4.75E-02	8.56E-01	1.36E-01
A_23_P82065	1.38	-1.13	1.16	1.26	1.53	1.89E-02	5.03E-01	2.70E-01
A_24_P35935	-1.13	-1.33	-1.05	-1.35	-1.41	4.22E-01	2.27E-03	3.99E-01
A_23_P330209	1.49	1.00	1.10	1.44	1.35	1.74E-01	9.67E-01	5.95E-01
A_24_P281853	-1.35	-1.05	-1.14	-1.17	-1.85	2.49E-01	7.25E-01	2.05E-01
A_24_P713185	-1.38	-1.42	-1.16	-1.10	-1.41	1.41E-01	3.53E-02	1.18E-01
A_23_P352535	-1.26	-1.44	-1.08	-1.03	-1.49	1.18E-01	2.40E-02	4.45E-01
A_23_P26367	1.23	-1.00	1.43	1.44	1.52	3.58E-01	9.86E-01	1.42E-01
A_24_P911788	-1.77	-1.25	-1.18	-1.19	-1.02	9.67E-02	9.90E-02	3.64E-01
A_23_P16648	1.08	1.25	1.23	1.12	1.89	5.42E-01	1.68E-01	1.57E-01
A_23_P428260	-1.11	-1.04	-1.13	-1.79	-1.25	4.96E-01	4.34E-01	1.11E-01
A_23_P206212	-1.57	-1.16	-1.18	-1.29	-1.92	1.38E-01	3.30E-02	3.16E-01
A_24_P393740	-1.38	-1.39	1.19	-1.28	-1.32	3.17E-01	8.16E-02	4.41E-01
A_32_P49764	-1.10	-1.43	-1.22	-1.36	-1.39	3.81E-01	5.64E-02	8.08E-02
A_24_P896765	-1.24	-1.35	-1.33	-1.29	1.25	3.26E-01	3.04E-01	1.01E-01
A_23_P211326	-1.06	1.33	1.65	1.09	1.28	6.95E-01	8.19E-02	1.72E-03
A_24_P348513	1.05	2.15	1.33	1.27	1.05	7.62E-01	3.21E-02	8.12E-02
A_23_P218928	-1.18	-1.20	1.03	-1.55	-1.31	4.71E-01	3.03E-01	7.77E-01
A_23_P114947	-1.15	-1.09	-1.12	-1.60	-1.64	8.17E-02	2.37E-01	1.38E-01
A_24_P376483	-1.20	-1.09	-1.09	-1.24	-1.81	1.24E-01	3.58E-01	4.00E-01
A_23_P251984	1.24	-1.03	1.16	1.12	3.74	1.31E-02	6.38E-01	6.74E-03
A_24_P482017	1.02	1.24	1.06	1.50	1.59	8.92E-01	1.77E-01	5.27E-01
A_24_P357572	1.10	-1.51	-1.29	-1.08	-1.28	6.30E-01	8.51E-03	2.09E-01
A_23_P130429	-1.09	-1.29	1.04	-1.65	-1.48	4.34E-01	3.04E-01	7.17E-01
A_24_P705167	1.10	1.23	-1.00	1.50	1.34	8.25E-01	1.74E-01	9.99E-01
A_23_P156907	-1.06	-1.28	-1.03	-1.35	-1.51	7.59E-01	1.99E-01	8.12E-01
A_24_P411561	-1.09	-1.68	-1.34	-1.03	-1.28	7.84E-01	1.13E-01	1.24E-01
A_23_P310911	1.60	1.02	1.14	1.19	1.59	1.31E-01	9.11E-01	3.73E-01

A_23_P206441	1.43	-1.23	1.11	1.45	1.28	1.06E-01	4.14E-01	2.81E-01
A_32_P111019	1.23	1.06	1.19	1.14	1.57	3.15E-01	7.44E-01	7.69E-02
A_32_P47643	1.10	1.26	1.27	1.18	1.21	3.95E-01	9.21E-02	2.05E-04
A_23_P344281	-1.25	-1.21	-1.30	1.01	-1.56	2.29E-02	5.86E-02	1.30E-01
A_23_P148047	-1.27	-1.19	-1.10	-1.30	-1.58	6.02E-02	1.50E-01	2.64E-01
A_24_P91094	1.40	-1.09	1.22	1.53	1.22	2.61E-01	6.42E-01	2.40E-01
A_23_P118095	1.18	1.40	1.30	1.16	1.11	2.38E-01	4.27E-02	8.73E-02
A_23_P32805	-1.52	-1.03	1.03	-1.24	-1.33	3.64E-02	8.91E-01	9.07E-01
A_24_P919850	1.56	1.03	1.03	1.57	1.11	1.55E-02	8.34E-01	7.47E-01
A_24_P68908	1.26	-1.04	1.17	1.22	1.56	1.67E-01	8.89E-01	1.30E-01
A_24_P200761	-1.10	-1.27	-1.35	-1.04	-1.67	4.22E-01	2.80E-01	1.47E-01
A_23_P114713	-1.09	-1.25	-1.35	-1.13	1.03	5.58E-01	2.91E-01	3.58E-03
A_23_P11032	-1.52	-1.42	1.06	-1.19	-1.22	1.89E-02	1.28E-02	4.76E-01
A_24_P188071	1.04	-1.06	1.15	1.55	1.41	7.68E-01	7.90E-01	9.04E-02
A_32_P21807	-1.18	-1.37	-1.23	-1.05	-1.17	2.03E-01	1.98E-02	1.02E-01
A_23_P425066	1.18	1.15	1.09	1.02	2.10	2.75E-01	2.78E-01	2.32E-01
A_23_P153320	-1.04	-1.62	-1.29	-1.16	-1.33	7.80E-01	4.91E-02	8.09E-02
A_23_P111724	-1.16	-1.38	-1.48	-1.08	1.25	4.04E-01	2.98E-02	1.10E-02
A_32_P162183	-1.09	-1.08	-1.13	-1.48	-1.23	6.77E-01	5.37E-01	3.28E-01
A_23_P211973	-1.08	-1.41	-1.18	-1.48	1.08	5.77E-01	1.55E-03	1.84E-01
A_23_P410159	1.41	1.23	1.01	1.38	1.09	4.81E-03	1.60E-01	9.63E-01
A_32_P147678	1.26	1.11	-1.03	1.38	1.66	1.93E-01	2.56E-01	6.37E-01
A_23_P119006	1.31	-1.03	1.17	1.17	1.79	1.15E-01	8.62E-01	3.91E-01
A_23_P108948	1.31	1.12	1.06	1.28	1.69	6.66E-02	1.27E-01	4.77E-01
A_32_P188921	1.26	1.34	-1.03	1.34	1.31	4.09E-01	2.08E-02	8.23E-01
A_24_P346762	1.70	1.09	-1.02	1.33	1.34	3.07E-02	2.43E-01	9.24E-01
A_23_P420442	1.49	1.22	1.35	-1.13	1.23	7.11E-03	4.48E-02	2.84E-02
A_23_P344694	1.22	1.21	1.28	1.23	1.17	4.84E-01	2.59E-01	2.02E-01
A_24_P334640	1.25	1.30	1.22	-1.10	1.58	1.99E-01	1.59E-01	8.84E-02
A_24_P230570	-1.60	1.05	-1.12	-1.10	-1.53	6.56E-02	8.20E-01	3.68E-01
A_23_P58676	1.33	1.20	-1.09	1.21	1.83	2.19E-02	2.18E-01	5.43E-01
A_23_P88095	-1.08	-1.62	-1.05	-1.19	-1.27	1.32E-01	2.24E-04	3.52E-01
A_32_P209208	-1.22	-1.46	1.01	-1.63	-1.04	1.17E-01	9.01E-02	9.57E-01
A_23_P30813	1.60	1.33	1.32	1.08	-1.07	8.54E-02	5.67E-02	2.21E-02
A_24_P163168	-1.58	1.05	-1.28	-1.18	-1.37	2.30E-02	4.94E-01	2.27E-02
A_24_P178723	1.48	1.19	-1.01	1.33	1.35	1.39E-01	4.19E-01	9.74E-01
A_23_P29922	-1.23	-1.52	-1.06	-1.17	-1.25	1.85E-03	5.23E-03	3.68E-01
A_24_P387514	1.05	1.22	1.23	1.47	1.10	7.48E-01	1.99E-01	2.05E-01
A_24_P137602	-1.14	-1.08	-1.17	-1.67	-1.27	3.69E-01	7.44E-01	1.07E-01
A_23_P9677	-1.14	1.22	1.37	1.42	1.07	6.01E-01	3.70E-01	9.90E-02
A_32_P135113	1.03	1.28	-1.07	1.35	1.78	9.03E-01	7.48E-02	6.99E-01
A_24_P392622	1.83	-1.05	1.12	1.45	1.33	6.78E-02	7.24E-01	2.44E-01
A_23_P214080	-1.37	-1.25	-1.20	1.07	-1.69	2.80E-02	2.70E-02	1.14E-01
A_32_P197340	-1.24	-1.24	-1.18	-1.48	1.22	1.53E-01	2.63E-01	2.13E-01
A_23_P393080	1.33	1.18	1.28	1.43	-1.15	2.28E-01	8.19E-02	8.37E-02
A_23_P59261	1.40	1.00	1.52	1.31	1.02	3.73E-02	9.92E-01	2.39E-07
A_23_P152620	-1.10	-1.19	-1.35	-1.23	-1.31	4.98E-01	2.04E-01	5.52E-02

A_24_P169092	-1.15	-1.39	-1.22	-1.13	-1.42	2.50E-01	5.45E-02	2.67E-01
A_23_P207939	-1.53	-1.47	-1.06	-1.17	-1.37	1.26E-01	1.08E-01	6.44E-01
A_24_P226278	-1.49	-1.36	-1.11	-1.08	-1.15	2.28E-02	4.21E-02	3.66E-01
A_23_P26965	-1.16	1.10	-1.33	-1.56	-1.15	4.56E-01	6.26E-01	1.90E-02
A_23_P340148	1.04	-1.61	-1.36	-1.36	-1.11	8.48E-01	6.69E-02	1.03E-01
A_23_P76658	-1.23	-1.51	-1.06	-1.18	-1.14	4.94E-02	2.06E-04	4.49E-01
A_23_P42116	1.76	-1.01	1.05	1.04	1.65	7.02E-03	9.18E-01	4.84E-01
A_24_P255965	1.15	1.06	-1.02	1.39	1.72	4.15E-01	5.69E-01	8.50E-01
A_23_P334328	-1.07	-1.11	-1.33	-1.02	-1.41	6.51E-01	4.53E-01	6.23E-04
A_23_P215778	1.11	1.37	1.16	1.15	1.49	4.67E-01	3.90E-01	3.69E-01
A_23_P121869	-1.27	-1.18	1.06	-1.01	-2.52	2.23E-02	2.95E-02	5.47E-01
A_23_P78405	1.20	1.20	1.12	-1.04	2.22	2.35E-01	2.37E-01	5.99E-01
A_23_P131435	-1.02	-1.32	-1.15	-1.39	-1.36	7.56E-01	4.64E-02	1.17E-01
A_24_P910833	1.28	1.19	1.04	1.43	1.30	2.24E-01	1.18E-01	6.74E-01
A_24_P302506	-1.28	-1.20	-1.40	-1.18	-1.19	1.91E-01	1.03E-01	6.13E-02
A_23_P38537	1.10	1.24	1.15	1.48	1.19	8.17E-01	1.97E-01	4.40E-01
A_23_P347027	1.35	1.16	1.27	1.36	1.01	3.09E-01	2.06E-01	1.17E-01
A_32_P387648	1.36	-1.22	1.15	1.33	1.74	1.85E-01	4.03E-01	2.13E-01
A_24_P367752	1.24	1.11	1.25	1.27	1.31	1.73E-01	4.86E-01	8.67E-02
A_23_P129188	1.22	1.25	1.04	1.18	1.61	1.09E-01	7.17E-02	5.97E-01
A_32_P54616	-1.06	-1.35	-1.09	-1.23	-1.38	7.56E-01	7.25E-03	2.63E-01
A_23_P77697	1.21	1.31	1.08	-1.23	1.44	3.13E-01	1.71E-01	7.58E-01
A_32_P150086	1.04	-1.14	-1.34	-1.48	1.34	8.99E-01	7.41E-01	1.28E-04
A_24_P123616	-1.21	-1.14	-1.01	-1.32	-1.77	7.14E-02	1.22E-01	8.78E-01
A_23_P170233	1.35	-1.19	1.29	1.43	1.27	6.31E-02	2.03E-01	2.38E-03
A_23_P150789	1.38	1.43	1.19	-1.19	1.43	3.48E-02	1.09E-02	6.23E-02
A_23_P9280	-1.26	-1.22	-1.13	-1.54	-1.13	9.60E-02	7.50E-03	8.28E-02
A_23_P328545	-1.39	1.34	1.06	-1.01	1.05	4.05E-01	3.04E-02	8.14E-01
A_24_P535380	1.06	1.36	1.33	1.37	1.08	6.71E-01	9.16E-02	5.54E-02
A_23_P319153	1.10	-1.01	1.06	1.40	1.60	5.66E-01	9.61E-01	7.33E-01
A_32_P32835	1.34	1.10	1.25	1.26	1.16	2.92E-01	5.50E-01	2.29E-02
A_23_P35597	-1.05	-1.36	-1.02	-1.45	-1.25	8.46E-01	4.98E-02	8.84E-01
A_23_P53126	-1.19	-1.22	-1.06	-1.31	-1.33	2.42E-01	4.11E-02	5.13E-01
A_24_P419017	1.07	1.51	1.14	1.56	1.08	7.20E-01	4.37E-02	1.73E-01
A_23_P29551	1.39	1.04	1.08	1.46	1.21	1.08E-01	7.44E-01	1.71E-01
A_23_P340848	-1.31	-1.92	-1.18	-1.12	1.03	2.36E-01	2.28E-02	1.81E-01
A_24_P38815	1.55	1.33	1.09	-1.05	1.50	1.22E-02	8.05E-02	2.23E-01
A_23_P114349	1.43	1.00	-1.04	1.36	1.61	6.87E-02	9.82E-01	7.63E-01
A_32_P234691	-1.43	-1.05	-1.23	-1.14	-1.47	4.02E-02	6.85E-01	3.99E-02
A_32_P155645	-1.12	-1.46	-1.11	-1.44	-1.07	4.16E-01	1.71E-02	2.21E-01
A_23_P168651	-1.19	-1.00	-1.21	-1.29	-1.52	2.48E-01	9.93E-01	5.28E-02
A_23_P100730	-1.46	-1.27	-1.09	1.01	-1.26	4.58E-02	6.71E-02	5.52E-01
A_24_P569791	1.33	1.35	-1.18	1.25	1.48	2.46E-01	9.10E-02	3.67E-01
A_24_P220771	-1.27	-1.09	-1.10	-1.29	-1.34	3.66E-01	5.91E-01	5.48E-01
A_23_P2674	1.10	1.16	1.54	1.03	1.29	7.07E-01	4.42E-01	1.25E-01
A_24_P289178	1.28	1.35	1.42	-1.02	1.14	2.26E-01	7.85E-02	3.01E-04
A_23_P152791	1.16	-1.04	1.45	1.42	-1.02	5.61E-01	8.22E-01	1.32E-03

A_23_P210100	-1.46	-1.21	-1.31	-1.17	1.29	6.89E-03	3.06E-02	1.98E-03
A_24_P156049	1.85	1.17	1.21	-1.09	1.21	5.80E-03	1.21E-01	6.28E-02
A_24_P375962	-1.00	-1.27	-1.16	-1.32	1.04	9.93E-01	3.33E-02	3.99E-01
A_23_P410613	-1.04	-1.18	-1.02	-1.75	-1.26	7.57E-01	5.84E-02	8.33E-01
A_23_P16944	1.05	1.29	1.02	1.37	1.44	7.07E-01	8.54E-02	7.65E-01
A_24_P265051	-1.28	-1.41	-1.27	-1.06	-1.01	3.39E-01	3.69E-02	1.80E-01
A_24_P98109	-1.08	-1.48	-1.03	-1.23	-1.12	7.26E-01	1.06E-02	8.33E-01
A_32_P9924	1.10	1.09	1.43	1.26	1.18	3.52E-01	3.54E-01	3.50E-05
A_32_P22679	1.02	1.40	1.20	1.49	1.24	8.73E-01	3.95E-02	8.57E-02
A_23_P161209	-1.39	-1.19	-1.27	1.10	-1.49	3.95E-02	4.69E-03	3.74E-02
A_24_P937319	1.10	1.09	1.05	1.44	1.58	4.80E-01	4.52E-01	6.04E-01
A_23_P44088	-1.09	1.33	1.21	1.36	1.53	3.83E-01	6.58E-02	1.56E-01
A_23_P166100	-1.40	-1.09	-1.16	-1.22	-1.34	5.09E-03	2.04E-01	6.93E-04
A_23_P44674	-1.49	-1.31	-1.17	-1.18	1.04	3.37E-02	7.48E-03	6.36E-02
A_23_P33511	-1.20	-1.76	1.02	1.01	-1.47	5.56E-02	9.76E-03	6.96E-01
A_32_P215556	-1.09	-1.49	-1.06	-1.53	1.01	7.55E-01	2.52E-01	7.20E-01
A_23_P170579	-1.13	1.21	1.28	1.31	1.73	4.44E-01	2.00E-01	2.05E-01
A_23_P11874	1.30	1.65	1.15	1.65	1.11	1.43E-01	1.29E-01	1.31E-01
A_32_P171793	-1.37	-1.31	-1.09	-1.22	-1.17	3.25E-02	9.25E-03	2.27E-01
A_32_P128368	1.13	1.21	1.10	1.20	1.42	5.77E-01	3.24E-01	5.93E-01
A_24_P170726	1.17	1.06	1.05	1.89	1.41	2.69E-01	7.48E-01	7.24E-01
A_23_P366125	1.17	-1.04	1.15	1.58	1.25	2.89E-01	7.63E-01	1.65E-01
A_23_P390097	1.37	1.03	1.09	1.50	1.26	4.15E-02	6.28E-01	2.97E-01
A_24_P357688	-1.12	-1.37	1.00	-1.42	-1.40	5.95E-01	1.49E-01	9.75E-01
A_24_P918527	-1.10	-1.23	1.02	-1.65	-1.27	2.96E-01	1.42E-01	8.23E-01
A_32_P73535	-1.38	-1.36	-1.64	-1.05	1.34	1.36E-02	4.82E-03	1.08E-02
A_23_P145024	-1.16	-1.29	-1.21	-1.09	-1.21	3.97E-01	1.44E-02	1.53E-02
A_24_P392146	1.27	1.17	1.06	1.35	1.32	4.21E-02	2.22E-01	3.35E-01
A_24_P822704	1.15	1.24	1.30	1.23	1.09	4.93E-01	1.76E-01	1.81E-01
A_32_P101420	1.15	-1.05	1.12	1.46	1.62	4.37E-01	7.19E-01	2.91E-01
A_32_P416161	1.33	-1.07	1.13	1.27	1.84	2.18E-01	7.50E-01	2.86E-01
A_23_P110430	1.02	-1.41	-1.18	-1.25	1.15	9.54E-01	7.80E-02	3.10E-01
A_23_P48513	1.20	-1.05	1.40	1.54	-1.33	3.37E-01	8.36E-01	2.08E-02
A_23_P208389	-1.21	-1.08	1.04	-1.42	-1.54	1.05E-01	3.85E-01	6.06E-01
A_32_P142128	-1.11	1.21	1.32	1.73	1.05	4.64E-01	1.17E-01	1.63E-02
A_23_P345118	1.25	1.35	1.05	1.51	-1.13	2.62E-01	2.85E-02	4.56E-01
A_32_P72394	1.11	1.19	1.04	1.48	1.34	4.33E-01	2.65E-01	6.91E-01
A_23_P69154	-1.11	1.04	-1.13	-1.26	-1.92	5.81E-01	8.31E-01	4.29E-01
A_23_P215944	1.38	1.03	1.12	1.13	3.04	3.57E-02	8.04E-01	1.64E-01
A_23_P56578	-1.40	-1.14	-1.02	-1.45	-1.41	1.83E-01	6.52E-01	8.58E-01
A_24_P399888	1.76	-1.06	1.23	1.41	1.04	7.50E-02	7.47E-01	1.59E-01
A_23_P121533	1.14	1.27	1.17	1.31	-1.10	1.01E-01	4.31E-03	1.85E-01
A_24_P404628	-1.22	-1.39	1.01	-1.43	-1.14	2.20E-01	2.22E-02	9.00E-01
A_24_P238666	1.26	1.37	-1.05	1.11	1.55	1.31E-01	1.40E-02	6.63E-01
A_24_P406006	1.16	1.20	1.08	1.01	2.18	5.74E-01	8.92E-02	7.29E-01
A_23_P142756	-1.41	-1.02	-1.08	-1.27	-1.31	6.43E-02	9.18E-01	6.71E-01
A_23_P360777	-1.31	-1.15	-1.18	-1.55	1.18	1.02E-01	3.07E-01	3.06E-02

A_32_P113472	1.62	1.02	1.28	1.25	-1.02	1.84E-02	8.84E-01	3.58E-02
A_23_P254165	-1.38	-1.35	-1.24	-1.37	1.32	1.44E-01	1.81E-02	3.54E-02
A_24_P933940	-1.07	1.30	1.10	1.08	1.88	7.20E-01	7.04E-03	5.23E-01
A_23_P91430	1.30	1.10	1.24	1.43	-1.03	2.19E-01	3.91E-01	6.96E-02
A_23_P717	1.31	1.13	1.25	1.24	1.35	1.53E-01	2.15E-01	9.49E-02
A_23_P47426	1.21	1.25	1.10	-1.01	1.58	2.83E-01	5.31E-03	4.46E-01
A_32_P165297	-1.33	-1.29	-1.18	-1.00	-1.42	4.46E-02	2.42E-01	3.19E-02
A_24_P350196	-1.18	-1.28	-1.01	-1.35	-1.24	1.21E-01	2.93E-02	9.29E-01
A_24_P46417	1.25	1.04	1.07	1.18	1.97	2.30E-01	5.79E-01	3.99E-01
A_23_P19754	1.26	1.04	1.25	1.43	1.53	2.89E-01	5.84E-01	1.47E-01
A_32_P191120	1.22	1.31	1.23	1.01	1.37	1.52E-01	6.47E-02	2.17E-01
A_32_P90709	-1.21	-1.15	-1.24	-1.39	1.10	2.37E-01	4.76E-01	4.07E-02
A_24_P90097	-1.23	-1.11	-1.02	-1.78	-1.11	9.92E-02	2.54E-01	8.29E-01
A_23_P217379	1.08	1.07	1.18	1.71	1.17	4.30E-01	2.11E-01	2.11E-02
A_24_P251962	-1.35	-1.01	-1.39	-1.25	-1.33	1.16E-01	9.57E-01	4.71E-02
A_23_P76480	-1.13	-1.51	-1.11	-1.08	-1.28	2.32E-01	2.87E-03	1.52E-01
A_24_P231057	-1.05	-1.22	-1.04	-1.58	-1.21	7.39E-01	8.45E-02	7.24E-01
A_23_P39898	1.17	-1.12	1.38	1.05	1.09	3.35E-01	7.59E-01	2.30E-02
A_24_P305933	-1.02	1.24	1.07	1.23	1.85	8.47E-01	2.01E-02	3.68E-01
A_32_P150632	-1.46	-1.36	-1.22	-1.31	1.25	6.49E-02	1.88E-02	2.00E-01
A_23_P382835	-1.19	-1.17	-1.03	-1.43	-1.29	1.83E-01	4.09E-01	7.04E-01
A_24_P944751	1.20	1.24	1.28	-1.01	1.44	1.03E-01	2.04E-02	1.12E-02
A_24_P282083	-1.09	1.36	1.25	1.39	1.23	5.99E-01	5.23E-02	1.08E-01
A_24_P354451	1.28	-1.04	1.29	1.46	1.12	1.08E-01	6.39E-01	3.17E-03
A_23_P130466	1.05	1.45	1.04	1.22	1.40	5.39E-01	5.31E-03	5.81E-01
A_24_P783679	-1.01	-1.31	-1.02	-1.55	-1.47	9.69E-01	1.46E-01	7.70E-01
A_23_P319640	1.08	1.41	1.11	1.09	1.39	5.55E-01	1.26E-03	4.40E-01
A_24_P418408	1.28	1.17	1.04	1.35	1.36	9.21E-02	7.15E-02	5.52E-01
A_24_P338788	1.79	1.01	1.00	1.35	1.46	6.39E-02	8.91E-01	9.73E-01
A_23_P59358	-1.04	-1.41	-1.10	-1.29	-1.32	4.99E-01	1.54E-03	1.59E-01
A_23_P103511	-1.22	-1.16	-1.26	1.05	-1.63	2.52E-01	1.46E-02	8.08E-03
A_23_P204937	-1.03	-1.23	-1.01	-1.40	-1.58	8.10E-01	6.16E-02	9.23E-01
A_24_P76759	1.35	1.13	1.10	1.35	1.25	2.24E-02	1.37E-01	1.02E-01
A_23_P30666	1.17	1.16	1.20	1.13	1.80	5.53E-01	1.30E-01	9.99E-02
A_23_P135878	1.58	1.18	1.14	-1.16	1.67	4.86E-02	6.87E-02	9.08E-02
A_24_P229936	-1.14	-1.68	-1.16	1.20	-1.38	5.49E-01	6.29E-02	3.22E-01
A_32_P90615	1.06	1.72	1.19	1.05	1.31	7.10E-01	4.21E-02	9.49E-02
A_24_P7121	-1.25	-1.34	-1.30	1.05	-1.28	1.35E-01	3.81E-02	4.05E-02
A_32_P3572	-1.26	-1.46	-1.03	-1.05	-1.95	6.48E-02	1.70E-01	7.84E-01
A_24_P51279	1.01	1.30	1.15	1.56	1.17	9.14E-01	2.56E-02	2.35E-01
A_24_P342279	-1.20	-1.10	-1.15	-1.05	-1.66	2.28E-01	4.93E-01	1.99E-01
A_24_P926783	-1.21	-1.13	1.03	-1.45	-1.54	4.48E-01	3.19E-01	7.92E-01
A_24_P826046	-1.49	-1.07	-1.12	-1.12	-1.32	8.28E-04	4.13E-01	3.75E-02
A_24_P304071	-1.24	1.02	-1.15	-1.51	-1.01	1.10E-01	9.50E-01	3.39E-01
A_23_P163697	-1.58	-1.34	1.03	-1.18	-1.29	5.68E-02	2.74E-02	6.90E-01
A_23_P131747	-1.07	-1.20	1.00	-1.46	-1.39	5.25E-01	9.43E-02	9.88E-01
A_23_P252306	-1.04	1.29	1.09	1.21	1.24	8.32E-01	3.55E-03	3.15E-01

A_24_P69654	-1.48	-1.17	1.02	-1.22	-1.43	1.77E-02	5.11E-02	7.68E-01
A_23_P46447	-1.07	-1.21	-1.14	-1.57	-1.17	4.80E-01	1.44E-02	2.30E-02
A_24_P62169	-1.62	-1.18	1.00	1.15	-1.36	1.19E-01	1.58E-01	9.93E-01
A_24_P762767	1.18	1.16	1.11	1.66	1.07	1.18E-01	4.95E-01	4.70E-01
A_23_P96623	1.21	1.32	1.08	1.13	1.30	1.49E-01	1.85E-02	4.32E-01
A_32_P800799	1.66	-1.03	1.10	1.41	1.22	1.61E-02	6.95E-01	1.71E-01
A_24_P612200	1.06	1.52	1.16	1.09	1.38	4.37E-01	9.11E-03	2.67E-01
A_23_P359052	-1.25	-1.13	-1.04	-1.53	-1.30	2.87E-01	5.95E-01	3.88E-01
A_23_P334173	-1.21	-1.09	-1.25	-1.33	-1.31	1.55E-01	6.15E-02	1.90E-02
A_32_P60709	1.48	1.05	1.25	1.24	1.29	7.06E-02	7.11E-01	1.66E-01
A_23_P134542	-1.12	1.04	-1.32	-1.02	-1.50	6.06E-01	8.47E-01	1.10E-01
A_32_P11372	-1.13	-1.26	-1.05	-1.36	-1.51	4.80E-01	5.16E-02	4.81E-01
A_23_P110851	1.18	1.25	-1.05	1.81	1.08	1.31E-01	5.29E-04	6.12E-01
A_32_P12282	1.96	1.06	-1.00	1.28	1.08	5.82E-03	5.39E-01	9.87E-01
A_24_P307580	1.13	1.02	1.30	1.48	1.18	3.39E-01	8.70E-01	2.30E-02
A_23_P435394	1.00	-1.20	-1.29	-1.24	-1.30	9.82E-01	1.50E-01	8.45E-02
A_23_P156185	1.32	1.35	-1.10	1.25	1.15	1.68E-01	3.37E-02	5.52E-01
A_23_P77201	1.16	1.22	1.16	1.05	1.59	2.76E-01	6.83E-02	1.15E-01
A_24_P161144	1.19	1.15	-1.01	1.49	1.32	3.30E-01	2.02E-01	9.49E-01
A_24_P10137	-1.02	-1.20	1.03	-1.44	-1.61	8.66E-01	5.45E-02	8.16E-01
A_23_P75056	-1.29	-1.39	-1.12	1.04	-1.45	1.47E-01	5.89E-03	9.42E-02
A_23_P388855	-1.29	-1.25	1.00	-1.36	-1.20	5.24E-02	5.23E-02	9.92E-01
A_24_P128741	-1.06	-1.56	-1.18	-1.16	-1.29	7.67E-01	6.85E-02	7.99E-02
A_23_P75129	-1.09	-1.31	1.06	-1.25	-1.63	3.65E-01	5.95E-02	6.65E-01
A_32_P110390	1.05	1.13	1.02	1.41	1.62	7.06E-01	2.08E-01	8.23E-01
A_32_P70483	1.38	1.02	1.01	1.63	1.27	1.16E-01	8.62E-01	9.26E-01
A_32_P220078	1.50	1.32	1.07	1.18	1.21	1.90E-02	7.63E-02	2.10E-01
A_23_P405707	1.05	1.17	1.25	1.37	1.10	7.30E-01	1.46E-01	1.07E-02
A_23_P153958	-1.62	1.08	-1.13	-1.28	-1.22	1.40E-01	7.81E-01	3.82E-01
A_24_P251764	-1.00	-1.67	-1.15	-1.15	-1.22	9.90E-01	1.57E-02	2.09E-01
A_23_P154962	1.04	-1.43	1.03	-1.32	1.02	8.92E-01	2.98E-01	8.78E-01
A_23_P395438	-1.12	-1.18	-1.11	-1.58	-1.02	5.99E-01	3.62E-01	3.90E-01
A_23_P18055	1.15	1.32	-1.03	1.57	1.16	4.85E-01	1.96E-02	6.80E-01
A_23_P31124	-1.22	-1.06	-1.35	-1.57	1.01	1.85E-01	6.15E-01	7.57E-04
A_23_P104804	-1.45	-1.09	-1.37	-1.26	-1.47	1.51E-01	1.57E-01	1.64E-02
A_23_P117302	1.56	1.15	-1.08	1.15	1.92	9.11E-02	1.16E-01	6.55E-01
A_23_P56288	1.07	-1.06	1.33	1.19	1.88	6.49E-01	7.89E-01	1.33E-01
A_23_P156443	-1.21	-1.38	1.04	-1.02	-1.51	1.03E-01	6.79E-02	7.70E-01
A_23_P372638	-1.35	-1.15	-1.01	-1.55	-1.14	8.76E-02	2.99E-01	7.62E-01
A_23_P208393	1.49	1.20	1.07	1.20	1.23	1.61E-02	3.15E-02	5.07E-01
A_32_P18034	-1.04	1.33	1.11	1.09	1.71	7.37E-01	9.39E-03	3.73E-01
A_32_P193218	-1.24	1.01	-1.12	-1.49	-1.16	3.43E-02	9.29E-01	4.76E-01
A_23_P94546	-1.15	-1.51	-1.12	-1.57	1.07	1.12E-01	5.52E-02	1.03E-01
A_23_P171385	-1.24	-1.22	-1.03	-1.12	-1.65	2.23E-01	2.32E-01	7.11E-01
A_23_P133438	-1.25	-1.24	-1.24	-1.37	-1.04	1.38E-01	1.11E-01	7.86E-02
A_32_P45351	-1.27	-1.31	-1.28	-1.39	1.28	9.95E-02	2.21E-02	1.51E-02
A_32_P919718	1.01	1.19	1.16	1.50	1.17	9.63E-01	1.34E-01	2.73E-01

A_23_P3643	1.39	-1.09	1.25	1.33	1.46	2.08E-01	4.93E-01	1.46E-01
A_24_P564462	1.59	1.14	1.06	1.31	1.17	1.06E-02	1.69E-02	5.16E-01
A_24_P320645	-1.39	1.03	-1.20	-1.07	-1.67	7.78E-02	7.67E-01	5.82E-02
A_32_P164477	-1.19	-1.37	-1.20	-1.26	1.15	3.88E-01	1.80E-01	1.72E-01
A_32_P137391	1.31	1.30	1.32	1.03	1.09	1.52E-01	2.69E-01	3.17E-02
A_23_P201837	-1.12	-1.09	-1.12	-1.31	-1.49	2.43E-01	2.83E-01	1.75E-01
A_32_P385	1.09	1.24	1.14	1.48	1.00	6.32E-01	3.52E-01	2.35E-01
A_23_P149390	1.20	1.07	1.16	1.27	1.73	3.33E-01	6.57E-01	3.17E-01
A_23_P319050	1.45	1.21	1.15	1.06	1.66	2.70E-01	3.60E-01	5.22E-01
A_24_P170295	1.00	-1.12	-1.10	-1.25	-1.69	9.89E-01	4.72E-01	3.05E-01
A_32_P129810	1.14	1.40	1.10	1.39	1.21	3.08E-01	8.85E-02	3.75E-01
A_24_P159515	1.31	1.11	1.15	1.20	1.58	5.81E-02	2.81E-01	3.67E-01
A_23_P359636	-1.12	-1.37	-1.00	-1.16	-1.45	3.59E-01	1.85E-02	9.85E-01
A_32_P105694	-1.26	1.27	1.10	1.47	1.36	3.14E-01	1.07E-01	6.16E-01
A_24_P126246	1.33	1.09	1.08	1.57	1.32	2.19E-01	7.34E-01	5.13E-01
A_23_P150189	-1.18	-1.07	-1.15	-1.45	-1.27	2.71E-01	5.43E-01	9.97E-02
A_24_P290623	-1.00	1.18	1.42	1.62	1.03	9.92E-01	4.19E-01	4.17E-02
A_23_P211064	-1.22	1.00	-1.15	-1.29	-1.35	2.94E-01	9.81E-01	2.39E-01
A_32_P66684	1.21	1.33	1.06	1.74	-1.04	3.13E-01	2.44E-02	4.59E-01
A_32_P13719	1.25	1.21	1.15	1.02	1.45	1.41E-01	8.55E-02	2.19E-01
A_23_P216199	-1.43	-1.07	-1.22	-1.12	-1.53	6.43E-02	5.87E-01	3.51E-01
A_24_P75543	1.65	1.01	1.05	1.30	1.33	2.46E-02	8.18E-01	6.81E-01
A_23_P39386	-1.34	-1.28	-1.10	-1.01	-1.19	8.13E-02	3.87E-03	3.35E-01
A_24_P2584	-1.12	-1.14	1.00	-1.21	-1.86	2.27E-01	3.40E-01	9.87E-01
A_32_P72553	-1.31	-1.03	-1.01	-1.18	-1.69	1.62E-02	7.46E-01	8.65E-01
A_24_P278552	1.17	1.15	1.57	1.45	-1.16	5.26E-01	1.34E-01	3.32E-02
A_23_P57474	1.18	1.24	1.07	1.28	1.47	4.98E-01	2.36E-02	4.61E-01
A_24_P943180	1.14	1.27	1.19	1.08	1.44	4.23E-01	1.47E-01	1.59E-01
A_24_P945113	-1.19	-1.08	-1.13	-1.32	-1.63	5.04E-01	2.25E-01	3.44E-01
A_32_P24382	1.28	1.33	1.19	1.16	1.01	4.79E-01	1.12E-01	5.42E-01
A_23_P216812	-1.07	-1.25	1.01	-1.27	-1.65	6.26E-01	7.00E-02	9.26E-01
A_23_P112187	1.47	1.01	1.11	1.15	1.24	2.01E-02	9.53E-01	5.38E-01
A_24_P59220	-1.11	-1.02	-1.01	-1.42	-1.59	5.26E-01	8.10E-01	8.73E-01
A_24_P179569	-1.30	-1.13	-1.19	1.13	-1.58	1.63E-01	4.06E-01	1.76E-01
A_24_P100277	-1.01	1.04	-1.29	-1.33	-1.53	9.07E-01	6.11E-01	9.31E-03
A_23_P154688	1.05	1.31	1.12	1.20	1.45	7.17E-01	5.31E-02	2.04E-01
A_23_P18246	1.38	1.20	1.09	1.16	1.22	7.71E-03	4.86E-02	2.58E-01
A_24_P412156	1.03	-1.05	-1.13	-1.34	-1.33	9.42E-01	6.99E-01	5.24E-01
A_32_P39093	1.16	1.48	1.06	1.06	1.41	2.18E-01	5.21E-03	2.72E-01
A_24_P868583	-1.01	-1.11	-1.40	-1.23	1.10	9.58E-01	7.29E-01	1.52E-03
A_24_P75456	1.60	1.01	1.03	1.44	1.31	5.47E-02	8.80E-01	7.44E-01
A_23_P323154	1.35	-1.02	1.07	1.30	1.52	4.97E-02	8.87E-01	4.98E-01
A_23_P52939	-1.54	-1.17	-1.25	1.05	-1.06	2.74E-03	9.12E-02	2.11E-03
A_24_P137563	-1.29	-1.52	-1.04	-1.24	-1.12	6.70E-02	2.43E-02	4.62E-01
A_23_P212552	-1.14	-1.17	-1.10	-1.76	1.00	3.12E-01	2.66E-02	1.70E-01
A_23_P17560	-1.18	-1.11	-1.15	-1.09	-1.72	2.50E-01	4.29E-01	2.32E-01
A_24_P79529	-1.35	-1.19	-1.06	1.37	-1.63	9.63E-02	4.01E-01	7.08E-01

A_24_P371670	-1.14	-1.24	-1.00	-1.20	-1.57	1.92E-01	2.95E-02	9.71E-01
A_24_P500621	1.13	1.19	1.29	1.18	1.35	2.36E-01	3.29E-03	3.34E-03
A_24_P557534	-1.32	-1.56	-1.06	-1.19	-1.01	1.93E-02	2.57E-03	2.77E-01
A_32_P82863	-1.22	-1.40	1.00	-1.49	-1.21	1.23E-02	1.61E-01	9.89E-01
A_23_P130027	1.41	1.13	-1.01	1.37	1.41	1.17E-01	3.65E-01	8.63E-01
A_23_P208866	-1.32	-1.29	-1.08	-1.02	-1.41	9.68E-02	1.07E-02	4.48E-01
A_24_P201702	-1.12	-1.49	-1.09	-1.08	-1.25	3.79E-01	2.94E-03	2.32E-01
A_23_P385034	1.19	1.19	1.41	-1.08	1.42	3.39E-01	3.05E-02	2.22E-03
A_24_P932293	1.15	1.04	1.62	1.18	1.12	3.09E-01	7.72E-01	3.02E-03
A_23_P82379	-1.03	-1.11	-1.21	-1.18	-1.70	9.02E-01	1.91E-01	9.89E-02
A_23_P303149	-1.19	-1.11	-1.18	1.00	-1.64	3.06E-01	2.84E-01	1.50E-01
A_32_P147505	1.01	-1.08	-1.14	-1.39	-1.46	9.08E-01	5.51E-01	5.36E-02
A_24_P284213	-1.44	-1.01	-1.03	-1.29	-1.38	6.24E-02	9.77E-01	7.47E-01
A_32_P192354	-1.18	-1.14	-1.33	-1.05	-1.28	4.83E-01	4.43E-01	4.39E-02
A_24_P226210	-1.08	-1.28	-1.20	-1.50	-1.17	3.74E-01	1.25E-01	1.70E-01
A_23_P501961	1.11	1.24	1.24	1.05	1.44	2.34E-01	9.45E-02	2.25E-02
A_23_P258504	-1.53	-1.14	-1.28	1.33	-1.38	2.97E-02	3.52E-01	1.91E-03
A_32_P68050	-1.12	-1.44	1.04	-1.51	-1.12	2.68E-01	1.99E-02	6.67E-01
A_23_P37954	1.13	1.37	1.04	1.24	1.39	4.88E-01	2.62E-01	7.21E-01
A_23_P51926	1.22	1.31	1.23	1.01	-1.09	1.37E-01	4.86E-02	3.66E-02
A_23_P34700	-1.32	-1.13	-1.43	1.02	-1.19	6.25E-02	3.17E-01	1.17E-04
A_23_P163467	1.18	1.04	1.14	1.34	1.28	1.14E-01	7.48E-01	7.31E-02
A_32_P112223	-1.72	-1.25	-1.16	-1.08	1.14	1.81E-02	2.93E-01	1.35E-01
A_24_P914590	-1.03	1.00	-1.10	-1.43	-1.85	8.13E-01	9.53E-01	2.84E-01
A_32_P12504	1.24	1.21	1.14	1.11	1.46	1.77E-01	9.97E-02	2.06E-01
A_23_P212050	1.16	1.13	1.23	1.03	1.45	3.83E-01	2.80E-01	5.14E-02
A_24_P247820	1.22	1.19	1.17	1.26	1.16	2.41E-01	8.97E-02	2.93E-01
A_23_P73747	-1.07	-1.23	-1.09	-1.45	-1.14	6.87E-01	1.58E-01	2.56E-01
A_23_P18818	1.49	-1.00	1.15	1.42	1.03	9.84E-02	9.90E-01	3.57E-01
A_24_P341863	1.29	1.19	1.10	1.07	1.52	1.14E-01	2.01E-01	6.07E-01
A_23_P204696	-1.37	-1.20	-1.13	-1.04	-1.57	1.46E-01	1.76E-01	2.22E-01
A_23_P412214	1.09	1.21	-1.02	1.26	1.76	6.14E-01	2.81E-02	9.00E-01
A_23_P46725	-1.41	-1.22	-1.01	-1.03	-1.51	7.98E-02	2.52E-01	8.94E-01
A_32_P206549	-1.01	1.28	1.02	1.23	1.67	9.71E-01	1.64E-01	7.05E-01
A_24_P935026	1.12	1.04	1.46	1.15	1.10	5.87E-01	8.00E-01	1.19E-02
A_32_P168442	-1.36	-1.45	-1.18	1.06	1.08	4.82E-02	1.58E-01	2.48E-01
A_24_P77904	-1.04	-1.22	-1.06	-1.28	-1.76	8.49E-01	9.62E-02	8.22E-01
A_23_P70660	-1.34	-1.22	-1.17	-1.20	-1.17	1.57E-02	4.40E-03	9.47E-04
A_23_P170608	-1.32	-1.16	-1.18	-1.09	-1.32	6.19E-02	3.95E-01	1.02E-01
A_23_P343826	1.41	1.18	-1.07	1.23	1.47	1.28E-01	7.71E-02	7.01E-01
A_24_P928765	1.06	1.15	1.39	1.36	1.13	8.16E-01	1.94E-01	8.20E-02
A_32_P45168	-1.08	-1.10	-1.06	-1.52	-1.35	4.45E-01	1.99E-01	6.13E-01
A_23_P35576	-1.16	-1.26	-1.04	-1.67	-1.09	4.39E-01	1.62E-01	6.41E-01
A_23_P332908	-1.18	-1.30	-1.08	-1.33	-1.26	3.63E-01	3.33E-02	2.45E-01
A_23_P335920	1.37	1.47	1.16	-1.04	1.11	4.39E-03	2.85E-03	1.72E-04
A_23_P86610	-1.47	-1.16	-1.14	1.00	1.15	1.69E-02	3.22E-01	3.93E-01
A_24_P896619	1.11	1.11	1.58	1.12	1.31	5.00E-01	4.21E-01	3.05E-02

A_23_P328022	1.07	1.17	1.00	1.53	1.37	6.15E-01	3.42E-01	9.89E-01
A_23_P409438	1.26	1.18	1.05	1.13	1.61	3.79E-02	2.28E-01	7.51E-01
A_23_P10591	1.15	1.25	1.02	1.21	1.83	3.20E-01	3.65E-02	8.22E-01

		Fold change	P value	PrimaryAccession	UniGeneID	GeneSymbol
AS	Ethnic	Meta analysis	Meta anlaysis			
8.18E-01	2.66E-05	4.14	1.77E-02	NM_002988	Hs.143961	CCL18
8.06E-02	9.63E-03	3.36	8.77E-03	NM_181534	Hs.55412	KRT25
1.87E-04	2.53E-02	-2.77	6.46E-04	NM_198956	Hs.195922	SP8
5.82E-01	4.87E-01	2.48	1.93E-02	NM_000550	Hs.270279	TYRP1
3.57E-01	9.47E-01	2.32	1.06E-02	NM_006928	Hs.95972	SILV
3.49E-02	5.12E-03	-2.24	3.29E-03	NM_006160	Hs.322431	NEUROD2
2.08E-01	8.55E-01	2.23	8.20E-03	NM_006928	Hs.95972	SILV
3.64E-04	3.93E-01	-2.22	2.26E-04	NM_176813	Hs.100686	AGR3
4.05E-01	1.32E-03	-2.12	3.99E-04	NM_133431	Hs.112208	XAGE1D
4.42E-02	2.79E-03	2.09	3.41E-02	BC010054		RPSA
1.33E-03	7.92E-01	-2.02	7.73E-03	NM_004086	Hs.21016	COCH
1.65E-01	2.82E-03	-1.97	6.41E-10	NM_005235	Hs.390729	ERBB4
1.59E-01	8.06E-01	1.94	3.27E-03	NM_152738	Hs.173337	C6orf218
4.38E-01	4.69E-01	1.93	3.53E-02	NM_030967	Hs.247934	KRTAP1-1
1.75E-02	4.94E-02	-1.90	2.78E-03	NM_080676	Hs.661576	MACROD2
4.31E-01	4.53E-01	1.90	2.55E-03	NM_000273	Hs.74124	GPR143
7.57E-03	9.25E-01	1.90	8.63E-03	THC2711870		
5.90E-03	2.99E-01	-1.89	8.63E-05	NM_000517	Hs.654744	HBA2
1.50E-03	7.83E-03	1.89	3.09E-02	NM_138813	Hs.306212	ATP8B3
3.06E-01	9.69E-01	1.89	2.00E-02	THC2675163		
5.63E-03	3.10E-01	-1.87	2.87E-04	NM_000517	Hs.654744	HBA2
8.42E-01	3.84E-01	1.87	4.28E-02	NM_000372	Hs.503555	TYR
4.61E-03	3.68E-01	1.85	5.66E-04	NM_181607	Hs.61552	KRTAP19-1
5.19E-01	5.32E-01	1.85	2.20E-02	NM_003991	Hs.82002	EDNRB
8.24E-02	1.75E-02	1.85	2.02E-02	NM_001004298	Hs.587663	C10orf90
5.27E-01	6.08E-01	1.83	3.63E-02	NM_002420	Hs.155942	TRPM1
1.93E-03	6.06E-03	1.82	4.08E-04	AF289567	Hs.684029	
4.27E-03	8.13E-01	-1.80	2.82E-02	NM_004086	Hs.21016	COCH
3.00E-02	4.20E-02	1.79	1.47E-06	NM_020299	Hs.116724	AKR1B10
4.05E-01	2.07E-01	1.78	4.18E-03	NM_025139	Hs.471610	ARMC9
3.03E-06	5.63E-02	1.77	4.10E-02	NM_003125	Hs.1076	SPRR1B
4.29E-04	6.32E-02	1.77	9.98E-03	NM_012206	Hs.129711	HAVCR1
3.26E-02	5.44E-02	1.76	7.41E-06	NM_020299	Hs.116724	AKR1B10
8.82E-05	6.69E-05	-1.75	1.76E-02	NM_004061	Hs.113684	CDH12
9.76E-02	3.72E-01	1.74	1.62E-02	NM_032588	Hs.279709	TRIM63
7.32E-01	9.12E-01	1.74	3.49E-02	NM_006877	Hs.484741	GMPR
9.20E-01	6.65E-01	-1.73	3.23E-02	NM_001926	Hs.711	DEFA6
3.16E-02	3.27E-03	-1.72	5.86E-04	AK054921	Hs.571748	CDR1
3.87E-01	2.73E-01	-1.71	3.00E-02	NM_016522	Hs.504352	HNT
5.79E-01	1.58E-01	-1.70	3.84E-04	NM_174914	Hs.348941	UGT3A2
1.06E-02	9.14E-01	-1.70	5.74E-03	NM_000558	Hs.449630	HBA1
2.54E-02	5.51E-01	1.69	6.91E-04	NM_178012	Hs.300701	TUBB2B
2.76E-01	5.52E-01	1.68	2.68E-03	BC008034		
2.49E-03	1.76E-01	1.68	1.33E-02	NM_181607	Hs.61552	KRTAP19-1
4.37E-05	1.82E-02	1.67	7.46E-06	NM_007210	Hs.505575	GALNT6
2.40E-01	4.46E-01	-1.66	7.68E-09	NM_001765	Hs.132448	CD1C

1.60E-02	1.03E-01	1.66	1.58E-08			
1.34E-01	8.92E-01	-1.66	5.76E-05	NM_001012415	Hs.120464	SOHLH1
7.39E-01	6.30E-02	-1.66	5.17E-03	NM_003054	Hs.654476	SLC18A2
4.61E-01	6.99E-01	1.65	8.01E-03	NM_016180	Hs.278962	SLC45A2
1.38E-03	4.29E-02	1.65	2.60E-03	D00044	Hs.514107	CCL3
9.54E-05	9.75E-02	1.65	8.39E-03	NM_016190	Hs.242057	CRNN
4.05E-01	5.42E-01	1.65	7.52E-03	NM_032524	Hs.307022	KRTAP4-4
1.37E-04	7.62E-03	1.65	1.80E-02	NM_175053	Hs.660125	KRT74
1.82E-03	1.60E-02	-1.65	2.00E-04	NM_004616	Hs.170563	TSPAN8
5.10E-03	4.72E-01	1.64	2.13E-02	NM_025139	Hs.471610	ARMC9
7.04E-04	8.77E-01	1.64	1.13E-02	NM_013364	Hs.449627	PNMA3
8.49E-05	7.12E-01	-1.64	2.80E-02	NM_178127	Hs.318370	ANGPTL5
2.99E-03	1.42E-01	1.63	7.73E-05	NM_013358	Hs.412941	PADI1
7.63E-01	2.66E-03	1.63	2.42E-03	NM_052906	Hs.705655	ELFN2
1.41E-03	3.80E-02	1.63	2.90E-03	AK124776	Hs.444290	
2.26E-03	2.50E-01	1.62	4.13E-04	NM_005987	Hs.46320	SPRR1A
5.33E-01	1.10E-02	1.62	6.88E-03	NM_173505	Hs.374774	ANKRD29
7.73E-02	6.47E-01	-1.62	1.42E-02	NM_000518	Hs.523443	HBB
3.45E-02	1.11E-01	-1.62	3.88E-03	NM_019029	Hs.233389	CPVL
1.90E-03	4.79E-03	-1.62	8.43E-04	NM_002023	Hs.519168	FMOD
5.27E-01	5.99E-04	-1.61	2.55E-02	NM_002121	Hs.485130	HLA-DPB1
1.94E-01	1.44E-01	1.61	1.04E-02	ENST00000345847	Hs.307014	
5.77E-03	1.57E-02	1.61	1.65E-02	THC2635964		
3.61E-03	3.17E-02	1.61	3.14E-02	NM_153646	Hs.510281	SLC24A4
2.04E-04	1.41E-02	1.61	9.57E-04	NM_001444	Hs.408061	FABP5
2.82E-03	6.43E-02	1.60	1.10E-04	XM_001125944		LOC344332
4.46E-02	3.02E-03	-1.60	2.68E-02	ENST00000308384	Hs.646975	
6.85E-01	3.01E-02	1.59	2.17E-03			
1.02E-01	5.21E-01	-1.59	9.83E-03	NM_000519	Hs.699280	HBD
2.31E-02	3.34E-04	-1.58	3.21E-02	NM_004378	Hs.346950	CRABP1
2.41E-02	7.40E-04	1.58	3.02E-02	NM_178434	Hs.490211	LCE3C
7.13E-02	1.75E-02	1.58	4.62E-02	NM_030649	Hs.535257	CENTB5
1.29E-01	6.61E-03	-1.58	6.70E-03	ENST00000383121	Hs.409934	
5.98E-02	3.33E-03	-1.58	1.23E-03	NM_002125	Hs.534322	HLA-DRB5
1.66E-01	1.59E-01	-1.58	3.39E-04	NM_006889	Hs.171182	CD86
1.12E-02	2.93E-03	-1.57	2.37E-03	THC2742812		
1.86E-02	1.86E-03	1.57	3.23E-02	NM_005416	Hs.139322	SPRR3
4.45E-01	2.14E-02	1.56	3.89E-02	ENST00000377006	Hs.628968	
3.37E-02	4.54E-03	-1.56	1.15E-08	NM_007102	Hs.32966	GUCA2B
7.20E-02	5.76E-02	1.56	1.30E-02	NM_033448	Hs.660007	KRT71
1.91E-01	8.01E-03	1.55	2.89E-06	NM_015210	Hs.650822	KIAA0802
7.62E-02	4.14E-01	-1.55	9.14E-03	NM_000032	Hs.522666	ALAS2
7.77E-01	1.15E-01	1.55	3.51E-02	NM_004183	Hs.705554	BEST1
1.80E-04	3.62E-01	1.55	6.22E-03	NM_001080494	Hs.112949	C1orf34
2.47E-01	5.16E-02	1.55	7.22E-03	NM_002279	Hs.32950	KRT33B
2.09E-03	3.01E-01	-1.54	6.66E-16	BI836406	Hs.130203	
5.30E-01	7.70E-01	-1.54	4.02E-02	NM_001926	Hs.711	DEFA6

6.03E-03	2.89E-01	1.54	1.33E-06	NM_023112	Hs.278815	OTUB2
1.10E-02	6.62E-02	1.54	3.33E-03	NM_002108	Hs.190783	HAL
1.93E-01	6.55E-01	1.54	1.02E-05	NM_000166	Hs.333303	GJB1
3.82E-04	2.81E-01	1.54	1.16E-04	DA727827	Hs.670082	
2.72E-04	8.88E-03	1.54	1.11E-10	NM_001099676	Hs.535190	C12orf56
3.69E-02	3.53E-02	1.53	3.71E-06	NM_006086	Hs.511743	TUBB3
1.31E-01	6.15E-01	1.53	4.47E-02	AX721193	Hs.635114	
7.27E-01	3.40E-01	-1.53	4.05E-02	NM_080676	Hs.661576	MACROD2
9.03E-02	1.24E-02	-1.53	1.54E-02	NM_002121	Hs.485130	HLA-DPB1
5.15E-02	1.85E-02	1.53	4.36E-03	NM_080869	Hs.352180	WFDC12
6.23E-03	2.03E-02	1.53	2.08E-02	AK091366	Hs.650266	FLJ34047
8.44E-03	4.61E-02	-1.53	7.24E-07	NM_144669	Hs.655668	GLT1D1
2.69E-01	1.38E-01	-1.53	1.08E-02	NM_020056	Hs.591798	HLA-DQA2
8.36E-01	4.08E-03	-1.52	1.91E-02	NM_001079529	Hs.646912	FAM153B
2.60E-02	2.16E-02	-1.52	8.07E-03	NM_022555	Hs.534322	HLA-DRB3
1.51E-01	2.26E-01	-1.52	2.21E-02	NM_002838	Hs.654514	PTPRC
9.36E-01	1.52E-02	-1.51	4.51E-02	NM_000246	Hs.701991	CIITA
1.84E-01	5.95E-02	-1.51	7.87E-04	NM_001763	Hs.1309	CD1A
1.20E-01	1.09E-03	1.51	1.12E-02	NM_012413	Hs.79033	QPCT
3.71E-03	9.87E-01	-1.51	2.43E-02	NM_001003679	Hs.705413	LEPR
3.44E-05	9.81E-02	-1.51	4.63E-03	NM_006682	Hs.520989	FGL2
9.68E-01	1.64E-03	-1.51	3.99E-02	NM_024867	Hs.298863	SPEF2
4.15E-01	3.13E-01	-1.51	8.00E-03	AW451533	Hs.610260	
4.18E-04	5.00E-02	1.51	1.08E-03	NM_173681	Hs.647092	ATG9B
6.61E-01	3.05E-01	-1.50	2.67E-04	NM_002089	Hs.590921	CXCL2
4.82E-01	1.35E-01	-1.50	1.52E-03	NM_003874	Hs.398093	CD84
1.18E-01	4.20E-02	-1.50	2.70E-05	NM_002123	Hs.409934	HLA-DQB1
5.87E-03	2.99E-01	-1.50	1.30E-03	NM_021958	Hs.74870	HLX
6.97E-02	2.81E-01	1.50	9.81E-04	NM_000392	Hs.368243	ABCC2
3.59E-01	3.36E-01	1.49	1.21E-02	THC2643957		
7.19E-02	7.49E-01	1.49	2.66E-02	NM_144677	Hs.144531	MGAT5B
1.68E-01	5.91E-01	1.49	1.12E-02	NM_000392	Hs.368243	ABCC2
5.21E-02	4.69E-01	1.49	1.53E-03	NM_205848	Hs.370963	SYT6
8.40E-03	1.00E-01	1.49	2.58E-05	NM_001012716	Hs.274959	C18orf56
1.32E-01	5.02E-03	-1.49	4.08E-02	NM_004001	Hs.654395	FCGR2B
7.64E-01	8.43E-03	-1.49	2.73E-03	NM_001079527	Hs.652193	FAM153C
4.92E-01	8.28E-03	-1.49	1.63E-02	NM_018690	Hs.200333	APOB48R
3.62E-01	3.05E-02	1.49	4.84E-03	NM_032539	Hs.320368	SLITRK2
1.23E-02	1.89E-01	1.49	4.63E-03	THC2633920		
4.77E-02	1.13E-03	1.49	1.18E-02	NM_012413	Hs.79033	QPCT
1.71E-01	5.26E-03	-1.49	1.24E-02	NM_021983	Hs.705372	HLA-DRB4
2.94E-04	7.42E-01	-1.49	7.73E-14	NM_175571	Hs.647121	GIMAP8
9.73E-01	2.09E-02	-1.49	3.55E-03	NM_199328	Hs.162209	CLDN8
6.18E-01	5.86E-02	-1.48	4.17E-07	ENST00000327506	Hs.361778	
6.24E-04	2.49E-02	1.48	4.03E-04	NM_001444	Hs.408061	FABP5
7.51E-01	9.63E-01	1.48	3.99E-02	BC034319	Hs.363526	
1.69E-01	1.06E-03	1.48	4.99E-02	AK095214		

7.42E-01	2.18E-02	-1.48	3.86E-02	NM_020056	Hs.591798	HLA-DQA2
1.04E-03	1.06E-01	1.48	1.10E-03	NM_025153	Hs.109358	ATP10B
1.56E-02	6.59E-03	-1.48	7.13E-03	NM_004538	Hs.21365	NAP1L3
3.68E-01	3.16E-02	-1.48	1.09E-05	NM_006762	Hs.371021	LAPTM5
6.04E-02	1.04E-02	-1.48	5.09E-03	NM_002124	Hs.534322	HLA-DRB1
1.60E-01	1.55E-01	-1.48	2.33E-02	NM_001003927	Hs.591198	EVI2A
1.06E-01	3.43E-04	1.48	1.79E-02	NM_001080407	Hs.436178	GLB1L3
1.88E-02	4.01E-03	1.48	5.51E-08	ENST00000326470	Hs.199763	
2.89E-01	3.69E-01	-1.47	1.31E-03			
5.95E-02	8.61E-02	1.47	3.50E-04	ENST00000309447	Hs.4280	KIAA1239
2.01E-05	8.64E-02	1.47	9.78E-03	NM_016490	Hs.107922	LOC51252
3.20E-02	7.80E-03	1.47	3.95E-03	NM_001001547	Hs.120949	CD36
3.10E-02	3.01E-01	-1.47	4.87E-03	NM_001763	Hs.1309	CD1A
4.16E-02	1.88E-02	-1.47	6.77E-03	THC2678294		
1.03E-01	8.40E-02	1.47	1.19E-04	S67044		CD36
7.01E-01	9.24E-02	-1.47	5.57E-03	NM_058186	Hs.473877	FAM3B
7.11E-02	2.37E-01	1.47	4.78E-02	NM_002344	Hs.434481	LTK
1.84E-02	1.17E-02	1.46	4.03E-02			
2.47E-01	1.17E-02	-1.46	3.57E-02	NM_001040033	Hs.443057	CD53
1.48E-02	3.51E-02	-1.46	4.77E-03	NM_002001	Hs.897	FCER1A
7.08E-04	7.01E-02	1.46	2.18E-04	NM_001444	Hs.408061	FABP5
1.84E-02	3.47E-02	-1.46	9.28E-03	NM_033554	Hs.347270	HLA-DPA1
4.92E-02	1.39E-03	1.46	1.12E-02	THC2624901		
5.43E-02	5.41E-02	-1.46	1.10E-02	BC106057	Hs.534322	HLA-DRB3
8.23E-03	8.90E-03	1.46	9.77E-03	NM_170587	Hs.368733	RGS20
1.34E-02	8.31E-01	-1.46	4.19E-03	CR593388	Hs.700704	
4.70E-01	7.10E-02	1.45	1.92E-04	NM_033059	Hs.307015	KRTAP4-11
1.57E-03	1.01E-01	1.45	3.07E-05	NM_001444	Hs.408061	FABP5
2.41E-01	6.22E-01	1.45	2.10E-03	BX537788	Hs.658305	
4.41E-01	9.30E-03	-1.45	4.02E-03	NM_175078	Hs.334989	KRT77
2.82E-01	2.93E-01	-1.45	2.65E-02	NM_001838	Hs.370036	CCR7
1.63E-02	3.28E-02	1.45	1.75E-02	XR_018726		LOC340888
1.65E-01	6.82E-02	-1.45	5.03E-04	NM_004288	Hs.270	PSCDBP
3.39E-04	3.55E-01	-1.45	4.17E-02	AW268902	Hs.709761	
1.43E-03	1.16E-02	-1.45	6.07E-05	NM_020650	Hs.567550	RCN3
1.47E-01	1.13E-02	1.45	1.85E-03	XR_037365		LOC10012925
3.66E-01	4.41E-01	1.45	4.21E-02	AK093351	Hs.297967	FLJ36032
1.12E-01	5.36E-01	-1.45	1.55E-02	NM_005504	Hs.438993	BCAT1
9.26E-01	3.47E-01	-1.45	8.02E-03	NM_001080507	Hs.671212	OOEP
2.68E-02	1.89E-02	1.44	1.98E-02	AK022489		MYO1B
2.96E-01	2.96E-01	-1.44	3.88E-03	NM_019043	Hs.310421	APBB1IP
1.46E-02	4.25E-02	1.44	3.27E-04	NM_198828	Hs.595458	MAST4
1.50E-01	5.23E-01	-1.44	1.71E-02	THC2650074		
1.26E-01	7.67E-01	-1.44	5.53E-03	NM_032944	Hs.309767	STK31
1.21E-05	1.60E-02	-1.44	2.97E-02	NM_203339	Hs.436657	CLU
4.56E-02	4.99E-03	1.44	2.38E-04	NM_014028	Hs.226780	OSTM1
9.07E-01	7.49E-01	1.44	3.59E-02	NM_152908	Hs.126830	SLC47A2

1.48E-02	3.68E-02	1.44	2.23E-03	BC014117	Hs.520757	TBXAS1
5.10E-03	1.46E-04	1.44	6.76E-04	NM_175839	Hs.433337	SMOX
8.84E-04	5.36E-03	-1.44	1.19E-02	NM_001449	Hs.435369	FHL1
1.36E-01	1.74E-02	-1.44	3.54E-03	NR_001435		HLA-DPB2
1.66E-02	2.87E-01	1.44	3.35E-04	NM_012253	Hs.102866	TKTL1
2.10E-01	2.79E-01	-1.44	4.99E-02	AK124946	Hs.162868	DPF3
6.52E-01	2.32E-02	-1.43	2.79E-02	AK000992	Hs.658833	
2.85E-01	1.23E-01	-1.43	1.10E-02	NM_015717	Hs.199731	CD207
2.41E-03	7.04E-03	1.43	1.65E-02	AK022479	Hs.658520	
9.50E-02	4.09E-01	-1.43	9.26E-03	NM_001025158	Hs.709190	CD74
2.51E-02	5.57E-02	-1.43	1.36E-03	NM_014737	Hs.631504	RASSF2
2.92E-03	1.76E-02	-1.43	2.96E-02	NM_005807	Hs.647723	PRG4
8.01E-01	2.96E-01	-1.43	6.47E-03	NM_001015880	Hs.524491	PAPSS2
3.23E-01	1.03E-01	1.43	3.23E-02	NM_003101	Hs.496383	SOAT1
4.83E-01	8.39E-02	-1.43	1.15E-03	AJ002788	Hs.460355	
9.23E-04	7.03E-01	1.43	3.75E-02	NM_032727	Hs.500916	INA
7.36E-03	3.11E-02	1.43	9.05E-03			
4.33E-01	8.27E-03	-1.42	2.10E-02			
7.00E-01	2.61E-02	1.42	5.10E-03	NM_207309	Hs.142076	UAP1L1
2.61E-02	2.05E-01	1.42	3.28E-02	NM_018092	Hs.444046	NETO2
4.28E-01	7.22E-02	-1.42	4.09E-05	XM_933621	Hs.355357	LOC643669
1.09E-01	9.59E-01	1.42	1.42E-02	NM_178557	Hs.318529	NAT8L
8.47E-01	6.69E-02	-1.42	4.45E-03	NM_033054	Hs.37617	MYO1G
3.14E-03	1.15E-01	1.42	4.48E-02	NM_003812	Hs.591643	ADAM23
4.50E-02	3.31E-01	1.42	8.22E-06	BC007360	Hs.416379	MGC16121
1.09E-01	3.11E-02	1.42	2.96E-02	XR_018702	Hs.647755	LOC646446
1.91E-01	7.51E-03	-1.42	1.37E-03	NM_002110	Hs.655210	HCK
3.81E-02	3.34E-01	-1.42	7.50E-04	NM_014485	Hs.128433	PGDS
4.89E-01	2.74E-02	1.42	1.24E-03	NM_005063	Hs.558396	SCD
1.31E-01	8.39E-01	-1.41	4.96E-07	NM_172174	Hs.654378	IL15
6.79E-02	8.04E-02	-1.41	9.99E-03	NM_002119	Hs.631991	HLA-DOA
9.28E-01	1.54E-02	-1.41	6.47E-03	NM_001803	Hs.276770	CD52
4.50E-03	5.38E-03	1.41	1.44E-02	AL713773	Hs.557850	DENND2D
7.15E-02	3.05E-02	1.41	2.10E-02	NM_002769	Hs.709206	PRSS1
8.58E-02	9.51E-03	1.41	1.41E-02	NM_025243	Hs.221597	SLC19A3
2.60E-01	5.33E-03	-1.41	1.28E-02	NM_006120	Hs.351279	HLA-DMA
6.97E-02	6.75E-01	-1.41	6.10E-04			
2.18E-02	1.33E-01	-1.41	5.91E-05	NM_181523	Hs.132225	PIK3R1
5.42E-01	3.43E-02	1.41	9.36E-03	NM_018140	Hs.591741	CEP72
2.05E-02	5.53E-01	-1.41	6.81E-03	NM_022469	Hs.98206	GREM2
2.79E-05	7.12E-02	1.41	7.72E-06	NM_052926	Hs.573567	PNMA5
1.60E-03	2.84E-02	-1.41	9.80E-03	NM_001776	Hs.576612	ENTPD1
1.09E-01	2.65E-01	-1.41	1.67E-05	NM_004472	Hs.519385	FOXD1
1.05E-04	7.22E-03	-1.41	1.30E-04	NM_138444	Hs.693617	KCTD12
1.09E-01	5.42E-02	-1.40	4.55E-02	NM_033554	Hs.347270	HLA-DPA1
2.34E-03	4.52E-02	1.40	1.31E-02	XR_037043		LOC392335
1.55E-01	2.92E-01	-1.40	2.72E-02	NM_002125	Hs.534322	HLA-DRB5

3.44E-01	7.12E-02	-1.40	2.28E-03	NM_001267	Hs.97220	CHAD
2.95E-01	5.23E-02	-1.40	1.19E-02	NM_005211	Hs.654394	CSF1R
2.49E-03	3.91E-03	-1.40	6.97E-04	NM_001312	Hs.534309	CRIP2
2.57E-01	4.55E-01	1.40	4.39E-02	NM_013942	Hs.42146	PAX3
1.05E-04	8.64E-02	1.40	2.85E-03	NM_025074	Hs.369448	FRAS1
8.40E-01	1.07E-01	1.40	6.16E-03	NM_006834	Hs.287714	RAB32
2.93E-01	4.01E-03	-1.40	8.05E-04	BC033366	Hs.334989	KRT77
3.00E-01	3.95E-01	-1.40	5.86E-04	NM_005615	Hs.23262	RNASE6
3.91E-03	9.27E-02	-1.40	7.46E-04	NM_152436	Hs.406728	GLIPR1L2
1.10E-01	1.13E-03	1.40	2.31E-03	BC037292		FAM62C
5.58E-01	1.94E-02	-1.40	6.51E-03	AL522024	Hs.381099	
1.23E-01	2.59E-02	1.40	8.73E-03	THC2485189		
8.68E-01	3.99E-02	-1.40	3.43E-03	NM_003332	Hs.515369	TYROBP
1.30E-01	1.23E-01	-1.40	2.21E-02	NM_019111	Hs.520048	HLA-DRA
8.22E-01	2.01E-01	-1.40	4.30E-05	NM_001039396	Hs.709459	MPEG1
1.16E-03	1.31E-02	1.40	4.25E-03	NM_004505	Hs.448851	USP6
6.21E-01	1.85E-01	-1.40	6.84E-03	NM_001009568	Hs.123659	SMPDL3B
2.04E-01	5.01E-01	1.39	1.19E-02	NM_001102566	Hs.433150	PCP4L1
8.95E-01	3.09E-01	-1.39	3.76E-02	NM_000559	Hs.705371	HBG1
8.88E-01	4.58E-01	1.39	4.39E-03	NM_003918	Hs.567381	GYG2
1.66E-02	7.94E-02	-1.39	8.05E-04	NM_002736	Hs.433068	PRKAR2B
5.74E-01	9.35E-03	1.39	2.08E-02	NM_012157	Hs.475872	FBXL2
7.89E-01	3.37E-04	-1.39	3.47E-02			
4.43E-04	5.47E-01	-1.39	3.49E-03	NM_003613	Hs.442180	CILP
1.68E-01	1.41E-01	1.39	9.42E-05	NM_153347	Hs.502100	TMEM86A
5.47E-02	8.67E-01	1.39	1.60E-02	NM_013347	Hs.659349	RPA4
7.54E-01	1.43E-02	-1.39	4.40E-03	AL117630	Hs.655683	FAM153B
7.08E-04	6.84E-02	-1.39	2.79E-02	NM_002404	Hs.296049	MFAP4
4.63E-01	4.25E-01	1.39	3.91E-02	NM_014241	Hs.114062	PTPLA
3.03E-02	8.63E-01	-1.39	3.70E-03	NM_173800	Hs.98288	FLJ90650
1.43E-02	9.98E-01	1.38	4.67E-02	NM_144957	Hs.72026	PRSS21
1.94E-01	1.10E-01	1.38	4.12E-02	AX721195	Hs.166262	
7.44E-01	1.71E-01	-1.38	2.59E-02	NM_003890	Hs.111732	FCGBP
9.82E-05	3.09E-01	-1.38	9.74E-04	NM_005909	Hs.637017	MAP1B
1.14E-03	3.40E-03	-1.38	5.83E-06	NM_014719	Hs.406492	FAM115A
3.40E-01	2.02E-01	-1.38	7.77E-03	AK091508		
1.82E-01	3.13E-03	1.38	3.01E-02	NM_001030005	Hs.187694	CPLX3
1.10E-01	9.71E-01	-1.38	2.23E-05	NM_002867	Hs.123072	RAB3B
3.46E-02	4.66E-01	1.38	2.48E-03	NM_025049	Hs.112160	PIF1
9.06E-05	1.35E-01	1.38	5.68E-04	NM_182639	Hs.404568	HPS1
6.81E-01	1.59E-02	-1.38	3.59E-02	NM_001040619	Hs.460	ATF3
5.66E-03	3.50E-02	1.38	1.22E-02	AK130099	Hs.235795	
8.19E-03	9.12E-02	1.38	1.13E-05	AK090910	Hs.44227	
7.12E-04	5.33E-02	1.38	1.37E-02	NM_198562	Hs.403828	C3orf62
2.20E-01	6.47E-01	-1.38	2.88E-02	M27126	Hs.705372	
1.61E-03	7.21E-03	1.38	3.19E-02	NM_003568	Hs.708113	ANXA9
3.54E-03	4.90E-01	1.38	4.37E-02	THC2676186		

7.84E-01	4.30E-01	-1.38	3.96E-02	NM_024575	Hs.709522	TNFAIP8L2
1.23E-03	6.02E-03	1.38	4.40E-02	THC2677780		
8.85E-01	1.17E-01	-1.38	3.31E-07	NM_033054	Hs.37617	MYO1G
8.03E-03	3.65E-01	1.38	4.40E-02	NM_007000	Hs.159309	UPK1A
2.58E-01	3.26E-02	-1.38	1.03E-06	ENST00000353323	Hs.661576	
4.75E-02	1.43E-02	-1.37	1.25E-02	NM_006120	Hs.351279	HLA-DMA
4.87E-02	8.62E-01	-1.37	2.35E-05	AK001062	Hs.522928	
9.34E-03	2.25E-03	1.37	1.43E-07	NM_020974	Hs.523468	SCUBE2
2.76E-01	7.39E-01	-1.37	1.23E-04	NM_005849	Hs.530902	IGSF6
1.86E-01	1.63E-01	1.37	4.41E-02	M14087	Hs.701974	
1.56E-02	2.02E-02	1.37	9.16E-04	NM_003834	Hs.65756	RGS11
9.03E-01	1.15E-02	-1.37	2.20E-04	AB018295	Hs.627298	FAM153A
7.78E-02	6.17E-02	1.37	4.03E-06	EL953211	Hs.672859	
9.26E-02	1.10E-03	-1.37	3.33E-03	NM_052880	Hs.26670	PIK3IP1
4.57E-01	3.76E-03	-1.37	2.57E-03	NM_004040	Hs.502876	RHOB
1.04E-01	1.89E-02	-1.37	1.63E-02	NM_006762	Hs.371021	LAPTM5
1.96E-01	8.86E-01	1.37	9.96E-05	AK124806	Hs.34871	LOC10012882
2.35E-03	6.92E-01	-1.37	2.12E-02	NM_030751	Hs.124503	ZEB1
5.31E-01	5.84E-02	1.37	4.23E-03	AF132203	Hs.597496	PRO1933
1.23E-02	4.29E-01	-1.37	9.10E-03	NM_144658	Hs.368203	DOCK11
5.67E-01	1.77E-03	-1.37	3.89E-04	NM_172099	Hs.405667	CD8B
3.76E-01	3.45E-01	-1.37	4.06E-02	NM_019043	Hs.310421	APBB1IP
1.33E-01	1.60E-01	-1.37	7.10E-03	NM_033130	Hs.284813	SIGLEC10
1.76E-01	2.57E-01	1.37	7.27E-03	NM_203391	Hs.1466	GK
1.29E-01	1.27E-02	1.37	6.46E-04	AK092668	Hs.483238	
1.20E-01	1.75E-01	1.37	1.83E-03	NM_002386	Hs.513829	MC1R
3.44E-04	7.33E-02	-1.36	1.89E-04	NM_006329	Hs.332708	FBLN5
5.93E-02	1.62E-02	-1.36	4.28E-06	NM_182826	Hs.128856	SCARA3
1.16E-01	4.21E-01	1.36	9.22E-03	NM_003636	Hs.440497	KCNAB2
4.30E-01	8.61E-01	1.36	4.05E-02	NM_152996	Hs.337040	ST6GALNAC3
1.82E-01	8.90E-03	-1.36	1.68E-03	NM_006202	Hs.89901	PDE4A
2.10E-02	1.43E-01	-1.36	4.36E-05	NM_001038633	Hs.135015	RSPO1
1.83E-04	1.90E-01	-1.36	4.85E-03	NM_004791	Hs.696554	ITGBL1
4.04E-02	3.72E-02	-1.36	1.31E-05	BC033331	Hs.606162	
9.48E-04	2.31E-03	1.36	2.92E-02	THC2744561		
1.23E-01	5.34E-02	1.36	3.53E-03	NM_138461	Hs.710321	TM4SF19
4.36E-04	4.77E-02	1.36	2.24E-02	NM_138788	Hs.504301	TMEM45B
1.04E-02	5.58E-01	-1.36	1.18E-02			
1.83E-01	2.95E-02	1.36	3.82E-02	BC012036	Hs.680381	
1.79E-02	2.64E-03	1.36	3.77E-02	NM_001007125	Hs.570316	LOC198437
2.67E-02	4.07E-02	-1.36	2.45E-03	ENST00000361227	Hs.631492	ND3
1.28E-04	6.30E-02	1.36	6.68E-03	NM_017947	Hs.405028	MOCOS
7.68E-04	8.02E-01	-1.36	2.69E-02	NM_006207	Hs.458573	PDGFRL
6.33E-01	1.39E-01	-1.36	8.79E-03	NM_020125	Hs.438683	SLAMF8
6.56E-03	2.68E-01	-1.36	3.72E-03	NM_012395	Hs.430742	PFTK1
4.71E-01	2.62E-02	-1.36	3.24E-02	BC038749	Hs.664957	
9.64E-01	4.10E-01	-1.36	2.14E-02	NM_006291	Hs.525607	TNFAIP2

5.34E-01	3.56E-03	-1.36	3.78E-04	AL833294	Hs.655519	SYNPO2
2.58E-01	8.50E-02	1.36	2.05E-02	NM_020777	Hs.479099	SORCS2
6.67E-03	1.73E-01	-1.36	2.64E-03	NM_016084	Hs.25829	RASD1
5.16E-01	4.44E-01	1.36	1.69E-02	THC2732746		
9.09E-04	9.61E-03	1.36	9.60E-03	AK022255		C8orf60
1.68E-01	7.56E-01	-1.36	4.03E-03	NM_001039396	Hs.709459	MPEG1
6.21E-01	1.23E-01	-1.36	1.62E-02	NM_001122965	Hs.376144	RPTN
5.06E-01	3.18E-01	1.36	5.69E-03	NM_002386	Hs.513829	MC1R
5.78E-02	2.69E-01	-1.36	2.38E-06	NM_001002811	Hs.654651	PDE4DIP
1.18E-03	4.33E-01	-1.36	3.74E-03	NM_004560	Hs.98255	ROR2
4.54E-02	1.66E-02	1.36	9.34E-03	NM_022910	Hs.322430	NDRG4
3.69E-01	1.08E-01	-1.36	5.98E-03	L34088	Hs.387679	HLA-DQA1
4.43E-01	3.64E-03	1.35	2.64E-02	AF086547	Hs.418279	
2.08E-01	2.40E-01	1.35	5.06E-05	NM_005883	Hs.446376	APC2
5.67E-01	6.92E-02	-1.35	1.03E-02	NM_005892	Hs.100217	FMNL1
9.49E-01	2.68E-01	-1.35	4.74E-02	THC2657355		
8.08E-01	3.08E-01	-1.35	3.78E-03	NM_181644	Hs.567714	MFSD4
1.74E-01	2.36E-04	1.35	2.79E-02	THC2685559		
1.41E-01	2.14E-02	1.35	1.57E-03	NM_014907	Hs.163990	FRMPD1
3.45E-01	1.50E-02	1.35	6.21E-04	ENST00000312734	Hs.8373	
4.56E-01	4.56E-03	1.35	2.76E-03	NM_017983	Hs.463964	WIPI1
2.50E-01	7.02E-01	-1.35	1.71E-02	NM_001252	Hs.501497	CD70
8.10E-01	2.74E-01	-1.35	1.22E-02	NM_007237	Hs.632549	SP140
8.80E-02	8.85E-02	-1.35	8.33E-03	NM_152748	Hs.208093	KIAA1324L
3.96E-03	2.88E-01	1.35	4.60E-05			
4.72E-02	4.55E-03	1.35	2.37E-02	NM_201520	Hs.118918	SLC25A35
3.80E-01	1.96E-03	-1.35	1.69E-02	BC022385	Hs.390599	LOC440335
1.74E-02	2.28E-01	-1.35	1.40E-09	NM_023926	Hs.235390	ZSCAN18
2.04E-03	3.11E-01	-1.35	5.39E-03			
8.07E-01	5.09E-01	1.35	2.29E-02	BC008001	Hs.639447	
1.88E-01	1.61E-01	-1.35	1.59E-03	NM_005985	Hs.48029	SNAI1
3.44E-01	2.09E-01	1.35	1.15E-02	NM_014862	Hs.459070	ARNT2
7.83E-01	3.45E-01	-1.35	1.31E-02	NM_003063	Hs.334629	SLN
1.33E-01	1.30E-01	1.35	6.28E-04	NM_002534	Hs.524760	OAS1
9.51E-01	5.50E-01	-1.35	3.19E-02	NM_006495	Hs.5509	EVI2B
3.91E-01	2.10E-01	-1.34	3.39E-03	THC2588113		
2.80E-03	7.01E-02	1.34	7.05E-05	NM_144765	Hs.116651	MPZL2
5.92E-03	3.40E-01	-1.34	2.95E-06	NM_053001	Hs.253247	OSR2
8.76E-01	1.62E-01	1.34	2.50E-02	ENST00000381826	Hs.271721	GDNF
5.45E-01	8.55E-02	-1.34	1.20E-02	NM_002298	Hs.381099	LCP1
3.98E-02	1.82E-02	-1.34	1.80E-04	NM_005822	Hs.440168	RCAN2
8.49E-01	3.32E-01	-1.34	3.86E-02	NM_002664	Hs.468840	PLEK
5.88E-01	3.16E-01	-1.34	9.41E-03	NM_003120	Hs.502511	SPI1
4.08E-01	2.95E-02	-1.34	4.07E-04	NM_003446	Hs.89897	ZNF157
4.11E-01	2.48E-02	-1.34	1.75E-02	NM_006290	Hs.591338	TNFAIP3
6.66E-01	1.18E-02	-1.34	1.67E-05	NM_002738	Hs.460355	PRKCB1
2.67E-01	6.53E-01	-1.34	1.11E-05	BQ706262	Hs.536218	

1.42E-01	2.00E-02	1.34	1.13E-07	NM_024051	Hs.530024	C7orf24
3.72E-01	6.38E-02	1.34	4.68E-03	NM_031439	Hs.709543	SOX7
7.65E-01	1.65E-01	-1.34	5.82E-03	U39657	Hs.463978	MAP2K6
2.56E-02	1.29E-02	1.34	6.31E-03	NM_002959	Hs.485195	SORT1
1.81E-03	4.60E-01	-1.34	2.06E-02	ENST00000361789	Hs.631491	CYTB
8.61E-02	3.01E-03	1.34	3.07E-02	NM_182553	Hs.437072	CNIH2
8.82E-03	6.97E-02	1.34	4.45E-03	NM_003383	Hs.370422	VLDLR
3.98E-01	1.90E-01	1.34	7.77E-03	NM_000922	Hs.656437	PDE3B
3.24E-01	2.27E-02	-1.34	2.41E-02	NM_002118	Hs.654428	HLA-DMB
2.78E-03	5.06E-02	-1.34	2.18E-05	NM_152380	Hs.146196	TBX15
4.53E-01	2.65E-01	-1.34	6.43E-03	NM_006639	Hs.201300	CYSLTR1
1.93E-01	2.55E-01	1.34	4.76E-02	NM_181535	Hs.59736	KRT28
1.52E-02	5.58E-01	-1.34	2.13E-03	NM_005609	Hs.154084	PYGM
2.02E-02	3.73E-01	-1.34	1.85E-05	NM_005076	Hs.519220	CNTN2
2.28E-01	1.48E-01	1.34	3.81E-05	NM_173681	Hs.647092	ATG9B
3.57E-01	3.24E-03	1.34	5.54E-03	NM_000908	Hs.237028	NPR3
1.89E-01	6.95E-02	-1.34	9.92E-03	NM_001554	Hs.8867	CYR61
1.29E-03	3.36E-02	-1.34	2.51E-02	NM_001454	Hs.651204	FOXJ1
4.63E-01	4.62E-01	-1.34	2.19E-02	NM_172249	Hs.520937	CSF2RA
3.82E-01	5.86E-01	-1.34	7.98E-03	NM_002072	Hs.269782	GNAQ
7.87E-03	2.66E-01	1.34	1.67E-03	NM_005987	Hs.46320	SPRR1A
1.88E-03	4.03E-02	1.34	1.81E-02			
7.10E-03	4.08E-02	-1.34	6.45E-03	AK024399	Hs.505141	
5.13E-03	1.77E-03	1.33	2.19E-02	NM_025225	Hs.654800	PNPLA3
6.74E-02	9.06E-03	1.33	6.51E-04	NM_000908	Hs.237028	NPR3
1.35E-02	5.87E-03	1.33	4.94E-02	NM_019618	Hs.211238	IL1F9
2.86E-01	1.14E-02	1.33	4.17E-02	BI910665	Hs.137007	
8.44E-01	1.62E-01	-1.33	5.79E-04	NM_033468	Hs.283900	ZNF257
6.01E-03	1.47E-02	1.33	8.32E-03	NM_031439	Hs.709543	SOX7
5.21E-04	2.43E-02	1.33	3.18E-02	AF095737	Hs.198003	SARDH
4.72E-02	1.69E-03	-1.33	1.12E-02	AK097322	Hs.631498	
6.12E-03	7.84E-03	-1.33	8.84E-05	NM_020405	Hs.125036	PLXDC1
1.21E-02	1.07E-01	-1.33	1.99E-02	NM_144966	Hs.709555	FREM1
1.82E-02	3.61E-01	1.33	8.95E-03	NM_001123225		LOC644186
5.48E-03	9.02E-01	1.33	1.22E-02	NM_018984	Hs.199763	SSH1
9.91E-04	2.50E-02	-1.33	2.17E-02	NM_001034841	Hs.648523	LOC162073
6.38E-01	5.49E-02	-1.33	1.72E-03	BC038371	Hs.657602	
2.07E-02	1.59E-01	-1.33	3.51E-06	NM_014988	Hs.335163	LIMCH1
5.34E-03	8.86E-02	1.33	1.06E-03	NM_001018053	Hs.282702	PFKFB2
1.10E-01	2.45E-01	-1.33	4.03E-09	NM_144722	Hs.298863	SPEF2
1.52E-02	8.92E-03	1.33	1.34E-09	NM_182728	Hs.632348	SLC7A8
7.52E-03	5.33E-01	1.33	2.50E-05	NM_198173	Hs.657920	GRHL3
1.38E-01	2.91E-01	-1.33	8.12E-05	NM_004923	Hs.145932	MTL5
4.29E-03	7.96E-02	-1.33	6.54E-05	NM_153635	Hs.121335	CPNE9
5.70E-02	3.04E-02	1.33	3.04E-03	NM_030899	Hs.656413	ZNF323
2.03E-01	6.89E-02	-1.33	1.18E-02	NM_001554	Hs.8867	CYR61
2.06E-03	1.73E-01	-1.33	1.26E-05	NM_152989	Hs.657542	SOX5

4.43E-01	2.23E-02	-1.33	4.77E-02	NM_032413	Hs.112242	C15orf48
3.18E-02	4.50E-02	1.33	1.14E-03	X91906	Hs.166486	CLCN5
2.73E-03	5.18E-01	1.33	2.15E-04	NM_005073	Hs.436893	SLC15A1
4.92E-02	1.61E-03	-1.33	7.26E-03	AK098143	Hs.192155	LOC283861
1.57E-01	6.37E-02	-1.33	4.87E-03	NM_018938	Hs.591250	PCDHB4
5.08E-01	1.80E-02	1.33	1.23E-02	NM_033300	Hs.576154	LRP8
4.48E-03	2.27E-02	1.33	1.42E-02	AF161533	Hs.525088	CCDC82
1.08E-03	4.06E-01	1.33	9.12E-06	BC024020	Hs.708260	TMEM49
9.50E-01	8.30E-01	1.33	5.94E-03	NM_000166	Hs.333303	GJB1
2.86E-01	3.13E-01	1.32	6.79E-03	NM_020704	Hs.489988	FAM40B
9.83E-04	5.59E-01	-1.32	6.01E-03	NM_004098	Hs.202095	EMX2
1.80E-03	3.21E-03	1.32	2.17E-02	AK124173	Hs.598050	LOC10013047
2.92E-01	1.03E-02	1.32	4.81E-03	AK021906	Hs.658795	
3.93E-02	1.45E-02	1.32	4.66E-04	NM_016354	Hs.235782	SLCO4A1
2.57E-02	7.90E-01	-1.32	2.24E-02	NM_012395	Hs.430742	PFTK1
6.52E-01	3.87E-02	-1.32	1.71E-02	AW952039	Hs.654803	
1.49E-02	4.92E-03	1.32	1.19E-03	NM_000623	Hs.654542	BDKRB2
1.24E-02	3.59E-02	1.32	3.92E-03	BF063428	Hs.546239	
1.35E-02	2.76E-03	-1.32	5.14E-05	NM_173632	Hs.109540	ZNF776
7.22E-02	4.89E-02	1.32	3.55E-02			
3.93E-02	1.59E-01	1.32	4.52E-06	THC2655140		
1.57E-05	2.59E-03	1.32	3.43E-02	NM_000359	Hs.508950	TGM1
1.64E-01	9.78E-02	1.32	1.18E-04	NM_018302	Hs.107527	C4orf19
1.17E-01	9.59E-03	-1.32	3.50E-02	AF212044		
4.74E-01	6.88E-01	-1.32	3.95E-02	NM_001045556	Hs.75367	SLA
7.78E-01	6.74E-01	-1.32	9.13E-04	NM_000878	Hs.474787	IL2RB
2.01E-02	2.49E-02	1.32	7.07E-05	NM_018941	Hs.127675	CLN8
1.58E-02	3.78E-01	-1.32	1.82E-04	NM_001150	Hs.1239	ANPEP
1.06E-01	5.07E-02	1.32	3.72E-02	NM_177483	Hs.591810	GPLD1
1.49E-02	4.61E-02	1.32	2.71E-02	NM_006665	Hs.44227	HPSE
7.71E-02	1.40E-01	1.32	2.07E-03	NM_003459	Hs.467981	SLC30A3
2.55E-01	1.65E-02	1.32	1.05E-04	ENST00000312734	Hs.8373	
7.64E-02	8.85E-01	1.32	3.38E-02	NM_002964	Hs.416073	S100A8
3.66E-03	3.44E-01	-1.32	1.84E-02	NM_000129	Hs.335513	F13A1
3.74E-01	6.79E-03	-1.32	3.33E-04	NM_053056	Hs.523852	CCND1
2.48E-04	7.54E-01	-1.32	1.64E-04	NM_175571	Hs.647121	GIMAP8
5.73E-01	2.20E-01	-1.32	5.28E-04	NM_002738	Hs.460355	PRKCB1
7.82E-01	9.55E-03	-1.32	3.19E-02	NM_005855	Hs.471783	RAMP1
6.52E-01	6.68E-01	-1.32	1.78E-03	NM_175881	Hs.144348	ODF3L1
4.52E-03	1.64E-02	-1.32	2.34E-02			
3.57E-01	4.74E-03	1.32	1.03E-03	AL355688	Hs.655029	
7.12E-01	3.02E-02	-1.32	3.79E-03	NM_005428	Hs.116237	VAV1
4.45E-01	5.83E-03	-1.32	6.31E-05	NM_032011	Hs.368160	PCDHGA3
9.86E-01	3.15E-01	1.32	1.67E-02	NM_006834	Hs.287714	RAB32
7.75E-01	5.92E-01	-1.31	1.18E-02	NM_024320	Hs.368260	ATAD4
5.96E-03	4.47E-02	1.31	2.69E-02	AK022348	Hs.369657	SPATA5L1
3.77E-01	2.58E-02	1.31	9.49E-04	AF086071	Hs.197962	

2.09E-02	2.91E-02	1.31	3.34E-03			
2.30E-01	1.57E-03	1.31	6.27E-06	NM_207627	Hs.124649	ABCG1
3.14E-01	1.22E-01	-1.31	1.26E-02	BE926212		
7.76E-04	7.15E-02	1.31	4.96E-02	NM_002770	Hs.622865	PRSS2
9.13E-01	3.25E-01	-1.31	2.87E-02	CB959193	Hs.97644	
3.43E-01	3.41E-02	1.31	3.07E-03	NM_005505	Hs.709216	SCARB1
6.72E-02	6.24E-02	1.31	8.10E-05	AK090639	Hs.13349	NFASC
3.79E-02	1.02E-01	-1.31	7.71E-03	NM_001337	Hs.78913	CX3CR1
5.38E-02	1.62E-01	1.31	1.26E-04	AB002454	Hs.106242	CYP4F3
4.43E-01	3.42E-02	-1.31	4.27E-03	NM_001037582	Hs.379191	SCD5
4.90E-01	9.82E-03	1.31	3.71E-02	NM_001039395	Hs.179615	C9orf68
5.77E-02	2.03E-02	-1.31	1.20E-02	NM_007034	Hs.13852	DNAJB4
3.80E-01	7.65E-02	-1.31	2.39E-02	N34499	Hs.655670	
2.61E-02	1.62E-02	-1.31	5.21E-04	NM_004079	Hs.181301	CTSS
5.70E-01	7.24E-01	1.31	4.13E-02	NM_004265	Hs.502745	FADS2
1.44E-03	1.03E-02	-1.31	3.30E-06	NM_025004	Hs.287555	CCDC15
7.38E-02	6.45E-02	1.31	4.68E-02	CD239706	Hs.688414	
7.32E-02	2.48E-01	-1.31	4.85E-03	AL833309	Hs.622596	
2.48E-02	8.34E-01	1.31	1.46E-02	NM_033229	Hs.591789	TRIM15
6.90E-03	8.69E-01	1.31	1.19E-05	L33930	Hs.694721	CD24
4.64E-02	4.37E-01	1.31	3.38E-03	NM_005553	Hs.709220	KRTAP5-9
8.00E-02	2.52E-01	1.31	7.94E-04	NM_003842	Hs.521456	TNFRSF10B
7.98E-04	1.52E-01	-1.31	2.57E-02	NM_000362	Hs.701968	TIMP3
3.44E-02	9.66E-01	-1.31	2.94E-04	NM_016952	Hs.38034	CDON
2.05E-01	6.30E-01	-1.31	6.60E-03	NM_181723	Hs.403594	EFHA2
6.34E-01	1.19E-01	1.31	2.15E-02	NM_016363	Hs.661752	GP6
5.99E-02	1.74E-01	-1.31	2.85E-02	NM_004522	Hs.660699	KIF5C
3.76E-01	6.95E-01	1.31	5.64E-05	NM_001007595	Hs.144372	FAM148B
1.85E-01	1.69E-02	1.31	1.31E-02			
6.66E-01	7.39E-02	-1.31	2.55E-02			
2.17E-02	9.60E-03	-1.31	1.58E-02	NM_007034	Hs.13852	DNAJB4
6.15E-01	2.76E-02	-1.31	1.03E-04	NM_001627	Hs.591293	ALCAM
1.17E-01	2.00E-01	-1.31	2.18E-04	NM_138731	Hs.660396	MIPOL1
6.86E-01	1.45E-02	1.31	3.57E-03	NM_023112	Hs.278815	OTUB2
4.42E-03	1.19E-01	-1.30	5.27E-03	THC2540738		
9.59E-01	4.75E-02	-1.30	9.59E-03	NM_002985	Hs.514821	CCL5
4.45E-03	3.05E-01	-1.30	4.22E-02	NM_005725	Hs.310458	TSPAN2
6.73E-03	9.80E-03	1.30	7.65E-04	NM_014028	Hs.226780	OSTM1
4.75E-01	1.05E-01	1.30	1.88E-02			
9.64E-01	5.79E-01	1.30	1.72E-04	NM_052899	Hs.150549	GPRIN1
2.64E-01	2.98E-02	1.30	8.84E-03	NM_025015	Hs.654682	HSPA12A
5.85E-02	2.21E-02	1.30	2.00E-02	AK092987	Hs.705482	ARV1
1.66E-02	3.96E-04	-1.30	5.91E-03	NM_183422	Hs.507916	TSC22D1
1.82E-02	4.41E-01	-1.30	3.02E-02	NM_033402	Hs.193115	LRRCC1
4.82E-01	5.61E-01	-1.30	2.53E-05	NM_001289	Hs.655445	CLIC2
3.44E-03	7.43E-02	-1.30	7.38E-07	THC2691142		
3.17E-04	4.24E-01	1.30	2.36E-03	AF256215		ARNTL2

5.46E-01	1.71E-01	1.30	5.95E-03	AW993939	Hs.520819	
5.88E-02	1.58E-01	1.30	1.58E-05	THC2579173		
1.50E-01	9.43E-02	-1.30	1.84E-02	NM_001554	Hs.8867	CYR61
1.32E-04	7.88E-01	-1.30	2.58E-02	NM_002615	Hs.694727	SERPINF1
1.69E-01	1.60E-01	-1.30	4.19E-02	X91815	Hs.468274	SLC8A1
1.33E-01	2.55E-03	-1.30	2.50E-03	NM_015319	Hs.6147	TENC1
3.27E-01	1.49E-02	1.30	1.95E-02	XR_037019		LOC10013386
1.99E-02	1.59E-02	1.30	3.25E-04	BX115087	Hs.668548	
1.10E-03	3.23E-02	1.30	2.89E-02	BC010126	Hs.654410	
9.14E-02	1.64E-01	-1.30	2.96E-06	NM_201431	Hs.590920	RASSF6
6.03E-01	1.98E-03	1.30	5.04E-03	NM_004425	Hs.81071	ECM1
9.41E-01	2.57E-02	1.30	2.87E-02	NM_020704	Hs.489988	FAM40B
2.85E-02	8.00E-01	-1.30	7.41E-03	THC2648227		
3.87E-02	3.51E-03	1.30	3.21E-02	NM_020349	Hs.73708	ANKRD2
5.33E-01	1.76E-03	-1.30	4.38E-03	THC2707284		
3.95E-02	1.01E-02	1.30	9.00E-03	NM_033300	Hs.576154	LRP8
6.12E-01	5.12E-01	-1.30	5.96E-03	NM_001629	Hs.507658	ALOX5AP
2.70E-01	3.79E-01	-1.30	1.63E-02	NM_032023	Hs.522895	RASSF4
1.48E-01	4.53E-01	1.30	1.97E-04	ENST00000244321	Hs.22049	
4.49E-02	3.37E-03	1.30	6.83E-04	NM_153347	Hs.502100	TMEM86A
8.27E-03	5.19E-01	1.30	1.16E-02	AB039791	Hs.664579	ARP11
4.14E-02	9.32E-01	-1.30	3.76E-03	NM_181795	Hs.486354	PKIB
7.67E-02	1.68E-01	1.30	2.91E-02	NM_004232	Hs.44439	SOCS6
1.96E-02	1.27E-01	-1.30	4.87E-03	NM_006475	Hs.136348	POSTN
5.12E-01	4.22E-03	-1.30	8.58E-03	THC2705456		
2.32E-03	9.00E-03	-1.29	5.29E-05	ENST00000361567		
1.48E-02	9.21E-01	1.29	1.03E-02	NM_174932	Hs.372939	BPIL2
2.94E-01	1.91E-02	1.29	4.74E-03	THC2534530		
9.89E-01	7.83E-01	-1.29	3.00E-02	NM_017899	Hs.525709	TESC
2.62E-01	3.21E-01	-1.29	1.20E-02			
6.01E-01	6.16E-01	1.29	3.12E-02	AW972815	Hs.290255	
3.28E-02	5.31E-03	1.29	2.79E-03			
5.96E-01	8.32E-02	-1.29	1.89E-04	NM_002030	Hs.445466	FPR3
5.80E-01	8.64E-01	1.29	4.85E-02	ENST00000390689	Hs.61552	KRTAP19-1
5.10E-02	5.37E-01	-1.29	4.18E-04	NM_003451	Hs.172979	ZNF177
1.09E-01	3.01E-02	-1.29	6.17E-04	NM_004588	Hs.129783	SCN2B
5.99E-02	1.91E-02	1.29	2.05E-02	THC2553305		
3.92E-02	3.04E-03	-1.29	6.90E-03	NM_005345	Hs.520028	HSPA1A
2.52E-03	2.48E-02	1.29	1.65E-02	THC2753968		
5.18E-06	2.62E-02	1.29	3.07E-02	NM_005046	Hs.151254	KLK7
3.51E-01	7.59E-04	-1.29	3.95E-02	NM_001006607	Hs.646568	LRRC37A2
1.05E-03	2.77E-02	1.29	2.47E-04	NM_015704	Hs.570455	FAM152B
2.86E-02	3.21E-03	1.29	1.22E-02	AK022407	Hs.636866	
2.42E-02	2.15E-01	1.29	4.25E-02			
3.62E-02	9.81E-01	-1.29	2.00E-02	NM_000300	Hs.466804	PLA2G2A
3.84E-02	9.27E-03	1.29	1.14E-05	AK024346	Hs.483816	LOC153346
1.29E-02	8.87E-01	-1.29	7.73E-04	NM_198560	Hs.56782	LHFPL4

1.25E-01	8.36E-01	1.29	3.25E-03	NM_032726	Hs.632528	PLCD4
3.76E-02	9.84E-01	1.29	1.78E-03	NM_003963	Hs.184194	TM4SF5
2.77E-02	8.59E-04	1.29	1.68E-02	NM_012166	Hs.709527	FBXO10
3.97E-01	5.14E-02	1.29	3.67E-05	AF131834	Hs.4892	
4.93E-03	2.19E-01	-1.29	2.89E-02	NM_006933	Hs.302742	SLC5A3
5.11E-03	1.15E-01	-1.29	3.17E-02	NM_201269	Hs.173001	ZNF644
4.38E-01	4.26E-02	1.29	2.96E-02			
4.84E-01	2.52E-01	-1.29	1.34E-02	NM_000061	Hs.159494	BTK
9.24E-01	4.69E-02	-1.29	3.06E-02			
8.86E-03	1.05E-02	-1.29	1.18E-04	AK097322	Hs.465808	
1.32E-01	3.80E-01	1.29	4.08E-05	CR593560	Hs.238964	LOC440934
9.25E-02	7.98E-03	1.29	2.05E-03	BC041366	Hs.524085	USP2
6.20E-02	4.52E-01	1.29	5.59E-04	BC111002	Hs.591252	ARSI
6.79E-01	2.90E-01	-1.29	5.92E-05	NM_002135	Hs.524430	NR4A1
3.57E-02	3.11E-02	1.29	4.49E-02	ENST00000306634		LOC643205
1.67E-01	2.26E-01	-1.29	8.10E-03	NM_024848	Hs.709528	MORN1
1.96E-01	1.31E-01	1.29	2.53E-02	THC2645080		
1.60E-02	9.58E-03	1.29	4.48E-02	NM_001897	Hs.513044	CSPG4
2.56E-03	6.05E-01	1.29	3.42E-02	ENST00000166133	Hs.248087	
5.25E-02	3.39E-01	1.28	7.41E-05			
7.78E-02	1.92E-01	-1.28	2.54E-02	NM_003151	Hs.80642	STAT4
8.40E-03	2.47E-01	1.28	4.06E-02	NM_001024594	Hs.61329	C1orf53
1.19E-01	2.54E-01	1.28	3.68E-02	NM_006541	Hs.42644	GLRX3
4.53E-02	2.37E-04	1.28	6.22E-03	NM_017893	Hs.591923	SEMA4G
5.02E-01	1.04E-01	1.28	4.30E-04	NM_006536	Hs.241551	CLCA2
2.91E-01	8.84E-01	-1.28	1.88E-03	NM_014505	Hs.525529	KCNMB4
5.68E-02	5.82E-01	1.28	6.28E-04	NM_018000	Hs.709755	MREG
3.30E-02	1.07E-01	-1.28	3.47E-02	NM_020872	Hs.12723	CNTN3
3.28E-02	3.15E-01	-1.28	1.66E-02	AK129724		
2.56E-03	6.56E-02	-1.28	4.50E-09	NM_152436	Hs.406728	GLIPR1L2
1.36E-01	1.79E-03	1.28	3.11E-02	BG571904	Hs.660990	
4.55E-02	3.15E-02	1.28	2.02E-02			
7.35E-02	2.87E-02	1.28	9.43E-05	BM471507	Hs.436973	
7.43E-01	4.74E-03	1.28	1.31E-02	NM_175062	Hs.190559	RASGEF1C
4.15E-02	2.16E-02	1.28	1.24E-02	NM_181538	Hs.647524	GJC3
7.45E-02	5.60E-01	-1.28	5.79E-03	NM_001040114	Hs.460109	MYH11
8.38E-04	6.56E-04	1.28	4.91E-02	BF088423	Hs.108973	
2.92E-01	1.80E-01	1.28	2.72E-02	NM_000259	Hs.21213	MYO5A
1.99E-01	9.99E-03	1.28	2.28E-07	NM_002760	Hs.632287	PRKY
5.77E-01	2.43E-01	-1.28	2.36E-02	NM_021965	Hs.307835	PGM5
1.77E-03	5.64E-01	-1.28	4.40E-03	NM_030925	Hs.87159	CAB39L
6.17E-03	7.65E-02	1.28	1.73E-09	NM_022740	Hs.397465	HIPK2
2.20E-02	3.61E-02	1.28	2.47E-03	AK021848		
1.58E-01	1.13E-01	1.28	2.81E-03	NM_022147	Hs.43388	RTP4
6.28E-01	1.18E-01	1.28	4.84E-03			
5.92E-03	1.97E-02	-1.28	6.09E-11	NM_001250	Hs.472860	CD40
1.03E-01	3.08E-01	1.28	1.15E-02	AK090762	Hs.531632	

3.56E-01	3.38E-01	1.28	4.15E-02	THC2608658		
1.12E-01	3.05E-01	-1.28	2.66E-02	NM_152703	Hs.489118	SAMD9L
1.02E-01	2.15E-03	1.28	5.33E-03	NM_022740	Hs.397465	HIPK2
2.21E-03	4.37E-02	1.28	2.82E-02	NM_052819	Hs.696253	CARD14
1.63E-01	5.40E-01	-1.28	9.66E-05	NM_016952	Hs.38034	CDON
3.85E-04	3.26E-02	-1.28	2.02E-03	NM_003062	Hs.604116	SLIT3
1.40E-01	2.79E-03	1.28	1.62E-02			
4.79E-02	7.35E-01	-1.28	3.14E-03	NM_004816	Hs.118003	C9orf61
5.70E-01	4.00E-02	1.28	3.17E-02	NM_004004	Hs.591234	GJB2
1.75E-01	1.59E-03	1.28	9.35E-04	NM_018144	Hs.112955	SEC61A2
1.49E-02	1.49E-01	1.28	9.17E-03	NM_000710	Hs.525572	BDKRB1
8.80E-01	5.65E-01	-1.28	7.35E-03	THC2719486		
1.94E-02	3.55E-02	1.28	4.11E-02			
7.96E-01	1.22E-01	-1.28	2.30E-02	NM_006864	Hs.631592	LILRB3
1.60E-01	7.40E-01	1.28	4.75E-02	NM_000226	Hs.654569	KRT9
2.01E-03	3.00E-03	1.28	1.63E-02	NM_002133	Hs.517581	HMOX1
1.11E-01	7.29E-02	1.28	1.57E-02	NM_002960	Hs.557609	S100A3
9.68E-04	9.60E-02	-1.28	7.04E-08	NM_001034841	Hs.648523	LOC162073
3.96E-01	2.58E-01	1.28	2.13E-03	AK094322	Hs.425633	CKMT1B
1.05E-01	5.77E-02	-1.28	1.48E-02	AV652851	Hs.20255	
5.34E-01	3.76E-01	1.28	2.03E-03	NM_006745	Hs.105269	SC4MOL
1.84E-02	5.49E-03	1.28	2.98E-02	BX281122	Hs.665091	
7.22E-01	6.44E-02	-1.28	7.76E-03	NM_032782	Hs.710500	HAVCR2
3.96E-01	6.74E-01	-1.28	2.14E-03	BC005008	Hs.466814	CEACAM6
2.69E-02	1.73E-02	-1.28	8.73E-03	NM_002017	Hs.504281	FLI1
6.31E-01	4.30E-02	-1.28	2.85E-02	NM_004271	Hs.653138	LY86
2.77E-02	1.37E-01	-1.27	9.91E-09	NM_033254	Hs.591318	BOC
8.11E-03	1.87E-01	-1.27	6.19E-03	NM_018151	Hs.655671	RIF1
2.79E-01	3.66E-01	-1.27	7.08E-06	NM_005076	Hs.519220	CNTN2
6.69E-01	6.91E-03	-1.27	3.83E-02	NM_002371	Hs.80395	MAL
4.93E-01	5.42E-02	1.27	3.49E-02	ENST00000267857	Hs.194710	GCNT3
8.98E-02	3.52E-03	-1.27	5.44E-04	NM_198439	Hs.101949	KBTBD3
1.13E-01	4.73E-03	1.27	9.86E-03	AA639753	Hs.547580	
3.07E-01	1.27E-01	1.27	3.84E-03	NM_031854	Hs.572443	KRTAP4-12
2.25E-02	1.21E-01	-1.27	5.56E-03	NM_006113	Hs.267659	VAV3
7.12E-02	1.27E-03	1.27	2.88E-02	NM_004577	Hs.512656	PSPH
1.25E-04	6.67E-01	-1.27	4.49E-02	NM_005086	Hs.709230	SSPN
1.15E-01	1.36E-02	-1.27	1.16E-03	NM_016270	Hs.107740	KLF2
2.63E-01	1.84E-02	-1.27	4.21E-03	THC2537179	Hs.257664	
1.86E-03	8.13E-02	1.27	4.19E-02	BC001742	Hs.679408	LOC90834
5.05E-03	3.02E-03	1.27	3.89E-03	NM_001719	Hs.473163	BMP7
7.95E-03	4.14E-02	-1.27	4.60E-04	BC006271	Hs.659341	
5.25E-01	8.87E-03	1.27	3.56E-02	BC028580	Hs.676966	MGC26597
3.66E-02	8.51E-01	-1.27	1.13E-02	NM_030756	Hs.593995	TCF7L2
9.78E-01	2.66E-02	-1.27	1.98E-03	NM_152586	Hs.657355	USP54
8.94E-02	7.55E-01	-1.27	8.71E-03	NM_002178	Hs.274313	IGFBP6
2.01E-03	7.07E-01	-1.27	2.92E-02	NM_000062	Hs.384598	SERPING1

1.65E-01	2.75E-02	-1.27	2.74E-05	NM_015147	Hs.709257	CEP68
9.18E-01	1.92E-02	1.27	2.45E-02	NM_203391	Hs.1466	GK
2.42E-01	4.33E-03	-1.27	3.87E-02	NM_018179	Hs.591151	ATF7IP
2.63E-01	1.42E-01	1.27	9.64E-09	BC017694	Hs.655067	FAM128B
2.15E-04	2.62E-01	1.27	4.17E-02			
7.53E-01	1.31E-01	1.27	1.74E-02	NM_001276	Hs.382202	CHI3L1
1.66E-02	3.07E-01	-1.27	4.99E-02	NM_015678	Hs.491172	NBEA
7.21E-03	1.40E-01	1.27	4.58E-02	THC2680492		
2.45E-01	3.55E-01	-1.27	3.39E-02			
5.57E-01	2.64E-01	1.27	1.44E-03	NM_002632	Hs.252820	PGF
1.40E-01	3.47E-01	1.27	4.37E-02	BC015987	Hs.709396	
1.81E-01	8.31E-01	1.27	3.06E-02	BC008001		
4.82E-02	5.62E-02	1.27	1.44E-02	NM_175747	Hs.195398	OLIG3
4.60E-01	1.32E-01	1.27	2.31E-02	ENST00000357816	Hs.528335	FAM123A
1.23E-01	5.71E-01	-1.27	3.03E-02	NM_152721	Hs.569915	DOK6
2.50E-02	2.02E-02	-1.27	1.38E-02	NM_006391	Hs.699345	IPO7
4.35E-03	7.94E-02	1.27	2.51E-02	AK057267	Hs.122927	CLIP4
8.39E-01	7.59E-02	1.27	1.52E-02	CR936670	Hs.369819	TBC1D16
9.98E-02	3.32E-04	1.27	1.76E-02	NM_002690	Hs.654484	POLB
1.18E-02	3.85E-01	1.27	4.32E-04	NM_139165	Hs.511818	RAET1E
1.86E-02	1.27E-02	1.27	2.57E-02	ENST00000360737	Hs.659113	
8.32E-01	8.61E-01	1.27	5.47E-03	NM_020722	Hs.596667	KIAA1211
5.30E-02	7.26E-02	-1.27	4.68E-06	NM_001001132	Hs.160324	ITSN1
1.32E-01	6.71E-01	1.27	1.52E-02	NM_198060	Hs.268788	NRAP
3.43E-03	1.28E-01	1.27	2.81E-07	NM_013314	Hs.665244	BLNK
1.19E-03	5.20E-02	1.27	8.16E-08	NM_025045	Hs.474822	BAIAP2L2
5.88E-02	2.71E-02	1.27	6.24E-04	BC000200	Hs.111286	MRPS11
5.28E-01	1.34E-02	-1.27	6.04E-03	NM_145867	Hs.706741	LTC4S
2.06E-02	2.41E-01	1.27	2.53E-02	BQ323779	Hs.655491	
3.23E-01	6.26E-01	-1.27	5.01E-09			
8.64E-03	3.41E-01	-1.27	4.37E-02	AK002107	Hs.123072	RAB3B
9.79E-01	2.05E-02	1.27	2.40E-02			
7.07E-01	5.31E-03	-1.27	1.78E-03	NM_145306	Hs.522992	C10orf35
1.95E-02	2.72E-01	1.27	5.18E-03	NM_020877	Hs.367649	DNAH2
3.35E-01	2.81E-02	-1.27	2.25E-03			
1.80E-02	7.21E-02	1.27	4.66E-04	NM_020375	Hs.504545	C12orf5
7.22E-01	9.60E-01	1.27	1.01E-02	NM_003658	Hs.591944	BARX2
5.98E-03	1.43E-01	-1.27	2.95E-03	NM_005596	Hs.709255	NFIB
1.02E-01	5.89E-02	1.27	1.26E-02	NM_000785	Hs.524528	CYP27B1
3.27E-02	4.02E-02	1.27	2.31E-02	BC042589	Hs.130853	
2.39E-02	3.67E-02	1.27	1.51E-02	NM_001005338	Hs.537383	OR5H1
1.75E-01	5.28E-03	-1.27	1.36E-07	NM_015975	Hs.592248	TAF9B
1.51E-02	3.89E-01	1.27	7.55E-04			
1.28E-04	2.37E-01	-1.27	2.07E-02	NM_007249	Hs.373857	KLF12
7.60E-01	4.09E-01	-1.27	1.68E-02	AK090602	Hs.130499	LOC283143
1.34E-02	3.67E-02	1.27	8.85E-03	THC2548576		
8.31E-02	3.83E-01	-1.27	6.28E-03	NM_000901	Hs.163924	NR3C2

8.45E-01	3.89E-01	1.27	4.46E-02	BC039117	Hs.524331	OVOS2
2.65E-01	1.91E-02	1.27	7.60E-05	AK024346	Hs.483816	LOC153346
2.70E-02	2.72E-01	1.27	1.73E-03	AK022390	Hs.656537	
3.33E-01	9.12E-02	-1.27	2.55E-02	NM_001623	Hs.76364	AIF1
5.01E-02	2.86E-02	1.26	3.51E-05	NM_012324	Hs.558180	MAPK8IP2
6.14E-03	3.53E-02	-1.26	2.26E-06	NM_001001415	Hs.709598	ZNF429
5.68E-02	5.49E-03	-1.26	1.86E-04	NM_015180	Hs.525392	SYNE2
1.75E-01	1.16E-01	1.26	5.50E-04	NM_013941	Hs.631997	OR10C1
7.04E-01	7.65E-01	-1.26	1.39E-02	NM_001629	Hs.507658	ALOX5AP
2.81E-01	4.80E-02	-1.26	1.19E-02	NM_002842	Hs.179770	PTPRH
1.94E-01	6.10E-01	-1.26	4.75E-04	NM_003436	Hs.85863	ZNF135
2.62E-01	7.13E-01	-1.26	2.09E-02	NM_001772	Hs.83731	CD33
1.18E-01	1.38E-02	1.26	6.53E-10	AF112968	Hs.655240	SLC25A15
1.12E-03	8.15E-02	-1.26	3.57E-04			
1.78E-02	9.39E-02	-1.26	1.28E-05	NM_000848	Hs.279837	GSTM2
3.26E-01	1.73E-01	-1.26	1.85E-03	AJ420378	Hs.503043	CPT1A
1.45E-02	6.55E-02	-1.26	4.34E-02	NM_014840	Hs.524692	NUAK1
7.67E-02	5.14E-03	1.26	9.35E-03	NM_024930	Hs.274256	ELOVL7
5.15E-01	2.15E-02	-1.26	7.44E-03	NM_014935	Hs.253146	PLEKHA6
5.22E-01	1.31E-02	1.26	4.48E-02	NM_198570	Hs.677488	VWC2
1.15E-04	2.15E-02	1.26	1.29E-02	NM_144505	Hs.104570	KLK8
9.15E-01	9.20E-01	-1.26	4.48E-02	NM_001768	Hs.85258	CD8A
8.65E-03	5.11E-02	-1.26	3.83E-03	NM_032184	Hs.670497	SYDE2
6.79E-04	2.82E-01	-1.26	1.42E-02	NM_016578	Hs.420229	RSF1
6.78E-01	5.32E-02	1.26	1.07E-02	THC2656826		
1.17E-02	1.24E-01	-1.26	3.29E-04	NM_007038	Hs.58324	ADAMTS5
9.03E-01	7.95E-02	-1.26	1.99E-03	NM_030802	Hs.514308	FAM117A
3.42E-02	1.19E-03	1.26	2.93E-03	NM_021214	Hs.459072	FAM108C1
4.90E-01	4.17E-01	-1.26	4.13E-03	NM_033328	Hs.131288	CAPZA3
3.33E-03	1.71E-02	1.26	4.01E-04	NM_001006641	Hs.5476	SLC25A25
1.26E-01	6.94E-01	-1.26	1.79E-02	NM_014879	Hs.2465	P2RY14
4.86E-02	6.71E-01	-1.26	5.39E-04	NM_005909	Hs.637017	MAP1B
1.40E-01	2.26E-02	1.26	9.39E-03	BC020341		
5.68E-01	3.18E-01	-1.26	6.72E-04	NM_013322	Hs.571296	SNX10
5.67E-01	5.62E-03	1.26	4.81E-02	BC029107	Hs.657649	FMN1
3.24E-01	6.14E-01	-1.26	8.46E-07	NM_003970	Hs.443683	MYOM2
8.99E-02	3.42E-01	1.26	2.32E-02			
6.42E-02	4.27E-02	1.26	1.25E-04	NM_078476	Hs.159028	BTN2A1
1.66E-02	7.46E-02	-1.26	2.57E-02	NM_019605	Hs.708143	SERTAD4
3.78E-02	2.93E-03	-1.26	7.70E-03	NM_007366	Hs.410477	PLA2R1
6.12E-03	1.67E-01	1.26	2.00E-02	NM_030576	Hs.591166	LIMD2
2.16E-02	5.36E-01	-1.26	5.51E-04	NM_052913	Hs.591341	TMEM200A
5.16E-03	8.78E-01	1.26	6.49E-03	AL137592	Hs.272813	DUOX1
1.04E-02	5.54E-01	1.26	2.15E-03	NM_017422	Hs.180142	CALML5
3.89E-02	6.32E-02	1.26	8.55E-03	NM_003839	Hs.204044	TNFRSF11A
1.99E-01	5.38E-01	1.26	7.44E-03	THC2659561		
2.31E-03	1.03E-01	1.26	4.46E-02	AK055963	Hs.647777	RP4-621O15.

3.97E-03	1.57E-02	1.26	3.98E-04	NM_022162	Hs.592072	NOD2
9.98E-01	9.79E-02	-1.26	1.94E-03	NM_017409	Hs.44276	HOXC10
2.72E-03	2.30E-02	-1.26	7.49E-03	NM_002184	Hs.532082	IL6ST
7.54E-01	5.44E-01	1.26	4.98E-02	AL390143	Hs.676449	
5.18E-03	6.10E-01	1.26	2.66E-02	NM_031948	Hs.332878	PRSS27
8.47E-04	3.33E-01	1.26	5.14E-03	AL832142	Hs.656585	
7.21E-01	2.95E-02	-1.26	3.47E-02	NM_033647	Hs.505941	HELB
1.08E-02	2.72E-01	1.26	5.34E-03	NM_003842	Hs.521456	TNFRSF10B
1.12E-01	4.45E-02	1.26	3.08E-02	NR_003666		LOC441251
1.29E-01	3.46E-02	1.26	4.95E-02	THC2732966		
1.07E-01	1.22E-02	-1.26	1.71E-03	NM_152989	Hs.657542	SOX5
2.22E-01	5.80E-01	1.26	4.61E-02	THC2659236		
2.73E-01	1.28E-01	-1.26	5.39E-06	NM_001031847	Hs.503043	CPT1A
1.10E-01	6.68E-01	1.26	2.83E-04	THC2684848		
7.87E-02	1.73E-01	1.26	4.34E-03	AF234262		
6.41E-01	4.16E-01	1.26	3.89E-02			
1.23E-01	3.84E-02	-1.26	2.57E-02	NM_001962	Hs.658451	EFNA5
1.22E-02	2.75E-02	1.26	1.42E-03	NM_016352	Hs.93764	CPA4
1.24E-01	1.11E-01	1.26	6.92E-03	CR601315	Hs.507783	NHLRC3
1.67E-01	6.15E-01	1.26	3.56E-04	NM_006238	Hs.696032	PPARD
1.01E-01	1.16E-01	1.26	2.62E-02			
2.25E-02	2.65E-01	-1.26	4.94E-02	NM_021205	Hs.647774	RHOU
6.29E-02	2.40E-01	1.26	6.66E-04	BC008026	Hs.676121	MGC16025
1.43E-01	1.53E-01	-1.26	1.74E-03	NM_016848	Hs.656806	SHC3
2.16E-03	4.33E-02	1.26	3.08E-02	NM_002658	Hs.77274	PLAU
4.01E-01	6.18E-01	-1.26	2.98E-02	NM_130782	Hs.440890	RGS18
8.98E-02	1.39E-01	-1.26	1.20E-03	NM_057168	Hs.272375	WNT16
5.55E-03	2.74E-01	1.26	1.26E-03	NM_033393	Hs.132629	FHDC1
5.23E-02	1.41E-02	1.25	2.46E-02	NM_003236	Hs.170009	TGFA
3.62E-01	7.82E-02	-1.25	8.69E-11	NM_024681	Hs.517597	KCTD17
6.80E-04	3.69E-04	-1.25	4.49E-02	NM_015710	Hs.421907	GLTSCR2
1.18E-01	2.98E-01	1.25	3.20E-02	NM_001103161	Hs.591522	SH2D5
2.91E-01	2.45E-01	-1.25	5.38E-04	NM_002214	Hs.592171	ITGB8
1.70E-04	2.34E-01	-1.25	1.72E-02	BC031314	Hs.26766	
1.45E-01	5.01E-01	1.25	2.87E-04	AW138098	Hs.539067	
1.37E-02	3.02E-02	1.25	8.97E-03	THC2743652		
4.67E-03	2.25E-02	-1.25	8.36E-03	NM_006283	Hs.279245	TACC1
2.63E-02	1.96E-01	1.25	1.37E-02	AV698803	Hs.540419	
1.14E-01	4.02E-01	-1.25	1.72E-02	NM_003106	Hs.518438	SOX2
5.45E-03	1.02E-02	-1.25	5.57E-08	NM_001967	Hs.518475	EIF4A2
1.40E-02	6.42E-01	-1.25	1.44E-02	THC2640099		
5.00E-02	1.31E-02	1.25	7.25E-05	NM_014830	Hs.591025	ZBTB39
4.65E-03	1.32E-02	-1.25	6.00E-03	NM_013262	Hs.484738	MYLIP
8.29E-01	7.37E-02	1.25	2.45E-04	BC027471		LOC440173
1.67E-01	3.99E-02	1.25	3.32E-03	NM_007235	Hs.85951	XPOT
1.34E-02	2.93E-01	-1.25	5.01E-05	NM_003278	Hs.476092	CLEC3B
1.47E-01	6.29E-01	-1.25	1.26E-02	NM_130810	Hs.126403	DYX1C1

1.86E-01	2.26E-01	-1.25	4.17E-06	NM_004117	Hs.407190	FKBP5
5.65E-02	6.64E-03	1.25	1.16E-04	NM_001896	Hs.82201	CSNK2A2
1.20E-02	4.54E-02	-1.25	6.51E-05	NM_153705	Hs.83286	KDELC2
8.63E-02	8.11E-03	-1.25	3.73E-02	NM_201269	Hs.173001	ZNF644
1.62E-02	3.93E-02	-1.25	8.94E-04	ENST00000361227		ND3
2.83E-03	7.03E-02	-1.25	4.64E-02	NM_006287	Hs.516578	TFPI
2.32E-01	2.60E-01	-1.25	3.86E-02	NM_032023	Hs.522895	RASSF4
6.88E-03	7.84E-02	1.25	8.88E-05	THC2639487		
2.36E-01	2.06E-01	1.25	2.78E-02	AK000347	Hs.272794	LAX1
7.22E-02	2.85E-02	-1.25	2.71E-04	NM_000390	Hs.496449	CHM
2.19E-03	5.28E-01	-1.25	1.63E-05	BC012984	Hs.657382	PARD3B
1.37E-01	7.15E-03	1.25	2.61E-02			
1.93E-01	9.01E-02	1.25	1.50E-04	NM_006504	Hs.127022	PTPRE
6.97E-02	2.03E-02	-1.25	1.91E-03	AF196185	Hs.131489	PARD3
1.03E-04	6.17E-03	1.25	5.71E-03	NM_015209	Hs.368823	RP1-21O18.1
1.77E-01	2.65E-01	1.25	8.70E-04	NM_000342	Hs.443948	SLC4A1
5.74E-02	9.54E-01	-1.25	2.83E-02	NM_032853	Hs.515016	MUM1
3.36E-02	1.08E-01	-1.25	4.84E-05	NM_004277	Hs.40510	SLC25A27
8.49E-01	2.58E-01	-1.25	7.02E-04	NM_001039948	Hs.474397	SGSM1
8.79E-01	2.52E-02	-1.25	4.23E-02	NM_020659	Hs.268728	TTYH1
5.57E-01	3.29E-02	-1.25	1.08E-02	NM_001106	Hs.174273	ACVR2B
8.81E-01	2.92E-02	1.25	1.48E-02	NM_020715	Hs.594236	PLEKHH1
4.66E-03	1.96E-01	1.25	1.76E-05	NM_022740	Hs.397465	HIPK2
8.02E-02	4.71E-01	-1.25	3.87E-02	NM_138409	Hs.370055	C6orf117
2.79E-01	1.21E-01	-1.25	3.32E-02	NM_002606	Hs.473927	PDE9A
8.91E-02	3.46E-02	-1.25	1.22E-06	NM_005612	Hs.631513	REST
4.15E-01	1.87E-02	1.25	6.91E-03	NM_023112	Hs.278815	OTUB2
5.79E-04	1.77E-01	-1.25	1.80E-04	AK131288	Hs.710569	LOC10013331
3.10E-01	5.48E-01	1.25	2.95E-02	M87790	Hs.449585	
2.16E-01	3.83E-02	1.25	1.45E-03	NM_173076	Hs.134585	ABCA12
4.34E-01	1.35E-01	-1.25	1.99E-02	NM_002483	Hs.466814	CEACAM6
8.08E-03	5.19E-02	1.25	9.61E-07	NM_004278	Hs.499793	PIGL
7.50E-01	5.72E-03	-1.25	2.93E-02	AK090418	Hs.559040	LOC349196
3.72E-02	6.62E-01	-1.25	1.90E-02			
1.50E-02	9.17E-01	-1.25	1.42E-03	NM_014710	Hs.710048	GPRASP1
6.47E-02	2.25E-01	1.25	2.61E-03	NM_004694	Hs.42645	SLC16A6
1.30E-02	7.21E-02	-1.25	2.01E-03	NM_173550	Hs.17267	C9orf93
1.50E-02	4.59E-01	-1.25	1.43E-02	NM_130759	Hs.647087	GIMAP1
1.84E-01	2.49E-01	-1.25	1.30E-06	BC042034	Hs.592178	C7orf46
5.58E-03	7.78E-02	1.25	4.33E-02	THC2695815		
1.64E-02	4.26E-03	-1.25	4.34E-03	ENST00000361453	Hs.631494	ND2
8.54E-02	1.48E-01	-1.25	1.02E-02	NM_001547	Hs.437609	IFIT2
5.04E-03	1.69E-01	-1.25	1.74E-03	NM_000633	Hs.150749	BCL2
7.48E-01	7.48E-02	1.25	6.49E-04	NM_001039547	Hs.135904	GK5
8.08E-03	1.52E-01	-1.25	2.76E-02	NM_000700	Hs.494173	ANXA1
2.18E-02	5.61E-02	-1.25	2.52E-03	NM_153609	Hs.370885	TMPRSS6
1.48E-02	3.01E-01	1.25	3.99E-02	AK130741	Hs.347034	

6.34E-01	9.86E-03	-1.25	2.57E-03	NM_006777	Hs.143604	ZBTB33
2.91E-01	3.04E-03	-1.25	3.42E-02	NM_005645	Hs.632426	TAF13
5.94E-03	5.25E-01	1.25	6.13E-04			
1.11E-01	2.14E-01	-1.25	1.20E-03	NM_002193	Hs.1735	INHBB
1.81E-01	5.83E-01	-1.24	3.72E-02	NM_001080412	Hs.518301	ZBTB38
2.14E-03	6.65E-03	1.24	4.64E-02	XM_292021	Hs.282121	LOC341346
5.24E-02	2.20E-02	1.24	9.61E-03	CR749646	Hs.491354	EXTL3
4.95E-03	1.50E-02	-1.24	1.72E-04			
6.99E-02	8.53E-01	-1.24	2.77E-02	NM_025190	Hs.532921	ANKRD36B
6.29E-01	4.77E-01	1.24	3.47E-02	BC008001	Hs.570804	
6.78E-03	1.31E-02	1.24	1.79E-02	NM_001407	Hs.631926	CELSR3
2.51E-02	5.94E-02	1.24	2.06E-02	NM_020959	Hs.590990	TMEM16H
4.56E-01	3.00E-01	-1.24	1.88E-02	NM_014571	Hs.472566	HEYL
8.46E-01	6.30E-02	-1.24	1.11E-02	NM_182529	Hs.650237	THAP5
1.52E-03	4.12E-02	-1.24	2.55E-02	NM_001733	Hs.524224	C1R
6.58E-03	6.18E-01	-1.24	5.68E-03	NM_001080412	Hs.518301	ZBTB38
2.18E-04	6.42E-02	-1.24	4.99E-03	NM_006738	Hs.459211	AKAP13
2.21E-01	9.51E-02	-1.24	3.05E-02	AA045093	Hs.130438	
5.08E-03	1.10E-01	-1.24	9.79E-03	NM_002310	Hs.133421	LIFR
5.94E-03	4.31E-02	1.24	1.27E-02	NM_006675	Hs.504517	TSPAN9
2.89E-01	1.46E-01	-1.24	1.20E-03	NM_003355	Hs.80658	UCP2
1.71E-01	5.82E-03	1.24	3.80E-02	AB071195		BCL2L11
3.78E-03	6.01E-01	1.24	2.19E-02	NM_001080472	Hs.632269	C20orf142
3.15E-03	3.30E-02	1.24	1.31E-02	AK094466	Hs.655875	TSEN54
2.89E-02	4.36E-04	1.24	1.09E-04	NM_018103	Hs.482087	LRRC8D
5.38E-03	2.34E-01	1.24	7.48E-08	NM_152384	Hs.233398	BBS5
9.27E-01	1.27E-02	-1.24	4.81E-02	NM_002198	Hs.436061	IRF1
1.05E-04	2.64E-01	-1.24	2.25E-02	NM_001920	Hs.706840	DCN
7.84E-02	5.11E-01	1.24	1.78E-03	NM_207380	Hs.32433	C15orf52
1.20E-04	8.06E-02	-1.24	4.51E-02	NM_001992	Hs.482562	F2R
2.56E-02	1.14E-01	-1.24	5.51E-06	NM_032470	Hs.485104	TNXB
8.08E-01	9.48E-02	-1.24	2.01E-03	NM_181644	Hs.567714	MFSD4
9.62E-03	1.40E-02	1.24	1.15E-10	BC034571	Hs.380225	PLA2G4D
1.04E-04	6.98E-02	1.24	7.76E-04	BC014983		TBC1D20
3.22E-01	5.88E-01	1.24	2.62E-02	BC030778	Hs.515951	SH3YL1
7.44E-02	1.07E-01	-1.24	9.58E-03	NM_144974	Hs.170849	CCDC122
8.33E-03	1.44E-02	1.24	7.35E-03	AK000707		
2.43E-01	5.24E-02	-1.24	1.38E-04	THC2535223		
6.32E-02	6.07E-01	1.24	8.63E-04			
8.57E-02	1.91E-01	-1.24	5.22E-03	NM_001848	Hs.474053	COL6A1
1.12E-04	5.53E-02	1.24	4.88E-02	AK125672	Hs.592102	
1.59E-01	7.31E-03	-1.24	2.20E-04	THC2542194		
2.36E-05	4.66E-01	1.24	2.15E-02	BC004449	Hs.153629	MEF2B
2.09E-03	3.20E-02	1.24	5.11E-03	NM_003273	Hs.31130	TM7SF2
1.50E-02	3.42E-01	1.24	2.00E-02	NM_017556	Hs.530101	FBLIM1
9.60E-02	8.76E-03	1.24	8.89E-05	BC013792	Hs.199763	
4.64E-01	1.62E-01	1.24	4.40E-03	NM_013332	Hs.710088	HIG2

5.56E-02	2.26E-02	-1.24	6.03E-08	NM_021963	Hs.66180	NAP1L2
1.89E-01	2.30E-01	1.24	7.56E-03			
6.53E-01	2.18E-02	-1.24	5.22E-03	NM_002162	Hs.654563	ICAM3
2.67E-01	3.95E-01	1.24	9.98E-04	NM_001025366	Hs.73793	VEGFA
8.85E-02	9.87E-02	1.24	1.15E-07	THC2659519		
6.71E-02	1.54E-01	-1.24	4.95E-13	NM_053056	Hs.523852	CCND1
8.09E-02	8.84E-01	-1.24	1.54E-03	NM_004816	Hs.118003	C9orf61
2.10E-02	8.95E-01	1.24	1.29E-02	AK125225	Hs.306212	ATP8B3
5.97E-03	6.56E-01	-1.24	9.22E-03	NM_000898	Hs.654473	MAOB
5.76E-02	1.40E-02	-1.24	1.24E-04	CR591210	Hs.476082	
2.71E-01	1.73E-01	1.24	3.26E-02			
3.30E-02	2.47E-01	-1.24	4.72E-04	NM_024302	Hs.380710	MMP28
1.23E-02	4.79E-02	1.24	3.73E-03	BC034222	Hs.410316	HRASLS5
8.88E-02	4.73E-01	-1.24	1.46E-06	NM_003436	Hs.85863	ZNF135
1.78E-02	2.16E-01	-1.24	8.76E-03	NM_001943	Hs.412597	DSG2
2.66E-02	2.76E-02	-1.24	4.81E-02	NM_003514	Hs.134999	HIST1H2AM
1.38E-01	8.00E-03	1.24	5.43E-03	AK123107	Hs.558076	
9.82E-01	4.61E-01	-1.24	7.16E-03			
4.93E-01	8.30E-02	1.24	1.14E-02	AK000041	Hs.675410	C14orf113
4.46E-01	1.06E-01	-1.24	3.36E-03	NM_004210	Hs.594708	NEURL
1.74E-01	2.39E-02	1.24	1.02E-02	NM_022726	Hs.101915	ELOVL4
2.37E-02	6.60E-02	-1.24	1.11E-03	AK055438	Hs.660989	
7.52E-03	6.49E-02	1.23	1.85E-02	NM_057178	Hs.13680	RFFL
6.87E-02	5.40E-03	-1.23	8.77E-03			
1.85E-01	7.15E-03	-1.23	2.87E-04	THC2595309		
7.90E-01	2.17E-02	-1.23	3.80E-03	NM_015568	Hs.45719	PPP1R16B
1.48E-01	1.99E-01	1.23	2.51E-02	AK022393	Hs.661121	FLJ12331
5.05E-01	9.40E-01	-1.23	7.72E-03	BC020226		HLA-DOB
3.84E-01	2.67E-03	1.23	9.15E-03	NM_017573	Hs.46884	PCSK4
3.99E-04	2.04E-01	-1.23	3.18E-02	NM_152999	Hs.489051	STEAP2
2.63E-01	5.15E-02	-1.23	2.34E-03	NM_003246	Hs.164226	THBS1
3.94E-01	3.75E-01	-1.23	3.35E-02	NM_001465	Hs.370503	FYB
1.15E-01	2.54E-01	-1.23	2.75E-04	CX788817	Hs.120377	
2.23E-01	5.16E-01	-1.23	2.20E-02	THC2667205		
4.31E-01	2.57E-01	1.23	3.25E-02	NM_031413	Hs.658723	CECR2
2.48E-01	6.41E-01	1.23	3.76E-02	CR627452	Hs.474233	C22orf25
1.67E-03	2.92E-01	-1.23	4.44E-02	NM_016613	Hs.567498	C4orf18
7.99E-03	1.85E-02	-1.23	1.86E-03	NM_002923	Hs.78944	RGS2
1.27E-01	3.54E-04	-1.23	8.39E-03	NM_002116	Hs.181244	HLA-A
2.84E-02	7.54E-04	1.23	1.02E-02	NM_004577	Hs.512656	PSPH
1.58E-02	4.32E-02	1.23	1.70E-02	BC001743		C7orf44
6.64E-01	2.09E-01	-1.23	3.10E-02	NM_182603	Hs.503438	ANKRD42
2.00E-02	2.82E-02	-1.23	3.98E-02	NM_005406	Hs.706819	ROCK1
1.87E-01	3.10E-01	1.23	3.50E-02			
1.15E-02	4.43E-02	-1.23	4.84E-03	NM_018013	Hs.445244	SOBP
8.70E-01	1.57E-01	-1.23	3.46E-02	NM_032782	Hs.710500	HAVCR2
3.61E-01	4.17E-02	1.23	1.33E-02	NM_000386	Hs.371914	BLMH

5.34E-03	9.84E-03	1.23	1.54E-02	NM_000135	Hs.567267	FANCA
1.27E-01	1.03E-02	1.23	2.07E-03	THC2737176	Hs.670210	
1.20E-01	1.90E-01	1.23	4.36E-09	CR601458	Hs.8379	FAM110C
9.75E-01	7.50E-02	-1.23	1.40E-05	NM_001010879	Hs.454830	ZIK1
1.81E-02	2.34E-02	-1.23	1.13E-05	NM_000958	Hs.199248	PTGER4
2.43E-02	3.73E-01	1.23	2.85E-02	NM_006695	Hs.500197	RUNDC3A
3.18E-01	5.48E-01	1.23	5.15E-04	NM_005061	Hs.657266	RPL3L
2.69E-01	3.65E-01	-1.23	1.71E-02	NM_017551	Hs.530653	GRID1
5.76E-03	5.27E-01	1.23	3.54E-02	NM_000710	Hs.525572	BDKRB1
1.09E-01	3.50E-02	1.23	4.09E-04	BX640843	Hs.128803	
7.98E-01	4.35E-02	-1.23	1.11E-02	NM_198887	Hs.510375	NUP43
4.51E-01	9.29E-01	-1.23	5.60E-04	NM_000779	Hs.436317	CYP4B1
1.87E-01	1.97E-01	-1.23	2.90E-02	NM_032591	Hs.496057	SLC9A7
9.55E-05	6.63E-02	1.23	3.57E-02	NM_032704	Hs.652390	TUBA1C
7.78E-01	1.51E-01	-1.23	6.97E-05	NM_020776	Hs.4045	KIAA1328
7.62E-01	2.78E-04	1.23	4.15E-02	NM_000496	Hs.373074	CRYBB2
2.36E-01	2.71E-01	-1.23	1.65E-03	NM_000201	Hs.707983	ICAM1
5.38E-01	3.82E-01	-1.23	1.32E-02	NM_138290	Hs.411488	RUNDC3B
5.26E-04	1.98E-01	-1.23	6.25E-03	NM_000063	Hs.408903	C2
1.10E-02	6.54E-01	-1.23	9.98E-03	NM_024800	Hs.657336	NEK11
1.94E-02	5.11E-01	1.23	3.17E-03	NM_178422	Hs.523652	PAQR7
9.72E-03	2.61E-03	1.23	2.79E-02	AK123430	Hs.445496	MAP3K9
5.24E-01	4.08E-02	1.23	2.05E-02	THC2614203		
3.78E-02	7.32E-03	1.23	1.94E-03	NM_018000	Hs.709755	MREG
7.38E-02	1.63E-01	1.23	3.67E-03	BC007606	Hs.700219	
9.60E-02	4.13E-02	1.23	1.17E-02	NM_025182	Hs.301696	KIAA1539
3.75E-01	5.43E-01	1.23	1.70E-02	NM_153618	Hs.511265	SEMA6D
3.65E-01	5.45E-01	1.23	2.25E-02	BC014505	Hs.709178	MLLT4
5.16E-01	3.70E-02	1.23	1.69E-02	NM_133367	Hs.239388	PAQR8
6.63E-01	5.40E-02	-1.23	2.91E-02	NM_004118	Hs.516971	FOXS1
1.86E-01	2.01E-02	1.23	1.95E-02	NM_024563	Hs.13528	C5orf23
1.33E-01	4.84E-02	-1.23	3.55E-02	NM_014832	Hs.210891	TBC1D4
1.15E-02	8.10E-01	-1.23	2.68E-02	NM_032606	Hs.407154	CAPS2
6.46E-01	7.59E-01	1.23	6.42E-03	NM_003541	Hs.528055	HIST1H4K
3.52E-01	1.49E-01	-1.23	4.23E-02	NM_016205	Hs.570855	PDGFC
7.92E-02	1.97E-01	1.23	1.05E-02			
1.57E-01	2.99E-01	-1.23	4.79E-04	NM_003265	Hs.657724	TLR3
9.37E-03	4.89E-01	1.23	1.26E-03	NM_182492	Hs.710309	LRP5L
1.70E-02	2.26E-01	-1.23	1.36E-03	NM_153223	Hs.483209	CCDC100
4.71E-02	6.17E-01	1.23	1.29E-02	NM_017789	Hs.516220	SEMA4C
9.40E-02	2.93E-02	1.23	2.85E-02	THC2584954	Hs.158497	
3.31E-02	1.48E-01	1.23	3.59E-02			
4.47E-01	3.92E-02	-1.23	1.66E-02	NM_001964	Hs.326035	EGR1
4.30E-02	4.86E-01	-1.23	3.49E-03	ENST00000375280	Hs.443729	LOC285141
1.18E-02	4.52E-01	1.23	3.22E-03	NM_005185	Hs.239600	CALML3
6.72E-03	6.40E-01	1.23	4.78E-02	NM_006670	Hs.82128	TPBG
7.79E-02	1.18E-01	-1.23	2.65E-04	NM_172088	Hs.54673	TNFSF13

3.17E-01	1.47E-01	-1.23	6.76E-04	NM_032427	Hs.428214	MAML2
2.60E-01	1.62E-01	-1.23	5.92E-03	NM_181482	Hs.149363	C18orf1
5.38E-01	5.15E-01	-1.23	1.66E-03	NM_015288	Hs.483419	PHF15
6.23E-02	5.66E-01	-1.23	1.21E-02	NM_005408	Hs.414629	CCL13
1.39E-01	3.92E-01	-1.23	1.30E-02	NM_021998	Hs.326801	ZNF711
1.43E-01	4.48E-01	-1.23	1.51E-02	NM_052818	Hs.161220	N4BP2L1
6.71E-01	1.61E-03	1.23	4.84E-02	NM_005155	Hs.635690	PPT2
2.40E-02	4.45E-03	1.23	4.08E-02			
9.30E-01	3.83E-01	-1.23	2.91E-04	NM_007356	Hs.62022	LAMB4
5.97E-01	2.53E-02	1.23	9.01E-03	NM_181581	Hs.97627	DUS4L
9.37E-01	3.91E-03	-1.23	4.44E-02	BC050737	Hs.654587	SMA4
8.66E-01	4.01E-02	1.22	4.04E-02	NM_006033	Hs.465102	LIPG
5.60E-03	5.54E-02	-1.22	1.40E-03	NM_014880	Hs.709212	CD302
8.76E-03	1.50E-01	1.22	5.50E-04	AF086305	Hs.660199	ZNF286A
1.67E-01	3.28E-01	-1.22	3.88E-04	AB032989	Hs.709892	AMIGO1
1.42E-01	1.98E-01	1.22	1.83E-02	NM_005557	Hs.655160	KRT16
6.34E-02	9.74E-01	1.22	2.56E-03	NM_018667	Hs.368421	SMPD3
1.09E-01	4.40E-02	1.22	4.00E-02	NM_002016	Hs.654510	FLG
1.78E-01	1.45E-01	1.22	1.57E-03	BC012888	Hs.222055	NDST1
2.25E-02	1.19E-02	1.22	1.41E-03	NM_033429	Hs.709550	CALML4
1.91E-01	9.55E-02	-1.22	3.55E-04	NM_020817	Hs.477159	KIAA1407
4.97E-01	1.13E-01	1.22	2.33E-02	AK131087		POL3S
8.81E-02	3.31E-01	-1.22	4.65E-02	ENST00000344538	Hs.633153	LOC375010
1.80E-02	2.50E-03	-1.22	5.32E-03	NM_005345	Hs.520028	HSPA1A
1.22E-03	1.95E-01	1.22	2.53E-02	NM_005213	Hs.518198	CSTA
1.15E-01	3.01E-02	1.22	4.98E-02	NM_007173	Hs.25338	PRSS23
4.68E-03	3.58E-01	-1.22	1.43E-05	ENST00000376347	Hs.651407	
9.67E-01	8.67E-01	1.22	1.53E-02	NM_014211	Hs.26225	GABRP
1.24E-01	6.60E-01	1.22	2.41E-03	AK025323	Hs.671557	
9.25E-02	2.32E-02	1.22	2.05E-02	AL512694	Hs.556986	NADSYN1
1.97E-01	5.96E-01	1.22	1.62E-03	NM_145274	Hs.353163	TMEM99
3.29E-02	5.35E-01	-1.22	1.21E-02	NM_007021	Hs.93675	C10orf10
4.61E-03	1.06E-01	-1.22	5.25E-07	NM_005574	Hs.34560	LMO2
8.75E-02	7.28E-01	1.22	4.64E-03	AK098478	Hs.683792	LOC10013025
1.73E-04	8.19E-02	1.22	1.72E-02	NM_018306	Hs.475502	TMEM40
2.76E-01	8.62E-01	-1.22	3.03E-02	NM_000960	Hs.458324	PTGIR
7.19E-01	1.53E-01	1.22	2.64E-02	NM_000391	Hs.523454	TPP1
8.45E-03	1.66E-02	1.22	4.16E-02	NM_130776	Hs.43879	XAGE3
3.09E-01	5.37E-02	-1.22	5.25E-04	ENST00000344759	Hs.444446	
2.34E-02	5.18E-01	-1.22	2.96E-03	NM_001040440	Hs.436121	CCDC112
6.79E-02	6.10E-03	-1.22	7.37E-03	NM_001259	Hs.119882	CDK6
9.61E-01	2.50E-01	-1.22	1.86E-03	NM_003726	Hs.316931	SKAP1
1.49E-01	1.15E-01	1.22	3.08E-02	AI682237	Hs.439122	
2.69E-02	1.50E-01	-1.22	1.87E-03	NM_032217	Hs.601206	ANKRD17
9.34E-01	2.61E-01	1.22	4.55E-02	NM_002272	Hs.654610	KRT4
7.98E-01	4.13E-01	1.22	2.29E-02	NM_206967	Hs.461655	C16orf74
2.65E-02	9.40E-01	1.22	3.43E-02	NM_004694	Hs.42645	SLC16A6

2.79E-01	1.11E-01	-1.22	4.12E-03	NM_019885	Hs.91546	CYP26B1
4.77E-01	2.01E-01	1.22	3.08E-02	NM_012319	Hs.79136	SLC39A6
1.76E-01	8.74E-01	-1.22	1.91E-03			
3.67E-04	9.61E-02	-1.22	4.34E-02	NM_152261	Hs.257664	C12orf23
4.24E-03	3.77E-03	1.22	1.23E-02	NM_001006946	Hs.224607	SDC1
6.34E-01	9.87E-01	-1.22	4.60E-03	NM_020911	Hs.511454	PLXNA4
4.07E-01	5.42E-01	-1.22	1.98E-02	NM_013322	Hs.571296	SNX10
6.73E-03	4.42E-02	1.22	2.00E-04	THC2525505		
4.90E-02	1.04E-01	1.22	3.35E-03			
4.37E-01	2.09E-02	-1.22	3.35E-03	NM_004747	Hs.654829	DLG5
1.27E-02	6.52E-03	1.22	1.47E-02	AK097197	Hs.514590	HGS
3.18E-02	8.81E-03	1.22	3.76E-02	BC004179	Hs.667436	MGC2780
1.71E-02	1.62E-03	-1.22	1.60E-06	NM_021156	Hs.169358	TXNDC13
3.60E-02	7.93E-01	-1.22	4.29E-05	NM_001311	Hs.70327	CRIP1
8.91E-01	1.02E-02	-1.22	4.73E-02	AX721087		
2.23E-02	9.65E-01	-1.22	3.61E-02	BC030122	Hs.559426	
6.82E-02	4.65E-02	1.22	3.71E-02	AK023048	Hs.54713	FLJ12986
6.86E-02	5.35E-01	1.22	1.70E-03	NM_003953	Hs.493919	MPZL1
1.12E-01	3.88E-01	-1.22	1.77E-05	THC2676635		
3.02E-02	2.52E-02	1.22	2.29E-04	H12329	Hs.519880	
2.20E-02	1.30E-01	1.22	3.59E-02	AK094407	Hs.683873	LOC645427
2.02E-03	9.56E-02	1.22	1.46E-02	ENST00000307394	Hs.7247	EME2
4.14E-03	7.92E-02	1.22	6.32E-03	NM_152574	Hs.563630	C9orf52
3.41E-02	5.55E-02	-1.22	2.84E-02	NM_015384	Hs.481927	NIPBL
9.76E-04	1.23E-01	-1.22	3.02E-02	M74720	Hs.644653	
6.98E-01	1.50E-01	-1.22	4.82E-02	THC2752681		
4.89E-01	2.20E-01	-1.22	1.74E-06	NM_000024	Hs.591251	ADRB2
8.09E-03	1.61E-02	1.22	1.76E-04	NM_020964	Hs.514843	KIAA1632
2.69E-01	7.64E-01	1.22	1.34E-02	NM_001005209	Hs.446664	TMEM198
5.83E-03	4.21E-02	1.22	3.20E-02			
1.86E-01	6.53E-03	1.22	2.33E-02	NM_212559	Hs.592216	XKRX
2.96E-02	6.37E-01	-1.22	1.85E-03	NM_002448	Hs.424414	MSX1
1.12E-01	4.03E-01	1.22	4.91E-02	NM_005532	Hs.532634	IFI27
8.60E-04	1.02E-02	-1.22	2.37E-02	NM_021913	Hs.590970	AXL
3.34E-03	7.51E-01	1.22	4.82E-02	NR_003611	Hs.652450	BMS1P5
3.06E-03	6.12E-01	1.22	3.13E-02	NM_002648	Hs.81170	PIM1
2.61E-03	1.74E-01	1.22	1.14E-02	NM_002735	Hs.520851	PRKAR1B
3.67E-02	1.44E-03	-1.22	2.97E-02	AL117530	Hs.146346	LOC729085
3.81E-01	1.39E-02	1.22	3.35E-02	NM_147780	Hs.520898	CTSB
3.67E-02	2.43E-01	-1.22	2.22E-02	NM_053276	Hs.137415	VIT
3.16E-02	8.76E-01	1.22	3.35E-02	NM_001002876	Hs.208912	CENPM
9.06E-02	6.92E-01	1.22	3.55E-08	NM_012445	Hs.302963	SPON2
1.43E-03	2.00E-01	-1.22	2.54E-02	ENST00000327423	Hs.438906	
5.11E-01	4.48E-02	1.22	2.01E-02			
9.72E-01	3.52E-02	1.22	4.15E-02	NM_024830	Hs.368853	LPCAT1
1.95E-01	9.82E-02	-1.22	6.34E-03	NM_017759	Hs.445036	FLJ20309
2.54E-03	4.24E-01	-1.22	1.75E-02	NM_013960	Hs.453951	NRG1

1.00E-02	8.76E-01	1.22	5.48E-03	CA314451	Hs.369574	
8.44E-03	1.23E-01	-1.22	2.39E-02	NM_021785	Hs.708804	RAI2
5.47E-01	9.12E-03	1.22	3.24E-02			
4.96E-03	8.80E-01	1.22	3.73E-03	NM_007238	Hs.654857	PXMP4
1.01E-01	1.10E-01	1.22	1.71E-04	NM_018252	Hs.445386	TMEM206
9.45E-01	1.20E-02	1.22	4.03E-03	NM_014384	Hs.14791	ACAD8
9.66E-01	1.77E-02	-1.22	1.57E-03	CR627122	Hs.291319	
9.93E-06	2.27E-02	-1.22	7.82E-04	ENST00000391372		
2.04E-01	8.45E-04	1.22	3.07E-02	NM_005990	Hs.519756	STK10
7.73E-02	4.33E-03	1.22	1.68E-02	NM_016352	Hs.93764	CPA4
9.58E-01	6.22E-02	1.22	1.42E-03	THC2744687		
4.39E-02	6.70E-01	-1.22	1.31E-03	BC045657	Hs.656959	C6orf204
9.06E-04	5.24E-01	-1.22	4.02E-02	NM_016824	Hs.501012	ADD3
2.13E-04	1.14E-01	1.22	1.40E-02	NM_033641	Hs.145586	COL4A6
1.75E-01	2.61E-01	-1.22	4.66E-03	NM_018936	Hs.533023	PCDHB2
5.43E-01	1.75E-01	-1.22	6.91E-03	BF213738	Hs.85201	
1.46E-03	2.03E-01	-1.22	1.63E-02	NM_148894	Hs.444517	FAM44A
8.70E-01	7.46E-01	1.22	1.75E-02	NM_005795	Hs.470882	CALCRL
1.61E-02	4.32E-03	1.22	1.15E-02	NM_020698	Hs.370410	TMCC3
3.75E-02	1.11E-01	-1.22	3.82E-02	ENST00000372234		ANXA11
2.55E-03	6.68E-02	-1.22	5.94E-03	NM_002563	Hs.654526	P2RY1
9.16E-01	8.53E-03	1.22	5.05E-04	NM_015264	Hs.592207	C22orf9
1.45E-01	2.73E-01	1.22	7.71E-03	AK097085	Hs.660415	
1.50E-04	3.91E-01	1.22	2.26E-02	NM_003501	Hs.479122	ACOX3
3.37E-02	2.51E-03	1.21	5.28E-03	NM_021089	Hs.590941	ZNF8
3.59E-02	3.65E-02	-1.21	3.63E-02			
3.70E-01	1.02E-01	1.21	7.28E-03	BC009264	Hs.516124	hCG_1811732
1.76E-03	4.07E-03	1.21	1.16E-03	NM_198552	Hs.38516	FAM89A
1.65E-02	1.40E-02	1.21	4.13E-02	NM_145203	Hs.512897	CSNK1A1L
4.42E-02	4.01E-02	-1.21	5.40E-03	NM_173830	Hs.632616	C6orf182
7.64E-01	3.67E-02	-1.21	1.02E-03	NM_001085375	Hs.447011	FLJ13137
9.76E-03	3.19E-02	-1.21	9.77E-03	NM_014059	Hs.507866	C13orf15
4.63E-03	4.99E-02	1.21	1.50E-05	BC021301	Hs.657318	FARP2
2.55E-01	2.44E-02	1.21	1.97E-03	NM_014452	Hs.443577	TNFRSF21
2.79E-01	2.89E-03	1.21	3.31E-02	NM_020148	Hs.515283	SPIRE1
5.35E-01	3.27E-01	-1.21	4.71E-02	U18288	Hs.701991	CIITA
8.73E-01	5.20E-01	1.21	9.02E-03			
6.65E-01	1.77E-01	-1.21	3.49E-03	NM_024677	Hs.590923	NSUN7
7.78E-01	6.53E-02	-1.21	3.71E-02	XM_001130623	Hs.116176	LOC645733
3.93E-02	5.46E-01	1.21	1.54E-03	AL833832		
6.47E-01	7.02E-03	-1.21	1.98E-02	NM_001079846	Hs.459759	CREBBP
8.38E-04	2.33E-01	-1.21	4.59E-02	AK001357	Hs.675463	
2.71E-01	3.35E-02	-1.21	4.80E-03	BC112296	Hs.529860	
7.60E-02	9.75E-01	-1.21	1.16E-02	NM_001547	Hs.437609	IFIT2
1.27E-01	2.59E-01	-1.21	2.00E-02	NM_016524	Hs.258326	SYT17
1.06E-04	1.40E-02	-1.21	2.21E-02	NM_020738	Hs.9873	KIDINS220
6.33E-02	1.38E-01	1.21	1.59E-06	NM_002165	Hs.504609	ID1

1.08E-02	2.09E-02	-1.21	3.55E-03	NM_001300	Hs.4055	KLF6
1.63E-03	2.18E-01	-1.21	2.84E-04	BX538051	Hs.149540	LOC730102
6.32E-01	8.40E-02	-1.21	8.18E-03	NM_130436	Hs.368240	DYRK1A
8.93E-03	5.86E-01	1.21	8.59E-03	AK022016	Hs.613667	
3.31E-01	9.37E-02	1.21	3.87E-05	NM_000513	Hs.247787	OPN1MW
2.02E-02	7.81E-02	1.21	2.60E-02	NM_133329	Hs.352633	KCNG3
5.63E-01	1.43E-01	1.21	1.87E-02	BF246504	Hs.632926	
1.69E-02	8.47E-02	-1.21	2.54E-02	NM_148894	Hs.444517	FAM44A
5.38E-03	4.00E-02	-1.21	1.45E-04	NM_002349	Hs.153563	LY75
2.07E-01	1.13E-01	1.21	4.20E-03	THC2663783		
9.19E-01	3.72E-02	-1.21	2.73E-02	NM_148898	Hs.656280	FOXP2
1.08E-02	1.23E-01	-1.21	2.36E-03	NR_003674	Hs.439341	KGFLP1
5.48E-04	2.12E-01	1.21	1.20E-02	NM_198253	Hs.492203	TERT
1.60E-02	6.29E-01	1.21	4.87E-02			
3.89E-03	2.46E-01	1.21	7.08E-03	NM_001098523	Hs.90753	HTATIP2
3.25E-01	7.45E-02	-1.21	3.55E-03	NM_000958	Hs.199248	PTGER4
5.44E-02	5.49E-01	1.21	4.35E-03	NM_133456	Hs.519574	SHROOM1
5.34E-01	8.92E-03	1.21	3.21E-03	NM_032499	Hs.48348	C15orf41
3.66E-03	1.99E-01	1.21	1.69E-02	BC036762	Hs.680805	MGC46336
9.59E-04	2.18E-02	-1.21	2.48E-02	NM_014059	Hs.507866	C13orf15
4.82E-01	3.26E-02	-1.21	2.52E-02	NM_001002295	Hs.524134	GATA3
5.98E-03	1.51E-01	-1.21	1.50E-03	NM_012330	Hs.35758	MYST4
4.35E-01	1.52E-01	-1.21	2.85E-03	THC2558699		
2.19E-01	1.21E-02	-1.21	2.77E-02			
3.80E-03	2.82E-03	1.21	1.93E-02	NM_173490	Hs.162246	TMEM171
1.86E-02	9.94E-02	1.21	3.88E-02	THC2712447		
1.55E-01	1.74E-01	1.21	1.13E-03	AK092751	Hs.635171	LOC286254
6.87E-03	4.24E-01	1.21	1.09E-05	ENST00000361907	Hs.659681	BCOR
7.68E-02	3.46E-01	-1.21	1.37E-02	NM_002193	Hs.1735	INHBB
2.76E-01	3.16E-01	-1.21	2.05E-02	NM_002090	Hs.89690	CXCL3
1.77E-02	9.49E-01	-1.21	1.03E-02	NM_015672	Hs.115429	RIMBP3
5.64E-03	8.85E-01	-1.21	2.61E-02	NM_053044	Hs.479119	HTRA3
9.38E-03	1.48E-01	1.21	3.72E-02	U88965	Hs.667161	C3orf51
1.21E-01	9.47E-01	-1.21	6.47E-03	NM_030820	Hs.47629	COL21A1
1.94E-01	4.37E-01	-1.21	4.52E-03	NM_006006	Hs.591945	ZBTB16
3.76E-01	5.29E-02	1.21	4.47E-02	AF354444	Hs.650087	
1.24E-01	2.10E-02	1.21	2.92E-02	NM_052925	Hs.502378	LENG8
9.12E-01	5.54E-03	-1.21	2.40E-02	NM_002269	Hs.182971	KPNA5
2.59E-03	2.12E-01	-1.21	2.85E-02	NM_025134	Hs.59159	CHD9
1.57E-01	8.32E-02	1.21	3.94E-05	BE671182	Hs.437497	
4.02E-01	8.49E-03	1.21	2.94E-02	THC2708710		
2.47E-02	3.43E-01	-1.21	1.58E-03	AK123506	Hs.592801	
7.87E-03	5.99E-01	-1.21	1.30E-02	NM_025211	Hs.522255	GKAP1
1.59E-01	9.79E-03	-1.21	1.25E-02	NM_032335	Hs.356501	PHF6
6.34E-02	7.73E-01	-1.21	4.44E-04	NM_019018	Hs.591751	FAM105A
3.65E-02	1.17E-01	-1.21	2.12E-02	AB037817	Hs.710590	ZNF471
1.75E-02	3.03E-01	1.21	8.78E-04	NM_178520	Hs.364191	TMEM105

2.82E-02	7.44E-02	1.21	4.26E-02	NM_001374	Hs.103503	DNASE1L2
2.23E-02	3.12E-01	1.21	7.30E-04	NM_020375	Hs.504545	C12orf5
4.75E-01	1.38E-02	-1.21	3.04E-02	NM_025154	Hs.438072	UNC84A
5.66E-02	5.36E-01	-1.21	4.23E-03	AI379175	Hs.493819	
8.38E-01	6.04E-01	1.21	5.01E-03	NM_175885	Hs.448218	MGC33846
2.49E-02	8.67E-03	-1.21	1.18E-03	CR602405	Hs.101840	MR1
9.00E-03	9.90E-01	1.21	8.56E-03			
2.47E-01	1.08E-02	1.21	1.33E-02	NM_020770	Hs.591464	CGN
7.10E-01	6.02E-02	1.21	4.19E-02	BC006408	Hs.656558	ZNF493
2.12E-02	2.68E-03	-1.21	1.41E-02	NM_007355	Hs.509736	HSP90AB1
6.09E-02	2.75E-01	1.21	1.95E-03	AK098511	Hs.633049	
2.48E-01	3.14E-02	1.21	5.36E-04	NM_014726	Hs.94790	TBKBP1
2.82E-01	3.26E-02	-1.21	6.07E-03	NM_144695	Hs.552608	C1orf58
3.20E-02	1.97E-01	1.21	4.51E-02	THC2705431		
6.04E-02	1.75E-01	1.21	1.73E-02			
7.61E-03	8.96E-02	-1.21	4.06E-04	NM_005590	Hs.192649	MRE11A
2.13E-02	8.57E-01	1.21	4.79E-02	AK091621		KIAA0913
4.33E-02	1.59E-02	-1.21	1.36E-03	NM_058191	Hs.706813	C21orf66
9.03E-03	7.27E-01	1.21	3.87E-02	THC2689970		
8.46E-01	2.31E-02	1.21	2.99E-04	NM_007235	Hs.85951	XPOT
4.38E-01	8.33E-02	-1.21	7.14E-03	NM_024607	Hs.458513	PPP1R3B
5.43E-02	6.69E-02	1.21	2.80E-02	NM_030940	Hs.449291	ISCA1
9.09E-01	2.48E-01	-1.21	1.84E-05	NM_014266	Hs.117339	HCST
1.36E-01	1.21E-03	-1.21	4.24E-02	BC065040	Hs.259412	C1orf63
2.50E-01	5.79E-03	-1.21	3.62E-02	NM_001034841	Hs.648523	LOC162073
1.00E-01	5.75E-01	1.21	3.35E-02	NM_005797	Hs.116651	MPZL2
1.23E-01	1.24E-01	1.21	5.79E-05	NM_030758	Hs.517546	OSBP2
6.05E-01	6.44E-02	1.21	3.00E-03	AK074160	Hs.656032	CDH23
7.25E-03	6.61E-02	-1.21	6.22E-03	NM_000020	Hs.591026	ACVRL1
5.26E-01	9.34E-01	1.21	4.90E-02	BC063625	Hs.406714	KRTAP2-4
1.67E-01	9.33E-03	-1.21	1.72E-02	NM_004936	Hs.72901	CDKN2B
5.34E-01	1.64E-01	1.21	1.11E-02	NM_032843	Hs.133205	FIBCD1
3.01E-03	1.71E-04	-1.21	4.87E-02	NM_001099771	Hs.580547	A26C1B
4.75E-01	8.59E-03	-1.21	4.05E-02	NM_000227	Hs.436367	LAMA3
2.57E-02	6.40E-03	-1.21	4.00E-02	NM_007326	Hs.700572	CYB5R3
2.13E-01	4.65E-02	1.20	3.17E-04	NM_032034	Hs.105607	SLC4A11
3.03E-01	1.62E-01	1.20	1.47E-05	NM_005283	Hs.248116	XCR1
1.76E-02	2.10E-01	-1.20	6.24E-03	NM_000609	Hs.522891	CXCL12
2.99E-01	7.05E-03	1.20	7.53E-03	NM_021214	Hs.459072	FAM108C1
1.62E-01	7.04E-01	-1.20	2.19E-02	NM_001012421	Hs.632663	ANKRD20A2
2.93E-02	1.03E-01	1.20	3.09E-02	XR_016123		LOC440063
1.17E-01	2.24E-02	1.20	1.56E-02	NM_032575	Hs.592087	GLIS2
7.19E-01	7.25E-01	-1.20	8.12E-03	NM_003627	Hs.591952	SLC43A1
1.94E-01	3.80E-01	-1.20	1.09E-02	NM_144643	Hs.654690	SCLT1
6.33E-04	9.86E-01	-1.20	1.95E-02	NM_024665	Hs.709397	TBL1XR1
4.77E-01	1.09E-02	-1.20	1.00E-02	NM_004798	Hs.369670	KIF3B
3.96E-01	8.79E-02	-1.20	4.99E-02	NM_001080848	Hs.522810	CSAG2

1.53E-01	3.86E-03	-1.20	1.42E-02	NM_006805	Hs.96996	HNRNPA0
4.17E-02	8.40E-03	1.20	1.95E-13	NM_022740	Hs.397465	HIPK2
9.31E-03	9.14E-01	-1.20	7.74E-03	ENST00000361789	Hs.631491	CYTB
3.01E-02	2.95E-01	-1.20	5.92E-03	BX538288	Hs.124047	ZNF829
3.30E-02	3.41E-03	1.20	2.87E-02	NM_017957	Hs.670090	EPN3
8.87E-01	1.30E-01	-1.20	1.17E-03	NM_004877	Hs.5210	GMFG
5.22E-01	2.04E-01	-1.20	1.26E-02	NM_005127	Hs.85201	CLEC2B
4.67E-01	7.52E-02	1.20	1.53E-02	NM_001949	Hs.269408	E2F3
2.08E-01	4.09E-01	1.20	1.32E-02	CR610954	Hs.65135	KIAA0913
3.08E-01	1.38E-02	-1.20	5.83E-03	NM_000722	Hs.282151	CACNA2D1
9.99E-01	4.64E-03	-1.20	1.79E-02	NM_000141	Hs.533683	FGFR2
5.91E-03	1.57E-03	-1.20	7.14E-03	CR616772	Hs.448229	
4.65E-02	6.49E-02	-1.20	1.27E-02	NM_177974	Hs.512867	CASC4
7.59E-01	1.46E-01	-1.20	8.98E-03			
1.67E-02	3.80E-01	-1.20	1.84E-03	NM_153223	Hs.483209	CCDC100
7.13E-01	4.29E-03	1.20	1.05E-04	NM_032107	Hs.709356	L3MBTL
1.45E-01	7.59E-02	-1.20	4.93E-02	BC063385	Hs.74647	TRA@
1.74E-02	4.90E-01	-1.20	3.56E-02	NM_012224	Hs.481181	NEK1
3.26E-02	1.07E-01	1.20	1.10E-03	NM_001761	Hs.1973	CCNF
9.61E-01	7.85E-01	1.20	5.26E-04	NM_000952	Hs.709174	PTAFR
8.08E-01	3.88E-01	-1.20	2.75E-02	NM_000364	Hs.533613	TNNT2
3.98E-03	2.41E-02	1.20	1.07E-05	NM_207380	Hs.32433	C15orf52
5.77E-01	6.31E-01	-1.20	4.04E-02	THC2533546		
1.11E-02	7.76E-03	-1.20	4.90E-02	BC002769	Hs.517134	C20orf43
5.66E-01	1.02E-01	1.20	1.03E-03	BC024745		
8.90E-01	4.05E-02	1.20	9.45E-04	NM_000055	Hs.420483	BCHE
5.77E-02	3.21E-01	1.20	3.40E-04	AK074633		ELF5
3.47E-03	3.79E-01	-1.20	3.13E-03	NM_014782	Hs.48924	ARMCX2
1.94E-03	8.01E-01	1.20	3.20E-02	NM_015455	Hs.654984	CNOT6
6.01E-01	2.95E-02	1.20	2.86E-03	NM_023946	Hs.158665	LYNX1
7.42E-01	1.11E-02	-1.20	5.69E-03	NM_004064	Hs.238990	CDKN1B
9.84E-02	6.00E-02	1.20	2.57E-03	NM_015085	Hs.499659	GARNL4
8.00E-01	1.70E-02	-1.20	3.85E-02	NM_025209	Hs.167805	EPC1
9.88E-02	2.23E-02	1.20	4.26E-02	BC035156	Hs.658127	
3.83E-01	5.87E-01	1.20	9.92E-03	BC005231	Hs.472838	STK4
7.64E-01	8.33E-01	-1.20	1.92E-02	NR_003716	Hs.197076	HOTAIR
2.08E-01	2.29E-01	-1.20	1.25E-02	NM_018951	Hs.592166	HOXA10
4.70E-02	2.01E-01	-1.20	1.82E-14	NM_017633	Hs.10784	FAM46A
4.84E-01	6.80E-02	-1.20	4.73E-04	NM_022117	Hs.136164	TSPYL2
2.40E-01	1.20E-01	1.20	1.61E-03	NM_033449	Hs.591257	FCHSD1
9.42E-02	5.99E-01	1.20	4.54E-03	BC032716	Hs.698373	
2.96E-03	2.79E-02	-1.20	9.56E-03	NR_002211	Hs.532082	MEIS3P1
8.93E-03	4.21E-01	-1.20	2.57E-02	NM_014803	Hs.657337	ZNF518A
2.52E-02	4.96E-02	-1.20	1.98E-04	NM_144982	Hs.527874	CCDC131
5.47E-01	3.16E-01	1.20	6.51E-03	NM_021135	Hs.655277	RPS6KA2
9.93E-01	6.58E-01	-1.20	2.23E-02	NM_014951	Hs.22653	ZNF365
5.89E-01	6.80E-02	1.20	8.88E-03	THC2635386		

4.76E-03	2.81E-02	1.20	4.92E-02	NM_152351	Hs.462418	SLC5A10
2.48E-01	5.80E-02	1.20	4.70E-04	NM_172138	Hs.567792	IL28A
1.03E-02	1.12E-02	1.20	5.59E-03	NM_001004431	Hs.591142	METRNL

GeneName	Cytoband
chemokine (C-C mot	hs|17q12
keratin 25	hs|17q21.2
Sp8 transcription fac	hs|7p15.3
tyrosinase-related p	hs|9p23
silver homolog (mou	hs|12q13.2
neurogenic different	hs|17q12
silver homolog (mou	hs|12q13.2
anterior gradient ho	hs|7p21.1
X antigen family, me	hs|Xp11.22
ribosomal protein SA	hs|3p22.1
coagulation factor C	hs|14q12
v-erb-a erythroblasti	hs|2q34
chromosome 6 open	hs|6p24.3
keratin associated p	hs|17q21.2
MACRO domain con	hs|20p12.1
G protein-coupled re	hs|Xp22.2
	hs|7q22.1
hemoglobin, alpha 2	hs|16p13.3
ATPase, class I, type	hs|19p13.3
	hs|15q21.1
hemoglobin, alpha 2	hs|16p13.3
tyrosinase (oculocut	hs|11q14.3
keratin associated p	hs|21q22.11
endothelin receptor	hs|13q22.3
chromosome 10 ope	hs|10q26.2
transient receptor p	hs|15q13.3
	hs|9q22.2
coagulation factor C	hs|14q12
aldo-keto reductase	hs|7q33
armadillo repeat cor	hs|2q37.1
small proline-rich pr	hs|1q21.3
hepatitis A virus cell	hs|5q33.3
aldo-keto reductase	hs|7q33
cadherin 12, type 2 (	hs|5p14.3
tripartite motif-cont	hs|1p36.11
guanosine monopho	hs|6p22.3
defensin, alpha 6, Pa	hs|8p23.1
cerebellar degenera	hs|16p12.3
neurotrimin	hs|11q25
UDP glycosyltransfer	hs|5p13.2
hemoglobin, alpha 1	hs|16p13.3
tubulin, beta 2B	hs|6p25.2
	hs|14q22.3
keratin associated p	hs|21q22.11
UDP-N-acetyl-alpha-	hs|12q13.13
CD1c molecule	hs|1q23.1

	hs|10q23.33
spermatogenesis an	hs|9q34.3
solute carrier family	hs|10q25.3
solute carrier family	hs|5p13.3
chemokine (C-C mot	hs|17q12
cornulin	hs|1q21.3
keratin associated p	hs|17q21.2
keratin 74	hs|12q13.13
tetraspanin 8	hs|12q21.1
armadillo repeat co	hs|2q37.1
paraneoplastic antig	hs|Xq28
angiopoietin-like 5	hs|11q22.1
peptidyl arginine de	hs|1p36.13
extracellular leucine	hs|22q13.1
	hs|3p21.33
small proline-rich pr	hs|1q21.3
ankyrin repeat doma	hs|18q11.2
hemoglobin, beta	hs|11p15.4
carboxypeptidase, vi	hs|7p15.1
fibromodulin	hs|1q32.1
major histocompatib	hs|6p21.32
	hs|17q21.2
	hs|20q13.33
solute carrier family	hs|14q32.12
fatty acid binding pr	hs|8q21.13
similar to hCG18120	hs|2q23.3
	hs|6p21.32
	hs|8q24.21
hemoglobin, delta	hs|11p15.4
cellular retinoic acid	hs|15q25.1
late cornified envelo	hs|1q21.3
centaurin, beta 5	hs|1p36.33
	hs|6p21.32
major histocompatib	hs|6p21.32
CD86 molecule	hs|3q13.33
	hs|16p11.2
small proline-rich pr	hs|1q21.3
	hs|19q13.33
guanylate cyclase ac	hs|1p34.2
keratin 71	hs|12q13.13
KIAA0802	hs|18p11.22
aminolevulinate, del	hs|Xp11.21
bestrophin 1	hs|11q12.3
chromosome 1 open	hs|1p32.3
keratin 33B	hs|17q21.2
	hs|4q22.1
defensin, alpha 6, Pa	hs|8p23.1

OTU domain, ubiqui	hs|14q32.13
histidine ammonia-l	hs|12q23.1
gap junction protein	hs|Xq13.1
	hs|9p24.2
chromosome 12 ope	hs|12q14.2
tubulin, beta 3	hs|16q24.3
	hs|18p11.31
MACRO domain con	hs|20p12.1
major histocompatib	hs|6p21.32
WAP four-disulfide	hs|20q13.12
hypothetical protein	hs|5p15.1
glycosyltransferase	hs|12q24.32
major histocompatib	hs|6p21.32
family with sequenc	hs|5q35.2
major histocompatibility complex, class II, DR beta 3	
protein tyrosine pho	hs|1q31.3
class II, major histoc	hs|16p13.13
CD1a molecule	hs|1q23.1
glutaminyl-peptide	hs|2p22.2
leptin receptor	hs|1p31.3
fibrinogen-like 2	hs|7q11.23
sperm flagellar 2	hs|5p13.2
	hs|1q23.2
ATG9 autophagy rela	hs|7q36.1
chemokine (C-X-C m	hs|4q13.3
CD84 molecule	hs|1q23.2
major histocompatib	hs|6p21.32
H2.0-like homeobox	hs|1q41
ATP-binding cassett	hs|10q24.2
	hs|17q25.1
mannosyl (alpha-1,6	hs|17q25.2
ATP-binding cassett	hs|10q24.2
synaptotagmin VI	hs|1p13.2
chromosome 18 ope	hs|18p11.32
Fc fragment of IgG, l	hs|1q23.3
family with sequenc	hs|5q35.3
apolipoprotein B48 r	hs|16p11.2
SLIT and NTRK-like fa	hs|Xq27.3
	hs|17q25.1
glutaminyl-peptide	hs|2p22.2
major histocompatibility complex, class II, DR beta 4	
GTPase, IMAP family	hs|7q36.1
claudin 8	hs|21q22.11
	hs|2q37.1
fatty acid binding pr	hs|8q21.13
	hs|8p12
	hs|9p13.2

major histocompatib	hs|6p21.32
ATPase, class V, type	hs|5q34
nucleosome assemb	hs|Xq21.32
lysosomal associated	hs|1p35.2
major histocompatib	hs|6p21.32
ecotropic viral integr	hs|17q11.2
galactosidase, beta 1	hs|11q25
	hs|12q24.11
KIAA1239	hs|4p14
hypothetical protein	hs|2q11.2
CD36 molecule (thro	hs|7q21.11
CD1a molecule	hs|1q23.1
	hs|3p24.3
CD36 molecule (thro	hs|7q21.11
family with sequenc	hs|21q22.3
leukocyte receptor t	hs|15q15.1
	hs|9p24.3
CD53 molecule	hs|1p13.3
Fc fragment of IgE, h	hs|1q23.2
fatty acid binding pr	hs|8q21.13
major histocompatib	hs|6p21.32
	hs|10q26.13
major histocompatib	hs|6p21.32
regulator of G-prote	hs|8q11.23
	hs|13q12.3
keratin associated protein 4-11	
fatty acid binding pr	hs|8q21.13
	hs|10p14
keratin 77	hs|12q13.13
chemokine (C-C mot	hs|17q21.2
similar to Akr1b10	hs|10q21.3
pleckstrin homology	hs|2q24.1
	hs|4p15.31
reticulocalbin 3, EF-h	hs|19q13.33
hypothetical LOC100	hs|19p13.12
hypothetical protein	hs|1q21.3
branched chain amin	hs|12p12.1
oocyte expressed pr	hs|6q13
myosin IB	hs|2q32.3
amyloid beta (A4) pr	hs|10p12.1
microtubule associat	hs|5q12.3
	hs|9q32
serine/threonine kin	hs|7p15.3
clusterin	hs|8p21.1
osteopetrosis associ	hs|6q21
solute carrier family	hs|17p11.2

thromboxane A synt	hs|7q34
spermine oxidase	hs|20p13
four and a half LIM d	hs|Xq26.3
major histocompatib	hs|6p21.32
transketolase-like 1	hs|Xq28
D4, zinc and double	hs|14q24.2
	hs|1q21.1
CD207 molecule, lan	hs|2p13.3
	hs|Xp22.31
CD74 molecule, maj	hs|5q33.1
Ras association (Ral	hs|20p13
proteoglycan 4	hs|1q31.1
3'-phosphoadenosin	hs|10q23.2
sterol O-acyltransfer	hs|1q25.2
	hs|16p12.1
internexin neuronal	hs|10q24.33
	hs|1p36.22
	hs|16q12.2
UDP-N-acteylglucosa	hs|9q34.3
neuropilin (NRP) and	hs|16q12.1
similar to mCG2980	hs|19q13.2
N-acetyltransferase	hs|4p16.3
myosin IG	hs|7p13
ADAM metallopeptid	hs|2q33.3
hypothetical protein	hs|Xq26.3
similar to hCG20403	hs|1q23.2
hemopoietic cell kin	hs|20q11.21
prostaglandin D2 syn	hs|4q22.3
stearoyl-CoA desatu	hs|10q24.31
interleukin 15	hs|4q31.21
major histocompatib	hs|6p21.32
CD52 molecule	hs|1p36.11
DENN/MADD domai	hs|1p13.3
protease, serine, 1 (t	hs|7q34
solute carrier family	hs|2q36.3
major histocompatib	hs|6p21.32
	hs|4q22.3
phosphoinositide-3-	hs|5q13.1
centrosomal protein	hs|5p15.33
gremlin 2, cysteine k	hs|1q43
paraneoplastic antig	hs|Xq28
ectonucleoside triph	hs|10q23.33
forkhead box D1	hs|5q13.2
potassium channel t	hs|13q22.3
major histocompatib	hs|6p21.32
hypothetical LOC392	hs|9p11.2
major histocompatib	hs|6p21.32

chondroadherin	hs|17q21.33
colony stimulating fa	hs|5q33.1
cysteine-rich protein	hs|14q32.33
paired box 3	hs|2q36.1
Fraser syndrome 1	hs|4q21.21
RAB32, member RAS	hs|6q24.3
keratin 77	hs|12q13.13
ribonuclease, RNase	hs|14q11.2
GLI pathogenesis-rel	hs|12q21.2
family with sequence	hs|3q22.3
	hs|13q14.12
	hs|20q13.12
TYRO protein tyrosin	hs|19q13.12
major histocompatib	hs|6p21.32
macrophage express	hs|11q12.1
ubiquitin specific pe	hs|17p13.2
sphingomyelin phos	hs|1p35.3
Purkinje cell protein	hs|1q23.3
hemoglobin, gamma	hs|11p15.4
glycogenin 2	hs|Xp22.33
protein kinase, cAM	hs|7q22.3
F-box and leucine-ric	hs|3p22.3
	hs|5q31.1
cartilage intermedia	hs|15q22.31
transmembrane pro	hs|11p15.1
replication protein A	hs|Xq21.33
family with sequence	hs|5q35.2
microfibrillar-associa	hs|17p11.2
protein tyrosine pho	hs|10p12.33
laeverin	hs|5q23.1
protease, serine, 21	hs|16p13.3
	hs|5q35.1
Fc fragment of IgG b	hs|19q13.2
microtubule-associa	hs|5q13.2
family with sequence	hs|7q35
	hs|9q12
complexin 3	hs|15q24.1
RAB3B, member RAS	hs|1p32.3
PIF1 5'-to-3' DNA he	hs|15q22.31
Hermansky-Pudlak s	hs|10q24.2
activating transcripti	hs|1q32.3
	hs|4q21.21
	hs|4q21.23
chromosome 3 open	hs|3p21.31
annexin A9	hs|1q21.2
	hs|2q31.1

tumor necrosis facto	hs|1q21.2
	hs|15q15.3
myosin IG	hs|7p13
uroplakin 1A	hs|19q13.12
	hs|20p12.1
major histocompatib	hs|6p21.32
	hs|10q11.22
signal peptide, CUB	hs|11p15.4
immunoglobulin sup	hs|16p12.2
regulator of G-prote	hs|16p13.3
family with sequenc	hs|5q35.3
	hs|5q33.1
phosphoinositide-3-	hs|22q12.2
ras homolog gene fa	hs|2p24.1
lysosomal associate	hs|1p35.2
hypothetical protein	hs|2q22.3
zinc finger E-box bin	hs|10p11.22
PRO1933	hs|10q24.31
dedicator of cytokin	hs|Xq24
CD8b molecule	hs|2p11.2
amyloid beta (A4) pr	hs|10p12.1
sialic acid binding Ig-	hs|19q13.33
glycerol kinase	hs|Xp21.2
	hs|1p22.1
melanocortin 1 rece	hs|16q24.3
fibulin 5	hs|14q32.12
scavenger receptor	hs|8p21.1
potassium voltage-g	hs|1p36.31
ST6 (alpha-N-acetyl-	hs|1p31.1
phosphodiesterase 4	hs|19p13.2
R-spondin homolog	hs|1p34.3
integrin, beta-like 1	hs|13q33.1
	hs|8p21.1
	hs|1q22
transmembrane 4 L	hs|3q29
transmembrane pro	hs|11q24.3
	hs|14q21.3
	hs|18q11.2
bA299N6.3	hs|20q13.33
NADH dehydrogenase, subunit 3 (complex I)	
molybdenum cofact	hs|18q12.2
platelet-derived grow	hs|8p22
SLAM family membe	hs|1q23.2
PFTAIRE protein kina	hs|7q21.13
	hs|7q31.2
tumor necrosis facto	hs|14q32.32

synaptopodin 2	hs|4q26
sortilin-related VPS1	hs|4p16.1
RAS, dexamethasone	hs|17p11.2
	hs|1p33
chromosome 8 open	hs|8q24.3
macrophage express	hs|11q12.1
repetin	hs|1q21.3
melanocortin 1 rece	hs|16q24.3
phosphodiesterase 4	hs|1q21.1
receptor tyrosine kin	hs|9q22.31
NDRG family membe	hs|16q21
major histocompatibility complex, class II, DQ alpha 1	
	hs|21q22.3
adenomatosis polyp	hs|19p13.3
formin-like 1	hs|17q21.31
	hs|7q22.3
major facilitator sup	hs|1q32.1
	hs|2p22.1
FERM and PDZ doma	hs|9p13.2
	hs|5q15
WD repeat domain,	hs|17q24.2
CD70 molecule	hs|19p13.3
SP140 nuclear body	hs|2q37.1
KIAA1324-like	hs|7q21.12
	hs|12q13.13
solute carrier family	hs|17p13.1
hypothetical gene su	hs|16p13.3
zinc finger and SCAN	hs|19q13.43
	hs|1p32.3
	hs|9p11.2
snail homolog 1 (Dro	hs|20q13.13
aryl-hydrocarbon re	hs|15q25.1
sarcolipin	hs|11q22.3
2',5'-oligoadenylate	hs|12q24.13
ecotropic viral integ	hs|17q11.2
	hs|20q11.21
myelin protein zero-	hs|11q23.3
odd-skipped related	hs|8q22.2
glial cell derived neu	hs|5p13.2
lymphocyte cytosoli	hs|13q14.12
regulator of calcineu	hs|6p12.3
pleckstrin	hs|2p14
spleen focus forming	hs|11p11.2
zinc finger protein 1	hs|Xp11.3
tumor necrosis facto	hs|6q23.3
protein kinase C, bet	hs|16p12.1
	hs|11q23.2

chromosome 7 open	hs|7p15.1
SRY (sex determining	hs|8p23.1
mitogen-activated p	hs|17q24.3
sortilin 1	hs|1p13.3
cytochrome b	
cornichon homolog	hs|11q13.1
very low density lipo	hs|9p24.2
phosphodiesterase 3	hs|11p15.2
major histocompatib	hs|6p21.32
T-box 15	hs|1p12
cysteinyl leukotriene	hs|Xq21.1
keratin 28	hs|17q21.2
phosphorylase, glyco	hs|11q13.1
contactin 2 (axonal)	hs|1q32.1
ATG9 autophagy rela	hs|7q36.1
natriuretic peptide r	hs|5p13.3
cysteine-rich, angiog	hs|1p22.3
forkhead box J1	hs|17q25.1
colony stimulating fa	hs|Yp11.32
guanine nucleotide b	hs|9q21.2
small proline-rich pr	hs|1q21.3
	hs|11q24.3
	hs|12p11.21
patatin-like phospho	hs|22q13.31
natriuretic peptide r	hs|5p13.3
interleukin 1 family,	hs|2q13
	hs|22q13.33
zinc finger protein 2	hs|19p12
SRY (sex determining	hs|8p23.1
sarcosine dehydroge	hs|9q34.2
plexin domain conta	hs|17q12
FRAS1 related extrac	hs|9p22.3
hypothetical protein	hs|22q13.33
slingshot homolog 1	hs|12q24.11
hypothetical protein	hs|16p12.3
	hs|5p13.1
LIM and calponin ho	hs|4p13
6-phosphofructo-2-k	hs|1q32.2
sperm flagellar 2	hs|5p13.2
solute carrier family	hs|14q11.2
grainyhead-like 3 (D	hs|1p36.11
metallothionein-like	hs|11q13.2
copine family memb	hs|3p25.3
zinc finger protein 3	hs|6p22.1
cysteine-rich, angiog	hs|1p22.3
SRY (sex determining	hs|12p12.1

chromosome 15 ope	hs|15q21.1
chloride channel 5 (	hs|Xp11.22
solute carrier family	hs|13q32.3
hypothetical locus L	hs|16q24.3
protocadherin beta	hs|5q31.3
low density lipoprot	hs|1p32.3
coiled-coil domain c	hs|11q21
transmembrane pro	hs|17q23.1
gap junction protein	hs|Xq13.1
family with sequenc	hs|7q32.1
empty spiracles hom	hs|10q26.11
similar to hCG20367	hs|6q23.3
	hs|15q24.2
solute carrier organi	hs|20q13.33
PFTAIRE protein kina	hs|7q21.13
	hs|1q44
bradykinin receptor	hs|14q32.2
	hs|7q22.1
zinc finger protein 7	hs|19q13.43
	hs|14q22.3
	hs|3q29
transglutaminase 1 (	hs|14q12
chromosome 4 open	hs|4p14
	hs|5q31.1
Src-like-adaptor	hs|8q24.22
interleukin 2 recept	hs|22q12.3
ceroid-lipofuscinosis	hs|8p23.3
alanyl (membrane) a	hs|15q26.1
glycosylphosphatidy	hs|6p22.2
heparanase	hs|4q21.23
solute carrier family	hs|2p23.3
	hs|5q15
S100 calcium binding	hs|1q21.3
coagulation factor X	hs|6p25.1
cyclin D1	hs|11q13.2
GTPase, IMAP family	hs|7q36.1
protein kinase C, bet	hs|16p12.1
receptor (G protein-	hs|2q37.3
outer dense fiber of	hs|15q24.2
	hs|Xp21.3
	hs|21q22.3
vav 1 guanine nucle	hs|19p13.3
protocadherin gamm	hs|5q31.3
RAB32, member RAS	hs|6q24.3
ATPase family, AAA	hs|17q21.32
spermatogenesis ass	hs|15q21.1
	hs|5q35.2

	hs|9q22.31
ATP-binding cassette	hs|21q22.3
	hs|4p13
protease, serine, 2 (t	hs|7q34
	hs|11q12.3
scavenger receptor c	hs|12q24.31
neurofascin homolog	hs|1q32.1
chemokine (C-X3-C r	hs|3p22.2
cytochrome P450, fa	hs|19p13.12
stearoyl-CoA desatu	hs|4q21.22
chromosome 9 open	hs|9p24.2
DnaJ (Hsp40) homol	hs|1p31.1
	hs|3p21.33
cathepsin S	hs|1q21.2
fatty acid desaturase	hs|11q12.2
coiled-coil domain c	hs|11q24.2
	hs|6p24.3
	hs|3q26.2
tripartite motif-cont	hs|6p21.33
CD24 molecule	hs|Yq11.222
keratin associated p	hs|11q13.4
tumor necrosis facto	hs|8p21.3
TIMP metallopeptida	hs|22q12.3
Cdon homolog (mou	hs|11q24.2
EF-hand domain fam	hs|8p22
glycoprotein VI (plat	hs|19q13.42
kinesin family memb	hs|2q23.1
family with sequenc	hs|15q22.2
	hs|4p15.32
DnaJ (Hsp40) homol	hs|1p31.1
activated leukocyte	hs|3q13.11
mirror-image polyda	hs|14q21.1
OTU domain, ubiqui	hs|14q32.13
	hs|4q21.1
chemokine (C-C mot	hs|17q12
tetraspanin 2	hs|1p13.2
osteopetrosis associ	hs|6q21
	hs|19p13.11
G protein regulated	hs|5q35.2
heat shock 70kDa pr	hs|10q25.3
ARV1 homolog (S. ce	hs|1q42.2
TSC22 domain family	hs|13q14.11
leucine rich repeat a	hs|8q21.2
chloride intracellular	hs|Xq28
	hs|16p12.3
aryl hydrocarbon rec	hs|12p11.23

	hs|7q36.3
	hs|2q33.3
cysteine-rich, angiog	hs|1p22.3
serpin peptidase inh	hs|17p13.3
solute carrier family	hs|2p22.1
tensin like C1 domai	hs|12q13.13
hypothetical LOC10	hs|7p22.1
	hs|10p13
	hs|12q24.22
Ras association (Ral	hs|4q13.3
extracellular matrix	hs|1q21.2
family with sequenc	hs|7q32.1
	hs|3p14.2
ankyrin repeat doma	hs|10q24.1
	hs|11q13.4
low density lipoprot	hs|1p32.3
arachidonate 5-lipox	hs|13q12.3
Ras association (Ral	hs|10q11.21
	hs|19q13.31
transmembrane pro	hs|11p15.1
actin-related Arp11	hs|7q36.1
protein kinase (cAM	hs|6q22.31
suppressor of cytoki	hs|18q22.2
periostin, osteoblast	hs|13q13.3
	hs|14q22.3
bactericidal/permea	hs|22q12.3
	hs|4p15.33
tescalcin	hs|12q24.22
	hs|10q26.13
	hs|17p13.2
formyl peptide rece	hs|19q13.33
keratin associated p	hs|21q22.11
zinc finger protein 1	hs|19p13.2
sodium channel, volt	hs|11q23.3
	hs|3q27.1
heat shock 70kDa pr	hs|6p21.33
	hs|6p21.31
kallikrein-related pe	hs|19q13.33
leucine rich repeat c	hs|17q21.32
family with sequenc	hs|22q13.2
	hs|22q13.33
	hs|16p11.2
phospholipase A2, g	hs|1p36.13
hypothetical protein	hs|5q33.1
lipoma HMGIC fusio	hs|3p25.3

phospholipase C, de	hs|2q35
transmembrane 4 L	hs|17p13.2
F-box protein 10	hs|9p13.2
	hs|2p23.3
solute carrier family	hs|21q22.11
zinc finger protein 6	hs|1p22.2
	hs|2p11.2
Bruton agammaglob	hs|Xq22.1
	hs|6p22.3
hypothetical gene su	hs|2q36.1
ubiquitin specific pe	hs|11q23.3
arylsulfatase family,	hs|5q33.1
nuclear receptor sub	hs|12q13.13
hypothetical LOC643	hs|4q21.1
MORN repeat contai	hs|1p36.33
	hs|4p15.33
chondroitin sulfate	hs|15q24.2
	hs|19p13.3
	hs|18q11.2
signal transducer an	hs|2q32.3
chromosome 1 open	hs|1q31.3
glutaredoxin 3	hs|10q26.3
sema domain, immu	hs|10q24.31
chloride channel, ca	hs|1p22.3
potassium large con	hs|12q15
melanoregulin	hs|2q35
contactin 3 (plasmac	hs|3p12.3
	hs|6p12.1
GLI pathogenesis-rel	hs|12q21.1
	hs|10q22.2
	hs|10q24.32
	hs|18q23
RasGEF domain fami	hs|5q35.3
gap junction protein	hs|7q22.1
myosin, heavy chain	hs|16p13.11
	hs|9q34.11
myosin VA (heavy ch	hs|15q21.2
protein kinase, Y-lin	hs|Yp11.2
phosphoglucomutas	hs|9q13
calcium binding prot	hs|13q14.2
homeodomain inter	hs|7q34
	hs|6q15
receptor (chemosen	hs|3q27.3
	hs|14q11.2
CD40 molecule, TNF	hs|20q13.12
	hs|19p12

	hs|1q25.2
sterile alpha motif d	hs|7q21.2
homeodomain intera	hs|7q34
caspase recruitment	hs|17q25.3
Cdon homolog (mou	hs|11q24.2
slit homolog 3 (Dros	hs|5q35.1
	hs|2q37.2
chromosome 9 open	hs|9q21.11
gap junction protein	hs|13q12.11
Sec61 alpha 2 subun	hs|10p14
bradykinin receptor	hs|14q32.2
	hs|11q21
leukocyte immunogl	hs|19q13.42
keratin 9 (epidermol	hs|17q21.2
heme oxygenase (de	hs|22q12.3
S100 calcium binding	hs|1q21.3
hypothetical protein	hs|16p12.3
creatine kinase, mit	hs|15q15.3
	hs|2q23.3
sterol-C4-methyl oxi	hs|4q32.3
	hs|6q22.31
hepatitis A virus cell	hs|5q33.3
carcinoembryonic an	hs|19q13.2
Friend leukemia viru	hs|11q24.3
lymphocyte antigen	hs|6p25.1
Boc homolog (mouse	hs|3q13.2
RAP1 interacting fac	hs|2q23.3
contactin 2 (axonal)	hs|1q32.1
mal, T-cell differenti	hs|2q11.1
glucosaminyl (N-ace	hs|15q22.2
kelch repeat and BT	hs|11q22.3
	hs|20q13.12
keratin associated p	hs|17q21.2
vav 3 guanine nucle	hs|1p13.3
phosphoserine phos	hs|7p11.2
sarcospan (Kras onc	hs|12p12.1
Kruppel-like factor 2	hs|19p13.11
	hs|12q23.3
hypothetical protein	hs|22q13.33
bone morphogeneti	hs|20q13.31
	hs|17q21.31
PIP5K1A pseudogene	hs|6p24.3
transcription factor	hs|10q25.3
ubiquitin specific pe	hs|10q22.2
insulin-like growth f	hs|12q13.13
serpin peptidase inh	hs|11q12.1

centrosomal protein	hs|2p14
glycerol kinase	hs|Xp21.2
activating transcripti	hs|12p13.1
family with sequenc	hs|2q21.1
	hs|7q34
chitinase 3-like 1 (ca	hs|1q32.1
neurobeachin	hs|13q13.3
	hs|8q24.21
	hs|Xq23
placental growth fac	hs|14q24.3
	hs|10p15.1
	hs|9p11.2
oligodendrocyte tra	hs|6q23.3
family with sequenc	hs|13q12.13
docking protein 6	hs|18q22.2
importin 7	hs|11p15.4
CAP-GLY domain con	hs|2p23.2
TBC1 domain family,	hs|17q25.3
polymerase (DNA di	hs|8p11.21
retinoic acid early tr	hs|6q25.1
	hs|22q13.31
KIAA1211 protein	hs|4q12
intersectin 1 (SH3 do	hs|21q22.11
nebulin-related anch	hs|10q25.3
B-cell linker	hs|10q23.33
BAI1-associated prot	hs|22q13.1
mitochondrial ribos	hs|15q25.3
leukotriene C4 synth	hs|5q35.3
	hs|4q34.1
	hs|22q11.23
RAB3B, member RAS	hs|1p32.3
	hs|Xq22.3
chromosome 10 ope	hs|10q21.3
dynein, axonemal, h	hs|17p13.1
	hs|22q12.3
chromosome 12 ope	hs|12p13.32
BARX homeobox 2	hs|11q24.3
nuclear factor I/B	hs|9p23
cytochrome P450, fa	hs|12q14.1
	hs|6p22.1
olfactory receptor, f	hs|3q11.2
TAF9B RNA polymera	hs|Xq21.1
Kruppel-like factor 1	hs|13q22.1
hypothetical protein	hs|11q23.2
	hs|11q13.1
nuclear receptor sub	hs|4q31.23

ovostatin 2	hs|12p11.21
hypothetical protein	hs|5q33.1
	hs|20q13.2
allograft inflammato	hs|6p21.33
mitogen-activated p	hs|22q13.33
zinc finger protein 4	hs|19p12
spectrin repeat cont	hs|14q23.2
olfactory receptor, f	hs|6p22.1
arachidonate 5-lipox	hs|13q12.3
protein tyrosine pho	hs|19q13.42
zinc finger protein 1	hs|19q13.43
CD33 molecule	hs|19q13.33
solute carrier family	hs|13q14.11
glutathione S-transf	hs|1p13.3
carnitine palmitoyltr	hs|11q13.2
NUAK family, SNF1-l	hs|12q23.3
ELOVL family memb	hs|5q12.1
pleckstrin homology	hs|1q32.1
von Willebrand facto	hs|7p12.2
kallikrein-related pe	hs|19q13.33
CD8a molecule	hs|2p11.2
synapse defective 1,	hs|1p22.3
remodeling and spac	hs|11q14.1
	hs|3p25.1
ADAM metallopepti	hs|21q21.3
family with sequenc	hs|17q21.33
family with sequenc	hs|15q25.1
capping protein (acti	hs|12p12.3
solute carrier family	hs|9q34.11
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microtubule-associa	hs|5q13.2
	hs|3q29
sorting nexin 10	hs|7p15.2
formin 1	hs|15q13.3
myomesin (M-protei	hs|8p23.3
	hs|2q21.2
butyrophilin, subfam	hs|6p22.1
SERTA domain conta	hs|1q32.2
phospholipase A2 re	hs|2q24.2
LIM domain contain	hs|17q23.3
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hypothetical protein	hs|1q42.13

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interleukin 6 signal t	hs|5q11.2
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tumor necrosis facto	hs|8p21.3
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	hs|Xq13.1
SRY (sex determining	hs|12p12.1
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ephrin-A5	hs|5q21.3
carboxypeptidase A4	hs|7q32.2
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peroxisome prolifera	hs|6p21.31
	hs|22q13.1
ras homolog gene fa	hs|1q42.13
hypothetical protein	hs|2q37.3
SHC (Src homology 2	hs|9q22.1
plasminogen activat	hs|10q22.2
regulator of G-prote	hs|1q31.2
wingless-type MMTV	hs|7q31.31
FH2 domain contain	hs|4q31.3
transforming growth	hs|2p13.3
potassium channel t	hs|22q12.3
glioma tumor suppre	hs|19q13.32
SH2 domain containi	hs|1p36.12
integrin, beta 8	hs|7p15.3
	hs|14q23.1
	hs|11p15.4
	hs|22q12.3
transforming, acidic	hs|8p11.23
	hs|16q24.3
SRY (sex determining	hs|3q26.33
eukaryotic translatio	hs|10q22.2
	hs|4p14
zinc finger and BTB d	hs|12q13.3
myosin regulatory lig	hs|6p22.3
LOC440173	hs|9q21.33
exportin, tRNA (nucl	hs|12q14.2
C-type lectin domain	hs|3p21.31
dyslexia susceptibilit	hs|15q21.3

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<tr><td>Ras association (Ral</td><td>hs|10q11.21</td></tr>
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<tr><td>NADH dehydrogenase, subunit 2 (complex I)</td><td></td></tr>
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cadherin, EGF LAG se	hs|3p21.31
transmembrane prot	hs|19p13.11
hairy/enhancer-of-sp	hs|1p34.2
THAP domain contai	hs|7q31.1
complement compo	hs|12p13.31
zinc finger and BTB d	hs|3q23
A kinase (PRKA) anch	hs|15q25.3
	hs|4q35.1
leukemia inhibitory f	hs|5p13.1
tetraspanin 9	hs|12p13.32
uncoupling protein 2	hs|11q13.4
BCL2-like 11 (apopto	hs|2q13
chromosome 20 ope	hs|20q13.12
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leucine rich repeat c	hs|1p22.2
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chromosome 15 ope	hs|15q15.1
coagulation factor II	hs|5q13.3
tenascin XB	hs|6p21.32
major facilitator sup	hs|1q32.1
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SH3 domain contain	hs|2p25.3
coiled-coil domain co	hs|13q14.11
	hs|19p13.3
	hs|6p22.3
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transmembrane 7 su	hs|11q13.1
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HRAS-like suppresso	hs|11q12.3
zinc finger protein 1	hs|19q13.43
desmoglein 2	hs|18q12.1
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ring finger and FYVE	hs|17q12
	hs|1p36.33
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ribosomal protein S2	hs|16q22.1
major histocompatib	hs|6p21.32
proprotein converta	hs|19p13.3
six transmembrane	hs|7q21.13
thrombospondin 1	hs|15q14
FYN binding protein	hs|5p13.1
	hs|2p25.3
	hs|14q32.31
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chromosome 4 open	hs|4q32.1
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Rho-associated, coile	hs|18q11.1
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hepatitis A virus cell	hs|5q33.3
bleomycin hydrolase	hs|17q11.2

Fanconi anemia, con	hs|16q24.3
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zinc finger protein in	hs|19q13.43
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RUN domain contain	hs|7q21.12
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forkhead box S1	hs|20q11.21
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tumor necrosis facto	hs|17p13.1

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glucuronidase, beta	hs|5q13.2
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CD302 molecule	hs|2q24.2
zinc finger protein 2	hs|17p12
adhesion molecule v	hs|1p13.3
keratin 16 (focal nor	hs|17q21.2
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N-deacetylase/N-sul	hs|5q33.1
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transmembrane pro	hs|1q32.3
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	hs|Xq26.2
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serine/threonine kin	hs|5q35.1
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adducin 3 (gamma)	hs|10q25.2
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HtrA serine peptidas	hs|4p16.1
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KIAA0913	hs|10q22.2
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protein phosphatase	hs|8p23.1
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hematopoietic cell si	hs|19q13.12
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cadherin-like 23	hs|10q22.1
activin A receptor ty	hs|12q13.13
keratin associated p	hs|17q21.2
cyclin-dependent kin	hs|9p21.3
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solute carrier family	hs|20p13
chemokine (C motif)	hs|3p21.31
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CSAG family, memb	hs|Xq28

heterogeneous nucle	hs|5q31.2
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fibroblast growth fac	hs|10q26.13
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armadillo repeat cor	hs|Xq22.1
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GTPase activating Ra	hs|17p13.3
enhancer of polycon	hs|10p11.22
	hs|8q22.3
serine/threonine kin	hs|20q13.12
Hox transcript antise	hs|12q13.13
homeobox A10	hs|7p15.2
family with sequenc	hs|6q14.1
TSPY-like 2	hs|Xp11.22
FCH and double SH3	hs|5q31.3
	hs|7q22.1
Meis homeobox 3 ps	hs|17p11.2
zinc finger protein 5	hs|10q23.33
coiled-coil domain c	hs|12q21.1
ribosomal protein S	hs|6q27
zinc finger protein 3	hs|10q21.2
	hs|6p22.3

solute carrier family	hs|17p11.2
interleukin 28A (inte	hs|19q13.2
meteorin, glial cell d	hs|17q25.3