

Supplementary Material. Full technical report of GeneChip Human Transcriptome Array 2.0

Microarray Unit

Request R1266 Analysis

In the following experiment, the transcriptional expression of two distinct experimental conditions profiled through the use of Affymetrix GeneChip Human Transcriptome Array (HTA) 2.0 was characterized.

The data analysis was carried out using the Partek Genomics Suite commercial software (hereinafter PGS), updated to version 6.6 [6.16.0812 for Mac]

Status	Condition
treated	R1266_A_(HTA-2_0).CEL
control	R1266_B_(HTA-2_0).CEL

Below are the parameters set in PGS for the import, summarization and normalization of CEL files with RMA algorithm:

Probes to Import: Interrogating Probes and Control Probes

Probe filtering: skip

Algorithm: RMA

Background Correction: RMA Background Correction

Normalization: Quantile Normalization

Log Probes using Base: 2

Probeset Summarization: Median Polish

Reference:

Bolstad, B.M., Irizarry R. A., Astrand, M., & Speed, T.P. (2003), A Comparison of Normalization Methods for High Density Oligonucleotide Array Data Based on Bias and Variance. *Bioinformatics* 19(2):185-193

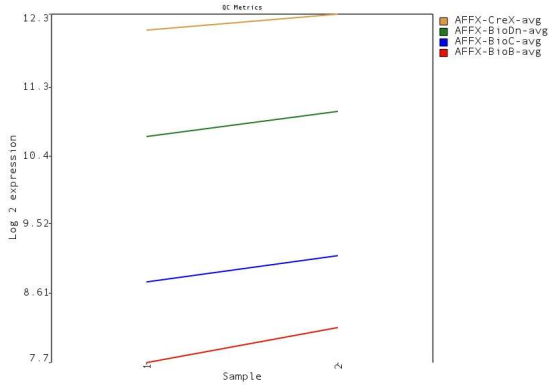
Irizarry, R.A., Bolstad, B.M., Collin, F., Cope, L.M., Hobbs, B., Terence, P., & Speed, T.P. (2003), Summaries of Affymetrix GeneChip probe level data *Nucleic Acids Research* 31(4):e15

Irizarry, R.A., Hobbs, B., Collin, F., Beazer-Barclay, Y.D., Antonellis, K.J., Scherf, U., & Speed, T.P. (2002) Exploration, Normalization, and Summaries of High Density Oligonucleotide Array Probe Level Data.

Wu, Z., Irizarry, R.A., Gentleman, R., Martinez-Murillo, F., & Spencer, F. (2004) A Model-Based Background Adjustment for Oligonucleotide Expression Arrays. *Journal of the American Statistical Association*, 2004 vol. 99 page 909.

Quality control:

Affymetrix arrays were processed by including in the hybridization mix 4 distinct control oligonucleotides exogenous to the test species that act as hybridization controls. The intensity value of the latter is expected to be homogeneous among the different samples being analyzed. The hybridization controls appear to have a variable expression level within an acceptable range in the different samples tested. (expression values are in log2 scale).



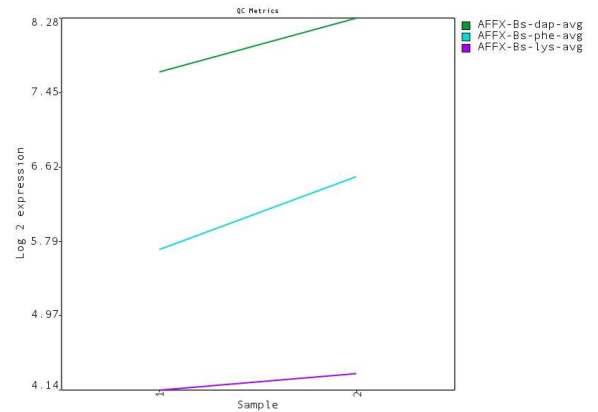
In addition to the hybridization controls, a series of non-related polyadenylated oligonucleotides are used as positive controls, which are amplified together with the biological sample being analyzed and act as (synthesis + hybridization) controls.

A reduced variability in the intensity value of these oligos between the different biological samples tested indicates a low level of bias introduced during the amplification procedure. Even from the synthesis controls, as from the hybridization controls, there is a moderate

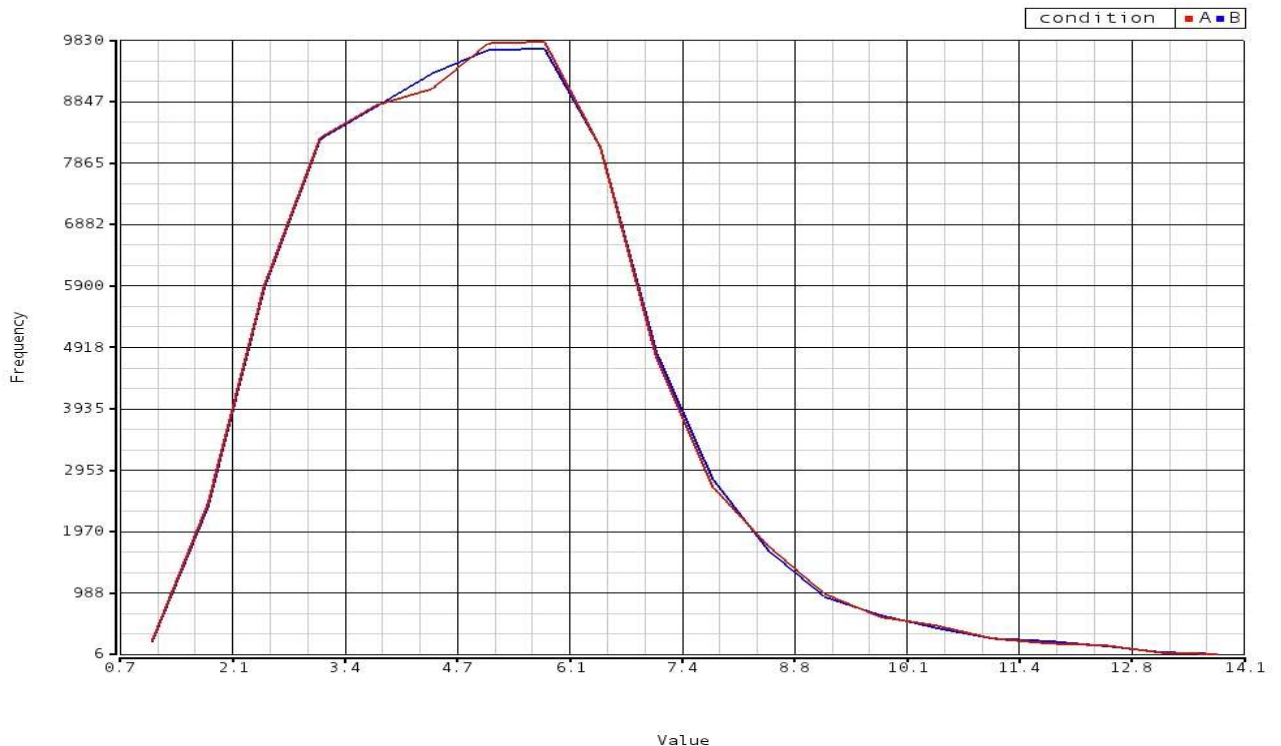
variability between the samples being analyzed.

The histogram of distribution of the signal intensity for the different samples tested was then evaluated, from which the image below is obtained.

Following the normalization of the raw data, there are no marked differences between the distribution profiles (also due to the effect of the normalization itself), so we proceeded with the analysis of the 2 experimental points.



Curva di distribuzione delle intensita' di segnale



PCA visualization (Principal Component Analysis)

No evaluation was made using PCA as it is not informative on a dataset of only 2 samples.

Identification of differentially expressed transcripts:

The initial list of 925000 probes synthesized on GeneChip array (and deriving from the exon-based analysis of the data) was collapsed to 70500 transcripts and subsequently filtered to eliminate the control probes.

The search for differentially expressed transcripts was conducted on 67500 transcripts belonging to the annotated nucleus with greater accuracy (main)

In the absence of experimental replicates it was not possible to use statistical criteria for the identification of differentially expressed transcripts; a criterion of 'regulation entity' or fold change set to numerical values equal to 2 has been adopted.

Below are the names of the comparative lists generated and the corresponding number of differentially expressed transcripts identified:

A_vs_B_fc2.txt

[163 transcripts identified]

Note:

In the comparison list, the experimental condition B represents the denominator.

The generated list was annotated using the latest version of the annotations for Affymetrix GeneChip Human Gene ST 2.1 provided by Affymetrix via the NetAffx portal [<https://www.affymetrix.com/analysis/index.affx>].

Supplementary data. Full list of transcripts differentially expressed between twin A and B (fc cutoff 2.0, GeneChip HTA 2.0 Affymetrix)

Column #	Transcript ID	category	gene_assignment	Gene Symbol	RefSeq	GO_biological_process	GO_cellular_component	GO_molecular_function	mrna_assignment	pathway	p-value(condition)	p-value(A vs. B)	Ratio(A vs. B)	Fold-Change(A vs. B)	Fold-Change(A vs. B) (Description)	Fold-Change(A vs. B) 95% lower limit	Fold-Change(A vs. B) 95% upper limit	p-value(B vs. A)	Ratio(B vs. A)	Fold-Change(B vs. A)	Fold-Change(B vs. A) (Description)	Fold-Change(B vs. A) 95% lower limit	Fold-Change(B vs. A) 95% upper limit	F(condition)	SS(condition)	SS(Error)	F(Error)
68045	TC14002222.hg.1	main	OTTHUMT00000326212 // IGHD3-22 // immunoglobulin heavy diversity 3-22 // 14q32.33 // 28	IGHD3-22	OTTHUMT00000326212	---	---	---	OTTHUMT00000326212 // Havana transcript // immunoglobulin heavy diversity 3-22 // gene_biot	---	?	?	7.64454	7.64454	A up vs B	1	1	?	0.130812	-7.64454	B down vs A	1	1	?	4.30544	0	1
15266	TC15001009.hg.1	main	---	---	---	---	---	---	DQ592463 // NONCODE // accn=DQ592463 class=piRNA name=piR-59575 ref=NONCODE v2.0 transc	---	?	?	6.44688	6.44688	A up vs B	1	1	?	0.155114	-6.44688	B down vs A	1	1	?	3.61429	0	1
969	TC01003512.hg.1	main	---	---	---	---	---	---	ENST00000455124 // ENSEMBL // havana:known chromosome:GRCh38:1:171247580:171251794:-1g	---	?	?	5.19802	5.19802	A up vs B	1	1	?	0.192381	-5.19802	B down vs A	1	1	?	2.82735	0	1
25351	TC01005583.hg.1	main	---	---	---	---	---	---	TCONS_12_0001306 -XLOC_12_000970 // Broad_TUCP // linc-ELTD1-11 chr1:-83485231-8356860	---	?	?	4.22713	4.22713	A up vs B	1	1	?	0.236567	-4.22713	B down vs A	1	1	?	2.16253	0	1
35752	TC05001631.hg.1	main	---	---	---	---	---	---	DQ597441 // NONCODE // accn=DQ597441 class=piRNA name=piR-35507 ref=NONCODE v2.0 transc	---	?	?	3.71759	3.71759	A up vs B	1	1	?	0.268992	-3.71759	B down vs A	1	1	?	1.79431	0	1
6129	TC01003722.hg.1	main	NM_002023 // FMOD // fibromodulin // 1q32 // 2331 // ENST00000354955 // FMOD // fibrom	FMOD	NM_002023	NM_002023 // GO:0005975 // carboxydrate metabolic process // traceable author statement // traceable author statement	NM_002023 // GO:0005576 // extracellular region // traceable author statement // NM_0	NM_002023 // GO:0008201 // heparin binding // not recorded // NM_002023 // GO:0048495	NM_002023 // RefSeq // Homo sapiens fibromodulin (FMOD), transcript variant 1, mRNA. //	---	?	?	3.59352	3.59352	A up vs B	1	1	?	0.278279	-3.59352	B down vs A	1	1	?	1.70275	0	1
19370	TC0X002032.hg.1	main	---	---	---	---	---	---	OTTHUMT000006060 // NONCODE // novel transcript [gene_bioty pe:lincRNA transcript_bioty	---	?	?	3.53592	3.53592	A up vs B	1	1	?	0.282812	-3.53592	B down vs A	1	1	?	1.66	0	1
31945	TC15001895.hg.1	main	---	---	---	---	---	---	DQ598152 // NONCODE // accn=DQ598152 class=piRNA name=piR-36218 ref=NONCODE v2.0 transc	---	?	?	3.3752	3.3752	A up vs B	1	1	?	0.296279	-3.3752	B down vs A	1	1	?	1.53996	0	1
62795	TC06000451.hg.1	main	---	---	---	---	---	---	DQ597264 // NONCODE // accn=DQ597264 class=piRNA name=piR-35330 ref=NONCODE v2.0 transc	---	?	?	3.35544	3.35544	A up vs B	1	1	?	0.298023	-3.35544	B down vs A	1	1	?	1.52513	0	1
26785	TC14002240.hg.1	main	OTTHUMT00000325964 // IGHD3-3 // immunoglobulin heavy diversity 3-3 // 14q32.33 // 2850	IGHD3-3	OTTHUMT00000325964	---	---	---	OTTHUMT00000325964 // Havana transcript // immunoglobulin heavy diversity 3-3 // gene_biot	---	?	?	3.34042	3.34042	A up vs B	1	1	?	0.299363	-3.34042	B down vs A	1	1	?	1.51385	0	1

5730	TC15001370.hg.1	main	---	---	---	---	---	---	DQ595419 // NONCODE // accn=DQ595419 class=piRNA name=piR-61531 ref=NONCODE v2.0 trans	---	?	?	3.30939	3.30939	A up vs B	1	1	?	0.30217	- 3.30939	B down vs A	1	1	?	1.49051	0	1
61360	TC0X002025.hg.1	main	S60973 // DMD // dystrophin // Xp21.2 // 1756	DMD	S60973	S60973 // GO:0002027 // regulation of heart rate // inferred from mutant phenotype	S60973 // GO:0005634 // nucleus // inferred from direct assay // S60973 // GO:0005634	S60973 // GO:0002162 // dystroglycan binding // inferred from physical interaction	S60973 // NONCODE // accn=S60973 class=mRNALike lncRNA name=NULL ref=H-invitational v7.	S60973 // GenMAPP // Striated_muscle_contraction	?	?	3.29608	3.29608	A up vs B	1	1	?	0.30339	- 3.29608	B down vs A	1	1	?	1.48049	0	1
29380	TC02004983.hg.1	main	OTTHUMT00000323143 // IGKV3D-15 // immunoglobulin kappa variable 3D-15 (gene/pseudogene)	IGKV3D-15	OTTHUMT00000323143	---	---	---	OTTHUMT00000323143 // Havana transcript // immunoglobulin kappa variable 3D-15 [gene_bio]	---	?	?	3.2704	3.2704	A up vs B	1	1	?	0.305773	- 3.2704	B down vs A	1	1	?	1.46114	0	1
63232	TC14002256.hg.1	main	OTTHUMT00000325667 // IGHV3-21 // immunoglobulin heavy variable 3-21 // 14q32.33 // 284	IGHV3-21	OTTHUMT00000325667	---	---	---	OTTHUMT00000325667 // Havana transcript // immunoglobulin heavy variable 3-21 [gene_biot]	---	?	?	3.26475	3.26475	A up vs B	1	1	?	0.306302	- 3.26475	B down vs A	1	1	?	1.45688	0	1
30263	TC17001827.hg.1	main	NM_080284 // ABCA6 // ATP binding cassette subfamily A member 6 // 17q24.3 // 23460	ABCA6	NM_080284	NM_080284 // GO:0006869 // lipid transport // not recorded // NM_080284 // GO:0008152	NM_080284 // GO:0016021 // integral component of membrane // inferred from electronic annotation // NM_080284 // GO:0005524 // ATP binding // inferred from electronic annotation // NM_080284 // GO:0005524	NM_080284 // RefSeq // Homo sapiens ATP-binding cassette, sub-family A (ABCA1), member 6	---	?	?	3.2316	3.2316	A up vs B	1	1	?	0.309445	- 3.2316	B down vs A	1	1	?	1.43185	0	1	
10550	TC04001036.hg.1	main	NM_052964 // CLNK // cytokine-dependent hematopoietic cell linker // 4p16.1 // 116449	CLNK	NM_052964	NM_052964 // GO:0006955 // immune response // not recorded // NM_052964 // GO:0006955	NM_052964 // GO:0005622 // intracellular // non-traceable author statement // ENST000	NM_052964 // GO:0005070 // SH3/SH2 adaptor activity // non-traceable author statement	NM_052964 // RefSeq // Homo sapiens cytokine-dependent hematopoietic cell linker (CLNK)	---	?	?	3.21623	3.21623	A up vs B	1	1	?	0.310923	- 3.21623	B down vs A	1	1	?	1.42024	0	1
37792	TC14000529.hg.1	main	---	---	---	---	---	---	DQ577549 // NONCODE // accn=DQ577549 class=piRNA name=piR-45661 ref=NONCODE v2.0 trans	---	?	?	3.01918	3.01918	A up vs B	1	1	?	0.331216	- 3.01918	B down vs A	1	1	?	1.27066	0	1
55868	TC02003403.hg.1	main	---	---	---	---	---	---	uc010fh.2 // NONCODE // accn=NULL class=lncRNA name=ref=UCSCGeneNoncode transcriptid=	---	?	?	2.9673	2.9673	A up vs B	1	1	?	0.337006	- 2.9673	B down vs A	1	1	?	1.23112	0	1
30781	TC15000564.hg.1	main	---	---	---	---	---	---	DQ576734 // NONCODE // accn=DQ576734 class=piRNA name=piR-44846 ref=NONCODE v2.0 trans	---	?	?	2.91286	2.91286	A up vs B	1	1	?	0.343306	- 2.91286	B down vs A	1	1	?	1.18955	0	1
50158	TC15000894.hg.1	main	---	---	---	---	---	---	DQ583486 // NONCODE // accn=DQ583486	---	?	?	2.88629	2.88629	A up vs B	1	1	?	0.346465	- 2.88629	B down vs A	1	1	?	1.16925	0	1

40507	TC10002327.hg.1	main	---	---	---	---	---	---	ref=NONCODE v2.0 transc NR_003252 // NONCODE // accn=NR_003252 class=lncRNA name= ref=RefGeneNoncode transcript	---	?	?	2.54334	2.54334	A up vs B	1	1	?	0.39318 4	- 2.5433 4	B down vs A	1	1	?	0.9068 3	0	1
44871	TC13001561.hg.1	main	---	---	---	---	---	---	AK129948 // NONCODE // accn=AK129948 class=mRNAlike lncRNA name=Human lncRNA ref=Jounra	---	?	?	2.47651	2.47651	A up vs B	1	1	?	0.40379 4	- 2.4765 1	B down vs A	1	1	?	0.8558 37	0	1
33348	TC15001439.hg.1	main	---	---	---	---	---	---	DQ585053 // NONCODE // accn=DQ585053 class=piRNA name=piR-52165 ref=NONCODE v2.0 transc	---	?	?	2.47161	2.47161	A up vs B	1	1	?	0.40459 5	- 2.4716 1	B down vs A	1	1	?	0.8520 99	0	1
2822	TC14001478.hg.1	main	NM_001098725 // TCL1A // T-cell leukemia/lympho ma 1A // 14q32.1 // 8115 // NM_021966 /	TCL1A	NM_001098725	NM_001098725 // GO:0007275 // endoplasmic reticulum // inferred from electron annotat	NM_001098725 // GO:0005515 // protein binding // inferred from physical interaction //	NM_001098725 // RefSeq // Homo sapiens T-cell leukemia/lymphoma 1A (TCL1A), transcript	---	?	?	2.42888	2.42888	A up vs B	1	1	?	0.41171 2	- 2.4288 8	B down vs A	1	1	?	0.8195 73	0	1	
26280	TC08000023.hg.1	main	NR_039803 // MIR4659A // microRNA 4659a // --- // 100616348 // NR_039803 // MIR4659A /	MIR4659A	NR_039803	---	---	NR_039803 // RefSeq // Homo sapiens microRNA 4659a (MIR4659A), microRNA. // chr8 // 100	---	?	?	2.38628	2.38628	A up vs B	1	1	?	0.41906 2	- 2.3862 8	B down vs A	1	1	?	0.7872 16	0	1	
27097	TC14001418.hg.1	main	---	---	---	---	---	DQ582474 // NONCODE // accn=DQ582474 class=piRNA name=piR-32586 ref=NONCODE v2.0 transc	---	?	?	2.3535	2.3535	A up vs B	1	1	?	0.4249	- 2.3535	B down vs A	1	1	?	0.7623 72	0	1	
23291	TC17001828.hg.1	main	NR_039750 // MIR4524A // microRNA 4524a // --- // 100616316 // NR_039750 // MIR4524A /	MIR4524A	NR_039750	---	---	NR_039750 // RefSeq // Homo sapiens microRNA 4524a (MIR4524A), microRNA. // chr17 // 10	---	?	?	2.31386	2.31386	A up vs B	1	1	?	0.43217 8	- 2.3138 6	B down vs A	1	1	?	0.7324 16	0	1	
17711	TC17001364.hg.1	main	---	---	---	---	---	ENST00000459539 // ENSEMBL // ncrna:snoRNA chromosome:GRCh3 7:17:33381407:3338 1513:-1 ge	---	?	?	2.28378	2.28378	A up vs B	1	1	?	0.43787 1	- 2.2837 8	B down vs A	1	1	?	0.7097 44	0	1	
5830	TC13000546.hg.1	main	---	---	---	---	---	DQ594776 // NONCODE // accn=DQ594776 class=piRNA name=piR-60888 ref=NONCODE v2.0 transc	---	?	?	2.28323	2.28323	A up vs B	1	1	?	0.43797 7	- 2.2832 3	B down vs A	1	1	?	0.7093 28	0	1	
12792	TC13000545.hg.1	main	---	---	---	---	---	DQ594776 // NONCODE // accn=DQ594776 class=piRNA name=piR-60888 ref=NONCODE v2.0 transc	---	?	?	2.28323	2.28323	A up vs B	1	1	?	0.43797 7	- 2.2832 3	B down vs A	1	1	?	0.7093 28	0	1	
32799	TC01000723.hg.1	main	NM_001083592 // ROR1 // receptor tyrosine kinase-like orphan receptor 1 // 1p31.3 // 49	ROR1	NM_001083592	NM_001083592 // GO:0005737 // cytoplasm 169 // transmembrane receptor	NM_001083592 // GO:0004714 // transmembrane receptor protein	NM_001083592 // RefSeq // Homo sapiens receptor tyrosine kinase-like orphan receptor 1	NM_001083592 // GenMAPP // Nuclear_Receptors // NM_005012 //	?	?	2.28128	2.28128	A up vs B	1	1	?	0.43835 1	- 2.2812 8	B down vs A	1	1	?	0.7078 62	0	1	

						protein tyrosine kinase signaling	NM_001083592	tyrosine kinase activity /		GenMAPP // Nuclear_Recept																	
30734	TC10000255.hg.1	m a i n	---		---	---	---	---	ENST00000450980 // ENSEMBL // havana:known chromosome:GRCh38:10:38247922:38333155:1 gen	---	?	?	2.26866	2.26866	A up vs B	1	1	?	0.440789	- 2.26866	B down vs A	1	1	?	0.698373	0	1
61497	TC09001248.hg.1	m a i n	---		---	---	---	---	DQ574826 // NONCODE // accn=DQ574826 class=piRNA name=piR-42938 ref=NONCODE v2.0 transc	---	?	?	2.26738	2.26738	A up vs B	1	1	?	0.441037	- 2.26738	B down vs A	1	1	?	0.697413	0	1
47190	TC12000130.hg.1	m a i n	NM_080387 // CLEC4D // C-type lectin domain family 4, member D // 12p13.31 // 338339 //	CLEC4D	NM_080387	NM_080387 // GO:000223 // stimulatory C-type lectin receptor signaling pathway // trac	NM_080387 // GO:0030246 // plasma membrane // carbohydrate binding // inferred from electronic annotation	NM_080387 // RefSeq // Homo sapiens C-type lectin domain family 4, member D (CLEC4D), m	---	?	?	2.24474	2.24474	A up vs B	1	1	?	0.445486	- 2.24474	B down vs A	1	1	?	0.680418	0	1	
44915	TC19002491.hg.1	m a i n	M76743 // CEACAM1 // carcinoembryonic antigen-related cell adhesion molecule 1 (biliary)	CECAM1	M76743	M76743 // GO:0005886 // plasma membrane // traceable author statement // M76743 // G	M76743 // GO:0005515 // protein binding // inferred from physical interaction // M767	M76743 // NONCODE // RefSeq // Homo sapiens class=mRNALike lncRNA name=NULL ref=H-invitational v7.	---	?	?	2.24454	2.24454	A up vs B	1	1	?	0.445526	- 2.24454	B down vs A	1	1	?	0.680266	0	1	
8621	TC03001082.hg.1	m a i n	ENST00000426468 // XYLT1-AS2 // XYLT1 antisense RNA 2 // 3q29 // 101410543 // ENST00	XYLT1-AS2	ENST00000426468	---	---	ENST00000426468 // ENSEMBL // XYLT1 antisense RNA 2 [gene_biotype:antisense transcript	---	?	?	2.24415	2.24415	A up vs B	1	1	?	0.445603	- 2.24415	B down vs A	1	1	?	0.679975	0	1	
23647	TC02004396.hg.1	m a i n	X93757 // IGKC // immunoglobulin kappa constant // 2p12 // 3514	IGKC	X93757	X93757 // GO:0001895 // retina homeostasis // inferred from expression pattern // X93	X93757 // GO:0005576 // extracellular region // non-traceable author statement // X93	X93757 // NONCODE // RefSeq // Homo sapiens lncRNA name=NULL ref=H-invitational v7.	---	?	?	2.23131	2.23131	A up vs B	1	1	?	0.448168	- 2.23131	B down vs A	1	1	?	0.670353	0	1	
19705	TC01000371.hg.1	m a i n	NR_002997 // SCARN1 // small Cajal body-specific RNA 1 // 1p35.3 // 677774 // ENST000	SCARN1	NR_002997	---	---	NR_002997 // RefSeq // Homo sapiens small Cajal body-specific RNA 1 (SCARN1), guide RN	---	?	?	2.2179	2.2179	A up vs B	1	1	?	0.450877	- 2.2179	B down vs A	1	1	?	0.660325	0	1	
628	TC02000684.hg.1	m a i n	---		---	---	---	DQ574014 // NONCODE // accn=DQ574014 class=piRNA name=piR-42126 ref=NONCODE v2.0 transc	---	?	?	2.19319	2.19319	A up vs B	1	1	?	0.455958	- 2.19319	B down vs A	1	1	?	0.641876	0	1	
27643	TC02002199.hg.1	m a i n	---		---	---	---	DQ587734 // NONCODE // accn=DQ587734 class=piRNA name=piR-54846 ref=NONCODE v2.0 transc	---	?	?	2.19319	2.19319	A up vs B	1	1	?	0.455958	- 2.19319	B down vs A	1	1	?	0.641876	0	1	

18654	TC11002231.hg.1	main	NM_002424 // MMP8 // matrix metalloproteinase 8 // 11q22.3 // 4317 // ENST0000023682 6 /	MMP8	NM_002424	NM_002424 // GO:0006508 // proteolysis // inferred from direct assay // NM_002424 //	NM_002424 // GO:0005576 // extracellular region // traceable author statement // NM_0	NM_002424 // GO:0004222 // metalloendopeptidase activity // inferred from electronic	NM_002424 // RefSeq // Homo sapiens matrix metalloproteinase 8 (MMP8), transcript varian	NM_002424 // GenMAPP // Matrix_Metalloproteinases // ENST00000236826 // GenMAPP // Mat	?	?	2.18205	2.18205	A up vs B	1	1	?	0.458285	-2.18205	B down vs A	1	1	?	0.633582	0	1
30061	TC15000553.hg.1	main	---	---	---	---	---	---	DQ583824 // NONCODE // accn=DQ583824 class=piRNA name=piR-50936 ref=NONCODE v2.0 trans	---	?	?	2.18179	2.18179	A up vs B	1	1	?	0.45834	-2.18179	B down vs A	1	1	?	0.633387	0	1
67166	TC04001038.hg.1	main	---	---	---	---	---	---	ENST00000410250 // ENSEMBL // RNA, 5S ribosomal pseudogene 156 [gene_biotype:rRNA trans	---	?	?	2.1683	2.1683	A up vs B	1	1	?	0.46119	-2.1683	B down vs A	1	1	?	0.623362	0	1
16571	TC06003963.hg.1	main	---	---	---	---	---	---	TCONS_00011605 // NONCODE // accn=NULL class=lncRNA name=Human lincRNA ref=BodyMapLinc	---	?	?	2.16004	2.16004	A up vs B	1	1	?	0.462955	-2.16004	B down vs A	1	1	?	0.617222	0	1
37068	TC15001139.hg.1	main	---	---	---	---	---	---	DQ575741 // NONCODE // accn=DQ575741 class=piRNA name=piR-43853 ref=NONCODE v2.0 trans	---	?	?	2.15186	2.15186	A up vs B	1	1	?	0.464714	-2.15186	B down vs A	1	1	?	0.611158	0	1
39233	TC15001173.hg.1	main	---	---	---	---	---	---	DQ575741 // NONCODE // accn=DQ575741 class=piRNA name=piR-43853 ref=NONCODE v2.0 trans	---	?	?	2.15186	2.15186	A up vs B	1	1	?	0.464714	-2.15186	B down vs A	1	1	?	0.611158	0	1
44194	TC15000185.hg.1	main	---	---	---	---	---	---	DQ575741 // NONCODE // accn=DQ575741 class=piRNA name=piR-43853 ref=NONCODE v2.0 trans	---	?	?	2.15186	2.15186	A up vs B	1	1	?	0.464714	-2.15186	B down vs A	1	1	?	0.611158	0	1
53793	TC15000960.hg.1	main	---	---	---	---	---	---	DQ575741 // NONCODE // accn=DQ575741 class=piRNA name=piR-43853 ref=NONCODE v2.0 trans	---	?	?	2.15186	2.15186	A up vs B	1	1	?	0.464714	-2.15186	B down vs A	1	1	?	0.611158	0	1
63796	TC15000159.hg.1	main	---	---	---	---	---	---	DQ575741 // NONCODE // accn=DQ575741 class=piRNA name=piR-43853 ref=NONCODE v2.0 trans	---	?	?	2.15186	2.15186	A up vs B	1	1	?	0.464714	-2.15186	B down vs A	1	1	?	0.611158	0	1
40827	TC04002263.hg.1	main	NR_036614 // DCLK2 // doublecortin-like kinase 2 // 4q31.3 // 166614	DCLK2	NR_036614	NR_036614 // GO:0006468 // protein phosphorylation // inferred from electronic annotation // NR_036	NR_036614 // GO:0005737 // cytoplasmic protein serine/threonine kinase activity // inferred from el	NR_036614 // GO:0004674 // protein serine/threonine kinase activity // inferred from el	NR_036614 // NONCODE // accn=NR_036614 class=lncRNA name=ref=RefGeneNoncode transcript	---	?	?	2.15173	2.15173	A up vs B	1	1	?	0.464742	-2.15173	B down vs A	1	1	?	0.611064	0	1
57940	TC15002079.hg.1	main	---	---	---	---	---	---	TCONS_00023303 // NONCODE // accn=NULL	---	?	?	2.14877	2.14877	A up vs B	1	1	?	0.465382	-2.14877	B down vs A	1	1	?	0.608869	0	1

14227	TC12000046.hg.1	main	---	---	---	---	---	---	---	class=lncRNA name=Human lincRNA ref=BodyMapLinc DQ584103 // NONCODE // accn=DQ584103 class=piRNA name=piR-51215 ref=NONCODE v2.0 transc	---	?	?	2.14861	2.14861	A up vs B	1	1	?	0.46541 8	- 2.14861	B down vs A	1	1	?	0.6087 47	0	1
3087	TC10000869.hg.1	main	NM_001243194 // INPP5F // inositol polyphosphate-5-phosphatase F // 10q26.11 // 22876 /	INPP5F	NM_001243194	NM_001243194 // GO:0005622	NM_001243194 // GO:0042578	NM_001243194 // RefSeq // Homo sapiens inositol polyphosphate-5-phosphatase F (INPP5F),	---	?	?	2.14222	2.14222	A up vs B	1	1	?	0.46680 6	- 2.14222	B down vs A	1	1	?	0.6040 16	0	1		
41736	TC0X002051.hg.1	main	---	---	---	---	---	TCONS_00017504 // NONCODE // accn=NULL class=lncRNA name=Human lincRNA ref=BodyMapLinc	---	?	?	2.12833	2.12833	A up vs B	1	1	?	0.46985 1	- 2.12833	B down vs A	1	1	?	0.5937 49	0	1		
42674	TC13001040.hg.1	main	---	---	---	---	---	TCONS_00021766 // NONCODE // accn=NULL class=lncRNA name=Human lincRNA ref=BodyMapLinc	---	?	?	2.11469	2.11469	A up vs B	1	1	?	0.47288 2	- 2.11469	B down vs A	1	1	?	0.5836 84	0	1		
65925	TC04001138.hg.1	main	NR_039966 // MIR4802 // microRNA 4802 // --- // 100616274 // NR_039966 // MIR4802 // m	MIR4802	NR_039966	---	---	NR_039966 // RefSeq // Homo sapiens microRNA 4802 (MIR4802), microRNA. // chr4 // 100 /	---	?	?	2.11219	2.11219	A up vs B	1	1	?	0.47344 1	- 2.11219	B down vs A	1	1	?	0.5818 42	0	1		
59811	TC03003258.hg.1	main	---	---	---	---	---	TCONS_00006729 // NONCODE // accn=NULL class=lncRNA name=Human lincRNA ref=BodyMapLinc	---	?	?	2.10889	2.10889	A up vs B	1	1	?	0.47418 3	- 2.10889	B down vs A	1	1	?	0.5794 1	0	1		
12409	TC0X002033.hg.1	main	---	---	---	---	---	OTTHUMT00000060661 // NONCODE // novel transcript [gene_bioty pe:lincRNA transcript_bioty	---	?	?	2.09321	2.09321	A up vs B	1	1	?	0.47773 5	- 2.09321	B down vs A	1	1	?	0.5678 75	0	1		
24179	TC16001441.hg.1	main	ENST00000050174 0 // ACSM3 // acyl-CoA synthetase medium-chain family member 3 // 16p13.1	ACSM3	ENST00000050174	ENST00000050174 // GO:0005759 // mitochondrial matrix // inferred from electronic annot	ENST00000050174 // GO:0005524 // ATP binding // inferred from electronic annotation //	ENST00000050174 // NONCODE // acyl-CoA synthetase medium-chain family member 3 [gene_bi	---	?	?	2.08237	2.08237	A up vs B	1	1	?	0.48022 1	- 2.08237	B down vs A	1	1	?	0.5599 24	0	1		
49283	TC02004724.hg.1	main	EF212156 // TTN // titin // 2q31 // 7273	TTN	EF212156	EF212156 // GO:0000794 // condensed nuclear chromosome // inferred from direct assay /	EF212156 // GO:0002020 // protease binding // inferred from physical interaction // E	EF212156 // NONCODE // accn=EF212156 class=mRNAlike lincRNA name=NULL ref=H-Invitational	---	?	?	2.06809	2.06809	A up vs B	1	1	?	0.48353 9	- 2.06809	B down vs A	1	1	?	0.5494 62	0	1		
47526	TC10002326.hg.1	main	---	---	---	---	---	NR_003251 // NONCODE // accn=NR_003251	---	?	?	2.06142	2.06142	A up vs B	1	1	?	0.48510 2	- 2.06142	B down vs A	1	1	?	0.5445 91	0	1		

		in								class=lincRNA name=ref=RefGeneNoncode transcript																		
26580	TC09002817.hg.1	main	---		---	---	---	---		linc_luo_610 // NONCODE // accn=NULL class=lincRNA name=Human lincRNA ref=Scripture Rec	---	?	?	2.05892	2.05892	A up vs B	1	1	?	0.485691	-2.05892	B down vs A	1	1	?	0.542768	0	1
48187	TC04001928.hg.1	main	---		---	---	---	---		TCONS_0008002 // NONCODE // accn=NULL class=lincRNA name=Human lincRNA ref=BodyMapLinc	---	?	?	2.05608	2.05608	A up vs B	1	1	?	0.486362	-2.05608	B down vs A	1	1	?	0.540693	0	1
52461	TC15000084.hg.1	main	NR_003303 // SNORD115-11 // small nucleolar RNA, C/D box 115-11 // 15q11.2 // 100033448	SNORD 115-11	NR_003303	---	---	---		NR_003303 // RefSeq // Homo sapiens small nucleolar RNA, C/D box 115-11 (SNORD115-11),	---	?	?	2.05186	2.05186	A up vs B	1	1	?	0.487364	-2.05186	B down vs A	1	1	?	0.537611	0	1
11275	TC15000112.hg.1	main	NR_003344 // SNORD115-29 // small nucleolar RNA, C/D box 115-29 // 15q11.2 // 100033803	SNORD 115-29	NR_003344	---	---	---		NR_003344 // RefSeq // Homo sapiens small nucleolar RNA, C/D box 115-29 (SNORD115-29),	---	?	?	2.05186	2.05186	A up vs B	1	1	?	0.487364	-2.05186	B down vs A	1	1	?	0.537611	0	1
25208	TC15000099.hg.1	main	NR_003358 // SNORD115-43 // small nucleolar RNA, C/D box 115-43 // 15q11.2 // 100033817	SNORD 115-43	NR_003358	---	---	---		NR_003358 // RefSeq // Homo sapiens small nucleolar RNA, C/D box 115-43 (SNORD115-43),	---	?	?	2.05186	2.05186	A up vs B	1	1	?	0.487364	-2.05186	B down vs A	1	1	?	0.537611	0	1
53196	TC15000105.hg.1	main	NR_003358 // SNORD115-43 // small nucleolar RNA, C/D box 115-43 // 15q11.2 // 100033817	SNORD 115-43	NR_003358	---	---	---		NR_003358 // RefSeq // Homo sapiens small nucleolar RNA, C/D box 115-43 (SNORD115-43),	---	?	?	2.05186	2.05186	A up vs B	1	1	?	0.487364	-2.05186	B down vs A	1	1	?	0.537611	0	1
47383	TC03002827.hg.1	main	---		---	---	---	---		AK098488 // NONCODE // accn=AK098488 class=miRNAlike lincRNA name=Human lincRNA ref=Jounra	---	?	?	2.05079	2.05079	A up vs B	1	1	?	0.487617	-2.05079	B down vs A	1	1	?	0.536835	0	1
19979	TC07001921.hg.1	main	---		---	---	---	---		ENST0000459596 // ENSEMBL // ncrna:snRNA chromosome:GRCh3 7:7:140075363:140075466:-1g	---	?	?	2.04512	2.04512	A up vs B	1	1	?	0.488969	-2.04512	B down vs A	1	1	?	0.532702	0	1
4030	TC19000134.hg.1	main	NM_174918 // MCEMP1 // mast cell-expressed membrane protein 1 // 19p13.2 // 199675 ///	MCEMP1	NM_174918	---	NM_174918 // GO:0016021 // integral component of membrane // inferred from electronic a	---		NM_174918 // RefSeq // Homo sapiens mast cell-expressed membrane protein 1 (MCEMP1), mRNA	---	?	?	2.03345	2.03345	A up vs B	1	1	?	0.491776	-2.03345	B down vs A	1	1	?	0.524212	0	1
31458	TC07002696.hg.1	main	---		---	---	---	---		TCONS_00013649 // NONCODE // accn=NULL class=lincRNA name=Human lincRNA ref=BodyMapLinc	---	?	?	2.0301	2.0301	A up vs B	1	1	?	0.492587	-2.0301	B down vs A	1	1	?	0.52178	0	1
35656	TC01004449.hg.1	main	AK000776 // ROR1 // receptor tyrosine kinase-like orphan receptor 1 // 1p31.3 // 4919	ROR1	AK000776	AK000776 // GO:0005737 // cytoplasm // GO:0007169 // transmembrane receptor protein tyrosine	AK000776 // GO:0005737 // cytoplasm // GO:0007169 // transmembrane receptor protein tyrosine	AK000776 // GO:0004714 // traceable membrane receptor protein tyrosine	AK000776 // NONCODE // accn=AK000776 class=miRNAlike lincRNA name=Human lincRNA ref=Jounra	AK000776 // GenMAPP // Nuclear_Receptors	?	?	2.02947	2.02947	A up vs B	1	1	?	0.492739	-2.02947	B down vs A	1	1	?	0.521326	0	1	

41268	TC06001641.hg.1	m a i n	---	---	---	---	---	---	ref=NONCODE v2.0 transc DQ587590 // NONCODE // accn=DQ587590 class=piRNA name=piR-54702 ref=NONCODE v2.0 transc	---	?	?	0.488742	-2.04607	A down vs B	1	1	?	2.04607	2.04607	B up vs A	1	1	?	0.533395	0	1
47809	TC09001017.hg.1	m a i n	---	---	---	---	---	---	uc022bfp.1 // UCSC Genes // Annexin II and uses thereof. // chr9 // 100 // 100 // 0 //	---	?	?	0.487186	-2.0526	A down vs B	1	1	?	2.0526	2.0526	B up vs A	1	1	?	0.538157	0	1
844	TC02004976.hg.1	m a i n	OTTHUMT000003 23274 // IGV1D- 33 // immunoglobulin kappa variable 1D-33 // 2p12 // 28896	IGKV1D -33	OTTHU MT0000 032327 4	OTTHUM T000003 23274 // GO:0006 898 // receptor - mediate d endocyt osis // traceabl e author s	OTTHUMT00 000323274 // GO:0005576 // extracellular region // non- traceable author statem	OTTHUMT0 000323274 // GO:0003823 // antigen binding // 1D- 33[gene_bio	OTTHUMT000003232 74 // Havana transcript // immunoglobulin kappa variable 1D- 33[gene_bio	---	?	?	0.487103	-2.05296	A down vs B	1	1	?	2.05296	2.05296	B up vs A	1	1	?	0.538413	0	1
68903	TC10002567.hg.1	m a i n	---	---	---	---	---	---	TCONS_00017955 // NONCODE // accn=NULL class=lncRNA name=Human lincRNA ref=BodyMapLinc	---	?	?	0.484151	-2.06547	A down vs B	1	1	?	2.06547	2.06547	B up vs A	1	1	?	0.547549	0	1
61799	TC14002234.hg.1	m a i n	OTTHUMT000003 25960 // IGH3- 10 // immunoglobulin heavy diversity 3- 10 // 14q32.33 // 28	IGHD3- 10	OTTHU MT0000 032596 0	---	---	---	OTTHUMT000003259 60 // Havana transcript // immunoglobulin heavy diversity 3- 10[gene_bio	---	?	?	0.476355	-2.09927	A down vs B	1	1	?	2.09927	2.09927	B up vs A	1	1	?	0.572333	0	1
355	TC18000391.hg.1	m a i n	---	---	---	---	---	---	DQ583164 // NONCODE // accn=DQ583164 class=piRNA name=piR-50276 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.574914	0	1
792	TC14000014.hg.1	m a i n	---	---	---	---	---	---	DQ591735 // NONCODE // accn=DQ591735 class=piRNA name=piR-58847 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.574913	0	1
2219	TC02000838.hg.1	m a i n	---	---	---	---	---	---	DQ570062 // NONCODE // accn=DQ570062 class=piRNA name=piR-30174 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.574914	0	1
4793	TC02002302.hg.1	m a i n	---	---	---	---	---	---	DQ573684 // NONCODE // accn=DQ573684 class=piRNA name=piR-41796 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.574913	0	1
7295	TC18000390.hg.1	m a i n	---	---	---	---	---	---	DQ573684 // NONCODE // accn=DQ573684 class=piRNA name=piR-41796 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.574913	0	1
8440	TC14000024.hg.1	m a i n	---	---	---	---	---	---	DQ591735 // NONCODE // accn=DQ591735 class=piRNA name=piR-58847 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.574913	0	1

15302	TC14000866.hg.1	main	---	---	---	---	---	---	DQ573684 // NONCODE // accn=DQ573684 class=piRNA name=piR-41796 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.574913	0	1
17549	TC22000442.hg.1	main	---	---	---	---	---	---	DQ573684 // NONCODE // accn=DQ573684 class=piRNA name=piR-41796 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.574913	0	1
23099	TC02000835.hg.1	main	---	---	---	---	---	---	DQ591735 // NONCODE // accn=DQ591735 class=piRNA name=piR-58847 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.574913	0	1
23282	TC21000020.hg.1	main	---	---	---	---	---	---	DQ591735 // NONCODE // accn=DQ591735 class=piRNA name=piR-58847 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.574913	0	1
24527	TC09001343.hg.1	main	---	---	---	---	---	---	DQ573684 // NONCODE // accn=DQ573684 class=piRNA name=piR-41796 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.574914	0	1
30626	TC15001030.hg.1	main	---	---	---	---	---	---	DQ573684 // NONCODE // accn=DQ573684 class=piRNA name=piR-41796 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.574913	0	1
30627	TC15001029.hg.1	main	---	---	---	---	---	---	DQ583164 // NONCODE // accn=DQ583164 class=piRNA name=piR-50276 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.574914	0	1
36194	TC14000863.hg.1	main	---	---	---	---	---	---	DQ573684 // NONCODE // accn=DQ573684 class=piRNA name=piR-41796 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.574913	0	1
36314	TC14000020.hg.1	main	---	---	---	---	---	---	DQ591735 // NONCODE // accn=DQ591735 class=piRNA name=piR-58847 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.574913	0	1
37049	TC02000833.hg.1	main	---	---	---	---	---	---	DQ591735 // NONCODE // accn=DQ591735 class=piRNA name=piR-58847 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.574913	0	1
39201	TC22000450.hg.1	main	---	---	---	---	---	---	DQ573684 // NONCODE // accn=DQ573684 class=piRNA name=piR-41796 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.574913	0	1
43312	TC02000821.hg.1	main	---	---	---	---	---	---	DQ591735 // NONCODE // accn=DQ591735 class=piRNA name=piR-58847 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.574913	0	1

54404	TC02002305.hg.1	ma a i n	---	---	---	---	---	---	DQ573684 // NONCODE // accn=DQ573684 class=piRNA name=piR-41796 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.5749 13	0	1
55114	TC02002316.hg.1	ma a i n	---	---	---	---	---	---	DQ573684 // NONCODE // accn=DQ573684 class=piRNA name=piR-41796 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.5749 13	0	1
57210	TC14000860.hg.1	ma a i n	---	---	---	---	---	---	DQ573684 // NONCODE // accn=DQ573684 class=piRNA name=piR-41796 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.5749 13	0	1
60178	TCUn_gl00021300 0001.hg.1	ma a i n	---	---	---	---	---	---	DQ583164 // NONCODE // accn=DQ583164 class=piRNA name=piR-50276 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.5749 14	0	1
62124	TC02002315.hg.1	ma a i n	---	---	---	---	---	---	DQ573684 // NONCODE // accn=DQ573684 class=piRNA name=piR-41796 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.5749 13	0	1
63559	TC02002337.hg.1	ma a i n	---	---	---	---	---	---	DQ573684 // NONCODE // accn=DQ573684 class=piRNA name=piR-41796 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.5749 13	0	1
67205	TC22000445.hg.1	ma a i n	---	---	---	---	---	---	DQ573684 // NONCODE // accn=DQ573684 class=piRNA name=piR-41796 ref=NONCODE v2.0 transc	---	?	?	0.47556	-2.10278	A down vs B	1	1	?	2.10278	2.10278	B up vs A	1	1	?	0.5749 13	0	1
29774	TC19000574.hg.1	ma a i n	---	---	---	---	---	---	DQ590318 // NONCODE // accn=DQ590318 class=piRNA name=piR-57430 ref=NONCODE v2.0 transc	---	?	?	0.474356	-2.10812	A down vs B	1	1	?	2.10812	2.10812	B up vs A	1	1	?	0.5788 44	0	1
62885	TC02003402.hg.1	ma a i n	---	---	---	---	---	---	DQ187489 // NONCODE // accn=DQ187489 class=mRNAlite lncRNA name=NULL ref=H-invitational	---	?	?	0.468983	-2.13227	A down vs B	1	1	?	2.13227	2.13227	B up vs A	1	1	?	0.5966 59	0	1
21865	TC02000935.hg.1	ma a i n	---	---	---	---	---	---	uc021vqx.1 // UCSC Genes // Rfam model RF00189 hit found at contig region AC068551.6/16	---	?	?	0.467626	-2.13846	A down vs B	1	1	?	2.13846	2.13846	B up vs A	1	1	?	0.6012 36	0	1
55959	TC22001445.hg.1	ma a i n	OTTHUMT000003 21828 // IGLV3-1 // immunoglobulin lambda variable 3-1 // 22q11.2 // 28809	IGLV3-1	OTTHU MT0000 032182 8	---	---	---	OTTHUMT000003218 28 // Havana transcript // immunoglobulin lambda variable 3- 1 gene_biot	---	?	?	0.463762	-2.15628	A down vs B	1	1	?	2.15628	2.15628	B up vs A	1	1	?	0.6144 35	0	1
67324	TC14002211.hg.1	ma a i n	OTTHUMT000003 26459 // IGHA1 // immunoglobulin heavy constant alpha 1 // 14q32.33 // 349	IGHA1	OTTHU MT0000 032645 9	OTTHUM T000003 26459 // GO:0001 895 // retina homeost asis // inferred from	OTTHUMT00 000326459 // GO:0005576 // extracellular region // traceable author statement	OTTHUMT0 0000326459 // GO:0003823 // antigen binding // not recorded //	OTTHUMT000003264 59 // Havana transcript // immunoglobulin heavy constant alpha 1 gene_b	ENST00000 390547 // GenMAPP // Inflammat ory_Respons e_Pathway	?	?	0.463286	-2.1585	A down vs B	1	1	?	2.1585	2.1585	B up vs A	1	1	?	0.6160 79	0	1

26730	TC07001299.hg.1	main	OTTHUMT00000338400 // TRGV4 // T cell receptor gamma variable 4 // 7p14 // 6977	TRGV4	OTTHUMT00000338400	---	---	OTTHUMT00000338400 // Havana transcript // T cell receptor gamma variable 4 // gene_biotype	---	?	?	0.459211	-2.17765	A down vs B	1	1	?	2.17765	2.17765	B up vs A	1	1	?	0.630309	0	1
55343	TC17001281.hg.1	main	---	---	---	---	---	DQ592978 // NONCODE // accn=DQ592978 class=piRNA name=piR-33090 ref=NONCODE v2.0 trans	---	?	?	0.45741	-2.18622	A down vs B	1	1	?	2.18622	2.18622	B up vs A	1	1	?	0.636687	0	1
25554	TC16000387.hg.1	main	---	---	---	---	---	AF209882 // GenBank // Homo sapiens immunoglobulin heavy chain variable region 194-6 mRNA	---	?	?	0.448651	-2.2289	A down vs B	1	1	?	2.2289	2.2289	B up vs A	1	1	?	0.668554	0	1
34861	TC02003396.hg.1	main	EF028213 // IGKC // immunoglobulin kappa constant // 2p12 // 3514 // S67637 // IGKC //	IGKC	EF028213	EF028213 // GO:0005576 // extracellular region // not non-traceable author statement // E	EF028213 // GO:0003823 // antigen binding // not recorded // EF028213 // GO:0003823 // E	EF028213 // NONCODE // accn=EF028213 class=mRNAlike lncRNA name=NULL ref=H-invitational	---	?	?	0.445914	-2.24258	A down vs B	1	1	?	2.24258	2.24258	B up vs A	1	1	?	0.678801	0	1
45595	TC19001436.hg.1	main	---	---	---	---	---	DQ595116 // NONCODE // accn=DQ595116 class=piRNA name=piR-61228 ref=NONCODE v2.0 trans	---	?	?	0.445132	-2.24652	A down vs B	1	1	?	2.24652	2.24652	B up vs A	1	1	?	0.681756	0	1
16495	TC11001599.hg.1	main	---	---	---	---	---	DQ592387 // NONCODE // accn=DQ592387 class=piRNA name=piR-59499 ref=NONCODE v2.0 trans	---	?	?	0.432212	-2.31368	A down vs B	1	1	?	2.31368	2.31368	B up vs A	1	1	?	0.732278	0	1
51244	TC15000672.hg.1	main	---	---	---	---	---	DQ587888 // NONCODE // accn=DQ587888 class=piRNA name=piR-55000 ref=NONCODE v2.0 trans	---	?	?	0.42504	-2.35272	A down vs B	1	1	?	2.35272	2.35272	B up vs A	1	1	?	0.761784	0	1
38837	TC11001628.hg.1	main	---	---	---	---	---	DQ582305 // NONCODE // accn=DQ582305 class=piRNA name=piR-32417 ref=NONCODE v2.0 trans	---	?	?	0.424402	-2.35626	A down vs B	1	1	?	2.35626	2.35626	B up vs A	1	1	?	0.764464	0	1
48853	TC02003394.hg.1	main	---	---	AF103542 // GO:0005576 // extracellular region // non-traceable author statement // A	AF103542 // GO:0003823 // antigen binding // inferred from electronic annotation // A	AF103542 // NONCODE // accn=AF103542 class=mRNAlike lncRNA name=NULL ref=H-invitational	---	?	?	0.417002	-2.39807	A down vs B	1	1	?	2.39807	2.39807	B up vs A	1	1	?	0.796164	0	1	
47704	TC13000540.hg.1	main	---	---	---	---	---	DQ590719 // NONCODE // accn=DQ590719 class=piRNA name=piR-57831 ref=NONCODE v2.0 trans	---	?	?	0.402752	-2.48291	A down vs B	1	1	?	2.48291	2.48291	B up vs A	1	1	?	0.860717	0	1

28454	TC11001686.hg.1	m a i n	---	---	---	---	---	---	DQ575274 // NONCODE // accn=DQ575274 class=piRNA name=piR-43386 ref=NONCODE v2.0 transc	---	?	?	0.400634	-2.49604	A down vs B	1	1	?	2.49604	2.49604	B up vs A	1	1	?	0.870729	0	1
29152	TC11001707.hg.1	m a i n	---	---	---	---	---	---	DQ582888 // NONCODE // accn=DQ582888 class=piRNA name=piR-33000 ref=NONCODE v2.0 transc	---	?	?	0.393831	-2.53916	A down vs B	1	1	?	2.53916	2.53916	B up vs A	1	1	?	0.903638	0	1
47897	TC12000141.hg.1	m a i n	---	---	---	---	---	---	ENST0000459276 // ENSEMBL // U7 small nuclear RNA [gene_biotype:snRNA transcript_biotype	---	?	?	0.388988	-2.57077	A down vs B	1	1	?	2.57077	2.57077	B up vs A	1	1	?	0.927797	0	1
3123	TC12002599.hg.1	m a i n	---	---	---	---	---	---	TCONS_00020585 // NONCODE // accn=NULL class=lncRNA name=Human lincRNA ref=BodyMapLinc	---	?	?	0.38017	-2.6304	A down vs B	1	1	?	2.6304	2.6304	B up vs A	1	1	?	0.973408	0	1
3625	TC22000444.hg.1	m a i n	---	---	---	---	---	---	DQ573684 // NONCODE // accn=DQ573684 class=piRNA name=piR-41796 ref=NONCODE v2.0 transc	---	?	?	0.363742	-2.7492	A down vs B	1	1	?	2.7492	2.7492	B up vs A	1	1	?	1.06436	0	1
9714	TC15001033.hg.1	m a i n	---	---	---	---	---	---	DQ573684 // NONCODE // accn=DQ573684 class=piRNA name=piR-41796 ref=NONCODE v2.0 transc	---	?	?	0.363742	-2.7492	A down vs B	1	1	?	2.7492	2.7492	B up vs A	1	1	?	1.06436	0	1
10609	TC02000859.hg.1	m a i n	---	---	---	---	---	---	DQ583165 // NONCODE // accn=DQ583165 class=piRNA name=piR-50277 ref=NONCODE v2.0 transc	---	?	?	0.363742	-2.7492	A down vs B	1	1	?	2.7492	2.7492	B up vs A	1	1	?	1.06436	0	1
22259	TC14000865.hg.1	m a i n	---	---	---	---	---	---	DQ573684 // NONCODE // accn=DQ573684 class=piRNA name=piR-41796 ref=NONCODE v2.0 transc	---	?	?	0.363742	-2.7492	A down vs B	1	1	?	2.7492	2.7492	B up vs A	1	1	?	1.06436	0	1
22374	TC14000022.hg.1	m a i n	---	---	---	---	---	---	DQ599717 // NONCODE // accn=DQ599717 class=piRNA name=piR-37783 ref=NONCODE v2.0 transc	---	?	?	0.363742	-2.7492	A down vs B	1	1	?	2.7492	2.7492	B up vs A	1	1	?	1.06436	0	1
22932	TC15001019.hg.1	m a i n	---	---	---	---	---	---	DQ573684 // NONCODE // accn=DQ573684 class=piRNA name=piR-41796 ref=NONCODE v2.0 transc	---	?	?	0.363742	-2.7492	A down vs B	1	1	?	2.7492	2.7492	B up vs A	1	1	?	1.06436	0	1
29326	TC14000021.hg.1	m a i n	---	---	---	---	---	---	DQ599717 // NONCODE // accn=DQ599717 class=piRNA name=piR-37783 ref=NONCODE v2.0 transc	---	?	?	0.363742	-2.7492	A down vs B	1	1	?	2.7492	2.7492	B up vs A	1	1	?	1.06436	0	1
39202	TC22000449.hg.1	m a i n	---	---	---	---	---	---	DQ573684 // NONCODE // accn=DQ573684 class=piRNA name=piR-41796 ref=NONCODE v2.0 transc	---	?	?	0.363742	-2.7492	A down vs B	1	1	?	2.7492	2.7492	B up vs A	1	1	?	1.06436	0	1

64343	TC1400015.hg.1	ma ai n	---		---	---	---	---	---	DQ599717 // NONCODE // accn=DQ599717 class=piRNA name=piR-37783 ref=NONCODE v2.0 transc	---	?	?	0.363742	-2.7492	A down vs B	1	1	?	2.7492	2.7492	B up vs A	1	1	?	1.0643 6	0	1
65778	TC02000840.hg.1	ma ai n	---		---	---	---	---	---	DQ591735 // NONCODE // accn=DQ591735 class=piRNA name=piR-58847 ref=NONCODE v2.0 transc	---	?	?	0.363742	-2.7492	A down vs B	1	1	?	2.7492	2.7492	B up vs A	1	1	?	1.0643 6	0	1
4979	TC0Y000160.hg.1	ma ai n	---		---	---	---	---	---	HM222546 // GenBank // Homo sapiens isolate 1a61 immunoglobulin kappa light chain mRNA,	---	?	?	0.361722	-2.76455	A down vs B	1	1	?	2.76455	2.7645 5	B up vs A	1	1	?	1.0761 1	0	1
22211	TC02000692.hg.1	ma ai n	---		---	---	---	---	---	DQ586506 // NONCODE // accn=DQ586506 class=piRNA name=piR-53618 ref=NONCODE v2.0 transc	---	?	?	0.359038	-2.78522	A down vs B	1	1	?	2.78522	2.7852 2	B up vs A	1	1	?	1.0919 3	0	1
1274	TC04000772.hg.1	ma ai n	---		---	---	---	---	---	uc021xti.1 // UCSC Genes // Annexin II and uses thereof. // chr4 // 100 // 100 // 0 //	---	?	?	0.347163	-2.88049	A down vs B	1	1	?	2.88049	2.8804 9	B up vs A	1	1	?	1.1648 2	0	1
6629	TC09000447.hg.1	ma ai n	---		---	---	---	---	---	DQ594798 // NONCODE // accn=DQ594798 class=piRNA name=piR-60910 ref=NONCODE v2.0 transc	---	?	?	0.342304	-2.92138	A down vs B	1	1	?	2.92138	2.9213 8	B up vs A	1	1	?	1.1960 7	0	1
42928	TC07002894.hg.1	ma ai n	Z11232 // TARP // TCR gamma alternate reading frame protein // 7p15-p14 // 445347 /// Z	TARP	Z11232	Z11232 // GO:0006 955 // immune response // non- traceabl e author stateme nt /// Z11232 /	Z11232 // GO:0005887 // integral component of plasma membrane // non- traceabl e author s	Z11232 // GO:0004888 // transmembr ane signaling receptor activity // non- traceable auth	---	Z11232 // NONCODE // accn=Z11232 class=mRNAlike lncRNA name=NULL ref=H-invitational v7.	---	?	?	0.326491	-3.06287	A down vs B	1	1	?	3.06287	3.0628 7	B up vs A	1	1	?	1.3039 3	0	1
68648	TC22000467.hg.1	ma ai n	---		---	---	---	---	---	HM222546 // GenBank // Homo sapiens isolate 1a61 immunoglobulin kappa light chain mRNA,	---	?	?	0.322735	-3.09852	A down vs B	1	1	?	3.09852	3.0985 2	B up vs A	1	1	?	1.3310 2	0	1
37641	TC06000499.hg.1	ma ai n	---		---	---	---	---	---	DQ570403 // NONCODE // accn=DQ570403 class=piRNA name=piR-30515 ref=NONCODE v2.0 transc	---	?	?	0.303441	-3.29553	A down vs B	1	1	?	3.29553	3.2955 3	B up vs A	1	1	?	1.4800 8	0	1
12450	TC14001399.hg.1	ma ai n	---		---	---	---	---	---	DQ577137 // NONCODE // accn=DQ577137 class=piRNA name=piR-45249 ref=NONCODE v2.0 transc	---	?	?	0.285121	-3.50729	A down vs B	1	1	?	3.50729	3.5072 9	B up vs A	1	1	?	1.6386 9	0	1
17981	TC15001907.hg.1	ma ai n	---		---	---	---	---	---	DQ580631 // NONCODE // accn=DQ580631 class=piRNA name=piR-48743 ref=NONCODE v2.0 transc	---	?	?	0.21046	-4.75149	A down vs B	1	1	?	4.75149	4.7514 9	B up vs A	1	1	?	2.5276 1	0	1

Top Canonical Pathways		
Name	p-value	Overlap
Myo-inositol Biosynthesis	4.82E-03	20.0 % 1/5
Airway Pathology in Chronic Obstructive Pulmonary Disease	7.71E-03	12.5 % 1/8
B Cell Receptor Signaling	1.37E-02	1.1 % 2/186
D-myo-inositol (1,4,5)-trisphosphate Degradation	1.73E-02	5.6 % 1/18
1D-myo-inositol Hexakisphosphate Biosynthesis II (Mammalian)	1.82E-02	5.3 % 1/19

Top Upstream Regulators		
Upstream Regulator	p-value of overlap	Predicted Activation
PRSS2	1.81E-03	
CRTC2	1.17E-02	
CEBPE	1.26E-02	
ITGB3	1.26E-02	
SMARCD3	1.35E-02	

Top Diseases and Bio Functions		
Diseases and Disorders		
Name	p-value range	# Molecules
Cardiovascular Disease	3.61E-02 - 3.05E-04	3
Hereditary Disorder	3.61E-02 - 3.05E-04	3
Organismal Injury and Abnormalities	4.83E-02 - 3.05E-04	16
Skeletal and Muscular Disorders	3.61E-02 - 3.05E-04	8
Inflammatory Response	1.35E-02 - 3.53E-04	4
Molecular and Cellular Functions		
Name	p-value range	# Molecules
Cell-To-Cell Signaling and Interaction	1.35E-02 - 3.05E-04	4
Cell Death and Survival	4.15E-02 - 9.66E-04	3
Cell Morphology	4.17E-02 - 9.66E-04	2
Cellular Assembly and Organization	4.17E-02 - 9.66E-04	2
Cellular Compromise	1.35E-02 - 9.66E-04	2
Physiological System Development and Function		
Name	p-value range	# Molecules
Humoral Immune Response	6.75E-03 - 3.53E-04	2
Cardiovascular System Development and Function	2.77E-02 - 8.15E-04	3
Organ Development	1.63E-02 - 8.15E-04	2
Organ Morphology	1.92E-02 - 8.15E-04	2
Skeletal and Muscular System Development and Function	1.92E-02 - 8.15E-04	2

Top Tox Functions		
Cardiotoxicity		
Name	p-value range	# Molecules
Cardiac Arrhythmia	2.77E-02 - 3.05E-04	2
Cardiac Dilatation	3.61E-02 - 8.84E-04	3
Cardiac Dysfunction	1.92E-02 - 9.66E-04	1
Cardiac Enlargement	1.92E-02 - 1.92E-02	1
Heart Failure	2.07E-01 - 2.07E-01	1
Hepatotoxicity		
Name	p-value range	# Molecules
Hepatocellular Carcinoma	6.88E-02 - 6.88E-02	3
Liver Hyperplasia/Hyperproliferation	3.38E-01 - 6.88E-02	12

Top Networks	
ID Associated Network Functions	Score
1 Cellular Function and Maintenance, Cell Death and Survival, Gastrointestinal Disease	15
2 Cellular Development, Cellular Growth and Proliferation, Hereditary Disorder	3
3 Cellular Assembly and Organization, DNA Replication, Recombination, and Repair, Cell Cycle	3
4 Cell-To-Cell Signaling and Interaction, Cellular Compromise, Cellular Function and Maintenance	3
5 Ophthalmic Disease, Organismal Injury and Abnormalities, Gastrointestinal Disease	2

Top Tox Lists		
Name	p-value	Overlap
Reversible Glomerulonephritis Biomarker Panel (Rat)	2.30E-02	4.2 % 1/24
Cardiac Hypertrophy	4.28E-02	0.6 % 2/344
Increases Transmembrane Potential of Mitochondria and Mitochondrial Membrane	4.73E-02	2.0 % 1/50
Hepatic Fibrosis	9.59E-02	1.0 % 1/104
Liver Proliferation	2.00E-01	0.4 % 1/230

Top Analysis-Ready Molecules		
Expr Fold Change +		
Molecules	Value	Chart
IGHD3-22	+7.645	
FMOD	+3.594	
IGHD3-3	+3.340	
DMMD*	+3.296	
IGKV3D-15	+3.270	
IGHV3-21	+3.265	
ABCA6	+3.232	
CLNK	+3.216	
TCL1A	+2.429	
mir-4659	+2.386	
Expr Fold Change +		
Molecules	Value	Chart
TARP*	+3.063	
IGKC*	+2.243	
TRGV4	+2.178	
IGHA1*	+2.159	
IGLV3-1	+2.156	
IGHD3-10	+2.099	
IGKV1D-33	+2.053	
TRGC2	+2.005	

Supplementary figure 1. Significant networks associated with DEGs in twins A vs B identified by IPA.

Networks were scored based on the number of genes participating in any particular system and some of their associated functions are listed. This picture is generated automatically by IPA software. (ABBREVIATIONS: DEGs = Differentially Expressed Genes; IPA = Ingenuity Pathways Analysis)