Supplementary Data for:

iSyTE 2.0: a database for expression-based gene discovery in the eye

Atul Kakrana[1,†], Andrian Yang[2,3,†], Deepti Anand[4], Djordje Djordjevic[2,3], Deepti Ramachandruni[4], Abhyudai Singh[1,5], Hongzhan Huang[1], Joshua W. K. Ho[2,3,*], Salil A. Lachke[1,5,*]

[1] Center for Bioinformatics and Computational Biology, University of Delaware, Newark, DE, USA

[2] Victor Chang Cardiac Research Institute, Darlinghurst, NSW, Australia

[3] The University of New South Wales, Sydney, NSW, Australia

[4] Department of Biological Sciences, University of Delaware, Newark, DE, USA

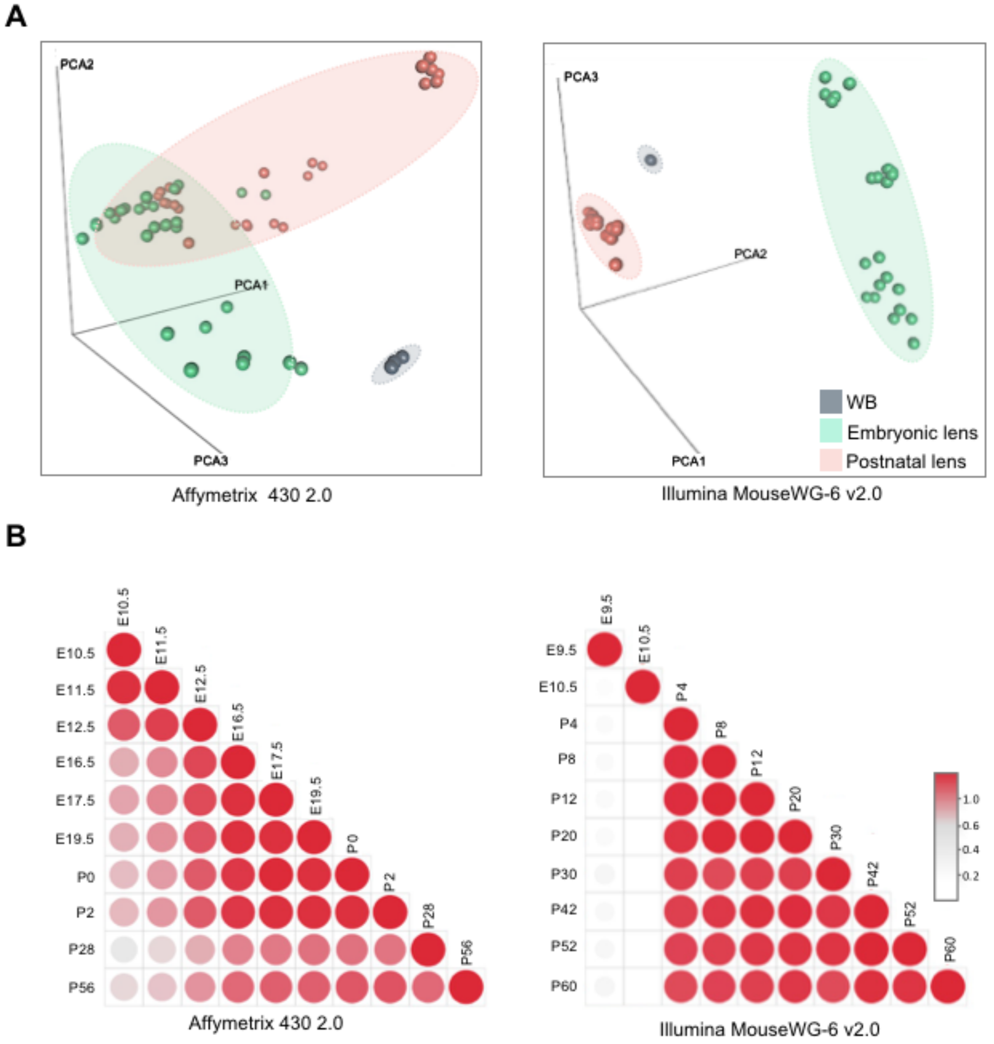
[5] Department of Electrical Engineering, University of Delaware, Newark, DE, USA

[†] The authors wish it to be known that, in their opinion, the first two authors should be regarded as joint First Authors.

[*] To whom correspondence should be addressed. Tel: +1 617 9599193; Fax: +1 302 8312281; E-mail: salil@udel.edu

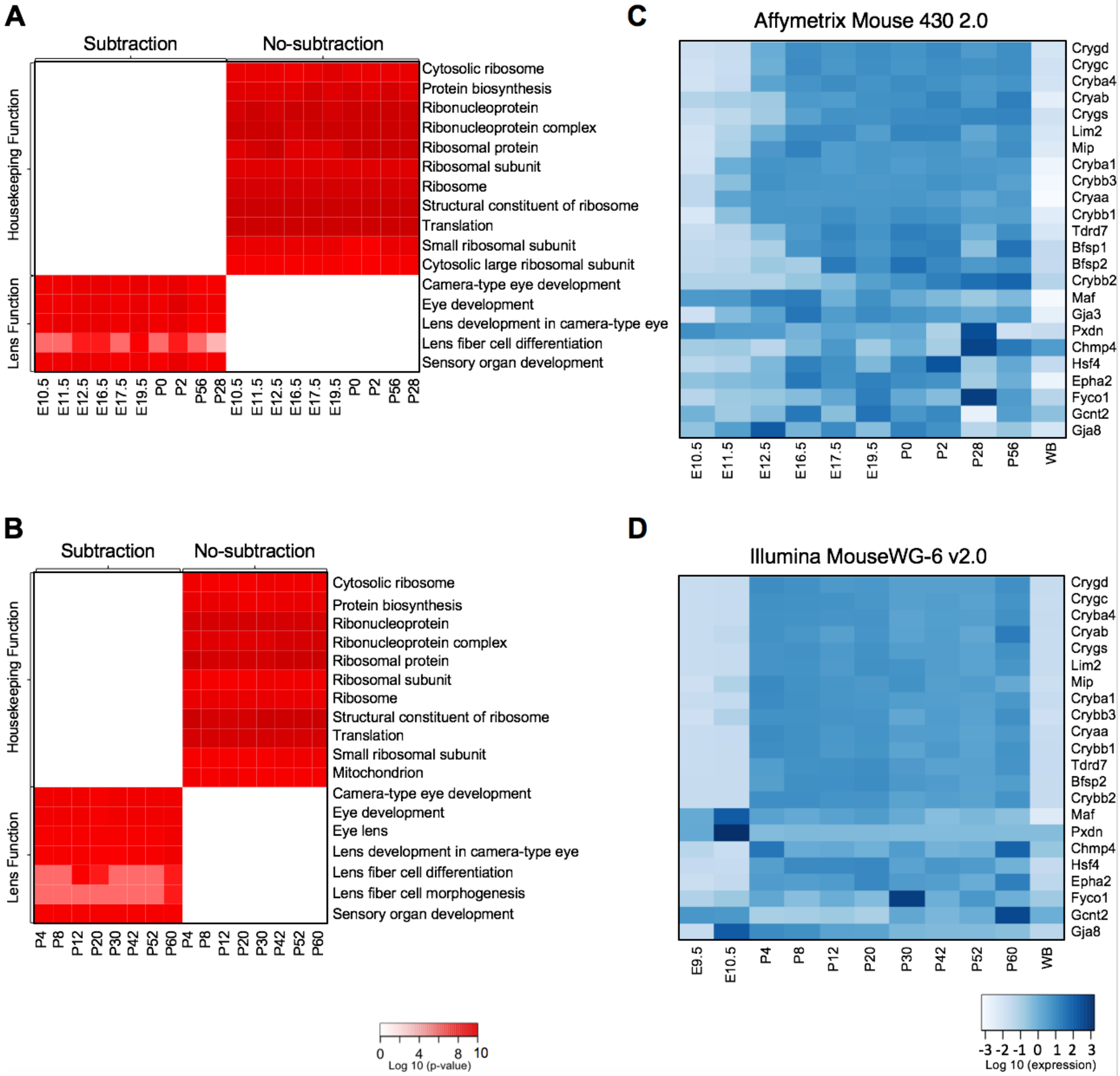
Correspondence may also be addressed to Joshua W. K. Ho. Tel: +61 2 9295 8645; Fax: +61 2 9295 8601; E-mail: j.ho@victorchang.edu.au

SUPPLEMENTARY FIGURE S1.



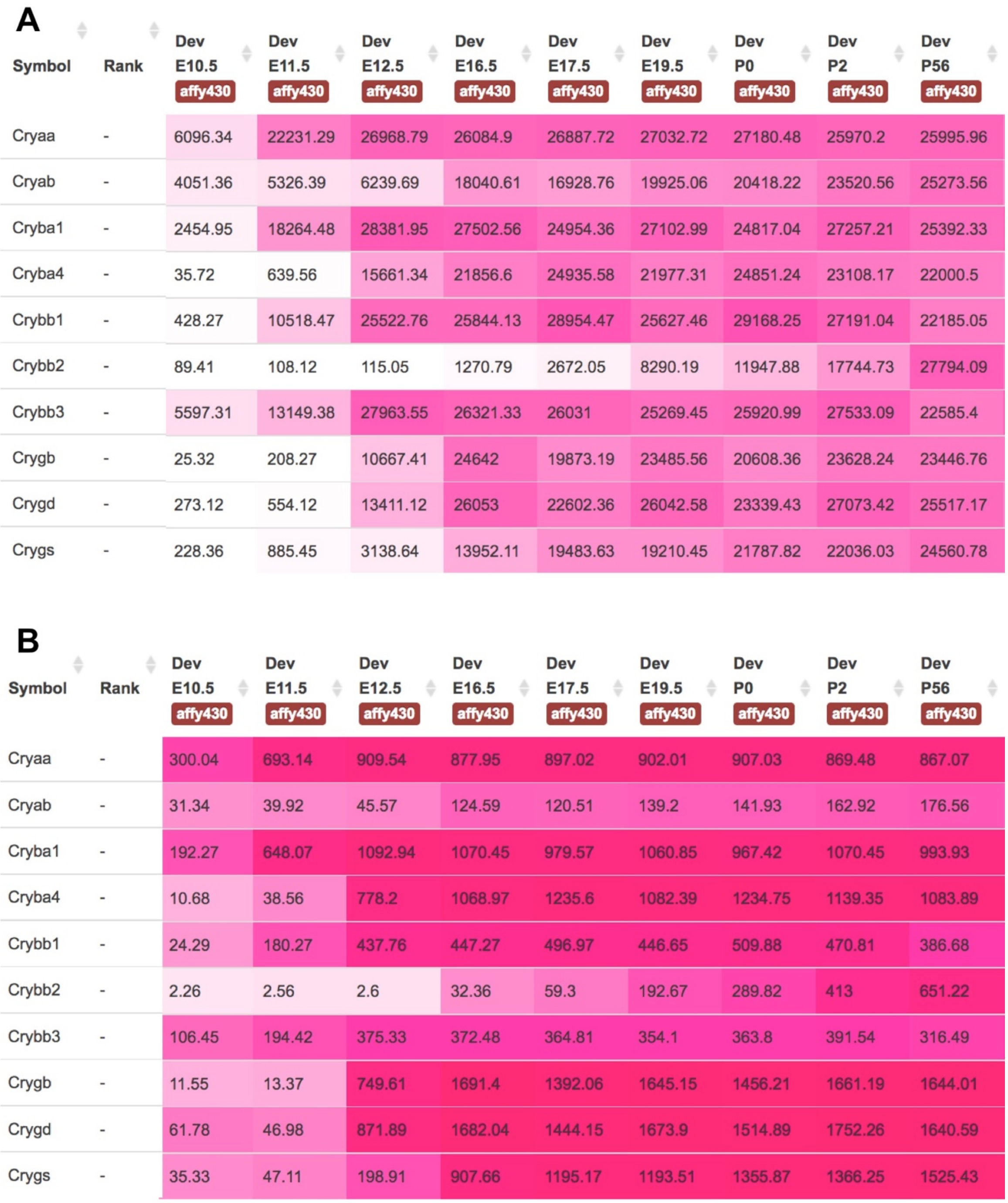
SUPPLEMENTARY FIGURE 1. Quality analysis of lens microarray datasets at embryonic, postnatal and adult stages. (**A**) Principle component analysis (PCA) of normalized data from Affymetrix Mouse 430 2.0 and Illumina MouseWG-6 v2.0 microarray platforms along with platform-specific embryonic whole body (WB) control datasets. The plots showed a segregation of data in three main groups corresponding to embryonic (green), postnatal (pink) and WB control (grey). The colored ellipsoid indicates specific data group. (**B**) Correlation dot plot representing Pearson's correlation values for all-versus-all comparisons of the normalized, processed data. The color and size of dots indicate degree of consensus between datasets.

SUPPLEMENTARY FIGURE S2.



SUPPLEMENTARY FIGURE 2. ***In silico*** **WB-subtraction identifies lens tissue-enriched genes in embryonic, postnatal and adult lenses.** The top 500 highly ranked genes with and without WB subtraction from (**A**) Affymetrix Mouse 430 2.0 datasets for isolated whole lens tissue at stages E10.5, E11.5, E12.5, E16.5, E17.5, E19.5, P0, P2, P56, and from isolated lens epithelium at P28, and (**B**) Illumina MouseWG-6 v2.0 datasets from isolated whole lens tissue at stages P4, P8, P12, P20, P30, P42, P52,P60, were tested for gene ontology (GO) functional categories. The obtained statistically significant GO categories (Fisher's exact test and Bonferroni corrected *p*-value ($p<0.05$)) with and without WB subtraction were visualized in the heat map. Heat map (red) intensity reflects statistically significant gene set enrichment. (**C**) Heat maps depicting expression of known genes linked to isolated (non-syndromic) human cataract cases in Affymetrix Mouse 430 2.0 lens datasets from stages E10.5, E11.5, E12.5, E16.5, E17.5, E19.5, P0, P2, P28 and P56 against the WB dataset and, (**D**) in the Illumina MouseWG-6 v2.0 lens datasets from stages E9.5, E10.5, P4, P8, P12, P20, P30, P42, P52, P60 against the WB dataset. Heat map (blue) intensity represents high to low gene expression.

SUPPLEMENTARY FIGURE S3.



A

Symbol	Rank	Dev E10.5 affy430	Dev E11.5 affy430	Dev E12.5 affy430	Dev E16.5 affy430	Dev E17.5 affy430	Dev E19.5 affy430	Dev P0 affy430	Dev P2 affy430	Dev P56 affy430
Cryaa	-	6096.34	22231.29	26968.79	26084.9	26887.72	27032.72	27180.48	25970.2	25995.96
Cryab	-	4051.36	5326.39	6239.69	18040.61	16928.76	19925.06	20418.22	23520.56	25273.56
Cryba1	-	2454.95	18264.48	28381.95	27502.56	24954.36	27102.99	24817.04	27257.21	25392.33
Cryba4	-	35.72	639.56	15661.34	21856.6	24935.58	21977.31	24851.24	23108.17	22000.5
Crybb1	-	428.27	10518.47	25522.76	25844.13	28954.47	25627.46	29168.25	27191.04	22185.05
Crybb2	-	89.41	108.12	115.05	1270.79	2672.05	8290.19	11947.88	17744.73	27794.09
Crybb3	-	5597.31	13149.38	27963.55	26321.33	26031	25269.45	25920.99	27533.09	22585.4
Crygb	-	25.32	208.27	10667.41	24642	19873.19	23485.56	20608.36	23628.24	23446.76
Crygd	-	273.12	554.12	13411.12	26053	22602.36	26042.58	23339.43	27073.42	25517.17
Crygs	-	228.36	885.45	3138.64	13952.11	19483.63	19210.45	21787.82	22036.03	24560.78

B

Symbol	Rank	Dev E10.5 affy430	Dev E11.5 affy430	Dev E12.5 affy430	Dev E16.5 affy430	Dev E17.5 affy430	Dev E19.5 affy430	Dev P0 affy430	Dev P2 affy430	Dev P56 affy430
Cryaa	-	300.04	693.14	909.54	877.95	897.02	902.01	907.03	869.48	867.07
Cryab	-	31.34	39.92	45.57	124.59	120.51	139.2	141.93	162.92	176.56
Cryba1	-	192.27	648.07	1092.94	1070.45	979.57	1060.85	967.42	1070.45	993.93
Cryba4	-	10.68	38.56	778.2	1068.97	1235.6	1082.39	1234.75	1139.35	1083.89
Crybb1	-	24.29	180.27	437.76	447.27	496.97	446.65	509.88	470.81	386.68
Crybb2	-	2.26	2.56	2.6	32.36	59.3	192.67	289.82	413	651.22
Crybb3	-	106.45	194.42	375.33	372.48	364.81	354.1	363.8	391.54	316.49
Crygb	-	11.55	13.37	749.61	1691.4	1392.06	1645.15	1456.21	1661.19	1644.01
Crygd	-	61.78	46.98	871.89	1682.04	1444.15	1673.9	1514.89	1752.26	1640.59
Crygs	-	35.33	47.11	198.91	907.66	1195.17	1193.51	1355.87	1366.25	1525.43

SUPPLEMENTARY FIGURE 3. Lens expression and enriched expression of cyrstallin genes in iSyTE 2.0. (**A**) Expression and (**B**) enrichment of ten crystallin-encoding genes in nine stages of lens (E10.5, E11.5, E12.5, E16.5, E17.5, E19.5, P0, P2, P56) as indicated by the processed Affymerix microarray datasets on the iSyTE 2.0 web-interface.

SUPPLEMENTARY FIGURE S4.

A

Symbol	Dev E10.5 affy430	Dev E11.5 affy430	Dev E12.5 affy430	Dev E16.5 affy430	Dev E17.5 affy430	Dev E19.5 affy430	Dev P0 affy430	Dev P2 affy430	Dev P56 affy430	Dev P28Epi affy430	Dev E15.5 affy430a	Dev P0a affy430a	Dev P0b affy430a
Chmp4b	-1.23	-1.31	-1.31	-1.15	-1.01	-1.22	-1.06	-1.2	1.09	1.28	-1.6	-1.71	-1.85
Fyco1	1.06	1.64	2.21	2.66	3.57	7.37	3.96	2.55	5.02	15.8	5.51	6.78	6.86
Gcnt2	1.01	-1.01	1.03	1.35	1.05	1.38	1.25	1.21	1.18	-1.32	6.6	15.26	11.73

Symbol	Dev E9.5 lumi1	Dev E10.25 lumi1	Dev E10.5 lumi2b	Dev E9.5 lumi2a	Dev E9.5 lumi2b	Dev E10.5 lumi2a	Dev P4 lumi2	Dev P8 lumi2	Dev P12 lumi2	Dev P20 lumi2	Dev P30 lumi2	Dev P42 lumi2	Dev P52 lumi2	Dev P60 lumi2
Chmp4b	-3.07	-2.12	-1.78	-1.54	-2	-2.02	2.71	1.48	1.54	1.37	1.8	1.33	1.41	3.14
Fyco1	-1.09	-1.44	1.06	-1.06	1.04	1.01	1.21	1.06	1.13	1.07	1.66	1.12	1.24	1.12
Gcnt2	1.54	-1.19	1.4	1.07	1.45	1.11	-1.13	-1.12	-1.1	-1.13	1.02	-1.03	1	1.32

B

Symbol	Brg1 E15.5 Mut affy430a	Pax6 P0 Mut affy430a	Tdrd7 P30 Mut lumi2
Chmp4b	1.01	1.08	1.51
Fyco1	-1.51	-1.14	1.47
Gcnt2	-1	1.65	-1.07

C

Symbol	Rank	Dev P0a affy430a
Gcnt2	1	15.26
Tfap2a	2	10.55
Nedd9	3	5.33
Hivep1	4	5.22
Gcm2	5	2.38
Pak1ip1	6	2.02
Slc35b3	7	1.68
Bloc1s5	8	1.45
Edn1	9	1.11
Adtrp	10	-1.43
Alpk3	11	-3.45

D

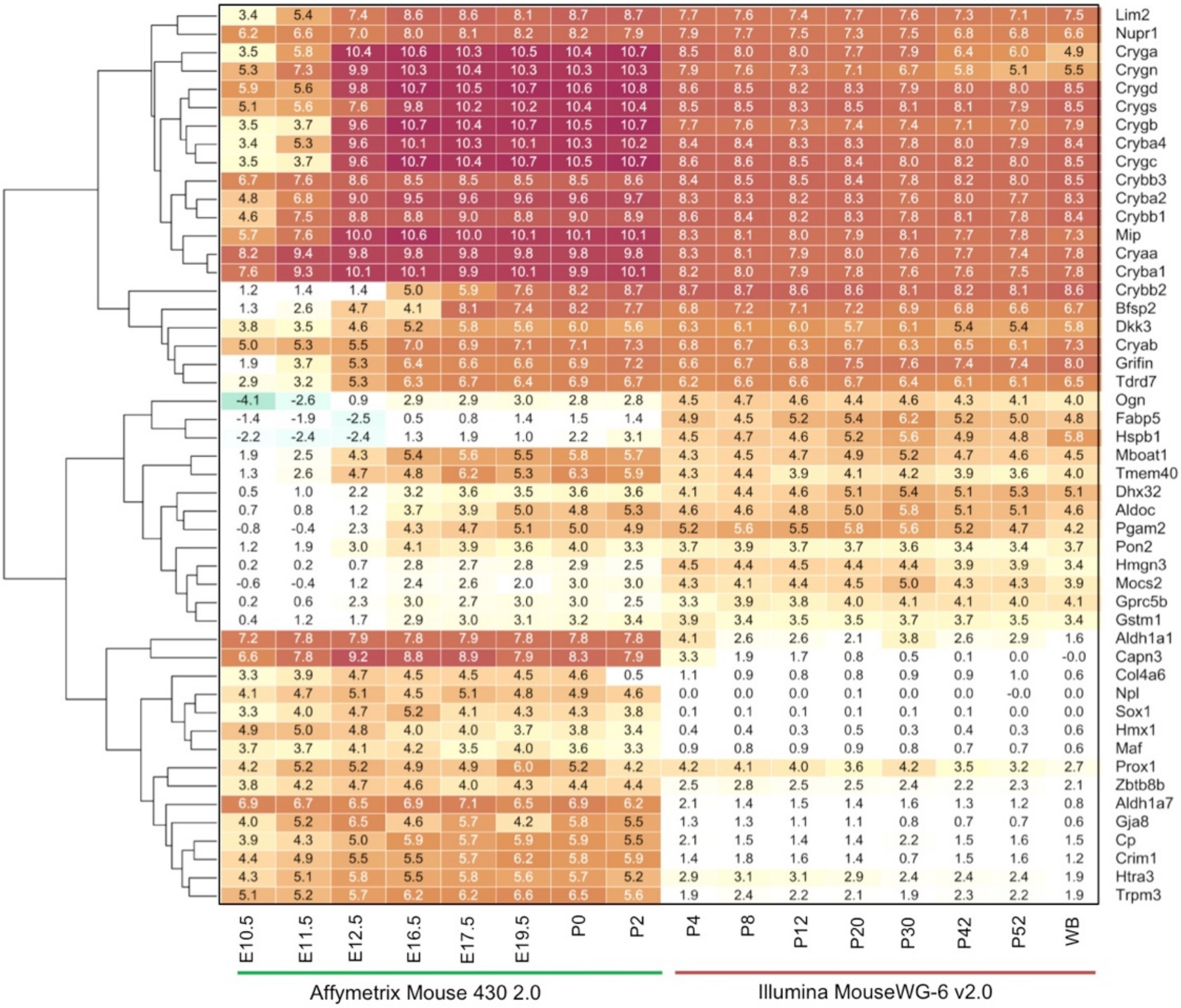
Symbol	Rank	Dev P56 affy430
Gnat1	1	21.84
Fyco1	2	5.02
Sema3b	3	4.67
Tcta	4	2.77
Nicn1	5	2.61
Zfp651	6	2.37
Slc38a3	7	2.2
Map4	8	2.15
Tmem42	9	1.96
Rnf123	10	1.53
Arih2	11	1.34
Cyb561d2	12	1.2
Dag1	13	1.12

E

Symbol	Rank	Dev E10.5 lumi2b	Dev P4 lumi2	Dev P8 lumi2	Dev P12 lumi2	Dev P20 lumi2	Dev P30 lumi2	Dev P42 lumi2	Dev P52 lumi2	Dev P60 lumi2
Gss	1	-1.03	9.03	8.04	6.56	6.93	5.75	6.17	5.85	5.53
Snta1	2	-1.02	4.83	3.17	3.78	4.8	6.57	5.84	5.14	5.59
Chmp4b	3	-1.78	2.71	1.48	1.54	1.37	1.8	1.33	1.41	3.14
Dynlrb1	4	-1.43	1.47	1.02	1.28	1.24	2.2	1.52	1.48	-1.16
1700003F12Rik	5	-1.05	1.79	1.79	1.68	1.57	1.22	1.19	1.11	1.07
Acss2	6	-1.22	-1.24	-1.13	-1.14	-1.11	-1.15	-1.14	-1.13	-1.16

SUPPLEMENTARY FIGURE 4. Analysis of the human non-syndromic cataract genes *Chmp4b*, *Fyco1*, *Gcnt2* in iSyTE 2.0. (**A**) Lens-enriched expression of the three cataract-linked genes in Affymetrix and Illumina microarrays. (**B**) Differential expression of *Chmp4b*, *Fyco1*, *Gcnt2* in *Brg1*, *Pax6* and *Tdrd7* mutant lenses. (**C-E**) Improved ranking of *Gcnt2*, *Fyco1* and *Chmp4b* in the original mapped intervals linked to cataract.

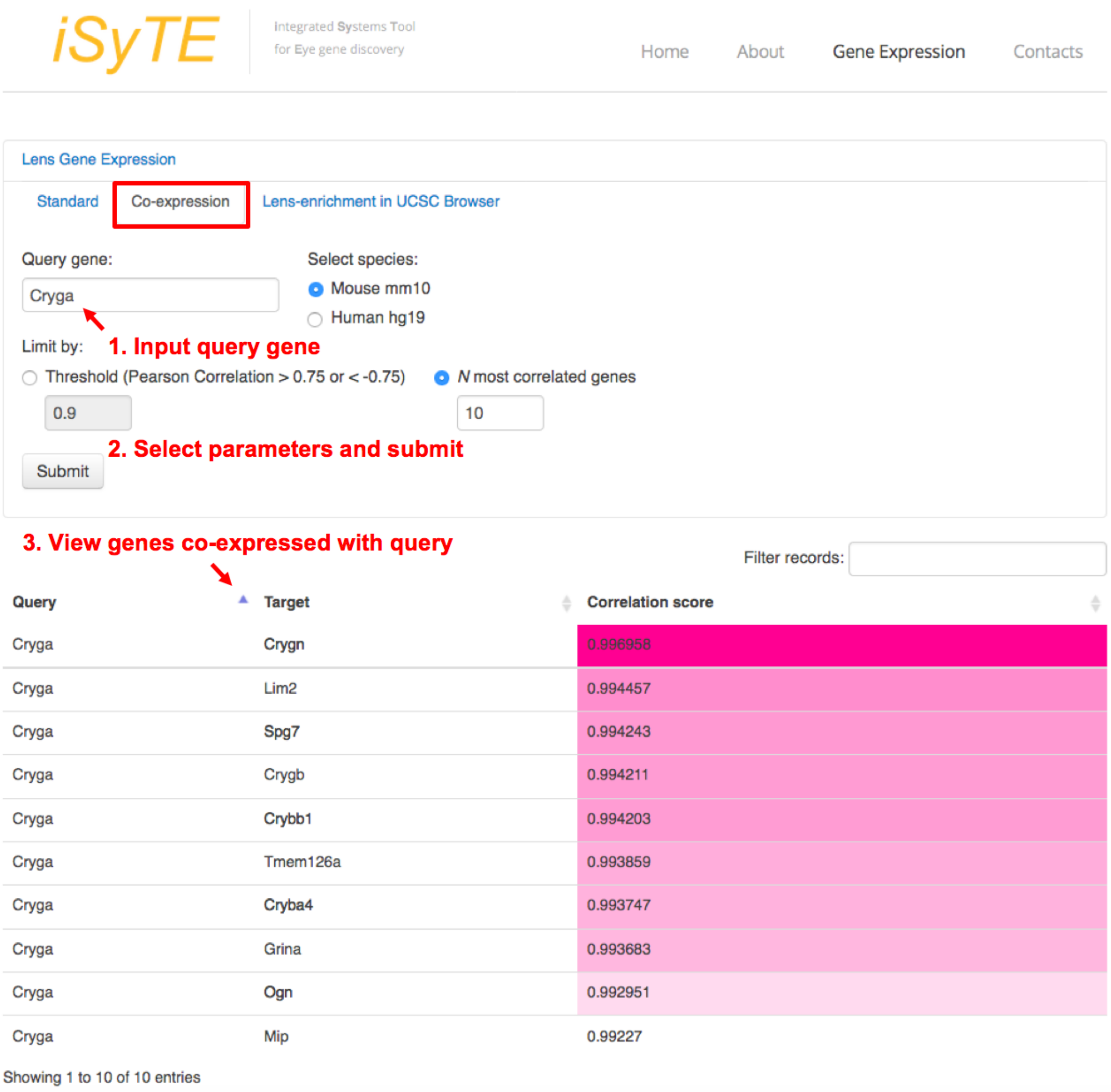
SUPPLEMENTARY FIGURE S5.



	E10.5	E11.5	E12.5	E16.5	E17.5	E19.5	P0	P2	P4	P8	P12	P20	P30	P42	P52	WB
Lim2	3.4	5.4	7.4	8.6	8.6	8.1	8.7	8.7	7.7	7.6	7.4	7.7	7.6	7.3	7.1	7.5
Nupr1	6.2	6.6	7.0	8.0	8.1	8.2	8.2	7.9	7.9	7.7	7.5	7.3	7.5	6.8	6.8	6.6
Cryga	3.5	5.8	10.4	10.6	10.3	10.5	10.4	10.7	8.5	8.0	8.0	7.7	7.9	6.4	6.0	4.9
Crygn	5.3	7.3	9.9	10.3	10.4	10.3	10.3	10.3	7.9	7.6	7.3	7.1	6.7	5.8	5.1	5.5
Crygd	5.9	5.6	9.8	10.7	10.5	10.7	10.6	10.8	8.6	8.5	8.2	8.3	7.9	8.0	8.0	8.5
Crygs	5.1	5.6	7.6	9.8	10.2	10.2	10.4	10.4	8.5	8.5	8.3	8.5	8.1	8.1	7.9	8.5
Crygb	3.5	3.7	9.6	10.7	10.4	10.7	10.5	10.7	7.7	7.6	7.3	7.4	7.4	7.1	7.0	7.9
Cryba4	3.4	5.3	9.6	10.1	10.3	10.1	10.3	10.2	8.4	8.4	8.3	8.3	7.8	8.0	7.9	8.4
Crygc	3.5	3.7	9.6	10.7	10.4	10.7	10.5	10.7	8.6	8.6	8.5	8.4	8.0	8.2	8.0	8.5
Crybb3	6.7	7.6	8.6	8.5	8.5	8.5	8.5	8.6	8.4	8.5	8.5	8.4	7.8	8.2	8.0	8.5
Cryba2	4.8	6.8	9.0	9.5	9.6	9.6	9.6	9.7	8.3	8.3	8.2	8.3	7.6	8.0	7.7	8.3
Crybb1	4.6	7.5	8.8	8.8	9.0	8.8	9.0	8.9	8.6	8.4	8.2	8.3	7.8	8.1	7.8	8.4
Mip	5.7	7.6	10.0	10.6	10.0	10.1	10.1	10.1	8.3	8.1	8.0	7.9	8.1	7.7	7.8	7.3
Cryaa	8.2	9.4	9.8	9.8	9.8	9.8	9.8	9.8	8.3	8.1	7.9	8.0	7.6	7.7	7.4	7.8
Cryba1	7.6	9.3	10.1	10.1	9.9	10.1	9.9	10.1	8.2	8.0	7.9	7.8	7.6	7.6	7.5	7.8
Crybb2	1.2	1.4	1.4	5.0	5.9	7.6	8.2	8.7	8.7	8.7	8.6	8.6	8.1	8.2	8.1	8.6
Bfsp2	1.3	2.6	4.7	4.1	8.1	7.4	8.2	7.7	6.8	7.2	7.1	7.2	6.9	6.8	6.6	6.7
Dkk3	3.8	3.5	4.6	5.2	5.8	5.6	6.0	5.6	6.3	6.1	6.0	5.7	6.1	5.4	5.4	5.8
Cryab	5.0	5.3	5.5	7.0	6.9	7.1	7.1	7.3	6.8	6.7	6.3	6.7	6.3	6.5	6.1	7.3
Grifin	1.9	3.7	5.3	6.4	6.6	6.6	6.9	7.2	6.6	6.7	6.8	7.5	7.6	7.4	7.4	8.0
Tdrd7	2.9	3.2	5.3	6.3	6.7	6.4	6.9	6.7	6.2	6.6	6.6	6.7	6.4	6.1	6.1	6.5
Ogn	-4.1	-2.6	0.9	2.9	2.9	3.0	2.8	2.8	4.5	4.7	4.6	4.4	4.6	4.3	4.1	4.0
Fabp5	-1.4	-1.9	-2.5	0.5	0.8	1.4	1.5	1.4	4.9	4.5	5.2	5.4	6.2	5.2	5.0	4.8
Hspb1	-2.2	-2.4	-2.4	1.3	1.9	1.0	2.2	3.1	4.5	4.7	4.6	5.2	5.6	4.9	4.8	5.8
Mboat1	1.9	2.5	4.3	5.4	5.6	5.5	5.8	5.7	4.3	4.5	4.7	4.9	5.2	4.7	4.6	4.5
Tmem40	1.3	2.6	4.7	4.8	6.2	5.3	6.3	5.9	4.3	4.4	3.9	4.1	4.2	3.9	3.6	4.0
Dhx32	0.5	1.0	2.2	3.2	3.6	3.5	3.6	3.6	4.1	4.4	4.6	5.1	5.4	5.1	5.3	5.1
Aldoc	0.7	0.8	1.2	3.7	3.9	5.0	4.8	5.3	4.6	4.6	4.8	5.0	5.8	5.1	5.1	4.6
Pgam2	-0.8	-0.4	2.3	4.3	4.7	5.1	5.0	4.9	5.2	5.6	5.5	5.8	5.6	5.2	4.7	4.2
Pon2	1.2	1.9	3.0	4.1	3.9	3.6	4.0	3.3	3.7	3.9	3.7	3.7	3.6	3.4	3.4	3.7
Hmgn3	0.2	0.2	0.7	2.8	2.7	2.8	2.9	2.5	4.5	4.4	4.5	4.4	4.4	3.9	3.9	3.4
Mocs2	-0.6	-0.4	1.2	2.4	2.6	2.0	3.0	3.0	4.3	4.1	4.4	4.5	5.0	4.3	4.3	3.9
Gprc5b	0.2	0.6	2.3	3.0	2.7	3.0	3.0	2.5	3.3	3.9	3.8	4.0	4.1	4.1	4.0	4.1
Gstm1	0.4	1.2	1.7	2.9	3.0	3.1	3.2	3.4	3.9	3.4	3.5	3.5	3.7	3.7	3.5	3.4
Aldh1a1	7.2	7.8	7.9	7.8	7.9	7.8	7.8	7.8	4.1	2.6	2.6	2.1	3.8	2.6	2.9	1.6
Capn3	6.6	7.8	9.2	8.8	8.9	7.9	8.3	7.9	3.3	1.9	1.7	0.8	0.5	0.1	0.0	-0.0
Col4a6	3.3	3.9	4.7	4.5	4.5	4.5	4.6	0.5	1.1	0.9	0.8	0.8	0.9	0.9	1.0	0.6
Npl	4.1	4.7	5.1	4.5	5.1	4.8	4.9	4.6	0.0	0.0	0.0	0.1	0.0	0.0	-0.0	0.0
Sox1	3.3	4.0	4.7	5.2	4.1	4.3	4.3	3.8	0.1	0.1	0.1	0.1	0.1	0.1	0.0	0.0
Hmx1	4.9	5.0	4.8	4.0	4.0	3.7	3.8	3.4	0.4	0.4	0.3	0.5	0.3	0.4	0.3	0.6
Maf	3.7	3.7	4.1	4.2	3.5	4.0	3.6	3.3	0.9	0.8	0.9	0.9	0.8	0.7	0.7	0.6
Prox1	4.2	5.2	5.2	4.9	4.9	6.0	5.2	4.2	4.2	4.1	4.0	3.6	4.2	3.5	3.2	2.7
Zbtb8b	3.8	4.2	4.7	4.6	4.0	4.3	4.4	4.4	2.5	2.8	2.5	2.5	2.4	2.2	2.3	2.1
Aldh1a7	6.9	6.7	6.5	6.9	7.1	6.5	6.9	6.2	2.1	1.4	1.5	1.4	1.6	1.3	1.2	0.8
Gja8	4.0	5.2	6.5	4.6	5.7	4.2	5.8	5.5	1.3	1.3	1.1	1.1	0.8	0.7	0.7	0.6
Cp	3.9	4.3	5.0	5.9	5.7	5.9	5.9	5.5	2.1	1.5	1.4	1.4	2.2	1.5	1.6	1.5
Crim1	4.4	4.9	5.5	5.5	5.7	6.2	5.8	5.9	1.4	1.8	1.6	1.4	0.7	1.5	1.6	1.2
Htra3	4.3	5.1	5.8	5.5	5.8	5.6	5.7	5.2	2.9	3.1	3.1	2.9	2.4	2.4	2.4	1.9
Trpm3	5.1	5.2	5.7	6.2	6.2	6.6	6.5	5.6	1.9	2.4	2.2	2.1	1.9	2.3	2.2	1.9

SUPPLEMENTARY FIGURE 5. Derivation of a molecular signature gene set for mouse embryonic and postnatal lens. Genes enriched (FC ≥ 10 fold) in embryonic or postnatal stages of lens development. Because a large number of embryonic lens microarrays were performed on the Affymetrix platform and a large number of postnatal lens microarrays were performed on the Illumina platform, these platform-specific datasets were analyzed to infer embryonic and postnatal lens molecular signatures, respectively. Values represent lens enrichment in log2 scale.

SUPPLEMENTARY FIGURE S6.



Query gene: Cryga

Select species:
● Mouse mm10
○ Human hg19

Limit by:
○ Threshold (Pearson Correlation > 0.75 or < -0.75) 0.9
● *N* most correlated genes 10

1. Input query gene

2. Select parameters and submit

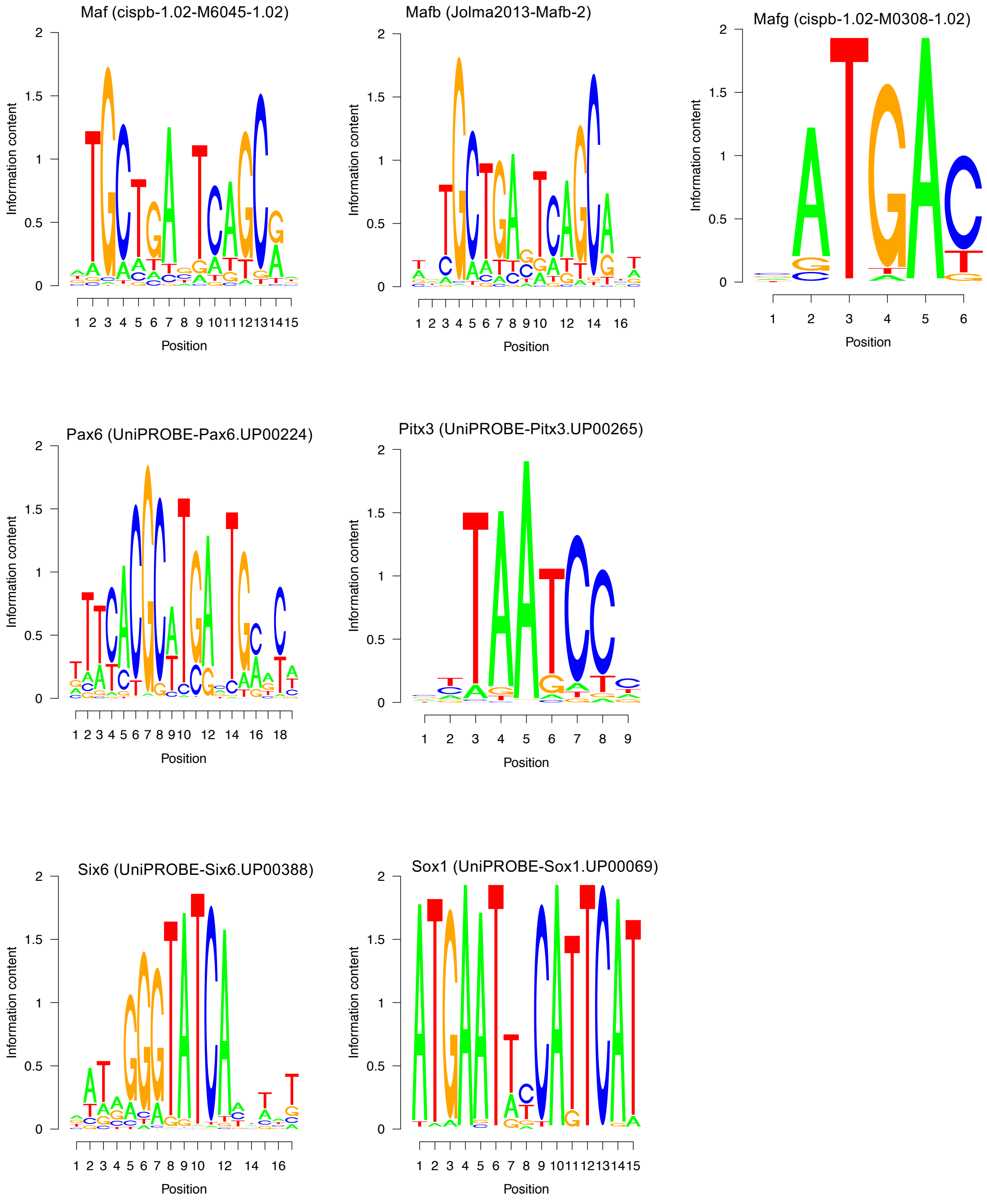
3. View genes co-expressed with query

Query	Target	Correlation score
Cryga	Crygn	0.996958
Cryga	Lim2	0.994457
Cryga	Spg7	0.994243
Cryga	Crygb	0.994211
Cryga	Crybb1	0.994203
Cryga	Tmem126a	0.993859
Cryga	Cryba4	0.993747
Cryga	Grina	0.993683
Cryga	Ogn	0.992951
Cryga	Mip	0.99227

Showing 1 to 10 of 10 entries

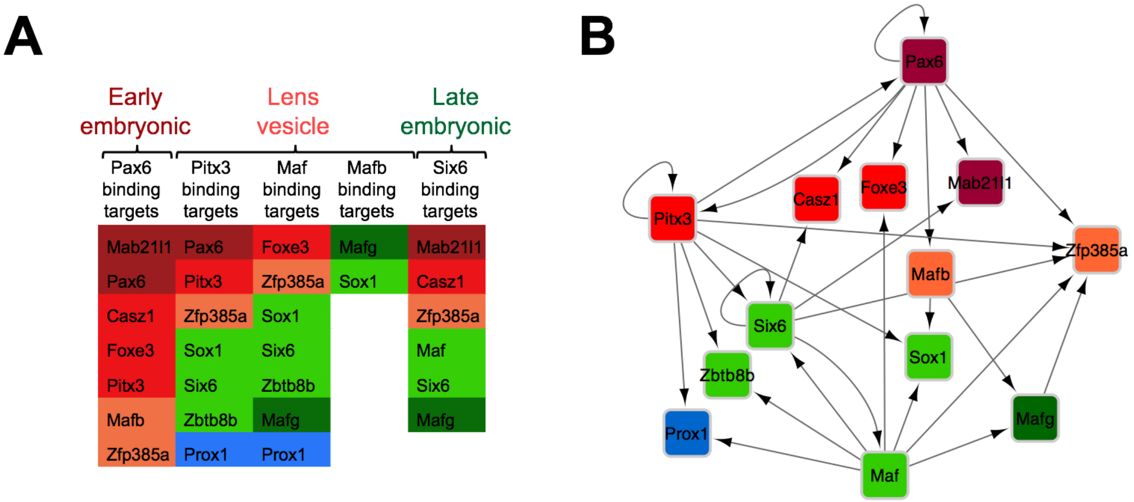
SUPPLEMENTARY FIGURE 6. iSyTE 2.0 has a new feature to determine co-expressed genes. Candidate genes that exhibit co-expression with a query gene can be searched using the Co-expression feature. This can be achieved by entering the candidate gene under the "query gene" (*Cryga* in the example above), and selecting the threshold for Pearson Correlation and the top number of correlated genes to be visualized as shown in steps 1-3.

SUPPLEMENTARY FIGURE S7.



SUPPLEMENTARY FIGURE 7. Transcription factor-Motifs used in expression-based gene regulatory network analysis. Transcription factor binding motifs for Maf, Mafb, Mafg, Pax6, Pitx3, Six6 and Sox1 were obtained from MotifDB and used to search the -2500bp upstream of the transcription start site in the 528 genes from the clusters identified by SOTA.

SUPPLEMENTARY FIGURE S8.



Early embryonic	Lens vesicle			Late embryonic
Pax6 binding targets	Pitx3 binding targets	Maf binding targets	Mafb binding targets	Six6 binding targets
Mab21l1	Pax6	Foxe3	Mafg	Mab21l1
Pax6	Pitx3	Zfp385a	Sox1	Casz1
Casz1	Zfp385a	Sox1		Zfp385a
Foxe3	Sox1	Six6		Maf
Pitx3	Six6	Zbtb8b		Six6
Mafb	Zbtb8b	Mafg		Mafg
Zfp385a	Prox1	Prox1		

SUPPLEMENTARY FIGURE 8. Transcription factor regulatory network predicted using iSyTE 2.0. Regulatory connections between the transcription factors in the SOTA clusters were investigated for new insights into the temporal dynamics of their expression and that of their targets in the lens. (**A**) Transcription factor binding motif analysis for the proteins Pax6, Pitx3, Maf, Mafb and Six6 identifies putative binding sites in the -2500bp region upstream of the transcription start site within other transcription factor-encoding genes present in six clusters. Notably, we find Pax6 binding sites upstream of majority of the transcription factor genes that exhibit peak expression early in lens development. Indeed, six of nineteen potential transcription factor targets of Pax6 are in the early lens development, lens vesicle or primary fiber differentiation clusters. Conversely, the lens vesicle cluster transcription factors Pitx3, Maf, and Mafb as well as the late embryonic cluster transcription factors Six6 have binding sites upstream of other transcription factor genes, majority of which exhibit peak expression in lens vesicle stage and beyond. (**B**) Network representation of transcription factors based on the presence of their binding motif in other transcription factors expressed in the lens. This analysis suggests their temporal hierarchy in the lens.

Supplementary Table S1. Mouse lens microarray datasets used in iSyTE 2.0.

Dataset	Mouse Stage	GEO accession	Tissue	Genotype	Microarray platform	Reference
Development	E9.5	GSE49227	Lens placode	Wild-type	Illumina WG-6 v1.1	(1)
Development	E9.5	GSE49223	Lens placode	Wild-type	Illumina WG-6 v2.0	(2)
Development	E9.5	GSE49229	Lens placode	Wild-type	Illumina WG-6 v2.0	(1)
Development	E10.25	GSE49216	Lens pit	Wild-type	Illumina WG-6 v1.1	(1)
Development	E10.5	GSE49218	Lens pit	Wild-type	Illumina WG-6 v2.0	(2)
Development	E10.5	GSE32334	Lens pit	Wild-type	Affymetrix 430 2.0	(3)
Development	E11.5	GSE32334	Lens vesicle	Wild-type	Affymetrix 430 2.0	(3)
Development	E12.5	GSE32334	Lens	Wild-type	Affymetrix 430 2.0	(3)
Development	E15.5	GSE22322	Lens	Wild-type	Affymetrix 430A 2.0	(4)
Development	E16.5	GSE47694	Lens	Wild-type	Affymetrix 430 2.0	(5)
Development	E17.5	GSE16533	Lens	*E2f2*-/- (no lens phenotype)	Affymetrix 430 2.0	(6)

Development	E19.5	GSE31643	Lens	*Notch2*$^{loxP:loxP}$	Affymetrix 430 2.0	(7)
Development	P0	GSE22362	Lens	Wild-type	Affymetrix 430A 2.0	(4)
Development	P0	GSE16533	Lens	*E2f2*-/- (no lens phenotype)	Affymetrix 430 2.0	(6)
Development	P2	GSE9711	Lens	Wild-type	Affymetrix 430 2.0	(8)
Development	P4	GSE25775	Lens	*Tdrd7*+/-	Illumina WG-6 v2.0	(9)
Development	P8	GSE100136	Lens	Wild-type	Illumina WG-6 v2.0	This study
Development	P12	GSE100136	Lens	Wild-type	Illumina WG-6 v2.0	This study
Development	P20	GSE100136	Lens	Wild-type	Illumina WG-6 v2.0	This study
Development	P28	GSE13402	Lens epithelium	Wild-type	Affymetrix 430 2.0	(10)
Development	P30	GSE25776	Lens	*Tdrd7*+/-	Illumina WG-6 v2.0	(9)
Development	P42	GSE100136	Lens	Wild-type	Illumina WG-6 v2.0	This study
Development	P52	GSE100136	Lens	Wild-type	Illumina WG-6 v2.0	This study
Development	P56	GSE47694	Lens	Wild-type	Affymetrix 430 2.0	(5)

Development	P60	GSE65500	Lens	*Mafg+/-:Mafk+/-*	Illumina WG-6 v2.0	(11)
Mutant	E9.5	GSE49227	Lens placode	*Le-Cre:Pax6*$^{loxP:loxP}$	Illumina WG-6 v1.1	(1)
Mutant	E9.5	GSE49223	Lens placode	*Le-Cre:Cbp*$^{loxP/loxP}$*:p300*$^{loxP/loxP}$	Illumina WG-6 v2.0	(2)
Mutant	E9.5	GSE49229	Lens placode	*Le-Cre:Pax6*$^{loxP:loxP}$	Illumina WG-6 v2.0	(1)
Mutant	E10.25	GSE49216	Lens pit	*Le-Cre:Pax6*$^{loxP:loxP}$	Illumina WG-6 v1.1	(1)
Mutant	E10.5	GSE49218	Lens pit	*Le-Cre:Cbp*$^{loxP/loxP}$*:p300*$^{loxP/loxP}$	Illumina WG-6 v2.0	(2)
Mutant	E15.5	GSE22322	Lens	*Brg1* dominant -ve	Affymetrix 430A 2.0	(4)
Mutant	E16.5	GSE47694	Lens	*Le-Cre:Klf4*$^{loxP:loxP}$	Affymetrix 430 2.0	(5)
Mutant	E17.5	GSE16533	Lens	*Cry-Cre:E2f1-/-:E2F2-/-:E2F3-/-*	Affymetrix 430 2.0	(6)
Mutant	E19.5	GSE31643	Lens	*Le-Cre:Notch2*$^{loxP:loxP}$	Affymetrix 430 2.0	(7)
Mutant	P0	GSE22362	Lens	*Hsf4-/-*	Affymetrix 430A 2.0	(4)
Mutant	P0	GSE16533	Lens	*Cry-Cre:E2f1-/-:E2F2-/-:E2F3-/-*	Affymetrix 430 2.0	(6)
Mutant	P2	GSE9711	Lens	*Cryaa-Foxe3* overexpress.	Affymetrix 430 2.0	(8)

Mutant	P4	GSE25775	Lens	*Tdrd7*-/-	Illumina WG-6 v2.0	(9)
Mutant	P28	GSE13402	Lens epithelium	*Sparc*-/-	Affymetrix 430 2.0	(10)
Mutant	P30	GSE25776	Lens	*Tdrd7*-/-	Illumina WG-6 v2.0	(9)
Mutant	P56	GSE47694	Lens	*Le-Cre:Klf4*$^{loxP:loxP}$	Affymetrix 430 2.0	(5)
Mutant	P60	GSE65500	Lens	*Mafg*-/-:*Mafk*+/-	Illumina WG-6 v2.0	(11)

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Supplementary Table S2. Expression-based clustering analysis of Affymetrix genes

Gene.Symbol	res.clust	Expression_E10.5	Expression_E11.5	Expression_E12.5	Expression_E16.5	Expression_E17.5	Expression_E19.5	Expression_P0	Expression_P2	Expression_P56	Enrichment_E10.5	Enrichment_E11.5	Enrichment_E12.5	Enrichment_E16.5	Enrichment_E17.5	Enrichment_E19.5	Enrichment_P0	Enrichment_P2	Enrichment_P56
Nupr1	1	1956.9	2464.7	3493.2	6979.6	7155.8	7761.3	7356.5	6505.3	10098.6	74.0	97.9	124.8	253.0	279.2	298.8	286.0	232.5	388.8
Grifin	1	158.9	788.4	2567.1	5023.6	5977.6	6204.7	7366.0	9442.2	17842.4	3.8	12.7	40.1	85.4	96.3	100.4	118.9	152.0	288.4
Sox2ot	1	229.3	351.7	481.3	202.5	503.2	719.7	651.7	656.5	1123.4	23.9	32.1	41.1	26.5	46.0	66.2	60.2	60.8	103.3
Cela1	1	386.5	518.5	1484.5	2347.4	2409.9	860.4	2491.5	1922.2	3120.6	11.5	15.7	42.6	65.7	70.0	24.9	72.2	54.9	90.4
Crybb2	1	89.4	108.1	115.0	1270.8	2672.0	8290.2	11947.9	17744.7	27794.1	2.3	2.6	2.6	32.4	59.3	192.7	289.8	413.0	651.2
Smco3	1	26.6	45.9	84.8	1048.3	1452.1	1225.2	1605.1	1784.5	2395.3	2.2	3.5	6.8	89.4	122.9	101.7	134.1	153.6	199.5
Clu	1	2023.0	2827.6	4907.8	7319.4	4053.7	4863.9	7096.4	8225.6	17433.7	8.9	10.4	21.7	33.2	18.0	21.9	28.7	37.7	78.6
Mboat1	1	138.7	329.4	1030.6	2089.8	2417.4	2238.7	2862.9	2709.0	5531.9	3.6	5.6	19.7	42.3	49.5	45.3	57.7	52.9	111.9
Gpr160	1	34.1	84.1	400.4	942.2	1543.7	829.2	1625.7	836.4	2788.7	2.0	3.3	19.1	43.5	72.4	39.2	75.2	40.5	131.4
Anxa1	1	2615.1	1784.2	1347.0	2686.0	2702.6	2096.5	2835.4	3050.6	7572.4	17.6	11.5	9.2	18.5	17.2	14.4	19.3	21.8	52.0
E130218I03Rik	1	185.3	167.5	155.3	201.0	205.2	180.9	217.3	75.3	1511.3	12.9	8.5	10.0	13.7	14.0	12.3	14.1	6.6	102.5
Ass1	1	1522.1	1646.5	822.5	1270.4	841.5	586.5	1183.9	2614.9	3086.2	23.4	26.0	12.4	17.8	11.5	7.9	15.9	36.3	43.3
Folr1	1	410.6	276.1	235.6	616.7	505.5	974.1	686.4	1358.3	2336.7	9.6	6.7	5.8	14.6	11.5	23.5	16.4	33.9	56.5
Cyp4v3	1	246.2	214.7	210.0	412.2	441.5	337.3	484.7	327.5	845.0	8.4	6.3	7.0	15.1	15.4	11.6	16.1	11.4	29.2
S100a4	1	75.6	43.7	90.3	1202.9	2560.1	2850.4	3802.8	3009.8	5760.6	1.7	1.0	2.8	31.1	67.5	74.4	99.6	79.7	149.3
Dnase2b	1	16.0	13.0	12.6	1260.5	1246.8	779.5	1752.7	1663.6	4441.2	1.4	-1.1	1.0	94.5	92.9	56.8	125.7	107.2	324.7
Metrnl	1	209.8	288.9	470.5	1057.8	1342.1	1108.4	1640.5	1117.2	4682.4	2.8	3.9	6.4	14.0	17.8	14.6	21.7	15.8	61.8
Dapl1	1	64.7	82.4	69.2	371.8	545.5	1696.4	465.5	1715.1	8734.5	1.8	2.0	1.9	10.5	15.9	47.9	11.7	54.4	246.1
Aldoc	1	215.5	249.9	314.3	1847.3	2162.9	4608.2	3928.1	5431.1	11351.0	1.6	1.8	2.3	13.0	15.3	32.8	28.0	40.2	81.0
Dtna	1	136.4	142.8	159.5	378.0	333.1	517.3	420.4	621.2	1673.8	4.4	4.1	5.0	11.7	11.4	16.7	13.7	20.0	54.1
Gpr137b-ps	1	634.2	895.2	1771.3	2153.7	1876.4	1949.5	2095.8	2044.7	3703.3	3.1	4.4	9.9	12.7	10.9	11.2	12.0	11.8	21.3

Necab1	1	70.3	32.3	32.1	82.7	96.6	87.9	123.8	83.6	348.0	6.2	3.4	3.0	7.7	8.7	8.2	11.5	7.9	32.5
Ngef	1	59.2	96.9	186.6	476.5	605.8	604.6	845.0	648.0	1400.5	1.5	2.5	4.9	12.5	16.5	16.6	23.0	17.4	38.6
Kcnj12	1	137.2	242.6	279.6	197.2	247.9	202.9	260.1	140.4	287.8	5.0	7.9	10.3	8.1	9.6	7.9	9.7	5.9	11.2
Myo6	1	196.3	301.2	296.4	308.1	322.9	329.5	363.4	214.1	532.1	4.7	5.6	7.0	7.0	7.0	7.6	7.7	4.9	12.3
2310030 G06Rik	1	153.8	104.8	82.1	155.0	164.7	207.4	228.2	148.9	1313.7	4.9	2.9	3.0	5.6	5.1	7.4	8.3	5.3	46.7
Dhx32	1	236.6	370.3	842.1	1705.9	2134.4	1994.1	2280.2	2267.8	5853.5	1.4	2.0	4.6	9.1	12.0	10.9	12.4	12.4	32.1
Ablim1	1	593.3	526.4	605.1	715.4	626.2	785.6	619.0	634.5	1092.9	4.8	4.6	5.5	6.4	5.6	7.0	5.2	5.8	9.7
P4ha1	1	959.7	946.0	956.9	1368.1	1524.9	2026.9	1008.3	842.8	2174.8	4.2	4.1	4.6	6.3	7.2	9.1	4.7	3.9	9.7
Fam134b	1	336.3	287.0	289.0	619.6	487.0	540.5	537.8	250.6	925.7	4.2	2.7	3.3	7.9	6.1	6.9	6.6	3.6	11.8
Ndrg1	1	34.0	26.4	127.5	2492.4	3020.5	4242.1	5322.6	3650.8	10818.6	-2.6	-4.3	1.0	20.6	23.7	34.3	44.0	29.4	87.4
Gstm1	1	251.0	455.3	665.7	1424.3	1698.7	1707.3	1884.1	2117.8	3579.5	1.3	2.3	3.3	7.2	7.9	8.5	9.1	10.5	17.7
Col4a4	1	14.4	17.2	16.9	96.7	263.4	590.3	847.9	726.0	1925.8	-1.2	-1.2	-1.0	5.8	12.7	30.3	42.7	38.0	100.6
Dct	1	65.0	148.6	84.3	89.4	293.4	604.7	169.0	549.6	973.7	1.6	3.9	2.2	2.2	6.7	14.6	4.2	13.9	23.4
Arsi	1	309.4	348.8	308.8	395.7	626.7	223.6	597.0	77.1	649.4	4.6	4.6	4.3	5.4	8.5	3.3	8.4	1.1	9.5
Lgals3	1	19.1	42.8	31.9	424.2	302.3	445.7	450.3	767.5	4834.2	-1.3	1.2	1.4	13.9	9.6	13.9	14.1	23.1	151.2
Fam169a	1	335.9	428.6	498.7	394.5	383.0	502.3	384.8	302.2	565.2	4.0	4.6	5.9	5.0	4.9	6.1	4.7	3.7	6.9
Birc7	1	45.8	38.1	50.3	477.1	675.2	826.3	963.4	762.4	2642.3	1.1	1.1	1.3	11.8	18.2	20.6	24.1	19.6	66.5
Oca2	1	21.4	52.7	53.8	80.6	125.0	218.9	142.8	110.6	287.2	1.2	2.7	3.0	4.4	6.4	12.3	8.0	6.6	16.0
Rilpl1	1	311.6	448.2	984.1	1222.3	1424.6	1295.9	1525.8	869.5	1928.6	1.7	2.4	5.8	7.2	8.2	7.4	8.6	5.0	11.1
Tpd52	1	1262.8	896.3	1007.2	1308.0	1555.4	1325.8	1652.7	1685.3	2318.0	4.7	3.0	3.6	4.7	5.7	4.8	6.0	6.1	8.4
Emb	1	1033.8	706.5	452.1	641.8	898.7	700.5	1327.4	1151.0	2122.1	5.9	4.1	2.6	3.5	4.9	3.9	7.6	6.1	11.9
Ephx2	1	131.7	72.2	74.5	181.3	184.9	201.8	217.1	123.6	409.9	3.8	2.1	2.4	5.7	5.9	6.6	7.0	4.1	13.3
Ptgds	1	149.5	263.0	345.7	505.9	987.5	3117.0	1165.7	3226.7	9600.2	-1.2	1.6	2.2	3.0	5.9	19.3	7.8	20.4	59.9
Prrt4	1	155.6	189.2	152.6	239.4	199.9	110.2	251.3	159.3	489.5	3.6	4.3	3.6	5.3	4.5	2.4	5.5	3.5	11.0
Dnajb2	1	187.3	215.1	401.1	1386.0	1732.9	1182.3	2162.7	1332.5	2920.9	1.3	1.5	2.4	9.0	11.4	7.8	14.3	9.2	19.2

Slc15a2	1	69.0	53.3	72.7	294.5	135.3	342.2	295.3	452.8	668.8	1.6	1.3	1.7	7.6	3.9	9.1	8.4	12.0	17.8
Hebp2	1	165.9	207.6	275.2	1132.3	2357.6	1367.8	2748.3	939.2	3020.3	1.2	1.3	1.9	8.2	17.1	9.8	19.6	7.3	21.8
Gprc5b	1	163.4	264.5	851.0	1278.1	1077.4	1304.8	1250.1	962.6	3031.9	1.1	1.5	4.9	8.0	6.7	8.0	7.8	5.8	18.7
Sqrdl	1	56.1	95.1	219.2	442.1	560.2	400.1	585.0	309.5	809.1	1.1	1.9	4.1	8.4	11.0	7.5	11.1	5.8	15.3
Suco	1	2337.1	2380.3	2500.9	2424.3	2443.6	2984.5	2739.5	1605.9	3057.6	4.4	4.6	4.3	4.3	4.4	5.4	4.9	2.8	5.5
Mypn	1	18.6	29.8	85.8	307.3	203.0	296.9	363.5	508.5	1078.8	-1.4	-1.1	2.7	9.8	6.5	9.4	12.4	15.3	34.8
Snta1	1	74.1	79.4	161.9	538.9	637.9	583.0	832.4	720.8	1265.1	1.1	1.3	2.6	8.8	10.0	9.2	13.1	10.5	20.1
S100a6	1	25.7	48.5	86.7	475.1	795.2	1483.8	1155.9	1475.5	3033.1	-2.2	-1.2	1.3	6.8	11.0	21.0	16.0	20.8	42.6
Nol3	1	45.7	67.6	154.7	374.7	492.9	400.0	497.2	346.0	2647.4	-1.1	1.2	3.2	7.3	10.4	7.8	9.7	7.0	51.5
Sned1	1	148.2	384.0	509.6	193.2	243.3	508.9	234.9	402.3	399.6	2.0	5.3	6.9	2.7	3.4	7.2	3.2	5.5	5.6
Snhg12	1	327.4	293.3	375.1	2380.3	1537.3	1905.5	1553.8	2821.0	4437.6	1.8	1.4	1.6	5.4	7.8	9.4	7.6	13.5	21.9
C920006 O11Rik	1	22.7	28.7	28.6	168.9	142.5	298.7	195.2	32.0	747.7	-1.0	1.6	1.4	9.8	8.8	17.3	12.6	1.8	43.3
D630024 D03Rik	1	26.7	32.5	45.3	242.7	280.1	266.7	271.0	118.8	400.2	1.1	1.3	1.8	8.3	10.5	10.1	10.1	4.8	15.1
Pgap2	1	164.3	199.2	198.9	1712.3	1786.7	1783.7	2115.3	1535.0	3680.0	1.2	1.1	1.1	10.4	11.1	10.7	12.8	8.7	22.2
Gpsm3	1	107.3	159.2	156.7	196.6	92.0	102.1	116.0	136.4	226.1	2.6	3.9	4.4	5.3	2.5	2.8	3.1	3.9	6.2
Jazf1	1	35.2	48.0	139.6	167.2	220.2	153.0	217.1	137.2	435.0	1.2	1.4	4.5	5.3	6.6	4.7	6.9	4.5	13.4
Tyrp1	1	30.5	40.6	31.5	53.1	201.1	372.9	191.3	300.1	336.9	1.1	1.5	1.2	1.9	7.7	13.9	7.0	12.0	12.5
Ing2	1	368.6	378.7	634.5	1286.5	1434.3	1461.3	1943.7	1734.4	3665.7	1.4	1.4	2.6	4.6	5.3	5.4	7.2	6.4	13.6
Amph	1	119.7	232.7	461.3	1236.7	1106.9	1684.0	1138.2	816.5	3282.9	-1.2	1.1	2.6	8.1	7.1	10.8	7.3	5.2	21.1
Fgf12	1	122.7	167.9	363.9	243.2	134.9	159.7	135.8	154.5	934.3	2.3	3.3	7.0	7.4	2.7	3.0	2.7	2.9	18.0
Slc4a5	1	28.8	37.4	30.9	32.2	54.7	190.9	52.3	144.2	177.8	1.7	2.3	1.9	2.0	3.3	11.6	3.0	9.8	10.8
Htra1	1	48.0	34.8	36.5	206.5	829.5	1347.5	1252.6	1785.3	5176.5	-1.7	-2.6	-2.6	2.3	8.5	14.7	13.4	19.1	56.4
Thrsp	1	12.4	12.1	26.0	85.1	66.3	107.6	104.5	71.2	281.6	-1.0	-1.1	1.9	6.0	5.2	7.9	7.5	5.4	20.7
Eif5b	1	585.3	630.4	736.9	3656.3	3739.8	2498.7	4240.4	4677.7	9517.5	1.3	1.4	1.5	7.7	7.8	5.2	8.9	9.7	20.0
Pcbd2	1	325.1	389.4	428.5	1056.6	1028.8	1121.8	1102.3	711.5	3038.0	1.5	1.8	2.1	5.2	4.7	5.3	5.1	3.2	14.3
Col4a3	1	27.4	24.2	26.4	59.8	76.1	175.1	245.3	229.5	934.8	1.2	-1.2	1.0	2.3	2.8	6.9	9.7	9.4	37.1

Ppl	1	44.9	44.7	51.0	75.3	120.1	207.1	409.8	245.1	446.9	1.3	1.4	1.4	2.4	4.0	6.4	11.9	7.2	14.4
Tfap2a-as1	1	128.7	85.1	64.5	56.8	58.7	48.9	61.8	35.1	180.9	5.0	3.6	2.7	2.4	2.6	2.1	2.6	1.5	7.7
Dync1i1	1	57.1	68.2	85.0	801.7	825.0	675.4	1071.0	670.2	2063.2	-1.6	-1.3	-1.0	8.5	8.8	7.3	11.4	7.1	22.3
Pla2g5	1	17.9	21.0	22.7	34.3	109.7	275.3	138.8	429.1	1414.5	-1.2	-1.1	-1.0	1.5	4.3	12.2	5.7	17.6	62.6
Pstpip2	1	35.8	40.5	51.6	218.9	187.7	213.4	325.8	216.6	622.2	1.1	1.1	1.4	6.3	5.5	6.2	9.1	5.8	18.1
Kcnh1	1	31.0	37.3	47.8	209.6	151.4	166.0	189.7	153.1	455.1	-1.0	1.0	1.3	6.0	4.3	5.0	5.5	4.8	13.7
Hmox1	1	128.5	122.9	159.6	1588.1	2242.9	403.3	4212.4	5799.6	5632.8	-1.2	-1.4	-1.1	9.8	13.6	2.4	25.0	33.2	33.1
Slc22a2	1	15.6	24.5	33.2	95.4	91.7	69.3	140.8	107.9	292.2	-1.1	1.2	1.6	5.2	5.2	3.7	7.6	5.1	15.5
Entpd1	1	15.6	23.3	42.2	124.5	175.9	119.3	209.4	199.6	676.0	-1.4	1.0	1.7	5.5	7.8	5.0	9.0	8.4	28.3
Car8	1	17.6	14.5	15.4	145.2	81.7	107.2	138.0	40.4	424.2	-1.1	-1.1	-1.1	7.2	4.3	6.3	8.0	3.0	24.4
Ank	1	275.2	975.1	1453.6	886.1	829.6	608.3	896.8	672.1	1830.0	1.2	3.3	5.1	3.2	3.0	2.2	3.3	2.6	6.7
Serpinb6b	1	129.8	117.6	90.9	136.3	55.6	53.5	60.3	40.9	1261.3	3.7	3.0	2.4	3.6	1.6	1.4	1.6	1.2	33.8
A430108G06Rik	1	10.6	11.8	15.9	44.2	34.8	58.6	69.1	36.6	345.3	1.0	1.2	1.7	4.7	3.6	5.7	6.4	3.5	34.6
Fas	1	69.2	57.7	61.4	69.7	71.1	54.6	84.6	98.0	894.1	2.3	2.0	2.1	2.3	2.5	1.9	2.9	3.4	30.6
Pacsin3	1	209.0	170.1	244.2	492.5	780.0	461.7	1295.9	725.2	3645.1	1.3	1.2	1.4	2.9	4.8	2.9	8.3	4.4	22.9
Il18	1	29.0	68.8	155.9	361.0	351.3	506.6	428.3	296.8	1473.8	-2.5	-1.3	1.7	4.3	4.5	6.4	5.6	3.8	18.6
Paqr3	1	27.9	42.5	87.9	221.6	120.4	181.8	159.4	70.0	440.8	-1.0	-1.0	2.4	6.4	4.1	5.8	5.2	2.1	14.1
Ephx1	1	27.0	48.8	46.4	125.0	112.1	126.3	141.4	136.5	1082.4	-1.3	1.2	1.4	3.3	3.0	3.4	3.7	3.5	28.9
Pygl	1	121.0	132.4	158.5	422.2	416.6	426.8	475.3	203.3	2286.7	1.1	1.0	1.4	3.6	3.9	3.6	4.2	1.7	19.3
Scel	1	26.7	27.1	29.1	69.7	73.4	117.5	103.0	72.9	1071.9	-1.1	1.0	1.1	2.6	2.6	4.2	3.9	2.6	38.7
Cd44	1	15.4	15.8	19.3	296.3	271.1	456.9	638.8	116.9	3607.5	-4.8	-4.2	-3.8	4.5	3.8	6.3	9.0	1.7	49.9
Casq1	1	17.2	30.1	31.6	57.9	134.2	240.7	294.1	399.2	1432.4	-2.4	-1.4	-1.3	1.3	3.2	5.6	6.8	8.8	33.6
Optc	1	26.3	20.0	22.2	40.4	161.5	303.3	244.2	779.3	445.6	1.0	-1.2	-1.2	2.0	5.7	10.3	6.6	26.0	15.1
Cubn	1	19.5	23.2	32.1	34.8	25.9	23.1	26.8	22.9	324.7	1.2	1.4	2.0	2.0	1.7	1.4	1.7	1.5	20.5
2310043M15Rik	1	22.5	33.5	29.3	84.9	76.3	80.4	96.9	111.5	406.7	-1.4	1.1	1.0	2.7	2.4	2.8	3.3	3.5	13.8
Neat1	1	58.7	47.8	46.5	61.4	56.9	97.9	55.0	73.1	546.2	1.5	1.4	1.4	1.8	1.8	2.9	1.6	2.2	16.2

Clic5	1	17.9	14.6	13.3	38.7	40.5	60.1	153.1	113.9	1282.0	-1.2	-1.4	-1.6	2.0	2.1	2.7	7.9	5.7	63.1
Ankrd24	1	133.4	137.8	149.3	205.7	211.7	151.8	159.5	141.6	3949.1	1.5	1.3	1.7	2.2	2.2	1.6	1.8	1.5	42.8
Lrrc66	1	23.3	18.9	20.3	20.0	21.4	19.2	22.8	20.9	172.9	1.8	1.6	1.6	1.5	1.7	1.5	1.7	1.7	13.7
Hspb1	1	124.1	112.4	119.8	1600.6	2295.6	1289.6	2970.7	5058.0	22002.9	-4.5	-5.3	-5.2	2.5	3.6	2.0	4.7	8.3	34.7
Rrh	1	89.9	17.3	21.1	27.9	31.0	65.3	22.8	203.8	91.4	4.5	-1.1	1.2	1.4	1.6	3.7	1.4	9.7	5.2
Tcp11	1	197.0	195.5	172.9	313.7	464.8	293.8	655.2	751.1	6910.5	1.1	1.1	1.1	1.8	2.6	1.6	3.8	4.3	39.7
Nrl	1	21.9	25.9	25.7	26.1	26.7	24.3	39.4	316.7	169.0	1.1	1.2	1.3	1.2	1.3	1.2	1.9	14.3	8.3
Vsnl1	1	13.2	12.2	10.1	66.4	45.9	61.1	59.8	47.2	407.3	-1.6	-1.7	-2.2	3.1	2.2	2.9	2.8	2.5	19.3
Cadm2	1	10.1	13.5	13.3	19.6	39.8	108.8	41.4	119.8	305.1	-1.9	-1.4	-1.4	1.0	2.1	5.6	2.1	6.1	15.5
Atp1a2	1	9.9	10.0	10.7	71.6	80.8	255.5	120.4	160.6	2246.3	-4.8	-5.0	-4.8	1.5	1.8	5.3	2.5	4.0	47.5
Gnat1	1	15.8	19.0	15.5	25.1	15.6	16.1	15.7	17.5	302.0	1.2	1.4	1.3	1.8	1.2	1.2	1.2	1.3	21.8
Ackr4	1	11.2	12.4	11.0	12.0	46.1	30.0	62.7	22.9	331.2	-1.2	1.0	-1.2	1.0	3.9	2.3	4.8	1.7	25.7
Fxyd1	1	87.0	151.6	284.3	355.1	379.5	660.1	493.1	1123.2	2904.2	-2.6	-1.6	1.5	1.8	1.9	3.3	2.5	5.3	14.3
Abi3bp	1	7.3	9.1	12.2	36.3	33.3	118.0	103.9	29.4	468.5	-2.7	-2.4	-1.9	1.7	1.7	5.6	5.0	1.5	22.7
Pdc	1	25.6	26.0	24.5	27.3	36.4	29.1	42.3	529.5	492.7	-1.1	-1.1	-1.1	-1.1	1.3	1.0	1.8	17.0	16.9
Aqp5	1	31.2	32.2	38.4	69.9	77.3	55.8	105.6	125.0	2875.1	-1.3	-1.2	-1.0	1.5	1.8	1.3	2.5	2.8	68.0
Srd5a2	1	23.3	25.8	24.0	32.0	26.7	24.9	57.6	114.9	1176.9	-1.0	1.2	-1.0	1.3	1.1	-1.0	2.3	4.2	46.6
Sh3bgr	1	11.0	14.5	15.0	127.0	240.0	234.5	354.3	312.0	987.6	-6.7	-4.7	-5.2	1.6	3.3	3.2	4.9	4.0	13.5
Aldh3a1	1	8.0	8.7	8.9	8.6	7.5	6.6	7.1	8.2	2552.5	1.1	1.2	1.2	1.1	1.0	-1.1	-1.0	1.1	347.8
Wdfy4	1	32.9	43.8	56.1	82.9	71.6	61.9	85.1	82.3	518.8	-1.0	1.2	1.5	2.1	1.8	1.6	2.1	2.3	13.6
Sord	1	62.1	105.1	92.5	380.4	423.8	418.4	465.3	273.2	3171.9	-2.3	-1.5	-1.9	2.5	2.8	2.6	2.9	1.7	19.7
Chrdl1	1	26.6	33.6	37.1	73.6	74.7	109.9	84.4	58.0	723.2	-1.4	-1.5	-1.2	1.8	1.7	2.5	2.1	1.5	17.2
1700020 N01Rik	1	13.7	13.4	13.9	31.0	40.3	15.6	53.9	12.1	848.7	1.1	1.0	1.0	2.2	3.2	1.2	3.9	-1.1	65.3
Tinag	1	19.1	18.6	21.2	20.0	18.3	22.6	22.5	26.5	341.7	1.2	1.1	1.2	1.4	1.2	1.4	1.5	1.7	21.5
Sbspon	1	22.5	17.2	23.3	30.5	30.8	72.2	41.5	33.3	413.4	-1.2	-1.5	-1.2	1.2	1.2	2.8	1.6	1.5	15.9
Slc24a2	1	29.3	32.1	40.0	60.1	53.2	45.1	68.7	38.4	562.2	-1.2	-1.0	1.1	1.6	1.5	1.3	1.9	1.1	16.2

Chpt1	1	70.3	112.6	128.9	253.6	224.7	213.9	316.7	252.7	1913.3	-1.8	-1.3	-1.1	2.1	1.8	1.7	2.6	2.0	15.6
Cdkn2b	1	50.7	197.2	374.1	49.9	56.7	53.2	60.1	58.2	445.9	-1.2	3.1	5.7	-1.2	1.0	-1.1	1.0	1.0	7.5
Ces5a	1	180.3	249.7	275.0	318.5	258.0	269.8	290.5	211.9	5534.9	-1.1	1.2	1.2	1.6	1.2	1.3	1.4	1.0	26.8
Otud1	1	29.7	29.0	21.8	45.9	33.8	50.0	57.2	37.2	523.5	-1.1	-1.1	-1.2	1.5	1.1	1.7	2.0	1.3	17.6
Cldn2	1	28.3	30.7	29.1	31.2	30.8	46.8	43.0	33.5	570.1	1.1	1.1	1.1	1.1	1.2	1.7	1.6	1.3	21.1
Rgs4	1	10.1	10.6	10.9	68.4	216.3	116.6	152.8	192.1	2570.9	-9.4	-9.3	-9.8	-1.5	2.1	1.1	1.6	1.8	24.7
Slc26a4	1	27.9	31.3	38.6	33.7	31.6	32.4	34.2	41.7	629.3	-1.1	1.0	1.2	1.1	0.0	-1.0	1.1	1.4	19.3
Gm4850	1	23.7	25.6	23.4	25.5	20.6	21.6	27.8	26.6	595.1	1.0	1.1	1.0	1.1	-1.1	-1.1	1.1	1.2	24.5
Il33	1	8.0	8.0	9.2	10.6	10.0	22.3	14.7	23.0	387.1	-1.7	-1.8	-1.5	-1.4	-1.4	1.6	1.1	2.1	27.6
Abca8a	1	10.1	10.2	10.6	7.7	10.7	9.6	10.9	10.3	168.4	-1.1	-1.1	-1.1	-1.4	-1.0	-1.2	1.0	-1.0	15.1
Zfp354b	1	14.9	21.8	20.5	26.6	21.9	27.8	18.7	21.3	291.2	-1.4	-1.1	-1.2	1.4	1.0	1.3	-1.1	-1.0	14.2
Gp2	1	13.0	14.3	14.6	12.9	14.3	12.2	17.6	12.1	183.2	-1.1	1.1	1.1	-1.0	1.0	-1.1	1.2	-1.2	13.4
Mup4	1	8.2	7.9	8.2	7.2	7.4	7.3	7.8	11.1	137.9	-1.0	-1.1	-1.0	-1.2	-1.2	-1.2	-1.1	1.2	15.7
Emp2	1	59.7	45.3	36.4	62.0	54.9	68.8	67.4	81.9	2221.4	-2.0	-2.6	-3.2	-2.0	-2.2	-1.7	-1.8	-1.5	18.5
Prox1	2	528.6	1283.3	1261.9	929.3	940.8	2071.2	1222.2	606.6	891.3	18.3	37.1	37.8	29.3	28.9	62.3	36.6	18.3	27.1
A830021 M18Rik	2	19.3	96.4	192.4	275.8	1404.2	1389.9	1296.9	404.1	31.2	3.6	8.4	20.6	34.4	143.4	154.0	133.5	41.4	3.1
2900017F 05Rik	2	127.8	46.7	79.4	15.7	574.4	302.1	696.3	36.6	31.2	10.5	6.3	7.4	1.5	56.1	27.6	63.8	3.6	2.8
Rnf113a1	2	364.8	361.3	398.2	1076.1	2204.3	3395.1	2729.8	1494.2	121.0	4.6	4.4	5.4	14.3	28.4	43.4	35.3	17.8	1.5
AU02176 0	2	126.3	102.8	84.3	28.4	404.5	395.0	542.9	22.5	31.0	11.2	10.4	8.5	2.3	34.9	32.4	44.7	1.7	2.5
2310014F 06Rik	2	152.1	212.1	249.1	282.9	372.0	452.4	331.9	225.7	140.7	4.6	6.1	7.5	8.5	10.9	13.4	9.9	6.4	4.1
Stx3	2	449.0	339.4	407.2	571.0	570.5	803.1	679.1	405.2	379.5	5.9	4.1	5.1	6.4	7.0	10.0	8.4	5.0	4.7
D230019 N24Rik	2	68.9	59.4	69.5	41.8	348.1	455.6	408.8	25.5	40.9	4.5	4.0	4.9	3.1	24.9	32.2	29.7	1.9	2.9
D430033 H22Rik	2	117.0	51.5	49.5	24.1	239.6	349.2	158.1	24.9	32.0	8.3	4.9	4.6	2.2	17.1	26.0	11.3	1.9	2.2
4930406 D14Rik	2	84.2	116.3	98.9	55.6	174.6	206.6	175.4	62.7	69.1	4.0	5.8	5.1	3.1	8.8	9.9	8.6	2.8	3.3
Lama1	2	563.1	590.2	381.8	335.8	622.0	655.1	607.7	395.2	158.5	7.3	7.1	5.1	4.3	7.5	7.7	6.8	4.6	1.9
9230108I 15Rik	2	192.0	130.3	304.8	68.9	417.4	369.2	423.3	126.2	125.9	4.3	3.9	6.7	2.0	8.8	8.4	9.6	2.8	2.9

9930031P18Rik	2	157.8	46.6	47.3	26.3	235.9	250.5	164.5	32.8	27.5	8.5	4.0	3.7	1.8	13.9	14.9	9.4	2.0	1.6
Tmem37	2	685.3	561.5	513.1	608.3	557.4	743.8	485.3	826.2	424.2	4.6	3.9	3.3	4.4	3.8	5.2	3.4	5.6	2.9
D5Wsu152e	2	151.0	63.7	55.4	27.1	202.0	227.5	164.3	28.1	45.8	7.5	3.9	3.7	1.7	11.5	13.3	9.7	1.6	2.6
2900073C17Rik	2	340.0	189.5	157.1	59.4	329.5	292.5	283.4	73.8	47.4	11.4	7.2	5.4	1.6	10.3	8.8	8.4	2.1	1.4
6430537K16Rik	2	516.7	149.4	117.1	46.8	476.1	607.6	421.7	64.5	27.9	11.8	5.6	3.8	1.2	13.4	16.4	10.6	1.7	-1.3
4930578M01Rik	2	111.9	62.9	57.9	45.0	98.0	84.3	89.0	87.0	27.1	6.2	4.2	3.6	2.5	5.6	5.0	5.4	4.8	1.6
Dmd	2	346.8	293.1	310.8	307.6	308.4	319.8	380.7	290.0	337.2	4.5	4.0	4.1	4.0	4.2	4.2	5.0	4.0	4.5
Kcnq1ot1	2	199.6	135.5	119.3	42.9	353.4	409.1	277.6	137.9	54.9	5.0	4.3	4.1	1.3	9.3	10.7	7.1	3.4	1.4
5430406J06Rik	2	165.0	144.6	98.4	159.6	156.8	539.6	220.1	106.8	75.8	4.1	3.7	2.7	2.9	4.1	13.6	5.6	2.4	1.9
A130004G07Rik	2	70.0	17.6	18.9	16.2	74.2	149.0	42.6	14.3	20.3	6.1	2.5	2.0	1.8	7.3	16.8	4.8	1.6	2.2
D15Wsu126e	2	103.6	69.9	61.0	25.9	192.6	448.7	177.2	28.9	27.8	4.4	3.7	3.0	1.5	8.9	21.3	8.1	1.3	1.3
5730409N24Rik	2	26.1	25.7	27.6	24.7	195.4	385.8	207.8	37.5	16.6	2.2	2.0	2.4	1.9	16.1	31.2	17.1	2.6	1.4
9030425L15Rik	2	59.0	37.1	34.8	24.8	241.2	430.9	269.2	27.5	42.8	2.8	2.1	2.2	1.3	12.2	21.8	14.0	1.4	2.2
2900011L18Rik	2	66.1	34.8	37.3	18.3	162.4	373.7	124.3	16.5	18.1	4.5	2.7	2.5	1.2	11.3	26.8	8.9	1.2	1.2
D530037H12Rik	2	40.8	20.3	45.2	14.9	111.3	154.0	98.3	18.4	12.2	4.1	2.2	4.5	1.4	10.6	15.0	9.9	1.6	1.2
A430102J17Rik	2	172.4	79.4	91.7	23.8	224.0	370.7	197.7	48.5	33.3	6.1	3.9	3.2	-1.2	8.5	14.1	7.4	1.7	1.3
2810043O03Rik	2	69.6	24.6	22.1	11.6	97.1	203.5	87.7	11.1	13.6	7.7	2.9	2.4	1.2	9.4	19.2	8.3	-1.0	1.3
9430011C21Rik	2	93.6	45.9	36.9	23.3	331.9	290.7	325.6	18.7	32.3	5.2	2.3	2.0	1.2	17.4	15.4	16.3	-1.1	1.7
9330156P08Rik	2	33.1	22.2	26.0	25.7	69.5	147.7	80.0	11.0	27.5	3.0	2.0	2.3	2.2	6.4	13.1	7.1	1.1	2.5
D230044B12Rik	2	57.6	26.6	25.2	14.1	121.6	197.4	105.9	19.4	17.9	4.6	2.4	2.3	1.2	8.8	14.4	7.2	1.4	1.3
B930068K11Rik	2	131.5	55.6	39.9	25.6	156.0	190.2	143.0	31.6	29.0	5.8	3.3	2.1	1.2	7.3	8.8	6.4	1.5	1.3
3110005L21Rik	2	45.9	17.5	16.1	14.0	122.9	132.3	98.9	13.4	14.9	4.4	1.8	1.9	1.5	12.7	13.8	10.0	1.4	1.5
8030447M02Rik	2	124.8	46.7	52.1	36.3	274.8	397.5	232.3	45.1	33.1	4.5	2.0	2.1	1.3	9.7	14.1	8.6	1.5	1.2
Scfd2	2	127.3	105.7	194.5	105.1	98.4	563.4	91.6	53.4	61.9	2.9	2.5	4.2	3.2	5.4	13.4	3.4	1.3	1.5
Taf15	2	81.5	66.8	48.3	46.8	63.3	104.1	43.6	17.4	13.4	6.8	4.2	3.0	2.6	4.1	7.0	3.0	1.0	-1.1
5430434G16Rik	2	95.0	44.5	31.1	22.3	65.9	95.5	83.2	19.4	10.2	5.8	3.1	2.3	1.8	4.4	6.5	5.4	1.3	-1.4

B230214O09Rik	2	13.6	9.9	16.3	51.5	473.2	361.9	304.9	8.2	55.1	1.2	-1.1	-1.0	5.2	34.4	26.0	19.0	-1.5	3.9
Gm19313	2	122.5	52.9	55.6	33.0	154.5	178.3	128.4	46.6	35.9	4.7	2.9	2.6	1.4	6.2	7.1	4.9	1.7	1.4
D5Ertd798e	2	65.8	31.7	22.7	11.4	66.2	106.0	56.3	22.2	14.7	6.2	2.7	1.9	1.0	5.5	9.0	5.0	1.8	1.2
LOC101056057	2	650.7	411.9	281.7	144.9	376.8	823.7	592.0	201.7	88.1	5.8	3.6	3.1	-1.0	3.5	7.3	4.7	1.8	-1.3
Mid1	2	163.4	69.1	69.9	29.7	82.4	166.5	73.5	47.7	72.6	5.9	2.4	2.8	1.0	2.8	5.8	2.5	1.6	2.5
4732423E21Rik	2	42.6	19.7	13.4	8.6	50.0	68.7	36.1	9.8	9.3	5.1	2.7	2.0	1.1	6.4	8.7	4.6	1.2	1.2
Atoh7	2	33.2	48.9	85.6	362.5	534.3	686.1	61.4	559.0	22.7	-1.1	1.6	3.0	8.6	12.0	19.9	2.3	14.1	-1.5
C130015C19	2	112.2	67.3	39.6	25.2	120.1	217.8	95.7	26.3	17.3	5.1	3.4	2.2	1.2	5.7	10.7	4.7	1.3	-1.2
2310035P21Rik	2	59.4	37.8	33.9	15.0	46.7	66.1	48.5	15.3	18.8	5.1	2.6	2.5	1.1	3.4	5.0	3.5	1.2	1.4
D9Ertd306e	2	133.0	55.2	46.7	16.6	103.1	74.8	88.6	35.9	18.1	5.7	2.8	2.3	-1.4	5.0	3.6	4.1	1.7	-1.2
AA415038	2	102.5	49.1	40.7	20.8	79.9	223.6	54.6	27.1	20.9	4.8	2.7	1.8	1.0	4.0	10.9	2.7	1.4	1.0
H3f3b	2	61.6	62.3	46.0	32.5	228.1	426.2	116.3	39.0	41.7	2.2	2.1	1.7	1.2	7.7	15.0	4.0	1.3	1.5
C430003N24Rik	2	68.3	27.4	35.3	16.8	103.4	140.2	75.6	19.2	17.9	4.2	1.7	2.1	1.1	6.4	8.5	4.3	1.1	1.0
A730059M13Rik	2	44.9	23.2	19.6	11.7	33.1	107.4	33.3	14.8	11.8	4.8	2.2	1.8	1.0	3.2	9.6	3.1	1.3	1.1
Fn3krp	2	8.2	10.9	12.7	63.1	19.7	616.3	95.1	14.8	31.0	-1.0	1.1	1.5	6.6	1.9	61.7	6.2	1.4	3.1
LOC75771	2	86.8	62.5	34.5	26.4	55.9	71.9	85.5	20.0	27.0	4.3	2.8	1.7	1.3	2.8	3.6	3.8	1.1	1.3
Slc16a4	2	141.8	59.8	34.6	22.0	79.1	175.8	72.0	39.1	17.5	5.8	2.7	1.5	0.0	3.5	7.4	2.9	1.5	-1.4
6330415B21Rik	2	8.2	8.6	8.3	8.5	100.2	128.0	122.2	10.2	21.0	1.1	1.1	1.1	1.2	13.3	16.9	15.9	1.4	2.8
1110012L19Rik	2	237.5	192.6	206.3	300.3	1674.5	1679.4	2001.3	221.9	300.1	1.3	1.0	1.2	1.8	9.3	9.7	11.9	1.3	1.7
D1Ertd564e	2	14.1	12.0	9.1	7.9	52.1	109.5	89.1	9.5	11.2	1.8	1.4	1.1	1.0	6.3	12.7	10.3	1.2	1.3
B430203I24Rik	2	18.9	14.8	16.4	12.4	91.9	162.2	119.5	15.1	13.9	1.5	1.1	1.3	1.1	7.4	13.0	8.6	1.2	1.1
4930447C04Rik	2	10.1	10.6	10.8	9.0	19.0	104.0	18.0	20.9	12.0	1.3	1.4	1.3	1.4	2.6	12.8	2.0	2.4	1.5
2610027H17Rik	2	16.3	11.1	9.1	11.2	25.1	105.1	16.3	12.6	13.4	1.9	1.3	1.2	1.4	2.8	12.5	1.9	1.4	1.6
A330076H08Rik	2	9.5	10.7	11.4	9.6	24.7	125.9	28.9	10.8	9.4	-1.1	1.0	1.1	-1.1	2.4	12.3	2.7	1.0	-1.1
Xist	3	970.6	329.6	372.6	115.3	1037.2	1073.6	602.0	267.3	108.3	134.2	51.1	60.3	16.4	23.4	19.3	15.9	35.1	14.9
Dmrta2	3	3203.7	1507.8	1463.6	1238.4	1458.9	1808.6	1865.4	638.6	2046.1	22.9	12.2	10.8	9.4	11.1	13.6	13.4	4.4	15.4

Pax6	3	3609.2	3160.2	2399.9	981.4	1384.7	2352.4	1232.2	1998.0	1572.6	24.6	19.7	14.4	6.3	8.7	15.2	8.1	13.1	10.2
Six3	3	2074.6	1517.9	1367.4	1426.0	1021.8	1620.8	979.9	572.3	676.7	20.3	15.3	13.3	14.1	10.1	16.1	9.8	5.8	6.7
Six3os1	3	436.2	257.4	200.8	237.9	240.2	257.5	263.1	208.7	78.7	19.2	11.4	10.4	11.5	10.9	12.3	12.6	9.8	3.7
Cdh1	3	2455.5	1496.9	1264.0	1107.2	926.5	860.3	809.3	435.1	817.8	16.9	11.1	9.0	8.2	5.6	6.3	5.9	3.4	6.0
Cx3cl1	3	967.8	424.4	274.1	309.3	223.1	100.6	189.3	146.8	136.7	22.4	9.6	5.9	7.1	4.4	2.3	4.4	3.5	3.1
Mab21l1	3	2213.5	1624.8	1439.3	537.4	723.7	915.0	601.9	905.0	743.7	9.8	7.6	6.7	2.5	3.5	4.2	2.7	4.3	3.4
Edaradd	3	328.5	292.2	194.0	194.0	115.9	233.5	83.9	84.5	111.2	7.3	5.7	5.2	4.9	2.8	5.6	1.9	2.0	2.6
Ggt1	3	343.7	225.5	146.8	160.8	147.0	131.9	140.8	140.1	101.9	7.4	5.0	3.3	3.6	3.4	2.9	3.2	3.2	2.2
Cadps2	3	508.4	182.1	168.3	186.7	159.5	166.7	196.7	203.7	468.3	7.5	2.6	2.6	2.7	2.4	2.5	2.9	2.9	7.1
Leprel1	3	2027.8	1427.6	967.6	790.4	615.7	532.0	502.5	410.8	95.2	13.6	9.4	6.5	4.9	4.1	3.5	3.3	2.8	-1.6
Upp1	3	212.9	171.1	92.1	146.6	96.4	82.7	71.4	152.2	227.9	6.7	4.2	2.6	4.4	3.5	2.2	2.1	4.0	6.0
Eml5	3	549.4	246.0	180.9	121.3	225.1	276.8	230.5	190.6	91.5	9.2	4.6	3.2	2.1	4.0	4.9	4.0	3.2	1.6
Etv5	3	979.6	732.7	621.8	734.5	434.1	535.0	402.2	525.5	367.5	5.7	5.0	4.3	4.9	3.1	3.7	2.8	3.7	2.5
Atp1b3	3	6115.9	6422.6	5205.3	2431.5	3029.2	3357.4	3274.7	3213.0	7190.8	4.4	4.4	3.7	1.7	2.1	2.4	2.3	2.4	5.1
Elp4	3	1191.4	908.7	699.7	503.0	473.9	711.3	398.4	535.0	404.6	4.7	3.7	3.1	2.3	2.1	3.1	1.8	2.5	1.8
Tfap2a	3	1149.0	524.8	409.8	328.7	244.2	310.1	374.7	361.3	665.8	6.5	3.0	2.3	2.0	1.4	1.7	2.0	2.0	3.7
Abcc4	3	784.7	263.0	163.6	203.4	151.8	174.7	139.0	53.8	84.0	11.4	4.0	2.7	3.2	2.1	2.8	2.1	-1.3	1.3
Itga3	3	496.3	260.0	180.8	287.5	240.8	200.5	252.2	184.5	241.4	5.0	3.0	1.9	2.9	2.2	1.9	2.3	1.7	2.3
Sema4d	3	556.9	558.3	383.2	275.6	265.1	176.6	187.2	293.8	164.2	5.2	5.0	3.6	2.4	2.3	1.6	1.7	2.7	1.5
Aldh1a3	3	683.6	176.7	71.1	34.5	86.5	146.0	28.6	252.2	99.8	20.2	4.3	2.1	1.2	2.1	4.4	-1.1	7.6	3.0
Slc17a1	3	210.4	83.7	73.5	65.3	55.4	52.1	76.4	44.3	35.6	7.7	3.3	2.8	2.3	2.0	1.9	2.8	1.5	1.2
Steap1	3	331.3	180.9	131.0	91.1	91.7	110.0	87.9	139.5	262.0	5.0	2.7	1.8	1.6	1.5	1.8	1.4	2.3	4.2
Cyp26a1	3	449.7	355.6	250.4	158.0	115.5	104.5	146.8	166.1	351.6	5.1	4.3	3.1	1.6	1.4	1.2	1.7	1.9	4.1
Dnajc1	3	1035.2	472.9	507.4	325.4	248.9	265.7	196.1	102.1	161.4	8.0	4.6	4.2	2.6	2.0	2.2	1.6	-1.2	1.3
Plekha1	3	890.9	478.2	370.2	250.0	442.2	672.5	389.1	472.3	268.1	4.4	2.5	1.8	1.3	2.1	3.3	1.9	2.3	1.3
Col13a1	3	1363.0	479.7	351.4	160.4	178.7	132.5	136.4	83.3	54.9	15.1	5.8	4.2	2.0	2.1	1.6	1.7	1.0	-1.5

1700086L19Rik	3	85.5	45.3	24.1	83.9	42.0	27.7	35.2	18.4	23.2	5.8	2.9	1.4	5.8	2.5	1.7	2.2	1.1	1.4
Plch1	3	657.2	348.2	281.1	182.6	205.4	294.4	170.2	193.1	92.9	4.9	2.7	2.1	1.5	1.5	2.3	1.3	1.7	-1.4
A730062M13Rik	3	93.3	53.7	41.7	25.8	45.8	67.3	44.5	27.2	32.7	4.4	2.5	1.8	1.1	2.0	2.9	1.9	1.2	1.4
Cngb3	3	135.1	40.8	29.5	17.4	18.2	19.9	20.5	23.1	25.6	8.3	2.6	1.9	1.1	1.3	1.3	1.3	1.5	1.7
Stra6	3	1638.8	989.8	522.0	336.2	204.0	118.0	168.0	156.7	66.4	12.0	8.6	3.5	2.4	1.4	-1.2	1.2	1.2	-2.1
Pla2g4a	3	531.1	239.3	139.8	222.5	166.0	183.9	153.4	93.2	232.1	5.2	1.7	1.2	2.0	1.3	1.7	1.4	-1.0	2.1
Slc15a3	3	412.4	121.4	308.8	31.7	20.5	24.7	20.0	23.0	16.2	15.4	5.7	12.8	1.3	-1.1	1.1	-1.1	-1.0	-1.4
Mtcl1	3	1086.2	483.8	359.6	325.4	514.3	422.0	564.1	181.7	276.6	4.5	2.1	1.6	1.4	2.2	1.8	2.3	-1.3	1.2
D230021J17Rik	3	47.9	16.8	12.8	17.0	28.0	19.2	28.7	11.4	18.1	4.3	1.6	1.2	1.5	2.6	1.7	2.6	-1.0	1.6
2410127L17Rik	3	4498.0	2750.9	1773.7	1051.8	846.3	814.6	667.4	457.6	921.7	6.6	4.4	2.8	1.6	1.3	1.2	1.0	-1.3	1.4
Alpl	3	177.2	186.0	97.3	44.6	42.0	33.2	45.5	62.2	54.5	4.6	4.7	2.6	1.1	-1.1	-1.3	1.1	1.6	1.3
A030007N12Rik	3	50.2	40.8	39.5	11.0	28.2	15.1	27.9	9.6	11.3	4.5	3.5	2.9	-1.1	2.2	1.2	2.2	-1.3	-1.1
BC023969	3	612.0	532.7	273.5	188.6	120.5	227.9	143.7	114.9	53.4	5.7	4.6	2.7	1.4	1.0	2.0	1.3	-1.0	-2.2
D10Ertd755e	3	64.8	24.7	19.1	12.6	27.4	23.3	23.4	12.2	13.9	4.7	2.0	1.8	1.0	2.1	1.9	1.8	1.0	1.1
Npvf	3	141.5	49.1	32.7	59.7	42.0	34.3	40.7	40.6	59.9	4.6	1.7	1.2	2.0	1.4	1.2	1.4	1.5	2.0
Gm4354	3	3098.0	2189.6	1678.8	205.3	930.6	816.5	1051.6	303.0	601.7	4.4	3.2	2.5	-2.9	1.3	1.2	1.5	-2.2	-1.2
Nav1	3	1390.4	1038.0	668.4	170.1	259.7	215.1	215.5	94.4	269.4	6.2	4.8	2.8	-1.4	1.1	-1.1	-1.1	-2.4	1.1
Csn3	3	1895.1	39.1	29.6	23.9	18.1	20.2	16.7	16.7	32.0	75.0	2.1	1.5	1.2	-1.1	1.0	-1.1	-1.2	1.5
Kcnk1	3	891.9	194.3	73.0	82.9	111.5	205.1	77.9	82.3	299.9	6.7	1.5	-1.6	-1.2	-1.0	1.7	-1.5	-1.3	2.4
Frem2	3	645.9	226.5	119.4	37.3	86.4	190.9	119.7	33.5	89.8	5.5	2.0	1.1	-3.5	-1.3	1.7	-1.0	-3.3	-1.3
Prtg	3	1006.3	462.3	222.8	95.0	112.3	120.4	114.8	56.5	91.6	6.3	3.2	1.5	-1.5	-1.3	-1.2	-1.3	-2.7	-1.6
2610028L16Rik	3	249.9	109.8	50.9	22.0	59.0	74.6	66.5	25.0	30.5	4.9	2.0	1.1	-2.2	1.1	1.4	1.3	-2.3	-1.7
Kcne3	3	82.6	36.7	35.7	47.4	14.8	12.8	9.2	9.1	8.0	4.3	2.5	1.5	2.0	-1.4	-1.6	-2.1	-1.9	-2.5
Phlda1	3	1637.1	464.1	340.6	648.4	337.2	471.0	287.0	138.5	111.0	4.2	1.4	-1.0	1.7	-1.1	1.3	-1.3	-2.8	-3.3
Crym	3	420.9	323.7	60.6	18.1	16.8	16.4	15.3	92.2	19.6	4.8	3.7	-1.4	-4.3	-4.7	-5.1	-4.8	1.0	-4.1
Cbln2	3	900.1	164.9	57.2	26.9	34.1	26.8	29.7	66.5	42.7	10.0	1.8	-1.5	-3.1	-2.7	-3.2	-3.0	-1.4	-2.0

Dleu7	3	92.8	16.0	14.4	15.6	12.9	20.7	12.7	15.0	22.1	4.5	-1.2	-1.4	-1.3	-1.6	-1.0	-1.7	-1.2	1.0
Lin28a	3	511.1	228.7	26.2	10.7	8.1	10.6	7.8	7.0	10.6	5.0	1.9	-3.3	-9.3	-12.6	-9.6	-13.2	-13.3	-9.8
Hmx1	4	2618.8	2908.8	2473.2	1368.7	1381.9	1127.8	1230.9	936.3	443.8	30.3	32.3	27.3	15.6	15.5	12.8	14.0	10.4	5.0
Pitx3	4	1191.0	1522.6	1333.9	1080.3	936.5	511.9	971.1	642.4	521.5	14.7	18.6	16.1	11.7	10.7	5.9	11.1	7.0	6.0
Camk1d	4	521.5	565.3	488.7	337.8	341.9	347.7	360.1	167.0	89.5	13.9	15.1	11.2	8.8	8.2	8.7	9.0	4.2	2.3
Foxe3	4	1097.0	1962.6	1077.4	379.3	398.0	122.3	322.5	373.3	196.0	19.8	33.3	20.3	7.1	7.8	2.5	6.3	7.8	4.0
Slc38a3	4	411.6	618.4	585.2	372.3	430.1	371.1	517.0	416.4	149.6	5.8	9.2	9.5	5.6	6.1	5.5	7.4	6.0	2.2
Fam198b	4	788.7	1916.8	3410.7	1326.8	1049.5	960.2	953.7	591.2	9.6	6.3	14.6	26.0	10.2	7.7	7.3	7.1	4.7	-13.7
Plekhg1	4	1670.5	1665.6	1921.5	1592.9	1546.9	421.9	1806.0	1188.6	514.1	6.8	6.2	7.6	5.9	5.8	1.6	6.8	4.6	2.0
Tox2	4	1533.5	1986.3	1685.3	1622.2	1760.2	1405.1	1766.2	1348.2	1048.6	4.1	4.9	4.3	4.2	4.6	3.6	4.5	3.5	2.7
Fam19a4	4	126.2	203.6	126.8	133.9	136.8	132.8	143.2	95.5	67.9	3.7	4.9	3.8	4.1	4.1	3.8	4.1	2.6	1.9
4632427E 13Rik	4	292.8	308.6	285.1	79.4	242.5	269.1	215.5	116.2	63.2	5.0	5.0	4.8	1.1	4.0	4.4	3.5	2.1	1.0
Casz1	4	101.9	138.7	130.1	120.1	118.5	97.9	116.9	94.3	41.2	2.8	4.0	3.2	3.0	2.9	2.3	2.7	2.1	-1.0
Cgnl1	4	522.5	678.8	494.9	555.3	445.7	437.3	378.5	375.3	196.4	2.9	4.1	3.0	3.2	2.5	2.6	2.2	2.3	1.2
Bid	4	502.8	541.8	472.4	361.4	249.3	268.4	217.7	198.3	190.9	4.0	4.5	4.2	3.0	2.1	2.3	1.8	1.7	1.6
Trib1	4	318.6	395.1	463.8	227.7	261.6	227.4	206.9	328.4	129.4	3.3	4.1	4.6	2.2	2.6	2.2	2.0	3.1	1.3
Gata3	4	226.2	283.8	245.1	280.0	136.4	152.2	111.7	87.8	32.0	3.4	4.7	3.6	4.3	2.0	2.3	1.8	1.3	-2.0
Parm1	4	1310.1	1664.1	1375.4	733.8	762.1	835.4	741.3	591.6	441.6	3.1	4.0	3.4	1.8	1.8	2.0	1.8	1.5	1.1
Myb	4	1170.5	554.4	422.0	313.7	479.6	473.9	200.2	1069.6	47.3	5.0	2.8	2.1	1.3	1.9	2.1	-1.0	4.4	-4.7
Scube3	4	872.6	908.8	564.3	267.7	215.1	186.7	178.8	118.5	70.4	5.1	5.7	3.4	1.6	1.2	1.1	1.1	-1.4	-2.3
Tmem132 a	4	1588.8	1733.2	1546.9	810.6	667.6	514.2	495.2	496.4	239.0	3.3	4.1	3.4	1.8	1.5	1.1	1.1	1.1	-1.9
Sfrp2	4	11545.0	9058.9	5124.8	333.1	188.9	246.3	28.3	144.3	13.9	8.7	6.7	3.8	-3.3	-7.6	-5.5	-42.0	-8.4	-96.5
Aldh1a1	5	6288.4	9761.0	10899.4	9764.9	10791.8	9837.6	9976.7	10209.8	7555.0	144.7	221.3	244.9	220.1	241.4	219.6	221.5	230.6	168.7
Capn3	5	1931.7	5817.5	16518.9	12196.0	12435.3	6296.0	8434.2	6584.5	31.7	98.5	215.3	608.5	455.1	467.2	232.2	307.6	236.2	1.2
Htra3	5	1352.7	2260.0	3419.5	3146.7	3658.0	3159.8	3523.5	2524.0	936.9	20.2	33.9	54.5	46.6	54.7	47.1	53.4	36.9	14.1
Gja8	5	461.0	1058.2	2613.2	688.0	1443.6	533.3	1623.1	1319.3	412.7	16.3	37.7	88.4	24.8	50.5	18.4	56.2	45.9	14.2

Npl	5	1867.4	2757.5	3553.8	2484.8	3527.3	3011.6	3136.3	2544.5	1856.4	17.6	26.5	33.4	23.3	34.0	28.5	29.5	23.7	17.6
Sapcd1	5	821.0	1282.6	1520.5	1469.4	1116.7	1251.2	1142.8	872.8	835.1	14.9	22.8	26.8	26.4	20.1	22.1	19.8	15.7	14.8
Rbm24	5	542.4	3358.7	4207.0	2916.7	2113.0	2538.5	2376.2	1574.3	2063.3	6.4	19.6	32.6	24.5	18.2	21.8	20.5	13.4	17.8
Adamts18	5	190.3	455.6	898.9	698.6	746.4	909.2	829.0	312.9	400.2	5.5	11.2	23.8	18.5	19.4	24.1	21.3	7.9	10.6
Sowaha	5	66.2	212.5	702.3	287.2	144.1	215.8	175.1	95.6	74.6	7.0	18.4	65.5	27.4	14.3	20.4	16.9	8.8	7.2
Col4a5	5	1392.1	3120.6	4840.3	3618.0	2824.5	3455.5	2655.8	1825.7	2373.6	6.7	10.5	17.3	15.4	11.8	14.3	11.1	8.0	9.8
Prx	5	165.9	713.8	1949.1	1057.3	2103.3	1655.1	2132.2	1632.5	425.9	2.5	8.0	23.4	14.6	24.3	20.1	23.8	17.8	5.2
Zfp185	5	197.5	511.3	821.9	553.8	738.4	583.9	764.0	473.2	358.9	3.9	8.6	16.3	12.4	14.9	11.8	15.1	9.4	7.3
Slc7a5	5	1964.1	4327.8	5145.7	3771.0	2633.4	2778.2	3051.8	2121.5	478.6	8.3	16.4	22.3	17.5	11.9	12.6	13.5	9.5	2.2
Ank2	5	629.2	2043.4	4077.0	4325.2	3022.6	3880.7	3413.8	2144.3	1312.7	2.6	7.8	15.8	16.0	12.0	14.9	13.1	8.2	5.0
Ezr	5	1912.9	2345.9	3110.5	2786.0	2419.6	2686.1	2432.2	1652.3	1761.0	6.8	8.0	10.8	9.9	7.9	9.3	8.2	5.8	6.1
Slc3a2	5	2975.7	4279.2	5541.5	4348.5	5788.5	4868.8	5812.1	4415.2	2783.9	3.9	5.0	6.7	5.3	6.9	5.9	6.8	5.4	3.4
S1pr5	5	22.9	62.2	140.1	95.0	72.6	60.1	57.8	37.0	17.6	2.3	5.3	14.4	8.8	7.0	5.9	5.7	3.7	1.7
Fam214b	5	277.2	454.4	945.9	890.2	956.2	753.7	975.4	450.6	347.7	2.4	4.0	7.6	7.3	7.7	6.2	7.9	4.0	2.8
Mafb	5	283.0	479.3	419.8	356.0	330.9	351.7	411.3	250.6	102.9	3.4	6.0	5.5	4.3	3.9	4.4	5.2	3.2	1.3
Pnpla6	5	175.5	293.1	565.0	403.8	370.7	490.3	388.9	409.7	156.7	1.9	3.0	5.7	4.5	3.7	5.0	3.9	3.7	1.6
Ddx26b	5	611.1	1781.5	2651.4	1029.1	1931.1	2337.8	1680.3	564.6	113.1	2.6	5.7	9.5	3.3	6.3	7.8	5.4	1.8	-2.7
Naaa	5	107.6	173.7	291.0	212.2	251.5	221.6	225.8	173.8	141.1	1.6	2.5	5.1	3.6	4.3	3.9	4.0	3.0	2.5
Crygd	6	273.1	554.1	13411.1	26053.0	22602.4	26042.6	23339.4	27073.4	25517.2	61.8	47.0	871.9	1682.0	1444.1	1673.9	1514.9	1752.3	1640.6
Crygb	6	25.3	208.3	10667.4	24642.0	19873.2	23485.6	20608.4	23628.2	23446.8	11.6	13.4	749.6	1691.4	1392.1	1645.1	1456.2	1661.2	1644.0
Crygc	6	25.3	208.3	10667.4	24642.0	19873.2	23485.6	20608.4	23628.2	23446.8	11.6	13.4	749.6	1691.4	1392.1	1645.1	1456.2	1661.2	1644.0
Cryba1	6	2455.0	18264.5	28381.9	27502.6	24954.4	27103.0	24817.0	27257.2	25392.3	192.3	648.1	1092.9	1070.4	979.6	1060.8	967.4	1070.4	993.9
Cryaa	6	6096.3	22231.3	26968.8	26084.9	26887.7	27032.7	27180.5	25970.2	25996.0	300.0	693.1	909.5	878.0	897.0	902.0	907.0	869.5	867.1
Mip	6	273.1	2431.3	12285.2	17325.8	11418.9	12722.5	12345.0	12850.3	14507.9	52.2	188.3	1024.7	1510.7	1011.3	1122.1	1095.2	1130.7	1282.7
Crygs	6	228.4	885.4	3138.6	13952.1	19483.6	19210.4	21787.8	22036.0	24560.8	35.3	47.1	198.9	907.7	1195.2	1193.5	1355.9	1366.2	1525.4
Cryba4	6	35.7	639.6	15661.3	21856.6	24935.6	21977.3	24851.2	23108.2	22000.5	10.7	38.6	778.2	1069.0	1235.6	1082.4	1234.7	1139.4	1083.9

Cryba2	6	276.9	3502.8	16897.9	23258.7	25397.8	24152.0	25170.9	25521.6	26123.5	27.0	111.6	527.9	737.2	802.3	765.9	799.0	811.8	828.3
Crybb1	6	428.3	10518.5	25522.8	25844.1	28954.5	25627.5	29168.3	27191.0	22185.1	24.3	180.3	437.8	447.3	497.0	446.6	509.9	470.8	386.7
Crybb3	6	5597.3	13149.4	27963.6	26321.3	26031.0	25269.5	25921.0	27533.1	22585.4	106.4	194.4	375.3	372.5	364.8	354.1	363.8	391.5	316.5
Gja3	6	329.3	2151.7	3472.3	6645.7	3993.7	5074.9	4478.8	3915.6	3911.5	49.4	153.5	334.3	640.5	378.5	481.4	424.9	382.9	376.6
Lim2	6	168.0	1906.1	7746.7	15812.9	15951.3	11452.0	17410.0	17222.7	14574.5	10.3	42.7	169.6	379.8	382.4	275.1	418.8	412.7	350.2
Mgarp	6	4386.9	4743.2	6962.7	7464.6	7365.8	9247.4	8277.2	9353.2	10036.7	56.9	63.8	94.4	99.0	97.0	121.8	109.2	121.7	132.2
Cryab	6	4051.4	5326.4	6239.7	18040.6	16928.8	19925.1	20418.2	23520.6	25273.6	31.3	39.9	45.6	124.6	120.5	139.2	141.9	162.9	176.6
Crygf	6	73.1	176.2	8083.8	21346.0	17170.6	20288.6	18117.6	19468.6	12774.1	8.9	3.7	164.3	459.2	369.6	431.7	385.3	413.6	271.9
Bfsp1	6	57.5	113.3	675.3	10137.9	12403.8	9699.6	13701.7	14716.5	18457.2	4.0	3.1	20.3	278.2	342.3	266.5	378.2	400.6	507.8
Tdrd7	6	645.1	1209.5	4162.8	8840.7	11917.8	9706.4	13043.7	11930.1	10403.6	7.5	9.4	38.2	79.3	107.4	86.6	115.8	103.4	92.8
Cp	6	629.3	934.9	1444.4	2454.1	2332.7	2606.0	2709.4	2064.9	3303.4	15.0	19.6	31.6	59.6	51.7	60.2	61.6	46.2	76.3
Bfsp2	6	111.2	251.1	1252.1	778.3	12317.5	8258.5	13957.8	9879.6	8511.6	2.4	6.2	25.6	16.8	265.2	173.6	296.3	213.9	181.0
Dkk3	6	1854.5	1531.6	3265.5	5086.8	7266.6	6631.9	8278.2	6169.8	7962.5	14.4	11.5	25.0	37.4	54.1	49.9	62.4	47.9	60.0
Tmem40	6	155.7	626.5	2511.6	2824.0	7381.6	3993.9	7848.0	5990.6	7251.7	2.5	6.2	26.4	28.2	76.0	40.1	79.8	59.5	72.6
Gpr137b	6	141.6	383.4	779.8	913.1	1088.9	449.3	1217.4	628.1	1046.1	6.1	11.9	29.8	38.5	48.0	19.4	54.3	26.2	45.1
Slc7a2	6	95.9	252.9	311.2	965.7	1146.7	1557.3	1452.6	1023.4	1293.1	3.8	7.5	10.7	32.0	37.5	49.5	47.3	32.0	41.1
Zbtb8b	6	579.7	770.0	1058.8	940.9	664.6	782.7	825.5	867.1	877.9	14.3	18.6	25.3	23.5	16.0	19.3	20.5	21.2	21.8
Cpeb1	6	24.9	74.6	192.3	491.9	390.6	575.3	437.5	400.6	455.6	2.4	5.2	17.0	41.2	30.3	48.9	38.3	33.1	38.6
Pla2g16	6	218.3	356.2	1516.1	6014.2	7426.1	8248.3	9047.2	7151.1	6329.6	2.1	2.6	10.7	38.8	53.8	55.9	60.9	51.1	42.9
Rsph10b	6	18.1	14.1	48.5	1083.5	849.5	1450.9	1284.0	819.3	1511.5	1.5	1.1	3.7	76.7	66.2	110.0	97.3	61.4	114.4
Gss	6	206.4	382.7	1170.8	2540.4	2678.5	1961.4	2798.9	2336.0	2049.0	2.9	4.6	12.8	28.0	30.2	22.1	31.1	26.1	23.0
Dock5	6	217.7	331.2	541.2	1285.4	2057.3	1373.9	2014.4	1016.8	1449.2	3.3	3.6	9.0	19.1	30.2	20.4	30.5	14.9	21.6
Synm	6	20.3	53.9	327.5	933.3	1792.3	1758.7	2363.2	595.5	1617.7	1.1	2.1	11.5	38.9	67.6	65.2	87.1	21.7	59.3
Usp15	6	38.6	160.4	526.1	1440.1	1020.9	1371.6	1216.3	1051.9	1108.7	1.4	2.8	8.8	35.9	25.6	33.8	31.1	24.6	28.0
Slc7a8	6	97.1	183.0	200.7	901.6	258.8	469.7	313.5	248.4	405.4	4.0	6.3	7.1	30.6	8.4	16.2	10.5	8.6	14.1
Sfrp1	6	666.3	2821.5	4311.3	5788.7	6541.3	3497.0	6692.4	5159.1	6171.5	2.2	7.4	11.2	16.7	17.4	9.4	18.1	12.8	16.7

Pon2	6	332.7	616.4	1368.8	2701.4	2281.1	1950.4	2634.2	1604.6	3193.2	2.3	3.7	8.1	17.3	14.5	11.9	16.2	10.1	19.8
Pkp2	6	352.1	370.8	889.6	1162.2	1398.6	1185.8	1311.8	924.1	1495.9	3.5	3.4	9.4	12.3	15.4	12.6	14.0	9.8	15.9
Malat1	6	365.4	314.0	755.8	692.7	1931.1	2801.2	1781.2	1234.3	1143.1	3.9	3.5	6.6	7.0	18.4	27.2	17.3	10.8	11.1
Fam89a	6	59.5	57.7	219.4	1244.8	2147.6	999.1	2863.8	1364.3	1722.6	1.6	1.1	4.2	24.6	44.7	20.6	57.2	27.9	35.5
Slc35f3	6	35.1	68.1	80.4	345.8	344.2	240.5	477.8	234.5	411.1	1.5	2.3	3.4	17.5	16.4	11.5	22.5	11.8	19.5
Susd2	6	151.8	97.1	94.8	234.4	226.5	250.3	289.7	177.8	259.0	5.7	3.9	3.7	8.9	7.4	9.2	10.1	6.9	9.6
Coro2b	6	224.8	218.5	463.1	2058.8	1812.4	2317.2	2121.5	1462.4	1555.2	2.3	1.6	3.9	20.3	17.1	22.5	20.0	13.4	15.1
Prkab2	6	132.1	170.7	208.9	805.7	1025.0	949.8	1498.9	811.9	1109.4	2.1	2.1	3.1	11.5	15.5	13.5	21.5	11.8	15.8
Mitf	6	75.7	125.2	137.2	391.2	554.5	764.4	568.5	464.9	666.1	2.2	3.5	3.8	11.4	15.6	22.0	16.3	13.2	19.2
Ypel2	6	515.0	1367.1	1654.9	1772.2	1778.1	1513.6	2192.6	1454.9	1828.1	2.7	5.2	7.6	9.4	9.3	8.0	11.7	7.7	9.7
Ptplad2	6	158.3	271.7	528.3	880.2	1137.4	834.0	1000.3	774.6	1052.2	2.0	3.2	6.2	10.4	13.6	9.9	11.7	8.7	12.5
Gstm6	6	35.8	64.1	71.9	328.6	191.8	301.3	215.7	276.6	150.1	1.9	2.8	4.5	18.5	10.8	16.7	12.2	16.4	8.3
1110059 G02Rik	6	265.0	258.0	523.1	1160.5	1112.6	886.4	1132.4	780.7	1061.7	2.9	3.0	6.1	14.1	13.0	10.4	13.2	8.8	12.5
Hfe	6	38.4	56.4	100.8	545.4	621.4	807.2	490.8	259.6	624.9	1.3	1.7	3.1	17.0	19.5	25.3	15.3	8.7	19.5
Nrcam	6	28.7	241.6	1384.7	2317.5	3748.9	2847.8	4166.6	3231.9	4553.8	-2.7	1.2	9.7	16.7	25.8	19.5	28.8	22.1	31.2
Ell2	6	1273.6	1624.1	3636.5	4834.0	2619.4	3003.2	2722.7	2559.3	3745.5	4.5	4.0	10.0	15.1	8.0	9.2	8.3	8.2	11.5
Six6	6	66.1	99.0	56.5	53.1	162.6	379.9	71.0	346.4	87.0	4.7	6.3	4.1	4.0	11.4	26.9	5.1	26.1	6.2
Pcp4	6	48.3	150.1	628.9	3805.7	4135.9	5007.8	5324.2	4597.2	4474.2	-2.0	-1.1	4.1	23.8	26.6	32.8	34.9	30.1	28.8
Rspo1	6	61.1	200.2	421.4	1070.2	1014.8	1073.3	991.5	668.9	1360.2	1.2	2.7	5.5	14.6	13.4	14.4	13.2	8.9	18.3
Crhbp	6	16.0	41.9	36.4	30.0	468.0	960.8	416.0	437.4	581.1	1.2	2.7	2.9	2.7	33.6	70.9	26.8	30.4	42.8
Rnf180	6	27.2	23.8	27.6	4669.5	3114.3	2616.9	3649.4	3543.8	4523.1	-1.1	-2.2	-2.0	88.8	58.5	50.4	72.8	70.7	87.1
Trpm1	6	105.7	182.6	69.8	85.8	184.0	263.7	139.0	232.1	190.0	4.4	6.6	2.8	3.9	7.8	10.9	6.1	9.2	7.9
Map3k5	6	85.4	94.8	89.8	418.4	617.7	813.8	717.3	926.9	1001.8	1.7	1.7	1.9	8.9	12.8	17.3	15.1	19.6	21.3
Katnal2	6	97.2	181.6	245.8	276.4	264.9	224.7	257.9	126.9	312.2	3.2	4.9	8.3	8.8	8.8	7.5	8.5	4.3	10.4
Palm2	6	35.4	28.0	68.9	1033.9	1795.0	1812.2	2048.2	1325.5	1060.9	-1.1	-1.6	1.5	21.7	40.6	37.7	44.1	28.0	23.7
Arhgap24	6	117.1	154.3	359.8	749.2	842.1	625.4	827.0	447.8	708.2	1.7	1.9	5.1	10.3	11.4	8.7	11.4	5.9	9.9

Hsf4	6	59.5	82.7	230.5	668.0	534.7	229.5	598.5	1144.1	339.8	1.7	1.8	5.4	15.6	12.2	5.4	14.1	25.8	8.1
Pmel	6	95.2	272.7	131.4	141.6	469.0	649.3	359.0	662.4	211.1	1.8	5.4	2.4	3.3	8.4	12.1	6.7	12.3	3.9
Vsx2	6	79.2	175.1	133.7	149.0	280.6	377.6	138.6	575.8	218.4	2.1	4.2	3.8	3.7	7.7	10.7	3.9	17.5	6.2
Ninj1	6	397.9	713.3	2064.3	4498.2	3513.6	4543.4	4329.5	4534.6	3141.5	1.2	1.6	4.3	11.7	9.0	11.6	11.2	11.6	8.1
Fam46c	6	361.1	739.5	1966.8	3857.5	3576.0	3729.9	3973.0	2965.1	3215.8	1.2	2.0	5.3	10.2	9.7	10.0	10.7	8.3	8.6
Gas7	6	72.0	65.6	102.9	312.4	242.3	501.4	338.5	208.0	257.7	2.0	1.6	2.8	9.0	7.0	13.5	8.9	5.2	6.9
Epdr1	6	97.3	443.0	911.1	1302.2	1028.4	1180.1	1031.3	1148.3	1663.5	-1.1	2.4	5.4	9.3	6.8	8.0	7.0	7.9	11.3
Glycam1	6	13.0	12.6	15.7	65.8	179.8	214.5	191.5	191.9	135.0	1.2	1.2	1.5	6.0	16.1	19.6	17.1	16.9	12.4
Rorb	6	42.1	54.7	41.2	87.5	160.4	194.7	64.4	648.3	38.2	2.7	2.9	2.4	5.3	6.4	10.0	3.5	26.4	2.0
Hspb2	6	212.0	161.5	237.7	837.9	620.7	657.3	846.2	977.5	631.7	2.1	1.7	2.4	8.2	6.5	6.7	8.7	10.0	6.4
Hist1h1c	6	225.4	327.1	432.0	1745.5	2193.9	2873.2	5115.2	1769.7	3072.1	1.1	1.3	2.1	8.0	10.0	13.6	23.7	8.5	14.5
Lrrc75b	6	21.5	42.7	48.0	1235.4	634.1	720.1	1097.0	1182.3	674.7	-1.4	-1.1	-1.0	34.2	18.0	19.5	31.1	30.4	18.6
Wbp2	6	354.8	625.0	738.1	1320.3	775.5	593.5	949.8	1010.5	1183.3	2.1	3.9	4.7	8.4	4.7	3.6	5.8	6.1	7.3
Gsn	6	178.5	159.8	1031.4	5777.5	4530.2	6339.5	4733.5	5278.4	4769.7	-1.4	-2.6	1.1	22.3	16.9	24.4	17.9	21.2	18.3
Cpeb3	6	23.6	22.0	36.6	410.8	335.8	418.1	452.1	384.7	527.5	-1.1	-1.1	1.4	15.9	12.7	16.3	17.5	14.3	20.6
Cpq	6	115.5	155.2	261.9	846.7	856.9	799.0	1137.6	932.3	1374.9	1.0	1.2	2.6	7.7	7.8	7.3	10.4	8.9	12.6
Scgn	6	97.7	114.2	142.2	258.3	264.2	321.3	329.8	479.1	341.9	2.1	2.2	2.7	5.7	5.4	6.6	6.7	9.4	7.0
Prkaa2	6	26.1	58.2	169.2	618.3	542.2	573.8	693.6	606.4	567.0	-1.5	1.0	3.6	13.0	11.8	12.2	15.0	11.7	12.2
Gabrg3	6	13.1	15.0	16.9	81.7	84.4	164.2	98.5	28.8	89.5	1.3	1.7	1.8	7.6	8.3	15.7	8.8	2.6	8.3
Qpct	6	17.2	24.4	38.2	353.6	420.3	319.7	594.7	353.5	447.1	-1.4	-1.0	1.2	13.3	15.2	11.4	20.9	13.2	16.0
Tom1l1	6	158.4	215.2	412.9	399.4	425.9	574.7	400.0	525.5	542.0	2.2	2.1	5.2	5.1	5.3	7.3	5.0	6.4	6.8
Tex2	6	81.5	91.2	215.8	1214.7	1179.4	1095.7	1280.0	1012.3	967.0	-1.2	-1.3	2.2	12.1	11.7	10.7	12.7	9.7	9.4
Sorbs1	6	111.2	516.1	1969.5	3316.8	2082.4	4290.2	2159.0	2260.9	3181.4	-1.8	1.1	5.9	11.3	7.2	14.7	7.6	7.7	10.9
Stk39	6	167.4	516.0	1343.2	2378.8	1235.3	1425.6	1080.8	1591.9	1380.6	-1.0	2.5	6.1	10.9	5.6	6.5	4.7	7.0	6.3
Gas6	6	50.6	74.0	214.2	981.6	809.9	639.0	898.2	970.9	1450.0	-1.8	-1.1	2.4	10.6	8.9	7.1	9.9	10.7	16.1
Add2	6	55.8	126.2	397.9	1440.6	1911.5	1687.5	1733.8	1441.8	1321.7	-2.1	-1.8	2.4	9.8	12.5	11.4	12.0	8.8	8.9

Acss2	6	15.3	16.1	25.0	65.9	222.1	47.5	244.8	68.0	179.4	1.3	1.3	1.8	4.7	17.2	3.7	19.2	5.3	13.7
Snx22	6	42.5	49.3	62.1	661.5	935.9	686.4	1257.2	831.3	1054.9	-1.4	-1.2	1.1	10.5	16.0	10.5	19.1	13.4	16.3
Grid1	6	15.5	24.3	54.0	201.6	162.6	280.6	204.9	112.7	129.8	-1.3	1.2	2.1	9.8	8.1	14.0	10.2	6.2	6.5
Rassf5	6	19.5	16.2	19.3	160.2	190.1	196.2	257.6	227.8	215.0	1.1	-1.1	1.0	8.8	10.3	10.8	13.8	12.3	11.8
Lpin1	6	24.0	23.5	48.0	319.2	458.0	371.7	725.8	290.2	578.0	-1.6	-1.3	1.2	7.8	11.7	9.3	18.3	6.6	14.5
Mapre3	6	48.3	107.5	118.3	454.2	164.0	171.7	194.0	269.3	288.6	1.0	2.3	2.8	10.5	3.8	3.8	4.6	6.9	6.8
Rbp3	6	30.9	59.7	82.4	310.8	114.4	65.1	94.0	423.6	182.8	-1.3	1.5	2.2	8.6	3.4	1.8	2.7	12.3	5.2
Rcan2	6	24.8	41.5	280.9	1111.9	1411.1	620.0	1692.0	1354.1	2283.1	-4.9	-5.3	1.6	7.0	8.3	3.8	10.1	8.4	14.0
Wfdc1	6	109.2	158.0	111.8	131.0	244.7	642.5	171.3	638.2	238.3	1.8	2.6	1.9	2.2	3.8	10.1	2.4	9.4	3.8
Slc6a15	6	17.2	29.3	102.5	229.8	463.9	635.1	420.6	853.9	63.6	-2.8	-1.9	2.0	5.4	8.9	14.1	9.5	19.3	1.4
Sfi1	6	76.2	103.3	124.8	83.2	90.9	114.7	95.6	442.7	45.9	2.4	3.1	3.7	2.7	2.7	3.5	2.9	13.2	1.4
Vwa5a	6	151.3	161.2	801.2	1470.1	1111.5	1637.9	1316.2	2179.8	1885.8	-1.7	-1.6	3.4	6.2	4.8	6.9	5.6	8.9	7.9
Hopx	6	64.8	78.0	103.7	2332.3	2304.1	2365.7	2436.7	975.9	1961.3	-2.4	-3.3	-2.2	10.3	10.0	10.6	10.6	4.3	8.8
Gadd45b	6	66.8	84.2	86.2	774.4	1356.9	1165.7	2169.0	2268.5	1146.9	-2.8	-2.0	-1.9	4.5	7.8	7.0	13.0	13.1	6.9
Col6a3	6	50.2	205.0	394.0	1303.1	1255.2	1594.6	985.8	3415.4	2437.4	-4.4	-2.2	1.1	3.6	3.8	4.3	2.8	9.6	6.9
Bend6	6	19.3	27.2	29.4	121.1	65.4	255.6	153.3	28.9	76.9	-1.1	1.2	1.4	5.1	3.2	11.8	7.6	1.3	3.6
Avp	6	38.2	43.2	48.8	213.4	121.5	187.9	161.8	2086.4	58.3	-1.1	-1.1	0.0	4.5	2.7	4.0	3.4	44.5	1.3
Cryga	7	16.6	1060.2	16528.3	18381.5	15757.5	18253.3	16181.9	20076.1	7291.5	11.6	55.3	1354.9	1517.0	1289.9	1492.0	1340.0	1646.3	595.9
Crygn	7	208.7	2360.1	14145.7	18754.4	19787.0	18829.7	18881.4	18756.2	2808.8	38.2	162.0	948.8	1280.1	1321.5	1285.4	1289.0	1272.1	191.3
Trpm3	7	820.2	782.2	1143.3	1592.9	1708.4	2158.4	2075.2	1058.5	1429.0	35.3	36.2	53.4	72.1	74.9	94.7	91.9	48.9	62.7
Vit	7	358.7	1181.0	2697.1	3116.5	3500.0	2594.0	3631.3	2762.9	2258.6	9.4	22.3	67.2	74.0	82.3	61.7	85.6	66.7	53.7
Crim1	7	1659.0	2448.0	3507.0	3698.3	3894.8	5738.6	4430.8	4926.9	2206.3	21.1	30.0	43.9	43.8	51.1	72.6	56.2	59.7	27.4
Pip5kl1	7	52.1	263.1	902.0	1010.0	1326.9	1139.9	1306.7	859.0	574.1	4.3	13.5	51.2	57.6	76.0	65.7	74.4	48.0	32.9
Caprin2	7	167.3	427.9	1642.7	4910.4	5903.2	3661.5	6658.6	2829.6	1334.2	3.1	4.3	17.7	54.9	65.0	40.4	73.8	31.3	14.7
Zfp365	7	19.1	129.0	517.6	1504.2	887.1	454.3	921.4	314.0	305.6	2.0	5.6	34.1	99.4	59.5	29.7	62.1	20.7	20.0
Gm17586	7	141.6	204.1	597.2	1407.7	1154.0	987.0	1070.3	623.8	338.4	3.6	4.8	14.7	37.7	28.2	25.1	27.3	16.5	8.6

Ptpru	7	347.8	639.7	1151.3	1326.6	1149.7	724.7	1320.9	1149.2	492.4	6.1	9.2	16.8	21.8	18.0	11.1	20.0	16.2	7.5
Slc16a12	7	54.7	181.8	525.6	786.8	408.3	447.8	385.8	483.7	375.6	2.0	5.2	16.8	29.2	13.3	15.4	13.5	15.4	13.0
Abca4	7	214.4	518.1	761.4	906.2	1032.6	677.9	935.3	644.3	463.3	3.3	7.9	11.8	14.2	15.6	10.6	14.1	10.3	7.2
Nid1	7	2697.6	5308.9	5020.2	8192.9	4391.5	6257.7	4469.0	4103.5	4901.1	6.0	10.4	10.1	15.3	8.2	12.2	8.7	8.0	9.5
Epb4.1l4a	7	574.7	866.1	1247.7	1353.6	1845.1	874.8	2061.6	1413.4	760.8	5.1	6.8	11.2	11.9	15.1	7.3	17.3	10.8	6.3
Bcar3	7	385.7	453.8	579.1	760.0	748.3	802.6	905.2	548.7	442.8	6.3	7.3	9.3	12.1	11.8	12.8	14.4	8.8	7.1
Slc24a4	7	34.9	46.4	172.5	959.6	1123.5	885.4	1579.9	828.4	662.7	1.1	1.5	5.4	28.9	35.4	27.2	45.5	23.9	20.3
Pla2g7	7	41.9	98.1	2246.7	3852.3	4400.6	3653.9	5172.1	5486.2	237.8	1.3	1.3	31.1	52.3	60.7	49.0	66.9	75.6	3.2
Cap2	7	192.5	572.4	1372.3	1317.5	2114.1	1808.9	1779.3	1112.4	1270.8	1.7	4.5	13.3	12.1	18.8	16.6	16.4	10.0	11.6
Ceacam10	7	23.0	20.8	21.8	1282.4	1089.4	721.8	930.9	849.9	664.1	1.7	1.1	1.0	65.5	57.6	36.7	50.7	42.2	33.8
Npnt	7	799.0	750.3	659.0	1297.9	1124.7	673.2	1178.3	530.5	891.9	6.2	4.4	4.3	9.8	7.6	5.2	9.0	4.3	6.9
Efcab1	7	99.2	283.9	717.6	1283.2	964.7	945.7	958.0	821.2	113.9	1.9	4.1	11.7	22.9	17.4	16.3	16.3	14.3	1.9
Lgi2	7	69.8	58.1	230.9	1364.9	1393.1	1560.7	1417.9	1282.8	246.8	1.5	1.1	4.1	30.0	30.0	33.8	31.1	29.3	5.3
Sptb	7	108.9	171.3	515.8	752.1	1223.9	576.7	1419.3	1164.6	680.0	1.2	1.9	6.9	11.8	16.8	8.0	19.9	14.0	9.5
Zfp536	7	216.8	204.5	356.4	491.8	674.3	628.2	753.3	283.7	306.3	3.4	3.3	5.6	8.0	10.9	10.4	12.2	5.1	5.1
Chrng	7	64.1	258.8	1264.9	1999.2	2381.0	1490.9	2554.9	1617.0	162.2	1.2	3.3	17.5	27.8	33.6	20.9	35.7	20.7	2.3
C030009J22Rik	7	10.7	8.9	46.4	171.3	199.7	269.1	234.4	77.2	109.4	1.3	-1.0	4.2	19.5	23.2	30.4	26.0	9.5	12.4
Tecrl	7	67.7	87.2	89.6	262.6	323.6	368.6	413.4	283.9	61.0	2.3	3.4	3.6	10.5	13.1	15.1	16.7	11.5	2.5
Pygm	7	38.9	33.2	184.1	1697.9	1251.6	1301.6	1306.5	1370.6	182.1	-1.2	1.0	4.3	50.2	33.5	35.6	36.3	34.6	5.1
Pgam2	7	56.2	99.8	824.9	3373.2	4488.0	5719.7	5255.9	4917.7	1303.3	-1.8	-1.3	5.0	20.0	26.3	34.4	32.2	30.2	7.8
Gcg	7	11.9	21.1	573.7	1429.6	2423.6	913.5	3111.8	871.0	52.0	-1.2	-1.3	18.4	47.1	72.8	30.4	99.9	28.3	1.7
Col4a2	7	1054.6	1861.8	2672.3	3007.6	3320.3	3404.9	3829.0	2900.6	1404.4	2.3	3.9	5.8	6.6	7.0	7.5	8.2	6.4	3.1
Col4a1	7	3237.3	5728.2	8030.3	7587.1	8523.5	7431.4	8831.3	5604.7	5745.6	2.6	4.7	6.3	6.0	6.6	5.9	6.8	4.5	4.6
Abcc8	7	104.5	184.4	278.5	328.2	479.6	540.4	622.3	518.6	84.0	2.4	3.8	5.6	7.1	10.0	11.1	13.1	9.5	1.7
Arntl2	7	16.0	19.6	107.9	296.9	84.4	131.7	73.3	122.0	26.1	1.4	2.0	11.2	32.2	9.1	13.8	7.5	12.3	2.7
Ggct	7	79.3	86.8	174.5	3122.9	2806.1	1687.6	3278.5	2388.4	670.0	1.1	-1.1	1.9	35.3	30.3	19.3	37.8	28.1	7.7

Optn	7	48.5	36.3	60.3	745.7	666.3	360.2	896.7	538.8	281.3	1.6	1.1	1.7	22.0	20.2	10.6	25.6	15.9	8.4
Drd4	7	54.9	69.7	304.4	620.5	737.3	535.6	716.0	517.9	256.4	1.1	1.3	6.0	12.5	14.5	10.3	13.8	9.6	4.9
Ctsf	7	267.2	480.2	647.6	457.5	489.9	658.3	613.6	592.8	463.5	2.4	4.3	6.4	4.2	4.7	6.1	5.8	5.5	4.3
E130119H09Rik	7	40.2	28.7	39.2	1262.3	1246.0	1195.6	980.6	825.2	608.6	1.2	-1.4	1.0	32.9	35.3	32.4	27.2	20.3	16.5
Sptbn2	7	347.0	883.7	1192.1	733.8	1066.6	924.0	1199.4	965.6	813.1	2.0	4.3	6.2	3.9	5.7	4.8	6.3	4.7	4.2
Stx11	7	10.8	13.6	14.6	485.9	645.7	556.9	861.4	593.7	349.0	-1.4	-1.3	-1.2	28.7	37.6	32.3	50.7	34.0	20.3
Tom1	7	475.7	517.8	1972.1	3713.3	4752.1	2764.7	4721.6	2352.0	2080.7	1.5	1.3	5.4	10.2	13.3	7.7	13.4	6.3	5.8
E330034G19Rik	7	42.0	21.2	27.1	711.7	553.3	631.0	1038.2	580.6	37.1	1.6	1.0	1.5	28.6	25.9	28.3	41.4	26.3	1.7
Cspg5	7	161.1	267.4	420.9	631.1	421.3	277.6	513.4	659.6	353.9	2.0	3.7	5.9	8.1	5.7	3.7	7.0	8.8	4.8
Tmprss5	7	39.1	46.8	86.7	319.0	383.1	365.9	489.7	261.2	79.6	1.3	1.6	2.8	10.6	13.0	12.3	16.3	8.2	2.6
Casp7	7	175.6	223.0	418.8	2150.6	1717.1	2047.1	2157.4	1905.2	589.5	1.3	1.4	2.6	14.1	11.2	13.3	13.8	12.5	3.8
Rnf123	7	176.1	208.7	590.2	1455.9	1904.9	1048.4	2130.8	1773.0	205.8	1.4	1.6	4.3	11.2	14.2	7.7	16.0	12.1	1.5
Dgkg	7	37.6	62.7	70.8	285.9	226.4	203.3	252.8	84.0	154.5	1.6	2.2	2.5	10.8	8.5	7.4	9.4	2.7	5.7
Pyroxd2	7	32.1	66.7	164.8	159.7	178.4	272.3	198.7	154.1	116.8	1.3	2.0	5.7	5.5	6.2	9.5	6.9	5.1	4.1
Myo7b	7	50.7	87.3	149.4	642.0	1109.7	395.6	1089.6	825.2	69.1	1.1	1.7	3.0	13.5	23.4	8.0	22.0	14.6	1.4
Nlrc5	7	23.8	20.6	23.2	341.1	437.0	529.6	351.6	173.4	124.5	1.2	1.1	-1.0	15.7	19.9	24.8	17.1	9.0	5.8
Pdlim7	7	386.8	648.9	1662.5	3170.0	3588.3	2754.0	3438.9	3203.1	680.6	1.3	2.2	4.4	9.2	10.0	7.8	10.0	8.9	2.0
Gm3515	7	224.3	39.8	73.7	1105.1	1267.4	1621.3	836.4	440.0	233.5	3.4	-2.0	1.3	17.0	20.9	27.5	14.3	8.3	4.0
6030439D06Rik	7	141.7	108.9	109.1	96.9	285.2	302.9	576.9	182.7	123.9	2.9	2.4	2.4	2.5	6.6	6.8	12.4	4.1	2.8
Tmprss11e	7	7.8	8.2	6.6	430.8	247.6	248.0	181.8	117.4	20.0	1.1	1.0	-1.0	56.6	30.6	32.1	22.3	16.6	2.4
Syt11	7	151.3	592.1	1323.0	2087.6	1811.0	1714.8	2002.9	526.9	640.7	-1.4	2.0	5.4	8.9	7.8	7.3	8.5	2.2	2.8
Nipal3	7	59.7	91.1	189.7	327.0	1361.3	225.0	1347.2	218.5	236.6	-1.1	1.5	2.8	5.4	21.9	3.5	21.2	3.4	3.7
Fgfrl1	7	344.6	649.0	1303.9	3241.4	5075.4	2854.5	5911.6	2108.0	1361.8	-1.1	1.3	2.7	7.7	12.8	7.1	14.5	5.1	3.4
Hlcs	7	84.2	155.0	324.1	297.8	313.0	240.4	292.3	255.3	176.7	1.5	2.6	5.4	5.1	5.2	4.2	5.1	4.6	3.1
Sdk2	7	31.5	95.5	179.0	1141.4	902.6	587.8	1015.8	562.4	161.2	-1.7	1.3	2.7	17.4	13.6	8.7	14.1	7.4	2.4
Tmcc3	7	103.6	106.6	747.7	1274.4	1294.8	1184.5	1281.1	673.6	767.8	-1.2	-1.7	5.0	9.1	9.6	8.7	9.3	5.1	5.6

Rsph3a	7	31.1	42.1	97.1	281.9	168.7	104.3	175.7	48.3	97.8	1.5	2.0	4.2	11.9	7.5	4.5	7.5	2.4	4.3
Cckbr	7	25.2	41.6	63.5	237.9	312.0	209.5	579.2	484.9	59.5	-1.1	1.4	2.3	7.2	9.7	6.8	19.2	14.8	1.9
Ggact	7	35.8	36.9	58.2	332.0	263.3	365.1	298.6	211.6	135.8	1.3	1.1	1.9	10.5	7.7	11.0	9.0	6.1	4.0
Gtsf1	7	16.9	21.1	23.2	251.1	292.2	322.9	360.3	209.1	101.6	-1.4	-1.1	-1.0	10.6	12.8	14.5	16.0	9.9	4.5
Fam189a1	7	21.3	54.4	60.6	396.8	411.5	316.1	403.3	178.4	260.2	-1.6	1.3	1.6	10.4	10.5	8.4	10.6	4.9	6.9
Hspb6	7	22.5	40.1	41.8	159.5	235.2	284.1	416.1	170.2	160.0	-1.2	1.3	1.0	4.8	7.3	8.7	12.9	5.3	4.8
Hspb3	7	24.6	47.4	137.8	618.8	721.6	751.7	772.9	745.9	142.5	-1.7	-1.2	2.3	10.4	12.4	12.8	13.1	12.0	2.4
Pappa	7	12.1	11.1	13.7	358.1	428.2	444.9	555.8	248.3	198.7	-2.5	-3.2	-2.2	11.4	12.6	13.1	17.1	8.2	5.9
Unc13c	7	21.9	16.9	80.4	299.5	311.5	182.3	244.9	88.5	27.5	1.2	-1.3	3.1	14.7	13.4	8.7	11.6	4.1	1.3
Bmper	7	57.0	265.5	833.7	1713.6	1841.9	862.6	1759.7	648.8	329.0	-1.9	1.4	5.7	11.6	12.9	6.0	11.9	4.5	2.3
Rgs8	7	45.6	57.8	312.8	633.2	358.7	179.3	199.9	173.5	181.3	-1.6	1.2	6.1	12.1	6.6	3.5	4.1	3.6	3.5
Lrrtm2	7	16.5	12.4	24.8	358.3	261.4	150.4	339.3	142.8	111.1	-1.2	-1.6	1.2	15.1	12.6	7.0	16.1	6.9	5.3
Scn11a	7	22.2	24.5	115.9	421.3	212.7	135.9	170.1	64.0	28.1	1.0	1.3	5.3	17.3	9.9	6.3	7.9	2.7	1.3
Cabp5	7	31.2	41.4	39.0	350.5	536.7	188.0	573.9	224.5	102.8	-1.1	1.1	1.0	8.7	14.6	5.1	15.8	6.0	2.8
Slc46a3	7	19.1	28.6	28.4	283.8	348.7	204.6	447.7	217.8	48.5	-1.1	1.0	1.2	11.9	14.7	8.3	17.3	8.3	1.9
1300017J02Rik	7	72.3	138.5	704.2	1024.6	1679.7	840.9	1449.9	877.8	168.2	-1.7	1.1	4.9	8.5	13.3	6.7	11.2	7.1	1.3
Ceacam1	7	16.9	17.3	19.6	105.6	168.9	64.9	199.6	127.5	30.4	1.2	1.2	1.3	6.9	11.3	4.2	13.2	8.5	2.0
Atp13a5	7	9.8	9.8	11.1	87.0	68.6	114.4	86.4	61.0	12.2	1.3	1.1	1.4	8.8	8.0	13.3	9.4	7.4	1.4
Syn2	7	40.4	49.5	218.6	228.2	339.4	394.7	594.3	207.8	54.2	-1.3	-1.0	5.4	5.3	7.6	9.2	15.1	4.5	1.3
Ccdc109b	7	12.3	11.9	9.7	94.9	235.0	80.1	282.4	243.8	62.6	-1.6	-1.5	-1.3	5.2	13.9	4.4	15.3	13.4	3.5
Ankrd66	7	18.0	15.4	17.9	201.0	177.6	194.8	173.6	216.2	25.3	1.0	1.1	-1.0	11.3	9.4	11.2	10.6	12.0	1.4
Rgs5	7	12.6	18.1	26.3	2242.6	1991.5	2398.9	2713.1	1745.6	67.4	-9.8	-8.5	-6.7	15.2	13.7	14.7	18.5	11.8	-2.4
Rmst	7	21.5	13.2	15.4	64.9	155.6	119.5	169.3	18.7	37.9	1.5	-1.1	1.1	4.9	11.8	8.4	12.1	1.3	2.7
Uox	7	20.1	22.2	26.1	231.4	292.6	22.2	440.5	224.5	119.6	-1.3	1.1	-1.0	9.4	12.0	-1.2	16.7	8.6	4.8
Wdr66	7	36.0	16.9	20.9	80.1	99.7	77.3	129.7	224.4	26.9	1.4	-1.4	-1.1	3.6	4.2	3.3	5.6	9.1	1.1
Rab42	7	23.8	22.3	32.6	327.6	67.9	110.3	27.4	51.6	28.5	1.1	-1.0	1.6	11.8	2.7	4.5	1.2	2.2	1.2

Gje1	8	41.6	600.6	4153.5	5535.8	2896.5	3166.2	2760.8	2435.9	206.0	19.2	69.5	742.9	1074.2	550.7	606.8	527.1	465.0	39.5
Sox1	8	571.2	1216.4	1898.7	2324.3	1111.7	1292.7	1267.6	880.6	730.3	10.0	16.1	26.0	36.2	17.4	20.1	19.9	13.8	11.2
Maf	8	6058.7	6137.9	7648.7	7956.6	4558.9	6626.4	4931.3	4056.6	4087.5	13.3	12.9	17.1	18.8	11.1	15.7	11.8	9.6	9.7
Med12l	8	514.2	736.1	880.4	978.8	725.4	1065.3	660.8	352.8	320.6	6.5	8.3	11.6	12.4	9.6	14.2	8.6	4.6	4.3
Ctnnd2	8	940.0	899.2	1386.7	1931.6	1262.2	1945.0	1146.2	879.6	520.0	6.4	6.1	9.7	13.9	8.6	13.2	8.1	6.3	3.5
Kcne1	8	74.4	98.1	94.0	165.8	117.9	115.4	78.0	65.3	32.0	5.4	7.1	6.6	11.4	7.9	8.0	5.4	4.5	2.2
Etl4	8	611.8	682.7	722.3	1013.7	614.2	819.3	610.5	271.9	538.9	5.3	5.3	6.1	8.2	5.0	6.8	5.1	2.3	4.5
Stxbp6	8	238.2	527.8	1000.5	1499.1	1062.9	1337.4	1128.5	202.3	337.2	2.0	2.8	7.8	12.4	8.7	10.9	9.3	1.6	2.7
Map6d1	8	43.4	57.5	166.0	229.8	130.3	93.9	90.7	60.8	46.9	1.5	2.0	5.6	7.6	4.4	3.2	3.1	2.2	1.6
Pik3cd	8	268.5	392.4	377.5	6218.8	161.2	5347.8	169.4	642.7	285.7	-1.1	1.2	1.2	22.4	-1.9	17.2	-1.8	1.9	-1.1
Aldh1a7	9	3452.0	2987.7	2558.7	3632.1	4205.7	2563.7	3469.4	2067.0	1334.6	116.3	101.4	90.1	123.4	134.3	88.1	121.5	74.5	45.8
Cntn6	9	73.7	183.4	207.4	253.4	227.8	286.9	281.0	135.8	72.5	5.5	11.1	14.9	18.2	16.8	20.5	19.9	10.3	5.0
Col4a6	9	450.4	837.9	1194.0	1038.1	1080.3	1091.5	1101.7	65.6	276.8	9.9	15.1	25.5	22.0	22.7	22.8	23.7	1.4	5.8
Adamtsl4	9	111.6	230.5	194.1	357.3	291.4	175.2	291.4	141.4	144.9	5.1	9.6	7.7	14.3	10.9	6.7	11.0	5.5	5.5
Ssx2ip	9	1751.7	2423.8	3532.5	4119.8	5843.5	3670.0	5345.2	3044.4	1314.4	3.8	5.0	6.6	8.3	11.5	7.4	10.8	6.4	2.6
Jag1	9	3203.7	3525.9	3806.0	3330.1	3425.4	3705.2	3179.0	1458.3	1171.5	6.5	6.9	7.4	6.7	6.9	7.4	6.3	2.9	2.3
Trpc6	9	12.5	27.5	96.2	192.1	200.9	111.1	116.5	69.7	14.2	1.4	2.5	9.7	19.3	20.6	11.0	11.9	7.2	1.4
Mafg	9	614.4	649.1	1049.0	1101.9	1056.8	1015.0	953.2	508.5	259.3	3.5	4.4	6.5	7.0	6.3	6.2	5.9	3.0	1.6
Cyyr1	9	71.3	83.9	173.8	1125.0	839.2	512.6	773.4	319.7	20.5	1.2	1.1	2.5	15.3	11.4	7.2	9.9	4.5	-3.5
Ptgfr	9	20.8	57.1	81.9	131.4	262.1	100.6	148.7	105.1	21.9	1.0	1.9	3.2	5.2	11.0	4.0	5.6	3.7	-1.2
Map7	10	1161.5	2233.0	2104.3	1201.0	1370.5	1090.1	1528.1	1156.4	1145.8	18.5	30.8	31.2	18.8	21.5	16.6	22.7	17.2	17.4
Bcl2l13	10	1070.8	1396.1	1902.7	1318.8	1371.5	1004.2	1344.1	1157.6	1031.0	4.1	5.2	6.8	5.1	5.1	3.8	5.1	4.3	3.9
Tpra1	10	479.2	859.9	925.4	518.7	725.9	541.3	639.2	381.0	333.7	3.6	6.1	6.8	3.8	5.5	4.0	4.6	2.9	2.5
Fam105a	10	145.2	252.7	213.5	210.7	237.8	135.7	239.4	189.4	184.4	2.8	4.6	4.0	3.9	4.1	2.4	4.3	3.4	3.2
Cpne7	10	223.6	564.9	617.8	195.4	154.2	163.7	149.4	204.1	49.8	5.9	13.6	14.0	4.7	3.7	3.8	3.6	4.5	1.2
Zfp385a	10	410.0	986.9	954.0	601.1	429.2	220.9	407.4	530.7	395.2	2.9	6.2	6.9	4.5	3.1	1.5	2.9	3.6	2.8

Gbf1	10	455.1	544.1	587.3	414.1	474.5	387.8	487.4	444.1	262.5	3.4	4.0	5.1	3.8	4.0	3.2	3.9	3.4	2.2
Fam43a	10	224.5	556.7	696.5	192.9	153.4	74.9	95.3	44.2	42.1	2.2	4.4	6.6	1.9	1.3	-1.5	-1.2	-2.1	-2.6
Sipa1l3	11	684.3	1156.8	1222.4	1193.2	821.1	746.5	856.1	645.6	609.7	5.8	9.3	10.3	10.0	6.5	6.1	6.9	5.2	5.0
Lacc1	11	301.2	374.7	463.0	406.7	339.8	143.8	348.6	65.6	361.6	8.0	8.1	11.2	9.9	8.2	3.5	8.2	1.7	8.7
Man1c1	11	777.0	786.7	836.9	991.4	708.4	725.8	794.1	582.6	588.6	6.3	6.7	6.8	7.9	5.7	5.8	6.1	4.8	4.7
Slc25a23	11	132.0	271.2	240.1	253.9	112.1	202.8	112.6	116.7	188.0	3.3	6.6	6.5	7.2	3.2	5.7	3.1	3.3	5.3
5830408B19Rik	11	364.8	671.1	698.0	673.5	533.0	421.1	433.2	384.7	295.3	4.0	5.3	6.4	6.5	5.3	4.2	4.1	3.7	2.9
Dgkb	11	118.2	166.2	159.8	102.9	73.3	79.7	46.3	51.1	176.9	5.6	6.9	8.4	5.4	3.7	4.1	2.4	2.5	9.0
Espn	11	47.6	85.8	97.0	68.9	28.5	25.5	28.5	33.7	29.1	4.5	7.1	9.0	7.2	2.7	2.5	2.6	3.3	2.8
Septin8	11	1160.4	1779.4	2152.7	976.9	861.0	1008.4	825.4	672.4	1353.3	4.1	6.0	7.0	3.3	2.9	3.4	2.8	2.3	4.5
Msi1	11	1041.8	1583.6	1778.7	2286.5	668.2	1171.6	802.8	696.5	431.3	2.6	4.4	5.2	6.0	1.8	3.0	2.1	1.8	1.1
Rgs13	11	19.2	91.3	84.3	50.1	13.1	9.7	9.8	7.2	11.0	3.1	8.7	12.8	6.6	1.8	1.4	1.4	1.1	1.6
Spp1	11	54.0	144.5	178.6	113.4	7.8	8.3	10.5	13.3	19.0	2.5	7.4	8.0	5.0	-2.8	-2.6	-2.1	-1.6	-1.1
Cyb561	11	151.6	251.1	177.3	93.4	39.5	28.2	31.8	18.9	29.6	3.2	4.2	4.0	1.9	-1.3	-1.7	-1.5	-2.5	-1.7