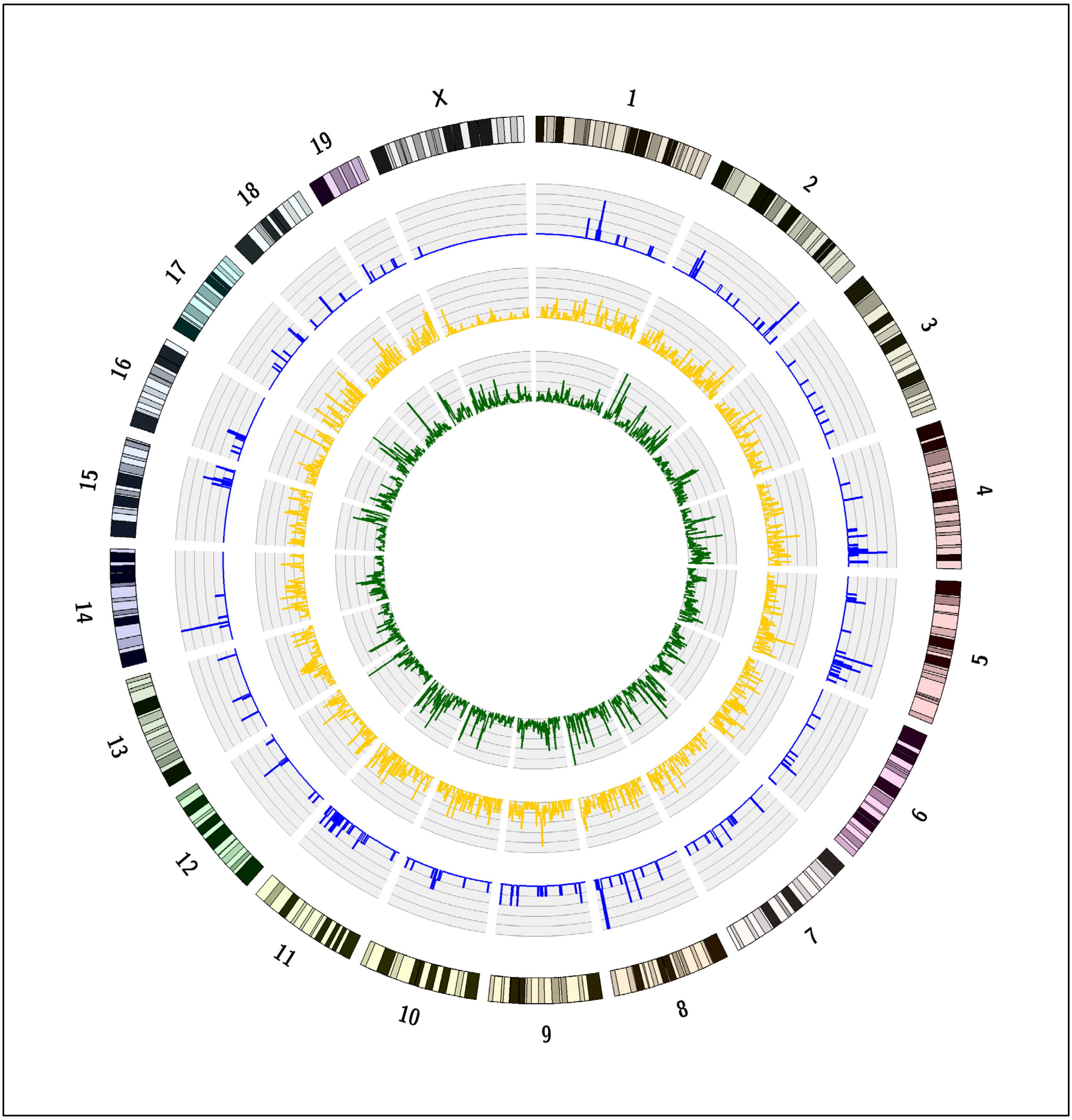

Figure S1 Locations of: annotated gene transcripts (green; genes per 1 MB genomic bin scale, scale 0-75), typical enhancers (TE; yellow, TE per 1 MB genomic bin scale, scale 0-15) and super enhancers (SE; blue, SE per 1 MB genomic bin, scale 0-5) relative to chromosomes (black).

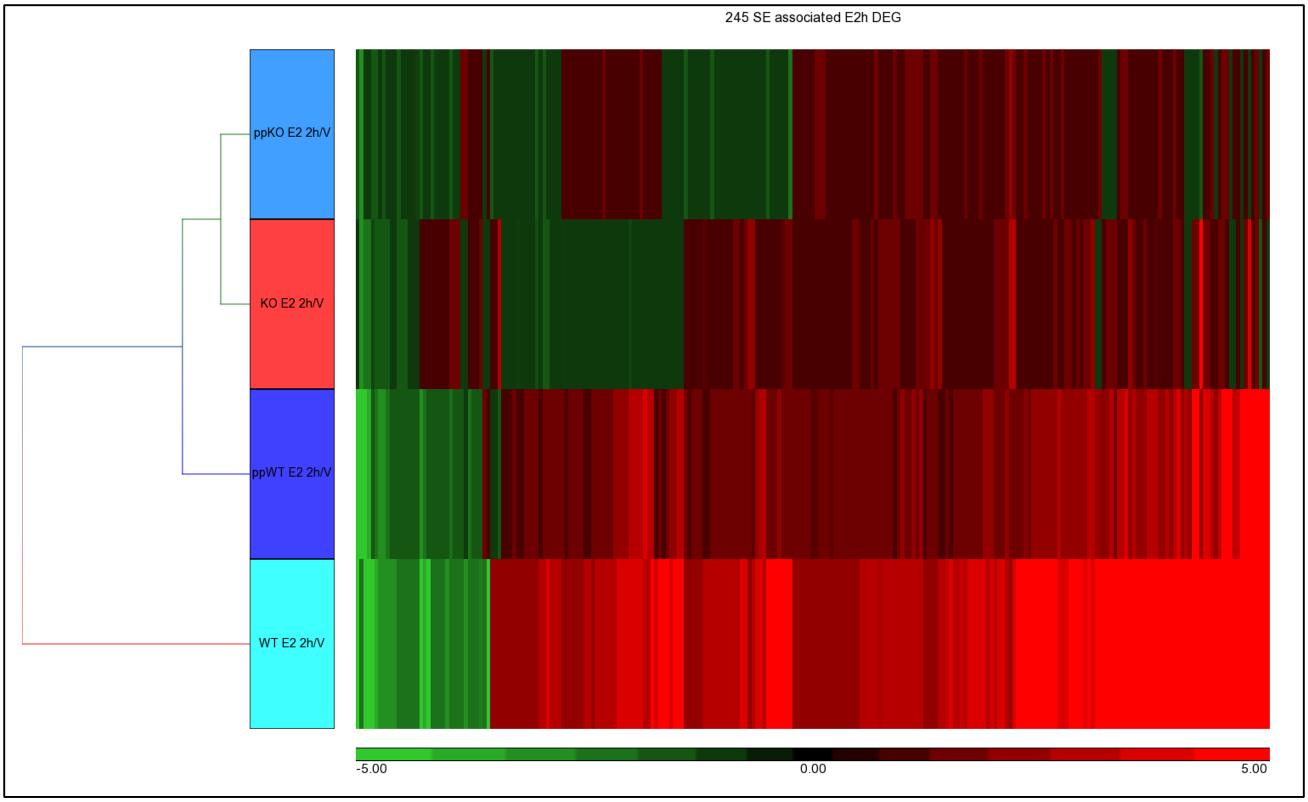

Figure S2 Hierarchical clustering of SE associated DEG reveals ERα-dependent E2 responsiveness is acquired as a result of pubertal development.

Microarray analysis of RNA isolated from uterine samples from adult ovex or 21-day old pre pubertal (pp) WT or ERαKO (KO) mice treated for 2h with V or E2. Each row shows the fold-change (E2 treated vs. V) of mean intensities derived from 3 replicate samples.

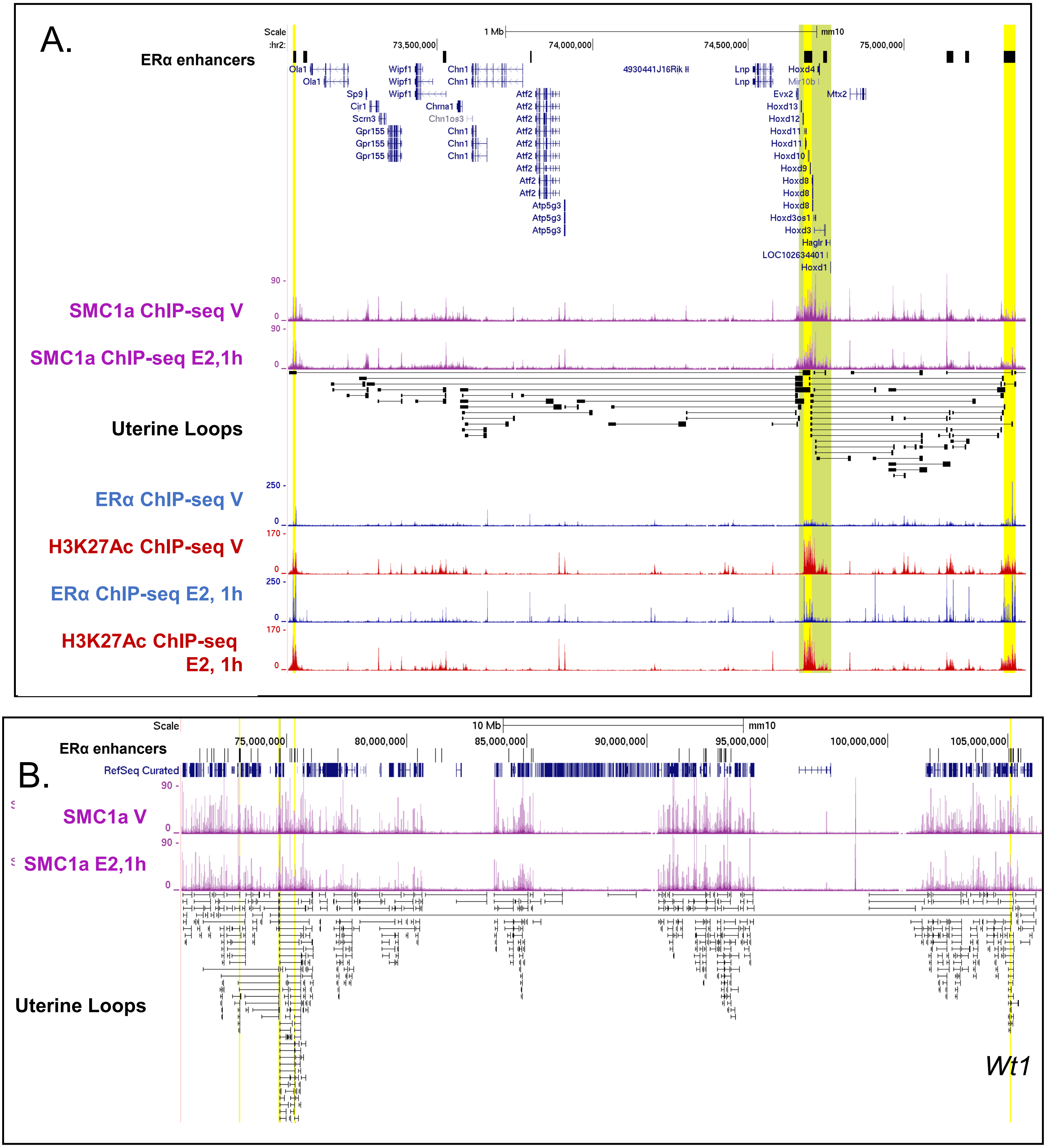

Figure S3 Chromatin loops of *Hoxd* cluster SEs with distal SEs

A. UCSC Genome Browser screenshot of *Hoxd* cluster (Chr2; mm10; chr2:73,022,009-75,418,655) near the SEs (yellow highlight) at and connected to the *Hoxd* cluster (green highlight). SMC1a ChIP seq tracks from ovex adult treated with vehicle (V) or with E2 for 1h are shown, with black lines connecting interacting regions called from the Hi-C analysis.

B. loop with SE 30 MB distal from Hoxd cluster (mm10; chr2:70,624,648-107,361,280)

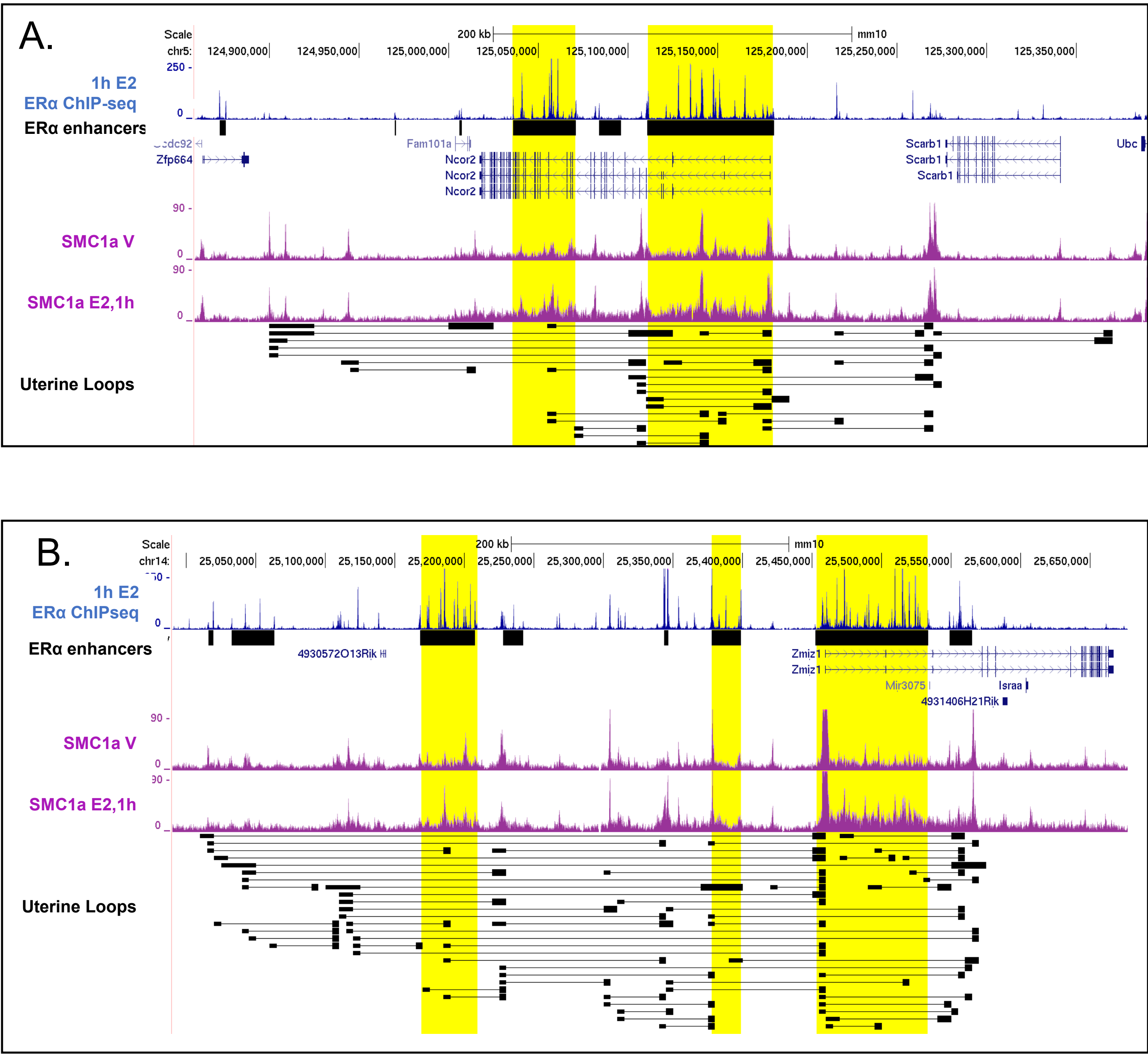

Figure S4

A. *Ncor2* (Chr5; mm10; chr5:124,858,420-125,390,828) SEs (yellow highlight).

B. *Zmiz1* (Chr14; mm10; chr14:24,990,067-25,676,917) SEs (yellow highlight) at or in loop to *Zmiz1*.

A.

Gene Symbol	average TPM	Gene Symbol	average TPM
Hoxa1	0.3	*Hoxd1*	0.1
Hoxa2	1.8		
Hoxa3	4.3	*Hoxd3*	7.3
Hoxa4	1.8	*Hoxd4*	71.7
Hoxa5	4.5		
Hoxa6	8.9		
Hoxa7	2.7		
		Hoxd8	45.5
Hoxa9	41.6	*Hoxd9*	35.3
Hoxa10	101.5	*Hoxd10*	73.0
Hoxa11	96.4	*Hoxd11*	23.8
		Hoxd12	0.0
Hoxa13	1.4	*Hoxd13*	0.0

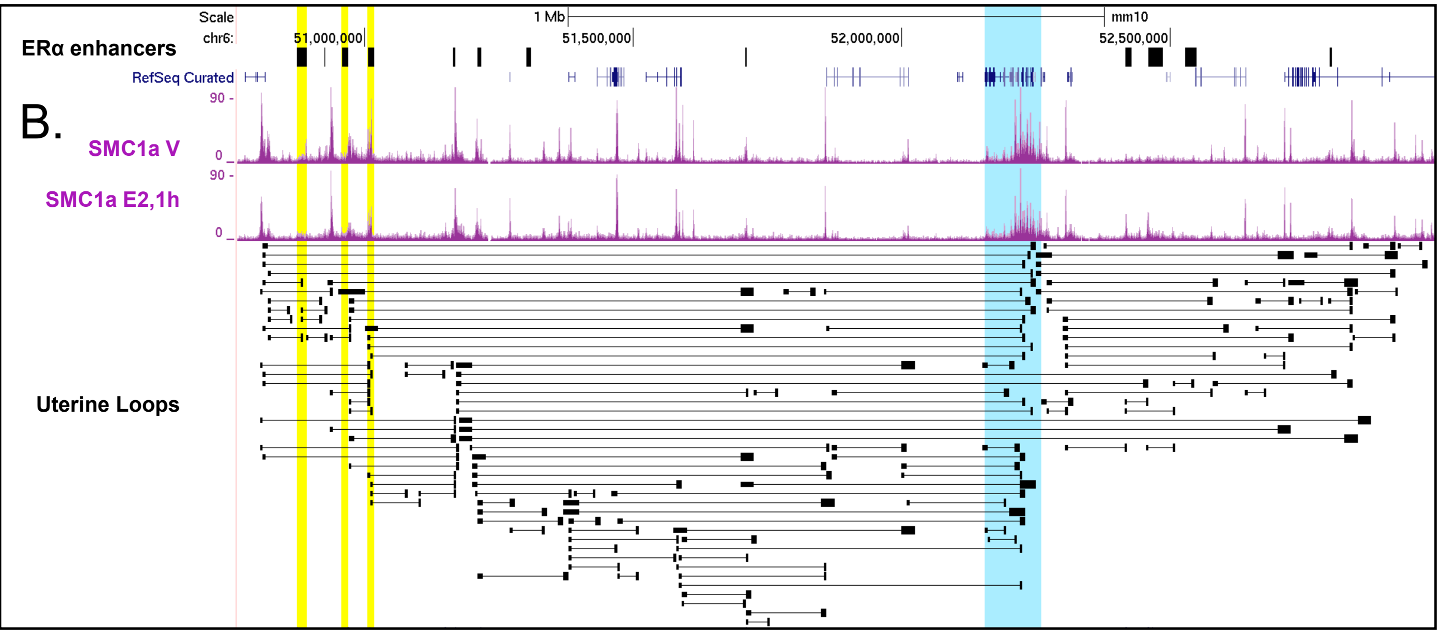

Figure S5

A. Expression of *Hoxa* and *Hoxd* genes in uterine RNAseq samples, average TPM across all 9 samples (3 replicates per each of 3 conditions V, E2 2h, E2 6h), giving an indication of the relative level of expression of each transcript.

B. *Hoxa* interactions with distal SEs. UCSC Genome Browser screenshot of Chr6 (mm10; chr6:50,762,332-52,994,317) near SEs (yellow highlight) connected to the *Hoxa* cluster (blue highlight).

SE by H3K4me1 signal							
sample	SE count	also SE by H3K27ac		top decile by H3K27ac		top quartile by H3K27ac	
Ovx E2	239	191	79.9%	219	91.6%	239	100.0%
Ovx Veh	236	205	86.9%	212	89.8%	235	99.6%
21dE2	275	180	65.5%	226	82.2%	273	99.3%
21dVeh	251	201	80.1%	212	84.5%	246	98.0%

Table S1 Comparison of SE called using H3K27Ac vs H3K4Me1

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr12:85815455-85824545	0610007P14Rik	58520	34.8	34.2	40.3	1.09987	0.411379	1.44587	2.83E-06
chr11:120348678-1203511	0610009L18Rik	66838	47.0	28.9	20.8	-1.4537	0.120263	-1.76345	0.0019887
chr11:70235204-70237914	0610010K14Rik	104457	31.5	32.1	39.2	1.14455	0.324599	1.55076	4.08E-06
chr17:25875500-25877163	0610011F06Rik	68347	64.9	57.6	35.4	-1.00699	0.960041	-1.46109	3.62E-07
chr4:107889899-10789780	0610037L13Rik	74098	82.7	86.5	86.2	1.17289	0.039586	1.30219	7.64E-06
chr4:101353783-10139918	0610043K17Rik	68400	15.0	10.9	3.9	-1.2246	0.548632	-2.83455	7.57E-06
chr16:90925811-90934849	1110004E09Rik	68001	24.2	23.2	35.7	1.08276	0.676637	1.8339	1.70E-07
chr7:116093380-11610521	1110004F10Rik	56372	127.7	126.2	167.2	1.10843	0.164644	1.63464	1.09E-20
chr2:156863122-15687356	1110008F13Rik	67388	54.6	67.5	112.0	1.38952	0.123124	2.48952	6.47E-09
chr2:32379101-32381915:	1110008P14Rik	73737	9.5	11.6	25.7	1.36141	0.083215	3.31413	3.84E-23
chrX:70385913-70389416:	1110012L19Rik	68618	46.0	38.6	15.2	-1.07609	0.726425	-2.37895	2.00E-11
chr4:41505009-41517333:	1110017D15Rik	73721	8.5	0.8	1.0	-6.22541	1.40E-05	-5.13195	6.66E-06
chr6:13871569-13896421:	1110019D14Rik	76311	7.0	5.6	1.5	-1.12466	0.638479	-3.48594	1.27E-12
chr17:84917182-84957710	1110020A21Rik	68531	3.0	1.7	0.5	-1.51067	0.20944	-4.26445	1.03E-07
chr9:50762828-50768152:	1110032A03Rik	68721	32.8	20.3	7.2	-1.44816	0.049412	-3.51048	3.08E-18
chr2:132690283-13275105	1110034G24Rik	73747	18.2	17.9	10.9	1.09377	0.519631	-1.32996	0.0033419
chr4:11485958-11551143:	1110037F02Rik	66185	56.6	54.3	54.4	1.07473	0.177862	1.20209	2.37E-06
chr17:34950236-34952471	1110038B12Rik	68763	81.0	121.2	382.5	1.66827	0.049745	5.42113	2.83E-18
chr15:76948544-76950731	1110038F14Rik	117171	45.5	46.8	58.8	1.15878	0.30005	1.60894	1.96E-06
chr13:33936032-33960181	1110046J04Rik	68808	8.9	6.3	2.4	-1.26327	0.40175	-2.79852	7.72E-07
chr2:91277828-91444642:	1110051M20Rik	228356	38.4	32.4	15.5	-1.05878	0.654363	-1.95796	1.20E-16
chr16:24392556-24393655	1110054M08Rik	68841	10.6	5.9	4.9	-1.60057	0.015586	-1.69976	0.0005885
chr1:23995939-24005640:	1110058L19Rik	68002	27.8	22.6	11.9	-1.11487	0.68241	-1.82973	0.0003846
chr4:124849485-12485073	1110065P20Rik	68920	23.3	18.5	28.8	-1.13339	0.44454	1.53096	8.13E-05
chr6:134929092-13495171	1190002F15Rik	381822	15.6	11.8	1.6	-1.18831	0.536243	-6.58325	9.45E-18
chr11:73047867-73083579	1200014J11Rik	66874	22.8	26.0	25.9	1.2859	0.145671	1.41173	0.008658
chr16:21794347-21809039	1300002E11Rik	1E+08	18.8	14.0	6.7	-1.20794	0.222437	-2.20453	2.01E-12
chr3:88822010-88832487:	1500004A13Rik	319830	3.1	1.7	0.7	-1.55711	0.179961	-3.08488	6.12E-06
chr2:127791377-12779248	1500011K16Rik	67885	29.5	25.9	37.5	-1.02462	0.887717	1.58219	3.77E-07
chr2:167062934-16706586	1500012F01Rik	68949	115.2	108.8	303.2	1.06171	0.723277	3.23805	1.96E-32
chr17:14943184-14945939	1600012H06Rik	67912	28.0	27.9	26.3	1.11617	0.188233	1.1746	0.0097737
chr8:103343878-10334753	1600027J07Rik	69794	0.4	0.5	3.5	1.27372	0.734711	6.12867	9.81E-06
chr5:30466077-30484087:	1700001C02Rik	75434	2.3	0.1	0.4	-5.51189	0.001968	-3.24725	0.0106026
chr17:47412734-47437375	1700001C19Rik	75462	3.0	0.2	0.3	-7.48201	4.99E-05	-4.95468	0.0001685
chr14:43342384-43347811	1700001F09Rik	71826	1.6	0.0	0.2	-5.60218	0.002247	-3.02739	0.0211585
chr5:146182450-14618530	1700001J03Rik	69282	8.2	2.4	2.3	-2.62805	0.02434	-2.45675	0.0080884
chr9:40050558-40053025:	1700001J11Rik	72224	6.0	0.3	0.8	-9.22286	3.68E-06	-3.92574	0.0012004
chr12:110667689-1106826	1700001K19Rik	66323	5.9	0.4	0.9	-6.68489	0.000104	-3.88618	0.0011742
chr13:68597439-68614231	1700001L19Rik	69315	2.5	0.6	0.2	-3.24419	0.014957	-5.40529	1.46E-05
chr6:83156404-83162975:	1700003E16Rik	71837	7.8	0.9	1.2	-5.84832	2.16E-06	-4.17294	1.03E-05
chr2:154548904-15455004	1700003F12Rik	75480	6.9	0.8	1.8	-5.3616	2.77E-05	-2.72984	0.0027733
chr3:124565891-12458109	1700003H04Rik	384775	2.1	0.1	0.4	-5.71932	0.001706	-2.71523	0.0341656
chr4:34711332-34730206:	1700003M02Rik	69329	12.9	1.4	1.7	-5.63917	9.58E-05	-4.33179	0.0001244
chr3:124401155-12442602	1700006A11Rik	71824	2.8	0.1	0.2	-7.83613	0.000114	-4.77354	0.0006973
chr11:101987056-1019922	1700006E09Rik	75437	3.1	0.2	0.2	-4.13863	0.016156	-3.70805	0.0058183
chr8:75448694-75984507:	1700007B14Rik	71831	1.9	0.2	0.3	-4.43844	0.003514	-3.20323	0.0056181
chr8:129067134-12918373	1700008F21Rik	75453	3.5	0.2	0.5	-7.87503	4.31E-05	-3.7783	0.0022138
chr17:49112264-49113533	1700008K24Rik	69311	11.0	0.5	1.4	-7.52242	0.00012	-3.77881	0.0035621
chr4:39450293-39451778:	1700009N14Rik	75471	5.1	0.2	0.7	-11.5618	1.70E-07	-4.22159	0.0002881
chr2:173719415-17372208	1700010B08Rik	75485	5.2	0.2	0.9	-7.0547	0.000191	-3.06287	0.0133586
chrX:95732590-95733265:	1700010D01Rik	76386	3.5	0.0	0.6	-6.86878	0.000435	-2.85088	0.0299176
chr17:8988333-9008319:+	1700010I14Rik	66931	12.3	3.5	3.0	-2.83356	0.004993	-2.88319	0.0004753
chr17:87389571-87427741	1700011E24Rik	75467	8.3	0.5	1.4	-8.12554	2.66E-06	-3.69387	0.0006424
chr14:49226359-49245428	1700011H14Rik	67082	2.9	1.4	0.4	-1.70341	0.264132	-3.73604	0.0002358
chr18:57533826-57731065	1700011I03Rik	75444	3.3	0.3	0.5	-5.57411	0.001185	-3.32456	0.006983
chr8:79210430-79248583:	1700011L22Rik	67687	6.8	1.4	0.9	-3.45827	0.004689	-4.58145	2.30E-05
chr6:32050288-32058915:	1700012A03Rik	76382	6.8	0.6	1.4	-5.82967	0.000292	-3.05151	0.0071294
chr11:109788291-1098280	1700012B07Rik	69324	3.6	0.4	0.7	-4.63946	0.003541	-2.87614	0.0156151

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr9:14758194-14771030:	1700012B09Rik	69325	3.0	0.0	0.3	-6.86279	0.000452	-3.61732	0.0068154
chr6:124347594-12435708	1700013D24Rik	76921	3.4	0.1	0.4	-5.22267	0.003621	-2.97358	0.0235327
chr3:108537584-10854469	1700013F07Rik	75504	8.8	1.3	1.1	-4.63939	0.000364	-4.61635	2.67E-05
chr4:137453296-13745546	1700013G24Rik	69380	7.6	0.4	0.7	-7.29347	0.000167	-4.68495	0.000681
chr1:170308861-17031212	1700015E13Rik	76925	6.1	0.4	0.8	-6.11008	0.000709	-3.77714	0.0033602
chr5:5437827-5479143:-	1700015F17Rik	381716	4.2	0.2	0.4	-5.30112	0.003501	-3.87111	0.0044221
chr7:52011680-52015716:	1700015G11Rik	1.01E+08	9.2	0.4	0.8	-8.79555	1.50E-05	-5.62738	5.87E-05
chr8:11654924-11678750:	1700016D06Rik	76413	1.6	0.1	0.4	-5.03358	0.004823	-2.43031	0.0662708
chr5:103648587-10365573	1700016H13Rik	74218	7.3	0.5	1.2	-6.50669	0.000152	-3.36526	0.0042975
chr11:75999912-76003569	1700016K19Rik	74230	4.6	0.4	0.7	-5.66499	0.000108	-3.95022	0.0002849
chr6:13413337-13415996:	1700016P04Rik	69413	4.9	0.3	0.7	-5.01897	0.004791	-3.28733	0.0120178
chr19:11096816-11130878	1700017D01Rik	69369	4.0	0.3	0.4	-5.38131	0.002699	-3.85	0.0039458
chr10:100592386-1006183	1700017N19Rik	66605	2.4	0.1	0.3	-7.09493	8.55E-05	-3.94143	0.0012373
chr8:121530784-12154195	1700018B08Rik	76405	4.5	0.1	0.5	-10.2803	2.59E-06	-4.89387	0.0001952
chr4:63607091-63622429:	1700018C11Rik	75524	5.2	0.2	0.9	-6.71921	0.000392	-3.09348	0.0145571
chr5:145042990-14504567	1700018F24Rik	69396	2.0	0.1	0.3	-6.52464	0.000583	-3.55955	0.0063145
chr19:29047483-29048729	1700018L02Rik	67329	1.9	0.8	0.2	-1.84132	0.285905	-4.03957	0.0009796
chr1:53158577-53187617:	1700019A02Rik	69397	5.9	0.5	0.7	-4.40495	0.010007	-3.62003	0.0058961
chr1:52925127-52952840:	1700019D03Rik	67080	10.4	1.6	2.1	-4.06198	0.004369	-2.9823	0.0070575
chr6:85899050-85904938:	1700019G17Rik	75541	6.1	3.3	2.0	-1.62677	0.032676	-2.36793	1.20E-06
chr6:5963897-5977393:-	1700019G24Rik	72249	2.7	0.1	0.3	-6.22891	0.000952	-4.05529	0.0029451
chr2:32777413-32784405:	1700019L03Rik	227736	3.0	1.1	0.4	-2.22371	0.029835	-4.72495	2.46E-07
chr12:96046621-96047222	1700019M22Rik	69423	11.4	0.5	1.1	-9.57834	4.14E-06	-5.31308	8.59E-05
chr19:58785803-58794414	1700019N19Rik	67507	10.3	0.9	2.2	-6.82458	7.60E-06	-2.97998	0.0033277
chr1:86426329-86428049:	1700019O17Rik	71863	2.4	0.1	0.3	-8.23628	1.64E-05	-4.81268	0.0001687
chr2:130405259-13040607	1700020A23Rik	75656	1.7	0.1	0.1	-4.00758	0.018145	-3.73759	0.0051578
chr19:5502769-5503787:-	1700020D05Rik	75555	13.1	3.5	2.9	-2.96284	0.003181	-3.08998	0.0001969
chr2:119594296-11960074	1700020I14Rik	66602	130.0	128.0	80.9	1.10083	0.18078	-1.28631	2.05E-06
chr11:83437694-83441232	1700020L24Rik	66330	1.7	0.2	0.4	-4.49368	0.003053	-2.6167	0.0189772
chr1:91404879-91406029:	1700020N18Rik	67086	3.8	0.3	0.4	-4.01103	0.018662	-3.64411	0.006128
chr10:43525121-43540994	1700021F05Rik	67851	37.5	38.7	54.1	1.16149	0.207265	1.79798	1.41E-12
chr2:173522592-17352850	1700021F07Rik	72221	3.8	0.2	0.6	-5.38448	0.002799	-3.0093	0.0198145
chr16:32821702-32868366	1700021K19Rik	1.01E+08	34.2	25.9	21.8	-1.18857	0.123056	-1.25093	0.0090083
chr5:24645453-24648860:	1700022A21Rik	72252	3.5	0.2	0.4	-6.05927	0.000732	-4.18883	0.0015084
chr10:61674527-61680290	1700022H01Rik	75539	1.5	0.1	0.2	-4.24521	0.013679	-3.51372	0.0079474
chr5:77016023-77061522:	1700023E05Rik	71868	3.2	0.1	0.4	-10.1218	1.19E-06	-4.89242	9.58E-05
chr11:103198944-1032085	1700023F06Rik	69441	2.4	0.2	0.2	-5.49613	0.001185	-5.02885	0.0002392
chr6:29985329-29993531:	1700023L04Rik	76419	4.5	0.9	0.4	-3.66839	0.003826	-5.38823	7.25E-06
chr13:98984090-98984565	1700024P04Rik	69382	7.4	0.4	0.8	-6.12588	0.000932	-3.98056	0.0028584
chr4:104913456-10501686	1700024P16Rik	242594	2.8	23.0	20.7	6.63737	8.37E-07	6.40521	3.26E-08
chr19:11139683-11165320	1700025F22Rik	69416	3.5	0.1	0.0	-6.16548	0.001085	-9.2466	1.49E-06
chr1:151884524-15209032	1700025G04Rik	69399	16.9	13.6	8.9	-1.11466	0.339022	-1.52601	1.32E-07
chr2:28692080-28699651:	1700026L06Rik	69987	12.9	1.2	2.0	-6.11024	4.63E-05	-3.86413	0.0003879
chr1:73016036-73025508:	1700027A15Rik	69449	15.5	1.8	1.6	-4.42972	0.007117	-4.31766	0.0011425
chr10:43746158-43765836	1700027J07Rik	69443	1.0	0.4	0.1	-1.86628	0.29766	-3.47432	0.0051844
chr7:44229930-44236122:	1700028J19Rik	70004	9.7	1.7	2.1	-3.9119	0.00045	-3.09274	0.0006105
chr19:23558760-23652812	1700028P14Rik	67483	44.9	32.1	1.8	-1.24696	0.376513	-16.6885	4.43E-45
chr13:97021864-97035254	1700029F12Rik	66479	8.1	0.3	1.0	-11.2572	5.77E-07	-4.30428	0.0005087
chr8:13550722-13562461:	1700029H14Rik	66501	10.6	1.0	1.9	-6.47117	5.94E-06	-3.5895	0.0003757
chr8:45953606-45975252:	1700029J07Rik	69479	26.3	18.6	4.3	-1.26878	0.20005	-4.71306	1.40E-29
chr4:135626655-13563019	1700029M20Rik	73937	4.0	0.1	0.4	-10.2577	3.16E-06	-4.6331	0.0004752
chr15:81980540-81981563	1700029P11Rik	66346	3.4	0.3	0.3	-4.87881	0.004852	-4.77712	0.0006842
chr6:117679207-11775176	1700030F04Rik	72263	1.5	0.1	0.1	-3.33017	0.041611	-3.40394	0.0082293
chr8:116969599-11697894	1700030J22Rik	69528	4.4	1.3	0.8	-2.71007	0.00428	-3.9267	1.71E-06
chr8:72443880-72460541:	1700030K09Rik	72254	22.1	20.1	14.0	1.01406	0.932422	-1.26104	0.0098656
chr15:98398445-98416135	1700031M16Rik	73302	5.3	0.3	0.6	-6.86145	0.000292	-4.12266	0.001816
chr12:52599984-52602322	1700031P21Rik	73278	2.5	0.0	0.4	-4.54311	0.00819	-2.52532	0.0561246
chr18:52646220-52663731	1700034E13Rik	78414	8.4	0.4	1.0	-5.83843	0.001599	-3.60527	0.0067363

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr3:40900199-40902543:	1700034I23Rik	73297	2.5	0.1	0.2	-11.3468	1.19E-06	-6.16909	2.60E-05
chr6:146951301-14695442	1700034J05Rik	73344	4.1	0.2	0.5	-8.82747	2.65E-06	-4.98525	6.05E-05
chr6:41684431-41685717:	1700034O15Rik	76606	7.8	0.5	0.7	-6.17007	0.000327	-5.1552	0.0001362
chr16:3905798-3908689:-	1700037C18Rik	73261	11.9	7.6	5.7	-1.38411	0.184549	-1.64166	0.007242
chr2:131146325-13116002	1700037H04Rik	67326	36.5	28.6	20.3	-1.12961	0.484979	-1.42723	0.003292
chr7:45282873-45288993:	1700039E15Rik	76713	4.2	0.1	0.5	-10.8948	8.44E-07	-4.62443	0.0002508
chr10:68430956-68541875	1700040L02Rik	73287	10.2	6.4	1.6	-1.40417	0.184572	-4.763	1.49E-14
chr9:57175275-57186110:	1700041C23Rik	67319	2.5	0.1	0.1	-3.98976	0.015727	-3.59323	0.0057655
chr4:116173372-11617429	1700042G07Rik	67323	7.9	0.5	0.8	-6.19972	0.000642	-4.47033	0.0009023
chr4:57359792-57364292:	1700042G15Rik	73349	2.8	0.1	0.4	-8.76818	1.04E-05	-4.20259	0.0007183
chr9:121937275-12194701	1700048O20Rik	69430	14.5	9.4	6.2	-1.35295	0.320845	-1.78537	0.0091694
chr6:147690241-14770237	1700049E15Rik	1E+08	0.2	0.3	1.6	1.34067	0.669268	5.13922	6.99E-05
chr7:27907392-27929430:	1700049G17Rik	73430	13.0	10.2	6.9	-1.15192	0.402613	-1.48992	0.0008519
chr10:71979885-71980690	1700049L16Rik	108950	3.5	0.1	0.4	-6.90299	0.000383	-3.61943	0.0059684
chr11:72266844-72268556	1700051A21Rik	73366	2.0	0.1	0.2	-4.92598	0.005393	-4.24361	0.0021138
chr11:105179021-1051814	1700052K11Rik	73431	9.7	8.5	12.0	-1.01846	0.925733	1.54535	1.47E-05
chr9:92309377-92357876:	1700057G04Rik	78459	1.8	0.0	0.2	-6.32211	0.00088	-3.79083	0.0051436
chr17:56875633-56888838	1700061G19Rik	78625	2.8	0.5	0.4	-3.5311	0.004498	-4.46426	3.91E-05
chr18:35726989-35730869	1700066B19Rik	73449	0.4	0.4	1.1	1.0069	0.991581	2.64413	0.0006877
chr13:58146949-58148975	1700066J03Rik	67339	2.3	1.5	0.0	-1.34353	0.644489	-6.47822	2.27E-05
chr1:57377620-57385422:	1700066M21Rik	73467	11.2	9.0	12.3	-1.1222	0.43505	1.36266	0.0021647
chr17:48089632-48090920	1700067P10Rik	68224	1.4	0.1	0.1	-4.37953	0.011742	-3.63374	0.0067704
chr6:40920460-40940557:	1700074P13Rik	73481	8.2	0.4	0.9	-9.69169	1.97E-06	-4.96702	0.0001199
chr9:105143344-10514508	1700080E11Rik	73532	3.8	0.4	0.2	-4.17777	0.014923	-5.31888	0.0003488
chr1:169928939-16993465	1700084C01Rik	78465	1.5	0.8	0.1	-1.49599	0.553549	-4.34436	0.0014085
chrX:91575211-91575911:	1700084M14Rik	73487	2.1	0.1	0.0	-4.45502	0.010287	-5.19097	0.0004201
chr12:74284276-74295950	1700086L19Rik	74284	4.0	1.7	7.2	-1.93329	0.074777	2.14314	0.0042834
chr18:38238405-38250565	1700086O06Rik	73516	6.2	5.4	7.2	-1.0366	0.876369	1.43853	0.0037003
chr15:79134655-79141251	1700088E04Rik	27660	12.4	9.0	2.7	-1.22127	0.460384	-3.47005	1.25E-10
chr11:23516203-23519942	1700093K21Rik	67358	4.6	0.1	0.4	-8.67689	4.08E-05	-4.63729	0.0007894
chr3:90062796-90068347:	1700094D03Rik	73545	15.5	11.3	6.2	-1.22737	0.081346	-1.98481	1.84E-14
chr5:112793292-11280170	1700095B10Rik	67360	1.6	0.1	0.2	-5.69581	0.001965	-3.46473	0.0088855
chr13:70573241-70576104	1700100L14Rik	73584	1.2	0.1	0.1	-3.29379	0.046112	-3.36753	0.009589
chr6:129532184-12953328	1700101I11Rik	1.01E+08	1.5	0.9	0.2	-1.48309	0.511517	-3.59257	0.0028352
chr17:10324602-10329312	1700110C19Rik	76634	6.7	3.6	2.0	-1.65738	0.120616	-2.50285	0.0002913
chr14:22019712-23056088	1700112E06Rik	76633	7.0	5.1	2.1	-1.23124	0.519935	-2.45654	8.40E-05
chr3:88171560-88177785:	1700113A16Rik	76642	7.2	4.2	2.3	-1.49728	0.162148	-2.33064	0.0001308
chr10:87058046-87230599	1700113H08Rik	76640	2.7	0.9	0.4	-2.45998	0.05344	-3.96622	0.0001647
chr6:96164503-96166205:	1700123L14Rik	78482	13.3	0.6	1.6	-11.85	9.69E-09	-4.80982	2.90E-05
chr14:54686171-54690742	1700123O20Rik	58248	30.2	35.2	37.8	1.30736	0.031292	1.55946	3.09E-06
chr14:59133040-59142893	1700129C05Rik	67932	4.7	0.2	0.5	-8.06664	7.30E-05	-4.28779	0.001377
chr7:145205818-14520811	1810010D01Rik	1E+08	5.3	3.7	1.8	-1.23857	0.604861	-2.14686	0.0065887
chr11:107028223-1070304	1810010H24Rik	69066	14.1	9.0	3.1	-1.39742	0.223293	-3.36982	3.74E-09
chr14:32785963-32817968	1810011H11Rik	69069	3.9	2.9	1.5	-1.19076	0.53387	-1.9917	0.0004978
chr10:86685527-86689954	1810014B01Rik	66263	11.7	8.4	4.3	-1.25252	0.364834	-2.08269	3.76E-05
chr15:89071198-89075854	1810021B22Rik	69120	9.3	7.4	3.9	-1.11512	0.731826	-1.85837	0.0025896
chr3:14606289-14611256:	1810022K09Rik	69126	178.9	217.8	343.9	1.36991	0.03373	2.36917	8.82E-15
chr7:73539798-73558395:	1810026B05Rik	69170	57.8	47.3	29.2	-1.09873	0.381294	-1.57794	8.93E-10
chr9:21592722-21595970:	1810026J23Rik	69773	32.2	34.4	42.6	1.20469	0.198788	1.63983	2.53E-06
chr11:116671660-1166757	1810032O08Rik	66293	19.7	26.9	39.1	1.52867	0.022558	2.42866	4.43E-10
chr13:64248700-64268145	1810034E14Rik	66503	4.0	3.0	0.7	-1.20981	0.532393	-4.28832	1.34E-10
chr3:122924397-12292619	1810037I17Rik	67704	69.0	79.2	72.3	1.28159	0.048747	1.30269	0.0069725
chr15:84379203-84447097	1810041L15Rik	72301	3.3	3.4	0.6	1.14316	0.68241	-3.86889	1.44E-10
chr10:77978650-77985438	1810043G02Rik	67884	27.3	18.9	10.0	-1.29554	0.10107	-2.14786	1.32E-10
chr11:120098934-1201004	1810043H04Rik	208501	30.1	31.2	49.0	1.16706	0.271579	2.0265	5.16E-14
chr19:3708333-3717881:+	1810055G02Rik	72056	18.4	28.2	58.2	1.71852	0.009803	3.79101	2.57E-16
chr3:36475937-36482299:	1810062G17Rik	72282	4.9	2.1	1.6	-1.98788	0.031549	-2.32229	0.0008089
chr9:22206786-22213860:	1810064F22Rik	69862	3.7	2.2	0.5	-1.52421	0.144193	-5.07384	4.62E-12

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr2:158070364-15809179	2010009K17Rik	72340	26.4	16.7	4.7	-1.39505	0.36596	-3.9221	2.34E-07
chr12:111961376-1119669	2010107E04Rik	70257	183.0	200.5	259.3	1.22354	0.087555	1.75898	7.34E-11
chr10:62107656-62111013	2010107G23Rik	69894	6.0	3.7	1.6	-1.45803	0.051702	-2.99657	5.24E-12
chr5:93206518-93213474:	2010109A12Rik	75610	3.9	2.2	0.4	-1.47251	0.456025	-4.50866	8.93E-05
chr13:62964893-63326096	2010111I01Rik	72061	66.6	53.1	41.9	-1.12566	0.302944	-1.26709	0.0045838
chr1:37611676-37719811:	2010300C02Rik	72097	7.3	4.5	3.7	-1.43901	0.068197	-1.52387	0.0062481
chr9:124291804-12431269	2010315B03Rik	630836	28.8	16.9	8.3	-1.5233	0.072915	-2.68442	2.30E-08
chr8:70776862-70777606:	2010320M18Rik	72093	21.9	15.4	8.8	-1.27308	0.370691	-1.92382	0.000721
chr11:5762150-5784710:+	2210015D19Rik	76508	13.2	13.5	19.7	1.14735	0.328072	1.84948	1.15E-10
chr13:58380046-58385225	2210016F16Rik	70153	26.0	27.0	39.6	1.16609	0.125126	1.89874	4.79E-19
chr7:98590606-98656569:	2210018M11Rik	233545	46.4	51.3	27.7	1.24651	0.083628	-1.33447	0.0032472
chr17:21879570-21909926	2210404O09Rik	70081	15.2	11.2	6.6	-1.22434	0.25027	-1.81696	3.32E-06
chr6:31220351-31337394:	2210408F21Rik	73652	6.0	4.9	2.8	-1.09805	0.761941	-1.6773	0.0084852
chr13:77135536-77613679	2210408I21Rik	72371	7.6	6.1	4.7	-1.11181	0.303845	-1.2821	0.0008921
chr9:63394447-63399244:	2300009A05Rik	69478	18.4	18.1	24.7	1.10258	0.609981	1.65914	2.13E-05
chr6:129232623-12923848	2310001H17Rik	76432	17.8	11.5	6.8	-1.38043	0.266428	-2.00938	0.0010725
chr11:120369562-1203787	2310003H01Rik	71885	27.3	26.1	33.9	1.08322	0.639799	1.55061	5.06E-05
chr1:138851979-13885685	2310009B15Rik	69549	13.6	11.4	17.2	-1.06376	0.803826	1.56861	0.0012934
chr7:90124836-90129936:	2310010J17Rik	78329	20.8	15.0	8.8	-1.24659	0.366494	-1.85727	0.000464
chr10:80318255-80320548	2310011J03Rik	66374	44.9	42.3	55.8	1.05439	0.540535	1.55127	8.32E-16
chr7:12927416-12931072:	2310014L17Rik	381845	1.1	1.2	3.2	1.18874	0.579148	3.38433	9.80E-11
chr12:80120546-80132844	2310015A10Rik	69548	18.0	10.4	6.9	-1.54654	0.089602	-2.0153	0.0003276
chr7:27553290-27582098:	2310022A10Rik	66367	9.2	8.0	9.6	-1.02449	0.87282	1.29899	0.00147
chr8:85026833-85030286:	2310036O22Rik	68544	101.6	120.7	155.3	1.33613	0.025964	1.89487	1.09E-10
chr17:46772635-46773407	2310039H08Rik	67101	24.9	22.5	36.1	1.01319	0.946269	1.79489	1.22E-09
chr6:86483376-86488227:	2310040G24Rik	381792	3.8	2.7	1.0	-1.25518	0.658741	-2.60343	0.005344
chr8:70139713-70147260:	2310045N01Rik	72368	106.1	82.9	50.9	-1.14391	0.229292	-1.6585	5.45E-10
chr7:131342718-13136269	2310057M21Rik	68277	13.9	15.1	19.8	1.22322	0.303885	1.75279	5.39E-05
chr17:35892677-35897378	2310061I04Rik	69662	9.3	10.2	24.6	1.2324	0.300206	3.22382	4.34E-18
chr11:115765433-1157990	2310067B10Rik	71947	29.4	25.3	10.2	-1.02331	0.918391	-2.26815	5.83E-12
chr6:82877866-82881853:	2310069B03Rik	69652	0.8	1.8	2.4	2.3285	0.015716	3.33264	8.77E-06
chr7:44246722-44252319:	2410002F23Rik	668661	88.9	115.6	153.9	1.46579	0.126029	2.09421	8.00E-05
chr3:145938032-14594427	2410004B18Rik	66421	30.2	39.9	35.7	1.48656	0.014343	1.46765	0.003122
chr18:33794892-33795989	2410004N09Rik	69749	66.1	64.8	83.6	1.09599	0.588345	1.5671	3.51E-05
chr11:62602877-62604806	2410006H16Rik	69221	229.3	206.3	269.4	-1.00079	0.997301	1.45957	0.0001865
chr12:83950608-83952953	2410016O06Rik	71952	9.3	15.1	23.1	1.80622	0.037044	2.91836	7.23E-07
chr15:8169106-8271158:+	2410089E03Rik	73692	50.1	35.0	15.2	-1.28378	0.153484	-2.57773	1.18E-13
chr19:18670780-18704792	2410127L17Rik	67383	20.7	22.2	33.2	1.2108	0.214474	1.99035	2.93E-10
chr5:118245227-11826311	2410131K14Rik	76792	19.5	22.7	22.9	1.31045	0.099262	1.45931	0.0024265
chr2:153341157-15334581	2500004C02Rik	72326	11.4	8.6	3.3	-1.19397	0.530061	-2.62743	4.76E-07
chr16:18836580-18840113	2510002D24Rik	72307	37.6	31.9	17.6	-1.05224	0.661873	-1.7034	1.13E-12
chr16:21649045-21694665	2510009E07Rik	72190	44.9	34.6	21.2	-1.17153	0.297142	-1.68672	1.34E-06
chr4:147940895-14794731	2510039O18Rik	77034	33.1	40.6	43.3	1.38166	0.04488	1.62052	9.31E-05
chr10:79064374-79097600	2610008E11Rik	72128	79.3	61.7	29.2	-1.15916	0.409252	-2.14051	6.35E-10
chr16:43889902-43964314	2610015P09Rik	212153	20.3	15.7	3.8	-1.162	0.384406	-4.19779	8.61E-32
chr16:11203383-11225796	2610020C07Rik	69918	4.8	4.4	1.6	1.00902	0.979013	-2.29745	8.78E-06
chr7:119794130-11984894	2610020H08Rik	434234	14.6	10.1	4.9	-1.28451	0.097706	-2.3561	1.09E-13
chr11:85791660-85832388	2610027K06Rik	69909	2.0	1.4	0.2	-1.24293	0.597324	-5.9588	4.09E-09
chr11:113043906-1132018	2610035D17Rik	72386	37.9	25.7	4.1	-1.32617	0.201151	-6.91022	4.14E-32
chr8:129216354-12923404	2610044O15Rik8	72139	33.5	26.7	14.3	-1.13928	0.629135	-1.8369	0.0005195
chr9:41581339-41592487:	2610203C20Rik	1E+08	72.2	42.1	22.8	-1.53176	0.093114	-2.42871	3.17E-06
chr13:28460034-28885422	2610307P16Rik	72518	40.6	30.7	6.9	-1.18432	0.329812	-4.56545	6.76E-35
chr3:45280439-45378260:	2610316D01Rik	72511	1.8	2.0	0.1	1.23425	0.695332	-5.62852	9.02E-06
chr16:17113398-17125106	2610318N02Rik	70458	16.4	1.9	3.1	-5.65448	9.56E-06	-3.41482	0.0003205
chr11:59197793-59202431	2610507I01Rik	72203	34.3	20.6	11.7	-1.49333	0.089523	-2.25921	4.56E-06
chr5:114821937-11482346	2610524H06Rik	330173	19.3	14.4	7.7	-1.20708	0.473485	-1.94142	0.0002927
chr8:60890451-60907572:	2700029M09Rik	72612	39.3	38.5	56.3	1.09608	0.366786	1.78499	8.74E-18
chr5:23850597-23855033:	2700038G22Rik	67194	6.8	12.5	23.7	2.01066	0.001199	4.09658	5.01E-16

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr18:62751674-62756347	2700046A07Rik	78449	13.6	6.2	0.5	-1.80483	0.251169	-11.5903	4.78E-11
chr12:71136848-71243303	2700049A03Rik	76967	30.7	21.3	6.8	-1.29056	0.177433	-3.50591	5.81E-20
chr17:13487021-13554094	2700054A10Rik	72578	4.3	2.7	1.5	-1.40614	0.150794	-2.19023	1.22E-05
chr14:19811402-19823823	2700060E02Rik	68045	151.9	141.4	156.7	1.04098	0.691416	1.28671	5.43E-05
chr18:24470871-24477767	2700062C07Rik	68046	34.5	31.7	38.6	1.03064	0.825951	1.39589	1.53E-05
chr6:133105239-13311089	2700089E24Rik	381820	76.5	67.8	80.3	-1.01037	0.91509	1.30989	1.28E-07
chr2:84669221-84670708:	2700094K13Rik	72657	54.7	45.8	30.2	-1.07354	0.676911	-1.44499	0.0007138
chr12:55045661-55080110	2700097O09Rik	72658	18.5	19.1	22.9	1.15831	0.237991	1.54423	6.05E-07
chr11:64079484-64083259	2810001G20Rik	66456	27.3	21.8	15.1	-1.11937	0.483202	-1.43699	0.0011966
chr2:94406707-94411680:	2810002D19Rik	66457	20.1	19.0	12.1	1.05753	0.690524	-1.3249	0.0018158
chr8:124839355-12486302	2810004N23Rik	66523	39.4	42.1	73.6	1.1991	0.085107	2.32365	4.41E-29
chr5:124328089-12434185	2810006K23Rik	72650	7.8	6.1	3.7	-1.15513	0.357902	-1.67225	5.16E-06
chr11:117076783-1170789	2810008D09Rik	76972	66.7	52.5	37.6	-1.13485	0.311121	-1.41412	0.0001262
chr8:123042575-12304460	2810013P06Rik	1.01E+08	22.8	17.1	10.6	-1.20043	0.253066	-1.71284	3.53E-06
chr11:58867240-58884338	2810021J22Rik	69944	15.0	10.4	8.0	-1.30031	0.162382	-1.48434	0.0053587
chr1:157412352-15742023	2810025M15Rik	69953	22.2	16.8	11.2	-1.19126	0.347294	-1.56226	0.0008797
chr12:111572317-1115744	2810029C07Rik	1.01E+08	3.8	1.7	0.8	-1.9121	0.087132	-3.15197	8.62E-05
chrX:108834478-10888689	2810403D21Rik	69964	9.6	5.5	2.5	-1.54873	0.062576	-2.96189	6.38E-09
chr11:69897358-69900986	2810408A11Rik	70419	12.6	4.5	1.6	-2.41844	0.000371	-5.74308	6.11E-16
chr2:165490112-16549331	2810408M09Rik	381406	17.7	23.2	38.2	1.47691	0.037444	2.63886	5.00E-12
chr11:120186650-1201898	2810410L24Rik	1E+08	9.9	5.2	2.8	-1.67023	0.110424	-2.62224	8.03E-05
chr8:70504296-70506739:	2810428I15Rik	66462	39.1	55.4	54.5	1.59007	0.00288	1.72294	1.90E-05
chr11:102619507-1026244	2810433D01Rik	77132	6.4	3.3	1.2	-1.66184	0.258671	-3.48118	0.0001675
chr17:25570811-25575043	2810468N07Rik	72834	6.6	3.2	1.3	-1.80805	0.021629	-3.76896	4.29E-10
chr5:113086323-11316331	2900026A02Rik	243219	21.5	19.0	9.6	1.00192	0.994268	-1.77576	1.13E-05
chr11:117611247-1176134	2900041M22Rik	78403	5.9	4.0	0.6	-1.29545	0.492623	-5.86785	1.66E-10
chr1:118458669-11845926	2900060B14Rik	68204	8.5	16.8	48.4	2.1364	0.015409	6.19492	2.19E-14
chr7:81523550-81531498:	2900076A07Rik	1.01E+08	40.5	30.0	22.9	-1.21003	0.188233	-1.40719	0.0015876
chr7:12512551-12556321:	2900092C05Rik	73090	1.4	0.1	0.1	-4.58562	0.0088	-4.72205	0.0009796
chr2:156388063-15639297	2900097C17Rik	347740	176.7	172.9	192.2	1.09877	0.264768	1.358	3.68E-07
chrX:152368572-15241670	3010001F23Rik	75693	4.5	3.5	1.5	-1.14123	0.660628	-2.32071	4.37E-05
chr11:50174851-50200115	3010026O09Rik	68067	10.7	8.1	4.0	-1.19856	0.631009	-2.02148	0.004691
chrX:123103559-12314329	3110007F17Rik	73061	11.4	9.5	2.1	-1.08511	0.828329	-3.89574	4.08E-09
chr4:108719649-10878190	3110021N24Rik	73133	3.7	2.4	1.1	-1.34865	0.362714	-2.61469	6.95E-05
chr4:35191282-35225880:	3110043O21Rik	73205	27.6	26.6	15.3	1.07749	0.332355	-1.44219	3.49E-11
chr17:21650611-21664966	3110052M02Rik	73229	12.0	10.5	7.2	-1.0294	0.869967	-1.33841	0.0040673
chr3:40894277-40936307:	3110057O12Rik	269423	12.6	8.5	3.5	-1.33455	0.150224	-2.84204	4.96E-12
chr5:139359739-13946053	3110082I17Rik	73212	14.0	15.1	28.8	1.2024	0.109323	2.55621	8.42E-33
chr2:115493513-11551220	3110099E03Rik	1E+08	4.8	2.9	0.4	-1.43966	0.405947	-7.03893	6.72E-10
chr17:5798657-5803242:+	3300005D01Rik	78512	1.3	1.4	0.3	1.17978	0.746119	-2.82979	0.0028104
chr14:49682019-49783367	3632451O06Rik	67419	41.7	28.7	2.5	-1.29805	0.082736	-12.7362	5.61E-96
chr14:12284203-12303231	3830406C13Rik	218734	35.9	26.0	17.2	-1.23947	0.024985	-1.6603	7.32E-12
chr13:107022570-1070335	3830408C21Rik	1E+08	4.1	2.0	1.3	-1.76879	0.012471	-2.35432	3.77E-06
chr19:28923064-28964154	4430402I18Rik	381218	8.1	2.7	1.1	-2.44557	0.031457	-4.63969	2.13E-06
chr10:60346851-60372684	4632428N05Rik	74048	45.2	38.5	22.4	-1.04671	0.864626	-1.60146	0.0019803
chr7:25376819-25566417:	4732471J01Rik	654804	5.2	3.1	1.5	-1.48505	0.049474	-2.72253	1.55E-10
chr11:113203315-1132096	4732490B19Rik	319871	5.7	2.5	0.4	-1.86482	0.123006	-8.36399	1.20E-11
chr5:25499797-25504473:	4831440E17Rik	320965	7.8	5.0	1.1	-1.3743	0.400478	-4.68649	5.44E-09
chr18:46850039-46905446	4833403I15Rik	74574	5.2	3.6	1.4	-1.30995	0.290581	-2.91279	1.22E-08
chr8:10899922-10902334:	4833411C07Rik	71624	20.2	11.2	0.7	-1.56362	0.30987	-14.0567	3.99E-16
chr7:67784538-67803496:	4833412C05Rik	73904	4.9	3.3	1.6	-1.31901	0.42906	-2.33762	0.0008411
chr11:95858817-95861046	4833417C18Rik	73906	5.0	3.4	1.3	-1.30898	0.453355	-2.71652	0.000104
chr17:87274886-87282814	4833418N02Rik	74597	7.9	4.4	2.2	-1.57014	0.147278	-2.66021	3.54E-05
chr18:4353547-4368945:+	4833419F23Rik	73915	15.0	10.2	2.7	-1.32235	0.461454	-3.91651	3.13E-07
chr13:119462759-1194861	4833420G17Rik	67392	93.9	73.7	29.8	-1.14156	0.243621	-2.4975	7.95E-30
chr13:54551218-54565382	4833439L19Rik	97820	49.1	64.8	103.0	1.48735	0.050378	2.55412	7.97E-10
chr12:57564115-57622109	4921506M07Rik	70846	1.1	0.0	0.0	-7.53256	0.00019	-6.70829	4.14E-05
chr6:50573304-50596590:	4921507P07Rik	70821	11.0	5.0	3.4	-1.88782	0.030616	-2.40434	0.0001301

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr18:6603633-6638966:+	4921524L21Rik	70901	1.2	0.1	0.1	-4.57576	0.008848	-4.00706	0.0032954
chr14:95881266-95882775	4921530L21Rik	66732	2.6	0.1	0.3	-8.5692	3.97E-05	-4.38774	0.0009871
chr2:179976853-17997901	4921531C22Rik	66730	8.3	5.3	2.1	-1.39818	0.175796	-3.0168	4.11E-09
chr11:3886088-3895126:-	4921536K21Rik	67430	1.3	0.2	0.4	-3.51167	0.008621	-2.1354	0.050792
chr4:103230445-10329086	4921539E11Rik	70941	1.5	0.0	0.2	-7.69981	0.000153	-3.41189	0.0090083
chr6:129322165-12933178	4922502D21Rik	381816	16.8	0.8	1.9	-10.207	1.03E-07	-4.91241	3.30E-05
chr2:130707853-13084011	4930402H24Rik	228602	57.3	48.7	33.1	-1.05454	0.622987	-1.38107	3.27E-06
chr15:82059151-82066538	4930407I10Rik	328573	3.5	0.1	0.3	-9.97722	2.33E-06	-6.0007	2.58E-05
chr4:9770585-9823411:+	4930412C18Rik	320152	3.4	1.7	0.3	-1.69712	0.141828	-7.62354	5.59E-13
chr6:72438683-72440615:	4930414L22Rik	78108	6.4	4.5	2.6	-1.28194	0.393025	-1.88524	0.0024075
chr11:11489266-11515190	4930415F15Rik	73862	2.4	0.1	0.6	-6.48714	0.00019	-2.51742	0.0264116
chr6:135658913-13568339	4930425L21Rik	75024	0.1	0.1	1.5	-1.01356	0.987505	6.51661	1.57E-06
chr12:113156421-1131654	4930427A07Rik	104732	4.5	3.3	2.2	-1.20361	0.330849	-1.58346	0.0009331
chr3:32365489-32367438:	4930429B21Rik	67576	0.7	0.6	4.0	-1.06501	0.906837	5.83633	1.81E-11
chr2:111193254-11122960	4930430A15Rik	67575	3.4	0.1	0.6	-9.50547	1.36E-05	-3.20063	0.0105159
chr10:100572274-1005892	4930430F08Rik	68281	14.1	9.8	5.4	-1.29897	0.281573	-2.02255	6.11E-05
chr9:3190269-3199813:-	4930433N12Rik	114673	2.9	1.6	0.2	-1.52902	0.41487	-6.24757	1.78E-06
chr16:38812205-38828749	4930435E12Rik	74663	1.1	0.0	0.2	-4.51728	0.009055	-2.59699	0.0484608
chr10:18797299-18831930	4930444F02Rik	73968	1.5	0.1	0.1	-6.86296	0.000392	-5.001	0.0005255
chr12:72881109-72917765	4930447C04Rik	75801	5.0	3.4	2.5	-1.31015	0.208747	-1.60497	0.003382
chr2:19344317-19352251:	4930447M23Rik	108871	3.9	3.4	6.4	-1.03167	0.900636	2.01546	4.21E-08
chr16:4964288-4978962:+	4930451G09Rik	74684	5.5	2.8	1.2	-1.71508	0.084499	-3.36254	4.25E-07
chr14:8431172-8666290:-	4930452B06Rik	74430	1.7	1.3	0.5	-1.1309	0.762268	-2.33108	0.0011477
chr14:79702920-79712930	4930452G13Rik	73989	1.8	0.1	0.0	-4.4485	0.00863	-4.52417	0.0010571
chr16:64766105-64770939	4930453N24Rik	67609	87.3	92.5	122.2	1.20198	0.424002	1.72167	0.0007297
chr1:161156843-16115931	4930469G21Rik	1.01E+08	2.2	0.3	0.2	-3.40277	0.044233	-3.96087	0.0036585
chr18:36106203-36109954	4930471G03Rik	74966	2.7	0.2	0.5	-4.81268	0.005845	-2.67418	0.0376062
chr14:69732784-69767113	4930480K23Rik	75016	5.8	3.4	1.6	-1.49886	0.165856	-2.65247	8.01E-06
chr19:5406815-5422847:+	4930481A15Rik	74931	24.3	12.3	1.3	-1.73754	0.022704	-12.935	7.34E-38
chr13:60842612-60864416	4930486L24Rik	214639	2.4	2.2	3.9	1.03425	0.928974	1.97845	0.0003251
chr8:93811694-93813555:	4930488L21Rik	75809	1.5	0.1	0.3	-5.8359	0.000794	-2.98763	0.0134816
chr5:149847747-14986428	4930500F04Rik	70969	0.5	0.4	5.2	1.03573	0.967215	6.79906	1.23E-05
chr3:146646259-14665131	4930503B20Rik	75015	9.5	1.3	1.2	-4.84513	0.000162	-4.58926	2.00E-05
chr18:70453140-70472480	4930503L19Rik	269033	30.0	26.0	18.0	-1.03757	0.823936	-1.3311	0.0036176
chr11:58446143-58452966	4930504O13Rik	403200	3.2	0.3	0.3	-4.13123	0.016079	-3.95448	0.0035748
chr11:30426006-30471829	4930505A04Rik	75087	4.5	0.8	0.7	-3.74477	0.004852	-3.85597	0.0004196
chr17:8293366-8311118:-	4930506C21Rik	75060	2.5	1.0	0.6	-2.02926	0.105521	-2.66025	0.0039309
chr4:109505332-10953129	4930522H14Rik	67646	1.4	0.0	0.1	-5.98755	0.001299	-4.31873	0.0019972
chr1:160044380-16007858	4930523C07Rik	67647	91.0	80.5	40.1	-1.03127	0.939148	-1.7607	0.0087785
chr13:67796594-67830985	4930525G20Rik	320163	2.4	1.4	0.6	-1.53128	0.121528	-3.10714	1.95E-07
chr14:86245970-86262042	4930529K09Rik	75155	1.0	0.3	0.0	-2.3713	0.167685	-4.08326	0.0027959
chr4:119205055-11921821	4930538K18Rik	75180	4.0	1.5	0.8	-2.1747	0.023506	-3.59166	3.52E-06
chr11:70615894-70616890	4930544D05Rik	668433	5.0	0.4	1.0	-5.43624	0.000843	-2.97361	0.0103797
chr6:65952571-65954014:	4930544G11Rik	67653	4.7	0.4	1.1	-6.28946	0.000108	-2.76947	0.0128103
chr17:4119446-4122102:-	4930548J01Rik	78043	1.6	0.6	0.2	-1.97998	0.27892	-3.54916	0.006595
chr9:53405286-53432803:	4930550C14Rik	75311	10.2	7.7	1.6	-1.18551	0.62893	-4.47029	2.69E-10
chr15:10714836-10790123	4930556M19Rik	75259	1.7	1.2	0.6	-1.25116	0.445867	-2.06601	0.0005881
chr13:23276204-23313407	4930557F10Rik	75322	1.0	0.0	0.0	-3.72484	0.018203	-3.25896	0.0088698
chr3:95386458-95402841:	4930558C23Rik	67654	3.0	0.2	0.5	-5.84467	0.001151	-3.35455	0.0082254
chr16:4835416-4867691:+	4930562C15Rik	78809	1.2	0.1	0.1	-5.9235	0.000956	-5.28473	0.0002345
chr16:92318763-92321441	4930563D23Rik	75328	4.0	0.3	0.6	-5.54841	0.00132	-3.63353	0.004272
chr17:44879704-44880885	4930564C03Rik	75341	1.4	0.1	0.1	-4.58868	0.00869	-5.22231	0.0004232
chr3:156546753-15656174	4930570G19Rik	329782	6.3	3.1	0.8	-1.74166	0.152896	-5.04319	2.42E-08
chr7:125368861-12537101	4930571K23Rik	75861	13.8	0.6	1.3	-11.1964	2.92E-08	-5.89234	3.42E-06
chrX:18418427-18461274:	4930578C19Rik	75905	9.3	5.7	3.4	-1.45536	0.147097	-2.12498	0.0001198
chr14:63971122-63987780	4930578I06Rik	67750	3.0	0.1	0.4	-6.96876	0.000306	-3.48647	0.0067512
chr3:138164135-13818671	4930579F01Rik	67741	1.8	0.1	0.3	-4.68326	0.007487	-2.75225	0.0343418
chr3:79629079-79632819:	4930579G24Rik	75939	7.2	7.4	9.1	1.14716	0.511436	1.55484	0.0015803

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr9:35116728-35130922:	4930581F22Rik	78934	15.1	9.7	5.0	-1.39852	0.125351	-2.34457	2.28E-07
chr5:26460070-26493314:	4930584F24Rik	75942	1.5	0.1	0.2	-4.90277	0.00557	-3.95568	0.0035196
chr6:91904233-91950725:	4930590J08Rik	381798	2.2	0.7	0.5	-2.63127	0.007285	-2.99182	0.0001786
chr9:15283337-15306448:	4931406C07Rik	70984	16.1	10.5	6.9	-1.37462	0.041218	-1.84299	3.20E-07
chr7:34236714-34285609:	4931406P16Rik	233103	48.8	48.1	27.8	1.10542	0.145825	-1.40113	3.58E-11
chr5:24543434-24555469:	4931409K22Rik	231045	1.4	0.2	0.4	-4.85309	0.001546	-2.36913	0.0402706
chr14:54583663-54605908	4931414P19Rik	74359	9.7	7.5	3.2	-1.16552	0.502409	-2.38468	3.01E-08
chr6:73468573-73469667:	4931417E11Rik	66740	1.3	0.1	0.1	-4.07859	0.016455	-3.48915	0.0083123
chr2:23207476-23267129:	4931423N10Rik	70981	1.2	0.1	0.1	-5.83529	0.000735	-4.50227	0.000584
chr8:105280409-10528952	4931428F04Rik	74356	3.1	1.6	1.4	-1.67598	0.025188	-1.70234	0.0033827
chr9:40894849-40964112:	4931429I11Rik	70989	1.1	0.4	0.1	-2.19836	0.1207	-4.38268	0.0001754
chr9:46303361-46319986:	4931429L15Rik	74361	1.8	0.1	0.2	-7.42948	0.000105	-4.62314	0.000537
chr7:104127913-10412982	4931431F19Rik	70980	1.4	0.1	0.1	-3.40725	0.044327	-3.62174	0.0068757
chr2:68657884-68748465:	4932414N04Rik	75721	2.7	0.3	0.4	-5.42433	0.000119	-3.8297	0.0003585
chr2:129798369-12980145	4932416H05Rik	654409	5.5	3.4	2.3	-1.44619	0.048377	-1.92141	6.51E-06
chr2:26271647-26294557:	4932418E24Rik	329366	7.8	4.2	1.7	-1.60961	0.081339	-3.34941	6.38E-09
chr3:36863106-37053033:	4932438A13Rik	229227	61.1	60.6	34.3	1.11654	0.338303	-1.41805	1.85E-05
chr3:135833694-13584026	4933401H06Rik	71038	1.1	0.0	0.1	-4.483	0.009483	-3.60342	0.0069064
chrX:62283499-62292078:	4933402E13Rik	74437	1.1	0.0	0.1	-7.32343	0.000176	-4.85676	0.0004859
chr8:87563907-87589197:	4933402J07Rik	330820	6.1	0.5	0.6	-5.64062	0.000968	-4.72375	0.0004294
chr5:59963119-59986002:	4933402J10Rik	71057	1.7	0.1	0.1	-5.07379	0.004649	-4.77683	0.0008914
chr11:69816566-69818440	4933402P03Rik	108803	6.2	0.3	0.5	-8.97537	6.85E-06	-5.61093	4.79E-05
chr16:16707687-16718121	4933404G15Rik	74066	1.0	0.0	0.1	-5.50153	0.002613	-4.20069	0.0024406
chr5:136919146-13693710	4933404O12Rik	66752	3.7	2.1	1.0	-1.51924	0.085362	-2.90726	1.43E-08
chr3:122882592-12292411	4933405D12Rik	74057	1.6	0.7	0.1	-1.83247	0.269269	-4.52781	0.0003332
chr7:50599190-50600528:	4933405O20Rik	243996	1.9	0.5	0.2	-2.41927	0.117782	-3.94939	0.0015836
chr12:32919384-32953789	4933406C10Rik	74076	6.7	3.7	1.5	-1.61988	0.013697	-3.37057	2.56E-13
chrX:75725458-75764699:	4933407K13Rik	74396	12.6	10.1	7.2	-1.1229	0.462777	-1.39368	0.0026141
chr18:34579846-34597468	4933408B17Rik	271508	3.5	2.1	1.5	-1.42673	0.175009	-1.81625	0.0026433
chr2:68582413-68616463:	4933409G03Rik	227998	4.5	0.2	0.5	-10.6609	4.60E-07	-5.12861	4.02E-05
chr10:117925459-1179483	4933411E08Rik	71067	1.2	0.4	0.1	-2.23812	0.098244	-6.3349	3.28E-06
chr19:42052228-42053628	4933411K16Rik	66765	33.8	5.2	5.4	-4.75568	8.26E-06	-4.12278	3.39E-06
chr10:116950562-1169632	4933412E12Rik	71086	11.1	8.7	4.0	-1.15245	0.413307	-2.2086	2.75E-10
chr1:23100474-23102253:	4933415F23Rik	66755	7.6	0.4	1.2	-7.6615	3.99E-05	-3.60098	0.0030165
chr10:116111664-1161139	4933416C03Rik	619332	3.1	0.1	0.4	-7.63981	9.64E-05	-3.64553	0.0042431
chr13:34924409-34953196	4933417A18Rik	66761	2.7	0.2	0.1	-5.42542	0.002909	-5.19718	0.0004528
chr1:71958998-72005195:	4933417E11Rik	71134	2.5	1.8	0.6	-1.28385	0.60395	-2.95588	0.0011478
chr11:72154097-72203371	4933427D14Rik	74477	31.7	29.6	18.7	1.05414	0.761941	-1.34943	0.0052204
chr7:120982509-12101478	4933427G17Rik	74466	2.8	0.9	0.8	-2.40108	0.032897	-2.56417	0.0034464
chr7:121587386-12158983	4933432K03Rik	75793	3.2	0.3	0.4	-4.57605	0.008115	-3.56745	0.006635
chr2:25212559-25214630:	4933433C11Rik	74472	2.2	0.1	0.3	-5.31204	0.003096	-3.50578	0.007696
chr11:59505685-59511067	4933439C10Rik	74476	31.8	25.7	13.2	-1.10684	0.296229	-1.91583	3.18E-20
chr7:125331782-12534978	4933440M02Rik	71208	1.7	0.1	0.3	-5.97681	0.000837	-3.4654	0.0059209
chr5:23431808-23434353:	5031425E22Rik	269630	60.3	50.5	36.5	-1.07436	0.563419	-1.32031	0.0007592
chr2:6922702-6928722:-	5031426D15Rik	68144	13.8	11.6	2.2	-1.08115	0.813016	-4.5677	1.93E-15
chr3:51559757-51567116:	5031434O11Rik	1E+08	9.7	6.9	1.4	-1.25268	0.578942	-4.70371	5.15E-08
chr15:84945720-84987971	5031439G07Rik	223739	40.9	46.1	54.4	1.27705	0.270793	1.63937	0.0022185
chr3:108458069-10853652	5330417C22Rik	229722	20.5	12.5	3.0	-1.37189	0.454106	-4.5372	1.70E-07
chr16:50726751-50732773	5330426P16Rik	68190	27.3	24.2	12.1	-1.01954	0.943292	-1.78196	5.62E-05
chr2:156852403-15686294	5430405H02Rik	74487	16.1	11.8	7.9	-1.22711	0.400239	-1.58976	0.0078629
chr5:100420842-10042953	5430416N02Rik	1.01E+08	39.0	60.0	78.7	1.71712	0.014113	2.43377	2.33E-07
chrX:105040854-10507012	5530601H04Rik	71445	15.7	12.7	5.1	-1.11222	0.555522	-2.41003	1.60E-13
chrX:13042015-13045295:	5730405O15Rik	70489	16.6	12.6	6.5	-1.18494	0.427578	-2.00492	5.42E-06
chr19:8888387-8888770:-	5730408K05Rik	67531	27.1	34.2	118.0	1.40696	0.04504	5.28391	1.97E-44
chr10:95417375-95428640	5730420D15Rik	70523	0.7	2.0	2.8	2.74454	0.024754	3.9859	6.62E-05
chr5:48395573-48414294:	5730480H06Rik	70592	7.4	5.7	3.2	-1.15392	0.534431	-1.81315	0.0001766
chr12:18514510-18535254	5730507C01Rik	236366	3.7	2.9	1.4	-1.14394	0.590184	-2.03979	3.03E-05
chr3:88777057-88829371:	5830417I10Rik	1E+08	13.1	12.1	12.6	1.03862	0.72442	1.19841	0.0067409

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr4:155400969-15542170	5830444B04Rik	641454	6.3	6.7	1.2	1.16273	0.607203	-4.10011	1.13E-12
chr5:128579130-12860068	5930412G12Rik	319616	18.1	12.7	4.2	-1.28145	0.152278	-3.36253	2.18E-20
chr5:148990056-14899521	5930430L01Rik	319982	18.5	10.3	5.8	-1.60463	0.04488	-2.47949	4.60E-07
chr9:58488603-58499742:	6030419C18Rik	319477	9.2	19.5	32.0	2.21082	0.040039	3.65159	1.19E-05
chr15:12808177-12824657	6030458C11Rik	77877	22.7	22.1	26.3	1.09635	0.309286	1.44851	4.29E-09
chr1:180432373-18048350	6330403A02Rik	381310	1.6	1.5	0.4	1.09991	0.776624	-3.02606	1.95E-07
chr11:71031941-71033617	6330403K07Rik	103712	48.8	41.4	9.0	-1.06012	0.844375	-4.10404	6.57E-17
chr4:63560360-63586353:	6330416G13Rik	230279	5.8	6.1	10.2	1.18309	0.510755	2.12645	8.44E-06
chrX:56374586-56378470:	6330419J24Rik	320237	3.8	1.7	1.6	-1.91912	0.009	-1.77569	0.0043347
chr7:139972303-13997875	6430531B16Rik	381933	2.3	0.4	0.3	-3.36098	0.020694	-4.21864	0.0005439
chr8:120114152-12016530	6430548M08Rik	234797	13.2	11.4	13.8	-1.03859	0.779055	1.30739	0.0008481
chr2:156000443-15600797	6430550D23Rik	320095	2.4	1.6	0.6	-1.3685	0.429288	-2.89032	0.0002383
chr8:36489191-36513013:	6430573F11Rik	319582	10.2	7.1	1.4	-1.28351	0.36596	-5.1859	7.87E-16
chr3:120454334-12088673	6530403H02Rik	320739	4.8	3.2	1.2	-1.32047	0.151315	-2.98605	3.22E-13
chr1:20888650-20890473:	6720483E21Rik	77741	1.1	0.6	0.1	-1.49928	0.515147	-3.65128	0.0032047
chr13:62603015-62624182	6720489N17Rik	211378	10.2	7.7	2.0	-1.19265	0.547379	-3.8238	1.06E-11
chr18:77633281-77714010	8030462N17Rik	212163	32.8	36.4	44.3	1.24939	0.090558	1.67721	1.22E-07
chr6:116650684-11665284	8430408G22Rik	213393	17.8	16.0	5.7	-1.01039	0.974823	-2.39257	8.56E-07
chr19:31213543-31216396	8430431K14Rik	78103	12.8	12.7	3.7	1.11873	0.631009	-2.63486	1.82E-10
chr10:43174699-43176565	9030612E09Rik	74530	1.5	1.2	0.4	-1.08479	0.856961	-2.96144	0.000125
chr12:100779123-1008726	9030617O03Rik	217830	11.7	9.5	3.5	-1.10278	0.444282	-2.62049	2.17E-25
chr12:24043202-24097269	9030624G23Rik	66808	2.5	1.8	0.9	-1.27435	0.385784	-2.24321	9.48E-05
chr7:118740271-11884149	9030624J02Rik	71517	67.9	55.6	37.5	-1.08944	0.29123	-1.443	1.67E-10
chr17:40875482-40880558	9130008F23Rik	71583	13.3	9.6	5.7	-1.24276	0.352256	-1.8291	0.0003086
chr7:127382260-12738716	9130019O22Rik	78921	15.4	15.2	10.1	1.10406	0.330234	-1.21514	0.0091473
chr7:128234451-12823803	9130023H24Rik	1E+08	9.8	7.8	10.7	-1.1169	0.35145	1.36402	0.0001293
chr7:25228723-25230264:	9130221H12Rik	77124	21.6	17.3	13.4	-1.11935	0.39822	-1.28117	0.009589
chr5:65987928-66004285:	9130230L23Rik	231253	0.2	0.8	2.2	2.52444	0.09558	6.1348	9.97E-06
chr15:58022271-58034294	9130401M01Rik	75758	28.5	29.7	44.6	1.16866	0.225968	1.94598	1.18E-13
chr9:8021672-8042823:-	9230110C19Rik	234912	15.0	10.5	8.4	-1.28046	0.12376	-1.40866	0.0052218
chr9:60523967-60545882:	9230112J17Rik	1.01E+08	2.2	1.4	0.5	-1.40324	0.298535	-3.26746	2.18E-06
chr6:128169700-12818380	9330102E08Rik	330427	2.8	0.7	0.9	-3.31267	0.000139	-2.24009	0.0026553
chr12:69197211-69199868	9330151L19Rik	414085	22.9	18.8	14.3	-1.08412	0.529988	-1.27574	0.0055251
chr10:29211643-29230779	9330159F19Rik	212448	1.2	0.7	0.1	-1.39083	0.521189	-4.65954	1.55E-05
chr9:88841798-88858870:	9330159M07Rik	319673	5.8	3.1	1.7	-1.63072	0.081103	-2.61716	7.39E-06
chr13:24937401-24939049	9330162012Rik	493800	4.5	3.2	2.0	-1.25413	0.392896	-1.70946	0.0055028
chr5:9266193-9480717:+	9330182L06Rik	231014	1.5	1.2	2.1	-1.0821	0.840971	1.78674	0.0096542
chr2:158353700-15836152	9430008C03Rik	68108	35.4	37.7	55.2	1.20206	0.106886	1.94496	1.12E-15
chr4:156109998-15612726	9430015G10Rik	230996	34.4	26.5	12.7	-1.16014	0.295518	-2.1397	4.73E-14
chr1:57406548-57415958:	9430016H08Rik	68115	27.6	30.3	36.0	1.23335	0.110362	1.62342	5.30E-07
chr18:4634929-4682869:+	9430020K01Rik	240185	40.6	33.3	19.2	-1.09334	0.373355	-1.69082	3.40E-14
chr9:88595325-88599243:	9430037G07Rik	320692	6.1	3.2	1.5	-1.65576	0.159776	-3.01294	4.05E-05
chr7:137375569-13741075	9430038I01Rik	77252	7.5	9.3	13.5	1.38737	0.307431	2.12961	0.0009784
chr6:53287295-53397216:	9430076C15Rik	320189	1.9	2.4	3.6	1.36682	0.323141	2.23318	0.0003069
chr13:51097738-51100727	9430083A17Rik	77428	5.2	2.4	0.6	-1.83816	0.149646	-5.11588	2.99E-07
chr8:111127444-11114549	9430091E24Rik	434350	10.6	8.0	3.0	-1.19491	0.426695	-2.71971	2.39E-10
chr6:92940582-93111749:	9530026P05Rik	330385	85.8	65.8	9.0	-1.17014	0.322607	-7.37857	1.53E-63
chrX:153037629-15307291	9530051G07Rik	319781	1.7	0.9	0.3	-1.63346	0.183808	-3.5052	7.89E-06
chr7:28129466-28164811:	9530053A07Rik	319482	1.9	0.5	0.3	-2.65864	0.061235	-3.18252	0.0041769
chr9:122572501-12258064	9530059O14Rik	319626	2.9	2.1	0.1	-1.16102	0.838506	-9.27068	1.58E-07
chr11:52396428-52408723	9530068E07Rik	213673	157.5	160.6	160.8	1.13442	0.125351	1.27278	9.14E-05
chr9:22411577-22444679:	9530077C05Rik	68283	11.1	6.0	1.8	-1.63062	0.040974	-4.65889	3.99E-16
chr17:23749236-23754065	9530082P21Rik	638247	10.9	7.0	4.1	-1.39717	0.08263	-2.11736	2.86E-07
chr9:68765346-68773322:	9530091C08Rik	320440	21.1	15.0	2.8	-1.25335	0.36628	-5.59311	2.46E-23
chr6:127085116-12710955	9630033F20Rik	319801	3.5	3.7	6.9	1.18499	0.378628	2.43435	3.14E-12
chr7:42609526-42642604:	9830147E19Rik	208111	18.3	16.9	10.1	1.02703	0.832731	-1.45108	3.79E-07
chr16:25059639-25069058	A230028O05Rik	319487	0.5	0.5	1.2	-1.04468	0.939148	2.48983	0.0013872
chr10:83543941-83596473	A230046K03Rik	319277	68.9	75.1	55.5	1.21982	0.008329	1.00554	0.939683

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr7:55962531-55980096:	A230056P14Rik	320845	7.2	6.5	2.1	-1.00256	0.994268	-2.62501	3.11E-08
chr7:61705850-61927574:	A230057D06Rik	319893	2.2	1.3	0.6	-1.48896	0.231211	-2.90279	3.36E-05
chrX:20961676-20987349:	A230072C01Rik	320742	11.2	9.5	5.7	-1.05372	0.791493	-1.55484	0.0002427
chr6:121636173-12167923	A2m	232345	6.1	4.8	2.7	-1.14729	0.613019	-1.77514	0.0013763
chr15:101221191-1012251	A330009N23Rik	380977	7.2	4.8	1.5	-1.34873	0.175535	-3.67722	9.70E-14
chr1:195017399-19503790	A330023F24Rik	320977	50.8	36.6	14.4	-1.23951	0.257855	-2.74512	5.85E-14
chr13:48044231-48262623	A330033J07Rik	320614	1.0	1.1	0.1	1.26334	0.702147	-3.52161	0.0016264
chr8:120204434-12022823	A330074K22Rik	434353	3.2	2.2	0.5	-1.30999	0.38828	-4.33902	5.76E-10
chr7:61943901-61982303:	A330076H08Rik	320026	2.3	1.9	0.3	-1.11727	0.758281	-4.65979	2.51E-09
chr4:128759258-12876929	A3galt2	215493	1.1	2.0	3.9	1.92526	0.137945	3.7489	5.32E-05
chr4:153957237-15396192	A430005L14Rik	97159	40.1	45.4	56.8	1.26597	0.052991	1.75671	4.45E-10
chr2:167690759-16769741	A530013C23Rik	329562	3.9	8.2	4.7	2.25386	0.004852	1.46703	0.122972
chr12:112489448-1124999	A530016L24Rik	319942	6.5	3.4	0.5	-1.51292	0.5038	-5.07263	0.0001164
chr13:67617001-67637753	A530054K11Rik	212281	27.7	28.0	18.7	1.133	0.056664	-1.17945	0.0012072
chr13:60029711-60116669	A530065N20Rik	328263	1.1	0.6	0.1	-1.61827	0.334674	-7.33888	1.55E-07
chr4:16164110-16266225:	A530072M11Rik	1E+08	2.2	1.3	0.6	-1.51349	0.333631	-2.64799	0.0021255
chr1:85717083-85736606:	A630001G21Rik	319997	10.0	7.5	5.7	-1.19922	0.26258	-1.4105	0.0039902
chr14:34051130-34102754	A630023A22Rik	105518	0.2	0.3	1.3	1.22636	0.783293	4.04529	0.0013228
chr10:7663371-7664623:+	A630066F11Rik	320642	7.0	3.6	3.2	-1.72316	0.00682	-1.72916	0.0007284
chr5:20950989-20956398:	A630072M18Rik	320770	7.7	5.5	3.6	-1.26936	0.24172	-1.70944	0.0003282
chr16:98062512-98082439	A630089N07Rik	320586	11.3	9.1	14.0	-1.10754	0.6592	1.53488	0.0033602
chr2:130872541-13090639	A730017L22Rik	613258	7.7	5.5	4.2	-1.25412	0.165984	-1.44415	0.0028854
chr3:121634936-12164645	A730020M07Rik	1.01E+08	2.7	1.9	0.6	-1.26216	0.479442	-3.16107	1.26E-06
chr9:62242596-62244100:	A730043L09Rik	330958	0.0	0.4	1.6	3.79406	0.019188	12.5637	3.72E-09
chr16:24529314-24534472	A730098P11Rik	624582	4.4	5.2	6.0	1.29851	0.215034	1.67256	0.0008341
chr5:107497745-10751255	A830010M20Rik	231570	11.5	8.4	4.0	-1.22397	0.380311	-2.23992	5.61E-07
chr18:32359057-32378284	A830052D11Rik	402767	1.7	0.9	0.3	-1.59604	0.297763	-3.69353	0.0001863
chr13:78198017-78236564	A830082K12Rik	320174	2.7	1.6	0.7	-1.53978	0.197954	-2.91194	2.94E-05
chr16:91465104-91470123	A930006K02Rik	1.01E+08	14.8	8.7	1.5	-1.48327	0.316902	-6.18047	4.87E-10
chr19:29503663-29521987	A930007I19Rik	77779	4.2	2.4	1.6	-1.52254	0.2237	-1.96699	0.0089666
chr18:44661665-44676271	A930012L18Rik	626275	1.1	0.6	0.2	-1.59726	0.208672	-3.20313	8.01E-05
chr5:122989354-12299834	A930024E05Rik	109202	7.3	3.0	1.0	-2.01843	0.107643	-4.40685	7.64E-06
chr17:33981492-33985358	AA388235	433100	3.7	2.4	0.2	-1.36887	0.361577	-9.30422	2.39E-17
chr4:119530315-11953876	AA415398	433752	9.5	6.6	3.9	-1.28392	0.358927	-1.88295	0.0012451
chr13:67589439-67609707	AA987161	1E+08	30.4	29.5	19.0	1.08047	0.493451	-1.28244	0.0013974
chr5:125475873-12551740	Aacs	78894	22.6	23.4	39.9	1.16843	0.595477	2.13928	6.60E-05
chr13:64291836-64312710	Aaed1	66129	147.0	115.8	30.9	-1.14143	0.32967	-3.74948	4.60E-43
chr7:97550331-97579497:	Aamdc	66273	42.7	35.3	19.3	-1.08707	0.573175	-1.75794	9.62E-09
chr1:74279840-74284738:	Aamp	227290	179.5	177.2	192.6	1.10971	0.202836	1.33997	7.54E-07
chr2:156547576-15656897	Aar2	68295	26.0	29.4	31.2	1.27673	0.113404	1.49145	0.0006108
chr15:52040107-52045722	Aard	239435	18.0	12.3	7.4	-1.30819	0.264803	-1.89234	0.0002923
chr8:111033842-11105556	Aars	234734	41.1	53.8	290.2	1.47541	0.042087	8.36192	3.07E-51
chr17:45506841-45520843	Aars2	224805	11.1	10.8	13.5	1.08759	0.432355	1.52116	3.03E-09
chr11:101406840-1014174	Aarsd1	69684	38.2	38.6	91.7	1.13667	0.396129	2.95841	3.28E-27
chr5:76875935-76905514:	Aasdh	231326	24.0	17.7	12.2	-1.21803	0.197907	-1.56022	8.04E-05
chr9:4294793-4309494:-	Aasdhppt	67618	35.8	35.6	46.7	1.1164	0.303565	1.62322	7.34E-11
chr11:84422856-84513501	Aatf	56321	56.5	56.3	125.0	1.11711	0.203386	2.75562	9.55E-65
chr11:120007316-1200471	Aatk	11302	2.8	1.9	1.0	-1.34847	0.116658	-2.1415	1.99E-07
chr16:8513429-8621567:+	Abat	268860	27.3	28.0	11.3	1.14299	0.392718	-1.91252	2.61E-09
chr4:53030789-53159895:	Abca1	11303	153.8	106.7	34.3	-1.29447	0.096475	-3.50987	1.73E-28
chr7:120203964-12032535	Abca14	67928	1.1	0.1	0.1	-5.62366	0.001208	-3.67872	0.003851
chr17:24352023-24410204	Abca3	27410	31.8	25.2	12.6	-1.13247	0.175796	-2.00505	1.89E-25
chr3:122044460-12218006	Abca4	11304	7.0	4.8	1.1	-1.25078	0.62635	-4.25974	9.13E-07
chr11:110269369-1103377	Abca5	217265	31.2	27.2	16.4	-1.02966	0.820502	-1.51967	1.80E-08
chr11:110176821-1102517	Abca6	76184	55.1	37.3	1.9	-1.32576	0.289367	-19.6429	1.47E-56
chr10:79997615-80015572	Abca7	27403	25.3	22.4	8.8	-1.00473	0.984749	-2.25519	2.53E-10
chr11:110025634-1100959	Abca8a	217258	129.2	88.4	3.0	-1.30314	0.365121	-27.9762	4.49E-62
chr11:109933406-1099958	Abca8b	27404	8.1	5.6	1.9	-1.301	0.242453	-3.24079	5.90E-13

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:110100822-1101681	Abca9	217262	47.5	38.3	6.7	-1.11724	0.501119	-5.54937	2.01E-55
chr8:123952459-12398312	Abcb10	56199	15.4	15.7	17.8	1.14978	0.261264	1.44231	3.66E-05
chr5:8660092-8748570:+	Abcb1a	18671	63.9	55.3	9.5	-1.03456	0.756755	-5.30049	1.08E-137
chr1:75171641-75180283:	Abcb6	74104	18.2	19.1	28.5	1.1856	0.342351	1.92928	1.38E-07
chrX:104280565-10441384	Abcb7	11306	22.1	21.5	28.4	1.08355	0.360222	1.59991	2.76E-15
chr5:124061857-12409579	Abcb9	56325	4.2	3.5	2.4	-1.07325	0.711524	-1.42426	0.0038392
chr17:46303230-46328023	Abcc10	224814	6.2	4.7	3.1	-1.18771	0.400164	-1.57865	0.0016963
chr8:86504841-86566590:	Abcc12	244562	1.7	0.1	0.2	-5.85609	0.000306	-3.73539	0.0015799
chr14:118482692-1187062	Abcc4	239273	23.7	22.1	12.0	1.03364	0.864763	-1.56612	4.17E-05
chr16:20331304-20426394	Abcc5	27416	73.3	54.8	18.8	-1.19742	0.109171	-3.0811	1.49E-42
chr6:142587862-14270227	Abcc9	20928	68.1	54.8	24.3	-1.10762	0.425911	-2.21764	6.18E-20
chrX:73716597-73738287:	Abcd1	11666	23.5	17.6	9.9	-1.19826	0.20232	-1.88418	8.97E-10
chr15:91145871-91191807	Abcd2	26874	11.7	5.4	1.4	-1.83235	0.123408	-5.21076	1.76E-08
chr3:121758910-12181521	Abcd3	19299	70.5	61.5	70.5	-1.02874	0.800841	1.24856	0.0008208
chr12:84602531-84617466	Abcd4	19300	19.5	13.5	7.4	-1.30075	0.226523	-2.05351	6.03E-06
chr8:79683442-79711740:	Abce1	24015	88.3	138.7	318.5	1.75635	0.009193	4.26974	8.02E-18
chr17:35956819-35969750	Abcf1	224742	71.4	76.1	111.1	1.20465	0.198656	1.93005	2.69E-10
chr5:24565341-24577467:	Abcf2	27407	47.0	79.0	152.4	1.86494	0.024243	3.7499	4.55E-10
chr17:31057694-31117981	Abcg1	11307	20.1	12.7	4.2	-1.41566	0.123671	-3.66057	8.26E-15
chr6:58596672-58692451:	Abcg2	26357	86.4	83.3	38.7	1.07163	0.563258	-1.77863	1.36E-13
chr9:44273190-44288244:	Abcg4	192663	5.7	3.5	1.9	-1.44465	0.126024	-2.34421	3.00E-06
chr17:84658234-84682923	Abcg5	27409	1.9	2.1	0.3	1.22564	0.700367	-3.88893	9.27E-05
chr5:30950066-30955095:	Abhd1	57742	13.0	9.4	4.7	-1.23563	0.305177	-2.14204	4.77E-07
chr16:45729725-45742955	Abhd10	213012	20.3	20.0	20.7	1.10329	0.23339	1.27541	3.63E-05
chr5:135009152-13501217	Abhd11	68758	28.3	23.5	42.4	-1.07834	0.539664	1.86559	5.53E-16
chr5:135012122-13501315	Abhd11os	69812	2.8	2.9	0.4	1.15506	0.789982	-3.72362	0.0003806
chr8:9977717-9992154:+	Abhd13	68904	33.8	38.7	42.2	1.28955	0.091981	1.54831	0.0001225
chr9:106440051-10644767	Abhd14a	68644	47.7	36.1	18.4	-1.18722	0.12474	-2.05261	1.09E-17
chr9:106448640-10645291	Abhd14b	76491	86.6	55.3	19.1	-1.40288	0.022388	-3.54969	2.03E-28
chr17:35089291-35102987	Abhd16a	193742	81.8	79.5	76.1	1.08971	0.147113	1.16443	0.0005613
chr10:80583649-80590341	Abhd17a	216169	43.5	42.6	46.7	1.09769	0.284989	1.34309	1.28E-06
chr19:21653309-21685637	Abhd17b	226016	36.5	41.1	42.5	1.257	0.015417	1.44848	4.66E-07
chr7:79273266-79361601:	Abhd2	54608	72.6	63.3	66.6	-1.02706	0.730615	1.14537	0.0046166
chr18:10644411-10706696	Abhd3	106861	6.8	6.0	1.7	-1.01122	0.962601	-3.08379	2.18E-15
chr14:54254129-54269169	Abhd4	105501	109.4	91.3	25.8	-1.07055	0.487749	-3.365	1.33E-75
chr14:8002902-8056555:+	Abhd6	66082	13.4	21.7	23.3	1.78643	0.071148	2.05242	0.0036436
chr2:22939989-23040241:	Abi1	11308	81.7	83.0	78.4	1.13797	0.13964	1.19699	0.0067215
chr11:95830072-95842476	Abi3	66610	4.9	5.2	5.7	1.20167	0.28881	1.4556	0.0024881
chr16:56477846-56690135	Abi3bp	320712	88.9	70.1	17.5	-1.13433	0.492055	-3.95817	8.66E-30
chr2:31688537-31804362:	Abl1	11350	66.8	51.2	37.4	-1.16661	0.107074	-1.4224	7.79E-07
chr1:156558787-15664961	Abl2	11352	20.0	20.5	24.7	1.15683	0.146577	1.54775	2.63E-09
chr19:57033264-57216032	Ablim1	226251	57.5	49.1	23.7	-1.04523	0.666736	-1.93247	2.55E-25
chr5:35757880-35884979:	Ablim2	231148	3.4	2.5	1.1	-1.21695	0.282498	-2.45276	1.17E-10
chr18:61799393-61911852	Ablim3	319713	8.1	8.2	4.3	1.13381	0.540535	-1.49249	0.0043087
chr10:18011260-18023252	Abracl	73112	70.1	63.7	75.9	1.01172	0.944052	1.34768	0.0005539
chr13:23418361-23423866	Abt1	30946	12.0	14.5	15.4	1.36789	0.057356	1.59022	0.0002226
chr6:88835914-88841935:	Abtb1	80283	81.5	60.0	6.2	-1.22209	0.299031	-9.82604	1.34E-60
chr2:103566310-10371842	Abtb2	99382	8.8	9.1	3.7	1.1638	0.274116	-1.88464	5.36E-10
chr9:119341294-11935029	Acaa1a	113868	93.6	75.9	41.3	-1.10737	0.392146	-1.79895	1.03E-12
chr18:74779212-74806207	Acaa2	52538	113.6	91.3	55.8	-1.11478	0.178266	-1.626	1.36E-16
chr5:114165518-11425075	Acacb	100705	9.6	7.4	2.8	-1.14814	0.49094	-2.62333	1.01E-12
chr5:121621029-12166051	Acad10	71985	11.1	6.7	2.5	-1.47837	0.116492	-3.30049	1.84E-10
chr9:104063703-10412764	Acad11	102632	27.4	23.2	13.0	-1.05294	0.719876	-1.66884	6.89E-09
chr5:121598281-12161893	Acad12	338350	13.2	8.4	1.1	-1.40389	0.144193	-8.92618	1.20E-31
chr9:26974139-26999549:	Acad8	66948	58.8	50.9	30.9	-1.04225	0.830635	-1.51321	0.0002418
chr3:36066000-36092857:	Acad9	229211	36.4	31.5	34.0	-1.03289	0.733275	1.16904	0.0078474
chr3:153922353-15394464	Acadm	11364	94.2	75.9	31.5	-1.11562	0.329844	-2.37218	4.40E-28
chr5:115110299-11511934	Acads	11409	37.9	30.0	17.2	-1.13705	0.369417	-1.75528	2.14E-08

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:70010183-70015428	Acadvl	11370	105.4	99.5	100.0	1.05479	0.467797	1.1835	0.0008353
chr16:31092413-31201238	Acap2	78618	72.2	69.6	44.6	1.08608	0.468199	-1.29175	0.0011605
chr4:155891875-15590725	Acap3	140500	19.8	19.0	21.7	1.07323	0.580604	1.36425	0.0001927
chr1:180726043-18075420	Acbd3	170760	46.0	53.6	63.8	1.31526	0.081746	1.71782	4.72E-06
chr11:103101688-1031121	Acbd4	67131	85.9	61.5	20.5	-1.25612	0.198026	-3.27111	1.68E-20
chr2:23068201-23114512:	Acbd5	74159	43.3	40.4	28.4	1.03819	0.687357	-1.22043	0.0006872
chr1:155558120-15568723	Acbd6	72482	29.1	25.1	32.3	-1.03284	0.763654	1.38476	1.73E-07
chr2:93833467-93849943:	Accs	329470	15.4	9.6	2.9	-1.43989	0.226478	-3.85882	6.27E-10
chr11:105967945-1059899	Ace	11421	11.4	8.0	5.6	-1.27771	0.109383	-1.6123	3.50E-05
chr11:105994675-1060054	Ace3	217246	1.4	0.1	0.1	-5.34457	0.003298	-4.1146	0.0028475
chr7:98213660-98309527:	Acer3	66190	20.2	23.0	30.9	1.27653	0.10473	1.88733	1.05E-08
chr1:173331886-17333350	Ackr1	13349	3.2	6.1	7.9	1.88083	0.157111	2.60912	0.0042624
chr9:121898355-12191107	Ackr2	59289	3.6	14.7	6.9	4.02662	9.73E-06	2.20273	0.0051026
chr1:90203980-90215722:	Ackr3	12778	24.1	66.0	105.8	2.77686	0.006151	4.48819	5.09E-07
chr9:104098138-10412664	Ackr4	252837	2.6	2.2	0.5	-1.05073	0.910235	-3.30723	3.91E-06
chr4:40143265-40199009:	Aco1	11428	50.5	39.7	53.0	-1.13898	0.15476	1.31115	5.90E-05
chr15:81872463-81915137	Aco2	11429	173.6	168.1	204.2	1.09164	0.50758	1.46761	1.56E-05
chr12:84009502-84017669	Acot1	26897	37.1	27.2	18.2	-1.2253	0.228702	-1.60967	0.0001222
chr15:20665214-20666750	Acot10	64833	1.5	0.4	0.6	-3.08229	0.004759	-1.89398	0.0420304
chr13:24817955-24831489	Acot13	66834	49.4	43.6	19.8	-1.0109	0.945466	-1.98285	2.89E-15
chr2:164792768-16480488	Acot8	170789	21.7	22.0	25.5	1.13358	0.28855	1.46392	3.21E-06
chrX:155262500-15529750	Acot9	56360	60.8	63.5	88.0	1.16761	0.105201	1.80152	1.69E-17
chr2:91202912-91214098:	Acp2	11432	48.2	40.3	30.4	-1.07625	0.50045	-1.26646	0.0015389
chr9:22126727-22135746:	Acp5	11433	23.5	14.9	8.5	-1.39092	0.208972	-2.1338	9.03E-05
chr3:97158777-97176576:	Acp6	66659	50.5	38.1	21.6	-1.18444	0.069844	-1.8597	1.48E-18
chr9:104288240-10433772	Acpp	56318	43.3	34.7	6.6	-1.12549	0.719149	-4.81585	2.42E-15
chr15:89568326-89574585	Acr	11434	3.4	0.6	0.8	-3.56402	0.007117	-2.75225	0.0083716
chr6:125049927-12506326	Acrbp	54137	29.0	18.0	6.6	-1.4255	0.090687	-3.38981	8.85E-15
chr9:36693220-36698837:	Acrv1	11451	5.4	0.3	0.6	-6.04297	0.000843	-4.01712	0.0023167
chr17:56843104-56874447	Acsbg2	328845	3.5	0.2	0.4	-8.60213	5.18E-06	-4.85959	0.0001137
chr11:94557102-94601786	Acsf2	264895	19.2	14.8	5.8	-1.16592	0.223159	-2.63273	3.19E-25
chr8:46471037-46536051:	Acsl1	14081	68.3	31.4	19.4	-1.82129	0.132563	-2.49478	0.0024379
chr1:78657825-78707743:	Acsl3	74205	32.0	32.3	44.7	1.1377	0.38718	1.73823	7.28E-08
chr19:55253369-55296628	Acsl5	433256	62.7	59.2	83.5	1.05721	0.598237	1.65939	2.90E-14
chr7:119760923-11978489	Acsm3	20216	0.9	0.7	0.1	-1.18326	0.797834	-3.04226	0.0059704
chr2:150618111-15066824	Acss1	68738	31.1	19.1	7.7	-1.46118	0.004689	-3.17519	9.91E-27
chr2:155518043-15556274	Acss2	60525	44.0	30.9	9.5	-1.26631	0.492095	-3.38172	1.44E-07
chr10:106936164-1071236	Acss3	380660	46.2	36.4	4.2	-1.14128	0.452854	-8.45313	1.28E-67
chr8:123891758-12389477	Acta1	11459	23.5	21.1	87.9	1.02831	0.948404	4.26133	6.09E-11
chr19:34240336-34255373	Acta2	11475	####	2024.0	2633.7	1.02767	0.885581	1.4916	0.0001356
chr5:142903116-14290672	Actb	11461	####	4246.9	8694.8	1.25354	0.089192	2.81249	2.08E-26
chr11:120345690-1203484	Actg1	11465	687.7	1068.5	1690.9	1.73808	0.029078	2.91982	3.42E-08
chr6:83512909-83536251:	Actg2	11468	287.0	300.2	727.4	1.15752	0.380029	3.09447	1.85E-23
chr9:107928469-10793246	Actl11	67722	3.2	0.1	0.3	-11.2209	2.44E-07	-5.59027	2.21E-05
chr3:32708546-32726971:	Actl6a	56456	50.2	56.1	94.8	1.259	0.114504	2.33478	1.78E-15
chr4:56743422-56744925:	Actl7a	11470	7.4	0.4	0.7	-6.08205	0.001022	-4.34854	0.0015926
chr4:56740005-56741425:	Actl7b	11471	11.5	0.7	1.5	-8.53394	2.89E-06	-4.43582	0.0002028
chr17:33432899-33434267	Actl9	69481	11.4	1.2	1.2	-5.45395	0.000414	-4.86792	0.0001064
chr12:80167542-80260371	Actn1	109711	155.7	174.2	296.3	1.25806	0.06981	2.3552	4.42E-20
chr19:4861216-4877909:-	Actn3	11474	2.5	2.3	0.7	1.00831	0.980821	-2.78289	1.96E-07
chr7:28893254-28962280:	Actn4	60595	139.7	129.5	206.9	1.04364	0.713814	1.8459	1.42E-18
chr12:70937857-70964717	Actr10	56444	46.5	48.0	70.8	1.16275	0.23104	1.89097	1.03E-12
chr19:46376814-46395735	Actr1a	54130	113.9	118.5	127.3	1.17264	0.245271	1.39104	0.0009616
chr1:36699202-36709925:	Actr1b	226977	75.2	76.5	112.5	1.14281	0.122165	1.86467	1.31E-23
chr11:20062304-20112951	Actr2	66713	104.3	106.7	165.0	1.14818	0.273926	1.96082	2.87E-14
chr1:125392905-12543572	Actr3	74117	160.3	180.4	330.0	1.26314	0.090035	2.53689	3.03E-20
chr5:25760026-25850341:	Actr3b	242894	7.6	6.2	3.6	-1.09852	0.675265	-1.66156	0.0004958
chr14:29978337-29993221	Actr8	56249	83.8	72.3	53.8	-1.03145	0.765372	-1.24214	0.0006105

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr4:154666428-15466786	Actrt2	73353	10.6	0.3	1.1	-10.7896	2.33E-06	-4.65645	0.0005202
chr3:30597073-30599870:	Actrt3	76652	1.2	0.1	0.2	-5.38542	0.001058	-3.09373	0.0081525
chr2:58267453-58357758:	Acvr1c	269275	3.4	1.3	0.4	-2.04732	0.161671	-4.71794	4.67E-05
chr9:119402501-11943350	Acvr2b	11481	22.3	14.3	2.5	-1.38782	0.302848	-6.19975	1.89E-15
chr15:101128522-1011453	Acvrl1	11482	35.5	32.6	38.5	1.03211	0.79622	1.35201	2.66E-05
chr9:106432981-10643823	Acy1	109652	17.2	14.4	17.5	-1.063	0.617452	1.27607	0.0014224
chr19:3986570-3990005:+	Acy3	71670	10.4	7.2	1.7	-1.2891	0.301232	-4.60764	1.23E-15
chr12:85272398-85280435	Acyp1	66204	42.3	31.7	15.7	-1.19361	0.265571	-2.12766	1.03E-10
chr2:163726571-16375023	Ada	11486	4.5	4.4	6.5	1.09055	0.646466	1.78201	1.86E-07
chr3:37063656-37111512:	Adad1	21744	5.1	0.3	0.8	-8.71543	1.42E-06	-3.94783	0.0004041
chr11:102761439-1027802	Adam11	11488	4.2	2.9	0.9	-1.26772	0.249006	-3.59373	2.47E-16
chr7:133883199-13422509	Adam12	11489	14.8	14.0	27.2	1.05743	0.761941	2.25965	4.66E-14
chr12:21323509-21373632	Adam17	11491	47.2	46.7	47.4	1.10091	0.289959	1.2513	0.0005902
chr8:24602246-24674755:	Adam18	13524	2.5	0.1	0.2	-9.14519	1.26E-05	-4.91881	0.0002775
chr11:46054502-46147347	Adam19	11492	31.4	27.8	38.4	-1.01568	0.951078	1.51405	0.0020026
chr5:121518604-12152169	Adam1a	280668	19.3	15.0	9.9	-1.13844	0.479698	-1.53001	0.0007951
chr5:121500097-12150298	Adam1b	280667	1.6	0.0	0.1	-13.1267	2.39E-07	-6.3421	1.43E-05
chr14:66027329-66077733	Adam2	11495	6.3	0.3	0.7	-10.5788	3.59E-07	-5.00385	6.39E-05
chr8:40793273-40797303:	Adam20	384806	1.0	0.1	0.0	-4.38659	0.011667	-4.75061	0.0009227
chr5:8072352-8368081:-	Adam22	11496	23.0	20.9	6.3	1.01928	0.927902	-2.84248	3.21E-21
chr8:40675094-40682199:	Adam24	13526	1.7	0.1	0.2	-8.10728	7.36E-05	-3.46534	0.0068038
chr14:68604998-68655842	Adam28	13522	8.5	3.9	1.4	-1.87705	0.017233	-4.30399	2.19E-12
chr8:24677234-24725825:	Adam3	11497	17.7	0.9	2.1	-10.0295	2.72E-07	-4.68787	9.14E-05
chr3:98160812-98163173:	Adam30	71078	1.5	0.1	0.3	-6.04655	0.000321	-3.16092	0.0063979
chr8:24836143-24948804:	Adam32	353188	8.5	0.7	1.6	-7.1257	3.00E-06	-3.32937	0.0011464
chr2:131050817-13106381	Adam33	110751	16.9	15.3	3.9	1.00363	0.99288	-3.31075	1.59E-10
chr8:24727093-24824369:	Adam5	11499	16.9	3.5	1.7	-3.72045	0.000203	-6.39262	6.39E-10
chr12:113543908-1135464	Adam6a	238406	1.7	0.1	0.2	-9.15608	1.99E-05	-4.25608	0.0012716
chr12:113489565-1134918	Adam6b	238405	1.3	0.0	0.0	-13.0037	6.18E-07	-10.359	1.79E-07
chr8:24949611-25016922:	Adam9	11502	43.8	48.0	74.5	1.21288	0.219719	2.09582	4.41E-11
chr14:68563387-68582072	Adamdec1	58860	8.7	10.3	2.1	1.28268	0.407776	-3.05809	1.98E-07
chr16:85793828-85803115	Adamts1	11504	50.3	188.6	560.2	3.95807	1.00E-08	12.0382	4.06E-33
chr17:33524196-33553782	Adamts10	224697	98.3	69.4	18.3	-1.26573	0.102923	-4.20734	7.07E-42
chr15:11064790-11346867	Adamts12	239337	22.8	17.6	2.4	-1.16628	0.548789	-7.12694	1.50E-31
chr10:61197112-61273438	Adamts14	237360	5.3	4.4	1.5	-1.07272	0.79462	-2.72633	6.94E-10
chr13:70727808-70841810	Adamts16	271127	1.4	1.0	0.5	-1.20181	0.589239	-2.35523	0.0002295
chr7:66839735-67152625:	Adamts17	233332	3.1	2.5	1.3	-1.10897	0.673824	-1.80847	0.0001808
chr11:50602085-50807573	Adamts2	216725	18.9	42.4	102.0	2.36246	0.015084	5.57846	4.06E-10
chr5:89673841-89883334:	Adamts3	330119	6.1	6.1	12.9	1.09566	0.762036	2.54553	1.93E-07
chr1:171250422-17125992	Adamts4	240913	4.1	99.8	122.3	10.5979	4.75E-07	13.0005	3.15E-10
chr16:85858157-85901125	Adamts5	23794	20.9	15.0	8.9	-1.25068	0.39947	-1.82807	0.0013082
chr13:104287873-1044947	Adamts6	108154	27.1	19.9	10.4	-1.22405	0.327646	-2.03812	1.16E-06
chr9:90162978-90200102:	Adamts7	108153	12.0	7.9	1.9	-1.36631	0.268776	-4.63058	3.30E-14
chr9:30942563-30962858:	Adamts8	30806	8.2	10.7	16.5	1.4733	0.21115	2.39099	0.0001173
chr6:92772699-92901441:	Adamts9	101401	17.7	33.7	56.4	2.10312	0.001764	3.74131	9.85E-12
chr4:86053915-86428382:	Adamtsl1	77739	42.7	35.3	14.9	-1.08437	0.660121	-2.25652	1.27E-12
chr2:27079381-27108613:	Adamtsl2	77794	0.4	6.7	10.0	5.33422	0.00211	7.36322	8.76E-06
chr7:82335694-82614448:	Adamtsl3	269959	6.5	6.2	3.1	1.07061	0.742498	-1.6569	8.49E-05
chr3:95676201-95687917:	Adamtsl4	229595	10.5	8.6	1.8	-1.1015	0.779176	-4.2871	2.03E-12
chr10:13552907-13563376	Adat2	66757	7.9	6.6	8.7	-1.0651	0.738091	1.35654	0.0064436
chr10:80602880-80607654	Adat3	1E+08	5.9	8.5	10.1	1.61533	0.002816	2.12158	3.36E-09
chr12:88360514-88461726	Adck1	72113	14.6	13.7	14.9	1.04357	0.727364	1.27477	0.0010361
chr6:39573876-39588769:	Adck2	57869	16.5	11.7	7.8	-1.26	0.209887	-1.65825	0.0001961
chr1:180165238-18019602	Adck3	67426	21.3	12.4	0.7	-1.52717	0.132508	-19.8406	3.22E-43
chr15:76576359-76595811	Adck5	268822	39.2	32.4	21.5	-1.08095	0.43409	-1.45181	6.29E-08
chr11:7063489-7178505:+	Adcy1	432530	2.7	3.3	9.3	1.36427	0.124566	4.17533	9.99E-23
chr1:165485183-16557677	Adcy10	271639	3.8	0.4	0.6	-6.59056	4.25E-06	-4.13309	7.45E-05
chr12:4133397-4213524:+	Adcy3	104111	17.1	13.5	9.0	-1.13212	0.310133	-1.50886	2.65E-06

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr14:55769092-55784019	Adcy4	104110	16.7	20.7	25.7	1.39646	0.282349	1.84735	0.0067289
chr16:35155636-35304549	Adcy5	224129	38.7	82.0	82.6	2.24006	0.03756	2.39089	0.0041086
chr15:98589986-98607633	Adcy6	11512	69.2	54.3	24.4	-1.13728	0.090035	-2.25416	7.22E-48
chr8:88272403-88329962:	Adcy7	11513	39.5	30.0	17.2	-1.1772	0.461454	-1.80926	0.0001001
chr15:64699035-64922296	Adcy8	11514	0.0	0.1	1.7	1.63615	0.42375	19.6007	9.16E-14
chr16:4284886-4420498:-	Adcy9	11515	23.6	25.8	10.2	1.23984	0.400887	-1.79953	0.0011691
chr6:55451978-55501455:	Adcyap1r1	11517	12.2	8.1	3.2	-1.34743	0.287787	-2.92689	7.80E-08
chr5:34573714-34632305:	Add1	11518	191.6	156.2	118.3	-1.10057	0.308804	-1.29241	0.0001459
chr19:53140443-53247326	Add3	27360	110.2	100.2	58.1	1.01498	0.860484	-1.51561	4.86E-19
chr10:10335703-10472314	Adgb	215772	1.5	0.7	0.4	-1.88052	0.043973	-2.95148	1.08E-05
chr3:138277645-13829069	Adh1	11522	202.1	359.9	1205.0	1.98632	5.62E-07	7.21024	1.26E-64
chr3:138415497-13843089	Adh4	26876	0.4	0.2	1.2	-1.6852	0.392257	2.8512	0.0096168
chr3:138437200-13845549	Adh5	11532	132.7	133.7	177.0	1.12903	0.129089	1.66379	1.31E-18
chr3:138217773-13823204	Adh7	11529	1.1	1.1	5.0	1.16326	0.70701	5.14855	3.86E-13
chr1:9548046-9577968:+	Adhfe1	76187	26.4	16.8	4.3	-1.39871	0.099105	-4.63096	9.61E-24
chr7:110627669-11062981	Adm	11535	23.6	62.8	88.2	2.91413	1.10E-08	4.43703	4.58E-20
chr18:80127135-80151482	Adnp2	240442	29.1	29.1	34.5	1.12644	0.303891	1.47926	1.70E-06
chr10:67544511-67548955	Ado	211488	35.8	31.8	36.6	-1.01179	0.94403	1.27683	0.0057283
chr1:134199215-13423545	Adora1	11539	6.1	2.4	0.5	-2.21893	0.005328	-8.84921	3.12E-20
chr9:59291572-59316200:	Adpgk	72141	26.1	23.9	50.8	1.02138	0.85023	2.4284	5.50E-52
chr16:38445399-38452689	Adprh	11544	67.2	64.6	89.9	1.07269	0.47356	1.66877	1.68E-15
chr4:126316351-12632170	Adprhl2	100206	52.2	58.7	74.9	1.26722	0.066836	1.78553	1.43E-09
chr11:67037880-67052618	Adprm	66358	35.1	35.7	18.7	1.14095	0.29762	-1.49527	1.29E-05
chr14:66635251-66771168	Adra1a	11549	5.4	5.5	2.4	1.15229	0.41649	-1.76214	6.05E-06
chr2:131545357-13156228	Adra1d	11550	1.2	1.2	2.3	1.09685	0.788043	2.29623	1.19E-05
chr19:54045182-54048982	Adra2a	11551	10.6	5.9	2.2	-1.58112	0.197527	-3.48729	1.72E-06
chr5:35278566-35281763:	Adra2c	11553	3.5	2.9	0.4	-1.0353	0.960068	-4.93837	1.88E-05
chr18:62177713-62179981	Adrb2	11555	42.0	87.8	12.1	2.32844	3.94E-08	-2.71397	3.22E-13
chr8:27225776-27229588:	Adrb3	11556	7.9	2.8	1.0	-2.08705	0.177654	-3.8823	0.0008598
chr19:4285999-4306222:-	Adrbk1	110355	48.5	56.1	71.3	1.30282	0.047981	1.82454	2.27E-09
chr2:180171588-18017628	Adrm1	56436	55.2	78.3	153.2	1.5927	0.061419	3.29273	1.37E-10
chr15:80948490-80970947	Adsl	11564	37.0	40.8	63.2	1.23881	0.050162	2.12628	1.06E-20
chr1:177763178-17779650	Adss	11566	83.3	86.4	106.8	1.16195	0.192462	1.5971	1.81E-08
chr11:5861866-5872225:+	Aebp1	11568	376.7	434.2	500.7	1.30501	0.269102	1.63302	0.005402
chr6:140622663-14067741	Aebp2	11569	34.7	38.6	40.7	1.258	0.109323	1.46163	0.0004517
chr7:78895927-78908833:	Aen	68048	18.1	34.7	98.3	2.11708	0.002181	6.18668	1.84E-20
chr7:28351540-28351633:	AF357399	1E+08	45.4	70.8	146.5	1.70504	0.099105	3.661	3.82E-08
chr8:13835231-13838089:	AF366264	231201	1.1	0.0	0.1	-8.22614	5.98E-05	-4.09034	0.0018116
chr9:89590035-89622986:	AF529169	209743	2.5	9.1	15.8	3.16546	0.015095	5.20427	9.95E-06
chr5:35893319-36003922:	Afap1	70292	35.7	33.3	22.9	1.04958	0.689438	-1.2462	0.0040629
chr18:61730262-61786662	Afap1l1	106877	36.1	34.4	22.3	1.06187	0.581304	-1.29048	0.0004107
chr11:53350767-53421830	Aff4	93736	104.4	119.1	132.7	1.28584	0.054347	1.58004	3.90E-06
chr8:123477862-12350391	Afg3l1	114896	23.5	22.0	28.2	1.05061	0.446423	1.50474	2.22E-22
chr18:67404764-67449136	Afg3l2	69597	52.3	52.2	75.2	1.12897	0.440613	1.78544	5.74E-08
chr8:53511702-53523422:	Aga	11593	46.6	32.2	19.4	-1.30357	0.07784	-1.90096	1.50E-08
chr1:89454811-89895282:	Agap1	347722	31.5	29.0	18.3	1.02797	0.751869	-1.37173	1.68E-09
chr2:90782744-90816231:	Agbl2	271813	3.2	1.4	0.4	-2.07007	0.005495	-5.65399	2.44E-14
chr5:30888852-30906666:	Agbl5	231093	17.4	9.5	5.8	-1.63615	0.004357	-2.33634	1.11E-09
chr1:82839483-82896275:	Agfg1	15463	68.8	79.1	86.2	1.29683	0.090035	1.55608	0.0001347
chr6:40325478-40396762:	Agk	69923	33.8	30.2	33.7	-1.00178	0.989592	1.2464	0.0008053
chr3:116739999-11680816	Agl	77559	23.8	21.7	24.6	1.01615	0.897258	1.28834	0.0002003
chr12:37241639-37581932	Agmo	319660	8.8	6.4	1.2	-1.23553	0.398631	-5.35814	4.15E-19
chr4:126435013-12646842	Ago1	236511	34.9	26.1	12.7	-1.19546	0.05847	-2.18443	1.48E-28
chr15:73101625-73184947	Ago2	239528	31.1	35.4	35.3	1.27916	0.078828	1.41483	0.0011657
chr4:126489543-12653345	Ago4	76850	10.7	8.5	1.9	-1.12655	0.319534	-4.40771	4.17E-60
chr17:34605861-34613449	Agpat1	55979	46.3	46.9	56.4	1.14242	0.279785	1.51974	1.58E-06
chr10:78271563-78351700	Agpat3	28169	52.7	47.3	51.7	1.0052	0.959762	1.22751	0.000123
chr17:12119284-12219640	Agpat4	68262	35.9	30.4	17.0	-1.0542	0.703048	-1.68599	1.15E-09

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr8:18846279-18884413:	Agpat5	52123	21.9	43.1	50.8	2.11739	0.036465	2.61633	0.0005519
chr8:23172946-23208453:	Agpat6	102247	63.5	67.0	91.5	1.19368	0.300714	1.78646	1.73E-06
chr5:100846229-10089910	Agpat9	231510	14.8	8.1	5.2	-1.62153	0.025139	-2.19595	2.91E-06
chr2:75832177-75931350:	Agps	228061	34.8	35.2	44.6	1.13233	0.032957	1.59924	1.60E-27
chr12:35992925-36004081	Agr2	23795	5.1	3.6	12.1	-1.25276	0.501119	2.79753	7.95E-07
chr4:156165290-15619748	Agrn	11603	44.2	35.3	16.3	-1.11925	0.274283	-2.15647	3.04E-26
chr13:30336356-30382867	Agtr1a	11607	64.8	39.2	8.7	-1.4736	0.244986	-5.2294	3.72E-12
chr4:148077061-14808806	Agtrap	11610	36.9	25.5	13.6	-1.30192	0.096507	-2.13795	1.23E-10
chr1:179744904-17980401	Ahctf1	226747	78.9	96.7	97.5	1.38455	0.07062	1.53033	0.0020739
chr2:155059312-15507449	Ahcy	269378	41.9	39.3	60.7	1.04211	0.791493	1.79737	7.53E-11
chr10:20952547-21080429	Ahi1	52906	15.8	14.4	23.5	1.01862	0.865181	1.85327	4.26E-27
chr19:8989284-9076926:+	Ahnak	66395	586.5	455.0	323.2	-1.15643	0.111266	-1.44935	4.40E-08
chr13:74211118-74292309	Ahrr	11624	1.9	1.1	0.1	-1.55508	0.165984	-8.92655	5.21E-16
chr12:87266728-87273952	Ahsa1	217737	160.1	224.9	244.2	1.57886	0.007017	1.88072	3.29E-06
chr9:55326949-55438344:	AI118078	244886	2.8	10.7	11.8	3.73938	8.52E-05	4.37312	2.74E-07
chr4:58800031-58912725:	AI314180	230249	113.7	105.6	109.2	1.04078	0.561143	1.19983	5.35E-05
chr17:27563769-27565727	AI413582	106672	31.5	27.8	15.7	-1.01929	0.931256	-1.60303	0.0001069
chr8:36993575-36995533:	AI429214	621080	10.9	6.4	2.2	-1.51841	0.22587	-3.57324	5.22E-07
chr4:41495601-41503075:	AI464131	329828	5.9	3.3	1.2	-1.57512	0.175744	-3.42262	7.91E-07
chr5:23692261-23712667:	AI506816	433855	1.7	3.1	12.4	1.94824	0.001706	8.34363	1.31E-38
chr4:141614370-14161560	AI507597	100165	6.3	0.4	0.6	-6.58751	0.000386	-4.76285	0.0005613
chr11:83223576-83226584	AI662270	1E+08	9.9	13.3	15.3	1.46319	0.147744	1.86547	0.0015527
chr6:48628167-48633688:	AI854703	243373	9.7	5.8	0.8	-1.46297	0.454807	-6.25746	1.58E-07
chr7:41372930-41393379:	AI987944	233168	24.3	19.5	12.4	-1.12032	0.459956	-1.55371	3.30E-05
chr1:183297060-18332450	Aida	108909	47.7	44.8	44.6	1.05	0.578798	1.16782	0.0078089
chrX:48474944-48513563:	Aifm1	26926	41.7	45.0	73.4	1.21596	0.133055	2.18576	9.27E-17
chr10:61715263-61739260	Aifm2	71361	15.6	10.8	5.6	-1.29887	0.092406	-2.21823	9.56E-12
chr16:17489677-17507485	Aifm3	72168	1.3	0.7	0.3	-1.58995	0.163425	-3.2433	1.09E-05
chr10:13652709-13868830	Aig1	66253	44.0	35.2	26.8	-1.1212	0.343698	-1.31088	0.0018604
chr3:132660498-13268387	Aimp1	13722	114.9	102.2	158.8	-1.00772	0.947566	1.7239	1.05E-20
chr5:143902704-14390983	Aimp2	231872	31.1	37.7	90.4	1.3596	0.086373	3.52668	2.91E-22
chr19:4113756-4125858:-	Aip	11632	47.3	44.7	46.0	1.0548	0.443728	1.21451	3.82E-05
chr17:12741311-12859884	Airn	104103	76.0	60.9	21.5	-1.12228	0.662413	-2.72126	1.38E-09
chr4:153373221-15348283	Ajap1	230959	2.9	4.2	9.9	1.55569	0.146122	3.87195	7.90E-10
chr14:54567469-54577661	Ajuba	16475	32.2	27.9	35.7	-1.03038	0.83223	1.382	6.41E-05
chr2:32621758-32635058:	Ak1	11636	17.9	23.4	54.9	1.46504	0.245338	3.49641	9.80E-08
chr9:8076633-8134294:-	AK129341	234915	8.1	5.9	3.4	-1.22799	0.288506	-1.89426	5.13E-06
chr4:128993224-12901152	Ak2	11637	56.3	64.9	79.3	1.29764	0.184663	1.73529	0.0001385
chr19:29020832-29047902	Ak3	56248	250.6	185.4	51.4	-1.21905	0.314731	-3.77328	3.35E-22
chr3:152462815-15266814	Ak5	229949	7.5	7.4	16.2	1.11182	0.546704	2.66825	3.71E-19
chr13:100651343-1006664	Ak6	1.02E+08	15.8	26.6	54.4	1.86625	0.011667	4.02916	3.10E-13
chr12:105705982-1057824	Ak7	78801	1.3	0.3	0.3	-3.46967	0.004445	-2.83654	0.0033526
chr2:28700161-28813165:	Ak8	68870	4.9	0.8	0.8	-4.08865	0.000709	-3.84113	0.000119
chr10:4266329-4359471:+	Akap12	83397	117.9	99.9	29.9	-1.04872	0.741172	-3.11487	1.66E-40
chr7:75455534-75754609:	Akap13	75547	109.9	87.9	39.0	-1.12369	0.475311	-2.22144	2.78E-13
chrX:36608183-36645414:	Akap17b	338351	9.6	6.3	3.7	-1.36949	0.387192	-1.97991	0.0086302
chr6:126853098-12687430	Akap3	11642	12.4	0.5	1.2	-11.2184	1.03E-07	-5.35009	2.86E-05
chrX:7067515-7078606:+	Akap4	11643	23.0	1.0	2.7	-11.2015	4.67E-08	-4.79357	6.33E-05
chr12:52699383-53151015	Akap6	238161	4.1	3.5	1.1	-1.03749	0.866982	-2.94551	9.39E-18
chr10:25169090-25299163	Akap7	432442	52.6	42.7	15.7	-1.10335	0.411379	-2.64312	5.04E-32
chr17:32321424-32350577	Akap8l	54194	155.7	136.0	58.8	-1.01184	0.956596	-2.08855	2.17E-11
chr5:3928186-4080204:+	Akap9	100986	84.6	76.9	48.8	1.02162	0.857771	-1.38219	1.21E-06
chr4:123735195-12375029	Akirin1	68050	32.9	67.1	88.5	2.21212	0.010233	3.06872	5.01E-06
chr3:108739658-10878230	Aknad1	329738	2.4	1.1	0.6	-1.89446	0.035009	-3.06787	3.70E-06
chr6:34384247-34396949:	Akr1b10	67861	47.6	36.0	12.7	-1.19066	0.382568	-2.91001	2.20E-14
chr6:34412362-34423137:	Akr1b7	11997	1.0	2.2	7.2	2.29201	0.027511	7.50249	2.90E-13
chr6:34354164-34368454:	Akr1b8	14187	28.0	20.4	36.1	-1.22854	0.214628	1.59632	7.88E-05
chr13:4059591-4090422:+	Akr1c14	105387	113.9	156.4	176.2	1.5289	0.000312	1.91799	3.77E-11

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr1:65013086-65032748:	Akr1cl	70861	2.7	0.6	9.4	-3.13869	0.006973	3.60185	5.86E-05
chr13:4592490-4609164:-	Akr1e1	56043	47.9	37.5	17.4	-1.14844	0.374502	-2.1755	9.26E-13
chr4:139310744-13931878	Akr7a5	110198	34.8	30.2	20.6	-1.03609	0.799878	-1.34446	0.0004097
chr12:112653821-1126742	Akt1	11651	120.3	170.8	258.4	1.59169	0.081687	2.55729	2.85E-06
chr1:177022115-17724876	Akt3	23797	103.2	87.7	38.3	-1.05457	0.585115	-2.14811	6.88E-35
chr8:91111781-91135494:	Aktip	14339	49.0	44.0	30.6	1.00487	0.97402	-1.27892	0.0019887
chr4:62505984-62520063:	Alad	17025	27.9	31.1	55.9	1.26159	0.304764	2.44135	2.25E-08
chrX:150547417-15057062	Alas2	11656	5.7	5.5	11.8	1.07083	0.900331	2.3077	0.0062234
chr5:90460889-90476603:	Alb	11657	2.2	0.7	0.2	-2.24646	0.144193	-4.19008	0.0006641
chr19:40550257-40588463	Aldh18a1	56454	29.0	28.7	108.6	1.09849	0.448627	4.61647	1.33E-80
chr9:71215789-71296243:	Aldh1a2	19378	39.3	87.7	388.1	2.37407	0.009546	9.88518	1.19E-18
chr7:66390893-66427477:	Aldh1a3	56847	37.3	26.4	3.1	-1.26585	0.340743	-8.88994	6.83E-36
chr6:90550848-90599171:	Aldh1l1	107747	12.1	8.4	3.7	-1.26317	0.569151	-2.36623	0.0016456
chr10:83487447-83534140	Aldh1l2	216188	2.6	2.2	6.0	-1.08864	0.767698	2.76362	9.09E-10
chr5:121567687-12159382	Aldh2	11669	165.4	121.4	64.4	-1.2193	0.007826	-2.04321	3.47E-34
chr19:3913491-3929716:-	Aldh3b1	67689	8.3	5.6	3.7	-1.32204	0.275376	-1.7727	0.0023339
chr13:24907579-24937661	Aldh5a1	214579	11.3	6.4	4.1	-1.59297	0.012457	-2.1494	2.06E-07
chr12:84430720-84450950	Aldh6a1	104776	160.9	125.1	23.4	-1.1544	0.356852	-5.34301	1.97E-55
chr18:56525736-56572939	Aldh7a1	110695	106.7	79.7	44.7	-1.19808	0.055886	-1.89796	1.04E-19
chr7:126795234-12680044	Aldoa	11674	447.2	411.0	647.9	1.03295	0.805568	1.80311	5.23E-15
chr4:72850583-72852634:	Aldoart1	353204	2.4	0.4	0.8	-4.21663	0.000359	-2.2666	0.015468
chr12:55565205-55566896	Aldoart2	79459	6.9	0.5	0.9	-7.1984	2.45E-05	-4.26029	0.0003407
chr16:5233621-5244907:+	Alg1	208211	34.6	29.6	49.0	-1.04333	0.68193	1.76493	5.43E-21
chr15:90224311-90230554	Alg10b	380959	42.3	41.8	53.9	1.10795	0.159385	1.59189	3.30E-19
chr8:22060721-22071627:	Alg11	207958	34.9	38.4	39.9	1.23671	0.010401	1.42442	5.64E-08
chr15:88805243-88819318	Alg12	223774	15.2	12.8	19.9	-1.06734	0.565909	1.62957	1.64E-12
chr3:121291817-12136201	Alg14	66789	36.8	30.3	41.3	-1.09055	0.449113	1.39709	9.17E-06
chr4:47469833-47474367:	Alg2	56737	27.9	22.6	55.4	-1.10665	0.259409	2.47767	6.67E-52
chr16:20605458-20610749	Alg3	208624	8.0	12.5	31.5	1.74898	0.015701	4.6603	1.59E-18
chr3:54735539-54749795:	Alg5	66248	35.5	33.4	48.8	1.05055	0.634948	1.70989	8.80E-18
chr4:99715630-99763460:	Alg6	320438	18.8	13.8	8.2	-1.22996	0.283036	-1.79523	2.49E-05
chr7:97371617-97392158:	Alg8	381903	16.0	15.6	28.0	1.09196	0.56281	2.17737	2.22E-16
chr9:50775225-50843639:	Alg9	102580	28.3	29.0	34.1	1.14657	0.062931	1.50508	2.23E-14
chr12:87428078-87443839	Alkbh1	211064	31.5	43.4	57.5	1.55011	0.024004	2.23384	7.40E-08
chr7:30308753-30314303:	Alkbh6	233065	43.8	46.6	48.3	1.18882	0.053546	1.37616	1.74E-06
chr12:28553756-28582483	Allc	94041	10.6	0.4	1.1	-10.3125	1.43E-06	-4.76286	0.0002318
chr6:85587531-85702751:	Alms1	236266	49.2	33.7	11.7	-1.31325	0.173528	-3.24082	4.43E-16
chr11:70315613-70322518	Alox12e	11685	4.3	3.8	0.9	-1.0214	0.960029	-3.44857	1.33E-07
chr6:116410071-11646117	Alox5	11689	4.7	2.4	1.1	-1.71623	0.028181	-3.2727	1.54E-09
chr11:69126377-69149115	Aloxe3	23801	1.4	0.7	0.2	-1.67765	0.187272	-3.842	1.38E-05
chr3:127670310-12778052	Alpk1	71481	27.1	22.4	13.3	-1.08246	0.561823	-1.61438	8.76E-08
chr4:137741731-13779638	Alpl	11647	1.9	5.7	25.1	2.85912	0.00842	11.0508	1.36E-14
chr9:110880174-11090053	Als2cl	235633	29.4	24.2	15.7	-1.07634	0.699086	-1.48929	0.0008072
chr1:59050506-59094900:	Als2cr11	73463	5.7	0.5	0.8	-6.77065	3.72E-05	-3.95055	0.0006042
chr1:58658120-58695989:	Als2cr12	108812	3.6	0.4	0.6	-4.38923	0.006171	-3.13928	0.0099197
chr11:120594516-1205983	Alyref	21681	82.3	124.1	241.7	1.69088	0.008774	3.52993	8.24E-16
chr1:171503478-17150475	Alyref2	56009	8.2	9.2	12.1	1.24836	0.121754	1.83583	1.72E-09
chr15:10981756-10996624	Amacr	17117	11.1	8.5	4.7	-1.18128	0.512221	-1.85016	0.0004035
chr10:93523338-93540033	Amdhd1	71761	1.8	1.6	0.4	-1.0012	0.998624	-2.99597	0.0001308
chr17:24155833-24163733	Amdhd2	245847	35.1	23.8	12.0	-1.32201	0.071538	-2.31158	9.84E-13
chrX:95420314-95444840:	Amer1	72345	28.5	17.3	8.4	-1.46554	0.27702	-2.49974	0.0003075
chr14:60378286-60381003	Amer2	72125	3.2	1.8	1.0	-1.54956	0.106858	-2.47348	1.63E-05
chr8:93971588-94012640:	Amfr	23802	100.3	103.6	182.3	1.16294	0.144388	2.25893	6.39E-28
chr15:102445367-1024546	Amhr2	110542	6.3	1.3	1.1	-3.60828	0.001332	-3.58767	0.0001346
chr3:108186289-10819228	Amigo1	229715	20.3	17.6	8.6	-1.03915	0.850716	-1.86256	6.98E-08
chr15:97244074-97247287	Amigo2	105827	18.6	19.9	4.3	1.16495	0.711011	-3.12629	7.72E-06
chr9:108053159-10805570	Amigo3	320844	2.3	4.0	6.7	1.91766	0.011893	3.41055	7.63E-10
chrX:142853474-14296672	Ammecr1	56068	11.7	10.8	12.0	1.02715	0.844993	1.2802	0.0013882

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chrX:145446424-14548763	Amot	27494	15.4	11.8	6.8	-1.16755	0.238904	-1.79524	6.49E-10
chr3:108074062-10808666	Ampd2	109674	27.7	22.1	41.4	-1.12106	0.075364	1.86229	5.54E-44
chr7:110768206-11081240	Ampd3	11717	33.9	70.0	92.4	2.28414	2.64E-15	3.36384	6.13E-37
chr13:18948351-19150919	Amph	218038	5.5	4.2	0.8	-1.1735	0.385326	-5.32471	1.27E-28
chr9:108296922-10830159	Amt	434437	39.9	28.2	13.1	-1.26742	0.256886	-2.37356	9.63E-09
chr3:113555952-11357775	Amy1	11722	27.8	20.0	4.5	-1.24186	0.346922	-4.64642	1.04E-20
chr11:109425946-1094381	Amz2	13929	59.2	50.7	34.4	-1.04488	0.63052	-1.37432	4.66E-08
chr2:128610083-12868739	Anapc1	17222	86.8	79.7	84.7	1.03073	0.717721	1.21908	0.0001208
chr8:79711820-79777321:	Anapc10	68999	13.6	16.0	15.8	1.32445	0.033671	1.44892	0.0002835
chr7:101881325-10189954	Anapc15	75430	20.1	21.3	50.6	1.19572	0.292513	3.09409	4.77E-23
chr2:25272466-25285916:	Anapc2	99152	68.9	59.6	42.3	-1.03067	0.799619	-1.29946	0.0002086
chr5:52834135-52866734:	Anapc4	52206	93.6	80.4	85.1	-1.04198	0.566854	1.13542	0.0077402
chr5:122787461-12282134	Anapc5	59008	434.8	379.2	254.2	-1.02102	0.849079	-1.36269	5.07E-07
chr14:51091077-51102009	Ang	11727	45.2	35.3	10.5	-1.14987	0.346949	-3.39243	6.06E-30
chr12:86700502-86726460	Angel1	68737	7.1	5.0	2.9	-1.25849	0.232029	-1.94463	2.64E-06
chr15:42424667-42676977	Angpt1	11600	18.5	15.4	1.9	-1.07703	0.578363	-7.60278	2.99E-95
chr8:18690263-18741562:	Angpt2	11601	12.3	16.8	12.7	1.53453	0.006428	1.28457	0.058169
chr2:151911332-15194465	Angpt4	11602	0.9	2.8	6.8	2.64241	0.042842	5.88104	1.02E-06
chr1:156839023-15686107	Angptl1	72713	2.8	1.7	0.3	-1.33657	0.653913	-4.52424	0.0003086
chr17:33774900-33781575	Angptl4	57875	14.5	38.8	45.1	2.53477	0.019262	3.23173	0.0001776
chr15:27466677-27594907	Ank	11732	29.1	24.2	14.4	-1.07592	0.507587	-1.60668	1.61E-10
chr8:22974836-23150497:	Ank1	11733	0.4	0.9	1.1	2.14093	0.085609	2.59745	0.0049266
chr3:126921607-12699845	Ank2	109676	23.8	19.8	5.2	-1.07609	0.663385	-3.56914	8.45E-34
chr10:69533708-70027436	Ank3	11735	24.8	20.0	7.8	-1.10169	0.340906	-2.51885	6.53E-39
chr1:72642980-72700564:	Ankar	319695	1.2	0.1	0.2	-5.89763	0.000678	-3.26174	0.0077775
chr2:136532321-13655585	Ankef1	319196	7.8	1.3	0.9	-3.95342	0.002462	-5.01428	1.67E-05
chr11:89421086-89538555	Ankfn1	382543	1.7	1.7	0.6	1.09826	0.819046	-2.23401	0.0019886
chr5:3689999-3803124:-	Ankib1	70797	35.5	37.0	61.5	1.16901	0.084119	2.15296	1.50E-31
chr1:92870129-92902906:	Ankmy1	241158	1.6	0.5	0.3	-2.58171	0.028413	-3.81241	9.22E-05
chr12:36157124-36197291	Ankmy2	217473	62.0	45.8	24.6	-1.21965	0.322152	-1.98077	1.58E-06
chr13:98263076-98274754	Ankra2	68558	25.8	21.3	15.0	-1.08745	0.584035	-1.36746	0.002093
chr19:36111965-36119844	Ankrd1	107765	0.6	0.4	1.7	-1.23134	0.718408	3.02665	0.0009218
chr8:11611581-11635757:	Ankrd10	102334	89.9	79.9	55.8	-1.00643	0.957008	-1.28607	4.51E-05
chr17:65967501-66077046	Ankrd12	106585	51.0	45.0	24.4	-1.00804	0.94649	-1.66525	1.25E-16
chr5:114775140-11480582	Ankrd13a	68420	60.1	60.6	83.8	1.13313	0.41296	1.73085	1.73E-07
chr11:77470487-77489678	Ankrd13b	268445	10.3	9.1	6.4	-1.01867	0.909548	-1.29533	0.0047207
chr3:157947466-15800683	Ankrd13c	433667	30.8	37.9	61.4	1.38435	0.060866	2.44392	4.09E-12
chr19:4270180-4283137:-	Ankrd13d	68423	9.4	7.9	3.3	-1.06085	0.753449	-2.27016	7.03E-12
chr2:11777753-11790323:	Ankrd16	320816	43.6	28.2	23.2	-1.38654	0.0099	-1.49631	7.01E-05
chr5:90227166-90366185:	Ankrd17	81702	52.3	53.2	59.7	1.14467	0.229541	1.42197	1.60E-05
chr1:36530534-36535729:	Ankrd23	78321	26.8	22.8	15.9	-1.05386	0.745319	-1.33985	0.0035704
chr10:81628540-81647612	Ankrd24	70615	18.3	14.2	4.9	-1.15034	0.385258	-2.89626	6.82E-21
chr7:35586247-35639237:	Ankrd27	245886	30.5	26.7	17.6	-1.02532	0.805897	-1.38493	4.47E-08
chr18:12252357-12305720	Ankrd29	225187	13.0	8.1	2.0	-1.41435	0.144977	-4.86478	1.12E-18
chr13:77043088-77135468	Ankrd32	105377	26.4	24.3	17.1	1.03013	0.821942	-1.23138	0.0082165
chr15:31291479-31367759	Ankrd33b	67434	2.3	1.8	3.2	-1.10932	0.725648	1.74621	0.0020319
chr3:96670131-96691034:	Ankrd35	213121	5.6	3.4	1.7	-1.45431	0.338185	-2.39434	0.0019818
chr11:5569684-5689337:+	Ankrd36	76389	4.2	0.2	0.5	-11.8866	2.34E-08	-4.78767	5.21E-05
chr8:45996908-45999850:	Ankrd37	654824	6.9	4.9	1.9	-1.27118	0.559733	-2.55838	0.000838
chr11:94328001-94341847	Ankrd40	71452	37.5	37.7	57.9	1.13063	0.102148	1.92902	1.94E-34
chr7:92584183-92637142:	Ankrd42	73845	12.9	7.0	2.9	-1.62122	0.001691	-3.40562	5.37E-21
chr1:54645340-54926387:	Ankrd44	329154	21.8	21.6	10.3	1.09973	0.630057	-1.67396	5.09E-05
chr1:161142712-16117050	Ankrd45	73844	1.1	0.3	0.3	-2.61946	0.011772	-2.78986	0.0008061
chr15:36477668-36496791	Ankrd46	68839	85.3	94.5	133.6	1.24972	0.196675	1.93153	1.41E-07
chr9:14780198-14782964:	Ankrd49	56503	37.9	38.3	65.5	1.12773	0.136089	2.15134	9.81E-43
chr3:38449261-38484816:	Ankrd50	99696	27.4	21.9	13.9	-1.11807	0.276998	-1.57357	5.71E-10
chr6:83762646-83768326:	Ankrd53	75305	1.2	0.2	0.2	-4.30468	0.005629	-3.22684	0.0062175
chr4:32804035-32950826:	Ankrd6	140577	19.1	17.5	9.3	1.02766	0.855745	-1.63438	5.99E-09

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr2:173568661-17357834	Ankrd60	70065	3.8	0.2	0.5	-4.94668	0.005352	-3.29006	0.012351
chr5:143890743-14389506	Ankrd61	66729	3.4	0.7	1.1	-3.5052	0.006006	-2.19316	0.0358436
chr17:43534174-43543639	Ankrd66	1E+08	1.1	0.6	0.2	-1.492	0.43266	-2.95491	0.0041548
chr6:18866318-18879584:	Ankrd7	75196	3.8	0.5	0.4	-4.08887	0.00863	-4.57954	0.0004478
chr1:75192160-75199385:	Ankzf1	52231	53.1	38.3	13.0	-1.24902	0.257308	-3.18012	1.01E-16
chr7:144588549-14473859	Ano1	101772	103.6	74.7	37.4	-1.22372	0.205504	-2.17838	1.16E-11
chr9:122175874-12229442	Ano10	102566	51.9	42.9	33.3	-1.08311	0.406113	-1.24365	0.0013216
chr6:125690419-12604012	Ano2	243634	7.3	4.6	0.4	-1.39302	0.332925	-10.7212	1.05E-20
chr10:88948994-89257790	Ano4	320091	82.2	61.5	13.1	-1.18918	0.252698	-4.88492	9.63E-50
chr7:51511029-51598707:	Ano5	233246	1.8	4.6	7.8	2.71213	0.000292	4.86262	5.83E-12
chr8:71476019-71486067:	Ano8	382014	14.5	12.5	7.0	-1.04541	0.827887	-1.64121	3.53E-05
chr9:62341343-62378805:	Anp32a	11737	173.1	156.1	95.6	1.00689	0.956596	-1.44634	1.10E-08
chr4:46451117-46472523:	Anp32b	67628	79.3	78.9	214.3	1.12391	0.509097	3.31282	1.69E-25
chr3:95929257-95947387:	Anp32e	66471	56.4	58.9	112.6	1.17534	0.115813	2.48086	1.33E-34
chr7:79821803-79842352:	Anpep	16790	185.5	127.3	79.1	-1.28841	0.114031	-1.85276	2.52E-07
chr6:87133853-87335775:	Antxr1	69538	96.1	79.9	26.8	-1.08174	0.540479	-2.84182	2.86E-36
chr5:97884688-98030962:	Antxr2	71914	143.2	124.9	42.9	-1.03993	0.884843	-2.60864	6.28E-11
chr14:34053470-34075999	Antxrl	239029	1.7	0.1	0.1	-9.12673	1.62E-05	-5.45459	0.000121
chr19:20373434-20390671	Anxa1	16952	284.9	253.5	144.1	-1.01367	0.958722	-1.574	0.000943
chr14:25842155-25886804	Anxa11	11744	65.4	53.5	41.4	-1.09856	0.341548	-1.2634	0.0009545
chr9:69453683-69491785:	Anxa2	12306	418.3	436.3	925.0	1.17331	0.409603	2.69519	6.01E-14
chr5:96793385-96845968:	Anxa3	11745	55.3	66.4	117.7	1.34828	0.202128	2.5637	2.50E-08
chr6:86736840-86793584:	Anxa4	11746	115.1	106.9	74.8	1.03512	0.758931	-1.23106	0.0026219
chr11:54978962-55033471	Anxa6	11749	345.6	382.5	419.5	1.24702	0.108205	1.50995	6.53E-05
chr3:95296094-95307176:	Anxa9	71790	29.7	21.0	3.1	-1.26391	0.063722	-7.44111	3.61E-76
chr6:48895255-48909187:	Aoc1	76507	0.2	0.3	1.9	1.50267	0.38846	9.68267	9.25E-15
chr11:101325063-1013296	Aoc2	237940	6.1	7.7	13.1	1.42605	0.144193	2.6118	5.72E-08
chr11:101330606-1013394	Aoc3	11754	27.2	17.9	10.6	-1.3584	0.204647	-1.99619	9.76E-05
chr1:58029969-58106410:	Aox1	11761	32.6	18.5	3.3	-1.56257	0.157104	-6.78606	1.03E-16
chr1:58113136-58200452:	Aox3	71724	107.3	68.7	5.2	-1.3987	0.24854	-14.0938	4.20E-38
chr3:127807265-12783749	Ap1ar	211556	50.6	48.1	51.8	1.05611	0.662975	1.2784	0.0020417
chr11:4947521-5042794:+	Ap1b1	11764	31.9	30.4	47.0	1.06666	0.348526	1.8396	2.39E-40
chr8:109778583-10986420	Ap1g1	11765	51.6	54.8	68.2	1.19888	0.173989	1.64259	3.51E-07
chr8:72240132-72257379:	Ap1m1	11767	78.1	75.0	84.7	1.07714	0.435227	1.35464	2.99E-06
chr5:137034994-13704606	Ap1s1	11769	46.8	42.8	56.7	1.02134	0.880111	1.51085	3.94E-08
chr1:79606876-79671972:	Ap1s3	252903	14.0	9.4	6.6	-1.34555	0.192913	-1.6729	0.0024694
chr7:44900373-44929490:	Ap2a1	11771	36.8	32.7	49.4	1.00143	0.993214	1.67507	4.69E-12
chr7:141562180-14163301	Ap2a2	11772	67.2	61.4	72.0	1.02246	0.736736	1.33857	8.77E-14
chr11:83302697-83405033	Ap2b1	71770	84.9	82.6	104.7	1.09515	0.468659	1.5365	4.28E-07
chr16:20535480-20544909	Ap2m1	11773	122.6	120.6	146.1	1.10576	0.380823	1.48503	6.57E-07
chr7:16738444-16749290:	Ap2s1	232910	106.3	111.6	136.0	1.17999	0.137297	1.5924	1.01E-08
chr7:81460399-81493925:	Ap3b2	11775	13.8	10.7	5.5	-1.1543	0.619553	-1.94499	0.0004215
chr10:80706978-80742211	Ap3d1	11776	109.1	101.8	113.4	1.0506	0.638162	1.29888	9.29E-05
chr14:21033742-21052442	Ap3m1	55946	36.9	36.6	57.1	1.11415	0.28709	1.92684	7.62E-21
chr8:22787354-22805654:	Ap3m2	64933	14.2	10.8	5.8	-1.18452	0.38135	-1.92017	1.67E-06
chr18:46741876-46790826	Ap3s1	11777	42.3	40.5	44.5	1.07057	0.507718	1.31087	7.73E-05
chr3:103809517-10382202	Ap4b1	67489	33.5	27.8	20.8	-1.08425	0.579603	-1.28698	0.009978
chr5:138172021-13817868	Ap4m1	11781	63.1	48.5	23.4	-1.16714	0.147278	-2.14171	5.54E-22
chr12:51690966-51738939	Ap4s1	11782	46.1	50.5	62.8	1.23104	0.074804	1.69645	7.42E-10
chr2:131210360-13121351	Ap5s1	69596	18.9	12.2	7.7	-1.38935	0.087415	-1.9295	7.01E-06
chr5:142463931-14247871	Ap5z1	231855	15.2	10.3	5.3	-1.32438	0.135761	-2.24929	7.10E-09
chr19:23758876-23949597	Apba1	319924	26.1	19.7	7.1	-1.18178	0.266976	-2.90364	1.59E-23
chr7:64501706-64753876:	Apba2	11784	3.3	3.0	0.7	-1.00233	0.994268	-3.86828	3.85E-15
chr10:81268172-81273247	Apba3	57267	37.4	50.0	72.7	1.50746	0.025	2.38389	5.42E-10
chr7:105558465-10558165	Apbb1	11785	38.3	24.4	5.8	-1.40569	0.20325	-4.87272	2.55E-16
chr5:66298725-66618817:	Apbb2	11787	25.3	22.5	14.0	-1.00261	0.985014	-1.43897	6.62E-07
chr18:34220984-34322190	Apc	11789	37.9	33.6	38.3	-1.00574	0.94423	1.26361	2.62E-08
chr10:80301820-80318256	Apc2	23805	2.1	1.5	0.4	-1.20872	0.5467	-3.43251	7.11E-09

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr18:62922327-62953195	Apcdd1	494504	115.7	58.3	18.1	-1.72076	0.164736	-4.28104	3.98E-07
chr14:50924949-50927188	Apex1	11792	64.2	75.2	121.4	1.31176	0.049729	2.33284	1.45E-16
chr9:66775487-66795423:	Aph1b	208117	13.5	10.7	6.1	-1.14522	0.556454	-1.75938	0.0002289
chr9:66814994-66834706:	Aph1c	68318	11.1	6.2	1.0	-1.59888	0.137685	-7.42787	1.74E-17
chr2:94411727-94438147:	Api5	11800	95.3	111.1	155.3	1.3147	0.054488	2.01775	4.19E-11
chr6:87628429-87672168:	Aplf	72103	15.1	11.9	6.2	-1.1404	0.47236	-1.92003	2.02E-07
chrX:48025146-48034852:	Apln	30878	2.7	4.5	10.0	1.79751	0.100841	4.02633	1.35E-07
chr9:31149557-31211815:	Aplp2	11804	321.4	278.3	176.8	-1.02842	0.79126	-1.451	1.83E-09
chr2:150583081-15060852	Apmap	71881	36.7	34.2	45.8	1.04105	0.731826	1.55755	1.92E-10
chr1:152750551-15275754	Apobec4	71281	1.8	0.2	0.1	-3.82236	0.025806	-4.37665	0.0018294
chr7:126585008-12658909	Apobr	171504	5.8	4.2	10.1	-1.22102	0.352413	2.14817	1.52E-07
chr16:31296192-31314808	Apod	11815	18.9	21.4	6.3	1.24424	0.397633	-2.3333	3.55E-06
chr15:77045075-77057108	Apol6	71939	4.3	4.8	22.9	1.2149	0.745319	4.80345	1.51E-05
chr15:77698889-77719288	Apol7e	666348	1.8	3.3	4.9	1.81127	0.199664	2.841	0.002269
chr15:77729072-77736382	Apol9b	71898	7.5	8.9	2.0	1.29341	0.488764	-2.65285	0.0001829
chrX:94367110-94417092:	Apoo	68316	4.5	4.2	6.5	1.05482	0.836697	1.79834	2.48E-05
chrX:112311408-11237243	Apool	68117	36.0	37.9	22.6	1.172	0.165366	-1.27339	0.0062079
chr16:84954436-85173707	App	11820	381.1	316.3	189.8	-1.08124	0.361108	-1.60196	1.21E-15
chr11:85191310-85235120	Appbp2	66884	51.0	58.6	67.5	1.29693	0.058508	1.64631	1.50E-06
chr10:83600034-83648664	Appl2	216190	144.0	107.4	19.2	-1.20089	0.102842	-5.90943	1.63E-101
chr8:122574637-12257690	Aprt	11821	172.0	152.4	232.3	-1.0086	0.941915	1.68444	5.60E-19
chr6:55336299-55348555:	Aqp1	11826	372.7	297.9	119.1	-1.12859	0.481234	-2.47316	2.52E-15
chr7:97726379-97738247:	Aqp11	66333	15.3	6.5	2.5	-1.97512	0.083677	-4.11427	2.27E-06
chr4:41033074-41048136:	Aqp7	11832	4.0	0.8	0.3	-3.1419	0.035325	-5.60739	4.50E-05
chr9:71110659-71163289:	Aqp9	64008	2.3	1.2	0.6	-1.63483	0.268357	-2.66931	0.0027504
chr2:114101161-11417533	Aqr	11834	53.1	51.7	68.9	1.09501	0.380311	1.61679	1.13E-11
chr7:101348069-10141258	Arap1	69710	90.0	63.9	31.7	-1.27009	0.317327	-2.20526	3.15E-06
chr18:37972623-37998969	Arap3	106952	20.6	18.2	12.3	-1.00806	0.945436	-1.33668	2.77E-06
chr9:44742144-44767808:	Arcn1	213827	147.4	184.1	312.6	1.40706	0.048174	2.59631	1.68E-13
chr12:84918149-84970886	Arel1	68497	33.5	31.1	39.5	1.04544	0.710884	1.47403	8.90E-08
chr11:59211412-59228267	Arf1	11840	248.5	269.6	419.5	1.21989	0.084215	2.09486	2.27E-18
chr11:103966725-1039853	Arf2	11841	46.2	59.6	98.4	1.45245	0.094175	2.5753	1.07E-08
chr14:26638197-26657258	Arf4	11843	109.0	124.5	244.4	1.28798	0.130385	2.74821	1.00E-16
chr6:28423640-28426499:	Arf5	11844	104.2	109.5	142.4	1.18012	0.269979	1.69243	7.99E-07
chr12:69372150-69375980	Arf6	11845	71.6	94.0	120.9	1.47487	0.030565	2.07279	1.18E-07
chr2:91265115-91277371:	Arfgap2	77038	95.0	92.6	99.8	1.09676	0.372653	1.31174	0.0001936
chr15:83299740-83350247	Arfgap3	66251	56.6	70.3	76.1	1.4002	0.113404	1.65432	0.0018575
chr1:10137507-10232670:	Arfgef1	211673	68.8	70.9	67.4	1.15839	0.142134	1.2224	0.0083065
chr2:166805581-16689805	Arfgef2	99371	20.2	20.5	23.9	1.14661	0.366078	1.47194	0.000291
chr10:18588011-18743758	Arfgef3	215821	0.9	0.9	1.8	1.11633	0.727681	2.35721	4.73E-06
chr3:84496093-84582625:	Arfip1	99889	55.6	54.4	62.2	1.09094	0.300296	1.39313	1.75E-08
chr7:105634201-10564041	Arfip2	76932	50.5	45.5	56.9	1.01254	0.9152	1.40671	3.32E-08
chr12:79130788-79156301	Arg2	11847	6.8	16.7	10.7	2.60618	4.80E-05	1.91476	0.0017658
chr18:6024450-6136098:-	Arhgap12	75415	56.0	46.0	26.7	-1.09801	0.526727	-1.66717	1.90E-07
chr7:123279149-12336991	Arhgap17	70497	24.3	24.5	26.9	1.13589	0.356678	1.37795	0.001048
chr19:41766588-41802084	Arhgap19	71085	10.3	7.6	4.4	-1.21972	0.304036	-1.85847	8.15E-06
chr9:51765352-51853059:	Arhgap20	244867	15.7	15.0	5.1	1.0729	0.58112	-2.45267	9.81E-27
chr11:103331484-1033636	Arhgap27	544817	6.4	6.9	9.3	1.19705	0.166059	1.79741	2.65E-10
chr17:67842708-68004108	Arhgap28	268970	21.0	20.6	6.6	1.09696	0.343271	-2.54543	1.74E-40
chr3:121953326-12201615	Arhgap29	214137	130.2	100.1	85.6	-1.16462	0.077356	-1.21712	0.0030005
chr9:32116136-32265511:	Arhgap32	330914	22.2	16.3	12.7	-1.22714	0.075136	-1.39345	0.0001474
chr7:30522226-30535060:	Arhgap33	233071	3.5	2.3	1.4	-1.36231	0.184663	-1.97163	0.0001016
chr7:16494473-16614993:	Arhgap35	232906	53.2	55.0	57.5	1.16556	0.235024	1.35023	0.001511
chr9:8994953-9239013:-	Arhgap42	71544	45.8	47.5	69.2	1.17076	0.362105	1.864	2.31E-07
chr11:65002039-65162961	Arhgap44	216831	16.2	12.7	9.0	-1.13943	0.518071	-1.43033	0.0099987
chrX:168795099-16930444	Arhgap6	11856	42.5	34.4	13.8	-1.11038	0.457195	-2.45095	3.41E-21
chr11:120577235-1205816	Arhgdia	192662	128.6	139.2	285.5	1.22071	0.155914	2.73842	2.48E-23
chr17:26199183-26201350	Arhgdig	14570	1.7	2.3	7.7	1.43114	0.225629	5.12937	4.73E-18

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr8:14911663-15001085:	Arhgef10	234094	28.7	24.6	12.1	-1.03222	0.872965	-1.87666	9.73E-09
chr4:140514485-14066590	Arhgef10l	72754	34.4	28.4	16.7	-1.07837	0.593584	-1.63437	8.50E-08
chr3:87618751-87738033:	Arhgef11	213498	55.4	45.9	30.0	-1.07662	0.365694	-1.47263	8.01E-12
chr9:42963842-43105718:	Arhgef12	69632	116.0	100.2	78.7	-1.03501	0.603918	-1.17915	0.0001357
chr11:68943154-68956858	Arhgef15	442801	9.8	7.1	9.9	-1.22741	0.035814	1.25727	0.0017241
chr3:88616207-88648052:	Arhgef2	16800	78.1	60.7	128.8	-1.15335	0.122833	2.05373	4.04E-27
chr10:127182521-1271900	Arhgef25	52666	150.7	115.4	50.9	-1.17394	0.383713	-2.32484	3.09E-11
chr3:62338777-62462221:	Arhgef26	622434	27.9	17.6	4.8	-1.39091	0.472036	-3.81026	1.97E-05
chr13:97898595-98206165	Arhgef28	110596	26.1	18.6	7.9	-1.25273	0.019288	-2.62732	3.55E-38
chr14:27143993-27403911	Arhgef3	71704	74.5	46.2	22.7	-1.4467	0.087848	-2.53675	8.01E-09
chr17:80307407-80388689	Arhgef33	381112	1.4	0.8	0.4	-1.50782	0.229196	-2.35129	0.000971
chr3:133159531-13323488	Arhgef38	77669	2.6	1.2	0.8	-1.84314	0.111162	-2.22842	0.0067662
chr1:34801722-34812754:	Arhgef4	226970	8.2	7.1	3.4	-1.01816	0.966587	-1.86496	0.0076693
chrX:57231485-57338729:	Arhgef6	73341	44.7	34.0	10.7	-1.1805	0.229587	-3.29043	2.30E-33
chrX:95048935-95166539:	Arhgef9	236915	11.6	9.0	3.5	-1.15639	0.414805	-2.63475	5.96E-15
chr17:4995074-5347656:+	Arid1b	239985	32.9	29.0	18.3	-1.00926	0.94185	-1.43234	3.52E-08
chr15:96287522-96405463	Arid2	77044	52.5	49.2	31.6	1.05474	0.661345	-1.32568	0.0002695
chr9:57790505-57834234:	Arid3b	56380	5.8	5.3	3.3	1.01891	0.927605	-1.41517	0.002185
chr12:71015967-71099351	Arid4a	238247	45.8	65.7	16.8	1.60557	0.147061	-2.05519	0.0035921
chr13:14063784-14199603	Arid4b	94246	66.0	63.6	35.6	1.08366	0.436304	-1.48071	2.82E-08
chr1:36307733-36324029:	Arid5a	214855	13.8	29.6	18.9	2.27621	0.002336	1.64958	0.0297676
chr9:108602943-10864938	Arih2	23807	54.1	60.0	61.4	1.25367	0.194561	1.41022	0.0083661
chr10:88731414-88743202	Arl1	104303	215.2	220.1	292.4	1.14782	0.166603	1.69081	2.50E-13
chr16:62793689-62847040	Arl13b	68146	35.3	35.9	18.9	1.13534	0.14493	-1.49243	7.33E-10
chr2:106962529-10697439	Arl14ep	212772	40.1	35.3	48.8	-1.01966	0.846049	1.51619	3.39E-14
chr13:113794508-1141574	Arl15	218639	35.9	32.1	19.8	1.00119	0.991328	-1.44692	1.04E-12
chr11:120464326-1204676	Arl16	70317	12.1	10.1	7.0	-1.07178	0.711569	-1.37116	0.0080775
chr8:94666600-94674457:	Arl2bp	107566	73.2	67.1	90.3	1.03381	0.830443	1.5354	1.36E-06
chr19:46531109-46573085	Arl3	56350	88.5	74.9	51.4	-1.05599	0.503179	-1.37565	7.56E-09
chr12:40033291-40037987	Arl4a	11861	43.4	33.4	21.2	-1.17298	0.456558	-1.6188	0.0012056
chr1:88698226-88702191:	Arl4c	320982	87.9	97.6	141.9	1.25462	0.375213	1.96165	0.0001823
chr2:15055362-15079191:	Arl5b	75869	29.6	31.1	30.1	1.1852	0.144914	1.26878	0.0069893
chr7:118118890-11812962	Arl6ip1	54208	147.8	145.8	94.7	1.10129	0.269461	-1.24861	0.0004695
chr5:124116108-12411819	Arl6ip4	65105	54.6	54.3	71.7	1.11557	0.191034	1.63921	2.41E-17
chr6:108783059-10882372	Arl8b	67166	86.5	84.0	92.7	1.09316	0.402063	1.33856	8.35E-05
chr3:19132144-19163065:	Armc1	74252	36.5	37.7	47.2	1.15747	0.029835	1.60989	1.12E-21
chr17:28530861-28538975	Armc12	67645	4.9	0.2	0.7	-9.06325	1.67E-05	-3.90234	0.0021847
chr10:41914990-42018382	Armc2	213402	3.5	2.6	0.3	-1.21209	0.505832	-7.71786	2.45E-21
chr2:19199118-19310243:	Armc3	70882	2.8	0.5	0.5	-4.26675	0.000348	-3.42401	0.0003339
chr7:128237357-12824510	Armc5	233912	7.4	7.2	13.9	1.10156	0.650886	2.29212	2.35E-10
chr8:70220193-70234422:	Armc6	76813	13.5	14.3	36.8	1.18668	0.074254	3.40911	3.05E-80
chr11:115475677-1154904	Armc7	276905	8.0	8.2	10.5	1.15495	0.371567	1.63171	8.62E-06
chr9:99478391-99568899:	Armc8	74125	30.0	31.2	39.8	1.17275	0.105001	1.65639	2.49E-12
chr1:86154780-86278284:	Armc9	78795	15.2	11.9	9.6	-1.14895	0.178226	-1.2606	0.0026728
chrX:134717938-13472191	Armcx1	78248	41.7	27.1	13.7	-1.3828	0.138187	-2.36548	1.08E-07
chrX:134804142-13480922	Armcx2	67416	46.2	44.2	71.2	1.06734	0.550054	1.91739	7.37E-21
chrX:134756568-13476145	Armcx3	71703	33.8	32.8	34.8	1.08534	0.37658	1.28539	0.0001002
chr7:84246275-84410038:	Arnt2	11864	23.3	15.9	12.1	-1.31601	0.050133	-1.52739	8.23E-05
chr7:113207465-11331412	Arntl	11865	15.6	35.3	37.0	2.50769	2.78E-35	2.94414	3.41E-52
chr6:146805530-14683352	Arntl2	272322	13.6	9.5	5.7	-1.29593	0.415038	-1.83441	0.0074525
chr5:145083869-14510875	Arpc1a	56443	85.0	90.9	99.1	1.20536	0.10876	1.45266	1.75E-05
chr5:145114256-14512818	Arpc1b	11867	160.9	168.6	260.6	1.17105	0.298936	2.00041	7.63E-11
chr1:74236550-74268213:	Arpc2	76709	186.4	188.5	281.1	1.13623	0.31471	1.8701	1.53E-12
chr5:122391928-12240617	Arpc3	56378	228.4	240.8	320.7	1.18042	0.296752	1.73463	1.00E-06
chr6:113378113-11339044	Arpc4	68089	52.8	57.4	81.2	1.22244	0.183837	1.90137	3.84E-09
chr1:152766542-15277558	Arpc5	67771	110.1	123.3	145.1	1.25634	0.215704	1.62365	0.0003316
chr2:39008139-39015872:	Arpc5l	74192	46.4	53.3	79.7	1.28998	0.084087	2.12101	3.72E-12
chr9:75037614-75060313:	Arpp19	59046	54.7	55.5	56.7	1.14077	0.180029	1.29308	0.0003985

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr7:99535486-99606771:	Arrb1	109689	78.2	69.9	26.6	1.00251	0.984057	-2.33411	4.59E-41
chr2:24925352-24935281:	Arrdc1	215705	37.9	30.2	14.7	-1.12745	0.302944	-2.05479	7.27E-18
chr8:70835138-70839720:	Arrdc2	70807	16.4	11.7	5.0	-1.26557	0.346949	-2.52875	1.85E-07
chr13:80883422-80896043	Arrdc3	105171	113.5	90.9	36.6	-1.13398	0.719508	-2.35876	6.99E-05
chr7:68736994-68749238:	Arrdc4	66412	30.1	40.8	45.3	1.49914	0.029415	1.84593	2.00E-05
chr17:56294111-56300286	Arrdc5	76920	2.6	0.2	0.4	-4.93182	0.005301	-3.25646	0.0127033
chr15:89472476-89477424	Arsa	11883	23.9	17.7	8.2	-1.2136	0.065314	-2.3225	5.46E-26
chr13:93771679-93943016	Arsb	11881	32.8	26.0	11.7	-1.12684	0.371567	-2.21235	1.20E-17
chr18:60912240-60917768	Arsi	545260	14.4	21.7	28.2	1.68785	0.022688	2.37163	1.14E-06
chr3:126363852-12644037	Arsj	271970	6.5	6.2	12.5	1.03373	0.945436	2.23668	0.0016545
chr13:76060422-76098660	Arsk	77041	44.2	38.5	9.1	-1.03155	0.826811	-3.85635	7.00E-60
chr5:92331841-92414627:	Art3	109979	23.2	13.2	3.9	-1.54126	0.144193	-4.37855	2.52E-11
chr6:136848451-13685760	Art4	109978	7.7	5.9	1.5	-1.16282	0.715358	-3.5398	1.08E-06
chr7:102096879-10210022	Art5	11875	4.1	1.8	0.2	-1.94773	0.119251	-8.97077	1.83E-10
chr8:124722139-12473412	Arv1	68865	21.3	24.3	31.4	1.28632	0.260037	1.8117	0.0002144
chr16:18348182-18407074	Arvcf	11877	10.5	9.8	4.0	1.04442	0.805155	-2.08491	2.11E-12
chr19:46707443-46741095	As3mt	57344	41.2	33.9	21.0	-1.09116	0.479241	-1.56267	1.16E-07
chr8:41340643-41374697:	Asah1	11886	153.2	132.1	97.4	-1.04369	0.764913	-1.25757	0.0094014
chr19:31984651-32103140	Asah2	54447	20.2	14.7	6.6	-1.24275	0.180682	-2.39633	1.64E-13
chr12:21111756-21270171	Asap2	211914	22.0	19.0	8.1	-1.03395	0.884604	-2.12383	2.25E-09
chr1:91540565-91559590:	Asb1	65247	16.0	23.3	28.2	1.6295	0.082034	2.11005	0.0004669
chr5:24532697-24540448:	Asb10	117590	1.0	0.4	0.1	-1.98782	0.258121	-4.42238	0.0009239
chr3:153844247-15385361	Asb17	66772	5.6	0.1	0.6	-11.0771	4.62E-06	-4.20343	0.0019818
chr11:30954398-31102704	Asb3	65257	37.3	34.5	19.2	1.03281	0.72427	-1.55028	5.95E-15
chr8:54550331-54587836:	Asb5	76294	0.6	0.6	1.6	1.08892	0.892768	2.65004	0.0042164
chr2:30823098-30828300:	Asb6	72323	26.3	35.5	39.4	1.51504	0.109883	1.81901	0.0024538
chr15:98134640-98165578	Asb8	78541	30.1	25.9	35.5	-1.03883	0.731921	1.46915	4.43E-09
chrX:164497903-16453975	Asb9	69299	2.3	0.0	0.2	-7.94654	0.000131	-4.0547	0.0030873
chr10:60002805-60099990	Ascc1	69090	31.9	25.9	13.9	-1.10543	0.528538	-1.81507	2.45E-08
chr11:4637793-4683386:+	Ascc2	75452	28.0	24.4	27.0	-1.02265	0.825575	1.20716	0.0012172
chr10:50592669-50851202	Ascc3	77987	51.7	53.0	71.4	1.14413	0.024817	1.72458	6.14E-34
chr8:25816001-25847694:	Ash2l	23808	53.7	48.7	56.7	1.02071	0.881395	1.32058	0.0002509
chr5:130011503-13002433	Asl	109900	49.0	53.1	60.5	1.22557	0.318124	1.5336	0.0036928
chr8:85017931-85025278:	Asna1	56495	68.7	72.8	105.7	1.19072	0.111936	1.91476	3.47E-16
chr6:7675171-7693182:-	Asns	27053	22.2	25.6	168.1	1.28582	0.140106	9.09237	8.64E-76
chr11:73304988-73324637	Aspa	11484	46.0	32.4	22.8	-1.27303	0.276606	-1.58423	0.0045677
chr12:112106683-1121275	Aspg	104816	27.6	25.6	4.2	1.03846	0.911442	-4.95183	3.69E-18
chr4:9449085-9669344:-	Asph	65973	39.6	31.2	19.4	-1.14256	0.40806	-1.62316	1.59E-05
chr5:112385445-11239221	Asphd2	72898	7.9	7.4	3.7	1.05318	0.807291	-1.68089	7.77E-05
chr9:105395392-10540575	Aste1	66595	11.5	14.3	14.2	1.39147	0.021194	1.53016	0.0001465
chr4:65380803-66404483:	Astn2	56079	26.3	23.5	8.9	1.00056	0.996946	-2.3635	1.53E-44
chr6:146549632-14657783	Asun	71177	53.2	57.1	79.1	1.20445	0.018509	1.85347	4.39E-25
chr2:153346139-15340400	Asxl1	228790	49.3	45.2	26.8	1.02281	0.873141	-1.46407	1.17E-06
chr12:3426857-3506849:+	Asxl2	75302	31.4	28.9	21.8	1.03056	0.579579	-1.15479	5.72E-05
chr18:22345089-22530227	Asxl3	211961	3.1	2.9	1.0	1.07626	0.68847	-2.42691	3.62E-14
chr19:32672563-32712298	Atad1	67979	80.4	84.0	132.0	1.17369	0.140378	2.03927	1.01E-19
chr15:58094047-58135082	Atad2	70472	35.2	33.8	19.9	1.07034	0.634589	-1.41057	0.0001882
chr4:155740640-15576109	Atad3a	108888	46.8	60.1	128.5	1.44948	0.041451	3.34684	5.43E-19
chr4:155761192-15576356	Atad3aos	70448	9.3	6.8	3.3	-1.21337	0.394015	-2.18435	2.37E-06
chr10:81194691-81208370	Atcayos	69678	68.6	33.6	25.0	-1.77504	0.041461	-2.09	0.0007348
chr7:130391494-13052036	Ate1	11907	57.7	54.3	56.6	1.05146	0.423884	1.22485	2.45E-06
chr15:100227859-1002612	Atf1	11908	34.4	40.8	60.3	1.33873	0.089531	2.16144	1.30E-09
chr1:191170297-19118333	Atf3	11910	16.0	47.9	36.9	2.94136	0.006487	2.49122	0.0050957
chr15:80255184-80257545	Atf4	11911	150.5	305.5	657.1	2.21291	0.005579	4.87693	3.63E-12
chr7:44812256-44816658:	Atf5	107503	59.2	70.3	253.7	1.34158	0.127779	5.15007	5.23E-32
chr1:170704457-17086777	Atf6	226641	30.7	29.8	48.7	1.08448	0.145004	1.97821	1.11E-68
chr17:34647146-34655074	Atf6b	12915	27.5	31.9	59.3	1.30717	0.107417	2.64447	9.99E-16
chr6:136518851-13660737	Atf7ip	54343	70.1	50.7	32.5	-1.24627	0.310449	-1.69676	0.0007299

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr13:90935349-91223987	Atg10	66795	13.1	10.4	5.0	-1.12747	0.428598	-2.0652	3.39E-11
chr15:101284301-1012909	Atg101	68118	35.0	36.5	17.3	1.17016	0.264472	-1.60954	4.29E-06
chr2:91674612-91710592:	Atg13	51897	23.7	19.1	8.0	-1.11192	0.430395	-2.33183	9.95E-20
chr14:47540893-47568434	Atg14	1.01E+08	26.0	21.1	7.8	-1.11193	0.558318	-2.62742	3.74E-16
chr1:87756011-87792428:	Atg16l1	77040	57.1	65.8	65.8	1.29877	0.05344	1.43412	0.0005168
chr7:101289616-10130208	Atg16l2	73683	48.5	47.0	25.8	1.07999	0.575644	-1.49859	7.73E-06
chr19:6241668-6262304:+	Atg2a	329015	21.4	18.6	12.5	-1.01738	0.909526	-1.35945	0.0002403
chr12:105613540-1056852	Atg2b	76559	28.4	29.0	32.1	1.1566	0.307232	1.41167	0.0007797
chr16:45158829-45188538	Atg3	67841	56.7	51.7	71.5	1.02121	0.820999	1.57592	9.35E-19
chr3:103643953-10364606	Atg4a	666468	7.4	6.8	8.1	1.03584	0.830391	1.37098	0.0006086
chr4:99193934-99259787:	Atg4c	242557	13.3	10.2	6.6	-1.17106	0.29585	-1.59565	1.81E-05
chr9:21265285-21274837:	Atg4d	235040	21.4	23.1	23.5	1.22115	0.165677	1.37071	0.0034485
chr10:44268358-44364291	Atg5	11793	36.6	40.0	56.6	1.22311	0.036614	1.92517	4.43E-20
chr5:24384181-24392143:	Atg9b	213948	0.4	0.5	1.3	1.60424	0.123161	3.97848	2.94E-11
chr7:140941581-14094765	Athl1	212974	91.6	67.0	29.9	-1.23083	0.316902	-2.39008	2.53E-09
chr1:71557156-71579403:	Atic	108147	78.2	75.0	179.4	1.07545	0.55196	2.84761	1.07E-41
chr12:69893105-69964085	Atl1	73991	16.0	13.4	8.2	-1.06645	0.689291	-1.54875	1.54E-05
chr9:53437122-53536671:	Atm	11920	41.0	31.5	12.1	-1.17406	0.313193	-2.66116	1.22E-18
chr6:72206177-72235577:	Atoh8	71093	13.0	7.6	4.1	-1.51133	0.016792	-2.48945	2.75E-11
chr11:43149877-43262286	Atp10b	319767	4.7	5.2	2.0	1.20152	0.558939	-1.85118	0.0036397
chr3:35754138-35856276:	Atp11b	76295	48.0	43.0	32.3	1.00593	0.956768	-1.18625	0.0028469
chrX:60223290-60403981:	Atp11c	320940	50.7	44.9	26.3	-1.01051	0.91975	-1.53518	4.12E-15
chr14:56365068-56388551	Atp12a	192113	5.8	7.4	15.1	1.41828	0.291715	2.99912	2.88E-06
chr8:69791163-69807748:	Atp13a1	170759	52.3	56.8	84.8	1.22592	0.109082	2.01401	5.19E-14
chr4:140986873-14100770	Atp13a2	74772	32.5	25.8	12.8	-1.12825	0.287409	-2.02412	1.59E-18
chr16:30312424-30388530	Atp13a3	224088	46.3	52.9	81.3	1.28856	0.066113	2.17386	3.02E-14
chr16:29231914-29378732	Atp13a5	268878	0.6	0.5	2.9	-1.0039	0.996596	4.27387	0.0001358
chr3:101576219-10160470	Atp1a1	11928	248.2	539.0	557.0	2.35773	0.002542	2.61456	4.04E-05
chr1:172271709-17229806	Atp1a2	98660	75.7	44.1	4.2	-1.52165	0.10655	-12.5049	3.62E-40
chr1:172223508-17225842	Atp1a4	27222	6.8	0.3	0.9	-9.15125	3.35E-06	-4.19464	0.0006503
chr11:69599750-69605960	Atp1b2	11932	13.5	15.1	5.7	1.25038	0.315205	-1.86531	0.0001141
chr9:96332675-96364299:	Atp1b3	11933	179.6	187.3	227.0	1.17187	0.119251	1.57442	1.42E-09
chr5:122453513-12250222	Atp2a2	11938	133.8	182.8	298.4	1.53965	0.007369	2.73688	1.92E-15
chr11:72961169-72993043	Atp2a3	53313	70.8	56.8	30.0	-1.11066	0.524379	-1.86168	1.29E-08
chr6:113745668-11404208	Atp2b2	11941	11.8	8.2	3.8	-1.2374	0.598372	-2.31721	0.0016202
chr8:119700009-11975771	Atp2c2	69047	0.1	0.7	0.7	3.3453	0.02132	3.68889	0.0016389
chr18:77773768-77782868	Atp5a1	11946	531.7	520.2	716.4	1.09623	0.316013	1.68003	3.85E-16
chr10:128083307-1280903	Atp5b	11947	620.2	684.8	1265.8	1.24149	0.040252	2.5332	1.88E-32
chr2:10056031-10080510:	Atp5c1	11949	214.2	191.3	224.7	-1.00305	0.979019	1.30945	7.26E-06
chr10:80142315-80145818	Atp5d	66043	154.1	161.6	223.1	1.17832	0.143213	1.80051	4.51E-13
chr2:174461075-17446410	Atp5e	67126	221.0	224.0	287.2	1.13311	0.332925	1.61464	1.02E-07
chr3:105942678-10596024	Atp5f1	11950	164.1	185.4	281.8	1.26975	0.062966	2.12629	2.17E-15
chr11:96072793-96075694	Atp5g1	11951	114.7	133.8	334.7	1.30993	0.009005	3.61538	4.10E-60
chr2:73908447-73911326:	Atp5g3	228033	200.4	209.6	360.0	1.17668	0.248513	2.22136	7.43E-16
chr11:115415697-1154199	Atp5h	71679	383.5	386.7	440.0	1.12811	0.14575	1.43017	3.39E-09
chr5:145183706-14519159	Atp5j2	57423	273.7	299.7	365.2	1.22872	0.109536	1.65713	1.15E-07
chr5:108433253-10843437	Atp5k	11958	247.5	235.2	340.1	1.06342	0.613851	1.71172	1.46E-12
chr9:44913248-44920742:	Atp5l	27425	170.2	181.5	237.7	1.19642	0.094783	1.73676	1.89E-12
chr16:91925223-91931630	Atp5o	28080	230.7	254.6	357.7	1.23844	0.036602	1.92808	9.39E-18
chr12:69724962-69744658	Atp5s	68055	15.3	13.5	7.2	-1.01273	0.956393	-1.68263	1.91E-05
chr7:25619414-25625550:	Atp5sl	66349	29.1	21.4	10.1	-1.2233	0.226997	-2.2644	1.46E-11
chrX:74297097-74304721:	Atp6ap1	54411	142.1	138.9	172.3	1.09751	0.304817	1.51221	7.18E-11
chr13:90883449-90905355	Atp6ap1l	435376	2.0	0.1	0.2	-5.25348	0.003171	-4.68812	0.0008714
chr11:101009452-1010637	Atp6v0a1	11975	41.2	33.8	23.2	-1.08796	0.397482	-1.41907	4.56E-07
chr5:124629052-12472445	Atp6v0a2	21871	25.7	30.1	52.4	1.32251	0.058884	2.51736	3.23E-17
chr6:38048483-38124586:	Atp6v0a4	140494	5.4	4.2	9.0	-1.12412	0.56561	2.08232	7.02E-09
chr8:105524470-10556604	Atp6v0d1	11972	93.1	81.7	99.7	-1.02026	0.82074	1.33662	6.21E-09
chr6:48537569-48541800:	Atp6v0e2	76252	53.0	38.3	24.8	-1.24535	0.219115	-1.68599	6.43E-05

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr8:69088736-69113717:	Atp6v1b2	11966	77.9	79.4	82.9	1.14082	0.220441	1.32476	0.000349
chr12:17284721-17324730	Atp6v1c2	68775	5.1	4.6	2.1	1.03034	0.9376	-1.90017	0.0023855
chr17:86944109-86947887	Atp6v1e2	74915	2.0	0.2	0.3	-4.57002	0.007278	-3.6185	0.0052996
chr4:63544765-63550701:	Atp6v1g1	66290	194.7	188.9	208.1	1.0855	0.381978	1.33332	1.03E-05
chr17:35236596-35238768	Atp6v1g2	66237	7.6	5.4	2.7	-1.23836	0.303769	-2.20513	3.57E-07
chr1:5083173-5162549:+	Atp6v1h	108664	57.1	67.9	94.1	1.33664	0.054137	2.03492	2.81E-10
chr8:21994348-22060074:	Atp7b	11979	4.0	3.1	0.4	-1.14744	0.841473	-4.50092	0.000157
chr5:67618139-67847431:	Atp8a1	11980	48.0	41.0	69.3	-1.04904	0.668113	1.79979	6.87E-18
chr14:59647741-60086834	Atp8a2	50769	1.6	0.7	0.6	-1.95635	0.061876	-2.12786	0.0067089
chr18:64528979-64661000	Atp8b1	54670	91.2	95.6	189.0	1.16487	0.368321	2.55149	7.97E-16
chr3:89939481-89963332:	Atp8b2	54667	55.2	56.8	62.7	1.15964	0.300833	1.41401	0.0007771
chr10:80519585-80539124	Atp8b3	67331	19.7	0.9	2.4	-11.1225	4.96E-08	-4.70141	7.95E-05
chr4:43267159-43373831:	Atp8b5	320571	1.5	0.6	0.5	-2.06389	0.011655	-2.45059	0.0001042
chr18:80734141-80934058	Atp9b	50771	65.0	58.7	70.8	1.01017	0.910766	1.36027	1.45E-10
chr4:115784814-11581231	Atpaf1	230649	12.8	12.7	14.5	1.10677	0.427382	1.41712	6.00E-05
chr11:60400624-60417099	Atpaf2	246782	27.8	26.0	29.0	1.0493	0.636711	1.30388	2.95E-05
chr4:132530555-13253365	Atpif1	11983	268.2	248.4	161.3	1.03328	0.759423	-1.32862	1.21E-05
chr5:31048640-31054633:	Atraid	381629	171.5	128.5	91.1	-1.19972	0.064389	-1.50209	4.13E-08
chr9:109059747-10907412	Atrip	235610	24.5	24.7	37.3	1.13286	0.227754	1.90248	3.35E-19
chr19:57611034-58133340	Atrnl1	226255	73.5	95.2	92.4	1.45971	0.031828	1.55495	0.0013567
chrX:105797615-10592937	Atrx	22589	159.3	143.8	89.6	1.00934	0.907935	-1.42122	3.56E-16
chr13:45549756-45964991	Atxn1	20238	42.9	37.6	12.4	-1.02269	0.892934	-2.73833	5.21E-29
chr15:85336381-85463836	Atxn10	54138	97.5	83.7	112.9	-1.0411	0.600439	1.44934	1.40E-14
chr12:101918901-1019582	Atxn3	110616	38.5	34.5	20.5	1.00034	0.998519	-1.49541	4.91E-10
chr12:33302515-33368277	Atxn7l1	380753	12.5	9.4	4.5	-1.19022	0.303768	-2.18299	2.04E-10
chr12:33147686-33251157	Atxn7l1	380753	11.4	10.0	6.2	-1.02286	0.899151	-1.46467	0.0001849
chr3:108202228-10821052	Atxn7l2	72522	9.2	8.2	10.7	1.00053	0.998614	1.45206	0.0008499
chr11:102289300-1022966	Atxn7l3	217218	39.9	57.3	61.4	1.60853	0.079442	1.85655	0.002897
chr10:112925428-1129290	Atxn7l3b	382423	119.6	111.4	122.5	1.0461	0.579976	1.27968	3.02E-06
chr12:105513433-1055152	AU015791	104932	0.4	0.7	4.4	1.5803	0.355844	9.19734	8.27E-13
chr9:50605240-50617464:	AU019823	270156	25.6	29.7	29.1	1.30734	0.069612	1.41363	0.0022286
chr16:5211819-5222299:-	AU021092	239691	39.9	26.0	9.5	-1.36044	0.15893	-3.25568	2.98E-13
chr13:52835110-52929677	Auh	11992	49.3	48.0	17.7	1.08425	0.453169	-2.22122	8.84E-26
chr6:83054521-83057682:	Aup1	11993	92.0	96.9	110.5	1.18608	0.113703	1.49708	4.77E-07
chr4:155831269-15583309	Aurkaip1	66077	66.5	71.3	97.6	1.20018	0.119251	1.81943	2.25E-12
chr5:131437682-13254234	Auts2	319974	9.3	8.6	4.0	1.02446	0.923368	-1.82772	8.34E-06
chr2:112492964-11263125	Aven	74268	23.0	19.6	38.6	-1.03873	0.8462	2.09121	4.69E-12
chr6:56714905-56761911:	Avl9	78937	43.2	42.9	23.2	1.11057	0.250909	-1.48372	1.66E-09
chr19:42123275-42128993	Avpi1	69534	23.7	22.8	34.4	1.08179	0.694183	1.79476	1.20E-06
chr4:156203284-15620602	AW011738	100382	8.9	7.0	4.7	-1.13318	0.555357	-1.50473	0.0043688
chr7:41478874-41499890:	AW146154	101835	16.0	12.4	4.0	-1.15908	0.540484	-3.10488	1.56E-12
chr13:14630245-14638202	AW209491	105351	16.3	15.1	19.8	1.03351	0.796493	1.51296	8.45E-09
chr5:119570129-11958035	AW549542	100993	9.1	6.7	3.3	-1.21072	0.341676	-2.16357	1.54E-07
chr15:3982035-3995752:-	AW549877	106064	89.1	69.1	37.5	-1.16023	0.225971	-1.88872	4.48E-13
chr9:39587396-39604124:	AW551984	244810	46.2	36.9	2.7	-1.13048	0.603847	-12.5037	3.84E-61
chr18:25169020-25467321	AW554918	225289	20.9	16.7	12.3	-1.12593	0.266527	-1.36205	6.21E-05
chr17:26138686-26195811	Axin1	12005	41.2	44.3	55.8	1.2151	0.168265	1.684	4.64E-07
chr7:25756500-25788733:	Axl	26362	176.4	163.2	80.8	1.03642	0.653734	-1.74487	1.14E-29
chr9:118040522-11806979	Azi2	27215	42.4	45.1	42.6	1.19183	0.050162	1.25256	0.0011268
chr15:38487430-38519266	Azin1	54375	44.8	70.4	118.1	1.75199	0.029399	3.10944	8.31E-09
chr4:128930233-12896245	Azin2	242669	17.2	10.3	4.3	-1.49563	0.036602	-3.08595	3.31E-14
chr7:70365383-70411146:	B130024G19Rik	434198	58.6	30.0	8.8	-1.67144	0.242846	-4.22427	5.86E-06
chr16:87496073-87504038	B130034C11Rik	414095	6.3	3.2	2.5	-1.71341	0.019059	-1.96675	0.0002037
chr2:101560781-10162898	B230118H07Rik	68170	19.7	15.5	7.0	-1.14385	0.315846	-2.22328	1.87E-16
chr6:142413431-14241974	B230216G23Rik	319552	0.5	0.7	1.5	1.49565	0.42426	3.26562	0.0004762
chr13:55693124-55703500	B230219D22Rik	78521	87.0	92.4	87.7	1.19198	0.042898	1.25838	0.0005929
chr2:180370858-18038588	B230312C02Rik	320485	13.8	11.1	4.3	-1.11039	0.722639	-2.44045	1.51E-06
chr6:83441755-83448322:	B230319C09Rik	320775	1.5	0.9	0.2	-1.45094	0.511252	-3.4154	0.0020406

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr3:69573919-69598960:	B3galnt1	26879	55.7	50.4	25.0	1.00466	0.98063	-1.77452	9.97E-09
chr13:13954674-13999068	B3galnt2	97884	48.1	49.0	48.9	1.14007	0.091589	1.27001	4.08E-05
chr1:143640697-14364993	B3galt2	26878	10.3	4.8	1.6	-1.79591	0.212527	-3.97172	6.17E-05
chr4:155989466-15599267	B3galt6	117592	9.1	10.0	21.9	1.22856	0.077983	2.98586	6.91E-41
chr9:26751562-26761338:	B3gat1	76898	1.0	0.6	0.2	-1.53156	0.274613	-3.61424	2.07E-05
chr19:8920393-8927236:+	B3gat3	72727	48.1	50.5	64.8	1.17917	0.171789	1.67579	2.89E-09
chr5:149678257-14976259	B3glct	381694	9.7	9.1	17.4	1.04911	0.592334	2.22583	5.70E-53
chr7:25627624-25629490:	B3gnt8	232984	5.3	4.2	2.6	-1.11968	0.688696	-1.61621	0.0085586
chr8:105252638-10525515	B3gnt9	97440	20.5	14.4	10.2	-1.28043	0.221155	-1.58188	0.0021777
chr11:121616208-1216731	B3gntl1	210004	20.4	13.9	8.0	-1.32486	0.29157	-1.97336	0.0004184
chr4:117873000-11788347	B4galt2	53418	22.6	21.6	25.5	1.06729	0.598624	1.40689	1.59E-05
chr2:167298445-16734917	B4galt5	56336	20.1	137.3	140.7	5.37633	6.69E-05	5.77393	1.34E-06
chr18:20684599-20746404	B4galt6	56386	10.7	9.0	12.2	-1.06589	0.569944	1.42753	6.02E-07
chr13:55600111-55609954	B4galt7	218271	22.9	21.5	24.2	1.04639	0.667463	1.31913	1.66E-05
chr19:5038826-5041134:+	B4gat1	108902	28.5	22.9	12.3	-1.12092	0.465653	-1.83507	1.58E-08
chr6:13625675-13677966:	B630005N14Rik	101148	38.7	34.1	22.4	-1.01843	0.853285	-1.37812	7.73E-09
chr17:10319919-10321141	B930003M22Rik	1.01E+08	8.6	5.8	4.2	-1.33344	0.228374	-1.61455	0.0074076
chr11:61505172-61512927	B9d1	27078	51.1	40.7	23.3	-1.12818	0.508225	-1.7299	9.99E-06
chr7:25681158-25686558:	B9d2	232987	18.1	15.3	8.1	-1.05478	0.754602	-1.76935	1.13E-07
chr16:97356728-97439012	Bace2	56175	6.7	9.3	23.0	1.54461	0.169276	3.90114	2.98E-09
chr16:87698954-87733346	Bach1	12013	46.8	41.8	22.2	-1.01372	0.962703	-1.6619	0.0012603
chr4:32417435-32586108:	Bach2	12014	6.9	5.6	0.8	-1.11682	0.514413	-6.61355	6.40E-54
chr4:40936398-40948294:	Bag1	12017	149.3	153.9	208.2	1.15894	0.169305	1.73632	9.86E-13
chr1:33745484-33757750:	Bag2	213539	23.5	47.6	48.7	2.18359	0.021926	2.38513	0.0012451
chr15:79258195-79285509	Baiap2l2	207495	4.5	2.2	0.2	-1.76002	0.055627	-12.3053	6.50E-20
chr17:25242659-25256364	Baiap3	545192	3.0	2.7	0.8	1.01721	0.953737	-2.74701	4.26E-10
chr17:27019812-27028626	Bak1	12018	25.8	26.6	37.0	1.15805	0.338421	1.77478	6.95E-08
chr18:3507957-3516404:+	Bambi	68010	16.5	10.4	7.0	-1.42563	0.191331	-1.8348	0.0026992
chr19:5364633-5366876:-	Banf1	23825	57.5	56.9	113.7	1.10848	0.269724	2.45967	7.44E-47
chr3:136053364-13632604	Bank1	242248	3.1	2.2	1.0	-1.21376	0.674216	-2.16228	0.0098656
chr8:121950492-12202926	Banp	53325	19.0	32.9	13.8	1.93954	0.000689	-1.09508	0.628304
chr9:31846044-31913285:	Barx2	12023	12.9	10.3	1.7	-1.07538	0.902653	-4.50902	5.03E-06
chr12:85686720-85709087	Batf	53314	6.3	15.9	17.1	2.66989	1.33E-06	3.20084	3.08E-11
chr7:45461695-45466898:	Bax	12028	65.8	77.9	157.6	1.33465	0.066272	2.94376	5.66E-21
chr12:54892989-54986336	Baz1a	217578	13.7	22.2	38.9	1.80023	0.035161	3.30175	1.89E-08
chr10:128092783-1281293	Baz2a	116848	32.4	28.0	18.5	-1.02227	0.907317	-1.38863	0.0017836
chr2:59899363-60125740:	Baz2b	407823	85.9	70.4	30.5	-1.09129	0.423502	-2.24129	8.07E-28
chr8:15041446-15046078:	BB014433	434285	5.1	0.2	0.4	-7.78399	0.000105	-4.91131	0.0005002
chr19:53929659-53944627	Bbip1	1.01E+08	26.6	27.8	29.5	1.17016	0.060839	1.38261	1.99E-07
chr19:4886882-4906627:-	Bbs1	52028	12.3	9.9	5.8	-1.11661	0.394489	-1.67778	1.12E-08
chr10:111298679-1113017	Bbs10	71769	14.4	9.8	5.2	-1.32027	0.396968	-2.0952	0.0014827
chr3:37312554-37321451:	Bbs12	241950	21.9	14.9	11.1	-1.31836	0.186363	-1.54888	0.0052618
chr8:94067954-94098811:	Bbs2	67378	53.7	43.2	12.0	-1.11352	0.392268	-3.54211	2.76E-47
chr9:59321966-59353508:	Bbs4	102774	26.4	22.0	11.1	-1.07696	0.680168	-1.87501	2.38E-08
chr2:69647255-69667569:	Bbs5	72569	20.3	16.7	12.3	-1.08469	0.587579	-1.3201	0.0057568
chr3:36573143-36613389:	Bbs7	71492	17.0	13.4	10.3	-1.13587	0.337741	-1.30909	0.005123
chr9:22475715-22888280:	Bbs9	319845	49.5	40.4	10.3	-1.09951	0.428631	-3.80906	2.22E-58
chr16:50191844-50432389	Bbx	70508	51.9	42.7	25.8	-1.08685	0.268538	-1.6062	3.99E-19
chr16:42955580-42956079	BC002163	170658	16.0	12.2	4.3	-1.18182	0.600439	-2.76521	3.32E-06
chr1:150361311-15039305	BC003331	226499	55.6	49.0	33.5	-1.01873	0.86963	-1.32305	1.03E-05
chr17:25184561-25187662	BC003965	214489	20.7	22.8	39.4	1.23442	0.079284	2.35522	6.02E-23
chr5:104508352-10452238	BC005561	1E+08	24.3	33.6	35.5	1.55926	0.02096	1.79871	9.98E-05
chrX:70460056-70477043:	BC023829	236848	29.5	29.8	30.5	1.12793	0.087917	1.2892	9.45E-07
chr7:27195781-27205386:	BC024978	414069	3.5	4.2	7.0	1.36561	0.208947	2.45168	3.62E-07
chr10:81606308-81609836	BC025920	268319	4.5	2.4	2.0	-1.64889	0.065099	-1.71823	0.0098904
chr1:157458582-15748873	BC026585	226527	20.8	18.1	5.2	-1.02966	0.891244	-3.0996	1.70E-19
chr16:44724301-44737284	BC027231	212547	14.9	21.9	51.0	1.64525	0.014098	4.08559	1.41E-19
chr2:25459488-25461094:	BC029214	227622	51.3	43.1	33.8	-1.06569	0.511426	-1.21534	0.0033491

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr2:155817732-15581920	BC029722	613262	44.1	31.0	24.6	-1.27673	0.01992	-1.4307	1.35E-05
chr10:86705811-86776843	BC030307	103220	3.0	1.6	1.1	-1.6896	0.023664	-2.16251	2.37E-05
chr7:120677620-12073485	BC030336	233812	32.2	36.6	39.5	1.27893	0.039458	1.52793	3.31E-06
chr18:75005900-75009933	BC031181	407819	80.5	95.3	116.7	1.33055	0.00403	1.80447	6.29E-14
chr15:4020111-4027406:-	BC037032	414066	1.6	1.0	0.4	-1.39541	0.350285	-2.74292	0.0001123
chr5:138259658-13826405	BC037034	231807	19.7	24.5	33.6	1.39276	0.001037	2.11386	3.29E-20
chr2:145701195-14575367	BC039771	408057	5.6	3.3	0.8	-1.52249	0.111198	-5.16903	2.03E-14
chr10:121739937-1217528	BC048403	270802	3.9	2.7	7.3	-1.31925	0.175487	2.28383	3.48E-09
chr6:90301270-90305448:	BC048671	243535	2.6	0.2	0.3	-4.50509	0.008696	-3.82082	0.0040526
chr7:81494274-81498330:	BC048679	210321	49.3	41.1	18.4	-1.08078	0.810974	-2.05647	0.0001847
chr4:42868003-42874203:	BC049635	277773	6.8	0.3	0.8	-9.72766	3.54E-06	-4.2817	0.0007257
chr6:136828843-13684055	BC049715	320135	4.1	0.9	1.6	-3.27578	0.004759	-1.86038	0.0724258
chr7:24709259-24714535:	BC049730	232972	1.7	0.2	0.3	-4.50098	0.00827	-3.20566	0.0122005
chr11:51253651-51262951	BC049762	193286	5.3	0.7	0.7	-4.2519	0.003137	-4.08869	0.0004741
chr17:34398820-34460734	BC051142	407788	15.5	2.8	2.0	-4.16766	9.10E-05	-4.88766	3.92E-07
chr17:33908182-33909178	BC051226	407803	11.2	7.3	2.8	-1.36139	0.325721	-2.9512	3.06E-06
chr2:181220016-18122285	BC051628	332713	3.6	0.3	0.5	-6.44008	1.16E-05	-4.526	2.82E-05
chr2:115581716-11577876	BC052040	399568	8.9	6.6	3.5	-1.20695	0.527264	-1.9743	0.0007888
chr4:106590909-10661723	BC055111	242602	1.1	0.1	0.1	-4.46514	0.007014	-5.92916	7.89E-05
chr1:163954008-16399478	BC055324	381306	15.8	12.9	6.1	-1.10063	0.673056	-2.012	1.13E-06
chr2:18699022-18749605:	BC061194	381350	3.3	0.5	0.5	-4.19811	0.003413	-3.60375	0.0014611
chr6:128993020-12900664	BC064078	408064	18.2	11.7	3.0	-1.39675	0.161372	-4.51477	1.29E-15
chrX:136742957-13680336	BC065397	436230	15.7	11.6	6.3	-1.20411	0.218899	-1.97413	7.33E-10
chr7:28284652-28291134:	BC089491	280621	2.9	0.3	0.4	-5.39562	0.000645	-4.27839	0.0004485
chr11:118332360-1183425	BC100451	58251	26.9	12.2	9.8	-1.93362	0.000932	-2.12677	5.99E-06
chr7:19756138-19770532:	Bcam	57278	111.1	103.9	119.6	1.04869	0.711318	1.34477	0.0001828
chr8:111710475-11174384	Bcar1	12927	20.9	28.3	38.3	1.52144	0.145072	2.189	0.0002753
chr3:103171711-10317915	Bcas2	68183	70.3	69.3	75.6	1.10966	0.341747	1.34126	0.0001443
chr11:85353164-85826058	Bcas3	192197	41.4	33.2	8.7	-1.10905	0.229057	-3.76105	1.57E-93
chr11:85766833-85775680	Bcas3os2	78420	1.9	0.6	0.1	-2.25335	0.166767	-5.41526	0.0001769
chr6:144993835-14507615	Bcat1	12035	35.5	76.0	91.2	2.25019	0.024165	2.8447	0.0002044
chr7:133709333-13372114	Bccip	66165	65.4	85.4	189.3	1.47106	0.032178	3.51838	1.19E-20
chr3:73635809-73708415:	Bche	12038	53.6	44.2	22.8	-1.10247	0.747826	-1.83493	0.0011154
chr7:25629852-25658761:	Bckdha	12039	98.3	76.6	13.5	-1.15052	0.309286	-5.69099	3.98E-69
chr9:83948781-84124240:	Bckdhb	12040	45.5	39.3	23.8	-1.03774	0.826686	-1.51837	2.49E-05
chr3:145924262-14593436	Bcl10	12042	37.2	50.9	48.6	1.53233	0.002181	1.61725	2.86E-05
chr11:24078056-24173558	Bcl11a	14025	1.6	0.9	0.6	-1.62114	0.142274	-1.92595	0.0091104
chr1:106538178-10671429	Bcl2	12043	62.4	49.8	15.5	-1.11908	0.281207	-3.18714	7.12E-57
chr2:128126038-12816254	Bcl2l11	12125	27.6	25.0	7.0	1.02616	0.916116	-3.06375	6.41E-18
chr6:120836230-12089284	Bcl2l13	94044	14.9	17.0	16.6	1.28912	0.124465	1.38535	0.009978
chr6:134396329-13443872	Bcl2l14	66813	11.9	3.8	3.2	-2.6723	4.31E-05	-2.77505	7.83E-07
chr7:19808462-19822755:	Bcl3	12051	6.2	26.5	27.9	3.77386	0.000495	4.38702	4.30E-06
chr16:23965052-23988612	Bcl6	12053	17.7	51.9	31.9	3.07719	7.43E-07	2.17608	0.0001174
chr5:123344448-12337408	Bcl7a	77045	26.2	17.7	6.6	-1.33112	0.063006	-3.10554	1.52E-22
chr5:135168372-13518185	Bcl7b	12054	33.6	36.5	59.9	1.22674	0.158006	2.2078	2.42E-14
chr7:127704978-12770876	Bcl7c	12055	43.1	43.2	52.7	1.12052	0.224372	1.52625	8.63E-11
chr10:20312469-20342501	Bclaf1	72567	187.6	214.5	204.5	1.28842	0.062917	1.35693	0.0036823
chr9:50533087-50555138:	Bco2	170752	3.5	2.6	0.8	-1.20368	0.490819	-3.20989	5.36E-09
chrX:48341358-48406728:	Bcorl1	320376	10.8	10.4	5.0	1.08999	0.593233	-1.70398	5.01E-07
chr1:74588361-74592443:	Bcs1l	66821	15.8	14.1	23.0	-1.00966	0.965178	1.8042	1.67E-07
chr16:31422297-31458901	Bdh1	71911	2.0	2.6	4.6	1.45963	0.165763	2.78225	1.72E-07
chr3:135281221-13530442	Bdh2	69772	84.3	64.2	5.0	-1.17701	0.371567	-12.6506	7.82E-77
chr12:105604091-1056054	Bdkrb1	12061	2.6	5.8	28.1	2.39235	0.002281	11.688	3.36E-28
chr12:105563172-1055930	Bdkrb2	12062	13.2	16.0	120.0	1.36073	0.256847	10.2681	1.38E-35
chr13:100017994-1001040	Bdp1	544971	39.1	51.5	54.7	1.48236	0.041997	1.72263	0.0002668
chr8:104170513-10421909	Bean1	65115	1.3	1.2	3.6	1.05335	0.91975	3.1349	1.95E-05
chr11:101288267-1013022	Becn1	56208	106.6	111.5	134.7	1.17714	0.173392	1.57298	2.13E-07
chr12:109032182-1090682	Begain	380785	1.0	1.3	1.6	1.48329	0.17596	1.95584	0.001531

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr10:43479140-43515417	Bend3	331623	6.2	6.8	16.6	1.23361	0.338185	3.23271	6.02E-15
chr5:67392147-67427799:	Bend4	666938	5.0	3.3	2.0	-1.3589	0.093707	-1.94146	1.58E-06
chr4:111415006-11146029	Bend5	67621	16.4	12.9	5.8	-1.14402	0.656003	-2.18937	5.24E-05
chr1:33852052-33907621:	Bend6	320705	3.1	2.8	1.3	1.00525	0.989894	-1.82961	0.0042215
chr2:4717831-4802146:+	Bend7	209645	8.1	6.8	3.3	-1.06104	0.77045	-1.94733	8.20E-08
chr19:9985172-10001633:	Best1	24115	10.1	6.1	2.1	-1.47208	0.296183	-3.43212	4.05E-06
chr6:4076904-4086927:-	Bet1	12068	42.6	40.6	46.9	1.06014	0.657913	1.37079	0.0001368
chr7:140853384-14085638	Bet1l	54399	56.6	60.3	55.3	1.19181	0.056207	1.21911	0.0052626
chrX:136213972-13621551	Bex1	19716	40.5	35.4	49.4	-1.01296	0.958004	1.52152	0.0008761
chrX:73483635-73495936:	Bgn	12111	121.0	84.3	36.3	-1.27893	0.174971	-2.62639	2.08E-13
chr5:144190286-14419444	Bhlha15	17341	0.3	0.5	2.8	1.55545	0.433707	6.30879	1.41E-06
chr6:108660629-10866692	Bhlhe40	20893	55.1	83.0	83.2	1.67455	0.037183	1.83657	0.0016216
chr6:145858243-14586542	Bhlhe41	79362	10.5	2.9	1.9	-3.04764	1.50E-05	-4.05998	2.96E-10
chr10:70925096-71159634	Bicc1	83675	53.6	53.5	32.4	1.12544	0.368248	-1.31898	0.0032492
chr6:120893119-12091682	Bid	12122	12.7	13.7	19.3	1.211	0.422421	1.85829	0.0001713
chr9:7818226-7835255:-	Birc2	11797	97.1	89.7	61.2	1.02717	0.835905	-1.26873	0.0016005
chr17:74528295-74703356	Birc6	12211	90.2	87.9	99.9	1.09541	0.279851	1.38318	5.53E-08
chr2:157556362-15756636	Blcap	53619	45.4	43.9	48.2	1.08795	0.502313	1.32561	0.0009128
chr14:63372837-63417187	Blk	12143	3.9	5.7	12.9	1.4904	0.398581	3.37887	0.0002291
chr11:76945656-76987389	Blmh	104184	80.4	77.0	93.1	1.07481	0.551042	1.44153	3.91E-06
chr10:128919914-1289235	Bloc1s1	14533	198.5	186.1	109.6	1.04303	0.712056	-1.44676	1.64E-07
chr19:44139247-44146446	Bloc1s2	73689	41.2	41.6	46.4	1.13453	0.199664	1.40683	1.06E-06
chr5:36747374-36748679:	Bloc1s4	117197	12.1	18.6	19.2	1.7025	0.035466	1.90875	0.0010037
chr7:27447978-27465981:	Blvrb	233016	66.9	56.4	39.5	-1.06381	0.589091	-1.35409	5.96E-05
chr1:164289800-16430748	Blzf1	66352	20.5	23.7	25.9	1.30449	0.067693	1.57091	3.97E-05
chr2:118528757-11854967	Bmf	171543	85.4	47.6	4.3	-1.50554	0.467645	-8.1127	3.91E-08
chr2:18677018-18686629:	Bmi1	12151	66.1	72.5	116.5	1.22954	0.076074	2.18312	7.08E-20
chr5:98854439-98880960:	Bmp3	110075	4.0	2.6	0.4	-1.3927	0.365556	-6.2292	1.25E-11
chr14:46383520-46390599	Bmp4	12159	35.6	27.3	14.7	-1.17191	0.490925	-1.90094	4.29E-05
chr9:75775365-75899017:	Bmp5	12160	3.1	1.6	1.1	-1.70516	0.104799	-2.07674	0.0038281
chr4:123312650-12334325	Bmp8a	12163	0.2	1.0	3.0	3.88073	0.010806	9.86414	3.78E-08
chr9:23223076-23485215:	Bmper	73230	4.1	3.1	8.8	-1.16065	0.689291	2.52185	5.04E-05
chr3:141837136-14216922	Bmpr1b	12167	4.6	4.1	1.9	-1.00826	0.974913	-1.89751	6.40E-06
chr1:59764279-59878081:	Bmpr2	12168	62.2	56.3	38.9	1.01097	0.91509	-1.28004	7.36E-06
chr6:118383381-11841941	Bms1	213895	57.1	56.4	79.2	1.11454	0.365614	1.72839	3.15E-11
chrX:164192842-16425819	Bmx	12169	7.1	5.6	2.7	-1.13876	0.511517	-2.10688	4.88E-08
chr4:84272542-84675086:	Bnc2	242509	44.6	42.5	66.0	1.0663	0.713651	1.83955	8.85E-09
chr17:26781079-26792521	Bnip1	224630	28.2	26.3	42.1	1.04312	0.723004	1.86219	2.11E-20
chr9:69989466-70011659:	Bnip2	12175	48.0	52.3	59.6	1.22393	0.020723	1.54704	7.64E-11
chr7:138890836-13890950	Bnip3	12176	97.8	80.6	16.9	-1.08626	0.39602	-4.57984	1.30E-104
chr14:66985240-67008877	Bnip3l	12177	118.0	96.9	19.1	-1.09731	0.547368	-4.85808	2.18E-56
chr3:95241293-95251193:	Bnipl	171388	11.2	8.7	4.9	-1.12525	0.727861	-1.7844	0.0068219
chr11:31665150-31671862	Bod1	69556	76.6	80.2	99.7	1.17884	0.178226	1.62022	5.00E-08
chr5:41787540-41844315:	Bod1l	665775	68.5	62.6	40.7	1.02535	0.801287	-1.34141	4.40E-07
chr3:96196588-96197586:	Bola1	69168	25.1	23.8	26.5	1.05355	0.764863	1.31699	0.0087444
chr7:126696000-12669669	Bola2	66162	95.7	94.8	147.2	1.11366	0.461156	1.90782	1.67E-11
chr6:83349484-83358392:	Bola3	78653	36.3	39.2	75.6	1.20751	0.078166	2.58976	2.23E-39
chr1:55300069-55363469:	Boll	75388	4.4	0.3	0.5	-5.9649	0.000383	-4.5514	0.0003814
chr15:76452996-76477269	Bop1	12181	25.9	38.0	122.8	1.64405	0.025242	5.56149	1.23E-24
chr6:34476356-34505610:	Bpgm	12183	17.0	12.7	20.1	-1.20375	0.243998	1.46574	0.000758
chr13:34037641-34074074	Bphl	68021	50.2	36.6	12.7	-1.23129	0.108922	-3.11994	2.14E-30
chr2:154130336-15413835	Bpifa3	73388	2.1	0.2	0.2	-3.68045	0.030895	-3.99359	0.0035329
chr2:154223742-15424090	Bpifb5	228802	2.3	3.2	34.8	1.54341	0.06704	17.6099	1.62E-73
chr1:185332159-18535776	Bpnt1	23827	27.4	34.8	68.2	1.43228	0.027246	3.05338	6.36E-20
chr5:150522621-15057014	Brca2	12190	7.1	4.7	2.8	-1.35284	0.143132	-1.98446	8.37E-06
chrX:75416628-75455701:	Brcc3	210766	24.3	22.6	28.8	1.04102	0.704328	1.47898	7.11E-10
chr17:34112019-34122607	Brd2	14312	109.5	123.3	161.9	1.27082	0.067468	1.83673	4.90E-10
chr18:34598615-34624863	Brd8	78656	69.5	64.0	47.0	1.03407	0.686827	-1.17929	0.0016575

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr5:107331194-10738705	Brdt	114642	6.5	2.8	1.0	-2.05492	0.010792	-4.87041	2.36E-12
chr5:144244437-14426457	Bri3	55950	36.8	28.5	18.4	-1.15314	0.269269	-1.59544	5.86E-07
chr11:86058136-86201193	Brip1	237911	2.7	2.6	1.2	1.06163	0.819562	-1.78418	0.0002386
chr15:10474779-10485937	Brix1	67832	37.2	54.9	82.2	1.65684	0.034695	2.65565	8.61E-08
chr6:113604772-11361695	Brk1	101314	162.4	156.2	175.6	1.07373	0.401695	1.34989	2.60E-07
chr12:55836366-55869735	Brms1l	52592	29.0	35.8	33.0	1.39208	0.04864	1.4147	0.0080473
chr1:183276342-18329700	Brox	71678	61.1	65.5	64.5	1.20677	0.136115	1.31509	0.0041074
chr6:113307137-11332486	Brpf1	78783	26.9	33.6	36.5	1.40764	0.062209	1.67511	0.0002235
chr4:129461679-12948843	Bsdc1	100383	65.1	71.1	21.7	1.22085	0.090687	-2.37883	7.67E-23
chr10:79704358-79711979	Bsg	12215	307.7	302.7	302.7	1.10132	0.144193	1.22872	2.64E-05
chr4:62480067-62497298:	Bspry	192120	25.9	24.2	32.8	1.05029	0.866909	1.56025	0.0075757
chr8:71534262-71537437:	Bst2	69550	141.6	193.9	253.7	1.53527	0.003402	2.21091	1.40E-11
chr19:36926079-37014057	Btaf1	107182	41.0	59.0	82.2	1.61787	0.023291	2.43391	5.37E-08
chr7:81792074-81829431:	Btbd1	83962	61.4	69.3	102.4	1.27159	0.074413	2.06527	3.19E-13
chr7:113315644-11336933	Btbd10	68815	22.8	35.6	57.7	1.73765	0.074804	2.93556	3.94E-06
chr10:85386814-85660292	Btbd11	74007	7.2	6.9	4.2	1.06685	0.714873	-1.37552	0.0044868
chr7:130774069-13082589	Btbd16	330660	2.1	0.2	0.5	-6.00158	6.52E-05	-2.7471	0.0087569
chr11:114790669-1147958	Btbd17	72014	0.2	0.2	0.7	-1.2593	0.716315	2.69381	0.0073131
chr4:117119218-11712572	Btbd19	78611	6.3	6.1	12.0	1.07442	0.601742	2.34749	8.81E-27
chr10:80642617-80657071	Btbd2	208198	36.3	28.0	19.0	-1.1617	0.253066	-1.51939	1.02E-05
chr2:138256584-13828742	Btbd3	228662	28.3	24.7	30.0	-1.02887	0.853387	1.32345	0.0013411
chr12:112976482-1129789	Btbd6	399566	22.5	15.4	8.6	-1.31477	0.07377	-2.07183	3.36E-10
chr5:107437997-10749159	Btbd8	1.01E+08	16.3	10.7	5.5	-1.3585	0.103397	-2.33236	4.82E-09
chr17:30215524-30576287	Btbd9	224671	17.1	15.9	27.2	1.04311	0.613602	1.98935	7.51E-42
chr5:91357261-91402994:	Btc	12223	4.0	2.8	1.3	-1.28686	0.308266	-2.34281	3.27E-06
chr14:31641057-31668197	Btd	26363	46.5	43.1	16.3	1.0253	0.901623	-2.25051	2.72E-13
chr13:98309897-98317006	Btf3	218490	446.8	449.6	668.0	1.12845	0.284003	1.85825	3.57E-15
chr4:108814295-10883358	Btf3l4	70533	41.1	34.1	44.6	-1.07762	0.256115	1.35695	1.65E-11
chr1:134074865-13407915	Btg2	12227	76.6	129.4	92.4	1.88433	0.000115	1.49325	0.0054736
chr11:49168325-49187089	Btnl9	237754	4.7	2.7	1.2	-1.55937	0.051851	-2.90319	3.93E-09
chr19:45363734-45533343	Btrc	12234	23.2	18.2	12.6	-1.14179	0.110929	-1.47476	3.56E-10
chr2:118598211-11864159	Bub1b	12236	27.4	23.9	7.7	-1.03345	0.911463	-2.7376	3.06E-10
chr7:131560391-13157189	Bub3	12237	75.8	85.2	106.5	1.26543	0.046675	1.74715	3.41E-10
chr9:46283012-46298783:	Bud13	215051	18.6	19.3	21.9	1.17417	0.357942	1.4634	0.0020907
chr5:145140397-14514807	Bud31	231889	115.3	159.2	220.1	1.54907	0.053542	2.3102	1.04E-06
chr10:45335762-45369708	Bves	23828	22.7	21.3	29.2	1.04332	0.798039	1.60046	7.51E-07
chr17:47599331-47611492	Bysl	53414	7.1	15.7	52.4	2.37512	0.003589	7.84879	2.97E-18
chr11:87760541-87785928	Bzrap1	207777	6.3	5.2	1.7	-1.09178	0.690284	-2.95641	3.87E-15
chr1:58393136-58406548:	Bzw1	66882	169.8	234.6	407.3	1.55197	0.024852	2.90642	9.52E-13
chr12:36091835-36156825	Bzw2	66912	88.2	91.9	229.8	1.15634	0.22762	3.21724	4.22E-44
chr19:27430037-27432631	C030016D13Rik	107372	4.5	3.3	1.4	-1.23652	0.338421	-2.41666	8.30E-08
chr7:27674661-27706482:	C030039L03Rik	112415	5.8	5.0	2.8	-1.04247	0.89317	-1.63003	0.005593
chr11:103697724-1037255	C130046K22Rik	399609	4.5	3.3	2.3	-1.20376	0.353803	-1.50365	0.0047053
chr1:184871926-18488303	C130074G19Rik	226777	79.1	43.4	21.0	-1.62958	0.036856	-2.88321	2.81E-09
chr11:17257618-17269176	C1d	57316	34.8	34.6	37.5	1.1093	0.251169	1.34059	5.37E-06
chr6:7845224-7872042:+	C1galt1	94192	39.2	39.6	52.5	1.12582	0.296788	1.66151	1.25E-10
chr11:70977846-70983026	C1qbp	12261	59.5	71.4	212.0	1.35262	0.072561	4.32931	4.59E-33
chr1:120340582-12034317	C1ql2	226359	12.0	9.1	3.6	-1.1701	0.478253	-2.6093	5.32E-10
chr2:13001887-13010864:	C1ql3	227580	1.5	1.3	0.3	-1.08214	0.871062	-3.08203	0.0001013
chr11:118428457-1184517	C1qtnf1	56745	12.4	14.6	5.8	1.33423	0.183376	-1.69531	0.0011616
chr15:10952332-10980162	C1qtnf3	81799	113.7	90.0	26.1	-1.14513	0.646697	-3.32734	8.63E-11
chr2:90885786-90890526:	C1qtnf4	67445	3.4	2.3	0.9	-1.29626	0.446114	-2.70982	7.06E-05
chr5:43515569-43616586:	C1qtnf7	109323	77.3	54.1	34.1	-1.28774	0.400239	-1.75963	0.0084492
chr14:60768134-60780869	C1qtnf9	239126	9.3	6.6	1.4	-1.26746	0.266101	-5.06269	7.65E-22
chr6:124512621-12452344	C1ra	50909	126.0	108.8	44.0	-1.04578	0.853682	-2.25235	1.99E-09
chr6:124493113-12451064	C1rl	232371	7.2	5.0	2.6	-1.28323	0.361577	-2.1321	0.0001068
chr6:124530344-12454235	C1s1	50908	498.3	445.5	162.6	-1.00914	0.962343	-2.43054	6.14E-19
chr6:124624625-12463608	C1s2	317677	3.0	2.0	0.7	-1.29402	0.260667	-3.40575	2.79E-11

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr17:34862602-34882100	C2	12263	40.2	33.5	15.2	-1.07991	0.814866	-2.04736	0.0001998
chr10:118920381-1189271	C230029M16	216377	4.4	4.6	0.8	1.1457	0.744652	-3.85021	4.08E-07
chr15:89476252-89484850	C230037L18Rik	1.01E+08	3.2	1.4	0.6	-1.96774	0.086257	-3.56742	5.70E-05
chr7:35392152-35396767:	C230052I12Rik	101831	8.3	8.1	10.4	1.09148	0.594181	1.56325	1.43E-05
chr9:44309237-44320282:	C2cd2l	71764	7.9	11.5	12.8	1.61994	0.082334	1.93956	0.0017732
chr7:100372233-10047015	C2cd3	277939	26.8	22.9	7.1	-1.0414	0.752078	-2.98136	1.27E-45
chr9:67830532-67832330:	C2cd4a	244911	6.2	2.7	1.1	-1.84218	0.242735	-3.18311	0.0027454
chr2:26136807-26140506:	C330006A16Rik	109299	47.0	39.4	48.4	-1.07037	0.588668	1.28679	0.0022493
chrX:36848544-36864246:	C330007P06Rik	77644	52.4	46.1	35.0	-1.01377	0.899134	-1.19487	0.0033034
chr15:100614140-1006151	C330013E15Rik	78445	4.0	2.4	1.2	-1.42518	0.3854	-2.30197	0.0053693
chr8:3567998-3584776:+	C330021F23Rik	546049	1.4	1.5	0.2	1.15342	0.807411	-4.1491	0.0001499
chrX:53053112-53057190:	C430049B03Rik	72575	10.3	5.5	4.3	-1.6628	0.023104	-1.86313	0.0004076
chr5:76840599-76873554:	C530008M17Rik	320827	2.8	0.5	0.6	-4.05054	5.81E-06	-3.25715	1.07E-05
chr7:16246743-16259540:	C5ar1	12273	4.8	6.2	12.8	1.37976	0.40938	2.93685	6.90E-05
chr15:4988762-5063773:-	C7	109828	3.3	0.6	0.3	-3.71037	0.004763	-5.05514	1.93E-05
chr4:129219578-12926140	C77080	97130	10.1	7.5	4.8	-1.20878	0.071121	-1.67239	1.08E-10
chrX:104077435-10420111	C77370	245555	1.0	1.5	4.0	1.57544	0.142826	4.35363	5.86E-11
chr6:86438398-86470387:	C87436	232196	35.1	30.0	22.6	-1.051	0.68264	-1.2378	0.005967
chr2:25498650-25501719:	C8g	69379	2.5	1.7	0.8	-1.2704	0.500148	-2.41075	0.0006999
chr9:78175914-78178882:	C920006O11Rik	320295	13.6	7.4	4.6	-1.62331	0.158326	-2.20364	0.0023073
chr17:36109030-36111676	C920025E04Rik	667803	1.9	3.0	6.4	1.71924	0.072086	3.89151	2.89E-10
chr1:85793447-85851577:	Cab39	12283	143.7	139.7	153.7	1.09497	0.503208	1.33326	0.0018782
chr14:59440981-59548903	Cab39l	69008	45.0	41.0	47.0	1.0183	0.889636	1.30449	0.0002047
chr18:11839274-11945627	Cables1	63955	15.7	11.7	2.4	-1.20853	0.455721	-4.92225	1.18E-19
chr5:87979451-87981541:	Cabs1	70977	13.8	0.9	1.4	-6.79509	0.000209	-4.61925	0.0005809
chr18:12741355-12755142	Cabyr	71132	5.3	0.8	1.2	-4.52573	0.000343	-2.94383	0.0026437
chr2:27009926-27021089:	Cacfd1	381356	22.5	21.5	22.9	1.07654	0.553279	1.27097	0.0037721
chr4:100776679-10100374	Cachd1	320508	31.7	24.6	11.3	-1.15578	0.483873	-2.18991	1.94E-08
chr14:30039941-30491156	Cacna1d	12289	14.6	11.6	4.0	-1.11979	0.496664	-2.84816	5.37E-21
chr1:154392519-15472592	Cacna1e	12290	9.0	7.9	3.2	-1.01886	0.954605	-2.20587	3.04E-06
chr5:15934691-16374511:	Cacna2d1	12293	72.7	60.1	26.4	-1.08833	0.629854	-2.17913	1.86E-12
chr14:28904943-29721864	Cacna2d3	12294	3.7	3.3	11.1	-1.00737	0.979523	3.62784	2.28E-20
chr15:98632328-98644536	Cacnb3	12297	40.4	29.3	8.5	-1.23841	0.153393	-3.71586	1.82E-32
chr2:52428320-52676609:	Cacnb4	12298	3.1	2.6	0.5	-1.04415	0.900299	-4.78168	1.64E-15
chr10:81321103-81326251	Cactin	70312	24.5	26.3	29.9	1.21478	0.18542	1.52116	9.83E-05
chr19:60524696-60581023	Cacul1	78832	34.1	35.9	33.8	1.18228	0.045589	1.2352	0.0010841
chr1:160202367-16021289	Cacybp	12301	49.5	81.1	129.1	1.83185	0.003361	3.13517	5.32E-12
chr5:31054780-31078479:	Cad	69719	18.7	18.1	46.9	1.08562	0.423352	3.12853	1.74E-64
chr9:47530352-47853385:	Cadm1	54725	71.6	62.9	24.8	-1.01184	0.942305	-2.29167	2.06E-23
chr6:23262774-23839421:	Cadps2	320405	13.8	12.5	6.0	1.0166	0.923231	-1.81894	4.87E-11
chr13:38006052-38036937	Cage1	71213	11.7	3.6	2.3	-2.67854	0.001312	-3.66854	3.61E-07
chr4:15881264-15906709:	Calb1	12307	38.2	31.8	6.6	-1.08632	0.887987	-3.70993	5.54E-05
chr15:102706777-1027221	Calcoco1	67488	116.4	89.7	11.7	-1.16244	0.238821	-7.72906	1.01E-108
chr6:34709444-34775469:	Cald1	109624	320.7	288.8	418.6	-1.00193	0.993734	1.61797	9.44E-06
chr19:47132232-47138294	Calhm2	72691	29.3	20.4	10.7	-1.29863	0.376749	-2.09758	0.0004038
chr13:3802893-3804318:-	Calml3	70405	0.9	1.4	5.4	1.53152	0.466183	4.54175	0.0001426
chr8:84842088-84846931:	Calr	12317	444.3	518.8	1319.8	1.31475	0.135721	3.60948	4.28E-22
chr8:72424183-72443778:	Calr3	73316	4.8	1.7	1.2	-2.2818	0.013627	-2.90923	6.62E-05
chr6:29348106-29376675:	Calu	12321	241.1	276.4	430.3	1.28791	0.044782	2.20824	4.01E-17
chr6:113334124-11334392	Camk1	52163	84.0	74.6	51.1	-1.01112	0.943183	-1.3147	0.0008211
chr1:193346346-19337028	Camk1g	215303	3.8	5.9	0.4	1.69356	0.220441	-5.10377	5.70E-07
chr18:60925632-60988152	Camk2a	12322	2.9	1.9	0.5	-1.33253	0.18037	-4.46652	3.41E-18
chr3:126596951-12684632	Camk2d	108058	34.5	32.8	20.5	1.06201	0.453758	-1.34592	6.27E-08
chr14:20734873-20794088	Camk2g	12325	50.0	49.7	55.8	1.12145	0.413838	1.3915	0.00078
chr4:138455148-13846012	Camk2n1	66259	28.6	24.2	5.6	-1.06367	0.736733	-4.0212	3.70E-35
chr16:20619215-20621278	Camk2n2	73047	0.7	1.3	1.9	1.89222	0.194839	2.79754	0.0044818
chr5:122731170-12277941	Camkk2	207565	18.8	17.8	36.7	1.06221	0.63795	2.42937	4.16E-30
chr8:3587450-3609075:+	Camsap3	69697	4.9	4.0	1.8	-1.07662	0.781464	-2.06608	8.01E-06

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr4:151059523-15186176	Camta1	100072	4.8	4.2	1.8	-1.01783	0.934232	-2.13215	3.12E-11
chr10:119198812-1192400	Cand1	71902	57.8	65.4	86.3	1.27728	0.107643	1.84807	5.20E-08
chr11:50293957-50325673	Canx	12330	296.3	308.5	660.8	1.17041	0.195855	2.76037	5.25E-32
chr4:122859048-12288605	Cap1	12331	205.9	197.3	246.5	1.07249	0.387314	1.4929	4.15E-13
chr19:5988545-6015825:-	Capn1	12333	54.4	42.4	22.2	-1.15533	0.284809	-1.94608	3.11E-12
chr17:25959556-25965505	Capn15	50817	20.6	24.6	28.6	1.3461	0.1207	1.7132	0.0001819
chr1:182467259-18251748	Capn2	12334	126.5	114.2	130.5	1.00606	0.957838	1.28585	1.94E-05
chrX:143802237-14382741	Capn6	12338	7.4	4.7	0.9	-1.39268	0.186363	-5.80611	5.48E-20
chr14:31336724-31371983	Capn7	12339	70.5	69.7	69.2	1.10798	0.121065	1.22542	3.80E-05
chr7:30186942-30195048:	Capns1	12336	265.6	234.9	251.5	-1.01081	0.911885	1.18222	0.0016456
chr2:103762945-10379764	Caprin1	53872	117.0	132.5	211.3	1.27755	0.098375	2.23129	1.89E-13
chr6:148842492-14889623	Caprin2	232560	31.9	25.9	7.4	-1.1036	0.553547	-3.35583	1.40E-28
chr10:112165676-1122165	Caps2	353025	1.3	0.6	0.1	-1.76393	0.13871	-7.76332	6.59E-10
chr15:9436028-9466035:+	Capsl	75568	19.0	14.2	5.9	-1.19976	0.283036	-2.51787	5.09E-13
chr3:104822785-10486450	Capza1	12340	69.0	83.0	106.0	1.35187	0.039179	1.89783	7.15E-09
chr6:17637098-17666536:	Capza2	12343	173.0	174.8	196.1	1.13061	0.289118	1.40885	3.36E-05
chr6:140041525-14004278	Capza3	12344	5.6	0.2	0.5	-9.61904	4.73E-06	-5.66802	5.29E-05
chr4:139192899-13929182	Capzb	12345	180.1	167.7	243.0	1.04335	0.412956	1.68555	1.11E-52
chr7:45699967-45704661:	Car11	12348	42.6	26.6	4.2	-1.43063	0.07416	-7.56006	3.60E-38
chr9:66713686-66766845:	Car12	76459	2.8	5.1	25.9	1.96311	0.055614	9.32968	9.12E-18
chr3:14641727-14663002:	Car13	71934	7.3	12.3	17.6	1.84835	0.004736	2.89099	8.18E-10
chr3:95897800-95904639:	Car14	23831	3.4	2.0	1.2	-1.49434	0.097695	-2.22859	2.79E-05
chr11:84957754-84966054	Car4	12351	6.9	4.2	0.5	-1.42573	0.316583	-9.02535	1.11E-14
chrX:163976822-16402801	Car5b	56078	12.1	8.3	2.7	-1.29206	0.439503	-3.24188	2.85E-07
chr8:104534700-10455034	Car7	12354	2.5	1.1	1.0	-1.88984	0.028667	-1.89232	0.0051252
chr4:8141493-8239041:-	Car8	12319	16.2	12.7	0.9	-1.14465	0.571428	-13.377	5.54E-57
chr15:5097439-5108533:-	Card6	239319	4.4	2.9	1.5	-1.38375	0.193602	-2.20767	2.03E-05
chr1:60098247-60153953:	Carf	241066	12.9	9.3	4.6	-1.25156	0.154763	-2.23371	5.57E-12
chr16:8658587-8672153:-	Carhsp1	52502	87.0	93.0	82.9	1.19794	0.00863	1.19187	0.0016408
chr9:21546894-21589465:	Carm1	59035	38.7	40.0	57.7	1.16527	0.295618	1.85076	1.87E-09
chr19:4164324-4175479:-	Carns1	107239	5.4	4.3	2.0	-1.13474	0.580979	-2.16128	4.85E-07
chr7:143557230-14360009	Cars	27267	28.9	33.2	85.2	1.29831	0.114971	3.60197	1.34E-26
chr6:145174872-14521097	Casc1	320662	3.9	2.2	0.8	-1.52599	0.194185	-3.54216	3.18E-07
chr11:98809808-98833807	Casc3	192160	39.2	41.7	44.0	1.1975	0.113017	1.40191	7.55E-05
chr2:121866970-12193620	Casc4	319996	56.7	49.4	60.6	-1.02521	0.816254	1.33632	2.56E-06
chr9:5345476-5373034:+	Casp12	12364	95.3	80.6	33.6	-1.07625	0.820781	-2.1984	3.01E-05
chr6:42265039-42282496:	Casp2	12366	65.2	47.4	19.2	-1.23999	0.342708	-2.63526	1.01E-09
chr8:46617291-46639698:	Casp3	12367	30.3	23.2	10.4	-1.1714	0.381873	-2.28053	6.40E-11
chr3:129901425-12991410	Casp6	12368	32.4	24.4	6.9	-1.1897	0.211333	-3.66547	1.97E-34
chr1:58795374-58847503:	Casp8	12370	26.3	28.4	31.4	1.20279	0.121009	1.48112	8.93E-06
chr4:32615473-32653265:	Casp8ap2	26885	25.5	32.8	29.6	1.44885	0.01108	1.44719	0.001672
chr4:141793612-14181597	Casp9	12371	19.6	14.3	7.4	-1.22883	0.054476	-2.11076	5.67E-20
chr13:74693294-74808760	Cast	12380	81.1	67.7	53.2	-1.07715	0.467918	-1.22038	0.0052414
chr4:148804392-14895489	Casz1	69743	7.7	6.6	2.5	-1.04854	0.854795	-2.40304	1.84E-09
chr2:103453904-10348515	Cat	12359	105.6	73.8	31.4	-1.28549	0.05886	-2.65665	6.21E-23
chr1:74362108-74369321:	Catip	241112	2.6	1.6	0.5	-1.45723	0.22201	-3.54899	1.90E-07
chr19:5335741-5344153:+	Catsper1	225865	1.4	0.1	0.2	-6.53984	0.000584	-3.86605	0.0036684
chr2:121394355-12141379	Catsper2	212670	8.7	3.8	3.1	-1.95992	0.02027	-2.15793	0.0007987
chr13:55784579-55809000	Catsper3	76856	3.3	1.2	0.9	-2.17338	0.058884	-2.61511	0.002589
chr4:134211968-13422738	Catsper4	329954	2.4	0.4	0.4	-3.96219	0.001593	-4.06844	0.0001103
chr12:101404673-1016260	Catsperb	271036	1.1	0.0	0.2	-7.28488	0.000158	-2.58289	0.038338
chr17:56628143-56664456	Catsperd	106757	4.2	2.0	1.2	-1.79391	0.030616	-2.53818	1.20E-05
chr7:29181532-29214033:	Catsperg1	320225	11.1	6.4	1.4	-1.52672	0.079883	-5.89571	1.88E-21
chr7:29697219-29727015:	Catsperg2	76718	2.0	0.1	0.1	-9.32547	1.83E-05	-6.10834	6.33E-05
chr6:17281185-17289130:	Cav2	12390	58.8	43.0	33.6	-1.22477	0.012368	-1.39858	1.49E-07
chr6:112459505-11247287	Cav3	12391	0.4	1.0	2.0	2.02189	0.183713	3.81798	0.0004974
chr2:154436484-15453935	Cbfa2t2	12396	30.1	25.1	20.3	-1.07377	0.337465	-1.18513	0.0014159
chr8:122625136-12269910	Cbfa2t3	12398	7.2	5.9	2.3	-1.0835	0.746604	-2.47707	1.90E-09

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr16:93607837-93610349	Cbr1	12408	72.1	51.5	28.6	-1.25532	0.025869	-2.00685	1.39E-18
chr16:93683219-93690991	Cbr3	109857	32.6	23.8	15.3	-1.23388	0.256225	-1.68719	0.0001054
chr8:61487734-61503500:	Cbr4	234309	29.0	20.6	9.8	-1.27042	0.262686	-2.31659	6.12E-08
chr17:31612623-31637205	Cbs	12411	13.9	16.3	35.9	1.32622	0.358726	3.03875	1.97E-07
chr19:24919916-24961616	Cbwd1	226043	20.2	22.1	25.3	1.22945	0.13582	1.55961	1.30E-05
chr11:119023029-1190312	Cbx2	12416	14.1	8.4	2.0	-1.50238	0.164971	-5.11757	4.67E-14
chr15:79823898-79834333	Cbx6	494448	70.8	54.5	36.2	-1.16674	0.243498	-1.55435	3.76E-06
chr15:79915807-79932646	Cbx7	52609	115.3	93.2	27.4	-1.10486	0.354178	-3.32372	1.54E-58
chr15:79659227-79667660	Cby1	73739	31.2	27.0	11.8	-1.03767	0.856251	-2.08598	3.09E-10
chr5:43662379-43740970:	Cc2d2a	231214	47.9	31.8	13.7	-1.35219	0.167077	-2.70958	4.07E-10
chr10:62743928-62792368	Ccar1	67500	83.3	97.9	100.2	1.32507	0.04707	1.49475	0.0002266
chr18:66056856-66291838	Ccbe1	320924	5.5	3.7	2.5	-1.30932	0.120071	-1.75554	1.79E-05
chr2:30185131-30205699:	Ccbl1	70266	32.1	27.0	13.3	-1.06004	0.788043	-1.90934	5.92E-07
chr3:142701048-14274491	Ccbl2	229905	17.2	13.5	6.6	-1.14754	0.638377	-2.00688	0.0002297
chr7:126649309-12667277	Ccdc101	75565	32.1	32.7	56.8	1.14891	0.334521	2.20053	6.20E-16
chr11:102881244-1028852	Ccdc103	73293	2.4	1.2	0.6	-1.73318	0.162368	-2.71487	0.0009262
chr10:78746924-78753067	Ccdc105	70976	1.8	0.1	0.1	-7.39463	0.000212	-4.92721	0.0005826
chr1:74902080-74935599:	Ccdc108	241116	2.6	0.1	0.3	-9.16302	6.71E-07	-4.45978	0.0001155
chr8:45934649-45944145:	Ccdc110	212392	1.6	0.0	0.2	-10.5156	2.03E-06	-4.48795	0.0003957
chr8:95534100-95558888:	Ccdc113	244608	4.8	0.3	0.5	-7.20602	5.39E-05	-4.63577	0.000253
chr7:45928398-45948956:	Ccdc114	211535	9.3	7.2	1.9	-1.15183	0.604077	-3.7211	5.98E-13
chr1:34436670-34439672:	Ccdc115	69668	24.6	29.0	59.4	1.32596	0.098004	2.95567	1.74E-18
chr11:5528888-5542217:-	Ccdc117	104479	43.9	82.8	41.3	2.07688	0.007116	1.16355	0.535951
chr9:110656503-11071159	Ccdc12	72654	63.6	65.2	87.4	1.14987	0.232072	1.70987	6.54E-11
chrX:7731714-7741324:-	Ccdc120	54648	7.1	5.2	2.9	-1.22635	0.181955	-1.93293	8.40E-09
chr1:181509633-18151145	Ccdc121	403180	0.6	1.2	0.1	1.90667	0.260577	-3.57093	0.004197
chr14:77036772-77112204	Ccdc122	108811	5.5	3.5	1.6	-1.37894	0.311817	-2.59272	4.65E-05
chr8:70868227-70873490:	Ccdc124	234388	40.0	45.8	111.6	1.29013	0.100289	3.42303	1.30E-28
chr6:49319353-49341581:	Ccdc126	57895	7.4	7.8	8.3	1.17199	0.181395	1.39634	8.67E-05
chr9:121797627-12183946	Ccdc13	1.01E+08	2.6	0.3	0.4	-5.39994	6.37E-05	-4.09529	8.79E-05
chr6:3498393-3603531:+	Ccdc132	73288	20.9	20.4	24.1	1.09349	0.296648	1.44314	7.47E-10
chr15:82127922-82142202	Ccdc134	76457	14.8	20.3	45.5	1.54973	0.062931	3.67087	7.72E-14
chr6:29398926-29426995:	Ccdc136	232664	49.2	27.7	17.4	-1.56795	0.00681	-2.22121	1.69E-09
chr11:120458129-1204643	Ccdc137	67291	31.6	38.4	52.5	1.371	0.030458	2.05562	6.95E-11
chr10:58497937-58576244	Ccdc138	76138	7.4	5.7	2.5	-1.16218	0.374532	-2.35943	5.52E-12
chr16:34690616-34725194	Ccdc14	239839	14.3	9.9	5.4	-1.2911	0.204819	-2.08021	6.95E-07
chr6:83101516-83109121:	Ccdc142	243510	15.3	10.9	6.3	-1.2671	0.452906	-1.85726	0.0051201
chr5:21292961-21424677:	Ccdc146	75172	3.1	1.5	0.6	-1.79382	0.072559	-3.94877	6.40E-08
chr2:58821698-59018606:	Ccdc148	227933	1.2	0.8	0.4	-1.40972	0.360382	-2.24985	0.003293
chr5:52374651-52471543:	Ccdc149	1.01E+08	7.6	5.7	9.6	-1.17851	0.158902	1.58344	9.26E-09
chr9:37275835-37348392:	Ccdc15	245902	19.9	14.9	8.1	-1.19742	0.262337	-1.95163	7.05E-09
chr1:54250683-54368727:	Ccdc150	78016	2.3	0.3	0.2	-4.30903	0.003943	-4.73179	0.000183
chr9:21989871-22002634:	Ccdc151	77609	1.7	0.4	0.1	-3.15029	0.004002	-6.55211	4.59E-08
chr7:45183676-45204892:	Ccdc155	384619	2.2	0.7	0.4	-2.50916	0.014073	-3.45232	4.18E-05
chr11:4141124-4160293:-	Ccdc157	216516	30.0	26.5	12.5	-1.00475	0.973355	-1.90243	4.19E-18
chr5:92608295-92675127:	Ccdc158	320696	3.1	1.9	1.1	-1.44943	0.201933	-2.11861	0.0005657
chr9:21927471-21935872:	Ccdc159	67119	17.5	11.4	4.4	-1.36164	0.119814	-3.08884	1.18E-13
chrX:52791200-52799468:	Ccdc160	434778	2.3	1.1	0.3	-1.75578	0.253585	-4.49593	5.39E-05
chr10:41538849-41606595	Ccdc162	75973	1.0	1.0	1.6	1.0086	0.984129	1.82179	0.0058457
chr4:116708930-11671510	Ccdc163	68394	71.3	47.5	16.6	-1.34293	0.072086	-3.34391	1.64E-22
chr17:29695977-29717017	Ccdc167	68597	16.2	11.6	8.4	-1.25448	0.18542	-1.52372	0.0009367
chr4:116596730-11660026	Ccdc17	622665	10.5	7.1	3.2	-1.32074	0.132115	-2.53102	5.36E-11
chr10:4509872-4561111:+	Ccdc170	1.01E+08	21.4	15.9	2.1	-1.20525	0.207419	-7.93346	1.11E-62
chr4:83525545-83864670:	Ccdc171	320226	19.6	15.0	4.0	-1.1669	0.095689	-3.82932	3.09E-74
chr2:69758057-69789486:	Ccdc173	75051	11.6	7.2	2.4	-1.43436	0.211944	-3.57036	3.11E-09
chr12:72101292-72185029	Ccdc175	73936	2.2	0.1	0.2	-7.4179	8.02E-05	-4.58375	0.0004825
chr12:84409068-84433780	Ccdc176	72873	5.3	2.1	1.5	-2.10473	0.02027	-2.50365	0.0002976
chr18:21810897-22171396	Ccdc178	70950	1.4	0.1	0.2	-5.97096	0.000739	-3.31364	0.0077571

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr5:108132914-10823294	Ccdc18	73254	5.5	4.1	1.2	-1.20155	0.282075	-3.64003	3.82E-23
chr1:164275598-16428784	Ccdc181	74895	35.5	21.5	11.9	-1.47844	0.032093	-2.33472	1.48E-09
chr2:25608629-25617678:	Ccdc183	77058	3.2	0.2	0.3	-6.74818	8.76E-05	-4.84802	0.0001453
chr1:182747126-18274918	Ccdc185	433386	3.7	0.1	0.4	-14.2995	9.71E-08	-5.01489	0.0001925
chr14:65837302-65866604	Ccdc25	67179	22.7	32.4	48.7	1.59607	0.007117	2.61613	1.93E-12
chr4:154026644-15404267	Ccdc27	381580	1.9	0.1	0.2	-7.29698	5.98E-05	-4.75511	0.0002137
chr10:18213685-18234981	Ccdc28a	215814	41.1	25.3	1.4	-1.44593	0.212253	-18.5834	8.24E-37
chr4:129619274-12962390	Ccdc28b	66264	86.5	57.2	11.2	-1.35878	0.248724	-5.66064	1.43E-19
chr4:119322893-11941552	Ccdc30	73332	4.2	1.2	0.5	-2.81117	0.005949	-4.9638	1.48E-07
chr9:58028682-58118823:	Ccdc33	382077	3.1	2.0	0.2	-1.37334	0.496818	-6.98346	2.87E-09
chr2:110017817-11004532	Ccdc34	68201	21.1	14.8	6.1	-1.27842	0.20473	-2.6763	4.66E-12
chr10:93540632-93584326	Ccdc38	237465	5.2	0.5	0.8	-6.78539	1.81E-06	-4.05451	6.23E-05
chr3:33812361-33844310:	Ccdc39	51938	13.7	7.7	1.5	-1.582	0.003412	-6.85741	2.60E-45
chr11:119228572-1192652	Ccdc40	207607	1.8	0.4	0.3	-3.50329	0.000735	-3.51054	5.77E-05
chr11:68587037-68597951	Ccdc42	276920	2.2	0.3	0.7	-4.65729	0.001191	-2.18753	0.0471535
chr11:102684688-1026977	Ccdc43	52715	27.4	32.8	42.6	1.34308	0.005268	1.93288	1.91E-15
chr11:106199356-1062163	Ccdc47	67163	108.7	106.5	149.1	1.1013	0.281692	1.7105	6.93E-18
chr16:27388956-27452218	Ccdc50	67501	88.7	87.0	89.2	1.09798	0.056491	1.25642	4.43E-10
chr16:50589859-50591154	Ccdc54	69339	9.0	0.5	1.0	-8.27842	6.79E-06	-4.79319	0.0001245
chr11:77044292-77078437	Ccdc55	237859	30.0	32.8	34.8	1.23403	0.136707	1.44775	0.0004651
chr11:120826542-1209328	Ccdc57	71276	20.4	13.7	6.8	-1.32412	0.142134	-2.33226	2.36E-09
chr16:36071660-36092118	Ccdc58	381045	24.8	26.2	39.3	1.18096	0.150025	1.96634	8.97E-17
chr10:105841479-1058475	Ccdc59	52713	62.6	65.9	78.1	1.18283	0.185772	1.55172	1.78E-06
chr5:116125581-11628898	Ccdc60	269693	9.7	3.7	1.9	-2.2248	0.002554	-3.6738	2.64E-09
chr7:18890884-18910404:	Ccdc61	232933	19.5	14.3	10.9	-1.21626	0.173085	-1.42246	0.0010485
chr5:123930689-12396989	Ccdc62	208908	9.4	5.4	2.9	-1.54714	0.033438	-2.52145	5.62E-09
chr5:122108052-12213806	Ccdc63	330188	3.0	0.4	0.7	-5.02078	0.000112	-2.95016	0.0023545
chr5:115649286-11573155	Ccdc64	75665	4.8	5.3	2.5	1.21579	0.322624	-1.51291	0.0062274
chr15:98708227-98723333	Ccdc65	105833	6.1	2.7	1.7	-1.78506	0.177433	-2.4634	0.0053913
chr9:15559864-15627933:	Ccdc67	234964	4.1	0.6	0.5	-4.78877	0.00015	-4.71909	1.13E-05
chr18:69925559-69969484	Ccdc68	381175	5.1	3.9	1.6	-1.17775	0.588411	-2.45175	1.60E-05
chr8:21970596-21974041:	Ccdc70	67929	4.6	0.2	0.5	-7.71614	6.36E-05	-4.50325	0.0005949
chr12:32378789-32382943	Ccdc71l	72123	22.8	22.5	40.8	1.09093	0.693625	2.19684	4.68E-09
chr16:17646470-17650738	Ccdc74a	72315	4.0	2.3	0.7	-1.47881	0.259897	-3.81378	6.75E-07
chr7:16994588-16996645:	Ccdc8	434130	38.3	37.4	47.2	1.10976	0.680846	1.52331	0.0090413
chr16:45094053-45127924	Ccdc80	67896	296.4	200.8	56.9	-1.33165	0.164836	-4.01615	8.95E-21
chr7:89866148-89903629:	Ccdc81	70884	3.7	0.7	1.0	-3.93407	0.00018	-2.64116	0.0018377
chr9:13246979-13292353:	Ccdc82	66396	61.0	55.0	36.1	1.00929	0.926113	-1.35004	1.05E-08
chr11:28385684-28584324	Ccdc85a	216613	1.7	1.5	0.7	-1.00575	0.986278	-1.85576	0.0005968
chr19:10941481-10949266	Ccdc86	108673	8.1	18.9	42.8	2.50646	0.001576	5.77816	1.24E-13
chr11:29374172-29510808	Ccdc88a	108686	32.4	32.4	30.8	1.11893	0.178869	1.18555	0.0065876
chr7:90426312-90428664:	Ccdc89	70054	4.7	1.3	0.6	-2.69899	0.023597	-4.44387	1.56E-05
chr7:16274042-16286795:	Ccdc9	243846	52.6	45.5	54.8	-1.02825	0.826811	1.30074	0.0003606
chr6:147475871-14763261	Ccdc91	67015	46.4	36.6	25.6	-1.13464	0.295216	-1.4448	2.09E-05
chr5:124834432-12486222	Ccdc92	215707	7.4	3.5	3.0	-1.82619	0.042842	-1.88548	0.0062284
chr1:121431067-12150646	Ccdc93	70829	36.7	29.9	14.7	-1.09616	0.198026	-1.9861	1.50E-40
chr17:55959187-55967951	Ccdc94	72886	30.2	30.2	32.5	1.12233	0.223393	1.34776	9.52E-06
chr5:36484588-36488171:	Ccdc96	66717	2.3	0.6	0.6	-2.85796	0.019169	-2.52624	0.0095581
chr7:25711117-25719053:	Ccdc97	52132	17.3	18.7	18.9	1.21919	0.20473	1.35999	0.0081818
chr10:97693059-97694926	Ccer1	66716	6.3	0.5	0.6	-6.74721	8.98E-05	-5.33386	6.37E-05
chr17:35517116-35531015	Cchcr1	240084	23.6	16.8	10.7	-1.25161	0.218363	-1.73741	3.52E-05
chr4:43983504-43985533:	Ccin	442829	4.6	0.3	0.9	-7.61538	9.74E-07	-3.31067	0.0007776
chr11:82057832-82062955	Ccl11	20292	18.1	27.0	112.9	1.58902	0.141296	6.79165	3.59E-17
chr11:82101845-82103399	Ccl12	20293	8.8	50.0	122.3	4.90157	1.07E-05	11.8078	1.26E-15
chr8:94810453-94812036:	Ccl17	20295	5.3	22.6	3.3	3.69021	0.001815	-1.21683	0.626515
chr11:82035577-82037452	Ccl2	20296	5.0	41.6	83.3	6.41861	9.16E-07	13.0528	4.10E-15
chr5:135569937-13557304	Ccl24	56221	3.2	5.2	0.5	1.58631	0.419083	-3.23593	0.0044418
chr8:4325210-4360020:+	Ccl25	20300	2.9	2.8	5.0	1.07199	0.83214	2.07285	4.01E-05

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:83647843-83649378	Ccl3	20302	3.0	7.1	8.9	2.16343	0.123805	2.87335	0.0056932
chr11:83662584-83664683	Ccl4	20303	3.7	9.0	17.7	2.34073	0.041461	4.77697	6.73E-07
chr11:82045712-82047523	Ccl7	20306	4.6	29.9	89.5	5.26135	5.73E-06	15.3537	3.07E-18
chr11:82115185-82116799	Ccl8	20307	26.5	50.6	64.2	1.93683	0.100105	2.61893	0.0016206
chr11:6546887-6596761:+	Ccm2	216527	39.6	42.3	53.0	1.19909	0.070946	1.66912	4.26E-12
chr3:55045469-55055055:	Ccna1	12427	2.8	0.3	0.4	-5.03118	0.001033	-3.95008	0.0008513
chr4:21727701-21759922:	Ccnc	51813	18.8	22.0	26.7	1.31361	0.015155	1.76485	5.43E-11
chr17:47505051-47599688	Ccnd3	12445	51.2	46.4	53.2	1.00946	0.9384	1.29773	3.80E-05
chr2:121008408-12101691	Ccndbp1	17151	66.6	58.6	20.7	-1.02209	0.889651	-2.54715	3.84E-27
chr7:38097984-38107490:	Ccne1	12447	1.8	2.4	4.5	1.48543	0.206248	2.93005	1.14E-06
chr4:11191351-11204779:	Ccne2	12448	2.9	4.2	4.7	1.59003	0.136078	1.93315	0.0050202
chr11:40748552-40755286	Ccng1	12450	94.7	96.3	157.4	1.12955	0.227396	2.06717	1.58E-24
chr5:93267573-93276231:	Ccng2	12452	76.8	54.7	5.6	-1.26832	0.451963	-9.45462	6.61E-26
chr13:85189477-85213723	Ccnh	66671	35.8	33.4	41.3	1.04054	0.778719	1.4392	1.20E-05
chr5:93181933-93206495:	Ccni	12453	207.1	164.2	87.2	-1.1334	0.258196	-1.88951	3.99E-16
chr19:40831279-40848570	Ccnj	240665	8.4	8.9	14.1	1.19543	0.4791	2.03638	3.04E-05
chr11:43528749-43586999	Ccnjl	380694	1.4	1.2	0.6	-1.05948	0.881439	-1.81381	0.0097524
chr1:64691345-64725642:	Ccnyl1	227210	16.0	23.7	34.6	1.65639	0.019691	2.6088	9.44E-09
chr7:118712611-11873701	Ccp110	101565	35.8	30.1	14.5	-1.0642	0.547996	-1.96801	1.59E-23
chr9:72985504-73016341:	Ccpg1	72278	80.8	67.2	15.3	-1.0768	0.42485	-4.19717	8.48E-111
chr9:72979725-72985376:	Ccpg1os	546143	30.6	21.0	5.9	-1.30759	0.16733	-4.00238	9.38E-20
chr9:124021971-12403168	Ccr3	12771	3.5	1.0	0.8	-2.73661	0.00871	-3.1052	0.0002544
chr9:124121543-12412718	Ccr5	12774	13.6	16.5	23.3	1.34105	0.331125	2.044	0.0009266
chr9:111054834-11105751	Ccrl2	54199	17.7	12.0	3.8	-1.32434	0.42875	-3.40115	7.12E-07
chr3:51224447-51251654:	Ccrn4l	12457	3.6	11.5	14.8	3.12541	0.000482	4.32898	8.61E-08
chr19:4825366-4839322:-	Ccs	12460	64.4	51.7	33.8	-1.11735	0.272224	-1.51882	9.23E-09
chr8:123840844-12386020	Ccsap	73420	3.4	2.3	1.6	-1.32526	0.225716	-1.71999	0.0018593
chr10:117050998-1170638	Cct2	12461	239.4	282.3	572.3	1.32672	0.054271	2.93862	3.54E-23
chr3:88297135-88321766:	Cct3	12462	206.7	302.1	670.0	1.64104	0.003976	3.92248	1.19E-23
chr11:22990593-23003336	Cct4	12464	268.3	302.1	507.4	1.26721	0.091149	2.33556	1.81E-16
chr15:31590884-31601804	Cct5	12465	414.4	463.1	764.8	1.2553	0.037204	2.29044	3.23E-24
chr5:129787356-12984644	Cct6a	12466	220.3	317.2	815.4	1.61806	0.007756	4.45434	3.15E-26
chr11:82719248-82764321	Cct6b	12467	7.2	1.7	1.2	-3.22664	0.002675	-3.86361	2.67E-05
chr6:85451505-85468477:	Cct7	12468	162.7	196.0	452.5	1.35647	0.023712	3.4232	8.68E-34
chr16:87483325-87495869	Cct8	12469	177.1	227.6	452.9	1.44618	0.026944	3.12199	1.76E-19
chr5:25516067-25518027:	Cct8l1	242891	1.9	1.0	0.3	-1.62629	0.321159	-3.87034	0.000209
chr5:143987909-14401485	Ccz1	231874	66.9	65.5	72.9	1.09649	0.275672	1.36069	2.26E-07
chr9:78615546-78716260:	Cd109	235505	10.0	8.6	2.9	-1.05043	0.707731	-2.72413	5.39E-33
chr7:141467362-14147148	Cd151	12476	134.4	122.8	173.2	1.01723	0.902942	1.60221	4.88E-10
chr6:124304651-12433052	Cd163	93671	3.4	1.8	0.6	-1.56428	0.248236	-3.82155	2.44E-06
chr7:140218267-14023114	Cd163l1	244233	5.3	10.5	32.0	1.6267	0.440871	4.05302	0.0014611
chr10:41519500-41531042	Cd164	53599	196.6	228.8	408.9	1.30893	0.024754	2.57216	1.70E-25
chr7:126408448-12641487	Cd19	12478	4.0	3.1	0.5	-1.10524	0.89727	-3.34147	0.005782
chr3:86995836-86999340:	Cd1d1	12479	36.3	23.5	4.7	-1.37242	0.223307	-5.63192	6.89E-20
chr18:89197427-89270327	Cd226	225825	4.8	8.2	11.5	1.69573	0.248164	2.53592	0.0056168
chr9:58524300-58540940:	Cd276	102657	6.9	4.6	4.0	-1.34813	0.048747	-1.39702	0.0044415
chr7:127191660-12719607	Cd2bp2	70233	55.2	63.0	84.5	1.28756	0.138273	1.88936	4.27E-07
chr11:102041511-1020556	Cd300lg	52685	7.5	4.9	1.8	-1.3712	0.225971	-3.23015	1.40E-09
chr2:60251993-60284484:	Cd302	66205	67.4	58.2	22.6	-1.04251	0.794378	-2.36755	7.35E-20
chr17:33843091-33849774	Cd320	54219	16.5	18.8	20.0	1.26866	0.027648	1.50259	7.28E-07
chr7:43527456-43533171:	Cd33	12489	6.3	5.4	2.2	-1.04535	0.892029	-2.19623	2.46E-05
chr1:194938821-19496129	Cd34	12490	262.0	261.6	438.3	1.1135	0.146685	2.08365	1.58E-43
chr5:17781690-17888959:	Cd36	12491	95.7	47.2	34.0	-1.73458	0.064835	-2.15708	0.0007661
chr5:43868827-43912374:	Cd38	12494	13.6	12.9	6.0	1.04959	0.872406	-1.80141	0.0005653
chr9:44981786-44987052:	Cd3d	12500	2.5	5.5	8.5	1.99625	0.181454	3.17887	0.0026581
chr9:44998743-45009590:	Cd3e	12501	2.4	5.4	8.5	2.0072	0.175796	3.22919	0.0022323
chr7:19356009-19359483:	Cd3eap	70333	15.5	24.5	55.7	1.76061	0.007965	4.25217	3.06E-18
chr9:44969572-44980431:	Cd3g	12502	10.0	24.7	46.6	2.12157	0.146328	3.96358	0.0003841

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr2:102811142-10290166	Cd44	12505	29.2	30.1	45.6	1.12563	0.716333	1.88159	0.0018116
chr1:195041900-19509224	Cd46	17221	20.7	12.4	4.0	-1.47491	0.237286	-3.71392	4.99E-08
chr2:104095801-10411541	Cd59a	12509	32.8	27.3	6.8	-1.0791	0.623085	-3.7836	5.31E-38
chr2:104071010-10408495	Cd59b	333883	4.9	3.4	0.6	-1.26063	0.574358	-5.03264	1.01E-07
chr10:128908919-1289128	Cd63	12512	293.5	273.8	391.4	1.04447	0.620634	1.6619	1.85E-20
chr6:129267325-12927536	Cd69	12515	1.3	3.5	3.5	2.4786	0.028415	2.81496	0.0013951
chr7:143052750-14306793	Cd81	12520	577.3	623.0	619.4	1.213	0.119632	1.33698	0.0020494
chr13:43785112-43803133	Cd83	12522	79.9	49.5	13.0	-1.43885	0.288031	-4.37955	1.07E-09
chr2:148436651-14844353	Cd93	17064	62.9	65.7	75.4	1.18029	0.348357	1.48786	0.0016566
chr16:46035657-46120248	Cd96	84544	3.0	5.7	7.3	1.80654	0.208934	2.50406	0.0088265
chrX:71420060-71492849:	Cd99l2	171486	55.1	46.4	26.2	-1.06943	0.646842	-1.66973	2.94E-08
chr4:138338528-13836795	Cda	72269	4.8	3.7	10.6	-1.13237	0.729672	2.61955	2.75E-06
chr14:59559388-59597959	Cdadc1	71891	24.6	19.2	11.8	-1.14895	0.154506	-1.66348	1.59E-12
chr13:64192545-64274988	Cdc14b	218294	15.3	11.5	8.8	-1.18672	0.213694	-1.37905	0.0015905
chr8:13757690-13781882:	Cdc16	69957	107.3	115.2	139.7	1.20875	0.094175	1.62019	8.81E-09
chr18:34631683-34651736	Cdc23	52563	60.0	58.6	67.1	1.09595	0.239388	1.39745	1.40E-09
chr9:109875579-10989389	Cdc25a	12530	16.1	15.5	22.9	1.08241	0.644489	1.7612	1.16E-07
chr2:131186948-13119851	Cdc25b	12531	52.8	31.0	9.8	-1.52443	0.025572	-4.13158	9.71E-23
chr11:104502526-1045506	Cdc27	217232	51.5	57.4	75.6	1.25366	0.083296	1.82056	6.13E-10
chr10:79682195-79688398	Cdc34	216150	41.5	60.1	108.6	1.62055	0.07287	3.08456	2.06E-08
chr9:21138541-21149906:	Cdc37	12539	108.4	101.4	133.0	1.05115	0.616871	1.53171	1.11E-11
chr4:137319696-13735775	Cdc42	12540	328.0	407.2	508.7	1.39494	0.011742	1.91966	2.71E-10
chr12:111292972-1113777	Cdc42bpb	217866	59.4	58.8	63.2	1.11618	0.362256	1.32703	0.0009428
chr11:113726850-1137518	Cdc42ep4	56699	51.8	49.8	29.1	1.07738	0.576406	-1.41695	7.23E-05
chr3:95228424-95236424:	Cdc42se1	57912	50.8	65.7	78.8	1.45465	0.109747	1.8898	0.0003169
chr11:54717415-54787703	Cdc42se2	72729	47.7	51.2	49.0	1.19933	0.05198	1.27976	0.0005893
chr16:18780447-18811972	Cdc45	12544	7.7	9.0	9.5	1.32242	0.138273	1.53244	0.0025127
chr17:45391888-45433707	Cdc5l	71702	80.1	91.6	105.9	1.28731	0.050378	1.64279	3.80E-07
chr11:98907889-98923942	Cdc6	23834	2.1	2.6	3.2	1.36185	0.268538	1.84155	0.0024465
chr5:106964322-10698443	Cdc7	12545	12.1	13.5	12.8	1.2513	0.025678	1.32461	0.0003129
chr12:112820235-1128293	Cdca4	71963	26.0	32.6	41.7	1.41458	0.060296	1.9791	8.88E-07
chr2:72476219-72486890:	Cdca7	66953	38.3	34.1	51.9	-1.01222	0.967035	1.66979	0.0010456
chr12:117843861-1178787	Cdca7l	217946	19.9	13.0	8.7	-1.36429	0.128147	-1.80174	0.0001301
chr8:118283755-11932344	Cdh13	12554	26.5	22.6	16.1	-1.04676	0.676637	-1.31655	7.58E-05
chr8:104601915-10462439	Cdh16	12556	39.8	32.1	18.4	-1.11473	0.702788	-1.68489	0.0035562
chr1:110889195-11097737	Cdh19	227485	3.4	2.7	0.5	-1.1312	0.721408	-4.70435	1.56E-11
chr18:16588877-16809049	Cdh2	12558	9.5	8.1	2.2	-1.04966	0.817847	-3.40822	1.95E-22
chr8:106510852-10655691	Cdh3	12560	14.6	19.6	40.6	1.50551	0.04546	3.34654	2.28E-15
chr7:126975914-12698050	Cdipt	52858	55.2	56.5	88.4	1.15658	0.423852	1.97301	4.68E-08
chr8:123224841-12323225	Cdk10	234854	83.3	66.6	48.1	-1.12298	0.442472	-1.37811	0.0023849
chr4:155624869-15564993	Cdk11b	12537	55.6	60.8	96.4	1.23697	0.250832	2.13461	8.40E-09
chr11:98203305-98253540	Cdk12	69131	39.9	41.9	50.3	1.18547	0.219414	1.56891	7.39E-06
chr13:17715962-17805097	Cdk13	69562	47.1	49.5	51.6	1.18627	0.18931	1.36429	0.00129
chr5:4803385-5380251:-	Cdk14	18647	27.5	21.1	10.9	-1.16087	0.135364	-2.01746	1.68E-21
chr1:59256907-59352369:	Cdk15	271697	3.3	2.0	0.4	-1.42189	0.40979	-4.71092	1.13E-06
chr10:93160876-93241342	Cdk17	237459	63.3	76.9	72.7	1.36403	0.000739	1.43155	3.28E-06
chr10:40349308-40483818	Cdk19	78334	35.3	28.6	7.2	-1.11025	0.363121	-3.89417	5.87E-64
chr13:64432553-64439721	Cdk20	105278	11.0	8.2	3.7	-1.21365	0.59618	-2.20655	0.0011089
chr5:124345439-12435462	Cdk2ap1	13445	40.3	49.7	96.8	1.3899	0.123805	2.90311	1.00E-11
chr19:4097351-4099017:+	Cdk2ap2	52004	54.6	59.1	75.9	1.19766	0.210605	1.72031	1.44E-07
chr11:116216002-1162202	Cdk3-ps	69681	3.7	2.1	1.3	-1.57005	0.103291	-2.22324	0.0002144
chr10:127063603-1270672	Cdk4	12567	245.0	246.1	383.9	1.12678	0.219719	1.95226	1.85E-22
chr5:24418242-24423530:	Cdk5	12568	51.2	39.4	20.0	-1.16604	0.200877	-2.03296	4.29E-16
chr4:70223024-70410367:	Cdk5rap2	214444	34.1	29.7	20.2	-1.02815	0.821941	-1.34929	3.18E-05
chr5:3344312-3522225:+	Cdk6	12571	46.5	35.1	18.6	-1.19417	0.502357	-1.94175	0.0002231
chr5:146231675-14630287	Cdk8	264064	46.6	46.1	47.3	1.10893	0.285907	1.26536	0.0007109
chr12:69746848-69790707	Cdkl1	71091	136.8	85.5	35.2	-1.40409	0.203558	-2.95225	2.18E-08
chr5:92006074-92043042:	Cdkl2	53886	7.0	4.7	2.9	-1.32937	0.089622	-1.87639	7.68E-07

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:52004221-52084667	Cdkl3	213084	13.3	5.9	6.3	-1.98125	0.000106	-1.65213	0.0009969
chrX:160784308-16099468	Cdkl5	382253	9.8	8.3	5.3	-1.06466	0.754602	-1.47941	0.0015977
chr17:29090986-29100722	Cdkn1a	12575	9.0	49.3	59.3	5.02918	3.67E-06	6.28836	1.39E-09
chr6:134920401-13492552	Cdkn1b	12576	153.8	110.6	40.8	-1.2561	0.34989	-2.89798	3.80E-10
chr7:143458339-14346105	Cdkn1c	12577	100.7	97.4	45.4	1.08483	0.66397	-1.75096	2.13E-06
chr11:51967631-51977336	Cdkn2aipnl	52626	43.4	45.4	51.4	1.17181	0.144193	1.47507	1.06E-06
chr4:89306289-89311032:	Cdkn2b	12579	1.9	2.0	2.8	1.15442	0.65352	1.82902	0.0018325
chr4:109660876-10966675	Cdkn2c	12580	31.2	19.5	9.2	-1.44038	0.074991	-2.63583	3.27E-10
chr9:21288464-21291209:	Cdkn2d	12581	15.3	15.4	8.5	1.11559	0.576979	-1.43723	0.0067151
chr2:3513065-3526376:+	Cdnf	227526	4.2	2.3	1.0	-1.60164	0.106505	-3.18654	2.40E-07
chr18:46713205-46728342	Cdo1	12583	68.2	46.2	11.1	-1.25902	0.714761	-3.36956	0.0020009
chr9:35452076-35507652:	Cdon	57810	65.5	45.2	37.9	-1.29563	0.065033	-1.38047	0.0028506
chr15:85806972-85811697	Cdpf1	72355	26.7	19.4	15.6	-1.24033	0.175253	-1.36747	0.0089809
chr11:115381916-1153961	Cdr2l	237988	14.7	26.1	31.2	1.94412	0.026714	2.48053	0.0001003
chr11:62951193-62993095	Cdrt4	66338	9.1	1.2	1.4	-4.71034	0.000936	-3.68397	0.0008989
chr5:101765130-10182385	Cds1	74596	5.3	3.2	2.7	-1.48373	0.049972	-1.54612	0.0053679
chr2:132263148-13231205	Cds2	110911	76.0	67.4	28.4	-1.01136	0.925733	-2.13363	7.21E-34
chr9:103353102-10336578	Cdv3	321022	66.1	85.7	144.6	1.4622	0.064554	2.65782	1.85E-10
chr8:116568724-11673299	Cdyl2	75796	4.5	3.5	2.8	-1.14827	0.289762	-1.28065	0.0097474
chr7:25461702-25477625:	Ceacam1	26365	6.9	6.2	10.0	1.02286	0.951078	1.76301	0.0035372
chr7:24777204-24784655:	Ceacam10	26366	4.7	2.2	0.8	-1.67089	0.380823	-3.19033	0.0059395
chr2:167688915-16769043	Cebpb	12608	10.3	61.1	29.0	5.19295	1.30E-05	2.89438	0.0014959
chr16:15887286-15889545	Cebpd	12609	10.9	54.3	18.6	4.11514	0.000732	1.85524	0.095063
chr7:35046422-35056566:	Cebpg	12611	39.1	46.3	58.2	1.33317	0.075358	1.84112	4.78E-07
chr17:78919003-78937070	Cebpz	12607	59.3	79.4	119.2	1.50849	0.021511	2.46115	5.49E-11
chr6:120666421-12077119	Cecr2	330409	6.7	4.3	0.5	-1.41039	0.204021	-8.70658	4.02E-27
chr2:90940397-91019497:	Celf1	13046	56.9	59.9	80.2	1.18491	0.057953	1.75894	1.54E-17
chr2:6539699-7396198:-	Celf2	14007	35.9	28.8	11.7	-1.11494	0.179908	-2.44422	1.47E-52
chr3:108390848-10841549	Celsr2	53883	6.5	4.3	3.4	-1.35349	0.04132	-1.54471	0.000144
chr7:83932857-84086505:	Cemip	80982	18.6	12.8	4.2	-1.30603	0.229853	-3.43157	1.19E-14
chr2:131177289-13118001	Cenpb	12616	166.4	157.1	227.3	1.06099	0.535225	1.70409	5.83E-18
chr1:189640614-18968808	Cenpf	108000	6.8	6.3	3.2	1.02558	0.930424	-1.65737	0.0012073
chr13:100759686-1007758	Cenph	26886	5.7	4.6	2.3	-1.10551	0.761941	-1.89098	0.0023589
chr14:56526761-56571846	Cenpj	219103	9.3	8.9	5.3	1.07022	0.545208	-1.40035	1.03E-05
chr12:4211672-4234294:-	Cenpo	52504	12.9	10.4	6.2	-1.10881	0.519631	-1.65323	3.48E-06
chr8:105844678-10585200	Cenpt	320394	18.4	21.6	26.7	1.32298	0.054137	1.79969	5.85E-08
chr8:46552069-46579584:	Cenpu	71876	4.8	3.2	1.8	-1.34802	0.273993	-2.02828	0.0004365
chr11:62524944-62539261	Cenpv	73139	43.6	34.8	22.7	-1.12403	0.400239	-1.52631	1.63E-05
chr10:30196009-30200540	Cenpw	66311	10.4	6.5	3.1	-1.41587	0.197325	-2.52971	4.07E-06
chr11:108425266-1088606	Cep112	76380	23.3	18.4	8.1	-1.1289	0.326812	-2.26999	1.10E-20
chr18:53681723-53744547	Cep120	225523	55.9	48.6	32.5	-1.02935	0.77149	-1.37264	1.10E-07
chr12:90998492-91384409	Cep128	75216	22.8	15.8	7.1	-1.29325	0.014555	-2.53628	2.63E-29
chr11:120064430-1200868	Cep131	12009	18.6	11.0	5.5	-1.51	0.032083	-2.60874	8.63E-11
chr9:87191963-87255532:	Cep162	382090	22.2	17.7	10.6	-1.12726	0.54819	-1.64445	0.0001828
chr9:45766946-45828638:	Cep164	214552	17.3	12.6	4.5	-1.23279	0.091181	-3.03883	1.52E-32
chr16:32099802-32108054	Cep19	66994	28.9	23.3	13.4	-1.11195	0.486294	-1.71705	2.15E-07
chr18:67800107-67885170	Cep192	70799	22.6	20.5	13.4	1.01471	0.882757	-1.34095	7.71E-08
chr2:155956558-15599890	Cep250	16328	34.8	22.8	12.5	-1.36648	0.075985	-2.1905	2.54E-09
chr10:100488289-1005736	Cep290	216274	21.0	17.4	9.5	-1.08663	0.561803	-1.76061	1.37E-09
chr8:56531522-56550566:	Cep44	382010	41.9	35.9	17.0	-1.05092	0.798752	-1.94704	7.70E-09
chr9:13807788-13827107:	Cep57	74360	53.0	42.9	31.2	-1.10684	0.263571	-1.3583	2.74E-06
chr10:41718840-41809868	Cep57l1	103268	14.8	10.6	3.5	-1.25552	0.258179	-3.30571	5.39E-16
chr9:102586578-10262612	Cep63	28135	56.8	40.5	35.7	-1.2529	0.0122	-1.26861	0.0009523
chr9:99243468-99300403:	Cep70	68121	36.5	26.0	10.2	-1.25976	0.069099	-2.81634	4.34E-27
chr13:74036495-74062285	Cep72	74470	7.8	4.4	1.4	-1.5925	0.048388	-4.11545	1.20E-14
chr18:67617397-67641336	Cep76	225659	7.4	9.4	14.9	1.43508	0.108056	2.44817	6.64E-08
chr10:94688790-94790336	Cep83	77048	38.0	37.0	35.7	1.09115	0.21221	1.17342	0.001798
chr10:94673493-94688613	Cep83os	67723	15.8	8.3	5.0	-1.69317	0.028799	-2.40237	2.63E-06

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr10:53278081-53379851	Cep85l	1E+08	131.2	103.2	39.3	-1.15022	0.768167	-2.40786	0.002436
chr7:35397093-35438684:	Cep89	72140	28.1	22.3	12.5	-1.1298	0.324712	-1.7816	5.84E-11
chr11:106789252-1068188	Cep95	320162	49.6	35.4	18.9	-1.25247	0.109247	-2.06953	3.14E-12
chr16:55899888-55934848	Cep97	74201	12.6	9.6	2.0	-1.18163	0.469587	-4.74501	2.70E-23
chr3:106502260-10654780	Cept1	99712	49.3	51.6	51.6	1.17212	0.058365	1.30483	2.78E-05
chr2:29869494-29882840:	Cercam	99151	19.9	13.0	7.5	-1.3702	0.08663	-2.08991	1.06E-07
chr2:79332491-79428988:	Cerkl	228094	2.2	0.9	0.3	-2.09934	0.058322	-5.0035	4.70E-07
chr3:95315252-95323568:	Cers2	76893	133.2	144.4	232.0	1.22338	0.148162	2.15454	3.64E-14
chr7:66743504-66823692:	Cers3	545975	6.5	3.2	1.3	-1.75596	0.070651	-3.67775	4.60E-08
chr8:4493405-4526079:+	Cers4	67260	41.4	28.5	19.3	-1.30571	0.143947	-1.69548	0.0001084
chr8:93020215-93048192:	Ces1a	244595	0.3	0.8	2.0	1.84609	0.342708	3.59207	0.005934
chr8:93166072-93197804:	Ces1d	104158	86.9	68.3	20.4	-1.14853	0.593233	-3.27723	1.10E-12
chr8:93201218-93229619:	Ces1e	13897	8.8	7.1	1.7	-1.11578	0.570384	-3.97103	1.26E-22
chr8:93256236-93279736:	Ces1f	234564	3.8	1.1	0.5	-2.21517	0.165645	-3.36231	0.0051266
chr8:104831644-10483865	Ces2b	234669	4.0	3.1	1.2	-1.15171	0.659221	-2.54176	1.31E-05
chr8:104961718-10496953	Ces2g	72361	13.2	9.5	5.2	-1.23287	0.381923	-1.99712	4.43E-05
chr18:9618419-9619469:-	Cetn1	26369	9.8	0.8	1.1	-5.88252	0.000654	-4.25418	0.0010282
chr3:37308627-37312446:	Cetn4	207175	11.4	4.1	2.5	-2.36527	0.00041	-3.40609	4.67E-09
chr1:171121661-17112696	Cfap126	75472	5.8	3.2	1.3	-1.56357	0.276253	-3.07714	0.0002263
chr8:95420250-95434869:	Cfap20	14894	82.6	68.7	40.5	-1.07212	0.414727	-1.62441	2.85E-16
chr19:47736857-47837361	Cfap43	1E+08	3.1	0.9	0.5	-2.69754	0.015973	-3.74858	5.26E-05
chr1:172521130-17254587	Cfap45	71870	4.8	0.6	1.0	-5.67011	3.74E-06	-3.31371	0.0002003
chr7:139600915-13968381	Cfap46	212124	1.5	0.6	0.2	-2.10593	0.081863	-4.57711	3.46E-06
chr11:67924806-67965642	Cfap52	71860	2.3	0.1	0.3	-7.00038	8.45E-05	-4.62408	0.0002928
chr18:74283100-74359984	Cfap53	74453	3.8	1.8	1.2	-1.76874	0.084572	-2.37611	0.0006838
chr4:118554551-11862040	Cfap57	68625	3.3	0.7	0.5	-3.5679	0.001081	-4.44836	4.86E-06
chr19:47937712-48035379	Cfap58	381229	1.9	0.1	0.2	-6.37838	0.000378	-3.87025	0.0023652
chr5:5580982-5664232:-	Cfap69	207686	13.6	8.5	3.1	-1.41455	0.072396	-3.33375	2.91E-16
chr14:20394190-20452225	Cfap70	76670	4.7	1.4	0.5	-2.81766	0.000145	-6.06178	5.03E-14
chr4:155409190-15544311	Cfap74	544678	4.2	2.8	1.0	-1.30716	0.106741	-3.23634	1.13E-18
chr8:46169556-46195590:	Cfap97	66756	31.0	22.2	17.7	-1.25177	0.074725	-1.3955	0.0005246
chr8:111768473-11185431	Cfdp1	23837	152.8	165.1	241.8	1.21323	0.049601	1.96902	1.35E-20
chr1:140085855-14018341	Cfh	12628	835.7	704.9	238.9	-1.06734	0.694329	-2.76547	2.32E-24
chr1:139810292-13985869	Cfhr2	545366	4.1	3.1	0.7	-1.21031	0.608309	-3.83343	2.17E-07
chr19:5490455-5494031:+	Cfl1	12631	480.8	525.4	1038.4	1.22679	0.080889	2.67123	1.60E-30
chr12:54858819-54862877	Cfl2	12632	107.0	100.2	117.0	1.04559	0.691203	1.36113	8.20E-06
chr1:58711491-58759209:	Cflar	12633	49.2	50.2	49.4	1.13752	0.042087	1.25523	2.42E-06
chr6:18170687-18322769:	Cftr	12638	3.4	2.6	5.8	-1.16863	0.68847	2.01327	0.0040468
chr16:64852085-64859491	Cggbp1	106143	81.1	90.3	92.8	1.25252	0.052068	1.42598	6.08E-05
chr3:94760070-94786515:	Cgn	70737	14.4	10.0	6.7	-1.28369	0.145357	-1.68785	4.52E-05
chr5:30933143-30945480:	Cgref1	68567	4.3	4.7	6.4	1.21209	0.391484	1.81582	7.81E-05
chr19:34473784-34475135	Ch25h	12642	4.2	10.8	25.5	2.40984	0.044031	5.62129	1.71E-07
chr11:30976707-30986365	Chac2	68044	6.9	6.8	11.7	1.1004	0.681809	2.09309	8.75E-08
chr11:94565074-94569127	Chad	12643	0.2	0.4	1.0	1.89362	0.239961	4.74671	3.53E-05
chr8:13869641-13881639:	Champ1	101994	35.3	38.0	50.7	1.21507	0.208786	1.78263	2.36E-07
chr14:20703027-20704425	Chchd1	66121	79.6	93.4	141.7	1.31536	0.087132	2.19042	2.72E-11
chr10:75935573-75937734	Chchd10	103172	70.0	53.8	33.1	-1.16314	0.254135	-1.67762	6.37E-08
chr5:129881161-12988747	Chchd2	14004	166.1	203.1	285.5	1.37412	0.02789	2.12293	7.03E-12
chr6:32792227-33060152:	Chchd3	66075	95.9	86.7	108.5	1.01192	0.899038	1.41306	2.75E-12
chr6:91464276-91473423:	Chchd4	72170	23.3	32.4	60.2	1.55357	0.019893	3.12671	2.08E-15
chr2:129129700-12913411	Chchd5	66170	25.1	18.8	10.3	-1.20602	0.422352	-1.90835	8.25E-05
chr4:3938888-3951382:+	Chchd7	66433	17.6	13.6	7.2	-1.15927	0.240459	-1.94094	4.78E-13
chr17:15704967-15772612	Chd1	12648	43.2	63.2	70.2	1.64257	0.037158	1.97746	0.000215
chr11:69340769-69342647	Chd3os	80515	8.2	7.2	4.8	-1.00334	0.987505	-1.3537	0.0082004
chr6:125096163-12513050	Chd4	107932	175.5	155.2	192.9	-1.00409	0.97568	1.37224	7.09E-06
chr4:152338651-15239019	Chd5	269610	2.6	0.6	1.3	-3.62629	5.27E-05	-1.60021	0.099133
chr2:160946978-16110908	Chd6	71389	83.2	68.9	31.8	-1.0834	0.479351	-2.07777	2.53E-22
chr5:110840017-11087413	Chek2	50883	19.1	12.0	2.8	-1.42003	0.183925	-4.95849	2.52E-16

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr8:72460483-72475233:	Cherp	27967	21.8	26.3	31.7	1.36365	0.149432	1.78814	0.0003015
chrX:103356476-10339611	Chic1	12212	22.9	17.5	11.2	-1.18141	0.235768	-1.62347	1.93E-06
chr5:75006424-75044626:	Chic2	74277	48.1	48.4	46.1	1.12859	0.175009	1.1979	0.0065319
chr7:141493136-14153985	Chid1	68038	24.5	20.4	31.8	-1.07953	0.508446	1.61941	1.65E-10
chr3:106147554-10616756	Chil3	12655	4.8	0.5	2.0	-4.31448	0.00495	-1.65824	0.259603
chrX:113040592-11318551	Chm	12662	31.0	32.6	32.3	1.17196	0.027246	1.29921	2.09E-06
chr1:175682238-17568835	Chml	12663	14.0	17.3	24.3	1.38666	0.002448	2.15808	3.84E-19
chr8:123204261-12321278	Chmp1a	234852	96.8	89.3	97.5	1.03377	0.733147	1.2582	0.0001111
chr7:13032006-13034777:	Chmp2a	68953	209.7	212.6	284.7	1.14109	0.228514	1.69003	1.67E-11
chr2:154657026-15469478	Chmp4b	75608	141.4	179.6	225.3	1.42824	0.004473	1.97481	1.03E-11
chr11:119913810-1199195	Chmp6	208092	37.0	34.5	66.3	1.04582	0.660121	2.23497	1.14E-41
chr2:73610660-73775346:	Chn1	108699	4.7	3.9	9.4	-1.06067	0.768167	2.48984	6.96E-16
chr6:54039932-54301812:	Chn2	69993	11.2	7.4	4.6	-1.34638	0.089284	-1.91846	8.77E-07
chr16:78930948-78951728	Chodl	246048	41.2	40.7	7.7	1.08244	0.821778	-3.94105	1.37E-11
chr9:18292267-18314000:	Chordc1	66917	73.4	119.5	127.0	1.81541	0.009	2.09421	5.34E-05
chr2:119547707-11958702	Chp1	56398	97.2	80.3	57.7	-1.08445	0.419995	-1.34627	2.13E-05
chr7:122219496-12222253	Chp2	70261	34.0	27.8	4.6	-1.0933	0.736736	-5.59441	9.85E-25
chr1:75474569-75479471:	Chpf	74241	27.1	30.8	49.7	1.28024	0.131475	2.2586	8.91E-12
chr15:73090412-73094075	Chrac1	93696	74.8	75.3	82.1	1.12233	0.136115	1.36849	2.00E-08
chrX:143285674-14339426	Chrdl1	83453	9.5	7.4	3.1	-1.13879	0.536825	-2.36552	7.56E-10
chr7:100006404-10003472	Chrdl2	69121	12.8	18.2	32.0	1.56949	0.236799	2.82697	0.0001749
chr7:63098692-63212526:	Chrna7	11441	1.8	1.4	0.7	-1.15873	0.700523	-2.04463	0.00461
chr11:70614883-70619194	Chrne	11448	1.4	0.4	0.1	-2.67464	0.053306	-4.9824	6.87E-05
chr2:92599707-92615252:	Chst1	76969	4.4	2.1	0.9	-1.73911	0.085935	-3.41595	7.74E-07
chr10:82985497-83195891	Chst11	58250	15.3	40.7	74.8	2.78802	0.001323	5.18911	3.65E-10
chr6:90308351-90325185:	Chst13	71797	0.5	1.6	10.8	2.3911	0.127854	10.5428	2.18E-08
chr9:95400926-95407270:	Chst2	54371	5.5	4.6	2.8	-1.07721	0.69615	-1.5579	0.0002204
chr8:110029075-11003933	Chst4	26887	5.8	1.7	1.0	-2.4645	0.072086	-3.47143	0.0012386
chr18:15452175-15718046	Chst9	71367	16.6	10.9	0.5	-1.31744	0.560969	-14.4799	1.32E-16
chr7:66109515-66173798:	Chsy1	269941	36.1	60.7	106.8	1.86827	0.016353	3.46488	7.64E-10
chr8:106883863-10689359	Chtf8	214987	131.6	144.9	149.8	1.23896	0.036542	1.42052	8.07E-06
chr3:90498539-90509498:	Chtop	66511	115.5	132.9	167.9	1.29676	0.048522	1.80384	2.77E-09
chr19:44073334-44107477	Chuk	12675	56.4	74.6	100.5	1.48899	0.03739	2.18057	8.79E-08
chr2:127240938-12724781	Ciao1	26371	51.0	45.9	28.7	1.00419	0.969817	-1.41888	2.64E-09
chr8:94819818-94838340:	Ciapin1	109006	8.4	11.9	22.4	1.59979	0.01599	3.23344	4.06E-15
chr3:95878505-95882228:	Ciart	229599	8.1	3.7	5.5	-1.89323	6.28E-05	-1.16229	0.275488
chr7:80227156-80232805:	Cib1	23991	25.0	22.2	32.9	-1.00393	0.982303	1.63941	1.75E-08
chr9:54545352-54560079:	Cib2	56506	23.1	23.0	12.0	1.11841	0.57873	-1.52361	0.0022213
chr18:67343564-67367794	Cidea	12683	1.5	1.3	0.3	-1.02428	0.968189	-2.9298	0.002457
chr6:113424634-11343576	Cidec	14311	67.4	24.5	5.2	-1.82487	0.348955	-3.94671	0.0028589
chr12:110872610-1108891	Cinp	67236	28.6	32.9	41.8	1.29469	0.048174	1.81278	1.16E-09
chr12:86947041-86965366	Cipc	217732	21.7	23.9	30.2	1.24461	0.272793	1.71593	0.00017
chr2:73283872-73312592:	Cir1	66935	53.0	41.1	11.8	-1.16161	0.347551	-3.52981	3.59E-29
chr8:106893640-10692309	Cirh1a	21771	35.3	55.3	114.7	1.74919	0.024754	3.81412	1.75E-12
chr10:71330494-71344849	Cisd1	52637	24.1	24.7	42.4	1.14308	0.32845	2.17437	1.64E-17
chr3:135406412-13542343	Cisd2	67006	28.8	28.9	43.8	1.12523	0.303845	1.89423	6.28E-16
chr10:17723228-17725674	Cited2	17684	25.2	14.1	6.8	-1.57589	0.18542	-2.72052	8.17E-05
chr4:120666563-12066782	Cited4	56222	7.4	16.7	20.7	2.42406	0.001124	3.23324	1.82E-07
chr2:32363010-32378313:	Ciz1	68379	50.6	40.3	33.3	-1.11893	0.218526	-1.21091	0.004691
chr8:22168152-22185819:	Ckap2	80986	5.7	6.8	8.2	1.32563	0.12837	1.79082	1.93E-05
chr10:84526305-84533888	Ckap4	216197	27.6	29.2	53.9	1.18827	0.213248	2.40923	1.91E-19
chr2:91546322-91620665:	Ckap5	75786	68.9	68.7	74.6	1.12091	0.113404	1.35499	1.23E-08
chr8:104250861-10426493	Cklf	75458	15.0	12.4	8.9	-1.08297	0.535892	-1.34851	0.0006293
chr2:121358641-12136373	Ckmt1	12716	6.5	9.5	11.5	1.60675	0.189879	2.06784	0.0071635
chr3:89415472-89418291:	Cks1b	54124	22.7	24.1	46.1	1.17943	0.29572	2.50061	3.70E-18
chr1:118389058-11860946	Clasp1	76707	46.6	39.7	29.1	-1.04739	0.576406	-1.27927	5.28E-06
chr9:113741473-11391969	Clasp2	76499	57.4	48.7	22.9	-1.05771	0.727681	-1.98814	1.54E-12
chr3:145004537-14503277	Clca1	23844	66.6	41.6	15.6	-1.39094	0.20232	-3.22509	3.87E-10

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr3:144730316-14476073	Clca3a1	12722	8.5	9.8	4.3	1.26516	0.316149	-1.57856	0.0084955
chr3:108653913-10867884	Clcc1	229725	50.3	44.0	33.5	-1.02501	0.816429	-1.2002	0.003872
chr16:20702966-20716636	Clcn2	12724	25.3	19.8	11.5	-1.14323	0.431473	-1.74304	2.44E-06
chr8:60910389-60983311:	Clcn3	12725	30.1	25.9	29.2	-1.0425	0.639459	1.21278	0.0006442
chr7:7282309-7300851:-	Clcn4-2	12727	47.2	47.6	53.5	1.13484	0.257419	1.4129	1.59E-05
chr16:26356646-26371839	Cldn1	12737	75.7	56.0	5.7	-1.19683	0.786428	-6.03426	4.76E-06
chr3:31149920-31164326:	Cldn11	18417	4.3	2.4	1.2	-1.53971	0.101009	-2.8127	5.63E-07
chr8:47824482-47825475:	Cldn22	75677	1.7	0.6	0.1	-1.96078	0.230329	-4.64505	0.0003225
chr16:18776847-18778262	Cldn5	12741	88.0	65.2	20.1	-1.22342	0.443347	-3.34282	1.67E-11
chr11:69964779-69967886	Cldn7	53624	26.1	34.5	45.0	1.47198	0.215398	2.05418	0.0017436
chr16:88560826-88563183	Cldn8	54420	26.1	19.9	8.4	-1.18746	0.673521	-2.30687	0.0012682
chr16:58727910-58734247	Cldnd1	224250	46.3	47.7	55.8	1.1573	0.271442	1.4969	2.11E-05
chr7:43440816-43443320:	Cldnd2	74276	3.5	1.1	0.8	-2.50077	0.047496	-2.7569	0.0049621
chr16:10545339-10744878	Clec16a	74374	14.5	15.9	18.8	1.22981	0.030875	1.6131	3.56E-11
chr6:129426684-12945200	Clec1a	243653	5.1	4.1	1.5	-1.13342	0.754718	-2.45567	0.0002894
chr9:123150946-12315743	Clec3b	21922	32.0	28.0	7.0	-1.02548	0.945108	-3.46202	1.50E-10
chr8:83389891-83426829:	Clgn	12745	8.3	0.4	1.1	-10.7981	1.01E-07	-4.43303	0.0001389
chr11:29547950-29578352	Clhc1	73324	1.3	0.9	0.3	-1.3179	0.517626	-2.70984	0.0011472
chr17:35050243-35058719	Clic1	114584	181.9	187.3	221.4	1.14903	0.252622	1.511	2.01E-06
chr4:135213970-13527276	Clic4	29876	191.8	198.4	212.0	1.15505	0.060625	1.37894	2.45E-08
chr11:45851964-45910625	Clint1	216705	69.6	75.6	131.5	1.22003	0.099262	2.34068	3.81E-22
chr5:123577794-12368436	Clip1	56430	79.1	68.7	55.0	-1.02955	0.698642	-1.14977	0.0031033
chr5:134489383-13455243	Clip2	269713	26.3	26.5	17.3	1.13461	0.199154	-1.21369	0.0089323
chr7:30291753-30308367:	Clip3	76686	41.7	32.3	9.9	-1.15703	0.44502	-3.2626	9.47E-20
chr1:58411988-58424088:	Clk1	12747	522.8	477.4	178.7	1.01535	0.928217	-2.32107	7.41E-22
chr11:51263171-51281764	Clk4	12750	198.1	176.7	118.1	-1.00201	0.980031	-1.3407	1.75E-12
chr12:104763114-1048650	Clmn	94040	11.3	6.1	2.5	-1.649	0.006472	-3.42588	3.47E-17
chr9:40685964-40784046:	Clmp	71566	80.6	64.1	45.9	-1.13128	0.478383	-1.39611	0.0057681
chr7:126571400-12658428	Cln3	12752	28.9	23.1	13.5	-1.12447	0.405752	-1.70389	6.18E-08
chr9:62838787-62852002:	Cln6	76524	24.8	15.2	10.4	-1.45922	0.1721	-1.84192	0.0032848
chr5:38706457-38876693:	Clnk	27278	2.8	3.4	7.6	1.2699	0.6179	2.91076	0.00051
chr7:97696657-97720793:	Clns1a	12729	32.5	34.8	49.4	1.2	0.039737	1.89594	1.37E-22
chr5:76209868-76304792:	Clock	12753	49.7	55.4	60.8	1.2481	9.95E-07	1.52839	6.48E-28
chr7:101663768-10179016	Clpb	20480	24.5	22.2	31.8	1.01997	0.922172	1.6176	6.15E-06
chr17:56990264-56996371	Clpp	53895	81.4	85.3	129.8	1.17865	0.107587	1.98553	1.29E-20
chr7:19631580-19665030:	Clptm1	56457	49.6	50.6	69.8	1.14938	0.219894	1.75331	3.65E-12
chr13:73604002-73620639	Clptm1l	218335	90.5	93.9	188.8	1.16468	0.069237	2.59767	5.78E-56
chr4:149586468-14964889	Clstn1	65945	111.8	94.0	56.5	-1.06067	0.535611	-1.57645	2.62E-13
chr4:44012643-44032848:	Clta	12757	209.6	201.0	216.2	1.07311	0.434354	1.28682	4.92E-05
chr13:54592939-54611272	Cltb	74325	38.9	45.8	102.0	1.32326	0.05637	3.22349	9.56E-28
chr11:86694653-86757492	Cltc	67300	198.7	212.1	342.1	1.19994	0.087965	2.13701	3.20E-22
chr11:74649495-74670847	Cluh	74148	36.2	45.8	91.4	1.43238	0.09271	3.05772	1.26E-12
chr10:33512334-33624600	Clvs2	215890	8.0	7.6	13.6	1.04055	0.918441	2.03913	0.0005843
chr14:122181694-1224022	Clybl	69634	19.6	14.0	6.3	-1.24459	0.256886	-2.42565	4.30E-10
chr6:142756686-14277571	Cmas	12764	41.8	36.5	41.3	-1.02693	0.823489	1.23344	0.0023667
chr15:31568912-31590119	Cmbl	69574	7.8	5.2	1.0	-1.33159	0.398631	-5.20996	1.32E-10
chr8:116888685-11692143	Cmc2	66531	12.0	10.7	5.8	-1.00608	0.97903	-1.63445	8.73E-05
chr5:113612355-11365039	Cmklr1	14747	14.7	47.9	122.1	3.21374	0.001626	7.80301	1.13E-11
chr6:85910154-85915677:	Cml1	66116	9.6	5.8	4.0	-1.46447	0.209715	-1.84637	0.0072457
chr6:85760631-85765744:	Cml3	93674	2.3	1.2	0.3	-1.64029	0.291607	-4.10703	5.63E-05
chr4:114960613-11498722	Cmpk1	66588	43.1	43.8	67.1	1.1399	0.265628	1.93268	6.83E-16
chr12:26469215-26479837	Cmpk2	22169	16.1	15.5	4.0	1.06663	0.829198	-3.06939	1.11E-10
chr8:104293542-10431014	Cmtm1	1.01E+08	1.7	0.1	0.1	-6.76062	0.000479	-4.72064	0.0008894
chr8:104281042-10429318	Cmtm2a	73381	17.0	1.3	1.6	-7.86824	1.80E-06	-5.881	2.46E-06
chr8:104322227-10433076	Cmtm2b	75502	8.6	0.5	1.3	-6.92761	0.000149	-3.64024	0.0033199
chr8:104340594-10434767	Cmtm3	68119	111.7	91.9	71.8	-1.08955	0.461395	-1.24316	0.0075772
chr9:114731203-11474934	Cmtm6	67213	65.0	65.7	71.6	1.1278	0.164817	1.3728	5.43E-07
chr9:114789345-11484415	Cmtm8	70031	11.8	9.4	2.2	-1.11754	0.719076	-3.9437	1.23E-11

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr17:29660601-29703359	Cmtr1	74157	90.7	86.0	87.9	1.06012	0.504803	1.21251	0.0011902
chr8:110217960-11022448	Cmtr2	234728	13.0	17.1	27.5	1.47563	0.006942	2.60448	1.54E-17
chr13:93040715-93144724	Cmya5	76469	9.5	7.3	3.0	-1.17942	0.396058	-2.46861	1.92E-11
chr2:156312473-15637563	Cnbd2	70873	10.8	5.0	4.3	-1.8955	0.000372	-1.96785	8.57E-06
chr6:87842615-87851106:	Cnbp	12785	456.5	522.5	659.6	1.28868	0.093324	1.78823	2.47E-07
chr18:84610509-84650095	Cndp1	338403	11.4	6.4	1.7	-1.57717	0.063506	-5.03827	1.74E-17
chr8:95239043-95306585:	Cngb1	333329	1.7	0.9	0.3	-1.64296	0.197941	-3.43445	1.85E-05
chr14:46775568-46788357	Cnih1	12793	42.8	53.5	105.7	1.40142	0.001118	3.05319	1.09E-41
chr1:181150931-18116899	Cnih4	98417	35.1	33.0	36.5	1.05156	0.57836	1.29869	7.25E-06
chrX:157821573-15804311	Cnksr2	245684	4.3	4.2	1.6	1.09715	0.767752	-2.02387	0.0002715
chr9:22099253-22109221:	Cnn1	12797	395.0	467.1	1146.6	1.31176	0.166922	3.49476	9.25E-19
chr10:79988600-79995400	Cnn2	12798	267.8	323.5	644.8	1.36362	0.092303	2.93996	1.66E-15
chr3:121426541-12145820	Cnn3	71994	265.5	236.3	162.7	-1.01128	0.943505	-1.30476	0.0014492
chr19:46761609-46878580	Cnnm2	94219	14.5	10.7	4.4	-1.21629	0.356475	-2.54752	4.43E-10
chr1:36511876-36528237:	Cnnm3	94218	28.6	18.7	6.2	-1.36575	0.148162	-3.52322	1.72E-15
chr1:39535802-39546877:	Cnot11	52846	27.9	28.6	28.6	1.15073	0.179962	1.27747	0.0015926
chr5:96070333-96161990:	Cnot6l	231464	38.6	31.4	17.1	-1.10345	0.236148	-1.80649	1.51E-23
chr1:75135215-75142368:	Cnppd1	69171	72.2	51.9	20.6	-1.25507	0.20207	-2.73995	3.81E-15
chr17:46735713-46752212	Cnpy3	72029	57.6	53.1	94.5	1.03196	0.784089	2.04593	3.42E-28
chr4:33924632-33948831:	Cnr1	12801	1.5	0.8	0.2	-1.71804	0.073967	-5.55505	5.55E-12
chr11:17051934-17079372	Cnrip1	380686	40.6	33.4	10.3	-1.10002	0.679347	-3.06289	8.38E-15
chr1:179546529-17962747	Cnst	226744	47.8	33.9	21.0	-1.27341	0.309506	-1.78944	0.0006932
chr11:101279203-1012887	Cntd1	68107	4.9	2.0	0.4	-2.15734	0.007053	-7.20679	2.45E-15
chr4:84884309-85131921:	Cntln	338349	31.8	27.8	14.1	-1.02635	0.84168	-1.79423	1.86E-15
chr1:132509425-13254294	Cntn2	21367	0.0	0.3	1.6	2.3131	0.183808	5.67702	0.0001932
chr6:102163306-10246466	Cntn3	18488	7.5	5.4	1.7	-1.2448	0.29123	-3.37646	6.00E-16
chr11:101176117-1011907	Cntnap1	53321	9.3	7.7	15.6	-1.08252	0.74858	2.05947	9.98E-07
chr6:45060061-47301371:	Cntnap2	66797	0.9	0.5	0.2	-1.5622	0.289501	-3.63389	3.50E-05
chr2:35109492-35178822:	Cntrl	26920	38.4	31.3	18.2	-1.10258	0.330948	-1.68373	1.18E-13
chr11:69299496-69323873	Cntrob	216846	14.5	11.4	7.3	-1.13639	0.448495	-1.5631	0.0001399
chr4:108328152-10834071	Coa7	69893	12.3	11.4	15.3	1.03454	0.794378	1.55058	2.27E-09
chr11:101082625-1010866	Coasy	71743	31.0	24.3	17.1	-1.14836	0.434892	-1.4406	0.0034014
chr12:51593341-51605773	Coch	12810	78.8	64.3	10.5	-1.09987	0.653537	-5.75099	7.43E-40
chr11:113649529-1136624	Cog1	16834	37.9	39.1	41.7	1.1624	0.218836	1.37378	0.0003806
chr8:124520767-12455200	Cog2	76332	46.3	47.3	48.0	1.14677	0.147449	1.29515	0.00024
chr14:75702351-75754493	Cog3	338337	60.8	65.6	86.0	1.21618	0.128498	1.7562	2.73E-09
chr12:31654869-31937630	Cog5	238123	57.0	51.3	34.5	1.00553	0.959326	-1.32042	7.06E-07
chr3:52982123-53017223:	Cog6	67542	40.5	34.9	44.6	-1.03597	0.700448	1.37631	6.10E-09
chr8:107048709-10705673	Cog8	97484	30.1	33.0	44.7	1.23932	0.137542	1.84318	6.61E-09
chr11:88973935-88991613	Coil	12812	19.8	16.5	21.3	-1.06682	0.549676	1.34733	1.72E-05
chr3:114030540-11422032	Col11a1	12814	3.0	2.2	1.0	-1.20511	0.347244	-2.41598	8.79E-10
chr9:79598987-79718722:	Col12a1	12816	17.6	13.4	27.3	-1.18167	0.539702	1.87798	0.000527
chr15:55307750-55520803	Col14a1	12818	70.8	47.6	17.1	-1.32203	0.247164	-3.19845	1.25E-11
chr10:77052179-77166530	Col18a1	12822	92.1	69.5	68.8	-1.18611	0.002697	-1.06928	0.176823
chr6:4505697-4541543:+	Col1a2	12843	514.2	355.6	236.2	-1.29551	0.144193	-1.7305	3.20E-05
chr15:71798476-72034227	Col22a1	69700	2.1	0.6	0.4	-2.8773	0.002026	-3.39984	1.66E-05
chr11:51289920-51583925	Col23a1	237759	10.9	9.8	51.1	1.01567	0.948404	5.7181	8.49E-48
chr3:145292472-14555200	Col24a1	71355	6.5	4.1	2.1	-1.37402	0.396519	-2.31286	0.0016005
chr3:130180845-13059988	Col25a1	77018	4.0	3.1	0.5	-1.14975	0.663569	-5.90658	1.60E-17
chr5:136741764-13688310	Col26a1	140709	1.7	2.0	0.1	1.27916	0.661345	-6.32485	1.01E-06
chr4:63215412-63334990:	Col27a1	373864	15.7	14.4	7.6	1.03466	0.884002	-1.63528	0.0001513
chr1:45311538-45349706:	Col3a1	12825	####	766.0	573.2	-1.32791	0.136048	-1.58034	0.0014084
chr8:11198423-11312826:	Col4a1	12826	167.1	162.1	311.5	1.0816	0.373193	2.32226	1.65E-45
chr8:11312829-11449287:	Col4a2	12827	91.8	85.0	177.8	1.03086	0.805063	2.40634	1.69E-36
chr1:82586921-82722059:	Col4a3	12828	5.9	6.7	12.9	1.26952	0.04488	2.71733	7.41E-31
chr13:96542735-96640167	Col4a3bp	68018	70.1	58.5	34.1	-1.07537	0.466707	-1.63988	1.83E-13
chrX:141475419-14168923	Col4a5	12830	60.2	51.7	18.8	-1.04585	0.694968	-2.55046	1.11E-41
chrX:141165403-14147407	Col4a6	94216	38.0	32.3	10.9	-1.04624	0.70543	-2.76427	1.88E-44

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr2:27886425-28039510:	Col5a1	12831	69.7	117.9	226.4	1.87356	0.015825	3.77322	4.71E-11
chr1:45374331-45503282:	Col5a2	12832	141.6	101.9	60.6	-1.25409	0.253857	-1.85151	1.63E-05
chr9:20770050-20815034:	Col5a3	53867	19.6	22.6	29.3	1.29213	0.260842	1.82589	0.000257
chr10:76708792-76726044	Col6a1	12833	560.2	557.0	1189.8	1.11258	0.123408	2.64543	4.53E-85
chr10:76595756-76623404	Col6a2	12834	247.6	294.0	966.2	1.33244	0.064835	4.74273	1.50E-42
chr1:90766860-90843971:	Col6a3	12835	156.0	238.3	657.4	1.70641	0.036367	4.87388	1.72E-16
chr9:105990318-10609669	Col6a4	68553	115.3	190.6	697.8	1.83747	0.025983	6.77876	2.31E-20
chr9:105856070-10596064	Col6a5	665033	4.7	2.1	12.4	-1.74905	0.23339	2.74765	0.0034094
chr9:105689417-10582808	Col6a6	245026	11.7	9.9	14.8	-1.0498	0.819046	1.57965	0.0002116
chr9:108953745-10898487	Col7a1	12836	10.1	6.9	3.2	-1.29796	0.132508	-2.47271	1.74E-12
chr16:57624256-57754737	Col8a1	12837	6.7	4.1	2.8	-1.45187	0.021212	-1.88636	5.68E-07
chr4:121039566-12105532	Col9a2	12840	3.2	2.4	0.5	-1.158	0.786079	-4.11459	1.95E-05
chr18:9707648-9877995:+	Colec12	140792	180.7	159.8	63.6	-1.01619	0.899646	-2.26217	1.32E-32
chr8:71611024-71624911:	Colgalt1	234407	94.9	89.0	102.5	1.0517	0.492826	1.34918	7.85E-10
chr11:22899728-22982284	Commd1	17846	74.4	73.3	94.3	1.10105	0.500968	1.57774	1.56E-06
chr3:57644349-57651684:	Commd2	52245	19.3	19.5	27.7	1.13562	0.296678	1.78488	5.80E-12
chr9:57155041-57158299:	Commd4	66199	57.9	52.0	35.4	1.00013	0.99998	-1.30782	0.0024272
chr14:101633766-1016404	Commd6	66200	46.7	45.7	48.9	1.09294	0.451963	1.30459	0.0009871
chr2:153616930-15363278	Commd7	99311	23.0	21.4	24.8	1.04417	0.729118	1.34591	8.88E-05
chr8:70373548-70382066:	Comp	12845	3.9	0.9	0.9	-3.26492	0.000847	-2.99871	0.0002203
chr16:18406882-18426716	Comt	12846	84.8	81.4	77.5	1.07334	0.271414	1.14172	0.004617
chr14:21845861-21848910	Comtd1	69156	6.0	5.9	9.0	1.10313	0.573175	1.86212	7.37E-09
chr1:172082529-17212233	Copa	12847	232.7	222.3	303.7	1.07496	0.502409	1.62782	8.30E-12
chr7:114215559-11425468	Copb1	70349	121.6	135.7	213.0	1.25628	0.105521	2.16481	8.39E-14
chr9:98563731-98588375:	Copb2	50797	159.8	176.0	326.2	1.24002	0.072711	2.52826	5.33E-26
chr8:70302785-70312990:	Cope	59042	143.4	150.4	232.6	1.18303	0.207793	2.0124	1.81E-13
chr6:87887940-87913594:	Copg1	54161	101.4	96.7	145.4	1.07313	0.523225	1.78775	7.63E-16
chr6:30747554-30896794:	Copg2	54160	50.8	42.3	31.4	-1.0753	0.499671	-1.2884	0.0005456
chr2:125830302-12585908	Cops2	12848	119.3	122.8	159.9	1.15631	0.189399	1.66743	1.46E-10
chr11:59817804-59839767	Cops3	26572	104.7	111.9	177.2	1.20389	0.16013	2.09737	7.49E-15
chr5:100518309-10054780	Cops4	26891	95.7	112.6	151.1	1.32542	0.06014	1.95455	2.20E-09
chr1:10024600-10038159:	Cops5	26754	78.3	77.1	124.3	1.10704	0.419079	1.97055	1.25E-15
chr5:138161102-13816398	Cops6	26893	68.2	65.0	113.7	1.06801	0.442474	2.07705	1.91E-40
chr6:124958411-12496552	Cops7a	26894	58.9	54.4	81.1	1.03579	0.70783	1.72142	7.54E-23
chr1:86587100-86606500:	Cops7b	26895	20.3	18.6	23.9	1.03025	0.809088	1.47279	2.39E-08
chr1:90603425-90613341:	Cops8	108679	77.5	93.4	115.4	1.35966	0.056602	1.84136	5.09E-07
chr15:103272918-1032998	Copz1	56447	108.4	104.1	139.3	1.07606	0.419079	1.60017	1.43E-14
chr11:96849876-96861202	Copz2	56358	69.2	55.7	36.7	-1.11519	0.374157	-1.50392	2.37E-06
chr1:55052770-55072702:	Coq10b	67876	25.0	83.5	73.3	3.22562	0.003434	3.03568	0.0007871
chr5:100654726-10067425	Coq2	71883	62.5	56.9	66.7	1.00999	0.958794	1.33169	0.0044952
chr4:21879675-21912126:	Coq3	230027	11.1	10.0	11.0	1.00392	0.978239	1.23793	0.0040401
chr5:115279702-11529697	Coq5	52064	34.7	39.5	43.7	1.28201	0.068646	1.56919	1.15E-05
chr12:84361968-84373796	Coq6	217707	38.2	40.1	44.5	1.18064	0.186139	1.45509	4.24E-05
chr7:118525062-11853331	Coq7	12850	22.1	21.8	26.0	1.10193	0.492584	1.46825	3.62E-05
chr7:126699774-12670481	Coro1a	12721	48.1	50.6	74.2	1.15054	0.702226	1.84025	0.008328
chr5:113842439-11390870	Coro1c	23790	78.2	89.5	113.0	1.29394	0.186363	1.7819	5.58E-05
chr9:62419492-62537044:	Coro2b	235431	3.1	4.5	4.9	1.5997	0.109154	1.899	0.0039944
chr11:77463913-77469501	Coro6	216961	11.7	8.3	2.0	-1.24319	0.605692	-3.92128	8.86E-07
chr11:63962627-64079472	Cox10	70383	10.6	10.0	23.8	1.06601	0.699862	2.7806	1.40E-26
chr16:38346999-38352763	Cox17	12856	90.5	94.9	110.0	1.17243	0.131563	1.51363	5.82E-08
chr5:90214725-90223996:	Cox18	231430	17.6	16.2	28.9	1.0328	0.852026	2.03669	7.63E-15
chr5:139337822-13934516	Cox19	68033	44.7	52.4	54.9	1.32196	0.111198	1.52211	0.0015301
chr1:178319153-17832269	Cox20	66359	109.3	98.4	64.1	1.00405	0.97522	-1.36051	1.26E-05
chr2:152754173-15276503	Cox4i2	84682	5.4	3.9	1.8	-1.22842	0.465901	-2.22253	0.0001455
chr9:57521232-57532426:	Cox5a	12858	64.0	74.2	184.3	1.30701	0.259791	3.44302	1.10E-13
chr1:36691487-36693388:	Cox5b	12859	224.4	256.2	377.0	1.28272	0.013548	2.08987	1.21E-21
chr5:115345654-11534895	Cox6a1	12861	233.8	262.3	375.5	1.25821	0.009913	2.00035	4.14E-24
chr7:30616974-30626151:	Cox6b1	110323	339.9	355.6	432.0	1.1728	0.119671	1.58331	1.03E-09

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr7:4751792-4753094:-	Cox6b2	333182	30.3	17.1	9.2	-1.56486	0.010615	-2.57616	3.22E-11
chr15:35931976-35938246	Cox6c	12864	594.7	566.2	607.8	1.06186	0.502357	1.27554	5.24E-05
chr9:79755241-79759853:	Cox7a2	12866	175.1	188.5	246.7	1.20861	0.132786	1.75079	1.25E-09
chr17:83501917-83514333	Cox7a2l	20463	569.4	495.1	175.8	-1.03387	0.817102	-2.57246	6.90E-31
chrX:106015700-10602245	Cox7b	66142	123.0	124.2	187.8	1.13078	0.293475	1.89598	2.84E-15
chr5:71442823-71548205:	Cox7b2	78174	5.1	0.3	0.8	-6.70572	0.00014	-3.66984	0.0020165
chr13:86044798-86046795	Cox7c	12867	407.8	388.6	455.1	1.06386	0.659233	1.3896	0.000214
chr19:7215158-7217616:-	Cox8a	12868	329.6	380.1	421.2	1.29562	0.011807	1.59307	7.09E-09
chr12:102899306-1029005	Cox8c	75483	8.2	0.5	0.9	-6.01655	0.001037	-3.91293	0.0031995
chr3:20215616-20242181:	Cpa3	12873	15.5	12.1	7.2	-1.14007	0.64607	-1.70728	0.0040523
chr6:30611010-30631521:	Cpa5	74649	1.2	0.0	0.1	-6.211	0.001003	-4.90705	0.0006946
chr11:76777208-76847008	Cpd	12874	83.8	69.8	40.5	-1.07769	0.403414	-1.65157	2.43E-16
chr8:64592551-64693040:	Cpe	12876	352.3	291.1	138.7	-1.08968	0.57574	-2.01823	1.03E-12
chr7:81347026-81454758:	Cpeb1	12877	32.9	20.0	13.9	-1.47709	0.057795	-1.86034	7.71E-05
chr5:43233463-43289724:	Cpeb2	231207	6.8	5.8	9.8	-1.04231	0.861201	1.7885	9.60E-06
chr19:37021291-37207471	Cpeb3	208922	5.8	3.8	1.7	-1.38744	0.23634	-2.63516	1.54E-06
chr11:31870940-31935635	Cpeb4	67579	23.8	45.8	26.9	2.11034	0.00771	1.38346	0.175693
chr6:21985910-22255606:	Cped1	214642	305.0	249.4	101.7	-1.09677	0.480079	-2.37591	2.04E-23
chr13:54371349-54383917	Cplx2	12890	23.1	16.6	11.0	-1.24401	0.111266	-1.66707	6.48E-07
chr10:117629500-1176873	Cpm	70574	24.4	26.4	2.7	1.21874	0.374562	-6.8695	3.89E-35
chr2:156071841-15611196	Cpne1	266692	58.1	46.2	69.2	-1.12758	0.191993	1.48642	1.75E-09
chr8:94533028-94570529:	Cpne2	234577	14.0	12.4	8.0	-1.01674	0.942101	-1.39106	0.007116
chr17:29156521-29237790	Cpne5	240058	15.3	12.1	3.1	-1.10703	0.716916	-3.7132	2.54E-14
chr15:90487481-90679388	Cpne8	66871	9.4	9.2	13.9	1.08078	0.79805	1.80166	0.0010605
chr16:58670208-58680389	Cpox	12892	11.8	10.4	13.1	-1.01678	0.904243	1.38078	1.17E-05
chr15:33083129-33594552	Cpq	54381	75.2	73.0	35.1	1.07866	0.615147	-1.70947	3.23E-08
chr15:76595808-76607591	Cpsf1	94230	49.7	44.9	58.1	1.01628	0.897258	1.46144	1.88E-08
chr12:101975974-1020059	Cpsf2	51786	28.1	34.9	58.0	1.39937	0.060267	2.52559	3.39E-12
chr4:155869567-15588910	Cpsf3l	71957	31.9	32.9	42.0	1.1568	0.06642	1.64506	4.33E-18
chr5:145167213-14518204	Cpsf4	54188	35.1	40.7	45.6	1.31036	0.13947	1.60786	0.0005185
chr11:113698171-1137100	Cpsf4l	52670	2.0	0.5	0.2	-2.52134	0.088409	-4.57023	0.0002907
chr19:10525244-10547735	Cpsf7	269061	86.1	88.5	91.8	1.16104	0.24052	1.3316	0.0021308
chr19:3323301-3385733:+	Cpt1a	12894	55.0	42.9	23.5	-1.14727	0.332217	-1.86451	3.71E-10
chr7:44959372-44974851:	Cpt1c	78070	34.8	26.3	18.8	-1.18684	0.31778	-1.46614	0.0020379
chr2:130390775-13039762	Cpxm1	56264	45.5	31.1	12.6	-1.29754	0.096144	-2.84061	3.28E-19
chr7:132042810-13215474	Cpxm2	55987	22.8	19.5	9.2	-1.04378	0.826655	-1.9688	2.13E-09
chr5:35502218-35525626:	Cpz	242939	9.2	5.4	2.0	-1.4708	0.240526	-3.38942	4.17E-07
chr1:195103788-19513157	Cr1l	12946	117.2	108.2	67.6	1.02573	0.839501	-1.38522	5.94E-06
chr6:127577975-12762993	Cracr2a	381812	15.3	11.5	2.8	-1.1924	0.440597	-4.08558	9.31E-17
chr7:141461094-14146660	Cracr2b	213573	27.1	20.2	6.6	-1.20079	0.23566	-3.23001	1.84E-24
chr10:95174746-95324097	Cradd	12905	10.5	10.9	12.9	1.15719	0.260266	1.52139	3.07E-06
chr17:24961226-25015230	Cramp1l	57354	25.0	22.7	11.6	1.02344	0.894463	-1.71758	1.65E-08
chr2:30400476-30415748:	Crat	12908	34.3	23.3	15.0	-1.30291	0.036219	-1.80773	8.13E-10
chr6:106778245-10680008	Crbn	58799	73.0	65.6	28.2	-1.00208	0.989681	-2.06161	2.34E-21
chr5:130029306-13006078	Crcp	12909	28.4	28.0	48.4	1.10271	0.307385	2.11799	1.56E-32
chr1:64532804-64604548:	Creb1	12912	54.4	56.5	46.5	1.16201	0.001405	1.06825	0.109699
chr2:91982328-92024170:	Creb3l1	26427	3.5	4.7	15.3	1.47186	0.109769	5.09883	1.71E-21
chr3:90237500-90243512:	Creb3l4	78284	13.1	4.7	2.0	-2.33438	0.006122	-4.48865	2.40E-09
chr16:4084048-4213404:-	Crebbp	12914	85.1	82.2	52.6	1.08646	0.551086	-1.28873	0.0068617
chr6:134830199-13485788	Crebl2	232430	51.6	39.6	6.8	-1.17498	0.427763	-5.82086	3.59E-36
chr17:26715650-26776626	Crebrf	77128	121.3	106.2	20.3	-1.0303	0.88773	-4.66607	2.46E-42
chr1:39618406-39651182:	Creg2	263764	4.3	2.2	0.5	-1.68863	0.083654	-6.05989	1.31E-14
chr6:113483569-11349333	Creld1	171508	17.1	15.6	18.3	1.01908	0.901564	1.33334	0.0005052
chr15:88819646-88826681	Creld2	76737	38.6	74.8	249.0	2.12292	0.005978	7.12567	8.04E-20
chr17:78200248-78376592	Crim1	50766	38.0	37.9	17.0	1.12916	0.511066	-1.76641	4.61E-06
chr12:113140236-1131455	Crip2	68337	117.5	107.3	52.0	1.02883	0.851364	-1.79824	5.63E-12
chr17:40764734-40794146	Crisp2	22024	47.9	3.1	5.8	-8.5317	1.12E-06	-4.7098	6.62E-05
chr1:17727417-17766207:	Crispld1	83691	18.1	13.1	2.0	-1.23835	0.317657	-6.68804	1.46E-34

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:75679259-75708428	Crk	12928	81.1	95.1	111.2	1.32153	0.062918	1.69887	2.83E-06
chr16:17451985-17487440	Crkl	12929	43.8	49.1	50.8	1.26483	0.091477	1.44391	0.0004974
chr8:70493156-70504081:	Crlf1	12931	0.6	1.9	7.5	2.34819	0.14937	6.57691	1.77E-05
chr5:109554709-10955899	Crlf2	57914	12.8	15.5	14.7	1.35564	0.046398	1.42744	0.0025125
chr2:132846666-13286676	Crls1	66586	27.3	31.7	45.2	1.30432	0.093997	2.04076	9.83E-10
chr4:141016637-14106054	Crocc	230872	14.6	14.0	5.2	1.08882	0.737542	-2.16516	6.47E-07
chr5:8966048-8997146:-	Crot	74114	68.7	58.8	22.7	-1.0543	0.818704	-2.37603	7.16E-11
chr19:42283037-42431783	Crtac1	72832	0.3	0.9	20.6	2.58373	0.033826	39.7585	2.43E-29
chr9:40972798-41004628:	Crtam	54698	1.7	0.7	0.6	-2.1522	0.043206	-2.21073	0.0071395
chr10:85131700-85185054	Cry1	12952	23.4	27.4	40.5	1.32234	0.161557	2.12808	2.29E-07
chr16:59490775-59555752	Crybg3	224273	65.8	48.1	21.8	-1.23115	0.276639	-2.36411	1.97E-10
chr7:120186384-12020198	Crym	12971	2.4	1.2	0.4	-1.77686	0.098122	-3.91975	2.04E-06
chr3:154596711-15462318	Cryz	12972	21.0	21.3	22.0	1.1289	0.39705	1.30371	0.0089868
chr16:91689322-91728802	Cryzl1	66609	71.2	57.4	34.6	-1.11394	0.269269	-1.64193	1.09E-12
chr10:128337832-1283624	Cs	12974	106.8	102.1	202.6	1.07537	0.567341	2.35509	1.97E-26
chr15:102176998-1021890	Csad	246277	46.0	32.7	12.5	-1.25765	0.053701	-2.90828	3.98E-32
chr15:81936759-81950941	Csdc2	105859	17.0	15.6	2.6	1.0129	0.965422	-4.88001	9.84E-23
chr3:103020546-10305818	Csde1	229663	414.7	408.6	523.3	1.10605	0.225629	1.57326	1.94E-14
chr2:166906096-16694638	Cse1l	110750	68.0	92.5	130.4	1.53078	0.016079	2.34959	4.87E-10
chr3:107741048-10776046	Csf1	12977	20.5	31.9	52.7	1.71614	0.008294	3.08838	2.39E-12
chr11:98701313-98703629	Csf3	12985	3.3	6.4	0.6	1.94063	0.170404	-3.28226	0.0014808
chr8:68356781-68735146:	Csgalnact1	234356	8.0	6.8	2.4	-1.0563	0.650693	-2.70197	1.59E-32
chr6:118107452-11813914	Csgalnact2	78752	44.9	43.9	50.4	1.09192	0.153909	1.40095	2.37E-14
chr10:99757705-99759658	Csl	71832	3.1	0.2	0.6	-6.82746	3.33E-05	-3.10829	0.0042035
chr4:127988044-12856765	Csmd2	329942	0.1	0.0	1.7	-1.20087	0.732848	21.6943	1.13E-27
chr18:61555582-61588299	Csnk1a1	93687	329.8	489.3	554.6	1.66193	0.039963	2.03463	0.0001971
chr11:120961741-1209913	Csnk1d	104318	103.4	110.6	127.4	1.2087	0.223393	1.5324	0.0001758
chr15:79417852-79442057	Csnk1e	27373	53.1	47.4	30.6	1.00081	0.995321	-1.38424	4.78E-07
chr10:80622780-80640771	Csnk1g2	103236	90.1	86.5	95.8	1.07766	0.27483	1.32877	3.40E-09
chr18:53862113-53955684	Csnk1g3	70425	34.6	30.6	32.6	-1.0135	0.856073	1.17681	6.83E-05
chr2:152226840-15228185	Csnk2a1	12995	103.7	109.7	138.9	1.18872	0.064554	1.669	1.52E-13
chr8:95446096-95488820:	Csnk2a2	13000	20.8	21.9	25.9	1.18928	0.238473	1.54894	3.68E-05
chr17:35116195-35122053	Csnk2b	13001	91.3	81.2	138.5	1.00745	0.973355	1.88131	4.16E-08
chr16:64477811-64479134	Csnka2ip	224291	1.6	0.1	0.2	-4.67029	0.007884	-3.47018	0.0092215
chr9:56865104-56899870:	Cspg4	121021	21.4	17.6	10.3	-1.08226	0.703612	-1.63484	0.0001402
chr9:110243783-11026257	Cspg5	29873	5.3	4.8	1.5	-1.00244	0.994012	-2.729	4.74E-11
chr9:119971166-11998465	Csrnp1	215418	6.8	19.6	18.8	2.95552	0.000739	3.07765	3.26E-05
chr2:65845767-66031546:	Csrnp3	77771	8.7	34.3	8.2	3.45926	0.00847	1.13944	0.767081
chr1:135729197-13575222	Csrp1	13007	####	1271.0	1636.8	1.17275	0.268538	1.67659	4.82E-07
chr10:110920176-1109395	Csrp2	13008	94.3	62.7	41.4	-1.35147	0.006324	-1.81633	1.42E-11
chr2:144369032-14440767	Csrp2bp	228714	26.2	22.8	32.3	-1.02535	0.787963	1.53759	2.64E-16
chr2:148789361-14879343	Cst12	69362	3.8	0.2	0.5	-6.34491	0.000441	-4.08187	0.001486
chr2:148820099-14883041	Cst13	69294	3.2	0.1	0.3	-6.95461	0.000352	-4.48529	0.0012005
chr2:148871732-14887546	Cst3	13010	596.3	605.6	348.3	1.12892	0.339233	-1.36881	0.0005437
chr2:148798839-14880558	Cst8	13012	8.9	0.2	0.7	-11.6517	9.16E-07	-6.1568	2.67E-05
chr2:148835147-14883873	Cst9	13013	7.8	0.5	0.7	-6.73831	0.000221	-5.22984	0.0001727
chr10:78425670-78427622	Cstb	13014	115.3	200.1	607.0	1.87711	0.07975	5.51518	1.61E-10
chr2:172371003-17238108	Cstf1	67337	45.8	49.7	57.0	1.22222	0.128332	1.54922	7.71E-06
chrX:134059176-13408682	Cstf2	108062	21.1	22.5	37.4	1.19538	0.068197	2.20875	6.96E-29
chr19:31082841-31086592	Cstf2t	83410	59.2	59.5	89.4	1.13171	0.403427	1.87239	6.32E-10
chr2:104590484-10466542	Cstf3	228410	18.0	18.3	31.1	1.14156	0.216625	2.14862	1.40E-24
chrX:65047644-65049017:	Ctag2	70062	2.2	0.1	0.1	-6.27777	0.000943	-4.81121	0.0008487
chr12:59129746-59190220	Ctage5	217615	77.7	71.6	69.8	1.02909	0.669336	1.12267	0.0068219
chr5:33247723-33275004:	Ctbp1	13016	128.1	140.3	214.0	1.22949	0.016489	2.07952	5.83E-29
chr7:132987011-13312348	Ctbp2	13017	63.6	53.4	40.8	-1.06706	0.542036	-1.24397	0.0022944
chr3:146450467-14646584	Ctbs	74245	23.1	16.6	13.2	-1.24899	0.083884	-1.39414	0.0006999
chr11:69015911-69036473	Ctc1	68964	30.5	22.0	10.8	-1.24266	0.076677	-2.23127	2.27E-18
chr8:105636538-10568292	Ctcf	13018	73.6	74.6	80.8	1.13896	0.169371	1.36988	5.95E-06

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:69981168-69990600	Ctdnep1	67181	43.6	51.7	65.6	1.33482	0.010816	1.8705	9.66E-13
chr18:80407959-80469667	Ctdp1	67655	25.0	31.4	44.9	1.42252	0.090687	2.20054	3.86E-07
chr10:126978717-1269999	Ctdsp2	52468	198.2	157.5	81.1	-1.13454	0.543035	-1.92179	1.80E-06
chr9:118926536-11904411	Ctdspl	69274	25.8	21.4	14.1	-1.07513	0.437169	-1.4553	4.92E-09
chr10:24595442-24598682	Ctgf	14219	50.3	35.4	20.9	-1.27282	0.242174	-1.89913	1.79E-05
chr18:75431221-75697696	Ctif	269037	8.8	8.5	9.1	1.08755	0.565807	1.29802	0.0072137
chr13:60934155-60936625	Ctla2a	13024	89.9	104.0	127.8	1.27471	0.300206	1.73131	0.0011569
chr13:60895351-60897447	Ctla2b	13025	14.7	22.9	19.7	1.71581	0.011257	1.63652	0.0042581
chr18:35118912-35254775	Ctnna1	12385	238.6	231.6	267.8	1.09339	0.49094	1.39844	0.0001412
chr10:63430098-65003667	Ctnna3	216033	11.8	10.4	5.0	-1.01367	0.944526	-1.89158	6.71E-10
chr2:157737401-15789190	Ctnnbl1	66642	38.3	35.8	40.5	1.05008	0.630057	1.3236	1.22E-05
chr11:73183133-73199019	Ctns	83429	29.4	23.6	9.9	-1.11845	0.375234	-2.3483	5.45E-22
chr4:120539868-12057027	Ctps	51797	30.6	81.0	216.1	2.82895	3.70E-05	7.76492	5.76E-22
chrX:162901560-16303454	Ctps2	55936	36.5	33.6	13.5	1.02537	0.811986	-2.15462	2.20E-36
chr7:111028951-11105637	Ctr9	22083	79.8	141.0	154.8	1.97002	0.000875	2.35136	4.82E-07
chr2:164832872-16484103	Ctsa	19025	122.0	97.8	52.4	-1.11915	0.161316	-1.86022	1.46E-26
chr14:63122462-63145923	Ctsb	13030	348.3	397.3	704.5	1.2837	0.281204	2.4451	5.08E-08
chr7:142375916-14238787	Ctsd	13033	772.5	697.2	373.4	1.00448	0.987208	-1.6454	0.0005311
chr1:131638314-13167550	Ctse	13034	1.6	1.4	2.8	-1.06211	0.901623	2.04628	0.0068352
chr19:4855129-4860912:+	Ctsf	56464	116.4	78.2	9.3	-1.33348	0.065314	-9.54554	1.28E-80
chr9:90054267-90076095:	Ctsh	13036	112.1	104.3	69.4	1.03658	0.815442	-1.29289	0.0050301
chr3:95499210-95509387:	Ctsk	13038	40.3	31.0	15.4	-1.16105	0.412429	-2.06711	1.02E-08
chr13:64363214-64370306	Ctsl	13039	333.4	295.1	172.1	-1.01571	0.931546	-1.54848	5.61E-06
chr3:81932616-81956725:	Ctso	229445	40.2	34.5	13.3	-1.04826	0.767598	-2.38697	5.63E-20
chr19:5465240-5468498:-	Ctsw	13041	11.8	12.4	18.7	1.15537	0.663901	1.90499	0.0022052
chr6:18366477-18514825:	Cttnbp2	30785	10.0	9.2	4.3	1.01555	0.958351	-1.84018	8.23E-05
chr7:43672031-43678297:	Ctu1	233189	14.3	14.7	17.7	1.1547	0.219719	1.54841	1.33E-07
chr8:122476143-12248309	Ctu2	66965	12.8	25.0	51.7	2.1317	0.010917	4.52058	8.65E-11
chr8:4257646-4259274:-	Ctxn1	330695	30.6	21.9	9.3	-1.25615	0.241061	-2.5818	2.48E-11
chr11:88099146-88194140	Cuedc1	103841	36.4	28.2	22.8	-1.15123	0.177367	-1.2728	0.0019794
chr6:47454324-47526139:	Cul1	26965	162.7	176.3	195.1	1.22106	0.108036	1.49234	1.67E-05
chr18:3383225-3436700:+	Cul2	71745	31.9	33.7	45.6	1.18572	0.137391	1.77697	5.21E-12
chr1:80266818-80340430:	Cul3	26554	128.4	133.9	149.2	1.17248	0.087967	1.44962	9.14E-08
chr8:13105721-13147939:	Cul4a	99375	88.8	84.4	108.0	1.06868	0.475247	1.51882	1.58E-11
chr9:53614582-53667507:	Cul5	75717	39.0	43.4	69.0	1.25263	0.060626	2.19241	8.38E-19
chr17:46650338-46664364	Cul7	66515	39.7	32.1	22.2	-1.10776	0.366047	-1.41991	1.05E-05
chr17:46500609-46546388	Cul9	78309	20.4	16.1	5.9	-1.13334	0.160878	-2.74016	1.75E-52
chr2:34874436-34892133:	Cutal	77996	5.0	3.3	0.9	-1.35013	0.287494	-4.13617	3.30E-11
chr19:43753023-43768638	Cutc	66388	21.2	14.9	10.1	-1.27928	0.26258	-1.65326	0.0018165
chr5:136248135-13656749	Cux1	13047	30.8	30.4	34.5	1.10781	0.219719	1.39695	2.40E-08
chr5:121860216-12204782	Cux2	13048	3.6	2.5	1.0	-1.29692	0.068049	-2.8659	1.82E-19
chr9:14500619-14510620:	Cwc15	66070	127.8	134.6	146.2	1.18121	0.119632	1.42545	8.64E-06
chr2:77895653-77946356:	Cwc22	80744	42.2	41.8	57.6	1.11671	0.402432	1.70037	4.11E-09
chr13:104631327-1048169	Cwc27	67285	44.6	41.0	52.7	1.0313	0.816429	1.47588	2.72E-07
chr9:3404085-3479236:+	Cwf19l2	244672	52.4	48.0	37.0	1.02488	0.700937	-1.13387	0.0017912
chr5:90891245-90893115:	Cxcl1	14825	1.7	17.8	3.3	6.52111	4.23E-05	1.93233	0.117345
chr5:92346639-92348889:	Cxcl10	15945	8.3	15.9	15.8	1.94694	0.08074	2.16198	0.0087227
chr6:117168535-11718136	Cxcl12	20315	158.2	120.8	72.5	-1.17341	0.401988	-1.72036	4.70E-05
chr13:56288643-56296551	Cxcl14	57266	83.7	70.0	17.6	-1.07781	0.813364	-3.58929	2.73E-12
chr11:70454234-70459984	Cxcl16	66102	39.7	57.5	56.7	1.61046	0.008988	1.75025	0.0001328
chr1:128588199-12859229	Cxcr4	12767	41.1	17.3	5.1	-2.0505	0.031991	-5.5321	2.63E-11
chr9:123806477-12381175	Cxcr6	80901	16.1	37.1	78.7	1.89407	0.273978	3.71473	0.0020009
chrX:53642489-53643763:	Cxx1a	66158	21.4	21.2	38.7	1.10983	0.388348	2.24658	3.25E-25
chrX:53669177-53670408:	Cxx1b	553127	30.1	26.1	35.2	-1.02837	0.865181	1.45602	3.07E-05
chrX:53607922-53609134:	Cxx1c	72865	46.3	32.9	16.3	-1.25876	0.0723	-2.25215	1.33E-16
chr3:134236495-13426208	Cxxc4	319478	1.6	0.7	0.1	-1.95227	0.136089	-9.65481	1.08E-10
chr11:105933704-1059441	Cyb561	13056	17.1	18.5	20.4	1.20902	0.218406	1.48137	0.000468
chr19:10577157-10590041	Cyb561a3	225912	23.0	18.0	9.8	-1.15216	0.311042	-1.87455	2.83E-10

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr9:107539011-10754186	Cyb561d2	56368	9.0	7.6	9.7	-1.05785	0.756577	1.34574	0.0058095
chr11:69393612-69395346	Cyb5d1	327951	53.4	46.6	54.6	-1.02322	0.860676	1.27505	0.0007674
chr11:72777232-72795839	Cyb5d2	192986	16.9	12.5	5.6	-1.20878	0.279851	-2.38354	7.62E-12
chr9:87022029-87077774:	Cyb5r4	266690	42.0	44.9	49.5	1.19532	0.001444	1.47009	8.38E-18
chr15:76343523-76345934	Cyc1	66445	90.3	104.1	216.3	1.29882	0.033906	2.96287	1.48E-32
chr6:50562563-50566474:	Cycs	13063	15.3	30.0	83.0	2.14905	0.005104	6.06133	7.49E-17
chr2:76353942-76360453:	Cyct	13067	2.3	0.1	0.3	-5.74007	0.00172	-3.68392	0.0054563
chr11:116645595-1166543	Cygb	114886	113.8	113.6	56.5	1.12846	0.494385	-1.59791	9.85E-05
chr15:76643395-76660208	Cyhr1	54151	40.1	37.6	25.2	1.04919	0.531365	-1.27322	2.39E-06
chrX:111110418-11112387	Cylc1	67407	1.3	0.0	0.1	-7.24223	0.000298	-3.77667	0.0052438
chr4:51216678-51229928:	Cylc2	74914	3.5	0.1	0.4	-9.7984	3.88E-06	-4.32568	0.0005741
chr8:88697028-88751946:	Cyld	74256	35.8	29.6	18.4	-1.0918	0.516512	-1.55189	1.21E-06
chr9:58015017-58027023:	Cyp11a1	13070	2.9	0.4	0.6	-4.78944	0.000196	-3.10695	0.0013648
chr19:46667165-46673000	Cyp17a1	13074	5.3	0.4	1.0	-6.80278	9.31E-05	-3.07649	0.0083594
chr17:79706953-79715041	Cyp1b1	13078	5.6	4.9	1.2	-1.03268	0.95713	-3.10819	0.0003189
chr1:60343372-60387387:	Cyp20a1	77951	60.6	55.9	69.3	1.02861	0.801823	1.42897	2.76E-08
chr19:37697808-37701536	Cyp26a1	13082	3.7	3.6	0.2	1.06298	0.923231	-8.69776	2.08E-09
chr6:84571414-84593908:	Cyp26b1	232174	3.3	2.5	20.1	-1.16306	0.65352	6.96085	1.02E-21
chr1:74713574-74737890:	Cyp27a1	104086	140.4	111.8	15.5	-1.12607	0.252055	-7.14385	4.65E-145
chr10:127048246-1270530	Cyp27b1	13115	0.4	0.6	1.5	1.69291	0.209389	3.95107	2.30E-06
chr19:44005022-44029247	Cyp2c44	226143	1.5	0.6	0.1	-1.88868	0.187727	-6.72671	6.09E-07
chr15:82370527-82380260	Cyp2d22	56448	66.4	44.8	6.9	-1.33102	0.268313	-7.05281	1.06E-26
chr7:140763832-14077497	Cyp2e1	13106	52.0	11.9	6.5	-2.57726	0.104557	-3.44119	0.0056236
chr7:27119955-27133660:	Cyp2f2	13107	8.4	6.5	1.6	-1.13034	0.799369	-3.50724	1.47E-05
chr4:96516138-96553651:	Cyp2j6	13110	17.8	12.7	5.0	-1.26188	0.283036	-2.78117	3.75E-11
chr4:96568429-96591485:	Cyp2j9	74519	35.4	26.7	1.7	-1.19342	0.562732	-13.9804	3.88E-37
chr17:43667372-43751431	Cyp39a1	56050	24.5	16.5	2.7	-1.32785	0.164116	-6.87796	2.25E-36
chr5:145345270-14539051	Cyp3a57	622127	0.6	0.6	4.2	1.02355	0.967806	6.75486	1.56E-12
chr12:108334381-1083622	Cyp46a1	13116	3.9	2.3	0.4	-1.46368	0.144624	-5.9967	2.01E-15
chr4:115624728-11564770	Cyp4b1	13120	33.4	22.4	3.3	-1.33508	0.238473	-7.48671	6.87E-29
chr17:32924688-32947361	Cyp4f13	170716	42.2	28.8	10.3	-1.31053	0.007193	-3.24728	2.60E-45
chr17:32506462-32528894	Cyp4f17	208285	36.9	24.5	7.6	-1.35278	0.08384	-3.78391	1.18E-23
chr8:45305802-45333196:	Cyp4v3	102294	41.0	33.9	8.3	-1.09622	0.728493	-3.79429	1.00E-16
chr5:4080674-4104697:-	Cyp51	13121	17.3	20.6	99.8	1.33917	0.24031	6.69791	8.72E-28
chr3:17948444-17948952:	Cypt12	75439	14.6	0.8	1.1	-7.61849	6.77E-05	-5.78786	6.19E-05
chrX:105499772-10550063	Cypt2	245566	2.8	0.2	0.3	-5.72608	0.001144	-4.59528	0.0006863
chrX:153558593-15355942	Cypt3	69361	4.4	0.3	0.3	-3.56329	0.032092	-3.46618	0.0079606
chr12:24665838-24681795	Cys1	12879	52.3	24.8	5.3	-1.86921	0.00425	-7.28777	4.76E-29
chr2:25238819-25239897:	Cysrt1	67859	1.1	0.6	0.2	-1.44364	0.525971	-2.97325	0.0090095
chr5:37735519-37739820:	Cytl1	231162	6.7	5.0	1.0	-1.1811	0.558963	-4.79439	1.22E-12
chr11:96944146-96965060	D030028A08Rik	319371	9.2	9.0	25.7	1.08413	0.510844	3.44644	3.20E-63
chr10:78162067-78169768	D10Jhu81e	28295	80.9	66.3	48.4	-1.09769	0.504578	-1.33258	0.0027107
chr10:83360221-83368835	D10Wsu102e	28109	38.6	37.7	46.6	1.09618	0.586966	1.50138	0.0002329
chr11:113684412-1136946	D11Wsu47e	276852	26.3	27.0	32.8	1.1466	0.400131	1.55266	9.88E-05
chr5:143758354-14376494	D130017N08Rik	320064	5.6	2.6	1.7	-1.89546	0.013413	-2.54198	7.19E-06
chr12:101082451-1010889	D130020L05Rik	319760	2.4	1.3	0.8	-1.65741	0.099495	-2.15893	0.0011049
chr8:69271080-69303375:	D130040H23Rik	211135	16.9	12.3	4.3	-1.23849	0.458088	-2.9734	4.38E-08
chr15:58415468-58457801	D15Ertd621e	210998	77.1	84.4	90.5	1.234	0.166272	1.45778	0.0008789
chr16:78540336-78576688	D16Ertd472e	67102	15.4	15.4	20.8	1.1132	0.477369	1.68407	2.68E-07
chr17:27751232-27820542	D17Wsu92e	224647	66.7	69.3	89.6	1.17014	0.110121	1.67595	7.85E-13
chr19:27388702-27429820	D19Bwg1357e	52874	48.5	59.1	130.5	1.37354	0.030023	3.30392	1.01E-27
chr1:186967416-18697062	D1Pas1	110957	2.7	0.1	0.4	-10.1353	2.33E-06	-4.04974	0.0010657
chr1:93825240-93852174:	D2hgdh	98314	21.8	15.2	4.5	-1.28418	0.154753	-3.77144	4.96E-24
chr2:30173447-30178459:	D2Wsu81e	227695	36.9	35.0	54.6	1.06545	0.589663	1.84376	7.12E-17
chr17:24409481-24414513	D330041H03Rik	654822	18.9	12.1	2.9	-1.391	0.288031	-4.68017	7.15E-12
chr19:5388336-5390069:+	D330050I16Rik	414115	7.1	5.8	3.7	-1.09653	0.690366	-1.50441	0.0061763
chr3:41742615-41758941:	D3Ertd751e	73852	17.7	13.0	4.4	-1.21937	0.088695	-3.20585	2.61E-38
chr2:104143075-10441033	D430041D05Rik	241589	1.9	1.1	0.2	-1.57571	0.160502	-6.00876	4.18E-13

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr7:125707876-12587479	D430042O09Rik	233865	31.5	24.0	13.6	-1.16819	0.079493	-1.8371	3.12E-20
chr2:158182533-15822922	D630003M21Rik	228846	11.9	8.4	1.4	-1.27267	0.477365	-5.83598	2.09E-14
chr9:43259879-43280075:	D630033O11Rik	235302	3.3	1.9	0.7	-1.50492	0.298403	-3.23076	0.0001753
chr7:4467245-4470884:-	D630041G03Rik	320749	1.5	1.0	0.2	-1.26061	0.572925	-4.57537	1.88E-07
chr7:134266262-13437682	D7Ertd443e	71007	3.1	1.1	0.5	-2.30324	0.012087	-4.02568	2.67E-07
chr6:17197751-17205695:	D830026I12Rik	319682	7.0	5.2	1.0	-1.20204	0.512062	-4.9916	1.03E-14
chr4:123403601-12341191	D830031N03Rik	442834	31.4	23.9	13.4	-1.17719	0.219414	-1.86471	6.97E-11
chr8:84246235-84249761:	D8Ertd738e	101966	179.3	210.4	247.6	1.32116	0.035161	1.71555	8.14E-08
chr8:36094828-36147787:	D8Ertd82e	244418	13.1	11.7	16.5	-1.00037	0.999383	1.57149	0.0005451
chr3:83898287-84040161:	D930015E06Rik	229473	35.2	29.0	8.2	-1.07642	0.580489	-3.39129	3.47E-45
chr5:104525735-10455421	D930016D06Rik	100662	16.4	22.1	24.5	1.51426	0.019661	1.8414	1.10E-05
chr11:51650954-51657681	D930048N14Rik	97775	11.5	6.4	4.4	-1.60931	0.012071	-2.04354	2.07E-06
chr12:71831068-71992376	Daam1	208846	41.4	35.6	26.6	-1.04052	0.689843	-1.24317	0.0004756
chr17:49456022-49564337	Daam2	76441	16.4	11.6	3.3	-1.26807	0.183589	-3.81855	1.02E-24
chr2:35558458-35730994:	Dab2ip	69601	32.1	53.8	57.5	1.84306	0.078521	2.09228	0.0057922
chr14:97786846-98169765	Dach1	13134	11.4	8.8	1.8	-1.16112	0.46877	-4.90292	1.31E-28
chr12:71309884-71320107	Dact1	59036	17.1	8.0	3.1	-1.83743	0.113017	-3.7614	4.37E-06
chr7:16875317-16887301:	Dact3	629378	26.6	22.6	13.6	-1.04683	0.756094	-1.55196	9.04E-07
chr14:54235485-54253929	Dad1	13135	31.4	32.6	46.7	1.16416	0.075136	1.85331	2.33E-23
chr1:130388528-13042299	Daf2	13137	5.3	1.0	0.8	-3.82272	0.000805	-4.2267	1.86E-05
chr9:108569892-10857277	Dalrd3	67789	98.4	85.1	41.3	-1.03068	0.750702	-1.8992	4.33E-29
chr5:74093083-74094336:	Dancr	70036	15.9	23.4	63.8	1.64408	0.022711	4.74892	1.57E-21
chr15:31224385-31274338	Dap	223453	42.4	33.1	28.8	-1.1475	0.079976	-1.17634	0.007036
chr13:60601947-60763191	Dapk1	69635	67.8	80.4	36.9	1.33381	0.025909	-1.46045	0.0001845
chr9:66158226-66272242:	Dapk2	13143	32.3	28.9	4.1	-1.00022	0.999723	-6.10063	2.72E-56
chr10:81183007-81193197	Dapk3	13144	26.1	31.3	43.6	1.3514	0.045757	2.06616	1.16E-10
chr1:128363707-12841741	Dars	226414	115.9	108.7	182.6	1.04614	0.716406	1.95778	1.10E-19
chr1:161040613-16107063	Dars2	226539	13.0	10.1	5.8	-1.15916	0.4022	-1.75795	5.43E-06
chr1:83159762-83210572:	Daw1	71227	1.2	0.6	0.1	-1.59469	0.454821	-4.70402	0.000495
chr10:80264991-80288413	Dazap1	70248	46.0	47.5	64.7	1.16429	0.296903	1.74669	5.31E-08
chr15:100615662-1006207	Dazap2	23994	210.2	188.4	123.0	1.00444	0.973597	-1.36625	9.86E-06
chr17:50279393-50293620	Dazl	13164	2.5	0.2	0.3	-6.84313	0.000119	-4.23453	0.0007777
chr2:27165507-27183204:	Dbh	13166	0.1	0.7	4.5	3.58181	0.021638	15.9658	5.89E-11
chr11:76217613-76218665	Dbil5	13168	42.1	3.1	5.0	-8.193	1.66E-07	-5.06957	3.61E-06
chr8:123504718-12351545	Dbndd1	72185	1.1	0.3	0.1	-2.72712	0.047519	-6.71494	2.56E-06
chr11:5788483-5800980:+	Dbnl	13169	59.8	61.7	96.4	1.16369	0.25027	2.00186	7.04E-14
chr7:45705247-45710203:	Dbp	13170	207.1	69.0	17.1	-2.54262	0.003182	-7.96937	3.31E-16
chr12:74297474-74300468	Dbpht2	386753	0.4	0.5	1.8	1.34579	0.495174	5.16859	1.15E-09
chr9:99575799-99584343:	Dbr1	83703	21.7	29.3	32.2	1.51707	0.074865	1.81355	0.0008467
chr3:116513079-11654998	Dbt	13171	33.4	28.9	38.8	-1.0406	0.818704	1.4461	0.0002538
chr4:45342101-45379722:	Dcaf10	242418	15.0	16.4	19.1	1.23547	0.154621	1.58296	2.94E-05
chr14:55560029-55570065	Dcaf11	28199	61.0	49.5	36.3	-1.10434	0.294832	-1.34081	1.52E-05
chr4:41291300-41314901:	Dcaf12	68970	47.8	45.6	26.7	1.06864	0.349288	-1.43103	7.47E-13
chr15:39112874-39146855	Dcaf13	223499	58.4	66.8	105.8	1.29026	0.094547	2.23721	5.81E-13
chr2:71055744-71099142:	Dcaf17	75763	17.9	12.3	7.1	-1.31295	0.186363	-1.97383	6.98E-06
chr12:83520466-83541992	Dcaf4	73828	28.3	20.1	9.1	-1.26955	0.306078	-2.40318	1.43E-07
chr1:165329501-16546046	Dcaf6	74106	71.1	58.2	27.6	-1.09361	0.26968	-2.05463	4.83E-36
chr11:106036872-1060593	Dcaf7	71833	54.6	51.6	60.2	1.06535	0.562657	1.37824	7.01E-06
chr1:172148015-17219639	Dcaf8	98193	188.8	146.6	92.6	-1.15706	0.172304	-1.62321	4.71E-10
chr11:102994056-1030171	Dcakd	68087	22.7	19.4	27.6	-1.04613	0.704148	1.51576	1.97E-09
chr16:58408535-58469745	Dcbld2	73379	33.1	46.1	59.7	1.56428	0.045755	2.18983	4.40E-06
chr18:71253632-72351069	Dcc	13176	2.3	1.6	0.2	-1.31727	0.511263	-8.47167	1.33E-13
chr13:25056004-25210706	Dcdc2a	195208	1.6	1.6	0.5	1.08139	0.855365	-2.42392	0.000376
chr4:129608331-12961425	Dcdc2b	1.01E+08	28.1	16.0	6.0	-1.54511	0.184644	-3.37351	5.71E-07
chr7:105752989-10578755	Dchs1	233651	41.6	32.4	18.6	-1.15197	0.383618	-1.77623	3.62E-07
chr5:88765013-88783277:	Dck	13178	7.8	8.6	9.0	1.22781	0.188788	1.42758	0.0019795
chr3:55242526-55539068:	Dclk1	13175	10.1	10.8	35.5	1.17515	0.395448	4.25409	1.12E-29
chr3:103800605-10380938	Dclre1b	140917	8.1	10.2	11.7	1.42263	0.007385	1.80279	1.31E-08

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr2:3424131-3461116:+	Dclre1c	227525	9.1	7.9	5.4	-1.02591	0.861354	-1.34007	0.0004828
chr10:97479500-97518162	Dcn	13179	####	3768.4	1039.0	1.00084	0.996946	-3.1798	3.14E-35
chr14:30479565-30527056	Dcp1a	75901	28.2	27.4	31.6	1.09526	0.42375	1.39811	1.93E-05
chr6:119175253-11922161	Dcp1b	319618	25.7	17.1	12.7	-1.34934	0.170404	-1.58764	0.0049415
chr3:89350235-89365239:	Dcst1	77772	1.2	0.1	0.2	-5.29393	0.000661	-2.89837	0.0089666
chr8:48099092-48141667:	Dctd	320685	7.8	6.3	14.8	-1.09465	0.560102	2.36894	2.55E-20
chr10:127266262-1272819	Dctn2	69654	160.8	134.5	159.4	-1.07134	0.273058	1.23833	1.51E-06
chr4:41714798-41723163:	Dctn3	53598	39.4	46.7	42.9	1.32733	0.000673	1.35866	1.06E-05
chr18:60526221-60558762	Dctn4	67665	99.9	97.7	91.6	1.09461	0.15368	1.14611	0.0042983
chr7:127256959-12726066	Dctpp1	66422	34.1	38.1	59.8	1.24781	0.14493	2.16572	8.73E-13
chr3:35892105-35932966:	Dcun1d1	114893	35.9	37.3	43.2	1.1714	0.224162	1.49782	1.85E-05
chr8:13255963-13288126:	Dcun1d2	102323	22.3	23.9	24.3	1.19754	0.0024	1.36148	6.71E-11
chr7:119853163-11989574	Dcun1d3	233805	14.9	16.7	17.5	1.26415	0.111162	1.46197	0.0006311
chr5:73481055-73560794:	Dcun1d4	100737	20.1	16.7	11.9	-1.07356	0.514537	-1.34667	5.43E-05
chr9:7184566-7207031:+	Dcun1d5	76863	101.8	116.0	150.1	1.28511	0.117505	1.82481	4.28E-07
chr11:120725373-1207272	Dcxr	67880	71.1	57.2	28.8	-1.11226	0.726992	-1.92009	0.0005533
chr8:71469194-71476097:	Dda1	66498	26.0	33.4	50.5	1.4495	0.039443	2.38483	1.42E-10
chr3:145758692-14589427	Ddah1	69219	2.2	1.9	6.3	-1.01774	0.952617	3.48968	2.96E-19
chr17:35059035-35062099	Ddah2	51793	95.4	82.2	43.6	-1.03271	0.867017	-1.74148	2.54E-07
chr19:10605625-10629821	Ddb1	13194	284.4	264.4	333.4	1.04702	0.697735	1.46256	1.51E-07
chr2:91211582-91237066:	Ddb2	107986	48.6	41.7	12.5	-1.03997	0.710888	-3.07102	2.76E-61
chr9:6265028-6266547:-	Ddi1	71829	4.8	0.3	0.5	-8.82086	3.00E-06	-5.4264	2.57E-05
chr4:141683563-14172341	Ddi2	68817	20.4	20.3	24.4	1.12432	0.410845	1.49036	5.18E-05
chr7:92857527-92874232:	Ddias	74041	4.2	3.0	5.3	-1.22664	0.400478	1.57236	0.0072448
chr10:127290793-1272962	Ddit3	13198	81.5	68.1	125.4	-1.06934	0.499573	1.92036	2.51E-25
chr10:40630011-40649931	Ddo	70503	24.3	16.9	4.4	-1.28495	0.291665	-4.16094	3.80E-17
chr4:138304738-13831261	Ddost	13200	148.3	137.4	245.8	1.0368	0.655624	2.06979	3.91E-50
chr1:169972307-17008894	Ddr2	18214	140.2	112.4	68.0	-1.12695	0.549159	-1.63359	0.0002137
chr2:130654083-13066464	Ddrgk1	77006	167.6	131.1	77.7	-1.14569	0.53036	-1.70777	0.0002376
chr10:75771233-75773374	Ddt	13202	56.8	36.9	26.4	-1.36508	0.02253	-1.70511	5.81E-07
chr12:13219307-13249174	Ddx1	104721	122.9	119.9	225.7	1.09449	0.317909	2.28628	7.27E-41
chr9:53098454-53248112:	Ddx10	77591	38.9	39.3	56.7	1.1334	0.09751	1.82073	1.81E-28
chr1:121553835-12156798	Ddx18	66942	46.4	56.8	109.7	1.37859	0.025163	2.90858	4.56E-23
chr8:110974991-11099782	Ddx19a	13680	32.3	32.3	42.0	1.12373	0.217849	1.62651	2.57E-13
chr8:111003186-11103175	Ddx19b	234733	14.5	11.4	19.8	-1.13712	0.237247	1.7007	2.64E-12
chr3:105678462-10568757	Ddx20	53975	39.5	42.8	50.4	1.22622	0.346595	1.57708	0.0033312
chr10:62580247-62602298	Ddx21	56200	51.7	98.9	326.6	2.09621	0.008764	6.94316	1.63E-18
chr15:98645507-98662889	Ddx23	74351	103.0	100.3	123.9	1.09495	0.296229	1.50425	1.67E-11
chr12:103407976-1034258	Ddx24	27225	84.3	102.2	128.0	1.36946	0.154607	1.86304	0.0001569
chr9:35541848-35558470:	Ddx25	30959	9.7	1.0	4.3	-6.18584	2.05E-06	-1.66454	0.142968
chrX:56454839-56507843:	Ddx26b	236790	148.2	128.4	27.8	-1.02895	0.844513	-4.21314	9.24E-71
chr2:167015313-16703494	Ddx27	228889	48.4	55.9	109.9	1.30368	0.078527	2.80063	1.06E-20
chr8:106009616-10601148	Ddx28	71986	14.5	17.6	22.4	1.36359	0.073134	1.90498	5.59E-07
chr2:28840406-28905575:	Ddx31	227674	14.7	21.0	40.3	1.60926	0.020696	3.31681	2.13E-14
chr8:83715177-83723351:	Ddx39	68278	35.8	47.9	166.5	1.50343	0.063216	5.49009	3.86E-26
chr17:35241746-35253707	Ddx39b	53817	235.9	223.3	356.4	1.06076	0.416174	1.88828	1.90E-39
chrX:13281022-13293983:	Ddx3x	13205	402.1	546.6	763.1	1.5273	0.043767	2.30655	1.55E-07
chr13:112598333-1126523	Ddx4	13206	7.0	1.2	2.2	-4.29769	0.00017	-2.28475	0.014344
chr13:55530410-55536658	Ddx41	72935	54.5	57.3	63.1	1.18565	0.257027	1.43884	0.0008382
chr11:106216926-1062491	Ddx42	72047	95.2	97.6	120.5	1.15679	0.293318	1.5748	3.98E-06
chr13:55634999-55681267	Ddx46	212880	66.1	62.2	73.7	1.05832	0.597926	1.39263	1.72E-06
chr8:70292866-70302452:	Ddx49	234374	39.8	47.4	85.2	1.3438	0.071414	2.62835	1.19E-15
chr10:62616023-62651198	Ddx50	94213	115.3	125.9	205.0	1.22902	0.081352	2.20473	8.41E-20
chr5:110653451-11066049	Ddx51	69663	15.5	19.1	24.9	1.39406	0.116492	1.97581	1.69E-05
chr11:83942090-83963086	Ddx52	78394	58.9	63.5	68.9	1.21408	0.182924	1.45455	0.0005015
chr5:120613130-12062859	Ddx54	71990	30.9	40.0	68.2	1.46181	0.027981	2.70815	2.61E-14
chr5:124552864-12456966	Ddx55	67848	14.8	13.7	26.5	1.03967	0.741675	2.23245	6.05E-34
chr11:6257545-6267729:-	Ddx56	52513	44.0	53.0	90.4	1.35959	0.060626	2.52976	2.13E-14

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr4:40203777-40239825:	Ddx58	230073	41.3	41.6	22.1	1.1241	0.424002	-1.48573	0.0001086
chr8:61928087-62037701:	Ddx60	234311	22.1	18.3	4.8	-1.09263	0.775894	-3.49545	1.12E-11
chr7:141297176-14133878	Deaf1	54006	29.1	23.0	16.0	-1.13642	0.37658	-1.4461	0.0003165
chr9:121710389-12171292	Deb1	26901	36.3	31.4	43.4	-1.03084	0.860765	1.4942	1.54E-05
chr4:15917240-15945507:	Decr1	67460	53.2	40.0	19.9	-1.20117	0.245287	-2.11836	2.94E-11
chr17:26081211-26090164	Decr2	26378	38.1	30.5	17.2	-1.12635	0.45764	-1.7522	3.42E-07
chr7:25202840-25219859:	Dedd2	67379	18.5	20.4	6.1	1.23089	0.109962	-2.38966	2.10E-17
chr8:123442956-12346389	Def8	23854	19.0	15.9	21.0	-1.06704	0.389075	1.38098	9.97E-11
chr1:182275770-18228275	Degs1	13244	115.1	111.5	177.7	1.0844	0.437323	1.91781	8.29E-21
chr2:37798990-38287384:	Dennd1a	227801	34.6	27.7	20.8	-1.11421	0.383509	-1.32188	0.0015285
chr4:86748555-86850602:	Dennd4c	329877	68.0	59.5	66.0	-1.02222	0.727681	1.21226	4.51E-07
chr14:26573858-26634322	Dennd6a	211922	39.4	30.8	20.3	-1.154	0.278866	-1.5485	3.73E-06
chr5:123907275-12392883	Denr	68184	38.7	35.4	75.5	1.03015	0.851797	2.41968	9.43E-25
chr5:32863721-32994233:	Depdc5	277854	18.3	15.8	10.1	-1.03807	0.670404	-1.4419	2.50E-11
chr15:55112317-55259273	Deptor	97998	36.7	29.5	3.0	-1.11954	0.638854	-9.1339	6.52E-49
chr15:57869502-57892418	Derl1	67819	90.4	86.8	104.7	1.07502	0.435254	1.4426	5.62E-09
chr11:71007440-71019841	Derl2	116891	25.9	25.0	34.7	1.08414	0.337901	1.67423	1.84E-19
chr1:75360292-75368579:	Des	13346	309.2	332.4	626.8	1.19623	0.293236	2.48173	2.35E-14
chr1:178187417-17825259	Desi2	78825	29.3	30.1	34.3	1.15342	0.023585	1.46123	1.08E-15
chr7:78827474-78847211:	Det1	76375	16.0	13.2	17.1	-1.08677	0.577976	1.32743	0.0035297
chr16:10530207-10543054	Dexi	58239	30.8	26.6	17.2	-1.02785	0.858309	-1.42775	5.24E-05
chr4:153964449-15397508	Dffb	13368	13.0	10.4	7.1	-1.11466	0.456982	-1.46168	0.0002043
chr6:50207403-50261769:	Dfna5	54722	4.4	3.6	1.5	-1.10587	0.798752	-2.17858	0.0012594
chr16:17840356-17891728	Dgcr2	13356	75.8	78.7	82.5	1.17311	0.235024	1.35953	0.0018611
chr16:18052860-18071632	Dgcr6	13353	30.7	23.6	19.7	-1.16254	0.142332	-1.24464	0.0048651
chr16:18253965-18289168	Dgcr8	94223	45.0	43.2	45.1	1.08027	0.47236	1.25325	0.0023095
chr12:37880705-38633410	Dgkb	217480	9.1	7.3	1.8	-1.10792	0.47152	-3.95844	9.53E-41
chr16:22466569-22657231	Dgkg	110197	2.3	2.3	4.2	1.12373	0.677259	2.23853	2.43E-06
chr14:78569609-78725089	Dgkh	380921	38.2	25.3	20.2	-1.3474	0.003096	-1.50445	6.63E-07
chr6:36846022-37299976:	Dgki	320127	8.3	7.7	2.5	1.02723	0.897269	-2.60317	4.00E-16
chr6:83480214-83506969:	Dguok	27369	77.0	66.3	41.5	-1.04515	0.767606	-1.48097	1.45E-05
chr4:106561038-10658911	Dhcr24	74754	5.9	11.8	43.8	2.15926	0.017355	7.80968	1.13E-16
chr4:133969057-13400086	Dhdds	67422	33.8	28.7	36.5	-1.05445	0.616247	1.34912	8.01E-06
chr7:45473563-45488796:	Dhdh	71755	22.7	14.1	4.8	-1.4393	0.127585	-3.60412	5.92E-13
chr13:92354783-92389053	Dhfr	13361	5.7	5.3	2.5	1.03475	0.906894	-1.80058	0.0003171
chr15:98893027-98898540	Dhh	13363	1.6	1.7	6.0	1.19994	0.706458	3.9351	2.50E-06
chr8:85071757-85075161:	Dhps	330817	31.9	28.7	38.2	1.01012	0.942093	1.49527	4.95E-09
chr14:55739020-55745684	Dhrs1	52585	44.6	34.6	20.0	-1.15866	0.313091	-1.77777	3.37E-08
chr11:84820728-84829003	Dhrs11	192970	9.4	9.9	13.9	1.18425	0.351311	1.83291	9.32E-07
chr11:78032313-78037864	Dhrs13	70451	6.8	7.9	13.6	1.31007	0.152278	2.46075	1.62E-11
chr4:144892827-14492764	Dhrs3	20148	110.9	127.6	44.3	1.27762	0.087965	-1.99064	1.49E-10
chr12:72650353-72664828	Dhrs7	66375	68.5	51.6	20.1	-1.19721	0.298011	-2.6785	1.06E-15
chr2:69380462-69403086:	Dhrs9	241452	1.9	3.4	7.3	1.86472	0.124566	3.92852	5.47E-06
chr4_GL456216_random:15	Dhrsx	236082	11.1	12.2	22.0	1.24269	0.150795	2.4516	5.35E-17
chr2:5898060-5942792:-	Dhtkd1	209692	14.6	7.6	1.7	-1.69145	0.041991	-6.36537	1.77E-20
chr5:52150203-52190546:	Dhx15	13204	158.7	195.5	261.2	1.38842	0.035838	2.03209	2.41E-09
chr17:35879778-35892668	Dhx16	69192	54.2	56.4	62.5	1.17365	0.134909	1.44081	3.97E-06
chr13:112927793-1129691	Dhx29	218629	18.1	20.9	50.8	1.29959	0.058391	3.45446	9.31E-35
chr9:110084319-11011761	Dhx30	72831	63.2	63.9	86.3	1.14139	0.262548	1.70452	1.52E-10
chr7:133720935-13378278	Dhx32	101437	31.5	33.4	38.8	1.19571	0.271876	1.52871	0.0002931
chr11:70984091-71004432	Dhx33	216877	31.8	36.2	51.5	1.28366	0.093966	2.00364	2.70E-10
chr7:16197221-16222032:	Dhx34	71723	16.5	12.0	8.0	-1.23731	0.226251	-1.63387	0.0001429
chr3:62468642-62506988:	Dhx36	72162	68.4	63.1	76.7	1.03205	0.658083	1.40089	1.22E-14
chr5:125414404-12543404	Dhx37	208144	16.9	21.7	30.7	1.45386	0.028875	2.24199	5.77E-10
chr8:109548024-10956560	Dhx38	64340	41.2	39.4	45.6	1.08231	0.631013	1.38199	0.0024062
chr11:86768849-86807660	Dhx40	67487	59.4	51.3	24.2	-1.04034	0.725676	-1.95476	7.30E-23
chr17:80238304-80290476	Dhx57	106794	45.0	35.6	22.4	-1.13504	0.244431	-1.59708	1.87E-09
chr11:101732956-1017673	Dhx8	217207	43.6	45.3	47.6	1.17281	0.276137	1.36386	0.0035811

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr1:153455758-15348766	Dhx9	13211	91.6	105.5	139.1	1.2978	0.033826	1.88616	9.08E-12
chr5:123511330-12352416	Diablo	66593	85.0	88.7	90.5	1.17367	0.082373	1.33009	3.89E-05
chr18:37844825-37935411	Diap1	13367	29.7	28.6	32.3	1.07456	0.49094	1.35407	1.54E-05
chrX:129749742-13046583	Diap2	54004	29.2	24.9	15.2	-1.04903	0.651563	-1.53336	1.23E-10
chr1:193104403-19313025	Diexf	215193	15.1	16.9	22.2	1.25376	0.006956	1.83389	7.96E-21
chr13:106947129-1069602	Dimt1	66254	30.2	35.2	47.9	1.31443	0.06415	1.96653	7.30E-10
chr4:107291465-10730714	Dio1	13370	6.7	7.9	1.3	1.23604	0.713766	-3.11544	0.0018321
chr12:90724552-90738438	Dio2	13371	72.2	111.9	378.3	1.63929	0.101859	5.79706	2.34E-15
chr12:110279230-1102810	Dio3	107585	4.4	12.9	7.8	3.13185	3.26E-06	2.13394	0.0005483
chr12:110275385-1102780	Dio3os	353504	28.9	25.8	7.5	-1.02168	0.963697	-2.81454	4.87E-05
chr10:76263049-76345291	Dip2a	64451	32.4	25.7	19.0	-1.12893	0.277736	-1.35957	0.0001369
chr16:35694903-35769356	Dirc2	224132	29.1	25.1	11.0	-1.03963	0.657272	-2.10616	1.18E-40
chr14:99076634-99099770	Dis3	72662	36.7	43.7	79.1	1.3419	0.055741	2.64938	1.09E-17
chr9:64306756-64341257:	Dis3l	213550	25.2	23.9	28.4	1.07082	0.617452	1.40743	0.0001031
chr8:125054195-12526115	Disc1	244667	4.1	3.1	1.9	-1.16602	0.512724	-1.65105	0.002179
chr9:50662753-50727984:	Dixdc1	330938	30.7	22.3	4.3	-1.23467	0.164836	-5.60722	9.28E-54
chrX:75095854-75109776:	Dkc1	245474	38.0	37.8	99.5	1.11209	0.271273	3.24667	5.20E-73
chr7:112116019-11215905	Dkk3	50781	96.0	90.2	16.2	1.04323	0.807291	-4.65403	1.11E-53
chr7:45207525-45211883:	Dkkl1	50722	24.7	3.6	6.7	-4.51007	0.000223	-2.48068	0.0103092
chr9:50634633-50659780:	Dlat	235339	28.9	27.6	32.7	1.07019	0.491946	1.41517	1.16E-07
chr12:31331562-31351471	Dld	13382	99.9	112.2	151.1	1.26572	0.085201	1.87512	5.91E-10
chr9:119102478-11914769	Dlec1	320256	2.1	1.3	0.4	-1.45795	0.10019	-4.50506	2.14E-15
chr14:61602836-61682373	Dleu2	668253	27.0	23.2	12.1	-1.041	0.700367	-1.78516	3.38E-18
chr14:62276229-62292979	Dleu7	239133	3.3	2.8	11.6	-1.07169	0.816964	4.18308	1.83E-21
chr7:91090786-92449246:	Dlg2	23859	1.2	0.9	0.2	-1.18538	0.467665	-4.37112	1.76E-15
chrX:100767722-10081841	Dlg3	53310	29.9	28.7	18.0	1.08112	0.605706	-1.32479	0.0049366
chr2:156613697-15676436	Dlgap4	228836	19.4	18.9	21.2	1.09677	0.444607	1.36619	0.0001744
chr17:15367354-15375823	Dll1	13388	4.3	7.0	10.7	1.8071	0.045068	2.91307	1.80E-06
chr2:119325784-11933566	Dll4	54485	14.6	15.3	5.4	1.18659	0.46411	-2.11526	3.50E-06
chr12:85110833-85134091	Dlst	78920	99.0	114.2	160.1	1.30259	0.076296	2.00191	3.92E-10
chr6:6863334-6867970:+	Dlx6	13396	27.2	17.4	14.4	-1.39376	0.103108	-1.49901	0.0096505
chr6:6820546-6869533:-	Dlx6os1	320038	10.7	5.7	4.2	-1.66354	0.059052	-1.9666	0.0011108
chr4:117674686-11768222	Dmap1	66233	53.1	48.6	54.4	1.02683	0.84913	1.27702	0.0020229
chr15:79561498-79605109	Dmc1	13404	3.5	2.8	1.5	-1.08529	0.770194	-1.79235	0.0010174
chrX:82948870-85205050:	Dmd	13405	156.7	138.3	86.3	-1.01407	0.950142	-1.44192	0.0020247
chr4:89688198-89694766:	Dmrta1	242523	1.1	1.1	4.8	1.17935	0.541907	5.45473	1.59E-26
chr4:107676290-10768416	Dmrtb1	56296	6.2	0.2	0.9	-10.6417	1.87E-06	-3.61195	0.0032609
chrX:102903221-10290868	Dmrtc1a	70887	2.3	1.0	0.3	-1.89272	0.134842	-4.22516	2.02E-05
chr7:24870057-24877651:	Dmrtc2	71241	1.6	0.1	0.1	-4.76346	0.006289	-4.34263	0.0016364
chr14:70602184-70636048	Dmtn	13829	7.0	5.2	2.1	-1.18427	0.325861	-2.61109	1.57E-14
chr18:49832997-49965473	Dmxl1	240283	60.7	65.2	63.0	1.20531	0.001359	1.2959	7.26E-08
chr10:62947029-62974188	Dna2	327762	4.6	4.2	5.3	1.01675	0.941476	1.42721	0.0021644
chr8:119575235-11959845	Dnaaf1	68270	8.6	0.3	1.1	-13.1407	1.30E-09	-4.67973	3.20E-05
chr7:4522957-4532442:-	Dnaaf3	436022	6.1	3.8	2.0	-1.4231	0.154824	-2.33978	6.48E-06
chr5:139150223-13918650	Dnaaf5	433956	9.1	10.9	13.5	1.35224	0.075726	1.84276	1.41E-06
chr14:31260375-31323896	Dnah1	110084	2.4	0.9	0.3	-2.32793	0.000131	-5.09623	2.46E-17
chr11:118021723-1181292	Dnah17	69926	2.5	0.3	1.2	-5.99693	5.30E-08	-1.60185	0.119283
chr11:69420809-69549108	Dnah2	327954	2.7	1.3	0.3	-1.80679	0.024004	-5.69843	3.68E-17
chr15:28203766-28472045	Dnah5	110082	2.0	2.0	0.1	1.08341	0.738252	-9.88572	6.95E-42
chr1:53397002-53706784:	Dnah7a	627872	1.2	0.2	0.2	-5.13648	0.00015	-4.71508	2.72E-05
chr1:46066738-46373550:	Dnah7b	227058	13.6	8.8	1.7	-1.37696	0.041529	-6.30178	3.35E-53
chr17:30626936-30875264	Dnah8	13417	11.7	2.4	1.6	-3.83708	3.70E-05	-4.78927	2.16E-08
chr4:41569794-41638158:	Dnaic1	68922	1.6	0.3	0.2	-3.47543	0.007369	-4.4647	7.77E-05
chr11:114727412-1147578	Dnaic2	432611	2.0	0.6	0.5	-2.55515	0.0186	-2.61758	0.0023551
chr4:40722468-40737151:	Dnaja1	15502	116.0	178.1	140.7	1.71943	0.001105	1.50116	0.004127
chr8:85537640-85555271:	Dnaja2	56445	91.1	113.4	157.6	1.40455	0.063305	2.12626	3.86E-08
chr16:4684070-4707693:+	Dnaja3	83945	44.8	47.7	68.8	1.1989	0.116718	1.9125	1.44E-14
chr8:83608175-83611903:	Dnajb1	81489	40.9	88.3	53.0	2.33714	0.004806	1.5625	0.0812904

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr16:22857845-22879634	Dnajb11	67838	28.1	40.9	136.5	1.63142	0.01832	5.7326	1.57E-28
chr10:59879591-59898016	Dnajb12	56709	33.8	36.1	34.5	1.19935	0.044256	1.27536	0.0004362
chr7:100503020-10051481	Dnajb13	69387	7.1	1.1	1.6	-4.31518	0.000351	-2.98136	0.0016068
chr3:137867675-13790893	Dnajb14	70604	24.7	19.7	27.6	-1.12311	0.379825	1.39386	0.0002597
chr1:75236423-75245692:	Dnajb2	56812	39.4	39.7	50.0	1.13236	0.308111	1.58155	8.98E-08
chr1:88204732-88205748:	Dnajb3	15504	14.9	3.3	7.2	-3.53109	0.000129	-1.58401	0.114693
chr3:152183871-15221008	Dnajb4	67035	54.1	73.4	75.7	1.52579	0.068197	1.71171	0.0025245
chr4:42953094-42958732:	Dnajb5	56323	16.3	18.5	42.8	1.26584	0.190913	3.18683	7.93E-20
chr15:81407088-81408273	Dnajb7	57755	5.2	1.4	1.0	-2.78566	0.039737	-3.27478	0.0022872
chr6:88222268-88223256:	Dnajb8	56691	10.8	0.8	1.2	-5	0.00477	-3.68301	0.0056967
chr12:44205897-44210068	Dnajb9	27362	47.9	49.6	87.8	1.15274	0.270281	2.26874	4.37E-20
chr2:18206333-18392830:	Dnajc1	13418	33.6	28.7	33.9	-1.04814	0.626732	1.26237	0.000169
chr4:151933720-15198195	Dnajc11	230935	46.5	48.8	79.8	1.18361	0.220855	2.12976	9.68E-15
chr10:63382443-63408840	Dnajc12	30045	8.7	7.7	1.8	-1.02294	0.94568	-3.67139	7.23E-12
chr9:104151597-10426293	Dnajc13	235567	60.2	59.3	56.5	1.10605	0.221852	1.17225	0.0095928
chr10:128805676-1288194	Dnajc14	74330	56.1	57.7	57.1	1.15763	0.186806	1.26941	0.0039144
chr14:77826217-77874917	Dnajc15	66148	57.9	55.8	69.8	1.08117	0.680168	1.49367	0.0006773
chr2:119172500-11920879	Dnajc17	69408	25.9	24.2	27.4	1.04539	0.741425	1.31925	0.0005562
chr3:34057280-34081354:	Dnajc19	67713	24.9	23.9	27.8	1.07118	0.497304	1.39262	7.35E-07
chr5:21757277-21785165:	Dnajc2	22791	43.6	47.3	104.2	1.22261	0.186477	2.94423	1.29E-23
chr15:10446763-10470516	Dnajc21	78244	34.4	43.7	63.2	1.4344	0.084572	2.24478	2.20E-07
chr4:59003193-59023398:	Dnajc25	72429	12.8	16.1	28.6	1.41463	0.076955	2.71939	3.41E-12
chr12:4082574-4110612:+	Dnajc27	217378	16.3	18.7	26.4	1.29861	0.110132	2.00961	7.14E-09
chr16:91614257-91618999	Dnajc28	246738	10.9	7.7	0.6	-1.27714	0.539702	-10.621	1.75E-18
chr14:118937932-1189817	Dnajc3	1E+08	70.6	91.9	203.4	1.46362	0.025875	3.50369	2.92E-22
chr5:135064206-13506536	Dnajc30	66114	24.2	23.1	24.9	1.07233	0.525971	1.29023	0.0004092
chr19:6987911-6992272:-	Dnajc4	57431	51.0	42.9	31.9	-1.06483	0.612272	-1.27579	0.0029911
chr2:181520485-18155288	Dnajc5	13002	64.2	72.0	95.6	1.26572	0.1133	1.84571	2.82E-08
chr3:19508595-19610862:	Dnajc5b	66326	5.6	0.3	0.6	-5.55943	0.002118	-3.87426	0.0037963
chr5:31108319-31112524:	Dnajc5g	231098	2.2	0.1	0.3	-6.51941	0.000372	-3.33746	0.007257
chr11:100582836-1006201	Dnajc7	56354	117.5	104.0	116.3	-1.00184	0.991162	1.23568	0.0081492
chr4:132535559-13255374	Dnajc8	68598	143.7	143.3	185.1	1.11911	0.305177	1.60432	7.89E-10
chr12:84114328-84143510	Dnal1	105000	14.5	12.8	6.3	-1.01159	0.956889	-1.82512	4.97E-08
chr4:125055339-12506565	Dnali1	75563	3.6	0.4	0.3	-5.47122	6.77E-05	-6.68678	2.47E-07
chrX:74273217-74282333:	Dnase1l1	69537	25.2	20.2	9.8	-1.12162	0.45401	-2.0359	2.33E-11
chr17:24440768-24443101	Dnase1l2	66705	15.0	12.9	5.5	-1.03854	0.89775	-2.11675	6.78E-06
chr8:84908624-84911461:	Dnase2a	13423	31.4	21.6	8.2	-1.3097	0.171645	-2.98572	6.53E-14
chr2:26348118-26352110:	Dnlz	52838	22.6	24.0	29.6	1.18923	0.042965	1.6343	6.13E-15
chr2:32308471-32353329:	Dnm1	13429	19.2	14.6	9.1	-1.18333	0.333698	-1.66203	4.36E-05
chr16:16312228-16359031	Dnm1l	74006	70.6	72.4	94.7	1.14931	0.070359	1.67235	8.26E-20
chr9:21424908-21507759:	Dnm2	13430	53.0	51.2	64.2	1.08745	0.341751	1.51257	1.06E-11
chr1:161987302-16247803	Dnm3	103967	8.2	6.6	3.2	-1.10604	0.483873	-2.03539	4.62E-13
chr19:43846819-43940198	Dnmbp	71972	35.0	37.9	18.6	1.23005	0.297628	-1.48487	0.0064629
chr9:20907206-20959888:	Dnmt1	13433	35.9	32.1	37.9	-1.00132	0.994268	1.32152	0.0013304
chr12:3806980-3914443:+	Dnmt3a	13435	34.4	26.3	17.1	-1.16844	0.074413	-1.59936	4.94E-13
chr2:153649449-15368773	Dnmt3b	13436	7.4	9.3	9.8	1.40824	0.064389	1.63599	0.0004757
chr10:78042287-78063622	Dnmt3l	54427	0.4	0.3	1.7	-1.28198	0.579587	4.75035	1.67E-10
chr17:46496789-46499618	Dnph1	381101	6.7	6.6	12.2	1.09299	0.647139	2.24399	2.82E-13
chr2:164746015-16476821	Dnttip1	76233	48.2	50.1	54.2	1.17097	0.284809	1.39996	0.0015453
chr3:122274414-12228527	Dnttip2	99480	75.5	95.9	122.7	1.4305	0.052163	1.99779	7.12E-07
chr11:75769090-75796057	Doc2b	13447	6.0	5.2	0.9	-1.02507	0.929375	-5.06127	4.56E-24
chr19:4003385-4007005:+	Doc2g	60425	6.3	4.6	2.2	-1.20031	0.396068	-2.23211	5.22E-07
chr7:134670687-13517364	Dock1	330662	79.8	64.8	35.6	-1.09995	0.242453	-1.7842	1.06E-23
chrX:35888832-36076562:	Dock11	75974	31.1	26.9	11.8	-1.04145	0.810974	-2.09327	4.86E-14
chr12:40446053-40846488	Dock4	238130	11.2	10.1	6.0	1.00329	0.984057	-1.47815	4.48E-06
chr9:21800180-21852635:	Dock6	319899	42.4	36.6	22.6	-1.0295	0.864597	-1.4921	2.90E-05
chr14:121542039-1217977	Dock9	105445	77.4	65.6	22.4	-1.05343	0.441373	-2.75661	6.26E-110
chr10:81384428-81388352	Dohh	102115	37.0	47.3	71.0	1.43783	0.010991	2.36549	5.96E-15

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr8:94863828-94876312:	Dok4	114255	14.1	16.2	28.5	1.28046	0.00682	2.50909	2.73E-41
chr2:170731807-17087977	Dok5	76829	1.1	1.1	3.1	1.11203	0.808828	3.25239	6.59E-07
chr2:30284229-30286354:	Dolk	227697	24.3	22.3	33.0	1.02964	0.825682	1.69472	5.59E-13
chr2:30392254-30400529:	Dolpp1	57170	11.5	11.0	19.8	1.07814	0.713814	2.12432	6.49E-10
chr9:86467154-86555806:	Dopey1	320615	39.2	40.2	45.6	1.15258	0.036547	1.45366	2.35E-13
chr16:93711907-93810588	Dopey2	70028	23.5	19.1	8.0	-1.09876	0.507405	-2.31969	4.73E-19
chr10:80130434-80139367	Dos	1.01E+08	8.1	8.1	10.7	1.10409	0.644136	1.62874	0.0003104
chr10:80755206-80794347	Dot1l	208266	14.1	17.3	23.6	1.38308	0.14847	2.0405	1.85E-05
chr9:44326845-44333600:	Dpagt1	13478	26.6	25.8	45.5	1.08926	0.47379	2.12198	1.67E-22
chr8:123186235-12320181	Dpep1	13479	4.3	3.2	1.4	-1.20115	0.530629	-2.30123	3.97E-05
chr8:105973520-10597941	Dpep3	71854	5.4	0.4	0.7	-5.87864	0.00044	-3.96434	0.0013343
chr19:5896516-5912871:-	Dpf2	19708	50.9	54.0	55.2	1.19812	0.099809	1.35468	0.0002442
chr12:83213751-83487736	Dpf3	70127	4.0	4.6	1.2	1.28417	0.456835	-2.44018	0.0001784
chr11:75177643-75190483	Dph1	116905	20.5	21.1	43.4	1.16024	0.176085	2.63501	1.24E-37
chr4:117888643-11789200	Dph2	67728	10.9	14.1	32.4	1.44767	0.064389	3.58002	2.84E-18
chr14:32080517-32085692	Dph3	105638	27.1	31.2	43.5	1.2957	0.005507	1.99877	1.94E-21
chr3:115888183-11592932	Dph5	69740	27.0	24.8	56.9	1.02616	0.829198	2.62126	3.35E-53
chr2:114516418-11465492	Dph6	66632	15.2	12.8	19.8	-1.05869	0.66547	1.62524	8.60E-10
chr2:24962422-24973471:	Dph7	67228	26.5	23.6	27.1	-1.00473	0.965255	1.27504	1.51E-05
chr19:4907229-4928287:-	Dpp3	75221	41.6	34.2	48.3	-1.09323	0.488764	1.44794	1.80E-05
chr2:62330073-62412231:	Dpp4	13482	30.2	23.1	9.8	-1.17719	0.220378	-2.4436	8.46E-21
chr5:26817357-27727500:	Dpp6	13483	3.6	3.6	4.6	1.11573	0.692789	1.58536	0.0080333
chr2:25352290-25356332:	Dpp7	83768	54.1	45.4	19.0	-1.07216	0.638948	-2.26359	5.38E-18
chr9:65032458-65082651:	Dpp8	74388	128.6	115.6	117.9	1.00708	0.936446	1.14582	0.0039343
chr17:56186682-56218889	Dpp9	224897	21.3	22.3	34.0	1.17301	0.107191	1.98442	4.97E-22
chr1:164796732-16482426	Dpt	56429	425.7	379.7	141.2	-1.01435	0.950837	-2.38451	2.18E-13
chr9:24557048-24696293:	Dpy19l2	320752	2.5	0.2	0.4	-7.59093	3.18E-05	-3.85261	0.0013461
chr4:11265079-11322131:	Dpy19l4	381510	47.5	42.3	30.9	-1.00862	0.942939	-1.22957	0.0010605
chr17:74299474-74323944	Dpy30	66310	47.9	49.9	56.0	1.16471	0.175796	1.45461	4.52E-06
chr3:118562178-11943291	Dpyd	99586	37.3	33.1	15.1	-1.01011	0.945436	-1.96783	6.70E-19
chr14:66802864-66868600	Dpysl2	12934	137.2	113.8	27.9	-1.08137	0.564024	-3.8822	3.08E-55
chr18:43320979-43438286	Dpysl3	22240	106.0	86.1	48.2	-1.11241	0.577976	-1.74297	8.65E-06
chr7:139086001-13910179	Dpysl4	26757	8.9	8.0	3.1	1.00728	0.968464	-2.24922	8.32E-15
chr5:30711895-30799369:	Dpysl5	65254	2.4	1.4	0.2	-1.46965	0.342173	-6.28132	7.12E-10
chr5:108268897-10828052	Dr1	13486	36.7	39.9	51.6	1.22526	0.121974	1.74808	7.56E-09
chr10:88322804-88357075	Dram1	71712	23.4	23.2	41.2	1.10678	0.686858	2.14363	8.10E-07
chr3:106547798-10657534	Dram2	67171	55.5	49.8	31.4	-1.00426	0.980021	-1.41333	0.0001034
chr19:5422804-5424979:-	Drap1	66556	128.0	119.0	165.7	1.04128	0.616732	1.61624	4.01E-22
chr5:30341663-30366708:	Drc1	381738	2.3	0.3	0.3	-3.74369	0.015701	-3.52224	0.0039836
chr8:95055103-95078141:	Drc7	330830	1.3	0.1	0.2	-7.78484	6.69E-05	-4.06449	0.0014812
chr11:3249922-3266386:-	Drg1	13494	123.8	119.7	162.5	1.08197	0.38774	1.63628	1.51E-15
chr11:60454617-60468705	Drg2	13495	87.2	86.9	115.2	1.11973	0.310133	1.64698	1.41E-10
chrX:134404780-13445657	Drp2	13497	2.0	3.9	8.4	2.11656	0.045803	4.44631	1.50E-07
chr16:96592079-97170735	Dscam	13508	0.3	0.3	1.7	1.07978	0.868056	5.74203	1.83E-13
chr16:94497724-94526629	Dscr3	13185	56.2	49.0	37.3	-1.02953	0.780972	-1.20435	0.0034688
chr1:111858702-11186491	Dsel	319901	40.5	30.1	18.7	-1.21809	0.388394	-1.70814	0.0009201
chr2:156995062-15700707	Dsn1	66934	8.9	6.9	3.9	-1.15684	0.413299	-1.78769	4.74E-06
chr1:33908225-34308662:	Dst	13518	146.1	121.1	54.5	-1.07868	0.43693	-2.13356	3.12E-31
chr2:144599953-14476874	Dtd1	66044	62.5	50.0	19.3	-1.11767	0.37075	-2.56061	9.80E-27
chr18:23310020-23659719	Dtna	13527	21.0	15.0	5.4	-1.2591	0.217152	-3.05618	7.97E-17
chr13:44922080-45002096	Dtnbp1	94245	54.7	45.5	68.1	-1.08013	0.561803	1.54824	2.81E-07
chr18:49696145-49755601	Dtwd2	68857	5.2	4.5	5.6	-1.01843	0.928961	1.34615	0.0055553
chr5:120680264-12071166	Dtx1	14357	13.5	9.1	3.3	-1.32329	0.020966	-3.23398	5.67E-33
chr10:127190378-1271957	Dtx3	80904	213.5	160.5	72.4	-1.18954	0.214071	-2.33187	2.20E-17
chr16:35926515-35939027	Dtx3l	209200	38.1	38.0	19.1	1.1112	0.425808	-1.58452	5.19E-07
chr19:12466336-12501996	Dtx4	207521	43.3	29.6	14.8	-1.31834	0.277736	-2.25738	7.99E-06
chr1:93792576-93801934:	Dtymk	21915	58.3	55.2	69.2	1.05718	0.578798	1.48129	5.36E-10
chr2:122280437-12229816	Duox2	214593	1.9	1.5	0.8	-1.08329	0.740292	-1.79643	0.0001672

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:120789202-1207963	Dus1l	68730	60.3	63.7	86.4	1.1881	0.144193	1.78332	1.43E-11
chr8:106011478-10605384	Dus2	66369	12.5	12.4	18.5	1.10751	0.46017	1.84432	8.93E-12
chr17:56764751-56770093	Dus3l	224907	48.5	43.7	49.9	1.00887	0.943292	1.28558	8.69E-05
chr12:31640055-31654826	Dus4l	71916	11.8	10.9	20.4	1.02408	0.915085	2.13503	3.08E-11
chr17:26505591-26508472	Dusp1	19252	18.5	39.5	29.0	2.32867	0.000845	1.88262	0.0034662
chr1:170874188-17088554	Dusp12	80915	41.8	38.4	49.5	1.02733	0.80015	1.47505	8.17E-11
chr14:21733395-21748622	Dusp13	27389	3.4	0.6	0.4	-3.91532	0.005384	-4.32551	0.0002512
chr2:80617214-80631661:	Dusp19	68082	17.0	13.3	9.0	-1.14713	0.436268	-1.50976	0.0009224
chr2:127336159-12733837	Dusp2	13537	6.5	17.0	9.3	2.80502	1.14E-05	1.73777	0.0090245
chr8:31089662-31097047:	Dusp26	66959	41.2	28.1	1.6	-1.31142	0.376423	-16.8422	3.47E-37
chr1:92906989-92908620:	Dusp28	67446	9.1	8.2	5.0	1.00549	0.983362	-1.45907	0.0077427
chr11:101971144-1019847	Dusp3	72349	37.7	32.4	62.2	-1.03831	0.794742	2.04355	4.95E-18
chr8:34807610-34819894:	Dusp4	319520	9.5	5.3	2.7	-1.6116	7.83E-05	-2.77304	5.56E-21
chr7:142079487-14209528	Dusp8	18218	2.6	7.1	7.7	2.66746	0.027592	3.01843	0.0015813
chrX:73639441-73643514:	Dusp9	75590	0.4	0.5	1.8	1.45332	0.391723	5.17028	5.75E-09
chr4:155847317-15585930	Dvl1	13542	65.4	81.4	100.6	1.40072	0.010883	1.90705	4.61E-10
chr11:70000626-70010109	Dvl2	13543	31.6	26.5	19.4	-1.06098	0.655616	-1.29797	0.0022829
chr17:34837019-34839186	Dxo	112403	38.4	37.7	36.8	1.10248	0.315283	1.19994	0.0093201
chr14:41072911-41092197	Dydc1	69496	1.2	0.0	0.2	-5.16454	0.004002	-2.95258	0.024615
chr14:41049209-41069074	Dydc2	71200	2.5	0.6	0.3	-2.6405	0.097062	-3.34593	0.0074277
chr18:75018772-75286966	Dym	69190	28.1	24.1	17.1	-1.04101	0.717681	-1.30998	9.45E-05
chr9:114688831-11472377	Dync1li1	235661	50.0	57.3	64.7	1.28929	0.010188	1.61223	6.30E-10
chr9:6928503-7177046:-	Dync2h1	110350	42.3	32.3	14.2	-1.17137	0.109883	-2.36284	1.43E-32
chr17:84626499-84655564	Dync2li1	213575	80.0	63.3	20.7	-1.13588	0.2635	-3.06382	9.50E-42
chr5:115297110-11530099	Dynll1	56455	120.7	179.8	220.6	1.67008	0.000888	2.24503	2.25E-10
chr2:155236533-15525027	Dynlrb1	67068	121.4	128.2	137.6	1.18306	0.028209	1.41505	2.26E-09
chr8:116505015-11651591	Dynlrb2	75465	3.7	0.6	0.4	-3.38697	0.035161	-4.29529	0.0013175
chr17:6306344-6317474:-	Dynlt1a	1E+08	2.3	1.4	0.8	-1.41668	0.090282	-2.30142	2.04E-07
chr17:6430112-6436295:+	Dynlt1b	21648	54.2	41.6	20.5	-1.17303	0.430611	-2.07929	2.16E-07
chr17:6646606-6655939:-	Dynlt1f	1E+08	4.2	3.4	1.2	-1.12625	0.74793	-2.52383	0.0001233
chr7:28179483-28187298:	Dyrk1b	13549	32.7	23.1	6.1	-1.26652	0.173432	-4.10875	2.96E-28
chr10:118859349-1188689	Dyrk2	69181	86.1	89.5	116.5	1.16086	0.244823	1.68488	1.08E-08
chr6:84008598-84211059:	Dysf	26903	9.6	8.3	24.6	-1.02892	0.839898	3.18007	3.40E-53
chr2:144470557-14452739	Dzank1	241688	11.4	7.4	1.4	-1.36869	0.127897	-6.08609	3.13E-31
chr14:118875520-1189254	Dzip1	66573	29.5	23.1	8.7	-1.1458	0.448257	-2.6517	1.13E-15
chr9:99629595-99669256:	Dzip1l	72507	20.4	12.1	10.6	-1.50501	0.035838	-1.51701	0.0064625
chr19:20492715-20556410	E030003E18Rik	320092	5.9	3.3	2.8	-1.57343	0.064835	-1.64608	0.0085648
chr11:97627387-97629716	E130012A19Rik	103551	0.3	0.5	0.8	1.90282	0.10954	3.27343	3.68E-05
chr4:101346524-10135624	E130102H24Rik	77866	163.1	111.3	15.5	-1.31145	0.449136	-7.11813	7.11E-16
chr10:39621411-39732007	E130307A14Rik	327744	20.0	15.4	11.4	-1.16571	0.394472	-1.39539	0.0098883
chr5:143301072-14331536	E130309D02Rik	231868	10.7	15.0	21.8	1.57536	0.032857	2.46899	2.20E-08
chr6:67036599-67080652:	E230016M11Rik	320172	9.9	7.7	3.5	-1.14561	0.477365	-2.21585	4.27E-09
chr18:36684923-36695925	E230025N22Rik	240216	1.1	1.0	0.1	-1.03018	0.956393	-4.4914	4.51E-06
chr13:29906575-29986063	E2f3	13557	4.8	4.3	6.0	1.00973	0.967389	1.54983	0.0004669
chr8:105297663-10530537	E2f4	104394	33.1	43.2	70.6	1.47261	0.027564	2.61225	5.17E-13
chr3:14578671-14606309:	E2f5	13559	31.8	34.7	36.9	1.21704	0.090188	1.44162	2.40E-05
chr12:16810965-16826752	E2f6	50496	31.3	57.8	50.3	2.03136	0.015242	1.91944	0.005522
chr6:40407498-40436133:	E330009J07Rik	243780	17.9	13.0	5.3	-1.23974	0.296678	-2.62286	8.90E-11
chr9:98748599-98820087:	E330023G01Rik	331011	0.2	0.3	2.2	1.58588	0.41181	9.67043	1.11E-10
chr7:78581066-78718220:	E430016F16Rik	414121	3.2	2.8	1.2	-1.03605	0.934399	-2.00633	0.0031589
chr7:127390836-12739362	E430018J23Rik	101604	20.7	15.8	7.2	-1.18183	0.458524	-2.23137	2.39E-07
chr17:24443778-24455392	E4f1	13560	39.7	37.6	25.1	1.06393	0.511517	-1.26225	0.0003052
chr14:31495079-31509858	Eaf1	74427	25.8	32.5	43.8	1.42243	0.053542	2.09078	8.06E-08
chr7:122038821-12206706	Ears2	67417	19.4	22.2	34.6	1.28266	0.004759	2.22538	4.03E-33
chr15:44619641-44641026	Ebag9	55960	26.5	25.9	31.4	1.09631	0.458483	1.47592	2.78E-06
chr11:44618100-45008096	Ebf1	13591	32.8	26.1	13.0	-1.12568	0.217844	-2.00682	6.91E-24
chr2:130295939-13037048	Ebf4	228598	25.3	22.5	15.4	1.00219	0.991756	-1.31384	0.0069308
chr4:118620799-11862777	Ebna1bp2	69072	52.2	60.5	117.4	1.30623	0.048944	2.77724	2.53E-24

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr14:61339763-61360445	Ebpl	68177	13.4	11.6	4.9	-1.04738	0.852801	-2.16469	7.41E-08
chr14:20319859-20348121	Ecd	70601	40.0	37.5	61.9	1.05136	0.665664	1.93252	5.89E-21
chr16:20611601-20645915	Ece2	107522	12.5	16.7	20.0	1.50088	0.163425	1.92531	0.002705
chr7:28825338-28832239:	Ech1	51798	265.1	243.4	153.8	1.01973	0.887987	-1.37806	2.94E-05
chr4:108165437-10817930	Echdc2	52430	145.6	124.7	38.3	-1.04309	0.641673	-3.01915	3.38E-80
chr2:6188465-6212994:-	Echdc3	67856	8.3	6.5	1.8	-1.15749	0.614454	-3.38987	4.40E-10
chr7:140105723-14011642	Echs1	93747	130.4	102.8	66.1	-1.14265	0.400239	-1.56634	5.32E-05
chr3:95734148-95739569:	Ecm1	13601	26.7	22.0	12.9	-1.08951	0.652775	-1.64237	4.74E-05
chr13:49504810-49532789	Ecm2	407800	56.6	42.0	7.1	-1.21209	0.198229	-6.16307	1.29E-62
chr18:35713089-35721491	Ecscr	68545	44.7	50.5	81.4	1.26427	0.033826	2.26066	1.10E-23
chr9:22072246-22085427:	Ecsit	26940	26.7	29.0	60.4	1.22328	0.147728	2.78915	2.97E-25
chrX:99975606-100400760	Eda	13607	7.8	6.7	2.6	-1.04103	0.779102	-2.3777	2.68E-22
chr10:58600788-58675696	Edar	13608	3.5	1.7	0.3	-1.71746	0.23031	-6.21758	4.78E-08
chr6:108828641-10885935	Edem1	192193	27.0	31.1	50.0	1.29205	0.070916	2.28779	2.69E-15
chr1:151755374-15182232	Edem3	66967	31.8	34.3	40.2	1.21274	0.071594	1.57027	1.60E-08
chr2:25557900-25562082:	Edf1	59022	182.8	183.6	254.6	1.12825	0.269345	1.73477	5.07E-13
chr13:88821472-89323225	Edil3	13612	5.8	6.6	1.1	1.24635	0.293475	-3.92404	1.93E-18
chr2:174760758-17478404	Edn3	13616	9.7	8.5	1.3	-1.01156	0.96991	-5.77042	3.47E-24
chr8:77663029-77724452:	Ednra	13617	36.9	33.5	46.7	1.00422	0.986678	1.56958	0.0005255
chr14:103814615-1038444	Ednrb	13618	14.8	15.2	17.1	1.13156	0.451981	1.42966	0.0016519
chr10:95940663-96045518	Eea1	216238	55.2	50.0	76.8	1.01252	0.887413	1.73438	1.81E-32
chr7:89954654-89980976:	Eed	13626	53.5	68.7	77.5	1.44584	0.015634	1.793	9.90E-07
chr1:63176831-63180486:	Eef1b2	55949	432.3	411.3	457.0	1.06279	0.566854	1.31815	7.56E-05
chr15:75894796-75909556	Eef1d	66656	193.7	173.5	194.0	1.00197	0.987927	1.25043	0.0008915
chr13:38645691-38659028	Eef1e1	66143	22.3	40.6	115.9	2.01197	0.004462	5.94968	3.54E-20
chr19:8967041-8978180:+	Eef1g	67160	737.9	698.1	1143.9	1.0581	0.550549	1.9329	1.39E-27
chr7:120842831-12090721	Eef2k	13631	37.1	21.5	11.3	-1.55092	0.031455	-2.55702	1.72E-09
chr6:88257334-88446539:	Eefsec	65967	29.8	26.9	30.3	1.00768	0.959587	1.26756	0.002548
chr9:25481597-25604110:	Eepd1	67484	16.0	9.1	2.9	-1.54233	0.135652	-4.02077	1.26E-10
chr12:33394854-33401269	Efcab10	75040	2.3	0.1	0.3	-4.86419	0.005828	-3.328	0.0110815
chr12:99717531-99883442	Efcab11	78767	1.3	1.0	0.4	-1.14106	0.719227	-2.32604	0.0007383
chr6:115810729-11583841	Efcab12	212516	3.9	2.4	0.4	-1.42008	0.119251	-7.54127	6.89E-22
chr1:178405881-17848324	Efcab2	68226	18.4	13.8	7.7	-1.19129	0.130385	-1.91017	1.18E-13
chr11:105092219-1051175	Efcab3	70894	4.2	0.7	0.8	-4.2824	0.000283	-3.47054	0.0002372
chr11:77089915-77188968	Efcab5	319634	3.9	0.6	0.6	-4.7408	3.26E-05	-3.87904	2.69E-05
chr15:83866712-84065349	Efcab6	77627	4.2	0.6	0.3	-5.32992	1.95E-05	-7.45913	3.38E-09
chr11:32522733-32527574	Efcab9	69306	6.0	1.4	1.1	-3.28809	0.00147	-3.59293	4.28E-05
chr6:87730869-87755911:	Efcc1	58229	5.1	4.5	1.1	-1.01988	0.956421	-3.60011	6.54E-11
chr11:28853205-28926743	Efemp1	216616	211.8	173.0	53.1	-1.10395	0.591262	-3.13858	2.07E-22
chr19:5474690-5481854:+	Efemp2	58859	84.6	73.7	98.8	-1.02874	0.780068	1.45779	1.44E-10
chr17:53398889-53463321	Efhb	211482	8.7	4.9	1.6	-1.58141	0.029292	-4.22649	1.50E-17
chr1:20951626-20990841:	Efhc1	71877	27.0	15.8	2.5	-1.51417	0.077889	-7.99466	2.07E-30
chrX:17132049-17319368:	Efhc2	74405	1.6	0.8	0.2	-1.83525	0.08384	-4.41315	2.45E-07
chr4:141858142-14187492	Efhd2	27984	33.9	32.4	41.4	1.06748	0.727681	1.51042	0.0003344
chr3:89271730-89280951:	Efna1	13636	46.3	31.4	16.2	-1.32928	0.290667	-2.20724	4.27E-05
chr3:89333393-89338028:	Efna4	13639	15.3	9.9	6.3	-1.38837	0.104002	-1.91836	2.13E-05
chrX:99136130-99148991:	Efnb1	13641	19.7	24.2	32.7	1.38821	0.301141	1.98558	0.0028225
chr15:65787041-65873812	Efr3a	76740	79.8	74.5	86.2	1.04324	0.514096	1.34881	1.83E-12
chr14:54916543-54926788	Efs	13644	29.9	19.6	15.2	-1.36621	0.136089	-1.5527	0.0056426
chr7:82648614-82777852:	Eftud1	101592	27.8	23.8	28.8	-1.04318	0.649335	1.29447	7.67E-06
chr11:102838472-1028809	Eftud2	20624	45.4	44.0	90.1	1.08854	0.399436	2.47181	1.34E-41
chr17:34613350-34615971	Egfl8	81701	9.0	9.1	3.7	1.13873	0.581954	-1.88801	0.0001051
chr15:7206120-7398395:-	Egflam	268780	34.9	31.0	4.8	-1.00387	0.982834	-5.6954	4.77E-76
chr11:16752203-16913907	Egfr	13649	46.1	61.5	62.1	1.49754	0.000504	1.67166	1.32E-07
chr18:34861207-34864956	Egr1	13653	14.7	30.0	53.4	2.23905	0.002642	4.18474	3.87E-11
chr10:67537869-67542188	Egr2	13654	4.7	6.0	14.3	1.42873	0.193959	3.59916	5.68E-11
chr11:22005826-22286795	Ehbp1	216565	63.4	50.9	16.5	-1.1183	0.422525	-3.02686	1.34E-31
chr19:5707374-5726317:-	Ehbp1l1	114601	53.3	57.6	67.2	1.21655	0.153669	1.56738	9.90E-06

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr19:6276896-6300096:+	Ehd1	13660	30.3	33.8	51.1	1.24657	0.161044	2.07698	1.42E-10
chr16:21761285-21787834	Ehhadh	74147	9.7	7.4	4.1	-1.15433	0.51317	-1.8633	3.25E-05
chr9:36779153-36797393:	Ei24	13663	77.4	73.1	91.7	1.05687	0.340103	1.48063	1.04E-23
chr2:125673100-12567564	Eid1	58521	101.7	82.9	55.4	-1.10633	0.50045	-1.4626	0.0001887
chr7:28267881-28269168:	Eid2	386655	15.9	18.7	25.5	1.31139	0.069237	1.97663	4.06E-10
chr11:100319996-1003220	Eif1	20918	185.2	250.8	318.2	1.5234	0.022008	2.10776	1.59E-07
chr18:46597704-46610225	Eif1a	13664	62.9	110.9	183.2	1.94611	0.00182	3.46265	8.63E-13
chr19:5366813-5371511:+	Eif1ad	69860	29.2	37.5	50.0	1.44836	0.061449	2.09951	6.43E-07
chrX:159372195-15938569	Eif1ax	66235	142.2	149.2	231.0	1.17662	0.049772	2.024	2.45E-31
chr9:120492606-12049532	Eif1b	68969	72.5	86.0	110.5	1.33814	0.105001	1.87818	2.43E-06
chr3:58525821-58557501:	Eif2a	229317	95.2	82.8	96.4	-1.03028	0.773781	1.264	0.0001612
chr5:143871862-14390271	Eif2ak1	15467	33.2	34.3	40.4	1.16401	0.157104	1.52041	8.21E-08
chr5:124570214-12457905	Eif2b1	209354	38.9	42.4	71.4	1.22825	0.18636	2.26397	1.95E-13
chr12:85219513-85226628	Eif2b2	217715	37.0	42.2	44.9	1.28615	0.100969	1.50954	0.000366
chr4:117019408-11708685	Eif2b3	108067	14.4	17.1	40.6	1.33415	0.089723	3.43802	1.38E-23
chr5:31187558-31193139:	Eif2b4	13667	38.0	35.4	47.6	1.04661	0.695427	1.56234	1.51E-10
chr16:20498817-20509325	Eif2b5	224045	60.2	68.5	117.0	1.28517	0.115634	2.39655	7.57E-14
chr1:131153207-13117347	Eif2d	16865	52.8	41.6	32.1	-1.13324	0.113777	-1.31217	4.87E-06
chr12:78862072-78887010	Eif2s1	13665	56.0	81.1	170.8	1.6244	0.009642	3.68054	3.97E-19
chr2:154871410-15489290	Eif2s2	67204	88.6	140.8	347.7	1.76853	0.030099	4.52576	3.46E-14
chrX:94188709-94212651:	Eif2s3x	26905	93.1	94.1	155.7	1.13498	0.281023	2.07592	3.80E-19
chr19:60761116-60790693	Eif3a	13669	203.8	245.1	461.8	1.35693	0.107587	2.76219	3.14E-13
chr5:140419305-14044335	Eif3b	27979	74.7	81.1	223.0	1.22485	0.259641	3.63383	8.77E-25
chr7:126546911-12656636	Eif3c	56347	245.1	239.4	518.8	1.09614	0.332315	2.63027	1.03E-50
chr15:77958998-77970824	Eif3d	55944	150.2	184.4	429.6	1.38418	0.055955	3.49021	2.70E-23
chr15:43250040-43282736	Eif3e	16341	373.2	360.7	424.3	1.08111	0.561143	1.41487	8.40E-05
chr9:20894349-20898590:	Eif3g	53356	189.4	205.2	419.1	1.22201	0.161413	2.7329	1.30E-22
chr4:129591974-12960064	Eif3i	54709	232.8	244.2	425.6	1.17504	0.152234	2.2669	5.71E-24
chr15:79075223-79094400	Eif3l	223691	199.5	205.0	283.7	1.15854	0.367124	1.76168	6.27E-07
chr2:104999657-10501702	Eif3m	98221	334.6	326.5	397.3	1.09269	0.482715	1.47719	4.86E-06
chr11:69666936-69672423	Eif4a1	13681	509.8	850.3	2216.1	1.85317	0.014181	5.00901	1.14E-16
chr16:23107468-23114132	Eif4a2	13682	583.8	634.7	647.2	1.22308	0.119488	1.37818	0.0010522
chr11:119288363-1193000	Eif4a3	192170	91.6	114.9	208.1	1.41568	0.098342	2.75841	6.16E-11
chr15:102073773-1020971	Eif4b	75705	469.2	377.7	299.9	-1.11346	0.250309	-1.24962	0.0010867
chr3:138526191-13855759	Eif4e	13684	62.1	86.1	156.4	1.55989	0.018662	3.05719	1.28E-14
chr1:87213914-87240488:	Eif4e2	26987	31.4	32.2	38.5	1.15284	0.141107	1.52921	1.65E-09
chr16:20672727-20692883	Eif4g1	208643	132.0	155.9	340.2	1.33403	0.109259	3.14491	3.19E-18
chr7:111067985-11108303	Eif4g2	13690	253.0	319.3	454.5	1.42225	0.01952	2.21519	7.30E-12
chr4:137993456-13820707	Eif4g3	230861	38.7	32.4	47.3	-1.06433	0.600418	1.52729	2.42E-08
chr5:134619876-13463932	Eif4h	22384	253.6	256.2	408.0	1.13609	0.215126	2.00403	1.44E-21
chr12:111538101-1115467	Eif5	217869	155.1	157.5	280.7	1.14548	0.350429	2.23725	9.41E-16
chr11:69916712-69921958	Eif5a	276770	153.3	173.5	495.2	1.27503	0.057303	3.97874	2.37E-49
chr3:28781311-28798846:	Eif5a2	208691	13.5	11.0	13.2	-1.08887	0.418896	1.22579	0.0054182
chr1:37998010-38055579:	Eif5b	226982	28.9	31.3	43.6	1.22312	0.245738	1.86425	5.47E-07
chr2:155819837-15582692	Eif6	16418	73.1	92.4	162.8	1.42261	0.024985	2.73818	2.55E-17
chr11:64979035-65002076	Elac2	68626	22.8	25.8	57.7	1.27881	0.081339	3.13062	5.02E-29
chr8:4284782-4325100:-	Elavl1	15568	41.2	48.0	72.2	1.3152	0.111011	2.15764	1.40E-09
chr11:16934709-16951282	Eldr	72735	2.5	2.4	0.4	1.04152	0.92137	-3.93586	5.34E-08
chr3:51252720-51340644:	Elf2	69257	57.5	59.9	35.3	1.17386	0.191657	-1.29849	0.0044555
chr1:135253574-13525847	Elf3	13710	19.4	40.0	42.9	2.12754	0.07416	2.39773	0.0073689
chr2:103412098-10345098	Elf5	13711	0.3	0.6	1.1	1.74957	0.30987	3.1514	0.0035887
chrX:20933395-20950608:	Elk1	13712	18.5	15.7	11.6	-1.05184	0.654932	-1.26935	0.0010564
chr1:132007605-13202568	Elk4	13714	51.1	50.9	58.6	1.1206	0.218899	1.43262	6.09E-08
chr2:121439027-12144260	Ell3	269344	4.1	3.1	0.4	-1.19666	0.643605	-7.04539	2.78E-12
chr13:20090507-20608356	Elmo1	140580	15.4	13.9	8.4	1.01368	0.913834	-1.46472	2.24E-08
chr8:83312632-83332486:	Elmod2	244548	18.8	14.1	9.9	-1.20399	0.318124	-1.51339	0.0020761
chr6:72565922-72598413:	Elmod3	232089	18.6	12.3	5.3	-1.35538	0.102148	-2.72237	1.03E-12
chr4:118428093-11843295	Elovl1	54325	34.4	41.4	68.3	1.3535	0.076031	2.4357	1.53E-12

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr13:41182382-41220403	Elovl2	54326	2.5	0.3	0.8	-4.95026	6.94E-05	-2.09511	0.034055
chr14:65530446-65593112	Elp3	74195	82.5	75.4	90.2	1.02191	0.816254	1.36669	4.18E-09
chr2:105700109-10590450	Elp4	77766	16.6	13.8	16.5	-1.07552	0.49094	1.24345	0.0022083
chr11:69968226-69981235	Elp5	54351	60.2	66.7	86.2	1.24861	0.0796	1.77741	8.23E-10
chr9:110305192-11032210	Elp6	72341	7.6	6.4	10.3	-1.06863	0.737417	1.67771	7.42E-06
chr13:117220573-1172744	Emb	13723	54.4	53.9	142.1	1.11271	0.794378	2.97631	6.19E-06
chr7:44489938-44496513:	Emc10	69683	64.9	59.0	62.3	1.0128	0.902942	1.19964	0.0015759
chr15:43477229-43527777	Emc2	66736	71.3	69.6	86.5	1.09126	0.265268	1.51077	2.25E-14
chr6:113514887-11353163	Emc3	66087	86.0	88.3	106.5	1.15177	0.090183	1.54335	1.27E-12
chr2:112363019-11236802	Emc4	68032	65.5	73.4	105.5	1.26217	0.098244	1.99587	2.02E-11
chr11:73175503-73177042	Emc6	66048	29.7	41.1	59.9	1.55559	0.011836	2.47417	3.01E-11
chr2:112455025-11246743	Emc7	73024	91.0	100.0	155.6	1.23629	0.124879	2.11644	9.85E-14
chr8:120653914-12066811	Emc8	18117	22.3	22.7	27.4	1.14699	0.380823	1.52528	0.0001146
chr14:55581524-55585254	Emc9	85308	12.3	7.7	2.8	-1.41678	0.132162	-3.3585	6.12E-11
chrX:74254687-74257893:	Emd	13726	60.4	71.4	133.4	1.33423	0.056491	2.71811	3.19E-19
chr17:24892152-24895087	Eme2	193838	49.6	49.8	65.7	1.13659	0.485428	1.64106	6.66E-05
chr6:124704370-12471217	Emg1	14791	142.8	167.8	258.1	1.32068	0.009663	2.2437	2.36E-22
chr17:71252176-71310965	Emilin2	246707	20.2	22.0	41.2	1.22302	0.238988	2.50745	2.33E-14
chr2:160906438-16091233	Emilin3	280635	1.9	0.9	0.3	-1.79403	0.173065	-4.16241	1.25E-05
chr12:108371153-1085395	Eml1	68519	104.2	80.7	58.8	-1.16114	0.296867	-1.41124	0.0008627
chr17:83350931-83480359	Eml4	78798	53.3	47.4	73.6	-1.00072	0.996919	1.72148	3.36E-13
chr12:98786604-98901484	Eml5	319670	9.6	6.8	4.7	-1.27343	0.137524	-1.60705	9.95E-05
chr11:29743051-30026033	Eml6	237711	7.6	6.1	4.0	-1.11221	0.442864	-1.51344	1.64E-05
chr6:135362931-13538317	Emp1	13730	114.9	124.6	164.3	1.21694	0.199413	1.76944	2.66E-07
chr16:10281749-10313968	Emp2	13731	89.5	74.9	50.3	-1.07268	0.56561	-1.41749	1.34E-05
chr19:59458690-59465357	Emx2	13797	50.4	49.0	63.0	1.08837	0.460319	1.55827	8.32E-09
chr1:181896386-18201998	Enah	13800	24.0	29.4	51.4	1.3815	0.101181	2.60248	4.92E-11
chr13:97241105-97253040	Enc1	13803	7.1	8.4	14.1	1.33053	0.122783	2.43662	3.98E-11
chr9:14353990-14381242:	Endod1	71946	22.1	19.5	29.3	-1.00987	0.942058	1.64945	1.29E-13
chr2:30171524-30174069:	Endog	13804	9.1	9.9	12.9	1.20961	0.25417	1.74973	1.08E-06
chr2:32646595-32682669:	Eng	13805	27.9	38.4	71.5	1.54501	0.113777	3.02256	6.25E-08
chr11:118476960-1184891	Engase	217364	6.0	3.9	9.0	-1.35825	0.185347	1.84091	0.0002601
chr4:41638144-41640302:	Enho	69638	9.1	7.2	1.6	-1.12405	0.678465	-4.13607	2.11E-13
chr2:21180731-21205365:	Enkur	71233	19.7	13.0	3.4	-1.35357	0.098342	-4.41389	8.84E-24
chr11:70657176-70662513	Eno3	13808	27.4	22.8	13.4	-1.07798	0.607051	-1.62916	3.55E-07
chr19:58943425-58971421	Eno4	226265	1.5	0.4	0.2	-2.91654	0.015455	-3.84051	0.0001486
chr5:100039994-10006876	Enoph1	67870	23.0	22.6	42.1	1.10351	0.529988	2.2618	3.70E-16
chr14:77156763-77721763	Enox1	239188	3.3	2.2	0.7	-1.3402	0.15462	-3.75448	3.69E-15
chrX:49009707-49288242:	Enox2	209224	18.4	14.6	7.8	-1.12376	0.313206	-1.8746	2.80E-14
chr3:129269177-12933274	Enpep	13809	47.3	38.6	23.0	-1.1074	0.652382	-1.62424	0.0008136
chr10:24641411-24712102	Enpp1	18605	53.1	39.8	14.4	-1.20024	0.282126	-2.89647	6.37E-19
chr15:54838679-54920146	Enpp2	18606	179.7	145.8	18.3	-1.10159	0.578828	-7.62665	8.76E-75
chr10:24773814-24836195	Enpp3	209558	90.8	64.1	11.9	-1.25435	0.484151	-5.47081	3.85E-15
chr17:44078846-44086561	Enpp5	83965	65.8	49.9	14.2	-1.18894	0.244532	-3.64446	4.77E-34
chr3:95624980-95632117:	Ensa	56205	103.3	109.5	108.4	1.19082	0.044947	1.30983	5.16E-05
chr11:120090522-1200987	Enthd2	78777	15.2	15.2	15.2	1.11892	0.31824	1.24668	0.0064752
chr2:25395874-25401323:	Entpd2	12496	19.3	14.6	7.6	-1.18556	0.244279	-2.00582	7.79E-11
chr12:84373876-84409029	Entpd5	12499	15.8	12.6	9.1	-1.1311	0.44502	-1.38223	0.0042869
chr2:25080323-25085719:	Entpd8	72090	5.0	3.6	1.0	-1.22403	0.636735	-3.52921	6.85E-06
chr15:44428111-44437685	Eny2	223527	42.7	38.9	48.1	1.01966	0.889716	1.40079	9.99E-06
chr15:81586214-81652077	Ep300	328572	46.7	43.9	27.8	1.06063	0.695575	-1.33478	0.0022493
chr4:131923427-13207531	Epb4.1	269587	35.4	29.0	16.6	-1.09357	0.234636	-1.70453	3.64E-23
chr2:156420909-15654321	Epb4.1l1	13821	24.3	20.8	28.4	-1.04412	0.578055	1.46237	5.98E-15
chr10:25359798-25523518	Epb4.1l2	13822	122.3	121.9	57.9	1.12817	0.463302	-1.67478	4.36E-06
chr17:69156810-69289987	Epb4.1l3	13823	52.2	46.4	26.6	-1.00426	0.981318	-1.56161	2.91E-06
chr13:19591708-19619830	Epdr1	105298	52.6	44.2	15.8	-1.07111	0.694329	-2.62188	2.60E-19
chr6:42358487-42373268:	Epha1	13835	6.6	5.0	3.0	-1.17118	0.301878	-1.78	2.61E-07
chr16:63545218-63864157	Epha3	13837	5.8	5.6	1.4	1.06257	0.742498	-3.27638	4.21E-22

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr1:77367185-77515088:	Epha4	13838	27.6	17.6	5.3	-1.39886	0.268538	-3.79225	6.24E-10
chr4:28813131-28967503:	Epha7	13841	11.9	6.9	3.3	-1.52166	0.165984	-2.70806	8.86E-06
chr9:101922128-10235469	Ephb1	270190	1.7	1.6	2.8	1.03275	0.926392	1.94624	0.0002112
chr16:21204795-21223304	Ephb3	13845	18.7	12.1	10.0	-1.37781	0.000616	-1.48529	4.56E-07
chr5:137350109-13737452	Ephb4	13846	54.3	50.5	61.0	1.0446	0.580719	1.40142	1.89E-11
chr6:41605482-41620507:	Ephb6	13848	21.2	16.5	4.3	-1.16188	0.436057	-3.81891	7.92E-24
chr1:180989556-18101749	Ephx1	13849	162.6	106.6	30.3	-1.3633	0.002235	-4.24655	1.20E-68
chr14:66084372-66124522	Ephx2	13850	11.5	7.8	2.4	-1.30668	0.390703	-3.55861	7.44E-09
chr5:107403513-10743003	Ephx4	384214	8.3	5.5	2.2	-1.34015	0.362966	-2.75542	1.41E-05
chr10:11343445-11457477	Epm2a	13853	16.4	10.4	5.4	-1.4076	0.216691	-2.29671	5.00E-05
chr7:5080235-5098178:+	Epn1	13854	53.3	51.1	57.7	1.07802	0.378426	1.35475	2.22E-07
chr15:76101488-76120195	Eppk1	223650	4.1	4.4	7.2	1.20609	0.259351	2.17563	2.33E-11
chr1:185363095-18542835	Eprs	107508	116.8	132.0	323.9	1.2717	0.018871	3.43569	1.44E-57
chr4:109280275-10938781	Eps15	13858	56.8	49.5	35.8	-1.02797	0.749334	-1.2709	4.62E-06
chr7:4464735-4480487:+	Eps8l1	67425	26.5	17.6	4.1	-1.31715	0.612288	-3.86555	0.0001317
chr7:141339002-14136301	Eps8l2	98845	21.8	17.8	5.8	-1.08961	0.524379	-2.95753	6.35E-32
chr5:30232618-30272430:	Ept1	28042	18.3	17.0	21.4	1.03875	0.62508	1.45634	3.99E-15
chr4:94907267-94928843:	Eqtn	67753	3.9	0.5	1.3	-5.19196	2.14E-05	-2.16047	0.0178201
chr11:78073376-78080383	Eral1	57837	34.9	35.0	37.3	1.12466	0.155701	1.33734	1.36E-06
chr13:74639872-74691875	Erap1	80898	58.0	61.7	80.7	1.18877	0.06369	1.73165	1.53E-15
chr11:98412484-98437716	Erbb2	13866	25.7	19.3	12.8	-1.18206	0.144193	-1.60595	2.27E-08
chr13:103818786-1039205	Erbb2ip	59079	185.9	157.0	100.2	-1.06327	0.516213	-1.48198	3.13E-10
chr10:128569368-1285895	Erbb3	13867	19.3	12.0	6.1	-1.42828	0.090687	-2.4465	1.49E-08
chr1:68039966-69108059:	Erbb4	13869	4.1	2.6	0.2	-1.26413	0.730877	-7.18251	2.67E-06
chr6:119570796-11984815	Erc1	111173	17.9	18.0	21.3	1.12672	0.135869	1.48793	7.40E-12
chr14:27622442-28478537	Erc2	238988	1.6	1.2	0.6	-1.18198	0.457233	-2.19543	1.33E-06
chr7:19345071-19356524:	Ercc1	13870	47.2	46.9	57.0	1.1164	0.19421	1.50862	6.13E-12
chr18:32240331-32270147	Ercc3	13872	34.7	35.1	46.6	1.13901	0.279324	1.67265	9.83E-10
chr14:32513521-32580989	Ercc6	319955	17.2	18.2	21.9	1.19208	0.093997	1.58851	2.22E-09
chr13:63815320-63900301	Ercc6l2	76251	32.7	27.4	33.5	-1.06792	0.357344	1.28141	4.64E-07
chr13:108158738-1081949	Ercc8	71991	14.4	20.6	33.5	1.60667	0.043923	2.80635	5.44E-09
chr17:26561512-26656933	Ergic1	67458	64.9	55.4	87.4	-1.05214	0.65352	1.67619	1.03E-13
chr6:148179318-14821237	Ergic2	67456	53.8	67.4	87.9	1.41195	0.030946	2.0148	9.44E-09
chr2:156008125-15601827	Ergic3	66366	171.7	147.8	103.1	-1.04213	0.65398	-1.33059	9.14E-07
chr12:80634023-80643861	Erh	13877	92.8	111.1	219.5	1.3445	0.035826	2.91027	2.07E-24
chr7:119783826-11979405	Eri2	71151	17.1	15.2	10.9	-1.0104	0.941097	-1.25058	0.0026204
chr4:117550324-11767429	Eri3	140546	82.7	70.4	55.5	-1.04806	0.497835	-1.19011	0.0002229
chr2:70508819-70540884:	Erich2	66748	10.2	5.2	2.1	-1.67412	0.188233	-3.26791	4.80E-05
chr3:154711133-15474901	Erich3	209601	7.5	1.3	1.2	-4.27745	4.35E-05	-4.088	4.10E-06
chr3:58616300-58637207:	Erich6	545527	1.0	0.1	0.8	-4.37384	0.00096	-1.0202	0.959316
chr11:30929784-30954131	Erlec1	66753	25.5	19.4	15.7	-1.17686	0.204516	-1.29264	0.0073831
chr19:44034943-44069785	Erlin1	226144	21.7	24.2	34.0	1.25651	0.134578	1.93251	3.42E-09
chr17:15041612-15064232	Ermard	381062	15.8	12.9	7.7	-1.0972	0.523605	-1.6271	7.70E-07
chr11:106397620-1064877	Ern1	78943	27.8	52.0	46.1	2.04191	0.027592	1.95596	0.0090434
chr14:45283087-45318572	Ero1l	50527	22.1	24.7	32.2	1.25669	0.009966	1.82021	1.76E-18
chr5:121444753-12145247	Erp29	67397	120.0	110.5	152.2	1.0327	0.728787	1.58304	4.48E-17
chr4:48193331-48279589:	Erp44	76299	42.7	43.5	71.3	1.14195	0.19421	2.07586	3.03E-24
chr4:150855091-15086888	Errfi1	74155	40.5	227.5	209.2	5.23133	1.55E-06	5.15379	5.17E-08
chr2:140119881-14017055	Esf1	66580	37.5	49.2	68.5	1.47738	0.067524	2.22575	6.06E-07
chr4:152120876-15215220	Espn	56226	3.4	2.8	0.8	-1.05651	0.896958	-3.19584	1.79E-06
chr10:4611989-5005633:+	Esr1	13982	237.2	198.0	145.7	-1.07141	0.475657	-1.29814	7.87E-05
chr8:106131183-10613697	Esrp2	77411	8.0	6.3	12.6	-1.13094	0.496818	1.94839	9.69E-09
chr12:116281222-1163730	Esyt2	52635	151.6	144.4	160.4	1.06377	0.531828	1.31952	2.50E-05
chr9:99309967-99358530:	Esyt3	272636	10.3	7.7	11.9	-1.19736	0.247528	1.44428	0.0009935
chr18:34902785-34932003	Etf1	225363	69.7	124.7	255.6	1.97106	0.01577	4.18201	5.28E-11
chr9:55454436-55512243:	Etfa	110842	72.5	69.5	91.6	1.07479	0.410219	1.57507	9.53E-15
chr7:43444072-43457800:	Etfb	110826	101.1	86.7	120.9	-1.04228	0.64395	1.49179	1.57E-13
chr3:79603788-79628767:	Etfdh	66841	57.8	58.5	83.6	1.1306	0.049893	1.80191	7.90E-39

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr7:24587543-24608926:	Ethe1	66071	26.3	32.6	13.3	1.39207	0.009027	-1.56413	1.93E-05
chr2:20289913-20810535:	Etl4	208618	23.9	17.9	9.9	-1.20017	0.25765	-1.9068	2.08E-08
chr13:59769966-59773680	Etohd2	13996	6.5	3.9	1.6	-1.49438	0.089325	-3.13326	3.25E-10
chr2:178023284-17803585	Etohi1	626848	45.8	37.0	27.9	-1.11284	0.44324	-1.31047	0.0057484
chr16:95702407-95721049	Ets2	23872	88.5	121.1	126.3	1.54249	0.017718	1.76322	8.15E-05
chr12:38780258-38868215	Etv1	14009	5.0	2.9	0.3	-1.5228	0.067	-10.4977	1.18E-31
chr3:87525578-87540158:	Etv3	27049	28.7	36.2	29.7	1.41032	0.00425	1.29131	0.0107437
chr11:101769742-1017853	Etv4	18612	2.0	1.1	0.6	-1.55137	0.133853	-2.68637	1.88E-05
chr16:22381313-22439570	Etv5	104156	34.0	20.4	13.6	-1.4944	0.109962	-1.94614	0.0004656
chr6:134035700-13427014	Etv6	14011	19.9	21.4	28.8	1.2029	0.190696	1.79926	7.92E-09
chr6:82041628-82093099:	Eva1a	232146	8.3	20.6	17.3	2.54293	0.017876	2.30612	0.0082719
chr4:126148003-12614987	Eva1b	230752	35.1	28.5	17.9	-1.10756	0.469066	-1.56483	4.32E-06
chr16:90830859-90904885	Eva1c	70967	14.7	12.3	6.4	-1.06154	0.766118	-1.82298	1.06E-06
chr5:37299171-37336881:	Evc	59056	52.0	46.3	13.8	1.00109	0.996254	-2.96823	5.80E-28
chr11:79526561-79530609	Evi2a	14017	6.6	6.2	11.6	1.04799	0.910121	2.08594	0.0011666
chr5:107744795-10787510	Evi5	14020	47.3	43.6	44.4	1.02987	0.620634	1.17132	3.11E-05
chr11:116220559-1162380	Evpl	14027	9.0	7.6	2.8	-1.03002	0.94404	-2.39489	8.58E-05
chr11:5069687-5099088:-	Ewsr1	14030	236.4	208.9	254.9	-1.00918	0.913317	1.34744	2.24E-11
chr12:80463095-80498135	Exd2	97827	50.8	41.4	17.1	-1.09856	0.405721	-2.3614	2.96E-28
chr13:30813918-30974047	Exoc2	66482	44.2	41.8	62.9	1.05952	0.470791	1.77552	5.69E-28
chr13:74169805-74208700	Exoc3	211446	52.8	54.6	69.2	1.16213	0.105272	1.63522	4.54E-13
chr8:105289924-10529609	Exoc3l	277978	4.7	3.3	1.8	-1.24994	0.189024	-2.08974	1.98E-08
chr14:49012144-49066667	Exoc5	105504	33.7	45.6	80.9	1.52244	0.006186	2.94306	3.74E-19
chr8:124890299-12489770	Exoc8	102058	13.9	14.6	14.7	1.17806	0.177433	1.32146	0.0020414
chr9:119444923-11946551	Exog	208194	7.3	6.7	8.6	1.04026	0.776887	1.46837	1.59E-06
chr19:41922980-41933314	Exosc1	66583	31.5	34.9	63.7	1.24757	0.104799	2.49946	1.10E-20
chr4:148558427-14858240	Exosc10	50912	82.7	86.3	128.3	1.17923	0.249784	1.92759	9.97E-11
chr2:31670737-31681307:	Exosc2	227715	43.9	52.7	94.0	1.35204	0.025869	2.65111	7.59E-22
chr4:45316630-45320603:	Exosc3	66362	34.2	39.2	64.1	1.2925	0.226523	2.29056	4.54E-08
chr15:76327397-76330670	Exosc4	109075	22.5	22.7	32.6	1.13072	0.217593	1.81112	3.72E-18
chr8:111056339-11105766	Exosc6	72544	7.4	16.8	25.2	2.42366	0.004455	3.79851	9.27E-08
chr9:123113231-12313612	Exosc7	66446	65.3	55.2	67.9	-1.05811	0.57836	1.29875	5.80E-05
chr3:54728679-54735364:	Exosc8	69639	64.5	62.6	71.6	1.08459	0.263358	1.38697	7.44E-11
chr3:36552606-36565727:	Exosc9	50911	41.8	45.5	86.6	1.22729	0.227547	2.54495	6.43E-15
chr9:53301670-53381158:	Exph5	320051	17.5	10.6	3.2	-1.40619	0.559354	-3.16482	0.003116
chr15:53068261-53346183	Ext1	14042	47.4	47.2	63.7	1.11718	0.359049	1.66953	7.66E-10
chr2:93695631-93822568:	Ext2	14043	54.3	46.4	50.0	-1.04766	0.499671	1.1511	0.0024927
chr14:65052059-65098106	Extl3	54616	60.2	59.8	58.1	1.11335	0.164736	1.20634	0.0011269
chr1:14168958-14310199:	Eya1	14048	1.2	1.0	0.2	-1.04003	0.934865	-3.27314	1.49E-05
chr10:23104168-23349903	Eya4	14051	1.2	0.3	0.3	-3.02038	0.000824	-3.03949	5.70E-05
chr11:101191115-1012264	Ezh1	14055	122.8	96.6	28.6	-1.14515	0.452138	-3.35795	1.25E-23
chr3:59146296-59153628:	F630111L10Rik	320463	0.6	1.0	1.6	1.79625	0.131699	2.98555	0.0001517
chrX:75172715-75380041:	F8	14069	4.1	3.5	1.3	-1.04337	0.794825	-2.55481	3.41E-20
chr18:60293380-60303016	F830016B08Rik	240328	10.1	9.5	1.8	1.04441	0.887963	-4.21318	1.60E-16
chr3:10204343-10208576:	Fabp4	11770	420.6	170.1	43.9	-1.71108	0.405096	-3.46464	0.0067608
chr3:10193624-10197283:	Fabp9	21884	38.1	2.1	4.6	-9.45871	3.49E-07	-4.80415	4.54E-05
chr19:10182888-10196872	Fads1	76267	63.9	48.8	39.5	-1.17115	0.195865	-1.28856	0.0054145
chr19:10064164-10101503	Fads2	56473	83.9	64.8	47.2	-1.15654	0.288883	-1.41414	0.0004645
chr4:109676627-10996396	Faf1	14084	41.0	39.2	72.1	1.07078	0.323141	2.19861	6.32E-65
chr13:54621784-54664063	Faf2	76577	42.9	42.5	58.8	1.10862	0.071549	1.71101	4.32E-39
chr7:84585159-84605942:	Fah	14085	22.8	16.4	6.6	-1.24257	0.277671	-2.67908	1.06E-11
chr2:127436215-12744456	Fahd2a	68126	27.0	21.1	12.6	-1.15088	0.298787	-1.70063	6.02E-08
chr9:98986373-99002019:	Faim	23873	20.7	21.3	35.8	1.15484	0.392103	2.13449	1.55E-11
chr11:76019195-76027782	Fam101b	76566	19.8	15.5	10.6	-1.14656	0.317368	-1.48545	5.57E-05
chr3:108970997-10902760	Fam102b	329739	145.6	137.1	42.3	1.029	0.941915	-2.62261	2.01E-06
chr7:81762953-81769490:	Fam103a1	67148	68.8	61.6	37.3	-1.00102	0.994268	-1.47135	1.13E-08
chr11:113661319-1136841	Fam104a	28081	18.3	18.7	23.7	1.14913	0.392718	1.59944	3.04E-05
chr14:8296278-8309776:-	Fam107a	268709	0.9	4.2	2.9	3.91028	0.0006	3.12622	0.0007799

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr5:121849028-12185459	Fam109a	231717	26.2	22.9	9.6	-1.02217	0.87275	-2.16552	3.45E-23
chr2:151969396-15198021	Fam110a	73847	6.2	5.8	16.8	1.06643	0.830635	3.25634	1.17E-12
chr4:5644179-5799944:+	Fam110b	242297	25.9	19.1	6.5	-1.2193	0.659221	-2.8318	0.0002891
chr12:31073968-31079940	Fam110c	104943	10.0	16.9	17.2	1.8553	3.53E-05	2.11178	4.48E-09
chr19:12573525-12589696	Fam111a	107373	15.9	16.5	27.4	1.15245	0.317884	2.1328	7.84E-15
chr5:64970075-65041901:	Fam114a1	68303	60.8	52.2	20.6	-1.04709	0.729406	-2.34764	3.31E-26
chr11:57482990-57518644	Fam114a2	67726	79.2	73.3	53.5	1.03721	0.652104	-1.18119	0.001391
chr11:95337018-95381872	Fam117a	215512	31.0	19.4	12.8	-1.43307	0.122444	-1.89309	0.0002858
chr1:59913006-59985348:	Fam117b	72750	29.1	27.0	13.0	1.04734	0.782316	-1.7873	4.77E-09
chr15:85037062-85062830	Fam118a	73225	80.9	63.0	34.4	-1.1562	0.424447	-1.85673	8.42E-07
chr9:35216965-35267805:	Fam118b	109229	17.5	15.9	22.8	1.0245	0.902942	1.61368	8.16E-06
chr13:48879217-48967828	Fam120a	218236	151.4	150.7	181.2	1.12264	0.328309	1.4931	1.58E-06
chr13:48968112-48969905	Fam120aos	68128	42.1	33.2	17.4	-1.13838	0.374502	-1.91582	2.25E-10
chrX:151344223-15147413	Fam120c	207375	17.7	14.7	8.5	-1.07836	0.473672	-1.66943	6.73E-13
chr19:24475779-24477474	Fam122a	68034	12.0	11.2	16.4	1.04494	0.775061	1.69862	9.54E-10
chrX:53243415-53269805:	Fam122b	78755	4.0	3.4	1.6	-1.05248	0.780139	-2.02703	8.87E-10
chr14:62555737-62608485	Fam124a	629059	13.6	10.4	3.2	-1.18502	0.653537	-3.11812	2.22E-06
chr1:58522806-58586333:	Fam126b	213056	29.1	24.7	18.6	-1.05669	0.531291	-1.25077	0.0001522
chr1:151571373-15171934	Fam129a	63913	33.9	30.3	18.5	-1.00582	0.971848	-1.46878	9.08E-06
chr2:32876134-32925253:	Fam129b	227737	51.4	48.8	82.2	1.07397	0.728071	1.97393	4.22E-08
chr6:42315305-42324640:	Fam131b	76156	5.5	4.2	0.8	-1.18479	0.49256	-4.9699	1.54E-19
chr5:3543833-3570546:+	Fam133b	68152	55.4	64.7	61.3	1.31732	0.064509	1.37813	0.0053281
chr1:75142786-75147909:	Fam134a	227298	86.5	74.6	46.4	-1.03772	0.620703	-1.48781	7.85E-17
chr15:25843298-25973696	Fam134b	66270	19.8	17.6	6.2	-1.01407	0.947566	-2.51106	1.17E-16
chr6:86365683-86370058:	Fam136a	66488	44.9	42.8	75.5	1.06402	0.581956	2.09192	3.97E-26
chr6:58933536-59024502:	Fam13a	58909	27.1	18.8	2.0	-1.2861	0.282075	-9.90037	3.41E-42
chr18:34442351-34506823	Fam13b	225358	69.3	76.6	74.8	1.24085	0.009845	1.34725	7.22E-06
chr10:70440668-70558732	Fam13c	71721	15.0	9.9	6.4	-1.3508	0.123124	-1.85417	2.62E-05
chr12:30884324-30893854	Fam150b	1E+08	0.5	2.3	2.2	4.24037	0.000501	4.31545	3.11E-05
chr4:106733915-10674829	Fam151a	230579	0.7	3.4	3.3	3.44166	0.018772	3.51847	0.0026539
chr13:92449620-92484031	Fam151b	73942	14.8	11.1	6.7	-1.19563	0.324712	-1.75239	2.08E-05
chr4:86444698-86558303:	Fam154a	75811	2.5	0.8	0.3	-2.38133	0.102537	-4.25917	0.0003811
chr7:82632960-82648528:	Fam154b	330577	6.1	4.1	1.0	-1.31721	0.389828	-4.18964	5.03E-10
chr11:23013387-23023741	Fam161a	73873	11.6	6.5	2.5	-1.57104	0.037204	-3.46937	3.41E-13
chr16:36043844-36071515	Fam162a	70186	95.4	86.0	106.6	1.00677	0.959921	1.39347	1.43E-06
chr2:25218745-25222281:	Fam166a	68222	5.9	0.4	0.9	-6.48779	0.000263	-3.39206	0.0054506
chr4:43427020-43429134:	Fam166b	329831	1.7	0.8	0.2	-1.65846	0.350282	-5.07745	6.38E-05
chr14:63436394-63465502	Fam167a	219148	1.0	0.7	2.4	-1.27592	0.398093	2.81891	9.52E-09
chr7:100706702-10084163	Fam168a	319604	34.5	27.8	19.3	-1.11423	0.40043	-1.42299	9.21E-05
chr1:34813218-34843050:	Fam168b	214469	114.6	111.6	138.1	1.09383	0.184891	1.50582	2.44E-17
chr13:97067287-97129522	Fam169a	320557	2.0	1.7	6.1	-1.02088	0.952743	3.6317	3.02E-14
chr7:68273839-68363092:	Fam169b	434197	3.0	2.3	0.8	-1.19144	0.674436	-2.72441	0.0002141
chr18:50278369-50283019	Fam170a	225497	1.7	0.1	0.3	-6.50589	0.000563	-3.24905	0.010975
chr14:32833962-32836788	Fam170b	105511	3.3	0.2	0.5	-9.44627	5.77E-07	-4.33405	0.000104
chr2:3118388-3227809:+	Fam171a1	269233	32.5	24.9	10.1	-1.17792	0.358006	-2.52152	8.67E-14
chr11:102436981-1024476	Fam171a2	217219	18.1	12.7	5.6	-1.28308	0.084587	-2.54952	1.32E-17
chr2:83812728-83881358:	Fam171b	241520	14.6	10.5	2.7	-1.25277	0.352409	-4.04217	4.27E-16
chr13:77708690-78166240	Fam172a	68675	30.1	26.2	20.8	-1.03014	0.727681	-1.15933	0.0056092
chr17:25790500-25792394	Fam173a	214917	94.2	66.7	40.2	-1.27107	0.203386	-1.84367	9.53E-06
chr1:95313628-95335284:	Fam174a	67698	18.0	16.4	10.3	1.02088	0.88749	-1.39619	4.96E-05
chr7:73740307-73776919:	Fam174b	1E+08	24.9	22.9	31.6	1.02126	0.870653	1.58039	4.38E-11
chr7:132859225-13288511	Fam175b	109359	45.8	46.2	46.3	1.12854	0.10419	1.26049	3.02E-05
chr1:36562696-36683183:	Fam178b	381337	5.1	1.1	0.8	-3.34032	0.004523	-3.8222	0.0001122
chr6:35312746-35326141:	Fam180a	208164	27.7	20.7	4.8	-1.19992	0.750684	-3.58474	0.0002743
chr12:103314959-1033170	Fam181a	1.01E+08	1.7	0.1	0.3	-5.31849	0.001968	-3.12649	0.0112573
chr7:93079879-93081721:	Fam181b	58238	5.7	2.5	1.8	-1.94829	0.074804	-2.31589	0.0036231
chr11:58792802-58801960	Fam183b	75429	3.7	0.4	0.6	-4.21729	0.011207	-3.26123	0.0099125
chr10:53633145-53750909	Fam184a	75906	9.6	7.0	4.2	-1.23919	0.351363	-1.78453	0.0004351

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr15:99271018-99287180	Fam186b	545136	1.7	0.2	0.4	-5.24826	0.000682	-2.98633	0.0080618
chr7:30973804-30989725:	Fam187b	76415	4.2	1.1	1.2	-2.98256	0.00052	-2.66389	0.000226
chr2:12347264-12419460:	Fam188a	66960	29.2	31.2	47.5	1.19703	0.053673	2.02493	1.57E-25
chr6:55203383-55320222:	Fam188b	330323	35.1	26.5	5.0	-1.19209	0.400221	-5.38992	1.19E-31
chr19:23972750-24031019	Fam189a2	381217	53.3	69.0	72.3	1.43373	0.001116	1.68711	9.97E-09
chr3:89183225-89189289:	Fam189b	68521	7.9	5.6	2.9	-1.26044	0.311053	-2.13049	4.92E-06
chr13:55539316-55571120	Fam193b	212483	74.5	58.4	23.6	-1.14307	0.364158	-2.49211	2.49E-19
chr17:25863698-25868738	Fam195a	68241	11.4	13.5	29.1	1.32587	0.142385	3.10025	2.65E-17
chr11:120542888-1205497	Fam195b	192173	74.3	70.9	120.2	1.06868	0.390503	2.01703	3.57E-44
chr9:121950988-12198020	Fam198a	245050	8.5	5.2	0.8	-1.45398	0.129064	-7.87185	2.51E-26
chr3:79885930-79946278:	Fam198b	68659	17.2	12.2	17.2	-1.26208	0.032186	1.25141	0.0081117
chrX:137049594-13708250	Fam199x	245622	17.2	15.6	17.3	1.01463	0.917575	1.25513	0.0027356
chr15:87544299-87759364	Fam19a5	106014	6.8	5.7	11.5	-1.06045	0.786428	2.10989	1.11E-09
chr19:60198586-60226697	Fam204a	76539	35.3	34.1	42.4	1.08518	0.387192	1.49756	2.45E-10
chr4:56802329-56809605:	Fam206a	230234	9.7	11.0	17.4	1.27134	0.135988	2.19785	1.39E-11
chr10:77486655-77515813	Fam207a	108707	30.3	34.1	43.8	1.26719	0.142274	1.78716	1.02E-06
chr14:27428847-27483554	Fam208a	218850	101.5	90.4	58.8	-1.00647	0.955929	-1.37976	5.17E-08
chr13:3566035-3611108:-	Fam208b	105203	58.1	61.8	84.6	1.19572	0.022711	1.81607	9.09E-24
chr2:172472554-17247431	Fam209	76426	8.5	3.7	2.9	-1.90808	0.084572	-2.18151	0.0070273
chr11:109672926-1097222	Fam20a	208659	12.6	9.2	5.5	-1.23023	0.464702	-1.76907	0.003985
chr1:156678571-15671891	Fam20b	215015	43.8	38.2	45.5	-1.02463	0.780715	1.30081	2.62E-07
chr5:138755081-13881006	Fam20c	80752	20.4	27.2	31.1	1.49053	0.159137	1.84222	0.0041981
chr6:116208033-11626267	Fam21	28006	93.0	76.4	39.7	-1.08749	0.219228	-1.87169	6.38E-38
chr18:68260185-68300333	Fam210a	108654	27.1	24.2	27.7	-1.00086	0.993758	1.27909	4.28E-07
chr2:172345577-17235574	Fam210b	67017	13.3	10.3	7.7	-1.15568	0.245271	-1.37001	0.0005597
chr4:154896430-15489904	Fam213b	66469	44.2	32.4	12.0	-1.2261	0.155369	-2.89381	6.65E-22
chr9:74953053-75032468:	Fam214a	235493	94.8	63.8	6.2	-1.33278	0.295286	-10.8091	1.69E-35
chr4:43032414-43046220:	Fam214b	230088	11.6	9.8	6.3	-1.05823	0.737542	-1.46711	0.0002626
chr5:122364584-12237196	Fam216a	68948	48.4	47.4	48.2	1.09721	0.405096	1.24373	0.0053047
chr13:34909964-34919992	Fam217a	71864	4.4	0.9	0.8	-3.43004	0.006607	-3.26741	0.0013515
chr9:57537528-57543187:	Fam219b	78323	33.6	32.7	51.5	1.09353	0.213471	1.9134	8.41E-40
chr5:143548706-14356452	Fam220a	67238	26.1	34.0	43.9	1.4594	0.037185	2.05778	1.71E-07
chr6:49367739-49389904:	Fam221a	231946	7.3	4.3	1.2	-1.50205	0.143211	-4.48871	3.18E-12
chr4:43659622-43668859:	Fam221b	242408	4.9	0.7	0.9	-4.89549	4.80E-05	-3.64185	0.000108
chr15:79609576-79658956	Fam227a	75729	6.2	3.4	0.4	-1.60489	0.109906	-9.70932	7.54E-23
chr2:125983483-12615200	Fam227b	75823	1.9	0.3	0.4	-4.13504	0.001824	-3.40395	0.0011058
chr12:4713805-4738383:-	Fam228a	74855	1.5	0.5	0.4	-2.31945	0.063198	-2.57849	0.0070011
chr12:4746216-4769267:-	Fam228b	207921	3.4	2.2	1.4	-1.34727	0.196675	-1.88846	0.0002594
chr4:129491190-12949195	Fam229a	68233	4.6	0.4	0.9	-4.91364	0.003052	-2.9991	0.0132983
chr10:39118808-39133895	Fam229b	66337	51.3	13.7	8.9	-3.09874	3.60E-05	-4.13402	1.65E-09
chr7:131334622-13133671	Fam24a	68223	3.8	0.0	0.5	-5.23637	0.003171	-2.88614	0.0271162
chr8:72219730-72223775:	Fam32a	67922	133.8	125.2	78.1	1.04356	0.774894	-1.36667	0.0005354
chrX:74384720-74393139:	Fam3a	66294	47.3	37.3	25.4	-1.13984	0.311225	-1.48352	2.11E-05
chr16:97471086-97504936	Fam3b	52793	1.2	0.4	5.0	-2.05561	0.096235	4.38653	1.28E-08
chr6:22306522-22356081:	Fam3c	27999	52.4	45.6	61.0	-1.02872	0.756793	1.45263	2.47E-12
chr16:30599723-30602797	Fam43a	224093	11.3	20.6	11.7	1.99376	0.003669	1.2856	0.227994
chr19:60811570-60836229	Fam45a	67894	41.5	37.9	40.3	1.0213	0.836028	1.21267	0.0009537
chr9:85320439-85327150:	Fam46a	212943	30.6	23.7	11.6	-1.16847	0.592493	-2.04699	0.0001727
chr12:12262139-12376361	Fam49a	76820	45.2	40.7	15.9	-1.01272	0.971848	-2.20042	2.77E-05
chr15:63929094-64060448	Fam49b	223601	25.4	28.9	44.0	1.28136	0.061626	2.14377	6.93E-15
chrX:74313033-74320149:	Fam50a	108160	48.7	39.4	46.0	-1.10366	0.256886	1.18063	0.0078595
chr13:34739642-34747622	Fam50b	108161	2.8	0.2	0.3	-5.70691	0.0017	-3.7284	0.0048444
chr5:33600353-33629635:	Fam53a	74504	32.3	26.6	37.5	-1.08664	0.389725	1.44713	1.10E-08
chr7:132712084-13281319	Fam53b	77938	22.5	17.1	10.3	-1.16272	0.316902	-1.73994	2.29E-07
chr11:76202056-76208257	Fam57a	116972	14.3	12.4	23.5	-1.02626	0.899151	2.03365	7.76E-12
chr11:78750506-78751729	Fam58b	69109	31.6	31.8	48.4	1.12594	0.30465	1.90677	1.71E-16
chr3:95282935-95296164:	Fam63a	75007	47.7	44.6	22.4	1.05419	0.775622	-1.68967	2.27E-06
chr9:70599014-70657174:	Fam63b	235461	23.7	22.6	13.8	1.06202	0.452526	-1.37516	6.37E-09

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr8:105605229-10562221	Fam65a	75687	16.2	12.8	9.4	-1.12456	0.447064	-1.36814	0.0038195
chr2:167980786-16801059	Fam65c	69553	4.2	4.5	1.0	1.15684	0.698199	-2.96196	6.49E-06
chr5:107908042-10798707	Fam69a	67266	36.5	24.0	9.0	-1.3631	0.323141	-3.01257	7.12E-07
chr2:26628457-26636497:	Fam69b	56279	23.9	19.7	11.7	-1.09739	0.693272	-1.61492	0.0012762
chr1:191162584-19116481	Fam71a	619288	2.3	0.1	0.2	-6.04509	0.001087	-4.39531	0.0014759
chr11:46404728-46407985	Fam71b	432552	2.0	0.1	0.2	-7.39906	5.89E-05	-4.47719	0.0004231
chr12:78691535-78734519	Fam71d	70897	8.2	0.7	1.0	-7.49548	3.85E-07	-4.95218	3.03E-06
chr7:44496588-44501134:	Fam71e1	75538	12.9	4.2	3.6	-2.58194	0.001384	-2.67153	7.20E-05
chr7:4753226-4771270:-	Fam71e2	243822	3.3	0.2	0.2	-7.75816	2.46E-05	-7.08801	2.96E-06
chr6:29319140-29336022:	Fam71f1	330277	7.0	0.2	0.7	-12.49	5.44E-08	-5.47632	2.22E-05
chr6:29281141-29290676:	Fam71f2	245884	14.0	1.9	2.0	-5.27198	4.43E-06	-4.66547	1.01E-06
chr2:30364233-30385519:	Fam73b	108958	27.6	29.4	37.7	1.20154	0.138031	1.69858	4.63E-09
chr4:132899213-13292255	Fam76a	230789	52.2	39.1	31.9	-1.19624	0.00822	-1.30865	6.58E-07
chr9:13827727-13846522:	Fam76b	72826	47.8	38.3	30.3	-1.12126	0.28349	-1.25994	0.0028978
chr9:70089310-70141557:	Fam81a	76886	2.0	2.1	0.6	1.13985	0.657842	-2.72082	1.50E-06
chr7:45721220-45729492:	Fam83e	73813	1.7	1.5	4.0	1.01981	0.972822	2.61243	0.0013343
chr12:14147598-14152038	Fam84a	105005	29.3	12.4	8.7	-1.97587	0.089531	-2.41088	0.0042185
chr8:124740257-12475180	Fam89a	69627	1.0	1.5	3.1	1.61579	0.251169	3.31887	4.01E-05
chr19:5728087-5729666:-	Fam89b	17826	64.9	49.5	34.1	-1.17546	0.046794	-1.51861	1.65E-11
chr4:12153722-12172015:	Fam92a	68099	74.7	72.0	85.5	1.0799	0.427884	1.42746	6.02E-08
chr9:66126611-66138968:	Fam96a	68250	55.2	53.6	58.5	1.08499	0.569238	1.3197	0.0034341
chr8:104639839-10464172	Fam96b	68523	50.3	60.9	73.9	1.35624	0.002776	1.82798	6.84E-14
chr17:75537086-75551946	Fam98a	72722	27.6	32.6	51.0	1.33069	0.062632	2.2816	3.64E-13
chr2:117249739-11727154	Fam98b	68215	18.1	16.6	21.8	1.03275	0.834392	1.50014	2.41E-06
chr7:29152510-29156210:	Fam98c	73833	30.5	22.0	13.9	-1.23356	0.079559	-1.74023	1.19E-09
chr13:63304709-63431745	Fancc	14088	43.8	27.9	10.2	-1.4023	0.145374	-3.25686	4.44E-12
chr6:113531682-11359628	Fancd2	211651	3.3	3.1	1.7	1.03319	0.899151	-1.56903	0.0023283
chr6:113596762-11360071	Fancd2os	70979	1.1	0.1	0.1	-3.83375	0.019599	-3.66796	0.0045179
chr7:51860577-51862267:	Fancf	1E+08	14.0	13.2	14.9	1.05212	0.764863	1.32597	0.0058524
chr4:43002337-43010301:	Fancg	60534	11.6	8.0	3.1	-1.30523	0.055627	-2.94997	1.20E-22
chr7:79392338-79450264:	Fanci	208836	2.3	2.3	0.9	1.12841	0.593985	-1.97027	1.64E-05
chr12:65075606-65132058	Fancm	104806	8.8	8.5	3.9	1.07839	0.456951	-1.80375	7.77E-17
chr7:133776891-13388153	Fank1	66930	3.9	0.5	0.8	-4.76224	0.000445	-3.19358	0.0020445
chr2:62500936-62574021:	Fap	14089	13.3	10.5	4.6	-1.13879	0.532642	-2.25837	6.37E-09
chr7:113513834-11357088	Far1	67420	97.1	105.6	136.9	1.22214	0.073921	1.75282	1.59E-11
chr8:84856986-84869257:	Farsa	66590	50.4	63.9	111.0	1.4289	0.017889	2.71052	4.31E-18
chr1:78417958-78488897:	Farsb	23874	64.7	69.8	139.9	1.20891	0.039375	2.68358	2.06E-48
chr5:24441040-24445235:	Fastk	66587	64.4	52.8	67.2	-1.09656	0.534276	1.30168	0.0085383
chr1:63730625-63753385:	Fastkd2	75619	25.8	29.4	37.8	1.27935	0.00098	1.82986	7.08E-24
chr13:68582248-68592279	Fastkd3	69577	18.5	21.3	21.7	1.29343	0.03955	1.46412	6.62E-05
chr2:130613838-13063002	Fastkd5	380601	19.9	26.0	28.0	1.47247	0.034415	1.7383	9.07E-05
chr8:44950208-45052257:	Fat1	14107	53.9	44.0	53.6	-1.09217	0.42426	1.24377	0.0050881
chr9:15910193-16378231:	Fat3	270120	7.3	6.9	2.6	1.06571	0.787918	-2.18979	2.08E-08
chr3:38886940-39011983:	Fat4	329628	28.4	21.2	11.2	-1.19446	0.406635	-1.99436	3.51E-06
chr11:116142285-1161681	Fbf1	217335	28.8	23.6	13.9	-1.08773	0.468673	-1.65155	1.88E-10
chr7:28169748-28179269:	Fbl	14113	68.7	85.9	234.7	1.40668	0.049902	4.14586	1.54E-28
chr4:141576062-14160605	Fblim1	74202	21.9	19.7	14.1	1.00423	0.977047	-1.24324	0.0057225
chr15:85206008-85286294	Fbln1	14114	241.3	196.1	75.0	-1.10834	0.474942	-2.54675	1.71E-22
chr6:91212764-91272540:	Fbln2	14115	47.2	64.0	187.9	1.5111	0.171998	4.50163	6.20E-12
chr12:101746565-1018191	Fbln5	23876	13.5	11.1	4.7	-1.088	0.582921	-2.2818	1.99E-16
chr2:128863932-12889703	Fbln7	70370	6.4	5.2	2.2	-1.09814	0.766958	-2.24213	3.31E-05
chr18:58008623-58209926	Fbn2	14119	7.0	8.0	10.3	1.2661	0.150068	1.80877	8.94E-07
chr13:62864753-62888282	Fbp1	14121	9.9	1.0	1.4	-5.31245	0.00068	-3.96242	0.0009546
chr9:20607475-20617271:	Fbxl12os	66662	2.2	1.5	0.6	-1.33122	0.383713	-2.65054	6.38E-05
chr5:21483847-21645605:	Fbxl13	320118	9.4	7.1	1.5	-1.17987	0.5822	-4.62361	3.87E-14
chr6:119479668-11948388	Fbxl14	101358	20.5	20.2	21.6	1.11034	0.374096	1.31455	0.0009576
chr19:46328184-46330446	Fbxl15	68431	4.4	5.9	7.8	1.47524	0.028865	2.18311	2.17E-09
chr17:25809085-25821265	Fbxl16	214931	3.9	3.8	1.7	1.09879	0.68752	-1.772	0.0001749

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr9:113976958-11402675	Fbxl2	72179	5.0	3.4	1.0	-1.29589	0.326535	-3.61566	4.82E-11
chr11:98082554-98149616	Fbxl20	72194	42.3	28.7	4.0	-1.32651	0.144193	-7.99653	2.56E-49
chr13:56522508-56537786	Fbxl21	213311	11.2	8.4	2.0	-1.19835	0.50045	-4.28824	1.07E-14
chr14:103080239-1030995	Fbxl3	50789	125.9	113.4	64.5	1.0021	0.986553	-1.55787	1.44E-12
chr5:43744618-43782149:	Fbxl5	242960	106.6	105.4	114.6	1.10601	0.150165	1.34107	1.01E-08
chr15:26540459-26895564	Fbxl7	448987	10.7	9.9	3.9	1.02594	0.921545	-2.14701	4.11E-08
chr8:105264648-10526932	Fbxl8	50788	5.6	4.4	2.3	-1.13611	0.636735	-1.89969	0.0003369
chr4:45034248-45084604:	Fbxo10	269529	19.5	14.2	7.5	-1.23367	0.200877	-2.04064	2.40E-09
chr17:87990859-88065285	Fbxo11	225055	67.1	62.4	42.8	1.04727	0.730877	-1.25229	0.0075445
chr14:65266701-65321502	Fbxo16	50759	6.3	3.6	1.9	-1.5583	0.062851	-2.53177	8.46E-07
chr2:11742573-11777527:	Fbxo18	50755	99.1	77.9	46.8	-1.1427	0.268912	-1.68574	1.10E-09
chr5:117976770-11801019	Fbxo21	231670	48.0	37.6	25.5	-1.14145	0.296713	-1.4963	8.73E-06
chr9:55208935-55224433:	Fbxo22	71999	48.6	54.9	65.8	1.27083	0.079095	1.68126	3.40E-07
chr5:137612505-13762507	Fbxo24	71176	2.8	0.5	0.5	-3.83802	0.002266	-3.44047	0.0006906
chr8:13907806-13940521:	Fbxo25	66822	36.9	32.2	10.7	-1.03269	0.874943	-2.70533	2.27E-18
chr1:182313102-18234160	Fbxo28	67948	33.0	33.0	34.9	1.12121	0.08401	1.32295	1.03E-08
chr2:104027799-10406323	Fbxo3	57443	64.0	54.6	43.9	-1.04578	0.597851	-1.16604	0.0063145
chr15:58175879-58214892	Fbxo32	67731	282.7	185.8	11.1	-1.35907	0.400436	-15.8046	6.94E-29
chr1:84839841-84900486:	Fbxo36	66153	7.0	2.9	1.5	-2.04361	0.024004	-3.33805	2.23E-06
chr11:72314444-72319419	Fbxo39	628100	1.7	0.3	0.2	-3.7513	0.01354	-4.55293	0.0004092
chr15:3963564-3979573:-	Fbxo4	106052	8.4	8.3	14.5	1.09105	0.516512	2.12204	5.42E-19
chr4:148152799-14816009	Fbxo44	230903	20.9	18.6	7.5	1.00941	0.974057	-2.1611	4.44E-07
chr16:32230112-32247025	Fbxo45	268882	22.2	24.8	26.9	1.25735	0.131118	1.50321	0.0003329
chr11:97854307-97884154	Fbxo47	72973	3.6	2.6	1.2	-1.24396	0.42179	-2.41807	1.19E-05
chr11:16951410-16954772	Fbxo48	319701	2.2	1.5	0.6	-1.31201	0.417434	-2.7394	5.06E-05
chr10:5799158-5805465:-	Fbxo5	67141	17.5	13.8	8.6	-1.14037	0.606487	-1.58664	0.0065339
chr4:148145716-14815213	Fbxo6	50762	26.9	23.3	16.7	-1.02951	0.764081	-1.29023	1.71E-05
chr8:56551134-56593939:	Fbxo8	50753	23.8	21.4	13.7	1.00054	0.997301	-1.3886	2.90E-06
chr11:62847123-62877462	Fbxw10	213980	5.4	1.8	1.0	-2.56188	0.002606	-3.78647	2.46E-07
chr11:32642555-32746814	Fbxw11	103583	54.4	58.2	71.5	1.20563	0.140405	1.63524	1.37E-07
chr13:50417877-50433769	Fbxw17	109082	36.9	39.1	80.4	1.18355	0.117782	2.69925	1.30E-38
chr2:34804364-34826235:	Fbxw2	30050	31.9	31.7	35.8	1.11751	0.228035	1.3987	3.97E-07
chr3:84815577-84979198:	Fbxw7	50754	21.1	20.0	26.7	1.06679	0.577976	1.57844	6.68E-10
chr5:118064981-11815545	Fbxw8	231672	50.0	48.3	68.0	1.08876	0.404748	1.70039	1.78E-14
chr12:84970930-84983303	Fcf1	73736	99.4	119.8	139.4	1.35276	0.007649	1.74404	4.37E-10
chr3:96282909-96293969:	Fcgr1	14129	5.0	8.0	10.9	1.76233	0.013985	2.6125	8.35E-08
chr7:45092993-45103822:	Fcgrt	14132	268.2	223.0	37.8	-1.07853	0.502409	-5.62504	2.37E-117
chr13:98723406-98815449	Fcho2	218503	63.9	55.6	23.5	-1.02886	0.817692	-2.16375	6.53E-28
chr18:37957434-37969731	Fchsd1	319262	15.6	13.1	5.9	-1.06688	0.676781	-2.08246	5.64E-14
chr2:25624667-25627974:	Fcna	14133	2.9	1.7	0.4	-1.43076	0.374468	-4.02889	5.25E-06
chr3:87250965-87263524:	Fcrls	80891	24.0	21.8	29.0	1.01722	0.948404	1.48799	0.0043676
chr14:63145150-63177793	Fdft1	14137	30.9	38.3	63.2	1.39893	0.228618	2.44632	9.53E-06
chr3:89093588-89101967:	Fdps	110196	26.9	31.8	107.0	1.32198	0.133995	4.82168	2.14E-32
chr9:51943025-51963602:	Fdx1	14148	13.1	13.0	12.9	1.11488	0.314573	1.22937	0.0080064
chr11:115268025-1152769	Fdxr	14149	14.6	13.0	7.5	-1.00125	0.995455	-1.53749	5.74E-05
chr18:64456550-64489066	Fech	14151	54.1	41.1	32.2	-1.17949	0.055166	-1.3404	7.68E-06
chr17:56256793-56263608	Fem1a	14154	24.5	31.7	51.7	1.46109	0.054446	2.57418	1.47E-10
chr9:62791830-62811648:	Fem1b	14155	52.3	57.6	71.0	1.24075	0.06052	1.6902	9.90E-10
chr19:10199132-10203943	Fen1	14156	18.6	17.1	27.7	1.02729	0.899039	1.84741	6.99E-08
chr8:121054882-12108311	Fendrr	68790	1.8	1.5	0.4	-1.05301	0.892971	-3.57543	6.57E-08
chr2:156019140-15605294	Fer1l4	74562	0.2	0.2	0.6	1.23603	0.609263	3.07165	6.43E-06
chr14:45458792-45530065	Fermt2	218952	228.2	222.6	247.2	1.09698	0.45203	1.35116	0.0003998
chr17:78369212-78418152	Fez2	225020	11.4	11.1	15.3	1.09039	0.373479	1.68204	9.55E-16
chr19:38097079-38114263	Ffar4	107221	0.9	1.0	2.0	1.21317	0.723507	2.39286	0.0085714
chr16:16416915-16599978	Fgd4	224014	40.9	35.2	22.5	-1.0457	0.74955	-1.45038	1.19E-05
chr6:91987110-92076005:	Fgd5	232237	19.6	14.8	8.4	-1.18687	0.027564	-1.87038	2.10E-25
chr10:94036001-94145339	Fgd6	13998	12.6	9.0	5.8	-1.24951	0.18416	-1.70785	1.46E-05
chr13:118714699-1187925	Fgf10	14165	8.6	5.4	1.6	-1.40523	0.334802	-3.80602	9.86E-08

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:69796068-69801716	Fgf11	14166	7.7	7.4	3.6	1.05777	0.787372	-1.69901	3.53E-05
chrX:59062146-59585572:	Fgf13	14168	1.0	0.7	0.2	-1.30958	0.454862	-3.54699	5.59E-06
chr11:33116978-33147400	Fgf18	14172	4.8	2.8	1.1	-1.48237	0.273003	-3.15617	1.72E-05
chr3:37348653-37404830:	Fgf2	14173	18.1	17.6	33.7	1.0838	0.661974	2.30253	6.80E-15
chr7:45613890-45615490:	Fgf21	56636	0.1	0.0	2.1	-1.08811	0.923231	11.8404	3.94E-08
chr14:58072686-58112720	Fgf9	14180	5.4	4.0	1.7	-1.16383	0.661345	-2.34046	0.0001346
chr8:25518759-25575718:	Fgfr1	14182	50.4	43.6	26.2	-1.03425	0.797423	-1.53441	2.58E-08
chr6:146577911-14659919	Fgfr1op2	67529	91.2	92.7	104.6	1.14287	0.178226	1.43033	7.48E-07
chr7:130162451-13026680	Fgfr2	14183	173.0	134.3	80.6	-1.15914	0.324635	-1.70508	4.72E-07
chr5:33721724-33737068:	Fgfr3	14184	3.8	6.6	8.8	1.9188	0.069612	2.6424	0.0003803
chr4:95557507-95926939:	Fggy	75578	20.3	16.8	3.8	-1.07432	0.626126	-4.18081	4.71E-46
chr5:21372673-21378386:	Fgl2	14190	326.3	273.2	157.1	-1.0819	0.76952	-1.63975	0.0025571
chr1:175601378-17562563	Fh1	14194	83.1	88.4	140.5	1.18821	0.019654	2.10579	1.10E-41
chr4:141890623-14201165	Fhad1	329977	3.7	0.7	0.6	-4.04922	0.000282	-4.07032	1.78E-05
chr14:9550094-11162032:	Fhit	14198	7.9	5.8	3.2	-1.21502	0.375201	-1.95161	3.77E-05
chr4:124700699-12470861	Fhl3	14201	10.4	11.9	36.0	1.28638	0.131605	4.21798	2.76E-35
chr10:85097019-85102495	Fhl4	14202	31.4	2.6	4.5	-7.48477	3.80E-07	-4.28295	3.04E-05
chr4:25199909-25242876:	Fhl5	57756	14.6	9.0	1.7	-1.43461	0.301522	-5.68167	1.75E-11
chr8:105329160-10534797	Fhod1	234686	15.6	11.3	5.5	-1.23541	0.25027	-2.23021	1.47E-09
chr18:24708623-25133507	Fhod3	225288	4.4	3.8	1.7	-1.01521	0.959742	-1.97644	1.81E-05
chr2:110360925-11036299	Fibin	67606	23.7	13.6	3.3	-1.52369	0.323764	-4.65457	4.05E-07
chr19:5460607-5465052:+	Fibp	58249	70.0	65.4	68.9	1.0473	0.545215	1.22914	3.31E-05
chr5:113735782-11374060	Ficd	231630	7.3	7.7	12.6	1.1947	0.228514	2.15634	5.54E-14
chrX:164373548-16440264	Figf	14205	17.2	12.4	5.0	-1.25236	0.420316	-2.62317	8.25E-07
chr15:101050192-1010543	Fignl2	668225	8.1	7.2	3.8	1.00196	0.993556	-1.69354	1.88E-06
chr5:74535482-74597124:	Fip1l1	66899	68.1	68.7	78.5	1.13202	0.111019	1.4415	1.52E-10
chrX:50555744-50635258:	Firre	103012	81.1	63.5	29.9	-1.13953	0.222695	-2.1547	7.27E-24
chr5:136953275-13696623	Fis1	66437	124.6	117.6	127.8	1.05671	0.64192	1.27941	0.0011509
chr2:163468703-16347262	Fitm2	228859	21.5	21.3	28.3	1.1104	0.501829	1.63322	1.87E-06
chr7:5007056-5014728:-	Fiz1	23877	26.6	30.9	32.1	1.30825	0.024985	1.50516	1.02E-05
chr11:100415694-1004248	Fkbp10	14230	43.2	33.1	49.3	-1.17307	0.189499	1.41648	8.44E-05
chr6:54577605-54593128:	Fkbp14	231997	20.0	43.9	40.7	2.31825	0.019445	2.30705	0.0035301
chr4:62300342-62360548:	Fkbp15	338355	47.7	44.9	46.8	1.05632	0.542068	1.22646	0.0006378
chr2:151542483-15156169	Fkbp1a	14225	67.7	76.1	116.9	1.2658	0.078309	2.13953	1.14E-14
chr19:6977739-6980461:-	Fkbp2	14227	62.1	55.9	93.5	1.00553	0.967389	1.87621	4.83E-21
chr12:65062432-65073938	Fkbp3	30795	124.2	115.8	127.2	1.04128	0.707387	1.27835	0.0002041
chr6:128430107-12843863	Fkbp4	14228	212.8	385.3	477.5	1.99251	0.020346	2.62236	3.45E-05
chr17:28398753-28486149	Fkbp5	14229	4.8	11.9	11.3	2.63168	0.000167	2.77868	3.25E-06
chr2:76663034-76673098:	Fkbp7	14231	69.8	61.1	19.9	-1.03009	0.861625	-2.77867	1.12E-25
chr6:56832059-56879360:	Fkbp9	27055	175.8	148.6	109.7	-1.06321	0.546111	-1.28184	0.0002395
chr7:16809267-16816732:	Fkrp	243853	19.6	24.2	34.8	1.38568	0.007843	2.19364	1.76E-16
chr3:89402673-89411863:	Flad1	319945	38.9	30.0	23.1	-1.16293	0.204471	-1.33941	0.0008957
chr11:59791408-59810039	Flcn	216805	52.1	40.7	24.7	-1.14678	0.084075	-1.68128	1.25E-18
chr11:60714146-60727263	Flii	14248	102.0	103.2	120.7	1.14022	0.22468	1.47627	5.84E-07
chrX:74223461-74246534:	Flna	192176	####	1251.4	1864.2	1.07807	0.561588	1.79026	2.99E-12
chr14:7817957-7951587:+	Flnb	286940	84.0	118.9	154.4	1.59003	0.04504	2.22514	5.95E-06
chr6:29433153-29461888:	Flnc	68794	44.3	72.0	163.4	1.81633	0.002381	4.39399	6.43E-21
chr19:7092011-7105729:-	Flrt1	396184	9.7	24.9	5.7	2.75071	0.000678	-1.32367	0.303006
chr2:140658198-14067147	Flrt3	71436	15.6	7.6	3.8	-1.75869	0.167841	-2.84086	0.0006326
chr5:147562196-14772598	Flt1	14254	13.4	14.0	20.0	1.17535	0.29409	1.84651	1.36E-08
chr7:45131189-45136432:	Flt3l	14256	33.1	21.8	9.8	-1.36373	0.123214	-2.62507	2.05E-10
chr17:23776918-23786077	Flywch2	76917	19.9	16.4	7.9	-1.08822	0.711569	-1.97835	3.34E-06
chr2:113327736-11371676	Fmn1	14260	4.7	3.4	2.5	-1.22564	0.06968	-1.53149	5.23E-07
chr2:52857868-53134202:	Fmnl2	71409	37.8	32.1	13.7	-1.04813	0.592725	-2.20535	3.62E-44
chr15:99317223-99370466	Fmnl3	22379	22.8	18.0	14.4	-1.13107	0.170274	-1.26753	0.0003941
chr1:162829561-16286654	Fmo1	14261	94.6	63.7	5.6	-1.3328	0.086141	-12.6879	4.47E-88
chr1:162875047-16289871	Fmo2	55990	148.4	83.9	6.7	-1.58107	0.000732	-16.802	9.44E-136
chr1:162793883-16281254	Fmo4	226564	1.1	0.4	0.1	-2.26054	0.10251	-4.38152	0.0001728

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr3:97628804-97655287:	Fmo5	14263	16.2	10.9	0.9	-1.32606	0.305734	-12.6695	7.00E-37
chr1:134037515-13404827	Fmod	14264	10.1	6.9	3.0	-1.29904	0.389906	-2.52894	1.57E-05
chr11:121434953-1214504	Fn3k	63828	9.1	4.5	0.1	-1.73393	0.190779	-25.8321	3.87E-24
chr11:121421373-1214307	Fn3krp	238024	34.8	28.4	13.3	-1.10132	0.555357	-2.06771	1.58E-11
chr2:31026206-31142008:	Fnbp1	14269	64.9	63.3	30.7	1.0983	0.447619	-1.67859	7.19E-10
chr3:122538719-12261971	Fnbp1l	214459	50.0	40.4	19.0	-1.10765	0.355837	-2.09481	4.73E-22
chr17:7738568-7804974:-	Fndc1	68655	19.8	14.4	6.1	-1.22424	0.413751	-2.5235	6.69E-08
chr5:31292246-31295877:	Fndc4	64339	19.8	20.7	35.3	1.1669	0.062344	2.22372	1.70E-43
chr4:129137060-12914459	Fndc5	384061	21.3	17.3	5.2	-1.10315	0.656718	-3.16767	2.24E-16
chr11:82892145-82900737	Fndc8	78919	1.8	0.4	0.2	-3.36553	0.012323	-4.97622	4.20E-05
chr11:54438179-54518241	Fnip1	216742	73.2	59.5	35.5	-1.10537	0.330333	-1.64668	4.15E-12
chr3:79455971-79567679:	Fnip2	329679	19.0	17.6	22.4	1.03548	0.84948	1.46631	0.0002411
chr8:25998722-26015601:	Fnta	14272	99.5	106.8	101.9	1.20598	0.111162	1.2767	0.006592
chr4:88094630-88411011:	Focad	230393	28.3	22.8	16.4	-1.10801	0.177041	-1.37944	7.18E-09
chr7:101839988-10185719	Folr2	14276	7.7	5.5	2.9	-1.24272	0.538733	-2.0159	0.003833
chr12:85473901-85477270	Fos	14281	7.2	94.5	48.3	8.57197	6.36E-07	5.17764	1.61E-05
chr19:5447698-5455938:+	Fosl1	14283	0.1	1.5	2.6	3.99138	0.019451	6.10247	0.0001014
chr5:32136472-32157839:	Fosl2	14284	42.5	129.9	161.3	3.24981	5.76E-07	4.36924	5.04E-13
chr13:31806646-31810635	Foxc1	17300	1.6	2.2	2.4	1.4714	0.144193	1.77632	0.0037076
chr11:116330704-1163353	Foxj1	15223	4.4	3.8	0.7	-1.05512	0.91883	-4.32899	4.54E-07
chr4:119539661-11962911	Foxj3	230700	40.2	39.1	40.0	1.09404	0.397021	1.24321	0.003732
chr5:142401497-14246201	Foxk1	17425	19.4	17.5	9.6	1.00898	0.954881	-1.60423	6.05E-09
chr11:121259987-1213098	Foxk2	68837	21.0	32.3	65.3	1.7202	0.003427	3.73818	4.15E-19
chr9:98955607-98958126:	Foxl2	26927	4.1	6.3	11.8	1.68825	0.140494	3.1984	9.42E-06
chr17:88440712-88490533	Foxn2	14236	24.5	39.9	54.1	1.80163	0.046675	2.58537	2.72E-05
chr12:99195094-99450074	Foxn3	71375	83.4	71.3	16.9	-1.04955	0.726992	-3.88667	1.52E-58
chr3:52268337-52350109:	Foxo1	56458	30.7	33.1	35.4	1.21734	0.245311	1.43405	0.0037198
chr10:42185786-42276742	Foxo3	56484	51.8	49.4	14.1	1.06902	0.561803	-2.90988	4.10E-45
chrX:101254528-10126087	Foxo4	54601	41.9	33.5	6.5	-1.12547	0.439966	-4.99815	5.42E-52
chr6:98925342-99435345:	Foxp1	108655	49.1	36.4	16.0	-1.2137	0.146131	-2.42832	7.19E-20
chr6:14901349-15441977:	Foxp2	114142	8.9	7.0	1.1	-1.13736	0.474942	-6.32262	1.78E-46
chr13:31558170-31560974	Foxq1	15220	1.9	1.2	0.4	-1.31098	0.619568	-2.98006	0.0026873
chr9:35204221-35211055:	Foxred1	235169	25.6	22.4	38.5	-1.0165	0.901981	1.87285	1.09E-19
chr15:77940522-77956722	Foxred2	239554	12.1	10.4	13.5	-1.03202	0.837573	1.39354	0.0001414
chr2:152931898-15293320	Foxs1	14239	5.1	38.5	39.2	6.29753	1.76E-06	6.73449	1.34E-08
chr2:32682609-32694175:	Fpgs	14287	25.4	56.1	86.4	2.31608	0.027712	3.61312	1.37E-05
chr19:38188479-38224132	Fra10ac1	70567	35.9	31.0	39.3	-1.03942	0.809604	1.36127	0.0009565
chr5:96373955-96784728:	Fras1	231470	5.8	4.9	1.5	-1.06106	0.829198	-3.0419	1.96E-12
chr19:41829970-41832583	Frat1	14296	6.9	3.5	0.7	-1.70475	0.162835	-6.17214	2.76E-10
chr19:41845976-41848132	Frat2	212398	6.4	4.4	0.6	-1.31742	0.393123	-7.25223	4.66E-16
chr4:82897920-83052167:	Frem1	329872	14.2	10.6	1.3	-1.19246	0.487215	-7.93578	7.90E-34
chr3:53513938-53657355:	Frem2	242022	16.3	10.0	1.5	-1.44944	0.107587	-8.10245	1.22E-34
chr8:41397454-41417118:	Frg1	14300	81.7	73.9	45.7	1.00918	0.948764	-1.42702	2.34E-06
chr2:4152863-4614043:+	Frmd4a	209630	12.6	10.9	8.3	-1.0282	0.783293	-1.21638	0.0013649
chr2:121545529-12180705	Frmd5	228564	1.6	1.4	0.6	-1.05425	0.882932	-2.03055	0.0007138
chr12:70825514-70902234	Frmd6	319710	38.8	36.0	80.7	1.03464	0.800645	2.58515	8.08E-36
chr19:5850974-5875208:-	Frmd8	67457	26.9	26.2	14.1	1.09357	0.31757	-1.51584	1.05E-10
chr17:47695207-47704286	Frs3	107971	7.6	5.3	3.5	-1.28738	0.326052	-1.70288	0.0045844
chr17:47699969-47701996	Frs3os	1E+08	1.5	0.0	0.2	-4.60079	0.007785	-3.09753	0.017728
chr5:150259930-15049775	Fry	320365	12.9	9.5	4.6	-1.21387	0.220441	-2.19439	5.63E-12
chr5:73020191-73256618:	Fryl	72313	49.6	38.0	21.7	-1.16531	0.129505	-1.81938	5.55E-16
chr2:80411970-80447396:	Frzb	20378	10.8	11.3	33.3	1.17376	0.304343	3.77742	7.13E-37
chr12:64471333-64474898	Fscb	623046	5.3	0.3	0.6	-7.81793	1.49E-05	-4.69977	0.0001832
chr5:142960355-14297318	Fscn1	14086	20.3	18.0	21.4	-1.01471	0.937512	1.3133	0.0057536
chr6:28427901-28438622:	Fscn3	56223	4.6	0.7	0.9	-4.43891	0.000904	-3.26278	0.0017366
chr17:55986511-55996881	Fsd1	240121	4.8	4.7	1.9	1.07159	0.83478	-1.97248	0.000737
chr4:53631471-53707009:	Fsd1l	319636	15.6	11.9	5.0	-1.18135	0.261605	-2.4758	8.95E-18
chr13:114452262-1144589	Fst	14313	1.6	2.6	18.5	1.68328	0.184099	11.2933	1.86E-18

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr10:79777274-79782630	Fstl3	83554	8.2	9.8	20.6	1.33204	0.363873	2.91727	9.79E-07
chr11:52764706-53187347	Fstl4	320027	8.4	10.1	11.1	1.33614	0.160576	1.63708	0.0013588
chr8:91313525-91668433:	Fto	26383	68.6	54.2	43.8	-1.13081	0.168265	-1.24911	0.0008378
chrX:8238668-8252406:-	Ftsj1	54632	17.3	19.6	23.8	1.2778	0.067368	1.7069	8.42E-08
chr11:106249144-1062558	Ftsj3	56095	69.2	110.0	285.1	1.77655	0.012826	4.82559	1.18E-18
chr3:152210458-15223683	Fubp1	51886	122.5	137.8	208.4	1.27187	0.14847	2.10031	1.20E-09
chr2:31572651-31617526:	Fubp3	320267	46.1	42.1	58.8	1.02567	0.845607	1.58923	1.59E-10
chrX:17556569-17572297:	Fundc1	72018	47.0	40.3	28.4	-1.04693	0.710983	-1.32166	0.0002987
chrX:75382399-75397158:	Fundc2	67391	41.1	35.3	40.9	-1.04328	0.700575	1.24351	0.0014007
chr7:140097815-14010244	Fuom	69064	17.1	15.1	6.9	-1.02964	0.930941	-1.94813	0.000244
chr7:80389194-80405431:	Furin	18550	30.7	35.4	35.0	1.29795	0.070251	1.41726	0.0015717
chr8:31187331-31261924:	Fut10	171167	23.7	19.2	5.6	-1.10946	0.543035	-3.28958	3.04E-26
chr7:45648591-45666394:	Fut2	14344	6.4	5.6	12.0	-1.0286	0.941301	2.24831	3.57E-05
chr9:14748459-14752122:	Fut4	14345	3.7	4.6	5.3	1.38426	0.144842	1.75401	0.0007099
chr4:25609333-25800003:	Fut9	14348	10.5	9.4	3.6	-1.01345	0.968189	-2.29453	3.54E-06
chr7:44896079-44900624:	Fuz	70300	56.9	38.5	15.6	-1.33017	0.177206	-2.82437	1.80E-11
chr4:147868979-14787035	Fv1	14349	29.5	30.2	17.2	1.14802	0.196781	-1.36435	0.0001227
chr7:31051678-31055656:	Fxyd1	56188	219.6	201.3	89.4	1.02052	0.873296	-1.95713	1.60E-21
chr6:117933559-11793733	Fxyd4	108017	101.0	78.6	11.5	-1.14324	0.780593	-5.66519	1.27E-09
chr7:31032723-31042331:	Fxyd5	18301	51.7	55.0	116.5	1.18317	0.41181	2.73468	4.51E-13
chr9:45370185-45396159:	Fxyd6	59095	161.7	139.6	54.4	-1.04052	0.730531	-2.3665	2.31E-35
chr7:31042515-31051454:	Fxyd7	57780	17.2	10.9	3.6	-1.4058	0.217871	-3.49435	2.83E-09
chr9:123789500-12385189	Fyco1	17281	47.1	36.3	16.7	-1.16485	0.342351	-2.22088	1.01E-12
chr10:39369799-39565374	Fyn	14360	70.8	66.0	73.3	1.03826	0.728521	1.29217	0.0001094
chr16:32877784-32908963	Fyttd1	69823	67.1	70.5	87.2	1.18612	0.317416	1.60886	9.49E-05
chr11:102604431-1026080	Fzd2	57265	35.0	24.2	8.1	-1.30138	0.112912	-3.38431	5.25E-23
chr14:65192441-65262463	Fzd3	14365	13.2	11.9	7.6	1.01059	0.939148	-1.38352	7.48E-06
chr7:89404366-89410110:	Fzd4	14366	16.2	12.2	6.8	-1.17327	0.43266	-1.89063	6.81E-06
chr10:81366879-81378370	Fzr1	56371	36.6	33.6	36.9	1.03502	0.787372	1.25996	0.0023991
chr1:193272160-19327318	G0s2	14373	38.5	19.5	5.7	-1.70055	0.162089	-4.44901	1.19E-07
chr12:51348230-51376986	G2e3	217558	26.7	24.8	17.4	1.03607	0.77149	-1.2248	0.0069725
chr11:55469752-55500887	G3bp1	27041	176.8	216.5	456.4	1.37987	0.067731	3.15102	1.17E-18
chr5:92052145-92083744:	G3bp2	23881	89.8	97.5	96.1	1.22255	0.097036	1.33304	0.0018001
chrX:169975043-16997891	G530011O06Rik	654820	0.3	1.1	1.2	3.43469	0.012064	3.86954	0.0005616
chr10:39946912-39960153	G630090E17Rik	1E+08	2.4	1.5	0.6	-1.36834	0.490921	-2.78495	0.00148
chrX:74409486-74429161:	G6pdx	14381	48.3	54.1	86.7	1.26141	0.223527	2.19991	8.24E-09
chr11:119267967-1192856	Gaa	14387	115.0	98.6	71.9	-1.04231	0.674866	-1.27492	9.32E-05
chr8:80764431-80880519:	Gab1	14388	44.8	27.0	7.8	-1.48716	0.016305	-4.43001	2.32E-31
chr6:129533192-12954233	Gabarapl1	57436	310.2	243.6	76.8	-1.15046	0.46177	-3.15464	2.20E-19
chr2:126628907-12667633	Gabpb1	14391	14.1	16.2	20.7	1.29463	0.075218	1.82538	2.50E-08
chr3:95181766-95217942:	Gabpb2	213054	52.2	50.2	53.2	1.07835	0.364374	1.27283	3.50E-05
chrX:72432676-72656246:	Gabra3	14396	12.5	8.5	3.7	-1.31068	0.113017	-2.68442	1.89E-14
chr5:71569734-71658308:	Gabra4	14397	1.7	1.0	0.3	-1.50799	0.06111	-4.0275	2.98E-13
chr5:71700016-72137244:	Gabrb1	14400	5.4	4.7	1.2	-1.01908	0.945529	-3.53699	3.38E-14
chr11:42419757-42632591	Gabrb2	14401	0.9	1.0	0.1	1.1763	0.708661	-5.58591	3.91E-09
chr4:155384979-15539806	Gabrd	14403	3.2	2.9	0.3	1.023	0.95616	-6.34959	6.05E-13
chrX:72257432-72274721:	Gabre	14404	6.2	4.0	0.9	-1.37661	0.22208	-4.92967	2.40E-15
chr11:33550781-33578957	Gabrp	216643	99.3	68.7	13.6	-1.28859	0.159861	-5.61489	8.78E-40
chrX:72825178-72842602:	Gabrq	57249	2.3	0.8	0.1	-2.33691	0.032709	-8.70075	1.22E-11
chr2:70489940-70563357:	Gad1os	68986	3.1	2.8	0.7	-1.02733	0.965734	-2.727	0.0047695
chr6:67035096-67037407:	Gadd45a	13197	28.2	88.6	94.5	3.26156	1.63E-05	3.77398	2.03E-08
chr10:80930091-80932204	Gadd45b	17873	20.4	36.9	34.9	1.94961	0.037374	2.01037	0.0055089
chr13:51846675-51848474	Gadd45g	23882	13.3	399.8	505.8	13.8738	2.74E-09	17.7161	1.41E-13
chr8:84832282-84835482:	Gadd45gip1	102060	31.8	39.0	61.4	1.37896	0.018507	2.38836	4.18E-17
chr5:108569107-10862977	Gak	231580	68.7	69.2	71.8	1.13789	0.339394	1.30498	0.006365
chr19:3409917-3414457:-	Gal	14419	0.0	1.2	5.1	2.53968	0.136964	6.28444	8.67E-05
chr11:3983636-3999328:+	Gal3st1	53897	2.4	1.8	0.9	-1.18572	0.620251	-2.01596	0.0027445
chr12:98202300-98259459	Galc	14420	17.7	16.8	8.7	1.06273	0.656678	-1.61683	3.86E-08

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr4:135965165-13596817	Gale	74246	4.7	5.1	37.4	1.2225	0.351768	9.4644	4.49E-62
chr11:116008357-1160127	Galk1	14635	32.2	26.5	42.1	-1.08896	0.394938	1.63175	8.23E-14
chr2:125859109-12598429	Galk2	69976	30.2	26.7	16.1	-1.01798	0.893238	-1.50374	3.24E-08
chr17:80127471-80185032	Galm	319625	20.8	19.6	5.1	1.04841	0.892618	-3.07604	7.88E-09
chr18:24205344-24286816	Galnt1	14423	92.8	86.6	111.3	1.04283	0.509817	1.49763	1.13E-22
chr11:57645442-57787500	Galnt10	171212	14.5	14.7	16.5	1.14678	0.202128	1.42385	5.04E-06
chr5:25222893-25265918:	Galnt11	231050	41.5	44.5	43.5	1.20542	0.084244	1.30835	0.0010827
chr17:73493751-73710451	Galnt14	71685	0.5	0.7	1.2	1.54991	0.29123	2.93367	0.0001687
chr14:32029103-32058326	Galnt15	78754	282.0	196.0	8.7	-1.28695	0.582842	-17.4359	1.72E-22
chr12:80518990-80603896	Galnt16	108760	33.2	32.8	14.0	1.09184	0.676269	-1.87854	1.73E-06
chr7:111471661-11177997	Galnt18	233733	27.6	29.6	44.5	1.2034	0.101012	2.00967	1.24E-17
chr8:124231394-12434572	Galnt2	108148	56.5	54.1	52.3	1.06963	0.354833	1.15774	0.0047978
chr2:66082766-66124793:	Galnt3	14425	4.1	6.1	9.8	1.59881	0.300865	2.54014	0.0046293
chr10:99108135-99113247	Galnt4	14426	19.8	18.0	21.3	1.01289	0.923985	1.34026	3.44E-05
chr2:57998155-58039171:	Galnt5	241391	2.5	2.2	1.2	1.00348	0.991172	-1.62841	0.0020558
chr5:25181480-25220289:	Galntl5	67909	7.9	0.5	0.9	-8.03426	2.45E-06	-4.98129	2.86E-05
chr8:57774052-58911627:	Galntl6	270049	2.5	1.5	0.5	-1.41926	0.069237	-4.02564	9.75E-18
chr11:116280939-1162839	Galr2	14428	3.1	2.2	0.4	-1.27729	0.43658	-5.35427	2.29E-11
chr4:41755228-41759224:	Galt	14430	28.2	25.6	13.8	1.02002	0.915411	-1.62847	1.52E-06
chr10:80258151-80260968	Gamt	14431	13.8	9.9	2.8	-1.25744	0.405947	-3.58843	2.36E-10
chr19:8898057-8916742:+	Ganab	14376	125.9	114.2	140.1	1.01809	0.857771	1.39006	2.32E-09
chr2:120403896-12046085	Ganc	76051	21.8	15.3	5.7	-1.28187	0.047017	-3.01258	7.28E-31
chr6:125161852-12516646	Gapdh	14433	393.7	500.0	982.2	1.43191	0.084473	3.01732	7.18E-13
chr7:30729779-30743681:	Gapdhs	14447	14.3	1.0	1.7	-7.20647	4.77E-05	-4.47216	0.000379
chr13:110352615-1103571	Gapt	238875	2.3	1.2	0.7	-1.67992	0.129258	-2.37526	0.0010508
chr2:34676983-34755232:	Gapvd1	66691	62.4	64.5	69.5	1.16649	0.255428	1.3884	0.0008537
chr3:129824912-12983139	Gar1	68147	14.8	20.8	42.8	1.5752	0.029835	3.48862	1.33E-15
chr2:32986366-33087204:	Garnl3	99326	12.9	10.1	4.5	-1.14345	0.508971	-2.24954	3.63E-09
chr6:55038001-55079504:	Gars	353172	75.8	86.5	270.0	1.28183	0.058832	4.37499	1.31E-53
chr16:91621397-91646972	Gart	14450	60.6	58.4	112.2	1.08342	0.562732	2.30061	2.98E-21
chr7:51879145-51994458:	Gas2	14453	6.2	4.6	3.6	-1.21497	0.199655	-1.36713	0.0060167
chr10:89408823-89443967	Gas2l3	237436	24.3	13.1	9.7	-1.66577	0.030392	-1.95803	0.0002506
chr1:161035166-16103853	Gas5	14455	219.3	278.4	698.0	1.42937	0.044318	3.85766	1.56E-24
chr8:13465374-13494535:	Gas6	14456	310.9	493.8	990.0	1.76961	0.043479	3.68765	9.39E-10
chr6:88198664-88207032:	Gata2	14461	61.7	49.7	36.7	-1.11476	0.50045	-1.33954	0.0086018
chr5:3639961-3647936:-	Gatad1	67210	62.5	58.2	66.1	1.04457	0.601856	1.32281	1.44E-07
chr8:69907069-69996384:	Gatad2a	234366	31.3	42.6	68.8	1.53201	0.062966	2.64853	1.46E-08
chr3:85574129-85654470:	Gatb	229487	18.9	16.8	9.7	-1.00969	0.956596	-1.54346	2.90E-06
chr5:115333242-11534116	Gatc	384281	18.1	17.5	19.3	1.08333	0.454807	1.33368	5.93E-05
chr2:122594473-12261127	Gatm	67092	17.3	10.8	4.8	-1.42366	0.087204	-2.82672	2.94E-11
chr5:134099748-13414175	Gatsl2	80909	6.6	5.6	1.0	-1.07251	0.732821	-5.14771	4.81E-33
chr11:4218251-4222409:+	Gatsl3	71962	9.8	6.6	4.8	-1.32592	0.112912	-1.61199	0.0004488
chr3:89202925-89208966:	Gba	14466	41.8	37.7	27.5	1.01149	0.917543	-1.21515	0.001198
chr16:70313949-70569720	Gbe1	74185	28.8	25.5	46.7	-1.01171	0.923047	2.02127	1.48E-31
chr19:46152558-46286510	Gbf1	107338	37.3	35.8	50.7	1.08211	0.585416	1.69523	1.36E-08
chr2:28496891-28505415:	Gbgt1	227671	27.0	21.6	9.6	-1.11749	0.630549	-2.19327	1.48E-07
chr5:105215699-10523953	Gbp10	626578	2.4	2.7	0.4	1.21954	0.621874	-3.8394	8.76E-07
chr5:105323026-10534647	Gbp11	634650	3.0	1.6	0.6	-1.5924	0.300296	-3.4885	0.0001462
chr3:142620663-14263800	Gbp2	14469	85.0	105.5	41.0	1.35893	0.14493	-1.6345	0.0020126
chr3:142560052-14257321	Gbp3	55932	52.5	58.8	8.4	1.23691	0.383387	-4.68093	5.25E-20
chr5:105115767-10513958	Gbp4	17472	15.7	16.6	7.6	1.16643	0.534886	-1.63012	0.0037813
chr3:142496934-14252234	Gbp5	229898	17.2	25.9	3.4	1.57913	0.223293	-3.4963	5.12E-06
chr5:105270702-10529369	Gbp6	100702	22.8	33.3	9.5	1.58901	0.062924	-1.8657	0.0011629
chr3:142530336-14255015	Gbp7	229900	53.7	51.8	13.9	1.06459	0.800485	-3.00515	1.67E-14
chr5:105078394-10511029	Gbp9	236573	42.5	41.9	10.6	1.09275	0.660121	-3.14211	1.03E-19
chr6:28416603-28421724:	Gcc1	74375	23.2	31.5	33.2	1.52554	0.029634	1.7576	0.0001869
chr10:58255526-58305592	Gcc2	70297	34.3	27.0	17.9	-1.13908	0.252334	-1.52242	2.63E-07
chr8:84886387-84893921:	Gcdh	270076	48.5	39.5	18.5	-1.10374	0.512431	-2.07682	3.87E-13

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr14:47153895-47189402	Gch1	14528	2.4	5.8	7.2	2.59678	6.06E-05	3.54181	3.40E-10
chr9:77754535-77794489:	Gclc	14629	40.3	51.3	62.9	1.42471	0.015095	1.92589	7.26E-09
chr3:122245557-12226721	Gclm	14630	23.1	18.4	32.3	-1.12821	0.34579	1.73447	1.84E-10
chr5:115565263-11562265	Gcn1l1	231659	45.5	46.1	67.6	1.14307	0.310449	1.84828	2.90E-11
chr19:17326141-17372844	Gcnt1	14537	30.5	23.6	7.4	-1.1649	0.704995	-3.00859	9.34E-06
chr9:70031496-70038088:	Gcnt3	72077	5.0	6.2	0.3	1.2561	0.728493	-5.48853	2.64E-05
chr8:116981828-11699344	Gcsh	68133	42.5	40.1	71.0	1.05462	0.590696	2.08134	1.77E-34
chr3:100162463-10020698	Gdap2	14547	19.1	25.6	25.4	1.50916	0.044766	1.63948	0.0018522
chr7:118688558-11870573	Gde1	56209	74.4	72.4	68.9	1.09055	0.225339	1.15788	0.0053322
chr10:128884546-1288917	Gdf11	14561	15.9	11.1	6.1	-1.28772	0.211309	-2.05398	1.42E-06
chr4:9844372-9862345:+	Gdf6	242316	0.8	0.8	8.4	1.15864	0.738099	10.7285	1.60E-21
chr11:53433286-53437902	Gdf9	14566	2.9	2.1	1.2	-1.26609	0.498726	-1.92181	0.0080333
chr13:3538075-3566261:+	Gdi2	14569	330.5	297.2	393.8	1.00349	0.97798	1.48469	9.50E-10
chr15:7810048-7837580:+	Gdnf	14573	2.8	1.7	5.1	-1.50937	0.037168	2.20508	2.05E-08
chr11:87033794-87074137	Gdpd1	66569	16.2	13.0	7.1	-1.11244	0.531365	-1.81818	1.88E-07
chr7:126766414-12677564	Gdpd3	68616	17.0	12.2	6.6	-1.25043	0.485575	-1.98824	0.0020409
chr12:59013393-59027988	Gemin2	66603	25.4	21.6	26.2	-1.05282	0.74606	1.28778	0.0085888
chr11:58120001-58168539	Gemin5	216766	22.9	32.5	45.3	1.5975	0.055741	2.38572	2.72E-06
chr17:80224489-80228497	Gemin6	67242	16.0	14.9	22.0	1.04282	0.785799	1.71521	2.35E-10
chr7:19564949-19573343:	Gemin7	69731	60.7	71.2	89.2	1.32123	0.131475	1.80969	1.47E-05
chrX:166170480-16619051	Gemin8	237221	16.7	12.6	6.2	-1.19167	0.444179	-2.11214	2.86E-06
chr5:139252324-13927005	Get4	67604	27.6	28.4	48.1	1.15865	0.23339	2.16243	3.08E-19
chr17:24693191-24696156	Gfer	11692	17.3	22.6	49.6	1.4711	0.057527	3.46236	1.02E-16
chr3:67430115-67475068:	Gfm1	28030	34.5	39.2	67.8	1.28147	0.065799	2.4364	2.10E-19
chr8:105716113-10575860	Gfod2	70575	14.4	17.8	18.8	1.35688	0.126511	1.60934	0.0015825
chr6:87042846-87092207:	Gfpt1	14583	34.4	34.3	54.8	1.1191	0.271041	1.98081	5.96E-22
chr19:58235581-58455398	Gfra1	14585	3.6	12.5	103.3	3.3257	0.00135	22.8515	7.44E-25
chr14:70890107-70979840	Gfra2	14586	5.5	5.5	2.3	1.11083	0.698345	-1.85312	0.0003608
chr15:78877190-78894585	Gga1	106039	31.1	29.7	38.3	1.07565	0.523411	1.53743	8.40E-09
chr7:121986722-12202119	Gga2	74105	32.3	29.5	18.7	1.03035	0.882498	-1.3782	0.0048616
chr6:54985095-54992867:	Ggct	110175	9.3	12.9	15.3	1.52116	0.026889	2.01731	1.18E-06
chr7:29170210-29173933:	Ggn	243897	3.2	2.0	0.7	-1.30746	0.559027	-3.06914	0.0003072
chr17:27018035-27036378	Ggnbp1	70772	30.0	13.2	5.5	-1.98282	0.001007	-4.15814	2.50E-16
chr11:84832361-84870738	Ggnbp2	217039	104.6	108.7	117.7	1.17245	0.210064	1.40196	0.0002827
chr13:14052445-14063401	Ggps1	14593	74.2	94.9	85.0	1.438	0.000611	1.4265	7.45E-05
chr15:3317755-3583352:-	Ghr	14600	64.8	52.2	35.6	-1.10829	0.549892	-1.44787	0.0012934
chr2:157329496-15734665	Ghrh	14601	0.0	0.5	1.7	1.75905	0.361577	3.35053	0.0069155
chr11:60417145-60445277	Gid4	66771	45.4	37.7	25.1	-1.07755	0.448322	-1.44123	5.83E-08
chr2:180710226-18072159	Gid8	76425	35.5	32.9	44.0	1.03831	0.636577	1.54731	3.22E-19
chr5:137518880-13752793	Gigyf1	57330	38.0	28.6	10.9	-1.18747	0.348182	-2.71976	4.05E-15
chr6:48676135-48678704:	Gimap9	317758	12.2	14.1	16.2	1.26912	0.249347	1.63445	0.0010027
chr10:7767947-7780917:-	Ginm1	215751	106.9	108.0	105.9	1.13245	0.131772	1.23683	0.0005857
chr8:23226610-23237668:	Gins4	109145	49.2	45.4	18.2	1.02848	0.840938	-2.14713	5.36E-21
chr8:83652678-83664789:	Gipc1	67903	50.1	47.4	55.1	1.0583	0.5659	1.37355	5.28E-07
chr3:152093841-15216590	Gipc2	54120	2.6	2.6	6.6	1.1321	0.70538	3.06197	1.54E-09
chr10:56377300-56390419	Gja1	14609	55.7	69.6	242.0	1.40093	0.111412	5.15296	1.97E-26
chrX:160902116-16090705	Gja6	414089	1.5	0.7	0.4	-1.67734	0.214628	-2.33698	0.0073036
chr14:57098602-57104702	Gjb2	14619	9.0	16.7	18.6	1.98081	0.057298	2.34579	0.0020845
chr4:127351086-12735408	Gjb4	14621	0.3	1.0	0.9	2.82384	0.034926	2.72871	0.0096346
chr11:102799478-1028196	Gjc1	14615	53.9	49.0	27.2	1.0281	0.899354	-1.56983	0.0002215
chr11:59175564-59183213	Gjc2	118454	7.3	4.8	2.2	-1.37276	0.388059	-2.48306	0.0005034
chr5:97455161-97457008:	Gk2	14626	11.5	0.6	1.5	-9.94918	1.29E-07	-4.59211	6.18E-05
chr9:96119429-96182953:	Gk5	235533	13.7	10.5	6.0	-1.16763	0.165763	-1.79813	2.87E-12
chr6:87383319-87388935:	Gkn3	68888	20.1	15.7	3.1	-1.13746	0.676781	-4.80368	2.24E-14
chr9:114401078-11447437	Glb1	12091	40.3	28.3	15.4	-1.28179	0.070359	-2.07153	1.59E-12
chr1:75198235-75210778:	Glb1l	74577	27.5	18.4	13.1	-1.33957	0.00527	-1.66809	1.24E-09
chr9:26763044-26806417:	Glb1l2	244757	18.7	11.7	2.6	-1.411	0.303565	-5.12883	5.88E-12
chr9:26817953-26860823:	Glb1l3	70893	1.4	0.1	0.2	-5.44269	0.001925	-4.00967	0.0023071

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr6:8509600-8597549:+	Glcci1	170772	17.6	12.1	8.0	-1.31298	0.208452	-1.73726	0.0005379
chr9:62057249-62070606:	Glce	93683	40.0	55.5	55.3	1.55961	0.058245	1.69134	0.0037685
chr2:29935409-29959432:	Gle1	74412	48.5	46.2	28.4	1.06442	0.316399	-1.3619	3.78E-12
chr8:111157558-11125920	Glg1	20340	101.6	86.8	59.0	-1.04758	0.530031	-1.37464	6.87E-11
chr13:15463723-15730025	Gli3	14634	16.5	13.1	10.2	-1.13165	0.360417	-1.29218	0.0083798
chr10:111985448-1119972	Glipr1	73690	25.3	34.0	46.8	1.47537	0.069099	2.24042	4.48E-07
chr10:112060189-1120785	Glipr1l1	69286	2.0	0.2	0.2	-4.61946	0.00766	-4.06474	0.0026655
chr4:43957702-43979118:	Glipr2	384009	23.9	29.4	74.5	1.36318	0.042456	3.79191	9.40E-33
chr19:28262448-28680077	Glis3	226075	32.3	27.1	15.3	-1.06035	0.70587	-1.68223	5.19E-08
chr3:88325023-88328631:	Glmp	56700	68.6	60.6	28.8	-1.01569	0.873072	-1.90253	1.18E-31
chr3:80843599-80913660:	Glrb	14658	42.4	33.9	2.9	-1.12239	0.511517	-11.2642	5.01E-85
chr7:137437648-13746859	Glrx3	30926	12.1	13.6	17.0	1.26008	0.090856	1.74515	2.14E-08
chr12:105032689-1050409	Glrx5	73046	31.8	34.9	56.5	1.23945	0.300593	2.17928	7.97E-08
chr1:52163450-52233232:	Gls	14660	71.2	71.5	71.5	1.12697	0.145357	1.25408	0.0002231
chr14:31001393-31012441	Glt8d1	76485	68.9	57.9	35.1	-1.06174	0.516056	-1.56511	2.85E-13
chr10:82650433-82690650	Glt8d2	74782	5.9	3.9	0.7	-1.36694	0.226523	-5.83719	2.26E-17
chr7:15971262-15999495:	Gltscr1	243842	9.0	8.1	5.0	1.00173	0.994231	-1.42362	0.0011934
chr17:46798116-46831413	Gltscr1l	210982	28.5	22.4	11.6	-1.13796	0.159385	-1.94659	3.38E-23
chr14:34310727-34345033	Glud1	14661	135.4	126.5	136.0	1.04688	0.549676	1.25417	6.57E-06
chr16:5013902-5049910:-	Glyr1	74022	116.0	117.9	129.7	1.14581	0.287827	1.3949	0.0002955
chr8:69371025-69395544:	Gm10033	378466	18.0	12.4	8.2	-1.30688	0.213007	-1.72787	0.0005687
chr7:27765673-27770972:	Gm10046	1E+08	5.1	4.4	1.1	-1.05105	0.910235	-3.1113	2.79E-05
chr13:12182717-12186488	Gm10336	328186	23.6	19.3	10.4	-1.09076	0.367354	-1.81341	1.68E-18
chr6:141340553-14134438	Gm10400	1E+08	10.4	6.3	2.4	-1.4543	0.380574	-3.04288	0.000226
chr5:109833501-10983414	Gm10416	667213	8.1	6.3	3.0	-1.1612	0.614625	-2.05289	0.000441
chr1:192136898-19215102	Gm10516	1E+08	3.6	2.3	1.8	-1.38624	0.089531	-1.62432	0.001042
chr4:156021645-15602382	Gm10560	1E+08	29.9	17.5	6.2	-1.50703	0.26258	-3.39157	4.31E-06
chr7:73808222-73816503:	Gm10619	1.01E+08	1.7	0.0	0.1	-9.92977	7.95E-06	-5.32576	0.0001751
chr8:86745699-86747060:	Gm10638	666945	7.9	6.0	1.1	-1.18067	0.749056	-4.48324	3.49E-06
chr3:40853476-40855285:	Gm10731	1E+08	1.6	0.1	0.2	-5.69415	0.001032	-3.99288	0.0018321
chr13:41865915-41913092	Gm10790	1E+08	1.8	0.8	0.5	-1.93675	0.097307	-2.73302	0.001202
chr19:6012620-6018459:+	Gm10814	1.01E+08	2.1	1.2	0.4	-1.51079	0.426895	-3.223	0.0017043
chr17:57092023-57105942	Gm11110	1E+08	7.4	5.4	3.1	-1.22785	0.397633	-1.87306	0.0003941
chr11:94755136-94761182	Gm11545	217122	6.1	3.8	1.1	-1.40333	0.314911	-3.88615	3.16E-08
chr11:104556789-1045621	Gm11665	1E+08	0.5	0.5	1.5	1.03112	0.965255	2.99772	0.001759
chr11:116657108-1166683	Gm11744	1E+08	6.9	7.0	1.8	1.12325	0.681851	-2.94189	1.11E-07
chr4:4527774-4529458:-	Gm11780	622019	4.7	0.3	0.6	-7.68477	2.70E-05	-4.40234	0.0003985
chr4:14930641-14953030:	Gm11837	1E+08	18.7	7.0	3.9	-2.29166	0.002209	-3.51454	2.39E-08
chr11:3309000-3320722:+	Gm11944	1E+08	24.5	14.5	8.0	-1.50891	0.060847	-2.37676	2.85E-07
chr11:6525591-6528760:-	Gm11974	1E+08	41.8	74.9	191.2	1.97366	0.011281	5.20754	2.04E-15
chr11:9048592-9069354:+	Gm11992	626870	2.1	1.1	0.1	-1.67819	0.259358	-7.22855	2.24E-08
chr11:53785489-53859256	Gm12216	622459	13.1	8.5	4.4	-1.37542	0.138273	-2.29965	3.94E-07
chr4:45762377-45764223:	Gm12409	1E+08	1.5	0.4	0.2	-2.36408	0.132025	-3.8414	0.0023394
chr3:95236920-95241109:	Gm128	229588	10.0	1.6	1.4	-4.57426	5.81E-05	-4.61515	2.53E-06
chr4:127126043-12712966	Gm12942	1E+08	28.5	21.0	4.8	-1.21946	0.282613	-4.55181	2.25E-27
chr4:131899478-13192002	Gm12992	545681	5.6	3.5	1.3	-1.43105	0.041854	-3.32508	3.25E-18
chr4:147175866-14751342	Gm13152	195531	17.9	13.3	7.6	-1.21432	0.34592	-1.85871	2.90E-05
chr4:147753974-14780978	Gm13157	1E+08	25.6	21.5	11.9	-1.07002	0.660336	-1.70781	4.22E-08
chr4:145617146-14562439	Gm13212	433801	9.6	7.1	2.8	-1.20681	0.234477	-2.73982	5.15E-16
chr4:146449030-14646944	Gm13251	433791	2.9	2.5	1.4	-1.03348	0.908214	-1.66364	0.0018596
chr2:20968874-20970348:	Gm13375	433408	4.2	2.5	1.4	-1.46446	0.177575	-2.27023	0.0001615
chr2:35549534-35558702:	Gm13446	1E+08	2.2	3.3	6.4	1.58859	0.312196	2.99936	0.0008038
chr4:34743788-34756259:	Gm136	214568	2.1	0.1	0.2	-6.82313	0.000343	-4.85176	0.0005304
chr2:117857291-11811120	Gm13986	329496	2.4	1.8	0.8	-1.22205	0.561956	-2.32077	0.0003629
chr2:128298663-12842935	Gm14005	1E+08	0.6	0.7	4.1	1.34725	0.396376	7.3368	1.54E-18
chr2:119321199-11932619	Gm14207	1E+08	5.9	2.9	0.8	-1.72657	0.137603	-4.61198	1.51E-07
chr2:176708353-17672181	Gm14305	1E+08	36.8	28.3	18.5	-1.17352	0.434892	-1.57567	0.0015695
chr2:177759288-17777327	Gm14322	626802	11.4	8.2	6.6	-1.25706	0.056669	-1.38072	0.0004642

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr2:177828991-17784031	Gm14325	329575	41.8	32.5	21.3	-1.15651	0.242765	-1.56713	5.57E-07
chr2:177498226-17751231	Gm14403	433520	16.0	11.3	6.2	-1.27558	0.062752	-2.04141	6.32E-13
chr2:177464742-17747919	Gm14420	628308	37.0	27.2	18.3	-1.22661	0.253939	-1.60456	0.0002754
chr7:104315031-10432483	Gm15133	622070	1.8	1.6	0.3	-1.0062	0.992975	-3.56457	0.0005185
chr13:111867936-1118719	Gm15326	1.03E+08	8.5	5.1	1.6	-1.46884	0.286236	-3.72185	6.90E-07
chr5:149006962-14901277	Gm15408	1.01E+08	4.1	6.2	8.4	1.68179	0.021412	2.47952	1.16E-07
chr3:89391864-89398779:	Gm15417	545539	3.9	3.1	5.9	-1.10245	0.684016	1.85973	5.64E-06
chr3:96555768-96566801:	Gm15441	1E+08	2.3	1.9	0.5	-1.11599	0.83015	-2.97273	0.0005336
chr7:44986900-44994601:	Gm15545	1.01E+08	9.2	6.6	3.7	-1.24701	0.443308	-1.90808	0.0016081
chr6:88842854-88847274:	Gm15612	1E+08	8.1	4.5	1.5	-1.58099	0.24265	-3.69092	4.97E-06
chr11:102665585-1026822	Gm1564	268491	1.9	0.1	0.3	-11.2096	9.82E-07	-3.86367	0.001719
chr16:31986831-31987791	Gm15694	1.02E+08	6.0	8.7	9.6	1.61556	0.080667	1.94521	0.0013671
chr5:144277061-14428051	Gm15708	1.01E+08	7.0	5.0	2.6	-1.24099	0.363176	-2.09071	1.88E-05
chr5:110167508-11017650	Gm15787	1.01E+08	7.1	5.7	1.5	-1.13305	0.690845	-3.60893	8.42E-10
chr5:121220219-12136857	Gm15800	269700	28.5	23.7	14.9	-1.06803	0.665042	-1.51523	1.45E-05
chr8:58698849-58700796:	Gm15881	1E+08	1.5	0.8	0.2	-1.63789	0.218406	-3.93451	1.64E-05
chr18:23750448-23752305	Gm15972	1.01E+08	5.3	3.3	0.1	-1.39938	0.547341	-7.79856	4.70E-07
chr4:155608297-15562475	Gm16023	1.01E+08	7.5	6.1	3.3	-1.11037	0.696666	-1.79272	0.0006158
chr1:17676027-17727646:	Gm16070	1.03E+08	1.4	0.8	0.2	-1.49212	0.318247	-4.67842	1.16E-06
chr8:25548673-25556083:	Gm16159	1.03E+08	1.2	0.0	0.2	-6.79996	0.00044	-2.86567	0.0268478
chr17:22776230-22817747	Gm16386	1E+08	15.0	11.1	6.4	-1.21248	0.502505	-1.81457	0.0025104
chr1:177991435-17804829	Gm16432	545391	2.1	1.1	0.5	-1.63631	0.113703	-2.96979	1.56E-05
chr15:79742698-79757394	Gm16576	1.01E+08	5.0	3.6	0.7	-1.23951	0.273993	-5.40037	2.46E-28
chr7:127582383-12758859	Gm166	233899	6.5	4.3	0.9	-1.34385	0.22014	-5.0885	8.63E-18
chr4:117213333-11725191	Gm1661	381544	2.5	0.7	0.3	-2.63396	0.075354	-4.24424	0.000564
chr5:33983474-33985006:	Gm1673	381633	5.8	6.7	1.7	1.2726	0.493366	-2.47505	0.0008967
chr9:22071002-22086131:	Gm16845	1.01E+08	5.5	5.0	2.3	1.02191	0.945108	-1.85437	0.000405
chr13:63289154-63297147	Gm16907	1.01E+08	5.8	3.4	1.6	-1.50001	0.196289	-2.71279	1.94E-05
chr14:105106728-1051146	Gm17066	1.01E+08	45.2	42.7	52.7	1.05674	0.511517	1.45538	8.13E-12
chr3:79345376-79464128:	Gm17359	1E+08	2.5	0.0	0.3	-7.15496	0.00031	-3.33533	0.0119109
chr5:104070060-10407760	Gm17660	1E+08	4.8	2.1	0.5	-1.93835	0.145222	-5.04599	9.24E-06
chr2:18027249-18030577:	Gm17762	1E+08	2.1	1.1	0.6	-1.72024	0.160576	-2.70584	0.0007002
chr10:77418376-77420939	Gm17769	1E+08	3.6	2.8	1.4	-1.16076	0.634653	-2.05187	0.0005543
chr9:67133561-67163788:	Gm19299	1.01E+08	0.0	0.0	1.0	0	1	11.8158	5.72E-08
chr8:109339800-10934090	Gm1943	384864	1.7	2.5	3.1	1.60584	0.164836	2.16318	0.0019875
chr1:133249852-13326980	Gm19461	1.01E+08	1.1	0.5	0.2	-1.81945	0.180776	-4.00797	6.19E-05
chr16:42884370-42912070	Gm19522	1.01E+08	2.5	1.4	1.0	-1.59103	0.092763	-2.02506	0.0009313
chr3:40846999-40875609:	Gm2011	1E+08	3.2	1.2	0.6	-2.1858	0.049339	-3.76928	3.78E-05
chr10:30603195-30606634	Gm20300	1.01E+08	24.5	19.2	10.6	-1.14798	0.341314	-1.82378	4.48E-09
chr1:164863121-16487143	Gm20743	433374	1.4	0.3	0.3	-3.36372	0.007785	-3.40261	0.0008711
chr10:92171301-92375373	Gm20757	627800	0.1	0.1	2.4	1.30138	0.704187	14.03	5.75E-12
chr17:94864918-94878321	Gm20939	1E+08	6.4	5.1	2.8	-1.1224	0.64441	-1.77792	0.0004338
chr7:73825924-73836549:	Gm21269	1.01E+08	2.9	0.1	0.5	-6.08902	0.001132	-3.01693	0.0201771
chr1:86351981-86352127:	Gm24148	1.02E+08	31.3	39.4	64.6	1.40364	0.331572	2.42121	0.0003103
chr9:15312611-15312669:	Gm25500	1.02E+08	52.6	65.6	134.9	1.38576	0.28243	3.03628	6.30E-08
chr12:111484609-1114858	Gm266	212539	5.2	3.9	1.3	-1.18278	0.755903	-2.77199	0.0025502
chr13:53393689-53455630	Gm2762	1E+08	4.4	0.3	0.5	-6.62766	0.000151	-4.70031	0.0003033
chr13:52569880-52573225	Gm2848	1E+08	1.3	0.8	0.2	-1.41937	0.560833	-3.03328	0.0087638
chr11:55097985-55113028	Gm2a	14667	81.1	71.4	37.2	-1.01316	0.934399	-1.73457	2.79E-11
chr9:8644078-8740988:-	Gm32014	1.03E+08	1.2	2.2	15.3	1.97611	0.004802	14.2449	5.49E-48
chr2:19655806-19657897:	Gm3230	1E+08	2.4	1.7	0.6	-1.26994	0.612139	-2.93511	0.0007269
chr2:18742709-18760862:	Gm3363	1E+08	3.9	2.0	0.5	-1.63442	0.36782	-4.06544	0.0003635
chr13:62367716-62383174	Gm3604	1E+08	10.2	7.9	3.1	-1.16643	0.610941	-2.4876	4.32E-06
chr12:81376991-81379486	Gm4787	214321	9.0	4.9	3.9	-1.60521	0.059221	-1.81032	0.0021729
chr18:60268301-60273267	Gm4841	225594	3.0	2.5	0.5	-1.09369	0.864972	-3.67792	2.01E-05
chr18:60212077-60247820	Gm4951	240327	18.4	17.6	3.4	1.04576	0.919915	-3.8499	1.47E-08
chr1:21285246-21298312:	Gm4956	241041	2.9	1.0	0.1	-2.27261	0.072074	-8.52633	1.57E-08
chr7:99624067-99627103:	Gm4980	1.01E+08	3.9	12.9	7.1	3.25049	0.001871	2.04278	0.0277676

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr1:180326969-18033054	Gm5069	277333	1.8	1.3	0.8	-1.21907	0.48812	-1.76997	0.0048679
chr13:97560000-97583994	Gm5086	328314	3.1	2.5	0.8	-1.08488	0.87275	-2.72182	0.0008796
chr7:30169922-30180209:	Gm5113	330503	6.4	4.6	3.0	-1.26169	0.208712	-1.68488	0.00015
chrX:102932047-10293422	Gm5126	331480	1.9	1.0	0.5	-1.66692	0.133009	-2.71964	0.0001668
chr13:62772200-62785808	Gm5141	380850	18.7	13.1	3.4	-1.28682	0.398962	-3.98482	3.06E-11
chr14:59158503-59178749	Gm5142	380907	3.6	0.0	0.5	-6.47533	0.000735	-3.29184	0.012934
chr3:37714190-37724360:	Gm5148	381438	1.5	1.4	0.1	1.0454	0.943196	-5.99824	2.61E-06
chr10:111500788-1115013	Gm5176	382421	10.0	10.6	15.6	1.18338	0.588655	1.89611	0.0014033
chr12:64917911-64924591	Gm527	217648	17.5	14.0	3.9	-1.12686	0.700726	-3.36591	5.42E-10
chr7:68618456-68620009:	Gm5334	384639	1.0	0.1	0.2	-4.89542	0.005629	-2.83017	0.0292516
chr14:19594138-19602587	Gm5458	432825	1.3	0.2	0.0	-3.20162	0.05823	-5.43501	0.0003052
chr6:87981683-87984180:	Gm5577	434064	12.8	8.0	1.0	-1.41051	0.193555	-8.397	4.26E-23
chr7:42660108-42692718:	Gm5595	434179	21.9	19.0	8.6	-1.03867	0.832491	-2.0268	1.00E-11
chr8:12385771-12436732:	Gm5607	434280	2.9	0.7	0.1	-2.39641	0.166372	-6.88537	3.65E-05
chrX:142297505-14229923	Gm5643	434858	0.9	0.9	1.8	1.11333	0.82934	2.27715	0.0031392
chr14:7323988-7332395:-	Gm5797	545013	1.3	0.0	0.3	-5.43391	0.002792	-2.39079	0.0722077
chr15:22713820-22714984	Gm5803	545091	2.0	2.7	3.9	1.48736	0.172304	2.30898	5.01E-05
chr6:85111416-85126094:	Gm5878	545861	1.1	0.1	0.2	-4.78707	0.000149	-3.36682	0.0004789
chr7:24818795-24840275:	Gm5893	545936	2.9	0.2	0.3	-6.51611	0.000259	-5.13976	0.0001754
chrX:92489949-92490679:	Gm5941	546347	2.9	0.1	0.3	-4.9618	0.005328	-3.34063	0.0117834
chr16:45416755-45492969	Gm609	208166	11.9	7.8	4.0	-1.35311	0.072854	-2.33372	6.80E-11
chrX:101261377-10126399	Gm614	245536	3.6	1.0	1.9	-2.91435	0.005422	-1.49843	0.18965
chr18:11821088-11839377	Gm6277	621998	4.0	2.2	0.2	-1.59442	0.183706	-11.622	8.34E-15
chr4:40720154-40722841:	Gm6297	622208	7.3	4.0	2.3	-1.61235	0.122832	-2.35162	0.0002948
chrX:109196756-10920044	Gm6377	622976	1.1	1.7	2.2	1.61307	0.213843	2.19704	0.0053822
chr14:48198716-48228413	Gm6498	624367	15.7	15.4	6.1	1.10328	0.720148	-2.00126	5.86E-05
chr7:73097752-73102068:	Gm6567	625243	1.9	0.5	0.2	-3.15211	0.009976	-4.71704	1.97E-05
chr19:30930386-30930962	Gm6642	625995	5.7	5.5	1.2	1.05862	0.891868	-3.33796	6.80E-06
chrX:64151405-64152198:	Gm6760	627470	3.5	0.1	0.3	-8.582	5.68E-05	-4.43182	0.0013073
chr4:141432672-14143610	Gm694	277744	0.5	1.0	3.7	1.91862	0.196421	6.70277	4.59E-08
chr13:119488039-1196104	Gm7120	633640	6.9	5.8	13.9	-1.05657	0.902942	2.37382	0.0004871
chr9:56027636-56031573:	Gm7444	665005	3.9	0.5	0.6	-5.94473	1.46E-06	-4.42454	3.69E-06
chr1:85199611-85213762:	Gm7609	665378	1.8	1.7	0.2	1.04284	0.942053	-4.94969	2.43E-06
chr1:170298193-17030633	Gm7694	665574	4.6	3.9	1.7	-1.03954	0.889766	-2.12126	2.24E-06
chr5:149154128-14915619	Gm8615	667410	1.4	0.6	0.3	-1.83033	0.198981	-2.82088	0.0037502
chr11:103534577-1036147	Gm884	380730	1.5	0.1	0.1	-7.55631	7.49E-05	-6.35753	2.47E-05
chr3:95985510-95986967:	Gm9054	668224	5.2	3.9	7.7	-1.16883	0.659981	1.80986	0.0058664
chr10:122078112-1220798	Gm9079	668272	6.0	4.4	7.6	-1.21654	0.306023	1.57697	0.0004443
chr1:59516264-59634509:	Gm973	381260	17.3	9.9	0.7	-1.54649	0.146974	-15.2054	3.05E-32
chr3:15296551-15332302:	Gm9733	751864	0.4	0.4	3.1	1.0328	0.966836	5.75535	2.05E-06
chr3:10088277-10092562:	Gm9833	1E+08	3.7	3.9	5.8	1.18751	0.40226	1.95894	5.65E-07
chr19:29067301-29069503	Gm9895	1.01E+08	12.5	8.9	2.5	-1.24909	0.449598	-3.67758	2.42E-09
chr17:7363712-7385305:-	Gm9992	667055	2.2	0.9	0.2	-1.87322	0.215126	-5.56456	9.07E-06
chr7:46976632-46987803:	Gm9999	629141	9.5	0.6	1.4	-7.04755	0.000131	-3.62607	0.0033252
chr13:31819586-32338544	Gmds	218138	15.1	14.3	37.9	1.06195	0.799717	3.05739	3.80E-17
chr4:132221025-13226154	Gmeb1	56809	13.7	14.2	17.6	1.17171	0.282126	1.60225	6.55E-06
chr2:181251451-18128796	Gmeb2	229004	20.5	23.1	27.2	1.27527	0.109931	1.64804	1.07E-05
chr9:108049290-10805193	Gmppb	331026	14.0	25.3	63.6	1.97272	0.019661	5.06597	3.53E-13
chr13:45507469-45546381	Gmpr	66355	77.9	53.5	12.5	-1.30883	0.165429	-4.79202	3.19E-28
chr3:63976143-64019078:	Gmps	229363	65.1	68.2	103.2	1.1833	0.276998	1.96436	6.20E-10
chr10:81528732-81545046	Gna11	14672	49.3	44.2	55.4	1.00517	0.959742	1.40732	3.58E-11
chr5:140759944-14083043	Gna12	14673	64.0	57.0	65.1	-1.00502	0.967215	1.27057	0.0001961
chr11:109362794-1094013	Gna13	14674	52.8	77.1	80.5	1.63799	0.039963	1.85546	0.0009043
chr19:16435667-16610818	Gna14	14675	22.2	18.8	10.2	-1.05803	0.756298	-1.72962	6.66E-07
chr5:18265135-18360413:	Gnai1	14677	41.4	36.7	17.0	-1.0166	0.943107	-1.92308	4.36E-08
chr9:107614138-10763534	Gnai2	14678	206.9	242.6	290.2	1.3225	0.093807	1.73374	1.08E-05
chr3:108107275-10814615	Gnai3	14679	137.7	151.5	191.6	1.23725	0.075136	1.72916	7.71E-10
chr18:67088298-67226791	Gnal	14680	5.8	4.3	1.2	-1.19626	0.587579	-3.4661	1.01E-08

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr8:93810838-93969388:	Gnao1	14681	5.6	4.0	2.1	-1.24114	0.270025	-2.0773	2.38E-07
chr2:174284320-17434674	Gnas	14683	226.3	205.1	224.3	1.01701	0.831538	1.23971	2.31E-06
chr4:155491361-15555926	Gnb1	14688	156.1	164.1	215.9	1.18215	0.080889	1.72251	1.43E-14
chr16:18498713-18566680	Gnb1l	13972	4.6	4.2	6.2	1.00543	0.975485	1.66995	4.05E-09
chr5:137528129-13753322	Gnb2	14693	221.2	215.0	270.6	1.09188	0.323298	1.52626	8.60E-12
chr11:48800360-48806241	Gnb2l1	14694	####	2247.3	2309.4	1.09013	0.358541	1.25306	0.0007214
chr3:32583528-32616535:	Gnb4	14696	60.1	45.2	8.8	-1.20012	0.289607	-5.27972	3.03E-42
chr9:75306288-75345923:	Gnb5	14697	22.3	17.5	8.9	-1.14967	0.333631	-1.98245	2.60E-11
chr4:44034075-44084177:	Gne	50798	13.8	10.4	18.2	-1.18859	0.159776	1.64789	1.53E-08
chr4:59035156-59041899:	Gng10	14700	63.1	64.4	68.2	1.1365	0.345097	1.34497	0.0021401
chr6:4003987-4008446:+	Gng11	66066	70.3	56.1	26.4	-1.13143	0.510252	-2.0993	4.29E-09
chr6:66896397-67021361:	Gng12	14701	94.3	128.9	482.2	1.5379	0.078285	5.93237	3.59E-23
chr14:19872559-19977249	Gng2	14702	31.5	28.4	13.7	-1.00216	0.994268	-1.8136	6.69E-05
chr3:146499836-14650554	Gng5	14707	208.4	252.5	305.1	1.36369	0.055233	1.80845	1.24E-06
chr10:80948624-81014925	Gng7	14708	3.9	3.6	1.6	1.02463	0.92663	-1.86258	2.23E-05
chr7:16891786-16895435:	Gng8	14709	4.8	3.4	1.8	-1.25363	0.451963	-2.03822	0.0011507
chr17:35979955-35989462	Gnl1	14670	33.7	35.8	52.5	1.19905	0.190965	1.93576	3.09E-11
chr4:125030014-12505538	Gnl2	230737	105.1	122.9	167.0	1.32102	0.122609	1.95814	5.20E-07
chr14:31012433-31019131	Gnl3	30877	80.8	179.8	338.0	2.40182	0.002816	4.64786	9.35E-11
chrX:150983133-15101732	Gnl3l	237107	36.2	38.5	59.4	1.19773	0.196978	2.03645	1.19E-12
chr17:46725664-46729165	Gnmt	14711	2.0	2.0	3.5	1.13092	0.762036	2.05735	0.0022107
chr18:38327537-38338993	Gnpda1	26384	17.9	12.5	6.9	-1.28108	0.124509	-2.05995	2.59E-09
chr5:69575002-69592285:	Gnpda2	67980	44.3	37.9	10.7	-1.05636	0.800645	-3.23457	3.85E-20
chr14:45376421-45388796	Gnpnat1	54342	17.5	17.6	36.3	1.1311	0.182289	2.58544	1.02E-52
chr17:25234318-25240116	Gnptg	214505	43.5	44.0	47.0	1.13399	0.123006	1.3494	4.64E-07
chr10:121365090-1213972	Gns	75612	102.4	88.5	71.3	-1.03433	0.66547	-1.14857	0.0057476
chr5:110176701-11022315	Golga3	269682	53.8	52.3	67.1	1.0973	0.47273	1.55608	4.10E-07
chr9:118506318-11858251	Golga4	54214	82.8	82.0	95.8	1.11828	0.399436	1.4436	7.52E-05
chr8:23241326-23257080:	Golga7	57437	74.6	77.7	93.5	1.17155	0.186742	1.56065	3.13E-07
chr16:36885011-36933085	Golgb1	224139	65.8	55.3	36.7	-1.05942	0.460996	-1.42947	1.32E-11
chr13:59634996-59675784	Golm1	105348	25.5	22.2	32.4	-1.03282	0.885369	1.57986	0.0002022
chr15:12321496-12351267	Golph3	66629	98.0	138.3	139.6	1.58066	0.085383	1.7294	0.0075444
chr1:133309823-13332302	Golt1a	68338	3.0	1.8	1.0	-1.43668	0.324682	-2.1427	0.0050421
chr6:142387243-14240385	Golt1b	66964	29.1	39.7	60.6	1.53016	0.001482	2.56358	3.62E-18
chr3:88835231-88910099:	Gon4l	76022	24.7	23.4	24.1	1.0651	0.489419	1.22015	0.0013951
chr10:52337024-52382124	Gopc	94221	30.9	26.2	30.9	-1.06066	0.61026	1.24905	0.0031813
chr1:163384909-16340364	Gorab	98376	24.0	21.8	29.4	1.01163	0.934899	1.52867	4.61E-09
chr2:70661509-70691725:	Gorasp2	70231	65.6	73.6	154.6	1.26799	0.145583	2.89538	2.06E-19
chr11:76726602-76763555	Gosr1	53334	40.9	42.6	44.8	1.17121	0.064835	1.36836	1.05E-06
chr11:103676849-1036977	Gosr2	56494	77.2	86.6	165.1	1.26452	0.086532	2.64137	3.26E-22
chr19:43499753-43524605	Got1	14718	13.7	30.1	69.4	2.3653	0.005121	5.50339	3.05E-12
chr8:95864137-95888365:	Got2	14719	71.6	62.3	94.2	-1.03069	0.79805	1.64307	1.92E-13
chr15:76331294-76334899	Gpaa1	14731	34.7	41.4	68.9	1.33924	0.00136	2.46838	1.07E-35
chr2:127425199-12743609	Gpat2	215456	1.7	0.3	0.4	-3.62546	0.007185	-2.82612	0.0075759
chr1:187215511-18735142	Gpatch2	67769	21.4	18.2	21.8	-1.04712	0.50645	1.2759	5.32E-08
chr12:86241878-86291368	Gpatch2l	70373	37.0	38.1	36.4	1.15779	0.096859	1.22876	0.0021021
chr3:88043106-88055994:	Gpatch4	66614	19.9	30.7	98.7	1.72619	0.003501	5.89791	1.74E-33
chr11:102475916-1025561	Gpatch8	237943	35.7	33.0	23.1	1.03743	0.717177	-1.23301	0.0009204
chr13:111425680-1114900	Gpbp1	73274	138.0	162.9	153.1	1.32996	0.070251	1.37786	0.0085537
chr4:116557727-11659388	Gpbp1l1	77110	110.0	106.0	53.6	1.08014	0.331838	-1.63891	5.37E-19
chr1:92831686-92860196:	Gpc1	14733	52.4	46.8	66.4	1.00625	0.969765	1.57586	1.43E-07
chr5:138273660-13827993	Gpc2	71951	11.3	10.0	4.1	1.01166	0.974513	-2.09888	0.0001472
chrX:52272427-52613974:	Gpc3	14734	68.2	54.8	24.1	-1.11552	0.42245	-2.25127	3.81E-18
chrX:52053018-52164923:	Gpc4	14735	16.2	13.8	9.5	-1.04944	0.781065	-1.36228	0.0036206
chr14:116925297-1179795	Gpc6	23888	12.8	11.1	5.3	-1.03169	0.883033	-1.93265	1.76E-08
chr9:114899339-11493398	Gpd1l	333433	40.5	31.5	22.4	-1.15712	0.31807	-1.43894	0.000536
chr5:139423179-13942780	Gper1	76854	6.3	2.9	0.7	-1.88037	0.021824	-6.35187	4.23E-16
chr12:78226655-78684769	Gphn	268566	33.3	30.5	39.2	1.02206	0.852194	1.46583	2.85E-09

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chrX:7697134-7710259:+	Gpkow	209416	26.3	29.6	33.4	1.26952	0.085386	1.57593	1.25E-05
chr13:24943152-24991936	Gpld1	14756	7.1	4.6	2.2	-1.37774	0.011257	-2.56856	6.95E-20
chr8:54779434-55060878:	Gpm6a	234267	23.5	15.4	7.1	-1.35162	0.182602	-2.56809	1.17E-08
chrX:166238943-16638903	Gpm6b	14758	35.4	32.4	41.9	1.02129	0.854346	1.47474	7.53E-10
chr5:31494761-31511627:	Gpn1	74254	43.1	49.2	77.8	1.28478	0.026551	2.2429	1.16E-21
chr4:133584373-13359173	Gpn2	100210	15.9	17.4	27.6	1.23766	0.187887	2.14709	2.19E-11
chr5:122372508-12238276	Gpn3	68080	48.0	43.0	28.4	1.0023	0.987837	-1.34763	0.0001422
chr6:49036518-49058182:	Gpnmb	93695	55.7	45.9	19.9	-1.07023	0.882498	-2.11896	0.0035477
chr8:27085841-27123436:	Gpr124	78560	71.4	47.1	28.9	-1.36294	0.144193	-1.93406	2.94E-05
chr10:14402585-14545036	Gpr126	215798	6.6	6.2	3.4	1.04527	0.792355	-1.56509	1.00E-05
chr12:72069618-72070991	Gpr135	238252	2.3	1.2	0.5	-1.60105	0.236256	-3.21521	0.0001425
chr13:13357620-13393624	Gpr137b	83924	17.5	14.2	4.2	-1.11078	0.688608	-3.24704	5.47E-13
chr13:12614065-12650395	Gpr137b-ps	664862	21.8	16.1	5.6	-1.2182	0.271164	-3.01852	1.14E-17
chr13:19749682-19824257	Gpr141	353346	0.5	0.7	1.8	1.53657	0.337089	3.61859	3.28E-05
chr4:152274362-15228533	Gpr153	100129	14.4	18.5	24.3	1.44438	0.101651	2.05679	1.79E-05
chr2:73341506-73386480:	Gpr155	68526	13.6	9.9	4.1	-1.242	0.297976	-2.62201	8.17E-11
chr4:150087503-15010592	Gpr157	269604	5.3	4.2	1.8	-1.13435	0.516512	-2.25409	1.18E-09
chr3:30855950-30897194:	Gpr160	71862	7.4	4.9	3.0	-1.32684	0.273465	-1.94227	0.0004531
chr3:59096448-59101821:	Gpr171	229323	3.1	4.8	4.5	1.69854	0.041997	1.76803	0.004907
chr2:118277098-11837341	Gpr176	381413	3.1	2.2	5.0	-1.24736	0.515565	1.92869	0.0039409
chr14:121952331-1219651	Gpr183	321019	3.8	4.5	6.7	1.28917	0.476144	2.08891	0.0026115
chr6:134869092-13489792	Gpr19	14760	13.2	7.4	4.1	-1.56789	0.161309	-2.4133	0.0002437
chr2:37516626-37519281:	Gpr21	338346	10.7	7.7	5.4	-1.24221	0.325309	-1.5725	0.0048389
chr6:99692679-99693818:	Gpr27	14761	6.9	8.3	15.6	1.35539	0.133312	2.7605	9.25E-13
chr6:25668523-25689980:	Gpr37	14763	1.4	0.6	0.1	-2.11412	0.093033	-9.04892	1.73E-09
chr8:94977109-95014208:	Gpr56	14766	19.7	28.9	23.7	1.65386	0.001095	1.49659	0.0020747
chr4:24973419-25009233:	Gpr63	81006	4.9	5.0	5.5	1.13986	0.398425	1.39363	0.0018042
chrX:160390690-16049807	Gpr64	237175	8.1	5.7	3.3	-1.27599	0.340977	-1.94678	0.0002834
chr12:98268635-98276722	Gpr65	14744	5.8	6.4	8.3	1.22724	0.510259	1.73409	0.0094162
chr12:100876682-1009081	Gpr68	238377	3.7	4.7	6.5	1.37874	0.285494	2.07729	0.0006913
chr9:14860254-14869499:	Gpr83	14608	0.4	1.2	4.6	2.77382	0.026292	9.33364	9.56E-11
chr3:96871066-96905298:	Gpr89	67549	38.1	36.4	44.5	1.06516	0.530061	1.4555	7.39E-09
chrX:135839034-13584473	Gprasp2	245607	59.7	58.2	31.7	1.10183	0.618948	-1.49244	0.0016903
chr7:118972040-11899521	Gprc5b	64297	30.1	19.7	5.5	-1.37361	0.325546	-3.99384	1.15E-09
chr14:34194441-34201633	Gprin2	432839	3.0	2.0	0.4	-1.34585	0.466707	-5.09119	9.33E-08
chr6:59352461-59426290:	Gprin3	243385	18.1	11.7	5.1	-1.37347	0.416099	-2.55705	0.0006274
chr11:120784272-1207891	Gps1	209318	92.4	110.8	212.0	1.35342	0.087281	2.8064	2.36E-15
chr11:69914192-69916591	Gps2	56310	90.3	89.5	98.9	1.11536	0.303652	1.36659	3.35E-05
chr2:26315533-26348237:	Gpsm1	67839	36.8	37.3	15.7	1.15062	0.506126	-1.84432	1.80E-05
chr3:108678638-10872229	Gpsm2	76123	69.7	52.4	25.4	-1.19639	0.303515	-2.16328	3.49E-10
chr15:76696764-76699675	Gpt	76282	13.8	9.5	4.9	-1.27821	0.47899	-2.12967	0.0016974
chr8:85492617-85527558:	Gpt2	108682	34.4	28.4	13.8	-1.09212	0.770114	-1.942	0.0002831
chr9:108339080-10834034	Gpx1	14775	294.4	459.7	555.6	1.7246	0.059295	2.23043	0.0002829
chr12:76792335-76795554	Gpx2	14776	11.8	10.7	44.9	1.00205	0.996919	4.38978	1.71E-12
chr7:100264544-10026556	Gpx2-ps1	14777	4.0	2.2	0.9	-1.62971	0.152579	-3.29686	1.08E-05
chr4:108400217-10840671	Gpx7	67305	25.2	18.5	12.2	-1.21943	0.272508	-1.64219	0.0001671
chr16:43980350-44027945	Gramd1c	207798	14.0	10.0	3.2	-1.25736	0.249347	-3.36072	5.02E-17
chr15:86057695-86137636	Gramd4	223752	28.5	22.0	15.6	-1.15726	0.019452	-1.46029	5.96E-15
chr15:101224207-1012327	Grasp	56149	27.4	24.1	16.2	-1.01377	0.910944	-1.3462	1.07E-05
chr2:64912482-65022766:	Grb14	50915	15.2	8.8	1.8	-1.52673	0.097246	-6.09592	7.12E-20
chr11:98446834-98455373	Grb7	14786	26.9	17.6	4.9	-1.36461	0.192401	-4.10998	5.36E-16
chr6:124739184-12474107	Grcc10	14790	213.3	201.0	112.3	1.04979	0.590025	-1.51909	1.25E-12
chr12:16670615-16800886	Greb1	268527	10.9	85.6	44.9	5.87752	4.80E-05	3.62574	0.0007289
chr4:44981411-44990696:	Grhpr	76238	20.1	15.8	11.8	-1.13741	0.345637	-1.34913	0.0024109
chr11:57011618-57330244	Gria1	14799	3.5	5.0	9.5	1.57808	0.027396	3.24424	3.66E-14
chrX:41401301-41678601:	Gria3	53623	6.8	5.8	3.7	-1.05539	0.783293	-1.4448	0.0020543
chr9:4417893-4796234:-	Gria4	14802	10.0	8.7	2.4	-1.0318	0.861354	-3.22487	8.20E-30
chr10:49099463-49788754	Grik2	14806	4.9	3.8	0.6	-1.17014	0.444792	-6.65538	2.17E-32

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr9:42520412-42944371:	Grik4	110637	2.8	2.4	1.1	-1.04661	0.854044	-1.96512	5.59E-06
chr6:135729805-13617351	Grin2b	14812	2.7	2.1	0.3	-1.14491	0.719033	-5.98412	8.71E-14
chr15:76246807-76249904	Grina	66168	159.1	130.1	84.3	-1.09333	0.293475	-1.50451	9.42E-12
chr10:119454034-1200872	Grip1	74053	4.3	2.6	0.8	-1.41155	0.113777	-4.21526	1.69E-17
chr6:91761510-91807393:	Grip2	243547	5.9	3.4	0.3	-1.53098	0.090687	-11.8244	1.87E-32
chrX:7789993-7820567:+	Gripap1	54645	30.4	33.0	40.3	1.21792	0.007965	1.65279	1.92E-18
chr5:34660379-34755303:	Grk4	14772	6.2	4.1	1.9	-1.36513	0.079559	-2.56961	4.26E-12
chr19:60889749-61092555	Grk5	14773	11.8	11.8	12.0	1.11892	0.267864	1.2735	0.0008344
chr6:110645598-11156723	Grm7	108073	5.8	6.0	1.1	1.14402	0.57515	-3.95306	8.46E-17
chr11:102430322-1024368	Grn	14824	144.8	112.2	44.4	-1.158	0.124426	-2.59423	3.51E-42
chr5:36465185-36474077:	Grpel1	17713	35.2	43.3	59.2	1.3848	0.035466	2.07283	4.98E-10
chr18:61712424-61726331	Grpel2	17714	29.6	29.0	36.2	1.10123	0.316243	1.5278	2.20E-10
chr8:13176869-13200624:	Grtp1	66790	14.7	14.5	4.8	1.11136	0.70194	-2.36149	1.00E-06
chr7:45825223-45830789:	Grwd1	101612	26.5	48.3	139.6	2.02644	0.002606	6.08216	5.96E-22
chr5:21186267-21291701:	Gsap	212167	31.9	26.7	10.9	-1.06913	0.550549	-2.32943	2.83E-30
chr15:75862339-75867404	Gsdmd	69146	87.4	78.8	47.5	1.00578	0.963429	-1.47036	8.71E-09
chr6:135237330-13525433	Gsg1	14840	34.3	2.4	4.6	-8.13194	1.20E-06	-4.40901	9.69E-05
chr7:125878419-12608241	Gsg1l	269994	0.3	0.4	0.9	1.53483	0.323174	3.0056	0.0002444
chr11:73135484-73138294	Gsg2	14841	10.6	2.5	3.7	-3.35428	8.25E-05	-2.12805	0.0047764
chr7:25228259-25237851:	Gsk3a	606496	53.3	57.5	64.1	1.21844	0.147278	1.49999	6.33E-05
chr12:105685352-1057030	Gskip	66787	18.5	20.0	24.1	1.2135	0.005969	1.62927	1.20E-19
chr16:11216241-11254325	Gspt1	14852	41.1	56.1	118.2	1.53545	0.033272	3.4621	2.92E-16
chr8:33653238-33698162:	Gsr	14782	41.2	37.8	69.9	1.02532	0.867165	2.10951	2.20E-20
chr1:21240585-21265575:	Gsta3	14859	8.8	4.3	1.2	-1.72148	0.228514	-4.34737	9.88E-06
chr9:78191966-78209349:	Gsta4	14860	75.9	55.5	22.8	-1.20547	0.423735	-2.58264	4.29E-09
chr3:132982551-13309174	Gstcd	67553	13.9	12.5	20.7	1.00777	0.961333	1.86012	5.34E-15
chr6:42245935-42250441:	Gstk1	76263	32.2	26.5	8.4	-1.0908	0.649579	-2.96953	6.01E-18
chr3:108012250-10801797	Gstm1	14862	485.1	360.8	125.1	-1.21125	0.224199	-3.04427	2.98E-23
chr3:107981702-10798643	Gstm2	14863	183.9	168.2	77.1	1.01317	0.956172	-1.88469	1.66E-07
chr3:108040408-10804485	Gstm4	14865	8.0	5.8	3.5	-1.23124	0.271876	-1.81577	2.08E-05
chr3:107895854-10789868	Gstm5	14866	146.9	89.5	72.9	-1.46196	0.03675	-1.59282	0.0010061
chr3:107926334-10793174	Gstm7	68312	101.8	97.2	45.7	1.05095	0.889766	-1.73507	0.0063316
chr19:47865545-47886305	Gsto2	68214	6.5	2.0	1.2	-2.57041	0.013794	-3.52072	4.08E-05
chr19:4035411-4037912:-	Gstp1	14870	140.8	132.9	193.1	1.05584	0.592243	1.71184	2.30E-17
chr10:75783813-75798584	Gstt1	14871	177.4	114.9	29.3	-1.38372	0.005054	-4.74771	3.27E-62
chr10:75831845-75834881	Gstt2	14872	90.8	43.1	9.9	-1.86426	0.006942	-6.68488	4.56E-25
chr10:75774122-75781414	Gstt3	103140	27.1	16.1	4.3	-1.50946	0.009709	-4.79505	4.96E-33
chr10:75814944-75822543	Gstt4	75886	10.8	1.7	0.7	-4.15199	0.003622	-7.12484	1.05E-06
chr12:87147165-87164723	Gstz1	14874	84.2	59.0	27.9	-1.27904	0.237466	-2.35375	1.09E-08
chr6:113067429-11307724	Gt(ROSA)26Sor	14910	24.4	32.9	38.7	1.51007	0.022363	1.94546	1.85E-06
chr12:91555262-91590487	Gtf2a1	83602	42.7	38.3	55.4	-1.00034	0.99847	1.61652	2.62E-14
chr17:88668660-88715150	Gtf2a1l	71828	5.7	0.4	0.8	-6.65946	0.000234	-3.71316	0.0030971
chr9:70012548-70022866:	Gtf2a2	235459	71.9	74.6	79.5	1.16559	0.1207	1.3796	1.15E-05
chr16:37509796-37539769	Gtf2e1	74197	17.6	20.1	30.0	1.28783	0.12795	2.09775	1.09E-09
chr17:57003402-57011288	Gtf2f1	98053	75.9	89.0	186.3	1.32173	0.069034	3.01656	1.01E-22
chr14:75896937-76010865	Gtf2f2	68705	66.7	77.0	118.2	1.29564	0.109747	2.18399	5.14E-11
chr7:46796094-46823800:	Gtf2h1	14884	59.6	67.1	78.4	1.26964	0.107808	1.63268	9.80E-06
chr13:100468577-1004926	Gtf2h2	23894	33.3	32.3	37.3	1.08644	0.324145	1.39829	5.76E-09
chr5:124579148-12459768	Gtf2h3	209357	26.2	26.2	36.2	1.12265	0.208212	1.72494	1.80E-17
chr17:35667728-35673743	Gtf2h4	14885	22.2	22.0	32.9	1.1074	0.332626	1.851	1.70E-18
chr17:6079828-6085485:+	Gtf2h5	66467	61.7	62.3	75.9	1.13068	0.119632	1.53392	4.36E-14
chr5:134237832-13431476	Gtf2i	14886	103.7	81.1	59.9	-1.14391	0.124039	-1.37991	7.56E-07
chr5:134357661-13445671	Gtf2ird1	57080	20.3	14.4	12.5	-1.26396	0.034543	-1.29186	0.0031385
chr5:134184038-13421814	Gtf2ird2	114674	20.7	18.6	20.4	1.00681	0.956596	1.23294	0.0010601
chr2:28822300-28840360:	Gtf3c4	269252	31.8	36.9	39.8	1.30997	0.093068	1.55273	0.0002928
chr2:28566245-28583279:	Gtf3c5	70239	23.3	22.3	25.1	1.0725	0.402179	1.34482	1.61E-07
chr10:40249203-40257665	Gtf3c6	67371	42.7	44.6	85.4	1.1762	0.239157	2.4774	1.68E-21
chr15:79690896-79721479	Gtpbp1	14904	36.4	37.2	39.7	1.15276	0.325695	1.35817	0.0033155

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr5:5537457-5559501:-	Gtpbp10	207704	22.9	21.4	26.1	1.04367	0.725676	1.42294	1.35E-06
chr17:46161032-46169370	Gtpbp2	56055	58.0	55.2	27.2	1.06885	0.506815	-1.69604	3.27E-15
chr8:71488103-71493400:	Gtpbp3	70359	26.5	24.3	30.3	1.02287	0.866328	1.42878	1.31E-06
chr13:8972478-8996012:-	Gtpbp4	69237	68.4	111.5	209.5	1.81222	0.023313	3.57676	2.32E-10
chr5:110103977-11010819	Gtpbp6	107999	46.0	53.0	48.4	1.2914	0.00688	1.31488	0.0003466
chr15:85859707-85876573	Gtse1	29870	2.3	2.9	4.3	1.39975	0.144193	2.22824	1.33E-06
chr15:103402459-1034304	Gtsf1	74174	11.5	0.5	1.6	-9.2628	5.64E-06	-3.93965	0.0013382
chr2:163087031-16308960	Gtsf1l	68236	10.8	0.5	0.9	-10.7774	9.08E-08	-6.62725	7.43E-07
chr17:47385393-47392967	Guca1b	107477	5.4	5.3	7.3	1.09378	0.767371	1.64588	0.0062468
chr9:3532349-3905787:+	Gucy1a2	234889	8.5	7.0	1.2	-1.09325	0.56312	-5.75962	6.15E-64
chr3:82092427-82145877:	Gucy1a3	60596	44.6	23.0	17.1	-1.71006	0.094311	-1.98537	0.0052515
chr3:82032004-82074711:	Gucy1b3	54195	30.4	21.5	14.4	-1.27786	0.28478	-1.66164	0.0022886
chr19:55198098-55241236	Gucy2g	73707	18.3	13.2	0.7	-1.23671	0.346595	-17.6492	6.92E-61
chr5:69556942-69573630:	Guf1	231279	49.4	34.9	24.4	-1.27476	0.110392	-1.60854	3.20E-05
chr11:59183855-59191952	Guk1	14923	52.4	49.6	55.1	1.05323	0.654918	1.31236	0.0001848
chr1:44551671-44796836:	Gulp1	70676	64.3	60.6	9.8	1.05006	0.66309	-5.17551	9.86E-113
chr6:100704734-10080508	Gxylt2	232313	12.0	8.1	2.4	-1.32573	0.141355	-3.89314	2.41E-19
chr18:52693679-52695593	Gykl1	14625	7.5	0.5	1.1	-8.37069	2.43E-06	-4.1283	0.0003086
chr18:32528320-32560034	Gypc	71683	40.4	27.2	17.4	-1.33886	0.20473	-1.82001	0.0004219
chr2:152669461-15270866	H13	14950	34.1	35.0	48.7	1.1532	0.130578	1.77728	4.47E-17
chr7:142575532-14257814	H19	14955	22.7	17.7	6.4	-1.14525	0.49359	-2.77619	3.04E-14
chr15:98255982-98257307	H1fnt	70069	13.9	0.7	1.1	-10.0202	3.18E-07	-6.53466	1.61E-06
chr6:87980421-87981482:	H1fx	243529	4.0	4.8	1.3	1.3317	0.489215	-2.30134	0.0055367
chr2:17996422-17996946:	H2afb1	68231	8.8	0.2	0.6	-8.14371	0.000106	-4.84498	0.0007943
chr6:136808248-13681007	H2afj	232440	17.1	16.9	22.9	1.10547	0.576391	1.6557	1.22E-05
chr11:6427226-6444443:-	H2afv	77605	77.9	69.9	20.7	-1.00056	0.997875	-2.97647	2.23E-39
chr9:44334715-44336073:	H2afx	15270	12.5	17.5	26.3	1.5512	0.098248	2.5068	3.23E-06
chr13:56073622-56135550	H2afy	26914	98.1	94.4	126.3	1.07889	0.451669	1.60609	2.19E-12
chr3:137864487-13786692	H2afz	51788	286.3	295.1	1097.6	1.14496	0.274698	4.71426	3.18E-74
chr17:35263094-35267497	H2-D1	14964	186.6	233.4	228.5	1.3781	0.095591	1.51384	0.0048444
chr17:33996012-34000333	H2-K1	14972	618.6	810.1	858.2	1.43992	0.078596	1.70552	0.000728
chr17:33974659-33978791	H2-K2	630499	41.2	30.7	5.6	-1.20892	0.615058	-5.11733	1.92E-11
chr17:35379617-35384674	H2-Q4	15015	97.1	134.2	147.1	1.53387	0.021088	1.86445	1.71E-05
chr17:36005695-36020560	H2-T24	15042	10.0	10.2	3.7	1.13004	0.703612	-2.0572	0.0003914
chr11:116021961-1160245	H3f3b	15081	869.5	777.2	992.2	1.00346	0.981407	1.42212	5.81E-06
chr10:3256208-3267771:-	H60c	670558	1.5	0.9	0.2	-1.37168	0.59144	-4.09266	0.000372
chr13:64161866-64186537	Habp4	56541	34.6	24.6	16.1	-1.25981	0.047017	-1.70532	1.63E-09
chr10:45577829-45712345	Hace1	209462	37.2	32.4	20.0	-1.02895	0.764215	-1.48781	3.53E-12
chr14:31607226-31640965	Hacl1	56794	19.3	14.1	2.1	-1.23361	0.419113	-6.6724	6.34E-25
chr3:131233420-13127210	Hadh	15107	93.9	64.9	26.3	-1.30195	0.109747	-2.80012	3.05E-17
chr5:30118304-30154980:	Hadha	97212	101.8	98.7	114.4	1.08581	0.148844	1.40528	1.40E-16
chr17:25779843-25785586	Haghl	68977	39.5	22.8	18.3	-1.55203	0.02789	-1.70364	0.0006613
chr11:100347327-1003561	Hap1	15114	8.4	5.8	2.7	-1.2723	0.331647	-2.38177	1.05E-06
chr13:89540636-89611832	Hapln1	12950	1.7	1.1	0.2	-1.4033	0.141296	-6.28907	1.80E-18
chr2:91710950-91721566:	Harbi1	241547	21.0	16.0	10.7	-1.17933	0.319241	-1.56063	0.0001932
chr18:36766528-36783205	Hars	15115	64.3	72.4	152.5	1.26722	0.038328	2.9359	2.31E-37
chr17:17843326-17855188	Has1	15116	0.7	16.1	19.7	16.9355	3.24E-20	22.3712	2.38E-27
chr15:56689944-56694460	Has2os	594843	5.6	3.5	1.8	-1.41006	0.368396	-2.30704	0.0033696
chr8:106870242-10688290	Has3	15118	4.0	2.0	1.0	-1.75304	0.084923	-2.99797	9.44E-06
chr2:71389260-71441622:	Hat1	107435	50.5	74.1	68.9	1.64445	0.015784	1.67697	0.001679
chr18:77757567-77767780	Haus1	225745	48.8	27.7	20.3	-1.57639	0.017679	-1.88878	2.58E-05
chr2:120609382-12062155	Haus2	66296	18.9	20.8	25.5	1.23819	0.089531	1.6781	2.49E-08
chr14:54541785-54554361	Haus4	219072	75.4	50.1	8.1	-1.35156	0.224052	-6.85902	4.97E-27
chr7:30653708-30664994:	Haus5	71909	29.8	23.9	13.9	-1.11639	0.41296	-1.70516	1.29E-08
chrX:73437315-73459029:	Haus7	73738	25.6	28.1	46.3	1.23958	0.14847	2.24273	3.30E-14
chr8:71251124-71272590:	Haus8	76478	21.5	26.9	12.5	1.39471	0.004972	-1.3686	0.0017604
chr3:89995446-89998716:	Hax1	23897	80.0	82.2	120.7	1.15459	0.150801	1.87802	1.33E-18
chr12:31926455-31950535	Hbp1	73389	137.5	107.9	24.7	-1.15431	0.56637	-4.24615	2.07E-19

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr10:21295979-21368889	Hbs1l	56422	38.9	35.8	42.7	1.0351	0.745702	1.37437	5.94E-07
chr5:123876736-12388002	Hcar1	243270	19.3	7.9	0.5	-1.94541	0.214551	-12.3196	9.14E-11
chrX:169311531-16932034	Hccs	15159	17.5	19.6	35.3	1.25485	0.053448	2.4968	4.32E-27
chrX:73942792-73966357:	Hcfc1	15161	40.8	39.8	42.7	1.10031	0.45046	1.30778	0.0023182
chr17:23673608-23675524	Hcfc1r1	353502	68.9	56.8	44.1	-1.08729	0.357079	-1.25037	0.0005534
chr10:82699007-82741392	Hcfc2	67933	42.0	45.5	55.9	1.221	0.065563	1.65962	2.92E-10
chr16:36934983-36963214	Hcls1	15163	19.7	20.9	27.7	1.1646	0.606487	1.70392	0.0062344
chr4:129516104-12954264	Hdac1	433759	62.1	65.0	97.2	1.17953	0.233185	1.93885	1.60E-11
chr15:89123303-89128700	Hdac10	170787	37.8	30.7	13.3	-1.1013	0.38828	-2.25118	3.03E-25
chr6:91156815-91174683:	Hdac11	232232	75.9	49.8	21.3	-1.37114	0.153428	-2.75815	4.17E-10
chr10:36974544-37001888	Hdac2	15182	136.6	137.9	197.0	1.13378	0.109393	1.79945	4.11E-25
chr18:37936971-37954988	Hdac3	15183	108.8	101.9	122.9	1.0501	0.600382	1.41197	6.17E-09
chr1:91932749-92148393:	Hdac4	208727	36.4	37.9	45.4	1.16582	0.149578	1.55618	1.33E-08
chr11:102195747-1022301	Hdac5	15184	78.8	57.2	16.8	-1.23947	0.165886	-3.68225	2.56E-31
chr15:97792664-97844502	Hdac7	56233	34.2	27.4	16.5	-1.11495	0.389435	-1.6447	1.42E-08
chrX:102284640-10250514	Hdac8	70315	34.9	26.5	6.7	-1.18103	0.207793	-4.09029	2.83E-44
chr12:34047582-34917095	Hdac9	79221	12.1	8.1	4.6	-1.34512	0.03002	-2.07016	3.50E-12
chr2:126593660-12661867	Hdc	15186	35.6	46.2	8.4	1.35449	0.568043	-2.74087	0.0045483
chr7:80343137-80346097:	Hddc3	68695	37.2	25.6	12.1	-1.30551	0.265809	-2.36755	7.08E-07
chr3:87906321-87916132:	Hdgf	15191	134.9	132.8	245.3	1.11045	0.499985	2.24937	2.11E-15
chr13:26768172-26770165	Hdgfl1	15192	3.3	0.4	0.6	-4.94587	0.001531	-3.0757	0.0080949
chr17:56079657-56100596	Hdgfrp2	15193	50.6	53.6	93.2	1.19723	0.212924	2.28336	7.31E-16
chr18:50567656-50568699	Hdhd1a	67365	2.1	0.0	0.2	-8.70251	5.27E-05	-4.90571	0.0006306
chr18:76944115-76972171	Hdhd2	76987	22.5	20.7	32.8	1.02942	0.770667	1.81697	2.67E-26
chr4:62499054-62502200:	Hdhd3	72748	8.0	6.2	13.2	-1.14405	0.51644	2.02745	2.76E-08
chr1:93405940-93478917:	Hdlbp	110611	133.6	157.0	330.2	1.3279	0.135768	3.00809	1.69E-15
chrX:111575204-11169707	Hdx	245596	3.8	4.0	5.4	1.16074	0.580979	1.72876	0.0019702
chr13:12395375-12438893	Heatr1	217995	28.7	46.5	111.8	1.80886	0.009027	4.57806	9.39E-18
chr8:88137885-88171943:	Heatr3	234549	31.0	38.7	88.0	1.40764	0.045223	3.46604	9.66E-23
chr17:78752906-78835381	Heatr5b	320473	21.3	18.4	14.1	-1.03551	0.757882	-1.20754	0.0070607
chr11:83753637-83783754	Heatr6	217026	18.0	17.8	19.3	1.10984	0.105641	1.3428	2.92E-10
chr11:83511679-83522099	Heatr9	629303	1.1	0.4	0.3	-2.11647	0.096678	-2.82277	0.0031677
chr6:135137519-13516821	Hebp1	15199	37.7	27.9	17.7	-1.21075	0.234239	-1.69568	7.27E-06
chr10:17900466-17948067	Heca	380629	62.9	52.4	14.6	-1.07979	0.575719	-3.41492	6.36E-44
chr12:51743722-51829536	Hectd1	207304	134.5	137.6	143.1	1.15077	0.196832	1.32651	0.0004287
chr4:116995348-11700527	Hectd3	76608	33.3	25.4	16.0	-1.17835	0.264993	-1.65331	1.99E-06
chr19:38930990-38968277	Hells	15201	11.6	12.6	15.6	1.2063	0.424651	1.65317	0.0022323
chr11:107547960-1076869	Helz	78455	31.3	27.6	18.6	-1.0112	0.948404	-1.34156	0.0013191
chr4:46393989-46404183:	Hemgn	93966	1.9	0.1	0.2	-7.48213	3.14E-05	-4.35438	0.0003404
chr9:107327082-10733835	Hemk1	69536	21.6	14.6	7.8	-1.32955	0.287787	-2.12186	9.88E-05
chr6:3457089-3494498:-	Hepacam2	101202	4.4	3.5	1.3	-1.11598	0.806437	-2.38705	0.0013353
chrX:96455436-96574484:	Heph	15203	22.4	19.1	12.1	-1.05484	0.678675	-1.48322	9.96E-07
chr7:56050155-56231798:	Herc2	15204	47.3	45.3	56.8	1.07696	0.542684	1.49577	4.77E-07
chr6:58833700-58920396:	Herc3	73998	23.3	16.9	8.7	-1.23788	0.36319	-2.07851	9.50E-06
chr6:57580992-57665136:	Herc6	67138	16.1	17.1	6.7	1.18272	0.207867	-1.91527	2.86E-11
chr9:25108130-25151781:	Herpud2	80517	37.6	30.2	20.7	-1.1185	0.426186	-1.44275	0.0001961
chr9:59539667-59565105:	Hexa	15211	120.7	92.1	48.0	-1.17389	0.189024	-2.00492	3.23E-15
chr13:97176331-97198357	Hexb	15212	100.4	83.5	40.0	-1.08175	0.578557	-1.99635	3.71E-14
chr11:121204433-1212226	Hexdc	238023	22.5	19.8	14.6	-1.01631	0.90825	-1.23417	0.0077657
chr10:30832359-30842783	Hey2	15214	8.5	6.0	4.2	-1.25985	0.229511	-1.59324	0.0010872
chr4:123233556-12324987	Heyl	56198	6.1	8.2	16.9	1.49979	0.322133	3.05208	0.0001312
chr13:23703841-23710811	Hfe	15216	40.1	33.3	11.2	-1.08141	0.536299	-2.82628	1.99E-33
chr5:106840197-10692589	Hfm1	330149	1.4	0.5	0.5	-2.56326	0.009027	-1.97935	0.0194317
chr5:16553495-16619439:	Hgf	15234	48.5	51.7	12.2	1.14125	0.792381	-2.77402	0.000681
chr15:76368898-76371411	Hgh1	59053	8.6	12.3	34.8	1.61445	0.02686	4.81883	1.58E-22
chr8:25944459-25976744:	Hgsnat	52120	61.5	50.7	41.0	-1.08908	0.330088	-1.1987	0.0041958
chr1:192512828-19277121	Hhat	226861	5.0	4.2	2.0	-1.08476	0.705465	-1.94967	1.44E-06
chr8:79965851-80058008:	Hhip	15245	0.8	0.6	2.4	-1.19708	0.616254	3.38999	3.41E-08

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr12:108306270-1083283	Hhipl1	214305	8.7	5.4	1.6	-1.43327	0.335568	-3.80287	6.13E-07
chr3:116631167-11666267	Hiat1	15247	68.5	85.4	108.0	1.40646	0.071377	1.9378	3.45E-06
chr6:52546230-52640300:	Hibadh	58875	106.3	85.8	65.6	-1.10925	0.197244	-1.29333	1.27E-05
chr1:52845046-52920860:	Hibch	227095	36.5	28.3	22.9	-1.15579	0.218899	-1.27018	0.0062688
chr11:115347709-1153677	Hid1	217310	7.5	5.5	10.0	-1.21876	0.206506	1.6656	3.13E-06
chr12:73907867-73947530	Hif1a	15251	102.9	162.3	286.2	1.76028	0.002678	3.34734	1.50E-15
chr9:121848560-12185800	Higd1a	56295	18.6	28.8	50.8	1.71975	0.075136	3.15488	4.78E-07
chr11:102836296-1028380	Higd1b	75689	13.8	11.5	1.6	-1.08476	0.815046	-5.90733	6.39E-15
chr11:94967661-94968456	Hils1	54388	19.2	1.1	2.5	-8.66335	3.14E-06	-4.35517	0.0002838
chr11:54866438-54870496	Hint1	15254	290.6	295.2	453.5	1.13486	0.280642	1.93698	5.01E-16
chr4:43654227-43656445:	Hint2	68917	57.0	48.2	32.0	-1.05697	0.653027	-1.42292	9.47E-06
chr10:30608207-30618366	Hint3	66847	44.8	36.8	25.3	-1.0921	0.562073	-1.41233	0.0007143
chr5:135406519-13554512	Hip1	215114	48.0	35.8	15.4	-1.20303	0.108383	-2.47659	6.65E-27
chr2:104426482-10449448	Hipk3	15259	90.6	97.6	103.8	1.2111	0.042909	1.42864	6.99E-07
chr16:18876750-18970308	Hira	15260	25.1	22.9	26.6	1.02302	0.835746	1.32177	7.02E-06
chr7:126861972-12686512	Hirip3	233876	22.6	18.5	23.3	-1.08823	0.524221	1.28686	0.0045861
chr13:23738807-23739531	Hist1h1c	50708	391.5	322.8	100.8	-1.09477	0.713579	-3.00513	1.70E-13
chr13:23621777-23622558	Hist1h1e	50709	268.3	223.8	127.6	-1.07904	0.705645	-1.66321	4.49E-05
chr13:23695811-23696545	Hist1h1t	107970	13.5	1.1	1.9	-5.38291	0.001367	-3.60084	0.0039343
chr13:23934462-23934913	Hist1h2aa	319163	6.0	0.1	0.8	-7.30082	0.000283	-3.39787	0.0104765
chr13:21753377-21753912	Hist1h2ak	319169	15.8	26.4	16.4	1.8392	0.001364	1.29115	0.133023
chr13:23933725-23934156	Hist1h2ba	319177	31.0	2.7	5.0	-6.73679	5.01E-06	-3.80415	0.0002393
chr13:23542923-23543444	Hist1h2bh	319182	19.8	27.6	28.0	1.52342	0.074413	1.73628	0.0021594
chr13:22043230-22043658	Hist1h2bj	319183	20.8	32.2	31.7	1.68996	0.01594	1.86807	0.0002712
chr13:23544052-23544954	Hist1h3f	260423	31.4	43.5	36.4	1.5282	0.006956	1.43653	0.0049415
chr13:23760795-23761249	Hist1h4a	326619	33.7	64.5	71.1	2.112	3.14E-05	2.56268	7.54E-10
chr13:23756937-23757386	Hist1h4b	326620	20.8	35.9	24.7	1.87994	0.00517	1.45877	0.0481514
chr13:23698084-23698458	Hist1h4c	319155	283.2	413.2	245.4	1.61766	2.77E-05	1.08235	0.475958
chr13:23531044-23531478	Hist1h4h	69386	169.8	275.0	116.9	1.7959	6.36E-05	-1.15852	0.284398
chr3:96219916-96220353:	Hist2h2ab	621893	17.3	23.7	27.7	1.52267	0.080152	1.94375	0.0002263
chr3:96220413-96220880:	Hist2h2ac	319176	71.0	98.8	86.0	1.55412	0.013005	1.50111	0.0045389
chr3:96221121-96223738:	Hist2h2be	319190	32.6	20.3	6.3	-1.43608	0.104991	-3.90579	2.56E-16
chr11:58954685-58955192	Hist3h2a	319162	131.6	114.9	47.7	-1.02928	0.876296	-2.17675	4.36E-14
chr11:58948911-58949372	Hist3h2ba	78303	18.2	12.7	4.2	-1.28114	0.439966	-3.17264	6.77E-07
chr6:136803993-13680443	Hist4h4	320332	113.3	124.9	44.0	1.21896	0.273693	-2.02767	7.49E-08
chr13:42052021-42185026	Hivep1	110521	31.5	27.4	13.3	-1.03788	0.861625	-1.86733	1.71E-07
chr10:13966379-14151378	Hivep2	15273	35.4	41.9	43.4	1.33393	0.020654	1.52826	1.28E-05
chr6:82725027-82774454:	Hk2	15277	11.7	20.2	31.0	1.90366	0.019661	3.09846	1.28E-07
chr11:90336535-90390917	Hlf	217082	34.5	18.1	4.7	-1.69202	0.042507	-5.34333	9.23E-18
chr3:20057811-20118491:	Hltf	20585	39.1	33.3	10.9	-1.05776	0.693272	-2.84816	2.61E-33
chr1:184727145-18473249	Hlx	15284	2.1	2.2	3.9	1.17361	0.634269	2.20332	0.0001545
chr14:64822218-64949847	Hmbox1	219150	45.1	37.7	25.1	-1.06843	0.493912	-1.43433	3.37E-08
chr9:44336348-44344228:	Hmbs	15288	24.8	24.5	51.5	1.10177	0.257855	2.58785	6.46E-66
chr1:150562502-15099343	Hmcn1	545370	11.0	9.0	1.7	-1.08832	0.464896	-5.08546	1.08E-91
chr10:81346046-81350457	Hmg20b	15353	23.3	22.5	30.6	1.08404	0.444607	1.63209	1.18E-12
chr10:120361275-1204769	Hmga2	15364	10.3	4.3	2.7	-2.0466	0.017704	-2.79455	1.55E-05
chr1:176834624-17683613	Hmga2-ps1	15365	2.4	2.1	5.6	-1.03674	0.934252	2.72103	4.12E-06
chr5:149047227-14905303	Hmgb1	15289	320.3	381.2	402.6	1.34094	0.093997	1.55624	0.0008806
chr8:33484311-33485757:	Hmgb1-rs17	628431	1.5	0.1	0.1	-5.50398	0.002159	-4.22949	0.0018373
chr4:128260212-12826089	Hmgb4	69317	14.8	0.4	1.1	-11.5082	9.16E-07	-5.90369	4.26E-05
chr9:76014977-76136350:	Hmgcll1	208982	4.2	3.4	1.1	-1.10565	0.632908	-2.9274	1.08E-13
chr13:96648962-96670936	Hmgcr	15357	22.4	32.4	67.3	1.62216	0.070359	3.52366	2.51E-10
chr13:119690351-1197082	Hmgcs1	208715	49.2	53.2	146.4	1.22188	0.412193	3.55766	2.19E-14
chr3:98280431-98310738:	Hmgcs2	15360	97.2	86.3	2.5	-1.03103	0.948404	-23.6318	6.98E-39
chr16:96121588-96127725	Hmgn1	15312	301.3	315.7	475.3	1.17551	0.070384	1.96413	6.78E-25
chr4:133964739-13396799	Hmgn2	15331	124.7	121.6	149.7	1.08858	0.385983	1.49843	1.52E-09
chr9:83109942-83146607:	Hmgn3	94353	35.2	29.8	16.1	-1.06328	0.724387	-1.73774	3.72E-07
chr18:61131277-61177050	Hmgxb3	106894	26.7	33.5	44.6	1.42008	0.052236	2.06211	1.10E-07

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:115497353-1155143	Hn1	15374	78.0	87.4	112.0	1.26128	0.130256	1.77976	3.55E-07
chr17:24942470-24960623	Hn1l	52009	45.1	51.6	91.1	1.2824	0.048851	2.50285	8.06E-23
chr11:83850869-83905917	Hnf1b	21410	3.5	2.0	1.4	-1.51867	0.087257	-1.88997	0.0007076
chr2:24002913-24049379:	Hnmt	140483	19.7	13.6	2.1	-1.30062	0.400524	-6.54184	3.74E-17
chr13:58125879-58128556	Hnrnpa0	77134	56.7	58.9	101.5	1.17086	0.267296	2.21504	1.23E-15
chr15:103240397-1032466	Hnrnpa1	15382	16.4	15.6	22.4	1.07753	0.707398	1.69437	1.26E-05
chr6:51460435-51469894:	Hnrnpa2b1	53379	449.7	496.2	651.4	1.24697	0.21848	1.78967	7.80E-06
chr2:75659259-75669407:	Hnrnpa3	229279	47.3	47.5	76.4	1.13043	0.274902	2.00644	5.28E-19
chr11:51600100-51606881	Hnrnpab	15384	148.4	199.4	451.2	1.51099	0.054928	3.64555	6.11E-16
chr14:52073380-52104028	Hnrnpc	15381	176.4	214.1	279.2	1.36783	0.04725	1.95548	1.92E-08
chr5:99955935-99978938:	Hnrnpd	11991	28.3	25.9	35.3	1.03018	0.855205	1.552	1.25E-06
chr5:100033579-10003922	Hnrnpdl	50926	131.3	132.3	259.3	1.13256	0.294625	2.4475	1.04E-27
chr6:117900340-11792562	Hnrnpf	98758	119.4	145.7	264.3	1.37328	0.07068	2.70684	1.88E-14
chr11:50377719-50386528	Hnrnph1	59013	720.8	852.8	905.2	1.33754	0.124214	1.55353	0.002161
chrX:134601286-13460705	Hnrnph2	56258	94.7	110.8	130.4	1.31565	0.028005	1.70955	1.98E-08
chr10:63014664-63023849	Hnrnph3	432467	106.1	103.4	61.7	1.10301	0.587579	-1.36756	0.0095927
chr13:58391132-58403343	Hnrnpk	15387	466.5	480.1	758.1	1.15981	0.2725	2.01508	1.66E-13
chr7:28810890-28822266:	Hnrnpl	15388	204.0	194.1	228.1	1.07002	0.46264	1.39654	8.11E-08
chr17:80029487-80062268	Hnrnpll	72692	58.7	63.9	62.2	1.22373	0.105427	1.32034	0.0034336
chr17:33646233-33685458	Hnrnpm	76936	219.7	238.1	275.5	1.22301	0.167052	1.55821	3.80E-05
chr4:136310942-13634597	Hnrnpr	74326	70.3	68.8	68.8	1.10096	0.324402	1.22298	0.0043234
chr1:178328300-17833778	Hnrnpu	51810	358.5	388.7	496.3	1.22627	0.227218	1.71476	1.09E-05
chr13:93304495-93405129	Homer1	26556	32.2	39.0	30.6	1.35939	0.00063	1.19122	0.0252689
chr8:84990595-85003364:	Hook2	170833	26.1	18.8	14.9	-1.24527	0.151973	-1.39077	0.0044323
chr3:95559677-95587860:	Hormad1	67981	2.3	0.1	0.3	-10.3548	2.73E-06	-4.31977	0.0006428
chr15:102944062-1029479	Hotair	1.01E+08	1.6	1.1	0.3	-1.26922	0.628179	-3.63018	0.0001242
chr6:52245243-52249769:	Hoxa11os	15397	61.0	35.3	22.3	-1.53969	0.150794	-2.0858	0.0011462
chr6:52169062-52213067:	Hoxa3	15400	6.9	3.7	2.1	-1.64748	0.18179	-2.3622	0.0021539
chr6:52215624-52218573:	Hoxa7	15404	3.9	1.7	2.3	-1.98432	0.007608	-1.36246	0.141718
chr11:96318267-96321638	Hoxb4	15412	10.4	7.4	4.5	-1.25527	0.413482	-1.79498	0.0030939
chr11:96303512-96306121	Hoxb5	15413	6.5	4.0	2.8	-1.43987	0.15226	-1.81379	0.002093
chr11:96299171-96301569	Hoxb6	15414	21.7	15.4	11.9	-1.26723	0.203487	-1.4502	0.0076536
chr11:96281905-96285325	Hoxb8	15416	3.4	2.6	1.5	-1.15937	0.605514	-1.78368	0.0027249
chr15:103034395-1030368	Hoxc4	15423	3.6	2.0	1.4	-1.54655	0.142216	-2.02076	0.0019644
chr15:103014008-1030174	Hoxc5	15424	6.5	3.9	2.0	-1.47529	0.149036	-2.48511	7.92E-06
chr15:103009562-1030118	Hoxc6	15425	13.8	8.6	2.9	-1.42388	0.194617	-3.51173	6.44E-10
chr2:74691891-74695106:	Hoxd10	15430	98.7	73.1	47.3	-1.21717	0.310449	-1.64995	0.0003295
chr2:74711993-74748271:	Hoxd3	15434	10.5	7.3	4.0	-1.28946	0.294552	-2.0544	4.00E-05
chr2:74710044-74716130:	Hoxd3os1	73429	3.2	1.9	0.9	-1.48135	0.374157	-2.371	0.008263
chr2:74721978-74729159:	Hoxd4	15436	114.2	71.5	29.4	-1.42733	0.164835	-2.95297	7.45E-09
chr2:74697763-74700208:	Hoxd9	15438	45.7	35.6	24.6	-1.15327	0.33906	-1.47985	0.0002364
chr4:138216612-13824468	Hp1bp3	15441	151.3	134.7	81.8	-1.00256	0.97799	-1.4773	2.50E-16
chr12:17690814-17791926	Hpcal1	53602	43.7	37.9	15.6	-1.03014	0.804376	-2.2218	1.57E-28
chr4:123183504-12319469	Hpcal4	170638	1.5	1.1	0.3	-1.17452	0.656199	-4.07643	1.62E-08
chr4:116819907-11682150	Hpdl	242642	0.3	0.5	1.6	1.65432	0.398425	4.30809	0.0003775
chr8:56294552-56321046:	Hpgd	15446	113.2	72.8	15.2	-1.38415	0.418896	-4.95569	7.14E-09
chrX:52988078-53021660:	Hprt	15452	69.9	73.5	153.3	1.17886	0.167866	2.71128	2.75E-32
chr19:42755196-42779976	Hps1	192236	13.3	11.0	7.3	-1.08351	0.44502	-1.45659	3.20E-07
chr7:141189934-14119400	Hras	15461	26.1	36.4	47.9	1.56919	0.035742	2.23555	9.24E-07
chr16:29209695-29230530	Hrasls	27281	1.5	0.1	0.6	-6.26707	6.99E-05	-1.83064	0.130991
chr19:7612569-7639238:+	Hrasls5	66727	19.1	1.2	2.6	-7.29144	4.65E-05	-3.96683	0.0011652
chr7:45335269-45338972:	Hrc	15464	1.7	0.9	0.1	-1.55758	0.23104	-7.70935	1.21E-10
chr13:54192129-54222432	Hrh2	15466	0.7	1.0	1.3	1.5001	0.276137	2.04166	0.0076053
chr5:118169764-11818947	Hrk	12123	1.1	1.9	0.2	1.85658	0.072037	-4.02251	9.79E-07
chr15:34484022-34495246	Hrsp12	15473	29.1	25.4	10.4	-1.02642	0.860765	-2.21903	3.21E-19
chr12:8313433-8343824:+	Hs1bp3	58240	28.5	17.5	5.7	-1.45864	0.110209	-3.78655	3.78E-14
chr3:144431107-14457021	Hs2st1	23908	33.7	39.8	67.3	1.31528	0.03052	2.46219	2.52E-21
chr11:64435332-64522835	Hs3st3a1	15478	1.8	1.1	0.7	-1.48606	0.175796	-2.03224	0.0014034

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr8:119344538-11934892	Hsbp1	68196	156.3	145.4	168.4	1.04539	0.708661	1.34411	4.91E-05
chr18:80229756-80247102	Hsbp1l1	66255	1.2	0.8	0.1	-1.32928	0.629535	-4.63752	0.0001892
chr5:110829070-11083977	Hscb	100900	31.9	22.9	7.1	-1.25266	0.228811	-3.46932	2.19E-18
chr8:105518746-10552398	Hsd11b2	15484	8.9	10.0	18.8	1.22245	0.466873	2.51919	5.94E-07
chrX:152001896-15200444	Hsd17b10	15108	142.1	128.4	79.2	1.00383	0.9827	-1.42913	0.000106
chr2:94032697-94157909:	Hsd17b12	56348	49.8	50.5	112.0	1.1314	0.308111	2.78584	1.96E-35
chr18:50128201-50196270	Hsd17b4	15488	85.7	70.6	57.9	-1.08907	0.329666	-1.18508	0.0074161
chr1:169949537-16996920	Hsd17b7	15490	3.6	4.7	28.3	1.46738	0.031533	9.34462	6.42E-68
chr8:119561978-11957520	Hsdl1	72552	40.1	31.4	24.9	-1.14912	0.278866	-1.28667	0.0072824
chr4:59581563-59618694:	Hsdl2	72479	36.9	35.5	23.5	1.07514	0.369481	-1.25798	6.60E-05
chr15:76477445-76500972	Hsf1	15499	65.9	68.4	81.7	1.16734	0.123571	1.54897	2.96E-09
chr10:57486385-57513143	Hsf2	15500	37.3	32.7	39.8	-1.01779	0.877715	1.3341	3.51E-06
chr11:87617164-87659542	Hsf5	327992	2.4	0.5	1.0	-3.30746	0.004369	-1.72469	0.123927
chr1:56636051-56637451:	Hsfy2	71066	2.2	0.1	0.3	-7.52474	7.57E-05	-4.18505	0.0009641
chr12:110691036-1106963	Hsp90aa1	15519	290.7	609.7	1072.0	2.29223	0.001267	4.22426	9.31E-12
chr17:45567778-45573261	Hsp90ab1	15516	956.1	1082.0	1805.5	1.27581	0.066993	2.33971	5.26E-18
chr10:86690841-86705444	Hsp90b1	22027	514.8	642.5	1357.0	1.40371	0.053035	3.21221	3.33E-19
chr16:75755191-75766818	Hspa13	110920	35.4	46.0	94.0	1.45597	0.00842	3.25207	1.69E-26
chr2:3488854-3512814:-	Hspa14	50497	21.8	22.6	29.1	1.16285	0.145825	1.66216	1.51E-11
chr17:34969359-34972156	Hspa1a	193740	7.0	20.8	11.0	2.98444	0.002554	1.80702	0.0568513
chr17:34956429-34959238	Hspa1b	15511	9.5	28.8	20.3	3.0916	0.000496	2.40898	0.0015717
chr17:34972703-34979228	Hspa1l	15482	10.8	1.5	2.7	-5.33481	5.00E-07	-2.83748	0.0003419
chr12:76404176-76406936	Hspa2	15512	66.1	58.4	29.2	-1.00785	0.96384	-1.79208	1.71E-10
chr11:53259814-53300479	Hspa4	15525	102.8	140.5	313.9	1.53747	0.036535	3.66825	4.36E-17
chr2:34772090-34776529:	Hspa5	14828	293.8	664.1	1906.9	2.4682	0.000153	7.28744	2.39E-23
chr9:40801273-40805199:	Hspa8	15481	####	2672.6	4645.9	2.34047	0.000135	4.31315	6.42E-15
chr18:34937415-34954351	Hspa9	15526	223.5	272.9	742.0	1.37767	0.055227	4.04292	9.60E-30
chr4:141420779-14142531	Hspb7	29818	20.2	39.3	64.1	2.05792	0.067146	3.36828	4.84E-05
chr5:116408495-11642286	Hspb8	80888	94.9	129.3	235.4	1.53025	0.022663	3.00914	9.97E-15
chr11:100713850-1007145	Hspb9	75482	18.4	1.7	2.6	-6.91535	6.18E-07	-4.44621	8.49E-06
chr16:35770386-35828462	Hspbap1	66667	5.3	5.5	6.0	1.17021	0.235264	1.40817	0.0003183
chr7:4660521-4684963:-	Hspbp1	66245	34.9	39.0	72.1	1.25854	0.049339	2.56875	1.38E-28
chr1:55077834-55087932:	Hspd1	15510	174.0	259.7	587.1	1.6747	0.014133	4.02682	8.74E-18
chr1:55088148-55091317:	Hspe1	15528	131.8	189.6	409.3	1.6137	0.015347	3.73415	3.69E-18
chr5:149616845-14963631	Hsph1	15505	25.9	114.3	123.6	4.18184	6.37E-05	4.74118	4.08E-07
chrX:57053570-57067182:	Htatsf1	72459	79.6	72.6	87.9	1.02258	0.829816	1.37954	4.96E-08
chr1:86099037-86111970:	Htr2b	15559	3.2	7.9	6.5	2.50352	0.005269	2.31383	0.0019114
chr7:130936203-13098565	Htra1	56213	94.9	97.8	177.6	1.16618	0.395448	2.30447	1.52E-11
chr6:83051267-83054571:	Htra2	64704	43.1	38.0	47.4	-1.02032	0.89729	1.36966	0.0002232
chr5:35652026-35679780:	Htra3	78558	56.3	78.7	19.5	1.57242	0.064539	-2.22559	1.74E-05
chr5:34761740-34912534:	Htt	15194	28.9	28.1	43.5	1.08982	0.408085	1.87768	3.43E-19
chr16:90386397-90499553	Hunk	26559	5.3	7.2	14.7	1.51888	0.083654	3.32859	1.35E-11
chr11:8993137-9011191:-	Hus1	15574	16.3	13.7	17.2	-1.07072	0.59424	1.31565	0.0009961
chrX:151803282-15193541	Huwe1	59026	118.2	112.2	125.1	1.06784	0.587407	1.32165	0.0004448
chr5:122209729-12224229	Hvcn1	74096	27.8	22.6	7.9	-1.10579	0.74694	-2.7006	1.47E-07
chr9:107569163-10757277	Hyal2	15587	34.5	43.4	56.7	1.41441	0.03313	2.0258	1.11E-08
chr6:24857997-24891958:	Hyal5	74468	1.7	0.0	0.2	-8.97457	2.87E-05	-3.89059	0.0027789
chr6:24733245-24745452:	Hyal6	74409	1.3	0.0	0.2	-10.8187	2.61E-06	-3.65012	0.0032205
chr8:110266977-11061025	Hydin	244653	1.1	0.2	0.2	-4.0179	0.001217	-3.53364	0.0004771
chr4:118359999-11836274	Hyi	68180	38.4	25.7	10.3	-1.34258	0.147731	-2.90096	3.29E-12
chr9:54917290-54949924:	Hykk	235386	8.2	6.0	1.6	-1.21796	0.324207	-3.93634	4.45E-21
chr9:35560821-35570069:	Hyls1	76832	13.7	11.2	3.9	-1.0987	0.671989	-2.70969	5.29E-12
chr9:44379490-44392369:	Hyou1	12282	49.1	71.0	337.0	1.62113	0.022746	8.01055	1.06E-38
chr2:121457088-12145844	Hypk	67693	98.3	100.1	142.2	1.14441	0.260919	1.79793	2.06E-12
chr19:34607957-34613401	I830012O16Rik	667370	17.3	14.5	2.0	-1.06988	0.866159	-5.96305	5.05E-15
chr12:21316392-21323607	Iah1	67732	81.7	67.2	31.9	-1.09783	0.641467	-2.02104	3.37E-08
chr13:49682130-49734267	Iars	105148	38.9	47.7	125.3	1.38045	0.046021	3.92931	2.41E-30
chr11:59155369-59163745	Iba57	216792	4.2	4.9	6.7	1.31994	0.018265	1.99069	2.92E-15

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr9:85687360-85749334:	Ibtk	108837	55.0	46.4	61.3	-1.06748	0.606368	1.38983	5.88E-05
chr1:59989068-60043087:	Ica1l	70375	1.5	0.4	0.4	-3.07441	0.002909	-2.95082	0.0004768
chr9:21015960-21028796:	Icam1	15894	34.7	119.4	157.5	3.40026	4.99E-05	4.88339	7.51E-10
chr11:106377656-1063826	Icam2	15896	17.9	18.8	22.2	1.17533	0.36875	1.52916	0.000718
chr9:69397998-69433074:	Ice2	93697	30.2	30.1	32.8	1.11862	0.353184	1.35515	0.0003645
chr9:78109192-78172109:	Ick	56542	19.2	14.4	6.2	-1.19915	0.345433	-2.408	7.05E-11
chr4:152297214-15230712	Icmt	57295	36.6	39.6	47.4	1.22312	0.120057	1.61443	6.33E-07
chr10:78069368-78079525	Icosl	50723	47.4	37.1	22.5	-1.14499	0.143798	-1.67674	3.74E-14
chr11:115403766-1154109	Ict1	68572	74.8	65.5	104.6	-1.01907	0.865181	1.74568	6.81E-22
chr12:25093799-25096092	Id2	15902	245.6	165.3	98.6	-1.33783	0.2224	-1.9458	0.000136
chr4:136143822-13614539	Id3	15903	196.0	156.9	66.8	-1.12215	0.551086	-2.31697	2.85E-11
chr19:37268741-37330613	Ide	15925	50.5	44.2	77.2	-1.01819	0.858174	1.90727	9.32E-33
chr7:80094847-80115350:	Idh2	269951	173.8	132.4	73.4	-1.18117	0.192007	-1.87934	8.19E-12
chr9:54586511-54604662:	Idh3a	67834	44.2	57.1	99.2	1.45617	0.103921	2.70889	5.64E-09
chr13:8885606-8892396:+	Idi1	319554	4.2	5.7	34.8	1.51417	0.198496	8.85427	8.56E-22
chrX:70343070-70365085:	Ids	15931	36.1	29.8	16.6	-1.08715	0.499671	-1.72646	4.11E-11
chr5:108660331-10868544	Idua	15932	30.2	21.8	13.5	-1.23797	0.181454	-1.77117	1.08E-06
chr8:84661331-84662852:	Ier2	15936	24.4	76.5	79.0	3.04154	0.006724	3.29142	0.0003486
chr17:35821713-35822911	Ier3	15937	42.4	170.6	174.9	4.00997	4.73E-06	4.43491	1.76E-08
chr18:76930027-76941614	Ier3ip1	66191	49.8	58.5	67.5	1.32218	0.055126	1.68163	2.22E-06
chr1:155096367-15509963	Ier5	15939	22.7	34.0	51.8	1.6754	0.003372	2.77806	4.09E-13
chr6:125145224-12516178	Iffo1	320678	20.7	18.0	10.4	-1.01167	0.962391	-1.57236	0.0006562
chr4:139530548-13962038	Iffo2	212632	13.3	13.8	15.1	1.17104	0.354228	1.41496	0.0043728
chr12:103434189-1034402	Ifi27	52668	205.5	198.4	116.9	1.07773	0.608165	-1.39667	0.0004825
chr12:103433873-1034436	Ifi27l2a	76933	79.2	91.3	29.1	1.27941	0.152741	-2.13473	3.79E-09
chr8:70762773-70766663:	Ifi30	65972	112.0	93.5	53.0	-1.07812	0.638377	-1.68485	3.10E-07
chr11:101448412-1014587	Ifi35	70110	68.9	79.6	77.7	1.29668	0.019661	1.4069	9.21E-05
chr3:151730923-15174995	Ifi44	99899	15.8	19.5	4.1	1.36232	0.216839	-2.89227	7.55E-09
chr2:62595793-62646255:	Ifih1	71586	27.6	24.5	13.1	-1.01029	0.959587	-1.67137	8.79E-07
chr19:34640889-34650009	Ifit1	15957	31.1	46.6	7.4	1.62767	0.112912	-3.094	1.01E-06
chr19:34550694-34576534	Ifit2	15958	35.7	26.1	6.8	-1.23184	0.387132	-3.97442	1.04E-16
chr19:34583529-34588982	Ifit3	15959	54.4	50.9	7.6	1.0389	0.917405	-5.21514	2.43E-17
chr7:140967429-14096982	Ifitm1	68713	548.6	457.6	115.5	-1.07835	0.738188	-3.67831	4.35E-22
chr7:140954839-14095596	Ifitm2	80876	920.4	839.6	510.1	1.01133	0.952053	-1.43704	0.0002175
chr7:141015812-14101689	Ifitm6	213002	4.0	3.9	7.2	1.07669	0.880223	2.10239	0.0051393
chr6:145397235-14543492	Ifltd1	74071	2.9	1.6	0.2	-1.56786	0.283036	-8.41402	3.93E-10
chr10:118441047-1184458	Ifng	15978	0.2	0.8	1.1	2.79907	0.059104	4.12046	0.0006031
chr4:135686457-13570818	Ifnlr1	242700	8.5	8.6	2.7	1.10046	0.818881	-2.34039	0.000588
chr12:40203129-40223189	Ifrd1	15982	56.8	76.9	164.3	1.52278	0.028878	3.49621	6.75E-18
chr9:107587718-10759303	Ifrd2	15983	38.1	51.7	107.8	1.52576	0.00293	3.4705	1.78E-28
chr6:115853528-11592669	Ift122	81896	49.0	37.3	16.3	-1.17498	0.229171	-2.37196	2.43E-19
chr17:25016086-25099497	Ift140	106633	24.6	15.8	4.0	-1.39221	0.041871	-4.76932	1.30E-36
chr5:31253279-31291114:	Ift172	67661	47.6	35.0	15.6	-1.21594	0.112588	-2.4077	3.80E-22
chr11:78536436-78541473	Ift20	55978	99.4	101.7	121.2	1.14965	0.287409	1.51737	6.98E-06
chr5:136908150-13691324	Ift22	67286	39.5	30.8	19.3	-1.14886	0.25765	-1.62377	5.84E-08
chr15:78159463-78174108	Ift27	67042	35.3	28.1	19.0	-1.12822	0.465901	-1.47689	0.0007138
chr12:86082561-86162459	Ift43	76411	59.5	50.7	61.9	-1.05484	0.710888	1.29444	0.0035704
chr9:44773009-44792714:	Ift46	76568	44.7	38.7	14.4	-1.02212	0.891244	-2.44859	2.32E-24
chr2:163017472-16304613	Ift52	245866	43.8	32.5	22.1	-1.20707	0.072846	-1.57747	8.06E-09
chr16:49699294-49765126	Ift57	73916	30.3	24.1	17.3	-1.12421	0.241203	-1.39837	3.86E-06
chr4:94614491-94693233:	Ift74	67694	38.9	33.2	20.8	-1.04698	0.611465	-1.48957	9.62E-12
chr3:68892499-69004570:	Ift80	68259	47.2	39.4	14.9	-1.07574	0.573175	-2.50362	5.09E-28
chr5:122550204-12261451	Ift81	12589	101.1	75.3	34.1	-1.20466	0.157218	-2.34872	5.06E-19
chr14:57424071-57517936	Ift88	21821	35.4	29.6	14.4	-1.06839	0.588668	-1.94851	4.76E-17
chrX:100494291-10051612	Igbp1	18518	127.0	104.5	67.6	-1.09205	0.389733	-1.50096	1.08E-08
chr9:65141189-65185870:	Igdcc3	19289	2.0	1.6	0.6	-1.10687	0.844993	-2.25177	0.0085449
chr9:65101486-65137947:	Igdcc4	56741	17.4	18.0	7.2	1.16561	0.414656	-1.89922	9.77E-07
chr10:87859056-87937047	Igf1	16000	47.1	67.2	433.1	1.59791	0.008081	10.8391	3.45E-68

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr7:67952257-68233667:	Igf1r	16001	79.3	66.4	17.0	-1.06614	0.646466	-3.66611	1.43E-51
chr7:142650768-14266103	Igf2	16002	5.5	4.6	2.6	-1.06562	0.746455	-1.69234	1.73E-05
chr6:49085218-49214954:	Igf2bp3	140488	1.3	0.2	0.2	-4.01252	0.012567	-3.25852	0.0086253
chr17:12682406-12769706	Igf2r	16004	142.4	106.4	50.9	-1.20713	0.324635	-2.1975	4.49E-09
chr11:7206091-7213923:-	Igfbp3	16009	602.7	622.0	140.6	1.1315	0.642884	-3.28534	8.04E-13
chr11:99041260-99052643	Igfbp4	16010	328.3	274.2	175.7	-1.07591	0.625247	-1.48545	3.98E-05
chr15:102144186-1021495	Igfbp6	16012	358.4	290.2	150.9	-1.11273	0.563545	-1.88233	1.56E-07
chr7:30565427-30567962:	Igflr1	101883	21.5	18.5	11.8	-1.04132	0.861303	-1.44419	0.0062464
chr18:36300101-36301478	Igip	109169	36.1	29.0	21.7	-1.11817	0.443755	-1.32873	0.0056563
chr7:43472907-43490023:	Iglon5	210094	3.3	2.5	0.9	-1.16088	0.585796	-2.87973	3.74E-08
chr3:59316735-59344256:	Igsf10	242050	39.7	36.6	41.0	1.0283	0.865144	1.28825	0.0068612
chr3:101377125-10146306	Igsf3	78908	35.9	28.1	8.3	-1.14571	0.244771	-3.43585	9.43E-50
chr1:172312407-17231983	Igsf8	140559	53.0	39.3	19.0	-1.21367	0.226335	-2.19664	9.37E-12
chr11:58199556-58207592	Igtp	16145	50.9	83.1	49.6	1.78429	0.003743	1.21214	0.274069
chr1:74945318-74951651:	Ihh	16147	3.5	10.7	11.4	3.03139	0.002352	3.51905	2.83E-05
chr18:60376029-60392629	Iigp1	60440	67.4	77.3	18.0	1.25818	0.353685	-2.86729	1.09E-09
chr18:36744656-36757639	Ik	24010	209.1	209.2	241.6	1.12372	0.208927	1.44081	4.77E-08
chr4:56749680-56802331:	Ikbkap	230233	46.0	45.6	53.8	1.12035	0.363711	1.45951	1.59E-05
chr1:131254602-13127956	Ikbke	56489	22.4	19.3	6.8	-1.04327	0.846424	-2.57248	3.33E-14
chrX:74393291-74453778:	Ikbkg	16151	32.1	26.2	19.6	-1.09764	0.29585	-1.3097	2.32E-05
chr1:69531210-69685960:	Ikzf2	22779	14.1	10.7	6.8	-1.18315	0.528462	-1.6219	0.0079254
chr10:128632415-1286459	Ikzf4	22781	2.6	7.7	5.7	2.93877	0.001498	2.49069	0.0014502
chr16:91406235-91425834	Il10rb	16155	55.6	43.1	25.1	-1.16247	0.365375	-1.75918	1.33E-06
chr8:70808449-70821423:	Il12rb1	16161	1.5	1.8	3.4	1.28897	0.621066	2.49875	0.0061533
chrX:36112139-36171261:	Il13ra1	16164	30.0	36.3	45.6	1.32389	0.217849	1.85755	0.0001967
chrX:147383478-14740383	Il13ra2	16165	1.9	1.9	0.4	1.07253	0.893302	-3.39504	0.0001245
chr8:82331624-82402586:	Il15	16168	30.6	18.8	6.8	-1.44458	0.336012	-3.1869	2.13E-05
chr2:11705293-11733985:	Il15ra	16169	15.2	10.5	5.8	-1.29119	0.426086	-1.99441	0.0023551
chr7:83643063-83735490:	Il16	16170	31.9	33.2	40.3	1.15321	0.319241	1.56984	8.69E-06
chr18:61687935-61692537	Il17b	56069	0.9	0.8	3.4	1.03979	0.9568	3.67772	0.0001867
chr14:57524829-57543166	Il17d	239114	14.4	13.4	7.7	1.0334	0.890987	-1.48912	0.0039439
chr6:120463197-12048372	Il17ra	16172	23.2	99.7	115.3	4.09966	8.57E-05	4.94298	2.01E-07
chr14:27039001-27107286	Il17rd	171463	28.6	20.3	6.9	-1.2672	0.082373	-3.27612	7.11E-32
chr9:50565368-50581837:	Il18	16173	12.2	10.5	4.5	-1.04188	0.898294	-2.10857	5.37E-05
chr7:102015077-10201815	Il18bp	16068	14.6	20.4	25.0	1.55379	0.034223	2.0881	3.62E-06
chr1:40515362-40551705:	Il18rap	16174	2.1	3.0	4.8	1.50535	0.301743	2.58492	0.0008363
chr1:40225080-40316177:	Il1r1	16177	32.9	38.5	43.0	1.28377	0.298349	1.60093	0.0071629
chr1:40084768-40125226:	Il1r2	16178	1.2	2.9	29.3	2.40434	0.002799	23.9182	5.86E-47
chr16:26581705-26725147	Il1rap	16180	10.3	8.1	4.0	-1.13992	0.349781	-2.06213	1.99E-13
chr1:40429570-40465414:	Il1rl1	17082	4.4	3.7	1.5	-1.05996	0.847874	-2.33783	1.19E-06
chr4:135728159-13575538	Il22ra1	230828	3.3	1.9	0.5	-1.49351	0.268755	-4.60196	8.23E-09
chr6:67422932-67491855:	Il23r	209590	1.7	4.3	4.9	2.22578	0.118152	2.75056	0.0099042
chrX:101264387-10126820	Il2rg	16186	18.5	23.4	29.1	1.3719	0.27762	1.88929	0.0025883
chr13:112522807-1125806	Il31ra	218624	1.3	3.5	3.1	2.80894	0.000569	2.76197	6.15E-05
chr19:29925114-29960715	Il33	77125	20.3	16.0	33.1	-1.12841	0.749222	1.93858	0.0043855
chr8:110741829-11080592	Il34	76527	3.5	2.2	0.3	-1.39721	0.30652	-7.01604	5.70E-13
chr7:125552282-12557947	Il4ra	16190	75.2	167.9	188.9	2.3544	0.000412	2.95752	1.07E-07
chr3:89869324-89913162:	Il6ra	16194	17.7	15.6	25.5	-1.02625	0.928106	1.76981	0.0001796
chr13:112464070-1125068	Il6st	16195	401.8	423.9	541.3	1.1793	0.021824	1.68008	2.40E-21
chr16:36693978-36726804	Ildr1	106347	7.8	7.9	10.2	1.12403	0.58813	1.63214	0.0004706
chr3:90476201-90488379:	Ilf2	67781	108.4	124.8	198.0	1.2976	0.048174	2.26161	9.41E-17
chr7:105736590-10574292	Ilk	16202	345.1	312.2	392.7	1.00965	0.93076	1.41981	1.31E-09
chr10:78574500-78584502	Ilvbl	216136	42.5	30.6	20.5	-1.24798	0.075934	-1.65217	9.36E-08
chr12:41024090-41955588	Immp2l	93757	12.0	10.7	5.8	-1.0156	0.952912	-1.64863	0.0004291
chr6:71831320-71875266:	Immt	76614	112.3	120.2	193.6	1.20067	0.003181	2.15136	3.54E-56
chr1:34439829-34445747:	Imp4	27993	39.3	50.8	75.7	1.457	0.021088	2.36972	4.96E-12
chr3:10313540-10331439:	Impa1	55980	39.3	44.8	55.3	1.27569	0.009312	1.74631	1.72E-14
chr18:67289223-67318841	Impa2	114663	19.0	12.9	6.7	-1.32984	0.30862	-2.17243	0.0001301

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr18:12972252-12992948	Impact	16210	98.6	88.7	115.0	1.00579	0.959665	1.45588	1.02E-10
chr4:4764351-4793306:-	Impad1	242291	79.7	74.5	78.6	1.04434	0.502807	1.23123	1.44E-06
chr6:29200437-29216364:	Impdh1	23917	17.7	15.5	26.1	-1.02317	0.843422	1.83993	2.22E-23
chr9:108560501-10856556	Impdh2	23918	207.5	207.1	496.3	1.1204	0.396497	2.95664	3.48E-33
chr4:98395826-98719603:	Inadl	12695	33.5	24.4	15.1	-1.22523	0.021843	-1.76242	7.94E-17
chr2:118745758-11874881	Inafm2	1E+08	16.1	23.0	27.0	1.59697	0.083303	2.01858	0.0006279
chr11:70688361-70700155	Inca1	103844	6.3	3.9	1.4	-1.43174	0.141296	-3.27965	1.10E-09
chr8:47667178-47675159:	Ing2	69260	11.4	12.2	5.3	1.20478	0.225056	-1.71193	2.97E-06
chr6:125039848-12504926	Ing4	28019	152.3	116.4	42.3	-1.17732	0.279023	-2.83373	9.41E-23
chr1:93803965-93822100:	Ing5	66262	32.8	34.7	34.5	1.18757	0.023824	1.31605	2.90E-06
chr1:75507077-75510354:	Inha	16322	11.3	5.0	3.1	-1.93115	0.098329	-2.58152	0.0018252
chr13:16014475-16027211	Inhba	16323	7.7	6.2	39.7	-1.09241	0.786141	5.96665	8.85E-23
chr1:119415465-11942224	Inhbb	16324	13.5	217.3	322.1	12.9989	1.90E-15	19.5816	1.35E-23
chr4:59769647-59783855:	Inip	66209	20.0	19.0	28.0	1.06586	0.76134	1.72638	1.34E-05
chr6:55170627-55174990:	Inmt	21743	348.5	295.7	80.5	-1.0532	0.805063	-3.37651	5.78E-24
chr2:119373042-11947762	Ino80	68142	36.5	38.2	52.5	1.17688	0.103806	1.79428	1.34E-15
chr18:24104761-24121819	Ino80c	225280	22.7	22.2	33.0	1.09508	0.391921	1.81267	3.07E-17
chr1:63114471-63158295:	Ino80dos	1E+08	10.8	7.2	6.0	-1.33941	0.076296	-1.43155	0.0046733
chr7:126852433-12686146	Ino80e	233875	55.3	54.5	75.5	1.11149	0.383431	1.70359	9.04E-11
chr1:52789420-52817688:	Inpp1	16329	28.3	18.1	10.8	-1.4055	0.108931	-2.044	7.74E-06
chr1:37299838-37410740:	Inpp4a	269180	29.1	27.6	12.6	1.07091	0.648072	-1.83096	1.50E-10
chr8:81342562-82127917:	Inpp4b	234515	25.5	22.3	6.3	-1.0299	0.809088	-3.22438	1.25E-61
chr2:26396249-26409219:	Inpp5e	64436	33.1	26.0	19.6	-1.13742	0.187946	-1.34114	4.65E-05
chr11:3494272-3504821:-	Inpp5j	170835	1.8	1.2	0.4	-1.33414	0.319427	-3.11008	3.12E-07
chr11:75631020-75648865	Inpp5k	19062	85.1	63.7	14.3	-1.19907	0.132487	-4.68671	6.14E-67
chr7:101822632-10183822	Inppl1	16332	57.2	58.0	31.3	1.14862	0.503338	-1.44809	0.0096352
chr5:28071412-28078662:	Insig1	231070	54.8	50.6	121.3	1.03752	0.867801	2.72438	9.40E-17
chr1:121304353-12133258	Insig2	72999	38.0	34.3	22.5	1.00265	0.986786	-1.34649	0.0003583
chr19:29321354-29325318	Insl6	27356	8.8	5.2	2.3	-1.48808	0.235862	-2.82554	4.48E-05
chr8:3150922-3279617:-	Insr	16337	66.0	55.7	19.9	-1.06294	0.645287	-2.62581	5.87E-32
chr8:68793929-68829410:	Ints10	70885	29.2	25.0	17.9	-1.04338	0.724132	-1.29963	0.0004466
chr11:86210683-86257568	Ints2	70422	21.4	20.3	31.2	1.06204	0.47273	1.82762	1.41E-28
chr7:97480956-97541398:	Ints4	101861	74.6	69.2	76.0	1.03627	0.630057	1.27423	1.90E-07
chr19:8892987-8897890:+	Ints5	109077	20.0	22.6	34.6	1.26647	0.027053	2.14723	7.47E-22
chr14:62676325-62761112	Ints6	18130	37.9	46.6	45.1	1.38562	0.081071	1.47505	0.0069331
chr1:191575734-19162169	Ints7	77065	34.9	32.6	37.2	1.04844	0.600354	1.33253	5.74E-07
chr4:11199158-11254259:	Ints8	72656	43.3	50.4	50.1	1.30982	0.025857	1.44036	0.0001099
chr4:48279760-48431953:	Invs	16348	24.3	22.1	12.5	1.01229	0.931219	-1.54726	6.03E-09
chr9:108002648-10804878	Ip6k1	27399	173.7	141.4	55.0	-1.10134	0.286096	-2.51345	1.35E-48
chr9:108795994-10880633	Ip6k2	76500	52.3	43.1	21.7	-1.08866	0.502357	-1.91031	2.81E-14
chr13:106794439-1069369	Ipo11	76582	37.7	35.5	41.6	1.05323	0.418682	1.37769	8.03E-14
chr4:117894493-11791499	Ipo13	230673	22.1	26.9	32.3	1.38008	0.125636	1.80511	0.0001837
chr14:55625629-55635678	Ipo4	75751	41.3	44.5	109.8	1.21692	0.257886	3.25545	1.85E-22
chr14:120911194-1209480	Ipo5	70572	102.9	109.5	249.9	1.20304	0.291665	2.97528	3.93E-19
chr7:110018425-11005511	Ipo7	233726	113.1	171.0	332.8	1.69418	0.00932	3.52899	1.76E-15
chr6:148770684-14883146	Ipo8	320727	40.7	39.7	38.8	1.09136	0.076637	1.19031	2.23E-06
chr1:135382315-13543049	Ipo9	226432	55.9	51.7	64.2	1.03976	0.684894	1.43748	6.14E-10
chr4:116507549-11653823	Ipp	16351	14.3	10.5	8.2	-1.22995	0.128634	-1.39163	0.0013841
chr13:49421223-49463060	Ippk	75678	21.1	31.1	32.9	1.65479	0.028209	1.90482	0.0003163
chr4:129615617-12961909	Iqcc	230767	39.8	26.4	14.1	-1.35135	0.288134	-2.16789	0.0001498
chr5:120589023-12060711	Iqcd	75732	4.9	2.4	0.6	-1.80704	0.030875	-5.40765	5.46E-13
chr5:140663505-14070237	Iqce	74239	27.7	17.9	9.1	-1.38959	0.057755	-2.39332	2.31E-11
chr9:106499967-10650225	Iqcf1	74267	5.6	0.1	0.6	-11.4526	2.80E-06	-4.38058	0.0011975
chr9:106543389-10656162	Iqcf3	68265	18.2	1.0	2.1	-9.33442	6.74E-07	-4.94921	4.68E-05
chr9:106568319-10657096	Iqcf4	67320	6.1	0.5	0.7	-4.89049	0.004957	-3.90999	0.0033233
chr9:106514573-10651600	Iqcf5	75470	3.7	0.2	0.3	-5.00216	0.005059	-4.08233	0.0029052
chr16:33014270-33056186	Iqcg	69707	2.6	1.6	0.3	-1.46391	0.16057	-5.31199	3.82E-14
chr9:63421620-63602448:	Iqch	78250	2.8	0.2	0.3	-6.87083	9.20E-05	-4.72241	0.0002485

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr7:118855775-11897265	Iqck	434232	2.0	1.0	0.7	-1.75704	0.097347	-2.18194	0.0029993
chrX:152144268-15222523	Iqsec2	245666	9.1	7.7	3.2	-1.0547	0.756577	-2.22206	2.38E-14
chr6:24444865-24515067:	Iqub	214704	2.7	0.5	0.5	-3.57969	0.001312	-3.55051	0.0001345
chrX:74013914-74023921:	Irak1	16179	50.9	47.2	78.1	1.04002	0.706857	1.91035	1.10E-25
chr10:120141654-1202015	Irak3	73914	18.8	60.5	29.2	3.12664	0.006186	1.75628	0.111803
chr11:53770014-53778374	Irf1	16362	64.2	100.4	48.9	1.72301	0.001135	-1.05015	0.764565
chr8:46739745-46847458:	Irf2	16363	26.1	22.4	14.4	-1.04696	0.830635	-1.44476	0.0036867
chr7:19004065-19006763:	Irf2bp1	272359	29.8	32.8	32.0	1.23989	0.125985	1.33797	0.0065087
chr8:126588296-12659343	Irf2bp2	270110	113.6	93.2	56.8	-1.09026	0.350285	-1.5944	3.79E-13
chr7:44997648-45002848:	Irf3	54131	95.0	89.0	90.1	1.0462	0.607039	1.18576	0.0030607
chr1:193153112-19317203	Irf6	54139	61.9	48.2	14.4	-1.15483	0.651827	-3.24471	3.80E-09
chr7:141263183-14126642	Irf7	54123	32.2	40.0	13.0	1.37024	0.269345	-1.90411	0.0020605
chr7:24431926-24445682:	Irgc1	210145	12.5	0.8	1.5	-9.59422	3.99E-08	-5.09998	5.75E-06
chr7:24530648-24538600:	Irgq	210146	15.4	13.6	8.7	-1.00925	0.921008	-1.41119	4.29E-12
chr1:82233105-82291439:	Irs1	16367	75.3	64.3	93.3	-1.05846	0.774582	1.53549	0.0003318
chr8:10986964-11008430:	Irs2	384783	39.5	32.0	3.1	-1.11846	0.817026	-7.89274	1.07E-13
chr5:137643032-13764571	Irs3	16369	2.5	2.6	0.6	1.15166	0.774582	-2.87538	0.0006552
chrX:141710998-14172521	Irs4	16370	2.1	1.0	0.3	-1.80294	0.087878	-4.88046	3.21E-09
chr12:84773270-84775089	Isca2	74316	51.1	49.8	53.9	1.088	0.390309	1.31601	4.42E-05
chr5:113772812-11377828	Iscu	66383	104.0	112.8	143.2	1.22012	0.113838	1.71113	7.09E-09
chr7:78913424-78920396:	Isg20	57444	13.1	13.5	17.9	1.15294	0.322151	1.70039	6.73E-08
chr3:87930314-87940686:	Isg20l2	229504	37.6	48.8	65.2	1.46146	0.066993	2.12179	1.37E-06
chr9:58156264-58159221:	Islr	26968	140.5	112.5	16.7	-1.12341	0.337248	-6.60552	5.98E-108
chr7:4877053-4895716:+	Isoc2a	664994	33.0	30.7	18.6	1.03971	0.83015	-1.4111	0.0014145
chr7:4844960-4866179:-	Isoc2b	67441	14.7	11.0	3.7	-1.204	0.549302	-3.02578	1.47E-07
chr6:87818448-87838759:	Isy1	57905	52.5	58.3	80.5	1.24342	0.044327	1.9041	1.01E-15
chr8:70594481-70597290:	Isyna1	71780	96.8	198.6	233.2	2.20632	0.022162	2.72657	0.0002211
chr2:155133481-15522685	Itch	16396	76.8	79.9	81.4	1.1719	0.218899	1.32088	0.0035326
chr8:85717557-85840949:	Itfg1	71927	63.7	62.8	60.8	1.10194	0.131605	1.1928	0.0002421
chr6:128409444-12842491	Itfg2	101142	31.0	25.8	37.7	-1.07144	0.496728	1.52052	1.81E-10
chr17:26212692-26244242	Itfg3	106581	41.3	32.4	24.0	-1.14116	0.124145	-1.37524	6.94E-07
chr13:114958081-1151019	Itga1	109700	67.4	56.3	36.6	-1.0813	0.711524	-1.46669	0.0038103
chr3:96645584-96664519:	Itga10	213119	8.0	5.9	3.9	-1.20654	0.347806	-1.59764	0.0011051
chr9:62677855-62783979:	Itga11	319480	10.1	9.4	2.0	1.04401	0.868056	-3.95693	1.51E-20
chr13:114835912-1149320	Itga2	16398	7.9	9.5	28.0	1.34733	0.039179	4.36634	5.07E-45
chr11:102453297-1024698	Itga2b	16399	7.6	6.1	3.7	-1.12449	0.652659	-1.63116	0.003833
chr11:95044482-95076714	Itga3	16400	26.7	24.6	31.9	1.03424	0.880223	1.47775	0.0017621
chr15:103344286-1033667	Itga5	16402	31.5	55.9	90.0	1.96483	7.05E-05	3.44957	5.34E-18
chr2:71786939-71858427:	Itga6	16403	41.0	45.9	90.3	1.26561	0.217871	2.69334	3.50E-13
chr2:12106660-12301920:	Itga8	241226	21.5	20.8	6.4	1.06355	0.811917	-2.63787	1.01E-10
chr9:118606709-11890100	Itga9	104099	29.2	28.8	48.0	1.1023	0.40778	2.03938	2.98E-19
chr7:127296260-12733513	Itgal	16408	7.7	9.5	14.2	1.32419	0.477201	2.1261	0.005893
chr8:128685654-12873357	Itgb1	16412	350.6	366.7	504.0	1.16797	0.110301	1.78508	4.22E-16
chr11:104608000-1046704	Itgb3	16416	17.7	32.5	61.5	2.00435	0.036639	3.86532	9.94E-08
chr4:99765402-99829118:	Itgb3bp	67733	8.5	6.3	3.7	-1.2073	0.307026	-1.81611	8.63E-06
chr14:123660140-1239740	Itgbl1	223272	5.3	4.0	0.9	-1.17147	0.65273	-4.1872	8.35E-10
chr14:30908574-30923587	Itih3	16426	0.7	1.2	1.9	1.77438	0.089345	2.89772	1.74E-05
chr2:10153543-10256529:	Itih5	209378	72.0	61.1	10.2	-1.06202	0.70194	-5.55847	2.06E-73
chr11:46325148-46389515	Itk	16428	2.7	4.8	5.7	1.84974	0.098568	2.403	0.0019505
chrX:107397195-10740336	Itm2a	16431	49.2	40.3	11.3	-1.10009	0.577976	-3.42704	8.29E-28
chr14:73362232-73385271	Itm2b	16432	####	1126.9	473.1	-1.06034	0.514537	-2.24949	9.75E-44
chr2:130667841-13068161	Itpa	16434	50.7	60.3	104.5	1.34108	0.136921	2.51515	1.45E-10
chr7:27207170-27228597:	Itpkc	233011	21.6	26.9	28.3	1.3933	0.005579	1.62817	3.63E-07
chr6:108213096-10855111	Itpr1	16438	91.5	82.6	37.0	1.01085	0.923231	-1.97104	1.37E-31
chr6:146108299-14650222	Itpr2	16439	55.7	44.8	12.2	-1.10592	0.610505	-3.54883	3.78E-24
chr17:27057304-27122223	Itpr3	16440	13.2	9.4	7.9	-1.25126	0.058877	-1.3318	0.0016995
chr12:4593008-4713952:+	Itsn2	20403	62.3	65.8	63.7	1.18745	0.014073	1.27775	8.68E-06
chr2:118862000-11888135	Ivd	56357	122.2	96.9	32.9	-1.12787	0.397298	-2.9232	3.41E-28

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr3:92570900-92573735:	Ivl	16447	0.1	0.1	0.8	1.09667	0.906624	5.34209	2.75E-05
chr1:151344498-15136444	Ivns1abp	117198	179.2	265.1	161.9	1.65016	0.00027	1.12594	0.352516
chr18:32067734-32104331	Iws1	73473	39.4	42.1	48.7	1.20326	0.102148	1.53911	3.05E-07
chr10:3540279-3554877:+	Iyd	70337	3.6	1.9	0.3	-1.61829	0.324528	-6.07968	7.25E-07
chr7:44708743-44719842:	Izumo2	75510	4.6	0.2	0.2	-7.632	0.000131	-6.6254	3.25E-05
chr10:80702693-80705382	Izumo4	71564	91.5	59.5	23.0	-1.37585	0.135737	-3.06751	1.30E-12
chr3:41555734-41616864:	Jade1	269424	42.2	32.8	22.2	-1.16067	0.419079	-1.50627	0.0015985
chr11:51813456-51857481	Jade2	76901	28.1	23.2	10.7	-1.08951	0.590184	-2.08905	7.31E-13
chr2:137081451-13711652	Jag1	16449	58.6	31.7	26.7	-1.65932	0.001013	-1.73722	1.86E-05
chr12:112908590-1129294	Jag2	16450	9.5	10.0	17.3	1.19295	0.519631	2.20263	1.50E-05
chr6:113442517-11344822	Jagn1	67767	34.8	43.0	75.0	1.38972	0.071879	2.63176	6.83E-13
chr4:101151974-10126528	Jak1	16451	126.9	131.4	140.8	1.15837	0.003087	1.38488	2.29E-16
chr8:71676383-71690577:	Jak3	16453	8.2	13.7	14.7	1.82225	0.022846	2.15092	0.0002083
chr5:37050857-37125298:	Jakmip1	76071	10.0	9.0	3.7	1.00243	0.994268	-2.08557	1.71E-05
chr16:84774123-84826375	Jam2	67374	50.6	45.1	25.4	-1.00902	0.96233	-1.58376	4.61E-06
chr9:27097384-27155421:	Jam3	83964	103.8	86.7	61.1	-1.0783	0.598624	-1.35753	0.001179
chr13:44730774-44921643	Jarid2	16468	31.0	24.9	19.5	-1.10488	0.333795	-1.27116	0.0012072
chr6:52768068-53068624:	Jazf1	231986	11.4	9.2	26.3	-1.11408	0.475657	2.85352	1.20E-27
chr12:85599105-85639878	Jdp2	81703	17.1	47.2	24.9	2.87732	0.000906	1.71888	0.051418
chr10:67127258-67256326	Jmjd1c	108829	120.6	101.1	66.8	-1.07547	0.70915	-1.43565	0.0030456
chr11:116837432-1168434	Jmjd6	107817	53.9	87.7	108.1	1.81201	0.024852	2.39276	2.27E-05
chr13:93430097-93499808	Jmy	57748	94.6	104.1	35.2	1.23044	0.103378	-2.12897	7.45E-16
chr15:79674250-79687872	Josd1	74158	43.0	44.0	42.1	1.14918	0.137347	1.22088	0.0047834
chr15:74702412-74709322	Jrk	16469	17.1	14.5	18.1	-1.06122	0.623414	1.32054	0.0003266
chr3:90231597-90235840:	Jtb	23922	63.9	68.9	68.9	1.20706	0.07044	1.34184	0.000187
chr4:95049036-95052222:	Jun	16476	60.0	100.2	45.2	1.85983	0.007965	-1.06148	0.785968
chr8:84976909-84978748:	Junb	16477	24.6	145.1	92.0	5.53932	1.75E-08	4.02522	2.36E-07
chr8:70697739-70700616:	Jund	16478	25.5	74.1	45.0	2.93061	0.003581	1.99922	0.0260751
chr16:33969073-34514027	Kalrn	545156	16.3	17.4	24.9	1.20429	0.308247	1.88712	9.00E-07
chr9:21766773-21798546:	Kank2	235041	92.8	82.1	52.2	-1.00938	0.954238	-1.41498	3.78E-05
chr17:33810523-33822914	Kank3	80880	43.7	35.5	19.3	-1.11157	0.577976	-1.78765	2.99E-06
chr4:98754892-98817537:	Kank4	242553	10.9	7.5	2.0	-1.29469	0.374705	-3.95899	1.49E-11
chr1:66719243-66817595:	Kansl1l	68691	65.6	54.2	25.3	-1.09438	0.697549	-2.03724	6.11E-07
chr15:98517658-98534269	Kansl2	69612	30.0	32.4	43.0	1.21831	0.155992	1.78184	1.28E-08
chrX:152294824-15232749	Kantr	72997	9.7	7.1	2.4	-1.23229	0.219901	-3.11067	3.00E-19
chr8:111993439-11201135	Kars	85305	116.4	117.8	220.1	1.13502	0.139523	2.3582	8.99E-45
chr11:100704746-1007124	Kat2a	14534	29.1	32.4	50.1	1.25605	0.117307	2.13093	1.17E-12
chr17:53566971-53672721	Kat2b	18519	60.8	47.0	26.1	-1.16925	0.459776	-1.83651	2.80E-05
chr14:21499770-21672478	Kat6b	54169	44.0	33.5	16.3	-1.18315	0.388008	-2.1139	2.85E-08
chr10:7726000-7763150:+	Katna1	23924	60.9	68.7	64.0	1.27177	0.068197	1.31253	0.007565
chr18:76993200-77047296	Katnal2	71206	2.6	0.9	0.3	-2.26887	0.056977	-4.90395	3.34E-06
chr8:95081201-95099874:	Katnb1	74187	16.1	11.3	8.4	-1.27806	0.124996	-1.52123	0.0005287
chr2:112379211-11241423	Katnbl1	72425	21.8	25.7	30.4	1.3242	0.077873	1.72259	5.26E-06
chr19:45076139-45079289	Kazald1	107250	9.8	5.1	1.2	-1.70521	0.068072	-5.77584	6.87E-14
chr8:15011025-15033332:	Kbtbd11	74901	7.3	9.1	3.1	1.39304	0.099973	-1.8392	7.59E-05
chr6:56777525-56797813:	Kbtbd2	210973	55.7	59.1	48.0	1.18948	0.002816	1.0792	0.13079
chr9:4309743-4331732:+	Kbtbd3	69149	13.8	11.4	6.7	-1.09275	0.667602	-1.64448	0.000171
chr14:79451835-79454816	Kbtbd6	432879	1.5	0.5	0.5	-2.68644	0.004369	-2.39654	0.0018722
chr6:95117880-95129793:	Kbtbd8	243574	1.9	4.1	7.3	2.3766	0.000331	4.52225	3.56E-14
chr6:72841114-72899979:	Kcmf1	74287	44.5	49.3	71.4	1.25074	0.095942	1.99325	2.79E-12
chr6:126636463-12664580	Kcna1	16485	1.0	2.7	3.6	2.79941	0.000152	4.01548	1.37E-09
chr3:107036162-10703812	Kcna3	16491	2.5	3.9	5.2	1.57753	0.294989	2.28788	0.0088441
chr6:126532551-12653555	Kcna5	16493	1.8	1.7	0.3	1.03085	0.959665	-3.28076	0.0002858
chr6:126708329-12674067	Kcna6	16494	1.7	1.2	0.2	-1.31225	0.243346	-6.29732	8.98E-20
chr3:65109368-65378225:	Kcnab1	16497	14.0	11.0	2.7	-1.13465	0.279965	-4.11609	1.51E-53
chr11:69326258-69333041	Kcnab3	16499	1.2	0.6	0.4	-1.64001	0.140293	-2.04492	0.0057764
chr1:15312452-15714214:	Kcnb2	98741	4.2	2.9	0.3	-1.30563	0.284483	-8.51179	2.38E-27
chr10:112271123-1124663	Kcnc2	268345	2.2	1.4	0.1	-1.35614	0.519935	-12.4593	4.69E-14

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr7:44590886-44604751:	Kcnc3	16504	0.3	0.5	1.0	1.68237	0.133895	3.39921	7.46E-07
chrX:7823843-7836503:+	Kcnd1	16506	1.5	1.2	0.3	-1.17741	0.72442	-3.18141	0.0001779
chr6:21216109-21729805:	Kcnd2	16508	3.8	2.8	0.5	-1.21074	0.393737	-5.54888	1.12E-22
chr3:105452330-10567400	Kcnd3	56543	17.3	15.7	22.1	1.02605	0.899099	1.58957	3.03E-05
chr7:100176670-10018486	Kcne3	57442	14.6	6.7	4.2	-1.91789	0.001074	-2.70942	2.35E-09
chr1:78816949-78820025:	Kcne4	57814	31.9	34.5	61.1	1.17936	0.585416	2.3011	2.27E-05
chr12:17172100-17176888	Kcnf1	382571	1.0	2.0	8.4	2.03806	0.110424	7.54194	7.12E-10
chr1:192190777-19251015	Kcnh1	16510	0.8	0.6	1.3	-1.08725	0.837405	1.92764	0.0044867
chr15:99224976-99242817	Kcnh3	16512	5.2	3.3	1.4	-1.42717	0.260006	-2.8256	6.79E-06
chr11:33629341-33993193	Kcnip1	70357	9.7	10.0	1.5	1.15393	0.358314	-4.78897	3.72E-36
chr19:45792346-45816063	Kcnip2	80906	14.5	11.4	3.6	-1.09831	0.814283	-2.94525	4.11E-06
chr2:127456498-12752209	Kcnip3	56461	9.1	8.2	5.1	1.00427	0.984813	-1.424	0.0036295
chr5:48389503-49285659:	Kcnip4	80334	1.0	0.9	1.7	-1.01001	0.983939	1.91656	0.0091173
chr11:111066164-1110768	Kcnj2	16518	11.4	10.1	4.0	-1.03217	0.94404	-2.17438	0.0011765
chr2:55437156-55595525:	Kcnj3	16519	1.0	1.0	0.0	1.14103	0.809088	-6.08824	2.21E-06
chr1:172321033-17232926	Kcnj9	16524	1.3	0.3	0.1	-3.41216	0.007965	-5.04284	1.91E-05
chr1:189207930-18940227	Kcnk2	16526	9.2	8.8	1.9	1.05944	0.844343	-3.64744	2.93E-14
chr5:30588170-30625270:	Kcnk3	16527	3.9	3.3	1.1	-1.0286	0.940015	-2.63351	1.64E-06
chr14:20140058-20181782	Kcnk5	16529	8.5	25.8	32.8	3.27003	8.61E-07	4.44303	8.89E-13
chr10:116418121-1164212	Kcnmb4os1	67342	3.4	0.1	0.5	-7.125	0.000242	-3.52689	0.0059607
chr8:70842049-70857008:	Kcnn1	84036	3.1	2.4	0.7	-1.15236	0.590184	-3.39181	2.69E-11
chr18:45560154-45685883	Kcnn2	140492	2.2	1.9	0.4	-1.01293	0.980068	-3.98044	3.29E-06
chr3:89520164-89672494:	Kcnn3	140493	21.1	21.6	8.4	1.14209	0.286791	-2.00591	3.57E-15
chr7:24370263-24385212:	Kcnn4	16534	6.6	5.8	8.9	-1.01746	0.961333	1.64979	0.0085727
chr15:65994915-66286224	Kcnq3	110862	1.5	1.0	0.2	-1.36728	0.381302	-5.78358	1.58E-09
chr4:120697473-12074717	Kcnq4	60613	12.7	12.7	3.3	1.13035	0.624073	-2.92494	6.06E-11
chr1:21398403-21961942:	Kcnq5	226922	4.0	3.8	1.7	1.05454	0.728881	-1.89564	6.26E-11
chr1:140246257-14061026	Kcnt2	240776	27.0	22.0	5.6	-1.09866	0.57515	-3.79935	5.60E-34
chr8:25849623-25937934:	Kcnu1	16532	5.5	3.6	0.3	-1.36971	0.189024	-11.3837	1.74E-31
chr6:29482036-29507952:	Kcp	333088	1.7	1.3	0.5	-1.15217	0.585416	-2.73438	3.76E-08
chr5:114363572-11438050	Kctd10	330171	85.5	101.5	110.4	1.3362	0.083296	1.59594	0.0002275
chr11:69878264-69880985	Kctd11	216858	17.0	18.5	20.8	1.20963	0.302104	1.51772	0.0016657
chrX:153685154-15369628	Kctd12b	207474	28.7	18.1	6.1	-1.42241	0.178398	-3.55755	2.81E-11
chr7:126928879-12694560	Kctd13	233877	11.0	7.8	13.5	-1.25199	0.154251	1.53249	0.0001347
chr18:40258361-40531184	Kctd16	383348	1.0	0.3	0.1	-2.41148	0.136429	-4.82282	0.0005091
chr15:78428564-78439303	Kctd17	72844	28.3	29.6	33.2	1.17031	0.045336	1.46506	4.06E-11
chr8:105382807-10541350	Kctd19	279499	7.3	0.4	1.0	-9.78286	1.21E-08	-4.66546	1.04E-05
chr7:97332323-97350216:	Kctd21	622320	13.7	10.7	4.4	-1.15036	0.397188	-2.46169	1.55E-14
chr1:188971098-18900784	Kctd3	226823	32.0	33.4	40.1	1.17892	0.198703	1.56284	1.49E-06
chr14:75955003-75965217	Kctd4	67516	20.2	11.4	4.6	-1.57075	0.183055	-3.19108	3.29E-06
chr17:24047720-24073485	Kctd5	69259	28.2	35.7	46.4	1.42608	0.037477	2.03042	4.53E-08
chr9:53384023-53401867:	Kdelc2	68304	57.9	45.4	20.7	-1.15191	0.467043	-2.20114	2.03E-09
chr7:45872840-45883726:	Kdelr1	68137	112.4	104.1	109.5	1.03774	0.723412	1.21608	0.0024986
chr5:143403820-14342190	Kdelr2	66913	115.3	121.8	237.3	1.18846	0.170027	2.54659	2.39E-25
chr15:79516408-79527739	Kdelr3	105785	25.4	28.2	36.2	1.23933	0.085211	1.76447	4.56E-10
chr13:47043499-47085279	Kdm1b	218214	21.9	18.8	12.8	-1.04398	0.702414	-1.36404	9.08E-06
chr6:71588970-71632917:	Kdm3a	104263	78.6	68.2	34.0	-1.02763	0.807291	-1.84231	1.60E-21
chr4:118137004-11818004	Kdm4a	230674	53.6	46.4	32.0	-1.02909	0.770925	-1.33636	9.04E-07
chr1:134560178-13463287	Kdm5b	75605	71.5	57.0	37.5	-1.12204	0.098651	-1.52283	2.92E-16
chrX:18162667-18279358:	Kdm6a	22289	92.6	83.0	47.7	1.00011	0.999657	-1.55134	9.69E-20
chr7:125444620-12546226	Kdm8	77035	13.4	11.2	16.9	-1.07812	0.682875	1.56476	7.11E-05
chr5:75933270-75978428:	Kdr	16542	44.4	36.1	85.8	-1.09229	0.46456	2.39555	3.95E-28
chr1:106720410-10675974	Kdsr	70750	23.3	18.0	5.6	-1.16941	0.372965	-3.24426	4.58E-22
chr9:21229730-21239332:	Keap1	50868	30.1	25.2	32.4	-1.07347	0.424271	1.34477	8.89E-07
chr1:21349677-21352199:	Khdc1a	368204	0.4	0.4	4.8	1.00628	0.99288	9.97166	8.81E-16
chr4:129703169-12974230	Khdrbs1	20218	74.0	71.4	84.7	1.08631	0.430045	1.42664	7.81E-07
chr15:68928420-69093518	Khdrbs3	13992	35.0	35.7	102.5	1.1355	0.222035	3.63236	1.12E-74
chr5:30921895-30931246:	Khk	16548	66.9	54.1	14.1	-1.10747	0.481947	-3.71224	1.46E-38

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr14:55884969-55896781	Khnyn	219094	84.1	71.5	29.2	-1.05599	0.730052	-2.28003	4.21E-18
chr17:57021049-57031507	Khsrp	16549	55.9	56.8	69.3	1.14543	0.257886	1.5458	3.46E-07
chr12:24974932-25059697	Kidins220	77480	114.1	93.2	49.9	-1.09603	0.194617	-1.82358	1.05E-32
chr13:46749088-46929718	Kif13a	16553	45.6	36.8	27.8	-1.10574	0.244301	-1.30824	1.69E-05
chr14:64652531-64806296	Kif13b	16554	48.7	39.4	20.2	-1.10928	0.356351	-1.92038	5.21E-17
chr2:142618345-14290146	Kif16b	16558	36.7	33.2	22.5	1.01385	0.91492	-1.30316	0.0001535
chr4:138262251-13830197	Kif17	16559	4.7	1.5	0.8	-2.53606	0.013679	-3.78314	9.42E-06
chr11:114765389-1147905	Kif19a	286942	2.3	1.7	0.6	-1.21572	0.479779	-3.10088	2.47E-08
chr1:93015455-93101874:	Kif1a	16560	11.8	8.4	1.4	-1.24344	0.136965	-6.55073	2.47E-62
chr4:149176319-14930773	Kif1b	16561	52.2	44.4	27.5	-1.04859	0.595101	-1.51546	3.35E-13
chr11:70700548-70731970	Kif1c	16562	56.1	50.3	65.6	1.00451	0.959035	1.45936	8.58E-18
chr19:34922358-34975731	Kif20b	240641	11.0	9.1	5.7	-1.07758	0.697735	-1.53064	0.0004162
chr4:41390748-41464848:	Kif24	109242	2.7	1.9	1.0	-1.26165	0.358541	-2.01048	0.0001296
chr13:58287516-58354862	Kif27	75050	6.3	2.5	0.8	-2.12753	0.033172	-5.09385	3.06E-09
chr11:91575286-91577555	Kif2b	73470	10.4	0.7	1.3	-8.20623	2.59E-06	-4.60623	9.94E-05
chr11:53567369-53604246	Kif3a	16568	39.2	32.8	13.2	-1.07298	0.59144	-2.36185	2.02E-24
chr2:153291416-15333338	Kif3b	16569	23.5	23.4	23.9	1.11964	0.295868	1.26852	0.0022932
chr12:3365132-3406494:+	Kif3c	16570	16.3	14.0	5.3	-1.05305	0.797423	-2.41074	8.88E-14
chr10:127225695-1272633	Kif5a	16572	7.2	5.3	1.8	-1.21451	0.45814	-2.97416	1.34E-09
chr18:6201005-6241524:-	Kif5b	16573	100.8	125.4	208.7	1.40076	0.040974	2.53833	5.26E-14
chr17:49615172-49909847	Kif6	319991	1.8	1.3	0.6	-1.26002	0.487215	-2.25866	0.0005541
chr7:79698098-79714186:	Kif7	16576	12.8	9.6	6.6	-1.18548	0.349628	-1.51846	0.0013617
chr9:110476958-11052517	Kif9	16578	6.9	2.7	1.3	-2.23023	0.004172	-3.82099	4.58E-09
chr1:163779679-16391710	Kifap3	16579	50.0	41.4	19.9	-1.08356	0.400478	-2.00031	5.98E-26
chr15:76660641-76668196	Kifc2	16581	22.5	15.9	4.0	-1.26244	0.187164	-4.39439	1.50E-29
chr10:79916971-79922272	Kiss1r	114229	2.8	2.4	1.1	-1.02579	0.92713	-1.96588	1.75E-05
chr5:75574987-75656721:	Kit	16590	7.2	11.2	17.1	1.73747	0.03346	2.81806	1.75E-07
chr2:146855889-14697008	Kiz	228730	85.9	67.6	12.7	-1.14233	0.285905	-5.29084	7.51E-77
chr5:65348411-65384003:	Klb	83379	1.8	1.3	0.2	-1.20137	0.794248	-3.55938	0.0029012
chr12:111758849-1118078	Klc1	16593	93.5	95.4	99.2	1.14521	0.141249	1.32472	4.00E-05
chr19:5107746-5118408:-	Klc2	16594	15.4	24.5	36.0	1.76832	0.059726	2.73244	1.18E-05
chr7:19394440-19404104:	Klc3	232943	13.6	9.4	2.9	-1.31031	0.245933	-3.572	1.34E-13
chr17:46630631-46645144	Klc4	74764	40.5	34.2	9.9	-1.06123	0.658249	-3.2302	5.09E-42
chr15:38291464-38300711	Klf10	21847	44.7	70.6	65.4	1.75838	0.003774	1.79084	0.0002731
chr12:24651371-24662782	Klf11	194655	36.9	34.6	10.9	1.01797	0.96991	-2.49776	0.0003205
chr14:99870640-10014979	Klf12	16597	7.3	5.3	0.9	-1.22398	0.257311	-5.89437	3.36E-38
chr7:63886351-63938915:	Klf13	50794	23.6	24.6	13.5	1.16884	0.140334	-1.39213	3.11E-05
chr6:90462626-90475209:	Klf15	66277	57.4	39.8	12.4	-1.28809	0.548632	-3.24519	2.51E-05
chr10:80567121-80577296	Klf16	118445	9.3	13.3	20.6	1.60188	0.101294	2.62689	6.80E-06
chr8:72319062-72321654:	Klf2	16598	18.9	32.6	24.0	1.91298	0.003216	1.55853	0.0167462
chr5:64803523-64830129:	Klf3	16599	65.1	48.2	31.9	-1.20881	0.010401	-1.62972	5.09E-17
chr4:55527137-55532475:	Klf4	16600	21.9	44.9	54.7	2.25373	0.001957	2.93703	5.92E-07
chr14:99298691-99313409	Klf5	12224	14.6	10.4	5.1	-1.2495	0.538222	-2.14671	0.0018458
chr13:5861489-5870393:+	Klf6	23849	100.3	98.4	62.3	1.08788	0.513438	-1.28721	0.0042212
chrX:153238045-15339613	Klf8	245671	4.6	3.8	2.2	-1.1094	0.57604	-1.65849	4.78E-05
chr19:23141226-23166911	Klf9	16601	92.7	116.1	39.1	1.38348	0.095112	-1.86291	2.17E-05
chr12:69241832-69283961	Klhdc1	271005	20.1	15.1	3.8	-1.19808	0.366747	-4.10754	1.72E-22
chr6:30401909-30455174:	Klhdc10	76788	37.3	33.8	36.7	1.013	0.886237	1.22985	2.73E-05
chr8:121796308-12182956	Klhdc4	234825	21.9	27.4	71.2	1.40735	0.014144	3.99425	7.83E-40
chr4:139962173-13996802	Klhdc7a	242721	10.5	8.4	1.9	-1.13048	0.705297	-4.16981	8.28E-13
chr1:171358449-17136079	Klhdc9	68874	5.1	2.3	0.5	-1.87237	0.143164	-5.94759	6.96E-08
chr11:100441924-1004570	Klhl10	66720	8.4	0.7	1.1	-7.21165	4.44E-07	-4.72291	4.62E-06
chr1:134455555-13449087	Klhl12	240756	28.5	33.6	32.7	1.33137	0.093296	1.4238	0.006852
chrX:23219271-23365082:	Klhl13	67455	42.2	40.3	7.6	1.05302	0.805081	-4.29939	4.87E-33
chr18:21550377-21652368	Klhl14	225266	3.4	2.4	8.4	-1.286	0.338421	2.93823	1.20E-09
chr4:156229044-15623485	Klhl17	231003	43.7	35.6	22.4	-1.09886	0.503777	-1.54751	4.49E-06
chr8:64739675-64849924:	Klhl2	77113	26.8	28.0	31.2	1.17206	0.173392	1.45226	1.22E-05
chr4:152008891-15201767	Klhl21	242785	33.1	23.5	11.3	-1.26109	0.098393	-2.30225	1.30E-15

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr16:20097554-20127744	Klhl24	75785	164.6	123.3	7.1	-1.20327	0.413541	-17.0031	1.09E-76
chr12:64942440-64965536	Klhl28	66689	37.3	36.1	22.5	1.08055	0.25908	-1.32494	1.71E-08
chr13:58004957-58102428	Klhl3	1.01E+08	6.3	4.9	1.1	-1.13502	0.649579	-4.24372	3.79E-14
chr4:24617273-24851086:	Klhl32	212390	8.0	8.7	17.2	1.21668	0.287827	2.63966	1.17E-14
chr14:50891389-50893255	Klhl33	546611	7.6	3.4	0.7	-1.87848	0.113017	-6.48169	1.34E-09
chr8:119862305-11987698	Klhl36	234796	16.3	11.6	7.5	-1.26033	0.208712	-1.72379	6.10E-05
chr15:58314573-58324169	Klhl38	268807	19.9	12.5	0.6	-1.41464	0.301565	-20.0965	5.21E-32
chrX:114474333-11456112	Klhl4	237010	16.0	12.7	7.9	-1.12982	0.436994	-1.61065	1.25E-05
chr5:65131231-65168142:	Klhl5	71778	37.0	28.1	17.2	-1.18457	0.101501	-1.71264	2.83E-12
chr7:43774617-43779262:	Klk11	56538	3.9	1.6	0.2	-1.82522	0.284243	-5.83754	1.75E-05
chr7:43950672-43954938:	Klk1b8	16624	1.8	0.2	0.3	-4.31821	0.009663	-2.94061	0.0184785
chr8:45269451-45294835:	Klkb1	16621	1.2	0.8	0.2	-1.33045	0.530321	-3.60601	9.68E-05
chr6:131219235-13124736	Klra2	16633	2.9	2.7	5.5	1.02684	0.956245	2.23623	0.000939
chr6:130291161-13030836	Klra23	79410	1.0	0.4	0.1	-1.86025	0.276253	-4.47906	0.0005787
chr6:128778485-12878864	Klrb1c	17059	5.4	4.6	2.0	-1.05585	0.87249	-2.05565	0.0002114
chr9:44803355-44881274:	Kmt2a	214162	37.3	36.2	20.5	1.09024	0.609263	-1.44704	0.0008436
chr5:25271794-25498783:	Kmt2c	231051	62.8	55.1	36.3	-1.01541	0.907736	-1.37949	8.33E-06
chr5:23434429-23504229:	Kmt2e	69188	70.3	68.2	39.9	1.09156	0.421	-1.40337	7.29E-06
chr7:118842218-11885599	Knop1	66356	38.0	34.5	39.9	1.01699	0.887946	1.31051	3.58E-05
chr2:118814003-11883621	Knstrn	51944	7.0	5.3	2.8	-1.17855	0.483873	-1.96195	3.38E-05
chr16:35983363-36036162	Kpna1	16646	29.6	47.6	89.0	1.79371	0.012664	3.55562	3.45E-12
chr11:106988629-1069995	Kpna2	16647	33.6	63.4	96.7	2.0702	0.011801	3.31291	1.37E-07
chr14:61365186-61439947	Kpna3	16648	37.0	50.5	69.9	1.53338	0.033639	2.29959	5.84E-08
chr3:69072221-69127092:	Kpna4	16649	67.1	85.0	120.7	1.42756	0.056257	2.20539	1.65E-08
chr4:129643979-12967276	Kpna6	16650	46.4	49.1	61.4	1.19619	0.295813	1.64033	5.24E-05
chr11:97159710-97187892	Kpnb1	16211	120.5	129.9	296.0	1.21483	0.110929	3.03864	3.70E-36
chr6:145216699-14525023	Kras	16653	22.4	32.5	44.7	1.62723	0.011667	2.424	4.67E-09
chr6:48395586-48419855:	Krba1	77827	27.4	18.0	10.6	-1.36231	0.075943	-2.03453	5.60E-08
chr11:5191553-5261610:-	Kremen1	84035	37.0	31.0	19.2	-1.0664	0.476144	-1.5333	2.31E-12
chr9:21273457-21287969:	Kri1	215194	43.0	45.6	60.1	1.19492	0.096507	1.74068	1.51E-12
chr5:3803165-3844515:+	Krit1	79264	30.9	35.0	35.0	1.27624	0.032648	1.40995	9.98E-05
chr10:111972695-1119884	Krr1	52705	35.2	41.2	50.0	1.3154	0.014503	1.76849	5.40E-11
chr11:99477973-99493110	Krt23	94179	6.8	10.3	9.8	1.65234	0.041654	1.77347	0.0027177
chr15:101412403-1014278	Krt7	110310	43.2	56.5	113.0	1.46574	0.225538	3.02446	1.19E-06
chr15:101929332-1019403	Krt79	223917	0.4	1.1	2.4	2.32618	0.065749	5.14643	1.39E-06
chr15:101459061-1014637	Krt81	64818	0.0	1.0	1.5	3.14137	0.062128	3.97856	0.0035481
chr3:89246438-89249722:	Krtcap2	66059	143.8	140.5	248.1	1.08847	0.474848	2.14101	6.06E-23
chr11:79014801-79146354	Ksr1	16706	19.4	51.2	70.7	2.7019	0.009672	3.807	1.28E-05
chr4:108847857-10884941	Kti12	100087	23.0	34.4	56.5	1.67655	0.005121	2.99042	5.71E-14
chr14:47649311-47736564	Ktn1	16709	124.5	110.8	86.4	-1.00247	0.979797	-1.15179	0.0064634
chr8:70513396-70523180:	Kxd1	75620	73.0	52.6	37.0	-1.24598	0.052991	-1.57039	1.75E-07
chr12:72073428-72085313	L3hypdh	67217	30.6	19.6	5.0	-1.40225	0.095796	-4.66874	2.03E-23
chr15:81663889-81688315	L3mbtl2	214669	11.6	13.6	20.1	1.32457	0.109781	2.1253	5.38E-09
chr10:26275452-26375185	L3mbtl3	237339	35.1	26.1	13.9	-1.20264	0.046398	-2.00683	4.36E-23
chr17:68273797-68780086	L3mbtl4	320858	2.0	1.7	0.4	-1.0245	0.954196	-3.66396	2.37E-08
chr14:77024201-77036617	Lacc1	210808	20.7	16.6	8.0	-1.12163	0.481063	-2.04545	1.41E-10
chr10:42312585-42478565	Lace1	215951	13.4	11.2	8.4	-1.07376	0.5567	-1.26424	0.0040955
chr9:66955393-66975484:	Lactb	80907	10.3	9.0	13.5	-1.01772	0.926837	1.62909	4.40E-07
chr1:13625900-13660509:	Lactb2	212442	24.9	21.8	24.0	-1.02067	0.85928	1.20387	0.0038448
chr6:124904359-12491170	Lag3	16768	12.8	9.5	1.9	-1.1953	0.492784	-4.99105	2.48E-18
chr17:67697265-67822645	Lama1	16772	1.9	1.9	0.5	1.06907	0.877916	-2.97467	9.48E-06
chr10:26981285-27616942	Lama2	16773	86.5	68.3	47.1	-1.13463	0.169305	-1.46656	1.15E-08
chr18:12334024-12583012	Lama3	16774	35.8	27.1	5.8	-1.164	0.479442	-4.7188	1.90E-27
chr10:38965515-39110188	Lama4	16775	122.5	89.2	53.5	-1.23965	0.342351	-1.79782	0.0002709
chr9:108479862-10849053	Lamb2	16779	150.9	124.0	72.5	-1.08804	0.38609	-1.66035	3.09E-14
chr1:153218922-15333278	Lamc1	226519	104.2	86.6	116.6	-1.07776	0.397633	1.395	4.79E-08
chr1:153122756-15318644	Lamc2	16782	16.5	21.0	46.2	1.41495	0.263358	3.24229	9.91E-08
chr7:101905837-10191190	Lamtor1	66508	93.1	84.9	114.0	1.02112	0.841771	1.52774	1.89E-13

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr3:137918555-13792876	Lamtor3	56692	74.6	85.9	111.2	1.29468	0.012858	1.85374	1.15E-14
chr1:67000517-67038872:	Lancl1	14768	44.0	33.3	11.2	-1.18595	0.206153	-3.10537	1.77E-31
chr5:45493374-45512691:	Lap3	66988	52.7	63.9	141.6	1.35822	0.030937	3.30181	1.63E-29
chr15:34238026-34284295	Laptm4b	114128	119.7	105.6	64.6	-1.01663	0.890054	-1.48	2.06E-09
chr11:58009064-58062032	Larp1	73158	53.7	74.1	110.3	1.55521	0.05814	2.48541	2.19E-07
chr15:99970065-10001635	Larp4	207214	52.1	71.8	126.6	1.55065	0.030119	2.94092	2.20E-12
chr13:9093905-9173090:+	Larp4b	217980	61.0	55.4	64.2	1.02049	0.889496	1.3118	0.0007733
chr9:60713121-60738801:	Larp6	67557	25.6	24.7	11.7	1.07589	0.700015	-1.7368	3.13E-06
chr3:127536714-12755334	Larp7	28036	50.4	54.1	86.4	1.21052	0.141808	2.12856	8.73E-16
chr18:42202349-42262071	Lars	107045	63.5	61.0	132.3	1.07505	0.396968	2.59211	2.10E-63
chr7:126363828-12636953	Lat	16797	6.5	13.8	23.6	1.97414	0.169213	3.42715	0.0008247
chr10:7681209-7716461:+	Lats1	16798	46.0	52.3	72.0	1.284	0.113453	1.93558	1.72E-08
chr9:51056780-51077094:	Layn	244864	17.2	12.3	4.9	-1.26328	0.231334	-2.74475	2.60E-12
chr2:158306493-15833285	Lbp	16803	104.6	81.6	51.1	-1.14235	0.634389	-1.61012	0.0091767
chr1:181815315-18184240	Lbr	98386	65.5	69.9	89.8	1.20181	0.098232	1.70811	6.14E-11
chr9:83391355-83441127:	Lca5	75782	8.0	5.9	3.1	-1.22043	0.289295	-2.03366	1.60E-07
chr16:96158406-96192257	Lca5l	385668	4.9	1.3	1.1	-3.08175	0.000165	-3.33598	2.37E-06
chr4:129548344-12957364	Lck	16818	7.8	10.8	11.1	1.48736	0.143466	1.71471	0.0087451
chr2:121137292-12114069	Lcmt2	329504	10.7	11.4	15.2	1.20272	0.192913	1.76629	1.90E-08
chr2:32384637-32387739:	Lcn2	16819	38.3	58.1	135.1	1.63852	0.046051	4.12914	1.53E-14
chr14:75131123-75230842	Lcp1	18826	57.7	58.3	80.5	1.11895	0.66342	1.70282	0.0012179
chr19:46032601-46045211	Ldb1	16825	166.5	155.7	84.9	1.0551	0.702147	-1.56106	2.33E-07
chr5:44472133-44799746:	Ldb2	16826	58.1	46.2	16.0	-1.12258	0.392218	-2.85327	3.31E-29
chr7:46845807-46855627:	Ldha	16828	215.2	234.5	536.0	1.21973	0.220833	3.0566	2.27E-22
chr17:5417323-5418767:-	Ldhal6b	106557	18.8	4.5	5.0	-3.36456	3.97E-05	-2.74579	7.42E-05
chr6:142490249-14250795	Ldhb	16832	280.6	228.3	87.3	-1.10664	0.573013	-2.52694	9.60E-16
chr7:46861263-46878142:	Ldhc	16833	75.2	3.0	8.0	-12.8853	2.63E-09	-5.32746	1.13E-05
chr8:111626271-11163032	Ldhd	52815	17.0	13.7	7.9	-1.11293	0.626745	-1.69974	0.0002149
chr9:21723576-21749918:	Ldlr	16835	14.2	19.4	92.3	1.5304	0.113184	7.34928	2.05E-24
chr4:107209180-10721791	Ldlrad1	546840	2.3	1.4	0.3	-1.415	0.533616	-3.73822	0.000825
chr2:101950201-10218646	Ldlrad3	241576	14.5	13.3	7.8	1.02855	0.836817	-1.48526	6.70E-07
chr18:67933257-68255549	Ldlrad4	52662	53.0	47.9	15.0	1.00512	0.978143	-2.79381	3.09E-26
chr3:131110297-13122435	Lef1	16842	8.4	5.2	2.5	-1.41553	0.046051	-2.60103	1.44E-12
chr3:65666228-65831162:	Lekr1	624866	5.0	4.4	1.5	-1.01942	0.945436	-2.64363	1.92E-10
chr3:92134994-92142754:	Lelp1	69332	6.8	0.4	1.0	-6.98655	0.000163	-3.6678	0.0033948
chr17:27189600-27204438	Lemd2	224640	46.6	46.6	63.7	1.12447	0.285755	1.70513	2.94E-12
chr3:89401896-89402650:	Lenep	57275	21.8	15.4	9.7	-1.26581	0.227838	-1.7706	8.87E-05
chr7:4148183-4149872:-	Leng9	243813	10.0	11.1	11.1	1.2458	0.099131	1.39265	0.0008792
chr9:75441524-75466432:	Leo1	235497	22.8	31.3	57.1	1.54547	0.002452	3.07738	7.57E-23
chr6:29060221-29073876:	Lep	16846	10.3	3.6	0.7	-1.76922	0.391165	-3.41195	0.009861
chr4:101717407-10181535	Lepr	16847	160.4	122.9	15.8	-1.17238	0.295531	-7.89012	1.15E-85
chr4:101647783-10165935	Leprot	230514	95.3	78.0	41.2	-1.10247	0.556111	-1.83862	1.88E-08
chr8:34135572-34146739:	Leprotl1	68192	35.7	37.4	47.6	1.17159	0.084392	1.65918	3.86E-14
chr5:33741352-33782704:	Letm1	56384	21.9	24.7	57.3	1.27447	0.135364	3.21255	1.46E-23
chr8:25578490-25597487:	Letm2	270035	31.3	18.1	4.1	-1.54274	0.07784	-5.67412	9.94E-21
chr15:78926725-78930465	Lgals1	16852	814.9	843.0	2071.7	1.16017	0.376623	3.10988	3.48E-23
chr7:28833794-28841703:	Lgals4	16855	2.7	1.6	0.6	-1.48473	0.24954	-3.14899	1.75E-05
chr13:12439402-12461738	Lgals8	56048	90.3	77.7	54.7	-1.04088	0.662433	-1.32149	1.42E-06
chr11:78962979-78984924	Lgals9	16859	76.2	89.2	107.9	1.31972	0.072231	1.75569	1.18E-06
chr19:38264782-38308939	Lgi1	56839	4.8	3.9	0.6	-1.1019	0.877468	-4.68973	1.13E-05
chr5:52537864-52566280:	Lgi2	246316	12.6	15.1	29.5	1.3442	0.346701	2.73224	4.95E-06
chr7:31059935-31070935:	Lgi4	243914	4.6	4.1	2.4	-1.01115	0.965279	-1.51928	0.0029451
chr1:134986353-13510527	Lgr6	329252	3.6	22.3	33.3	5.83564	6.52E-08	8.9826	1.12E-14
chr3:53041547-53261679:	Lhfp	108927	78.9	76.0	38.7	1.06511	0.738873	-1.62605	2.79E-05
chr13:94057796-94195409	Lhfpl2	218454	62.0	51.3	105.4	-1.07092	0.785548	2.08191	7.53E-07
chr2:36081953-36105408:	Lhx6	16874	1.0	1.3	1.6	1.36837	0.266661	1.83679	0.0024862
chr5:65391497-65409207:	Lias	79464	44.1	37.9	49.9	-1.04311	0.673824	1.4114	1.21E-08
chr11:4257568-4272514:+	Lif	16878	0.9	4.5	24.2	4.25131	0.000158	19.4182	1.70E-20

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr15:7129572-7197489:+	Lifr	16880	35.8	33.3	10.2	1.04875	0.858136	-2.72313	1.05E-11
chr7:13277313-13311427:	Lig1	16881	21.8	18.7	10.9	-1.04752	0.842384	-1.57176	0.0008313
chr11:82781109-82804274	Lig3	16882	38.0	35.9	52.7	1.06876	0.73091	1.72349	3.80E-06
chr8:9970020-9976323:-	Lig4	319583	3.9	5.0	11.3	1.42473	0.152366	3.43928	4.05E-12
chr5:66745840-67057159:	Limch1	77569	13.0	11.2	4.0	-1.04006	0.771836	-2.54193	1.15E-29
chr5:134656039-13468859	Limk1	16885	7.2	7.3	9.3	1.12522	0.466166	1.59729	1.55E-05
chr11:3343297-3409238:-	Limk2	16886	43.9	36.1	28.9	-1.08671	0.279728	-1.21414	0.0004787
chr18:31931507-31958619	Lims2	225341	80.9	65.6	32.4	-1.10812	0.541672	-1.98307	6.26E-10
chr12:84451508-84531533	Lin52	217708	28.9	27.9	15.6	1.08271	0.472364	-1.46776	5.55E-07
chr10:107271831-1074251	Lin7a	108030	11.3	8.4	1.3	-1.2005	0.328594	-6.8657	4.83E-45
chr2:109890878-10990093	Lin7c	22343	76.7	85.7	104.0	1.25939	0.091146	1.68346	3.13E-07
chr6:31093563-31218474:	Lincpint	232685	95.6	78.2	20.8	-1.10009	0.667556	-3.56478	2.82E-20
chr3:94399219-94404501:	Lingo4	320747	0.7	0.6	2.5	-1.01388	0.984129	3.54009	0.000386
chr7:66689889-66717256:	Lins	72635	8.2	9.1	9.7	1.22697	0.010211	1.46335	5.29E-10
chr19:34492316-34527474	Lipa	16889	60.1	44.2	26.3	-1.2189	0.343919	-1.81566	5.85E-05
chr7:25379527-25395987:	Lipe	16890	40.7	21.1	12.1	-1.65105	0.200434	-2.41376	0.0024397
chr19:33555281-33590311	Lipo1	381236	15.3	14.9	17.4	1.08669	0.573491	1.41364	0.0003078
chr16:10959273-10993121	Litaf	56722	92.8	198.6	173.6	2.33996	0.000461	2.23758	9.64E-05
chr17:17402686-17459388	Lix1	66643	5.6	4.2	0.7	-1.19194	0.62367	-5.71974	3.74E-13
chr3:96601133-96625352:	Lix1l	280411	86.0	68.5	29.5	-1.13479	0.56051	-2.27929	5.61E-09
chr10:120227060-1202320	Llph	66225	35.5	37.8	47.1	1.19621	0.275672	1.64057	2.25E-05
chr18:65980739-66002635	Lman1	70361	70.1	63.1	115.8	1.00362	0.972212	2.06179	1.43E-44
chr13:55343833-55362783	Lman2	66890	86.8	92.0	136.1	1.19066	0.058123	1.95337	6.02E-23
chr5:29229802-29378390:	Lmbr1	56873	21.5	18.0	11.0	-1.07004	0.324714	-1.56181	9.18E-20
chr15:98903921-98918098	Lmbr1l	74775	42.4	36.5	12.7	-1.03691	0.708613	-2.64556	2.81E-55
chr1:24678544-24766301:	Lmbrd1	68421	45.4	39.4	25.4	-1.03343	0.663906	-1.43004	3.50E-14
chr15:9140570-9197450:+	Lmbrd2	320506	24.5	24.9	29.0	1.13548	0.124566	1.47436	9.23E-11
chr6:112273758-11233042	Lmcd1	30937	17.2	18.0	18.0	1.16673	0.125418	1.3038	0.0003757
chr16:33062521-33125659	Lmln	239833	4.5	2.8	2.3	-1.40428	0.035814	-1.51284	0.0010099
chr3:88481148-88503352:	Lmna	16905	107.6	110.4	206.1	1.14766	0.134306	2.37788	1.91E-39
chr10:80901363-80918245	Lmnb2	16907	10.9	12.7	34.6	1.2996	0.004225	3.91619	1.64E-89
chr7:141210043-14121408	Lmntd2	72000	4.5	1.7	0.7	-2.20706	0.019235	-4.16151	1.52E-07
chr2:103957995-10398187	Lmo2	16909	31.1	22.9	37.9	-1.20926	0.162756	1.51087	2.97E-05
chr5:144100436-14418820	Lmtk2	231876	15.5	17.1	17.9	1.24349	0.116492	1.43472	0.0005722
chr7:45783947-45804142:	Lmtk3	381983	3.1	2.1	1.0	-1.30276	0.361105	-2.31569	5.43E-05
chr17:17527723-17624489	Lnpep	240028	129.1	104.1	69.1	-1.1146	0.30987	-1.49156	1.27E-07
chr5:147016655-14707657	Lnx2	140887	18.1	35.7	42.2	2.17667	0.001124	2.77417	2.67E-07
chr10:127032905-1270413	LOC100504608	1.01E+08	0.4	0.4	2.7	1.04503	0.956674	5.17502	2.42E-05
chr8:57304414-57320859:	LOC102636514	1.03E+08	240.8	180.4	55.7	-1.19237	0.116819	-3.41635	5.20E-48
chr17:56614298-56626903	Lonp1	74142	74.7	73.8	90.8	1.11127	0.289118	1.51849	2.18E-09
chr8:86624043-86716638:	Lonp2	66887	154.1	140.4	92.8	1.01084	0.947415	-1.32664	0.0010775
chr8:36216064-36249516:	Lonrf1	244421	21.5	13.2	10.4	-1.45576	0.00659	-1.64382	8.09E-06
chr1:38794509-38821215:	Lonrf2	381338	8.9	7.2	3.6	-1.11813	0.566854	-1.93143	3.25E-07
chr18:52516060-52529867	Lox	16948	48.9	40.3	17.9	-1.10147	0.751869	-2.12078	5.16E-05
chr9:58287723-58313212:	Loxl1	16949	20.2	20.1	31.5	1.11589	0.735557	1.87612	0.0016791
chr14:69609476-69695834	Loxl2	94352	22.5	22.6	62.4	1.12557	0.642674	3.31998	3.09E-14
chr6:83034224-83052564:	Loxl3	16950	23.7	16.7	6.7	-1.27676	0.190263	-2.75357	8.79E-14
chr19:42592279-42612806	Loxl4	67573	1.8	2.5	3.8	1.50591	0.109095	2.45776	1.76E-06
chrX:106920625-10693389	Lpar4	78134	8.3	4.9	1.9	-1.50838	0.223601	-3.23623	2.00E-06
chr5:107431549-10743503	Lpcat2b	70902	3.3	0.1	0.3	-9.4079	2.65E-06	-5.78491	2.28E-05
chr6:124663104-12470471	Lpcat3	14792	39.3	32.9	42.3	-1.07031	0.664363	1.34211	0.0031209
chr2:112239841-11224711	Lpcat4	99010	8.1	9.2	13.7	1.29111	0.423443	2.02712	0.0015011
chr5:81021593-81795730:	Lphn3	319387	39.2	34.0	10.0	-1.0344	0.783211	-3.10657	3.68E-55
chr12:16535669-16589770	Lpin1	14245	32.3	16.9	3.3	-1.68289	0.084087	-6.90816	5.37E-18
chr17:71183978-71249818	Lpin2	64898	18.6	19.9	20.8	1.19616	0.035838	1.39631	2.58E-07
chr8:68880555-68906932:	Lpl	16956	175.3	96.6	54.3	-1.5538	0.228811	-2.37876	0.0013018
chr3:117319146-11736087	Lppr4	229791	0.6	0.4	1.9	-1.31069	0.454083	3.66014	1.02E-08
chr3:117575461-11768950	Lppr5	75769	1.0	0.8	0.2	-1.14417	0.702147	-4.54166	4.36E-09

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr3:86224690-86782694:	Lrba	80877	35.4	31.2	23.2	-1.01492	0.899186	-1.21661	0.0028106
chr14:74754673-74947877	Lrch1	380916	38.6	36.0	15.5	1.04787	0.64228	-1.97764	6.65E-27
chrX:147471694-14755408	Lrch2	210297	15.7	12.0	8.3	-1.17188	0.436365	-1.50364	0.004494
chr17:56119678-56121946	Lrg1	76905	3.9	10.9	11.4	2.55502	0.032378	2.9367	0.0016645
chr6:34029448-34134034:	Lrguk	74354	1.7	0.5	0.2	-2.80836	0.000563	-4.84804	3.08E-09
chr3:106684987-10673657	Lrif1	321000	26.0	21.5	16.8	-1.08115	0.480079	-1.23377	0.0062752
chr6:94604529-94700145:	Lrig1	16206	42.8	59.8	98.7	1.56776	0.144193	2.70046	1.40E-05
chr10:125966219-1260153	Lrig3	320398	45.7	34.8	24.0	-1.18248	0.426998	-1.50229	0.0063964
chr15:39870603-39943757	Lrp12	239393	15.3	15.9	20.7	1.1637	0.316796	1.671	1.40E-06
chr8:46010602-46029476:	Lrp2bp	67620	1.1	0.2	0.2	-4.09179	0.00103	-3.89486	0.0001459
chr7:35200878-35215345:	Lrp3	435965	16.1	15.4	18.1	1.08325	0.590025	1.40323	0.0004597
chr6:134446478-13456691	Lrp6	16974	91.0	74.8	52.7	-1.09553	0.565227	-1.37458	0.0025958
chr4:107802259-10787684	Lrp8	16975	1.1	0.8	4.2	-1.24042	0.378908	4.63663	2.93E-23
chr17:84705247-84790786	Lrpprc	72416	56.0	55.4	91.8	1.11434	0.376388	2.03939	1.17E-17
chr9:77430823-77544852:	Lrrc1	214345	36.9	29.6	16.1	-1.11017	0.468105	-1.82102	9.42E-10
chr15:76710740-76715091	Lrrc14	223664	40.2	37.0	45.4	1.03107	0.736736	1.41172	1.18E-10
chr13:74359582-74364000	Lrrc14b	432779	3.2	1.7	0.6	-1.62878	0.261203	-3.24597	0.0002348
chr13:24012484-24280790	Lrrc16a	68732	20.1	16.9	10.8	-1.05963	0.652382	-1.48109	1.46E-06
chr14:55491093-55508264	Lrrc16b	268747	4.8	3.2	0.7	-1.33506	0.21737	-4.75737	3.69E-18
chr5:21543527-21575902:	Lrrc17	74511	136.0	95.8	19.0	-1.27846	0.467797	-5.06757	9.86E-13
chr14:32991382-33015292	Lrrc18	67580	12.8	5.0	1.5	-2.15673	0.047631	-5.56607	7.37E-09
chr9:110951545-11098406	Lrrc2	74249	1.4	1.0	0.2	-1.23912	0.638293	-4.94367	3.58E-07
chr10:61475833-61582228	Lrrc20	216011	5.8	4.1	1.7	-1.28903	0.26258	-2.63108	9.48E-09
chr6:124769869-12477972	Lrrc23	16977	9.6	4.7	1.1	-1.82584	0.004797	-6.14173	5.27E-21
chr7:139212988-13924297	Lrrc27	76612	10.4	2.4	3.0	-3.6025	5.15E-07	-2.56801	2.19E-05
chr7:67513410-67645236:	Lrrc28	67867	10.6	8.6	5.4	-1.10438	0.346337	-1.57707	1.48E-09
chr8:105312340-10532627	Lrrc29	234684	8.2	4.7	4.0	-1.53736	0.042867	-1.61531	0.0036629
chr10:77897576-77902536	Lrrc3	237387	4.7	3.1	1.5	-1.34539	0.141039	-2.48568	2.84E-09
chr7:98494222-98501830:	Lrrc32	434215	24.8	72.1	75.2	2.92814	0.004423	3.21307	0.0001539
chr3:30624267-30647818:	Lrrc34	71827	6.4	1.4	0.9	-2.98029	0.043294	-3.60015	0.0022932
chr8:105413622-10546408	Lrrc36	270091	7.2	3.4	0.4	-1.8548	0.008139	-12.9826	1.57E-30
chr6:28828126-28831747:	Lrrc4	192198	2.1	2.0	0.6	1.09892	0.719076	-2.44298	5.16E-07
chr4:116075465-11609704	Lrrc41	230654	55.7	84.7	141.7	1.69692	0.070661	2.97098	7.44E-07
chr4:107233514-10725353	Lrrc42	77809	28.1	21.9	30.0	-1.1489	0.137652	1.33533	1.58E-05
chr5:123489325-12350820	Lrrc43	381741	1.9	0.1	0.3	-8.23765	5.98E-05	-3.61224	0.0047199
chr11:120713953-1207211	Lrrc45	217366	73.2	53.2	26.0	-1.23419	0.149578	-2.22241	9.34E-14
chr11:97034602-97041369	Lrrc46	69297	14.1	0.9	1.6	-7.89585	3.30E-06	-4.82023	5.17E-05
chr4:154011803-15402151	Lrrc47	72946	24.4	30.8	40.3	1.4248	0.109171	2.01649	2.21E-05
chr11:60353380-60394333	Lrrc48	74665	12.8	8.7	2.8	-1.31318	0.129625	-3.48853	8.05E-19
chr9:60587235-60688134:	Lrrc49	102747	47.6	45.9	29.1	1.0814	0.361825	-1.30337	1.33E-05
chr7:44442487-44463344:	Lrrc4b	272381	6.4	4.8	2.2	-1.20317	0.413838	-2.24551	5.74E-07
chr2:96318169-97631664:	Lrrc4c	241568	6.2	4.1	2.8	-1.37254	0.093103	-1.74663	9.91E-05
chr7:101912989-10193385	Lrrc51	69358	32.4	16.2	7.1	-1.75345	0.015213	-3.44268	1.47E-11
chr2:85188071-85196699:	Lrrc55	241528	9.1	6.9	2.8	-1.18008	0.662297	-2.41677	0.0002858
chr7:141194130-14121005	Lrrc56	70552	7.9	4.0	1.4	-1.7243	0.035498	-4.14223	3.29E-12
chr11:94629824-94645216	Lrrc59	98238	48.4	68.1	231.4	1.57921	0.058518	5.56147	7.10E-22
chr15:66379858-66500910	Lrrc6	54562	2.2	0.5	0.4	-2.81381	0.060548	-3.27462	0.0055182
chr6:48554799-48570722:	Lrrc61	243371	8.6	5.3	2.6	-1.45389	0.089531	-2.56759	1.93E-08
chr14:75084303-75130883	Lrrc63	70859	1.7	0.1	0.3	-7.73717	8.22E-05	-3.19736	0.0097531
chr3:87736923-87748623:	Lrrc71	74485	3.3	1.6	1.1	-1.65462	0.175744	-2.23761	0.0040468
chr12:86734369-86763795	Lrrc74a	627607	3.2	0.2	0.4	-5.5094	0.002515	-3.46347	0.008843
chr16:17544465-17561247	Lrrc74b	74685	3.4	2.0	0.2	-1.46835	0.128634	-11.3594	5.39E-21
chr2:30237769-30263790:	Lrrc8a	241296	36.8	51.5	48.0	1.5756	0.009162	1.61564	0.0006565
chr5:105415775-10548618	Lrrc8b	433926	14.0	5.1	7.5	-2.32333	0.002995	-1.43655	0.138733
chr12:72441866-72510565	Lrrc9	78257	3.2	0.5	0.6	-4.62693	1.43E-05	-3.43493	5.31E-05
chr3:14533788-14572658:	Lrrcc1	71710	31.3	23.3	12.6	-1.21304	0.306877	-1.96071	5.49E-07
chr1:90998727-91128944:	Lrrfip1	16978	37.2	43.2	80.1	1.30975	0.079401	2.6502	6.81E-18
chr10:103063198-1032363	Lrriq1	74978	1.4	0.6	0.2	-1.83306	0.168544	-4.94113	1.93E-06

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr3:155093434-15519427	Lrriq3	74435	4.2	1.5	1.0	-2.31841	0.003239	-3.07063	1.97E-06
chr7:66258747-66388341:	Lrrk1	233328	40.7	29.8	14.7	-1.2207	0.0121	-2.19734	4.18E-37
chr15:91673224-91816124	Lrrk2	66725	25.1	19.4	7.2	-1.16	0.308471	-2.75634	4.19E-23
chr6:107529726-10757022	Lrrn1	16979	8.1	6.2	1.0	-1.17819	0.636771	-5.64723	1.69E-14
chr1:132880355-13294000	Lrrn2	16980	3.4	2.2	1.4	-1.3789	0.162899	-1.85093	0.0004179
chr6:77242717-77245517:	Lrrtm1	74342	3.3	0.8	0.1	-3.14648	0.011571	-9.61216	1.19E-09
chr2:32925215-32961255:	Lrsam1	227738	22.7	16.3	10.2	-1.25063	0.320409	-1.73909	0.000641
chr6:119315133-11933076	Lrtm2	211187	0.4	12.2	5.4	20.5181	1.68E-16	10.7155	4.60E-12
chr16:41533342-42146213	Lsamp	268890	18.6	15.4	4.3	-1.08639	0.489802	-3.43909	1.32E-44
chr16:30561369-30587589	Lsg1	224092	48.2	55.9	80.5	1.30782	0.068414	2.06729	2.96E-11
chr8:25785591-25803975:	Lsm1	67207	16.1	18.7	21.3	1.30921	0.053264	1.64389	2.10E-06
chr4:126096653-12609858	Lsm10	116748	38.1	29.1	18.7	-1.17862	0.347487	-1.61392	0.0001347
chr11:45928269-45944935	Lsm11	72290	9.1	8.4	9.4	1.03265	0.827887	1.29088	0.0029967
chr11:102163489-1021852	Lsm12	268490	31.2	40.2	92.1	1.44998	0.098678	3.52794	1.77E-14
chr17:34981854-34985893	Lsm2	27756	17.7	22.2	35.3	1.4171	0.135879	2.42817	2.13E-07
chr6:91516035-91522620:	Lsm3	67678	91.3	105.1	116.9	1.29246	0.080874	1.58902	2.72E-05
chr8:70673231-70678752:	Lsm4	50783	38.7	35.9	74.1	1.03678	0.780715	2.38226	2.67E-34
chr6:56701063-56704699:	Lsm5	66373	33.9	40.8	47.8	1.33942	0.058201	1.74294	1.26E-06
chr8:78804868-78821152:	Lsm6	78651	14.8	13.8	22.1	1.04342	0.658954	1.86093	4.05E-28
chr10:80852825-80855209	Lsm7	66094	100.8	101.7	147.7	1.12831	0.235833	1.82245	1.05E-17
chr7:30957770-30973469:	Lsr	54135	23.8	25.4	35.4	1.20753	0.44502	1.82607	0.0004175
chr10:76531627-76553934	Lss	16987	18.3	16.3	40.0	1.0014	0.996919	2.67828	1.40E-11
chr14:55765962-55768492	Ltb4r1	16995	2.1	2.6	5.4	1.34808	0.493366	2.8791	0.0002809
chr17:75005529-75392967	Ltbp1	268977	84.4	76.4	133.7	1.01351	0.934937	1.96984	1.56E-15
chr19:5740904-5758532:+	Ltbp3	16998	50.4	41.9	21.0	-1.07712	0.664147	-1.90107	1.82E-09
chr6:125306571-12531387	Ltbr	17000	61.6	100.8	142.6	1.82493	0.007224	2.77918	9.17E-09
chr11:50236472-50238471	Ltc4s	17001	5.3	2.9	1.3	-1.57019	0.301158	-2.7215	0.0021631
chr9:111019292-11104276	Ltf	17002	32.5	56.7	73.2	1.77223	0.145869	2.49474	0.0020739
chr2:119751326-11976043	Ltk	17005	1.4	1.3	0.5	1.03204	0.940946	-2.34838	0.0003666
chr10:13178638-13193137	Ltv1	353258	36.1	52.1	136.4	1.61745	0.027779	4.4794	8.33E-20
chr11:94291139-94321911	Luc7l3	67684	282.9	240.3	173.4	-1.04532	0.719076	-1.30256	0.0005329
chr10:97565501-97572703	Lum	17022	602.0	487.9	242.5	-1.1172	0.609991	-1.96405	1.41E-06
chr4:80910686-80954301:	Lurap1l	52829	36.2	35.6	49.0	1.10535	0.601742	1.67946	2.76E-05
chr4:136469761-13654931	Luzp1	269593	41.0	42.8	47.2	1.17928	0.286454	1.43311	0.0012837
chr7:54835245-55268888:	Luzp2	233271	13.7	11.0	0.9	-1.11334	0.521172	-11.0998	3.45E-81
chr3:67457999-67463907:	Lxn	17035	25.1	21.2	12.4	-1.06922	0.71401	-1.61531	2.98E-05
chr15:74994877-74998031	Ly6a	110454	104.9	160.2	207.5	1.67812	0.003946	2.41987	8.75E-10
chr17:35113946-35115400	Ly6g5b	266614	3.2	7.6	17.2	2.31547	0.030909	5.35029	1.25E-08
chr17:35071348-35074464	Ly6g6d	114654	5.4	4.3	0.9	-1.12498	0.810974	-3.77167	2.53E-05
chr5:38220482-38234306:	Lyar	17089	47.1	41.5	93.9	1.00582	0.985557	2.42865	6.12E-08
chr8:84701457-84704716:	Lyl1	17095	9.3	5.9	4.4	-1.39167	0.19925	-1.66497	0.0083465
chr15:74747856-74752979	Lynx1	23936	30.5	24.3	12.6	-1.12429	0.218899	-1.93519	1.10E-21
chr7:24864620-24869691:	Lypd4	232973	12.2	0.7	1.3	-6.76549	0.000283	-4.36896	0.0010985
chr2:49787686-49948846:	Lypd6b	71897	3.0	3.4	0.7	1.25561	0.565227	-2.90737	9.75E-05
chr1:4807893-4846735:+	Lypla1	18777	47.2	49.8	69.2	1.17836	0.006179	1.83013	5.68E-40
chr4:135968225-13597259	Lypla2	26394	42.3	48.4	77.8	1.29139	0.112678	2.26552	4.19E-12
chr1:186087732-18611731	Lyplal1	226791	9.4	7.8	4.6	-1.08308	0.741362	-1.61515	0.0016454
chr6:145211134-14521654	Lyrm5	67636	52.9	41.5	21.1	-1.15072	0.403427	-1.98304	4.69E-09
chr3:95134088-95139525:	Lysmd1	217779	6.4	4.8	2.1	-1.20053	0.347244	-2.37852	1.51E-09
chr13:81657806-81671890	Lysmd3	80289	35.5	42.1	37.5	1.32756	0.001937	1.31657	0.0003007
chr7:67222544-67228468:	Lysmd4	75099	15.5	11.9	9.5	-1.16609	0.273706	-1.30481	0.0099727
chr13:13590409-13777440	Lyst	17101	34.9	30.2	18.7	-1.04055	0.770925	-1.48814	1.14E-06
chr7:110850607-11086295	Lyve1	114332	39.0	69.2	64.3	1.98405	6.84E-12	2.04404	1.62E-15
chr18:4165832-4182236:+	Lyzl1	67328	2.4	0.1	0.4	-5.40969	0.002389	-2.9741	0.0192102
chr11:103631075-1036388	Lyzl6	69444	2.9	0.2	0.4	-4.91293	0.005104	-3.42277	0.0086437
chr4:149485333-14949666	Lzic	69151	30.2	30.5	46.5	1.14122	0.313401	1.91844	4.94E-13
chr9:123697593-12371755	Lztfl1	93730	43.1	40.4	15.7	1.05101	0.622987	-2.18644	2.87E-33
chr16:17508971-17526330	Lztr1	66863	89.0	80.1	57.8	1.00824	0.932968	-1.23012	6.87E-05

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr2:130632765-13064284	Lzts3	241638	23.0	18.9	11.1	-1.08145	0.742498	-1.63551	0.0008187
chr6:82946922-83030309:	M1ap	110958	1.0	0.1	0.2	-4.93246	0.001318	-2.81625	0.011304
chr6:122309010-12231767	M6pr	17113	185.5	183.9	220.2	1.11066	0.400211	1.47752	6.65E-06
chr16:38297754-38341860	Maats1	320214	2.9	1.3	0.6	-1.83307	0.050464	-3.55338	2.56E-07
chr3:101813076-10183622	Mab21l3	242125	40.5	27.0	6.3	-1.32325	0.573093	-4.06004	1.64E-05
chr19:7056768-7198062:+	Macrod1	107227	6.3	4.9	2.5	-1.13461	0.590112	-1.97938	2.62E-05
chr5:140008689-14032155	Mad1l1	17120	28.4	27.0	38.1	1.06334	0.546719	1.67399	1.33E-15
chr10:79664574-79668536	Madcam1	17123	0.2	0.7	3.6	2.37046	0.143466	8.78278	4.36E-07
chr5:33335572-33373294:	Maea	59003	96.5	104.0	125.2	1.21555	0.196919	1.60998	1.62E-05
chr1:166201385-16623874	Mael	98558	20.3	0.9	2.3	-11.5398	1.10E-08	-5.03841	1.72E-05
chr15:76351294-76354378	Maf1	68877	139.0	119.5	38.6	-1.04542	0.719182	-2.8618	9.01E-45
chr15:79347678-79359076	Maff	17133	9.7	29.4	51.1	3.12537	0.000147	5.65764	7.37E-12
chr11:120628351-1206335	Mafg	17134	36.4	41.6	41.1	1.2816	0.111266	1.40157	0.0044597
chr5:139791536-13980265	Mafk	17135	24.3	30.8	24.4	1.42657	0.001077	1.25401	0.0155551
chrX:94535474-94542074:	Maged1	94275	406.8	386.1	418.0	1.06727	0.615042	1.28307	0.0033173
chrX:150806421-15081433	Maged2	80884	100.4	89.0	58.9	-1.0106	0.943732	-1.36131	8.58E-05
chrX:153036166-15303756	Mageh1	75625	54.1	39.7	30.8	-1.22666	0.164882	-1.39607	0.0025169
chr6:93675453-94283917:	Magi1	14924	21.7	18.3	9.4	-1.05846	0.651563	-1.83734	1.01E-14
chr5:19227046-20704792:	Magi2	50791	8.9	6.4	4.4	-1.25008	0.255671	-1.60279	0.0010005
chr3:104013265-10422040	Magi3	99470	34.9	30.9	18.6	-1.01314	0.935473	-1.49443	2.37E-06
chrX:7673166-7681251:-	Magix	54634	3.8	2.0	0.4	-1.69942	0.087741	-7.06813	1.48E-14
chr4:107879755-10788742	Magoh	17149	95.6	131.7	228.2	1.54155	0.060143	2.8618	9.65E-10
chr6:131284389-13129324	Magohb	66441	21.5	25.5	42.5	1.3315	0.238988	2.38719	4.76E-07
chrX:105968085-10601189	Magt1	67075	43.2	43.2	91.7	1.11622	0.185039	2.64379	1.86E-63
chr13:41025120-41079706	Mak	17152	1.8	0.5	0.3	-2.66711	0.044208	-3.35636	0.0013998
chr8:31159468-31168724:	Mak16	67920	47.9	91.0	201.5	2.08184	0.011415	4.72498	6.61E-12
chr2:127633226-12765669	Mal	17153	25.2	30.7	45.8	1.36204	0.195865	2.21016	5.10E-06
chr2:127704390-12772989	Mall	228576	5.6	6.3	19.4	1.26467	0.36677	4.06434	8.31E-16
chr18:65430997-65478792	Malt1	240354	29.4	22.0	11.2	-1.20499	0.33413	-2.06795	9.68E-08
chr3:51687613-52105006:	Maml3	433586	20.0	15.1	2.7	-1.17615	0.220441	-5.65603	2.79E-69
chrX:71050256-71154717:	Mamld1	333639	8.8	6.8	4.6	-1.16181	0.360773	-1.51208	0.0004309
chr7:45639977-45645768:	Mamstr	74490	6.4	3.0	1.0	-1.86311	0.044542	-4.60853	3.76E-10
chr10:53906033-54075796	Man1a	17155	63.3	59.6	98.4	1.04113	0.852468	1.9126	8.08E-08
chr3:100562205-10068547	Man1a2	17156	64.4	61.9	70.2	1.06974	0.541251	1.3613	2.37E-05
chr7:80349097-80371375:	Man2a2	140481	50.9	42.4	22.2	-1.07608	0.449536	-1.82607	3.51E-20
chr5:36806813-36830649:	Man2b2	17160	33.5	27.6	18.1	-1.08144	0.477065	-1.47848	1.84E-07
chr9:57130777-57142210:	Man2c1	73744	74.5	59.0	44.7	-1.13029	0.123195	-1.33019	1.51E-06
chr3:135485611-13557140	Manba	110173	26.7	22.3	15.2	-1.07261	0.659211	-1.40315	0.0008813
chr2:157367594-15739676	Manbal	69161	43.3	38.4	61.8	-1.00634	0.957415	1.78228	1.84E-24
chr4:26324506-26346652:	Manea	242362	36.4	25.7	16.5	-1.2805	0.347487	-1.71983	0.0041778
chr9:106887415-10689193	Manf	74840	31.0	68.8	242.0	2.43076	9.08E-05	8.78312	1.98E-30
chr3:29891017-29924191:	Mannr	1.03E+08	10.0	6.9	3.0	-1.28395	0.568429	-2.3954	0.0030266
chrX:16709281-16817366:	Maob	109731	35.4	30.7	14.8	-1.03214	0.85543	-1.89976	4.71E-11
chr2:155276364-15527807	Map1lc3a	66734	97.7	107.7	166.7	1.24367	0.104066	2.11618	2.03E-14
chr8:121590468-12159804	Map1lc3b	67443	301.2	319.4	116.4	1.19971	0.307553	-2.04204	1.56E-08
chr8:70905974-70917529:	Map1s	270058	15.5	19.4	24.4	1.40569	0.059049	1.93791	1.08E-06
chr1:66175329-66442583:	Map2	17756	20.3	19.7	6.9	1.09376	0.539929	-2.32218	3.06E-18
chr9:64185793-64253605:	Map2k1	26395	55.5	106.8	124.6	2.0926	0.02174	2.58654	0.0001688
chr10:81105947-81124697	Map2k2	26396	48.8	58.1	113.6	1.34407	0.119494	2.83685	6.22E-14
chr11:60932057-60952803	Map2k3	26397	26.0	30.9	34.2	1.33838	0.074413	1.63333	6.99E-05
chr11:60920941-60931867	Map2k3os	24082	3.0	4.2	7.8	1.56348	0.096144	3.14165	2.39E-09
chr11:65688244-65788297	Map2k4	26398	44.6	49.1	50.3	1.24319	0.141314	1.40387	0.0023628
chr11:110399122-1105136	Map2k6	26399	34.3	20.3	5.9	-1.506	0.096175	-4.32046	1.78E-15
chr8:4238740-4247897:+	Map2k7	26400	56.0	57.4	56.7	1.15547	0.212378	1.26553	0.0061918
chr7:27656375-27674581:	Map3k10	269881	13.8	13.8	17.1	1.12326	0.252055	1.54563	7.09E-10
chr15:102497647-1025170	Map3k12	26404	16.1	11.9	6.3	-1.21896	0.317948	-2.01129	7.43E-07
chr16:21891969-21931877	Map3k13	71751	2.5	2.4	0.8	1.09824	0.761941	-2.50287	1.90E-06
chr11:103219764-1032674	Map3k14	53859	14.6	26.8	20.2	2.017	0.000617	1.692	0.0027606

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chrX:159988433-16012335	Map3k15	270672	2.1	2.5	3.1	1.33323	0.25493	1.81465	0.001026
chr11:106084902-1061554	Map3k3	26406	98.1	90.4	46.4	1.03184	0.578798	-1.68942	1.44E-46
chr10:19934526-20142750	Map3k5	26408	15.6	15.7	9.4	1.13087	0.334521	-1.33177	0.0019444
chr4:133240818-13325292	Map3k6	53608	5.7	13.2	10.6	2.45948	0.00063	2.20412	0.0004146
chr4:31964107-32023466:	Map3k7	26409	46.2	47.8	66.5	1.16516	0.165856	1.79051	2.60E-13
chr12:81714950-81781170	Map3k9	338372	2.1	1.3	1.1	-1.48972	0.024656	-1.50513	0.0034391
chr9:109931774-11008395	Map4	17758	44.6	38.4	50.2	-1.0372	0.664823	1.40361	6.70E-11
chr19:6341160-6355619:+	Map4k2	26412	38.1	31.5	14.8	-1.07878	0.602443	-2.04016	2.20E-14
chr7:99267447-99337137:	Map6	17760	7.3	5.8	4.0	-1.1336	0.345014	-1.46208	6.33E-05
chr3:82358072-82395268:	Map9	213582	5.6	4.0	2.5	-1.25918	0.207314	-1.79269	1.50E-05
chr16:16983382-17047453	Mapk1	26413	84.2	84.6	102.8	1.12802	0.084895	1.52474	2.12E-16
chr15:75993769-75999153	Mapk15	332110	4.3	2.2	0.4	-1.71205	0.041792	-6.92656	2.15E-16
chr7:138835818-13884626	Mapk1ip1	69546	56.2	45.8	15.3	-1.09776	0.443756	-2.90148	5.85E-36
chr14:47298314-47323091	Mapk1ip1l	218975	37.5	40.7	50.9	1.22696	0.165856	1.6867	1.36E-06
chr7:126759626-12676581	Mapk3	26417	130.1	94.0	54.7	-1.24495	0.068072	-1.89077	1.22E-12
chr18:73928486-74064949	Mapk4	225724	4.0	5.6	6.6	1.56061	0.00858	2.00529	1.81E-07
chr9:75386782-75410016:	Mapk6	50772	27.5	29.5	45.7	1.21588	0.361824	2.04282	1.79E-06
chr2:92383676-92401263:	Mapk8ip1	19099	28.0	21.3	12.0	-1.18102	0.1136	-1.85635	3.42E-15
chr15:89453911-89462447	Mapk8ip2	60597	2.8	1.2	1.2	-2.0407	0.001753	-1.79309	0.0019302
chr2:34406771-34624958:	Mapkap1	227743	43.4	41.0	46.1	1.05592	0.418135	1.32614	4.74E-10
chr1:131053704-13109754	Mapkapk2	17164	116.2	244.7	234.8	2.24178	0.02814	2.29491	0.0041802
chr5:121525051-12154589	Mapkapk5	17165	59.6	63.6	65.6	1.20519	0.208105	1.37008	0.0041769
chr2:153741287-15377331	Mapre1	13589	46.3	54.9	94.8	1.33641	0.052991	2.52339	9.95E-17
chr18:23752333-23893861	Mapre2	212307	46.6	32.5	11.7	-1.29013	0.163358	-3.09774	1.83E-17
chr5:30814756-30866106:	Mapre3	100732	19.4	13.4	8.8	-1.29053	0.201933	-1.73313	0.0001996
chr11:104231436-1043320	Mapt	17762	1.4	1.1	0.5	-1.08988	0.832305	-1.97649	0.0054899
chr1:184813068-18484584	2-Mar	67247	120.4	94.6	50.8	-1.14113	0.086323	-1.8904	8.49E-29
chr11:105360798-1054567	10-Mar	632687	6.3	0.3	0.7	-8.95471	3.14E-06	-4.61048	0.0002181
chr15:26309072-26409573	11-Mar	211147	2.9	0.3	0.4	-4.81253	0.004367	-3.56677	0.0051048
chr17:33685692-33718677	2-Mar	224703	52.8	49.8	37.0	1.05718	0.413299	-1.14064	0.0066205
chr19:37207545-37224457	5-Mar	69104	29.8	35.6	39.3	1.34693	0.103277	1.62942	0.0004069
chr6:116338022-11640954	8-Mar	71779	68.2	60.5	31.9	-1.0094	0.927577	-1.70502	2.59E-23
chr10:127056050-1270601	9-Mar	216438	6.5	6.4	7.6	1.10092	0.65243	1.44342	0.0065339
chr10:37133243-37138926	Marcks	17118	110.0	74.8	38.7	-1.32594	0.08464	-2.24205	3.15E-11
chr13:4248735-4249777:+	Marcksl1-ps4	111002	14.3	8.7	5.6	-1.46004	0.150068	-1.9544	0.0007797
chr16:14109166-14159274	Marf1	223989	89.3	75.3	29.3	-1.06197	0.468089	-2.42638	3.58E-58
chr12:111574510-1116562	Mark3	17169	82.7	100.7	131.0	1.37339	0.044565	1.95693	1.86E-08
chr10:127296221-1273117	Mars	216443	34.7	35.3	126.7	1.14559	0.199099	4.52099	2.99E-95
chr1:55237177-55240058:	Mars2	212679	12.8	13.8	20.7	1.21978	0.180506	2.0093	3.95E-11
chr19:42147389-42151703	Marveld1	277010	59.8	39.5	31.2	-1.36139	0.113404	-1.51675	0.0052345
chr16:23451785-23520590	Masp1	17174	4.2	2.8	0.4	-1.36475	0.258017	-6.64461	1.85E-17
chr4:148602544-14861548	Masp2	17175	1.4	1.2	2.7	-1.0474	0.927874	2.24126	0.0026226
chr4:116306760-11646418	Mast2	17776	25.8	32.1	78.5	1.40135	0.011772	3.73834	6.30E-38
chr6:72432799-72439558:	Mat2a	232087	154.1	269.9	539.7	1.9491	0.002819	4.12649	2.98E-15
chr11:40679314-40695203	Mat2b	108645	100.7	76.9	35.8	-1.1823	0.318124	-2.21776	1.52E-11
chr15:34306681-34436240	Matn2	17181	264.0	243.9	76.0	1.02739	0.866437	-2.74728	9.87E-31
chr18:35562158-35592045	Matr3	17184	283.7	288.7	317.5	1.14573	0.250787	1.39412	0.0001062
chr8:70016123-70042734:	Mau2	74549	91.6	89.8	57.9	1.10455	0.356419	-1.26075	0.0026613
chr7:127022137-12702647	Maz	17188	70.9	68.5	84.3	1.08122	0.329606	1.48486	7.58E-13
chr9:78430518-78443237:	Mb21d1	214763	4.4	6.5	8.4	1.62979	0.006253	2.33699	1.67E-09
chr16:28826176-28929698	Mb21d2	239796	14.3	13.4	17.3	1.04343	0.810974	1.51035	5.86E-05
chr10:80392541-80399479	Mbd3	17192	46.9	52.5	109.5	1.26252	0.139683	2.87213	1.49E-20
chr9:18478395-18485292:	Mbd3l1	73503	2.3	0.2	0.2	-3.854	0.024728	-3.45714	0.0095137
chr6:115840697-11585334	Mbd4	17193	21.5	14.2	4.7	-1.3583	0.23031	-3.44992	1.92E-11
chr2:48949508-49317069:	Mbd5	109241	21.7	18.4	10.4	-1.05769	0.613201	-1.65785	1.22E-12
chr13:81711417-81753275	Mblac2	72852	7.5	5.3	2.4	-1.26535	0.358726	-2.43839	1.02E-06
chr3:60472830-60629748:	Mbnl1	56758	253.2	216.3	373.2	-1.05131	0.623555	1.83486	1.67E-21
chr12:24831599-24960299	Mboat2	67216	27.8	38.2	41.9	1.53432	0.141107	1.81209	0.0070892

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:93886219-93946984	Mbtd1	103537	42.4	36.7	20.1	-1.03521	0.760994	-1.67974	1.97E-14
chr8:119508152-11955876	Mbtps1	56453	139.2	120.1	78.7	-1.03763	0.700539	-1.41005	4.68E-09
chrX:157547822-15759871	Mbtps2	270669	14.6	13.3	14.5	1.02275	0.865432	1.24059	0.0039378
chr18:68406899-68429320	Mc2r	17200	1.1	0.7	0.0	-1.38954	0.575267	-6.59359	5.85E-06
chr18:68337603-68339711	Mc5r	17203	3.3	1.6	0.6	-1.67804	0.364232	-3.25053	0.0043606
chr9:44134658-44142726:	Mcam	84004	221.7	166.2	117.8	-1.19547	0.133545	-1.4981	4.88E-06
chr18:44425060-44812182	Mcc	328949	15.2	14.3	7.0	1.04945	0.710314	-1.72047	9.87E-12
chr3:35959306-36000678:	Mccc1	72039	31.5	23.7	14.4	-1.19121	0.29585	-1.73166	4.55E-06
chr13:99948532-10001563	Mccc2	78038	51.1	37.0	22.5	-1.23694	0.197108	-1.79189	1.32E-06
chr7:64392771-64412119:	Mcee	73724	55.5	47.5	12.2	-1.04825	0.798039	-3.54751	1.91E-28
chrX:60055956-60179089:	Mcf2	109904	7.3	5.3	0.4	-1.22291	0.569544	-12.0004	2.28E-24
chr8:12915893-13020509:	Mcf2l	17207	12.0	10.2	3.0	-1.06146	0.720527	-3.17044	1.73E-28
chr17:87254443-87265947	Mcfd2	193813	86.4	80.0	125.5	1.03809	0.731502	1.80908	3.39E-20
chr6:88883474-88898780:	Mcm2	17216	20.0	21.5	25.9	1.20171	0.319159	1.60629	0.0003205
chr16:15623897-15637400	Mcm4	17217	39.6	46.1	44.1	1.30748	0.089439	1.38987	0.0065923
chr8:75109509-75128439:	Mcm5	17218	19.4	21.9	28.7	1.26312	0.174567	1.83846	1.20E-06
chr5:138164589-13817186	Mcm7	17220	103.7	82.5	34.8	-1.13077	0.57515	-2.32393	2.72E-09
chr2:132816141-13284418	Mcm8	66634	5.8	5.9	2.8	1.1261	0.509097	-1.64132	8.23E-05
chr7:128696459-12874042	Mcmbp	210711	57.2	60.8	75.0	1.19686	0.124465	1.63173	1.40E-08
chr8:3500519-3515231:+	Mcoln1	94178	46.5	33.5	19.4	-1.24712	0.132508	-1.89619	4.29E-09
chr15:99242817-99251961	Mcrs1	51812	78.9	71.4	102.9	1.01291	0.886992	1.62885	4.27E-25
chr13:76384961-77031810	Mctp1	78771	9.4	8.7	4.0	1.02471	0.918641	-1.87872	1.12E-06
chr7:72077830-72306595:	Mctp2	244049	5.5	4.1	2.8	-1.2043	0.332562	-1.54399	0.0017527
chrX:38600658-38613522:	Mcts1	68995	61.3	59.9	78.8	1.09419	0.455331	1.59761	5.21E-09
chr2:152687148-15268794	Mcts2	66405	26.5	33.9	53.4	1.43881	0.109323	2.4392	9.90E-08
chr10:59446984-59616692	Mcu	215999	19.5	19.1	22.2	1.09058	0.460662	1.41998	9.51E-06
chr17:47815328-47834691	Mdfi	17240	9.9	8.9	4.9	1.00417	0.983792	-1.59976	1.70E-05
chr6:15720661-15802169:	Mdfic	16543	30.5	45.4	57.2	1.66589	0.041361	2.25541	2.17E-05
chr1:63698827-63730318:	Mdh1b	76668	2.5	0.2	0.2	-6.1245	0.000366	-5.72234	5.20E-05
chr5:135778649-13579038	Mdh2	17448	134.2	142.5	294.0	1.19359	0.119632	2.71327	3.74E-34
chr10:118141787-1181689	Mdm1	17245	16.5	12.6	6.1	-1.17668	0.323298	-2.14422	8.93E-11
chr10:117688875-1177107	Mdm2	17246	58.1	60.9	78.9	1.17854	0.129614	1.69167	3.18E-11
chr1:132986105-13303058	Mdm4	17248	132.8	113.8	75.2	-1.0398	0.655347	-1.40829	3.50E-10
chr4:32657119-32775217:	Mdn1	100019	37.9	47.9	102.0	1.42774	0.05823	3.27397	1.88E-17
chr14:55657879-55660508	Mdp1	67881	31.8	29.7	50.2	1.04539	0.744702	1.96227	1.43E-17
chr18:73770040-73815392	Me2	107029	37.7	32.6	43.5	-1.03238	0.889246	1.4318	0.004861
chr7:89632818-89854359:	Me3	109264	10.5	13.4	25.5	1.42539	0.173302	2.88578	2.06E-08
chr17:46680453-46683126	Mea1	17256	77.0	67.1	93.7	-1.02092	0.905083	1.51675	1.03E-05
chr3:30236569-30509487:	Mecom	14013	35.3	27.8	16.2	-1.12224	0.69233	-1.70544	0.0038123
chr3:29951296-30013204:	Mecom	14013	58.0	45.9	31.4	-1.12738	0.700725	-1.45321	0.0626423
chr4:131843471-13186778	Mecr	26922	29.5	26.3	42.8	1.00125	0.994268	1.81138	1.52E-15
chr11:98152155-98193293	Med1	19014	41.8	44.5	54.3	1.19965	0.151592	1.61611	2.80E-07
chr13:69809882-69816094	Med10	28077	71.5	77.3	88.8	1.21805	0.224816	1.54187	0.0002542
chr11:70451931-70453726	Med11	66172	32.9	41.8	41.0	1.42139	0.000168	1.55085	2.24E-08
chr3:59006978-59318412:	Med12l	329650	6.1	5.0	9.2	-1.07108	0.697154	1.87926	2.63E-09
chr5:118560719-11876543	Med13l	76199	43.9	51.1	57.2	1.31376	0.099423	1.61679	0.0001186
chrX:12675371-12761973:	Med14	26896	28.0	25.8	31.3	1.03568	0.794301	1.3944	2.64E-05
chr16:17651208-17722947	Med15	94112	29.8	29.7	34.7	1.12355	0.35199	1.45229	2.08E-05
chr10:79894707-79908938	Med16	216154	23.6	22.1	26.8	1.05549	0.62635	1.42092	4.44E-07
chr9:15260351-15279867:	Med17	234959	33.4	31.3	36.2	1.05276	0.580932	1.35258	4.30E-07
chr4:132458729-13246392	Med18	67219	14.4	14.3	16.8	1.11261	0.46965	1.45055	0.0001796
chr2:84678402-84688215:	Med19	381379	25.7	29.3	40.5	1.27972	0.019661	1.95677	3.52E-17
chr17:47611596-47624418	Med20	56771	59.0	65.4	53.3	1.2442	0.005185	1.12836	0.0681626
chr6:146642579-14665060	Med21	108098	71.5	86.8	83.3	1.36784	0.023025	1.45209	0.0005581
chr2:26905267-26910642:	Med22	20933	43.5	42.0	54.8	1.0868	0.449598	1.57027	1.08E-09
chr2:29346810-29524790:	Med27	68975	14.5	16.2	31.5	1.25641	0.07407	2.69072	2.58E-27
chr7:28385247-28392690:	Med29	67224	15.0	16.5	25.4	1.24655	0.361824	2.06468	1.72E-05
chr12:81573564-81594958	Med6	69792	71.4	85.5	83.1	1.34472	0.013203	1.44959	8.76E-05

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:46436947-46442721	Med7	66213	23.2	28.1	34.5	1.35742	0.137557	1.81939	9.43E-05
chr4:118409337-11841582	Med8	80509	35.6	40.7	54.5	1.28815	0.101095	1.89503	2.07E-08
chr11:59948214-59963306	Med9	192191	17.5	17.1	18.8	1.08995	0.49509	1.336	0.0006728
chr5:149411806-14943170	Medag	70717	25.0	24.5	36.3	1.08827	0.616824	1.79229	4.83E-08
chr8:70152778-70167488:	Mef2b	17259	2.8	2.2	0.8	-1.14032	0.762055	-2.52028	0.0009871
chr13:83504034-83667079	Mef2c	17260	34.2	22.9	19.8	-1.3425	0.063874	-1.3744	0.0099366
chr2:3409043-3422648:-	Meig1	104362	37.2	2.5	4.6	-7.91745	4.74E-06	-4.52149	0.000145
chr17:24804382-24839787	Meiob	75178	1.7	1.0	0.5	-1.38924	0.477967	-2.38241	0.009071
chr7:16175395-16186508:	Meis3	17537	20.1	19.5	20.9	1.08579	0.421332	1.29709	0.0001932
chr17:74200700-74294863	Memo1	76890	44.1	45.2	72.8	1.15471	0.198342	2.05672	3.44E-20
chr11:101877510-1018943	Meox1	17285	4.7	4.9	8.2	1.14581	0.473902	2.12202	6.84E-10
chr5:137781906-13778670	Mepce	231803	48.7	48.0	30.3	1.10243	0.23036	-1.2797	3.63E-05
chr2:128698997-12880218	Mertk	17289	25.7	26.9	8.7	1.17144	0.364071	-2.31835	6.27E-12
chr7:83880495-83884341:	Mesdc1	80889	21.9	74.3	76.5	3.57405	1.21E-06	3.96601	1.72E-09
chr7:83892000-83901532:	Mesdc2	67943	76.7	97.1	125.3	1.42637	0.010693	2.02219	1.01E-10
chr7:79792241-79793590:	Mesp1	17292	1.2	0.0	0.2	-4.48604	0.009663	-2.76553	0.0350531
chr6:17463957-17573980:	Met	17295	40.0	37.0	16.2	1.04827	0.860765	-1.93251	1.32E-05
chr3:138458960-13848938	Metap1	75624	56.0	63.2	83.5	1.27212	0.137524	1.84353	3.02E-07
chr2:71453338-71525191:	Metap1d	66559	98.5	86.3	46.1	-1.02082	0.882513	-1.70099	4.03E-12
chr10:93858490-93891202	Metap2	56307	67.4	67.6	115.3	1.12935	0.264768	2.12775	2.90E-23
chr10:127041932-1270454	Mettl1	17299	28.4	35.7	121.7	1.413	0.005219	5.2694	8.37E-72
chr1:162533672-16254834	Mettl13	71449	23.6	17.9	33.4	-1.1823	0.255552	1.7636	3.87E-08
chr3:123368295-12338599	Mettl14	210529	28.0	25.2	33.9	1.0113	0.932551	1.51067	1.27E-09
chr2:109092300-10927829	Mettl15	76894	11.6	11.0	5.5	1.05577	0.763257	-1.67603	4.69E-06
chr11:74770863-74818692	Mettl16	67493	39.3	46.8	90.8	1.34478	0.067731	2.84171	2.08E-18
chr14:51884842-51891868	Mettl17	52535	61.1	41.8	31.3	-1.31285	0.097246	-1.54824	0.0004416
chr1:163994945-16399724	Mettl18	69962	30.9	20.0	8.5	-1.38495	0.24551	-2.74123	7.13E-07
chr11:105126425-1051411	Mettl2	52686	31.1	35.6	59.8	1.29016	0.057463	2.37892	1.60E-18
chr6:149141513-14915117	Mettl20	320204	70.5	63.3	23.9	-1.00227	0.991834	-2.33458	1.32E-16
chr16:8470813-8490197:+	Mettl22	239706	15.7	14.2	24.6	1.01476	0.93472	1.95207	2.44E-14
chr10:40683282-40811083	Mettl24	327747	32.4	24.2	14.6	-1.20415	0.453446	-1.7303	0.0015254
chr10:105763185-1058413	Mettl25	216292	18.2	16.3	20.9	-1.00484	0.977195	1.42741	3.63E-05
chr17:94727080-94749892	Mettl4	76781	33.0	28.9	17.2	-1.02532	0.867017	-1.52373	5.92E-07
chr2:69871195-69885615:	Mettl5	75422	30.2	27.9	35.1	1.03152	0.850825	1.44922	4.82E-05
chr14:31478798-31494977	Mettl6	67011	44.4	48.4	55.7	1.23033	0.193959	1.55885	0.0001479
chr15:100304817-1003143	Mettl7a1	70152	256.3	412.7	150.4	1.80229	0.000541	-1.35352	0.0429429
chr2:70964562-71055606:	Mettl8	228019	12.4	10.6	6.3	-1.04468	0.808463	-1.56561	3.20E-05
chr7:121034445-12107683	Mettl9	59052	73.9	73.4	100.2	1.10936	0.273693	1.68653	2.04E-15
chr3:88532395-88541394:	Mex3a	72640	10.4	9.7	15.2	1.04737	0.778385	1.82074	3.03E-10
chr7:82867333-82871576:	Mex3b	108797	59.5	39.2	10.3	-1.35722	0.419969	-4.02793	9.52E-08
chr18:73572705-73592578	Mex3c	240396	53.5	62.8	74.8	1.32457	0.098764	1.73034	1.75E-05
chr4:141010424-14101598	Mfap2	17150	48.1	31.1	8.2	-1.38154	0.024718	-4.55768	6.22E-39
chr8:60632825-60676731:	Mfap3l	71306	10.9	7.8	3.3	-1.26009	0.59162	-2.38083	0.0023708
chr11:61485444-61488704	Mfap4	76293	126.2	106.2	32.8	-1.0677	0.666095	-3.0497	3.22E-32
chr6:122513676-12252928	Mfap5	50530	86.9	87.6	23.5	1.12703	0.328594	-2.92896	7.22E-35
chr8:35587798-35679449:	Mfhas1	52065	24.7	22.1	22.9	-1.00048	0.996946	1.15764	0.0076143
chr3:32529482-32579225:	Mfn1	67414	47.9	40.8	30.0	-1.04886	0.582659	-1.27449	2.00E-05
chr4:147873586-14790490	Mfn2	170731	38.7	34.9	48.3	1.01496	0.914153	1.55453	1.40E-09
chr15:78755883-78773445	Mfng	17305	18.9	16.2	11.0	-1.04968	0.803409	-1.36768	0.0078089
chr3:67582768-67604231:	Mfsd1	66868	63.4	51.4	26.7	-1.10947	0.375516	-1.89245	3.69E-15
chr11:116854015-1168756	Mfsd11	69900	22.7	16.0	12.1	-1.27024	0.084154	-1.49269	0.0001402
chr4:122946851-12296118	Mfsd2a	76574	5.1	8.1	27.6	1.72375	0.118652	5.7569	6.65E-12
chr15:102279456-1022817	Mfsd5	106073	22.6	29.4	50.0	1.46406	0.075564	2.68064	5.60E-10
chr1:52656305-52727318:	Mfsd6	98682	20.2	14.9	8.5	-1.22049	0.060434	-1.884	2.24E-15
chr5:108441054-10844889	Mfsd7a	243197	12.0	9.0	2.5	-1.19901	0.467797	-3.59461	2.07E-13
chr1:191005832-19102619	Mfsd7b	226844	16.4	22.1	29.6	1.51324	0.012053	2.21674	5.99E-10
chr1:40772040-40790657:	Mfsd9	211798	5.4	2.8	1.6	-1.66973	0.16022	-2.41337	0.0013608
chr11:49244191-49263024	Mgat1	17308	44.5	41.7	46.6	1.04912	0.686858	1.30227	0.0003573

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr12:69184158-69186773	Mgat2	217664	43.4	58.2	157.9	1.49999	0.024169	4.37714	1.20E-27
chr15:80173721-80215519	Mgat3	17309	17.1	11.3	5.1	-1.3504	0.001764	-2.67203	2.40E-34
chr8:83348472-83379402:	Mgat4d	67555	1.5	0.0	0.1	-6.45476	0.000737	-4.12829	0.0028053
chr19:45750259-45783291	Mgea5	76055	141.9	144.1	86.7	1.13897	0.044961	-1.30933	4.79E-08
chr11:70130357-70137542	Mgl2	216864	20.9	26.6	36.3	1.41421	0.191993	2.09608	0.0001466
chr7:136894611-13712818	Mgmt	17314	17.2	15.4	6.1	1.0018	0.994268	-2.20485	1.18E-09
chr16:4886100-4938296:+	Mgrn1	17237	97.7	84.5	69.0	-1.03109	0.67517	-1.13167	0.0081634
chr1:167372384-16739379	Mgst3	66447	47.5	40.4	18.3	-1.05675	0.74419	-2.05646	9.76E-12
chr1:183326236-18336956	Mia3	338366	73.3	73.6	96.8	1.13186	0.242347	1.64686	3.27E-11
chr4:155654470-15566925	Mib2	76580	56.6	48.6	23.4	-1.03825	0.765334	-1.92298	2.11E-18
chr10:41476314-41487030	Mical1	171580	41.3	29.5	20.1	-1.26499	0.292402	-1.62347	0.0027883
chr7:112225836-11235519	Mical2	320878	40.0	49.9	47.0	1.39556	0.017704	1.4554	0.0007584
chr7:112368308-11241310	Micalcl	1.01E+08	7.1	3.3	3.3	-1.85564	0.010615	-1.65862	0.0096377
chr5:139706693-13973633	Micall2	231830	3.7	4.0	6.5	1.22284	0.520998	2.1146	0.0003421
chr10:59702563-59864134	Micu1	216001	57.2	55.7	67.6	1.08879	0.39234	1.47527	1.10E-08
chr8:40308051-40386304:	Micu3	78506	20.6	20.9	24.3	1.14234	0.275672	1.46811	9.22E-06
chrX:140678028-14076771	Mid2	23947	23.1	19.1	10.1	-1.09079	0.499036	-1.82818	2.36E-12
chr10:80148290-80158367	Midn	59090	27.1	74.1	69.5	2.76285	0.009683	2.75623	0.0014122
chr15:80234080-80253371	Mief1	239555	27.1	25.3	35.0	1.04575	0.581788	1.61647	2.70E-21
chr11:60728398-60732951	Mief2	237781	7.2	7.5	12.6	1.17114	0.478676	2.13947	2.71E-07
chr11:98437708-98438988	Mien1	103742	50.1	54.8	63.8	1.22626	0.08464	1.58397	1.31E-07
chr10:79540245-79555091	Mier2	70427	35.1	35.1	35.0	1.12479	0.251435	1.24761	0.0030646
chr10:75859353-75860250	Mif	17319	236.4	238.5	503.2	1.13879	0.506647	2.60755	8.83E-14
chr4:147860778-14786871	Miip	28010	42.0	31.4	13.8	-1.20662	0.43166	-2.35312	2.18E-07
chr7:18839966-18858653:	Mill2	243864	83.9	70.3	14.6	-1.07374	0.751176	-4.42129	8.76E-28
chr16:59471775-59492451	Mina	67014	29.8	27.8	51.1	1.03923	0.768258	2.13188	3.00E-24
chr11:70562881-70614482	Mink1	50932	24.5	20.3	16.7	-1.08027	0.324867	-1.17061	0.0056
chr4:139101814-13913111	Minos1	433771	31.1	31.1	37.7	1.12344	0.355845	1.50851	2.71E-06
chr19:32485769-32515370	Minpp1	17330	23.7	24.5	42.5	1.16101	0.087257	2.23885	4.36E-39
chr6:8209227-8236273:+	Mios	252875	41.8	37.8	43.2	1.01145	0.892309	1.29038	1.86E-08
chr9:41531425-41531504:	Mir100	723892	86.1	66.4	27.6	-1.14977	0.610351	-2.3944	4.67E-06
chr2:74726070-74726137:	Mir10b	387144	41.9	26.7	11.8	-1.37576	0.473902	-2.50223	0.0043855
chr10:92137140-92137223	Mir1251	1.01E+08	23.1	12.1	3.4	-1.59398	0.40778	-3.52875	0.0021931
chr6:51269812-51269910:	Mir148a	387166	6.1	8.3	16.2	1.35418	0.600439	2.65841	0.0084881
chr14:115044390-1150467	Mir17hg	75957	27.5	38.0	36.4	1.5537	0.009642	1.63969	0.0002962
chr14:115043851-1150439	Mir18	387135	14.8	29.0	24.9	2.08241	0.021088	1.98746	0.0066814
chr2:38852735-38852810:	Mir181a-2	387176	16.1	5.8	0.3	-2.03251	0.227754	-6.02919	5.95E-05
chr2:38853830-38853915:	Mir181b-2	723903	21.1	6.2	2.1	-2.49139	0.079401	-4.57181	0.0002047
chr1:160295864-16029597	Mir1927	1E+08	17.3	10.3	4.2	-1.43642	0.468199	-2.64212	0.0074042
chr18:35554567-35554636	Mir1949	1E+08	152.0	166.6	212.6	1.22656	0.29572	1.73254	5.46E-05
chr2:92191977-92192074:	Mir1955	1E+08	39.6	31.2	11.6	-1.13075	0.78977	-2.46497	0.0019321
chr8:70925525-70925618:	Mir1969	1E+08	2.0	7.5	12.7	2.40097	0.152841	3.7139	0.0043676
chr14:115044000-1150440	Mir19a	723891	32.9	46.7	55.6	1.56256	0.169258	2.01264	0.0035047
chr11:75461539-75466690	Mir22hg	1E+08	6.6	12.2	29.4	1.97116	0.049461	4.74123	1.88E-09
chr5:138165321-13816540	Mir25	723926	48.9	50.0	13.8	1.11018	0.832157	-2.49062	0.0026204
chr6:31062660-31062747:	Mir29a	387222	50.7	44.7	17.1	-1.03389	0.950545	-2.16874	0.009181
chr11:106782693-1067827	Mir3064	1.01E+08	####	1064.2	441.0	1.08249	0.60475	-1.96122	1.48E-11
chr5:139369650-13936974	Mir339	723898	16.9	8.1	3.7	-1.73325	0.21668	-2.92175	0.0019625
chr11:79726400-79726511	Mir365-2	723853	9.9	94.3	64.5	5.75688	0.000365	4.43582	0.0004024
chr16:43640655-43640737	Mir568	1E+08	121.7	117.2	27.9	1.07469	0.816841	-3.26177	1.68E-09
chr17:67026147-67026235	Mir5709	1.01E+08	15.0	10.4	3.4	-1.23746	0.699862	-2.72378	0.0071744
chr13:28710781-28710873	Mir6368	1.02E+08	24.7	14.2	2.2	-1.49164	0.430894	-5.23576	1.55E-05
chr2:94261300-94261399:	Mir670	735259	16.1	4.1	0.5	-2.6292	0.095028	-6.2606	4.29E-05
chr12:69763835-69763944	Mir681	751538	29.3	12.0	2.8	-1.99005	0.142891	-5.27034	6.97E-06
chr4:138316132-13831620	Mir7019	1.02E+08	27.6	17.7	3.8	-1.33223	0.593985	-3.95108	0.0003077
chr5:75176831-75176904:	Mir7025	1.02E+08	21.5	23.2	5.5	1.16352	0.779328	-2.52335	0.0096509
chr7:47083166-47083224:	Mir7056	1.02E+08	0.0	5.8	9.2	2.99692	0.073959	4.44273	0.0015234
chr8:123104975-12310504	Mir7079	1.02E+08	29.8	47.9	69.6	1.7329	0.123273	2.67854	0.0001774

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr8:84086099-84086186:	Mir709	735271	8.3	6.0	0.6	-1.17564	0.81585	-3.82883	0.0023199
chr10:120447991-1204481	Mir763	791076	6.6	2.6	0.7	-1.81036	0.350073	-3.35681	0.0092553
chr16:77329328-77558428	Mir99ahg	77994	25.4	16.6	9.6	-1.37456	0.271788	-2.04147	0.0006888
chr12:109734981-1097494	Mirg	1E+08	4.5	5.9	8.9	1.45305	0.277638	2.3212	0.0006178
chr9:41536716-41536811:	Mirlet7a-2	723965	70.6	53.0	19.1	-1.1884	0.549177	-2.79863	5.69E-07
chr11:71019611-71027134	Mis12	67139	24.1	29.3	33.0	1.36726	0.056499	1.69118	2.41E-05
chr16:90719312-90727371	Mis18a	66578	16.2	15.6	8.6	1.06656	0.783293	-1.50281	0.004872
chr6:97807058-98021358:	Mitf	17342	96.2	80.3	26.3	-1.0761	0.606572	-2.89433	4.35E-32
chr16:13256481-13417529	Mkl2	239719	30.0	23.7	13.0	-1.14053	0.492764	-1.82453	3.47E-06
chr6:31398828-31509477:	Mkln1	27418	88.7	95.2	106.3	1.20658	0.038307	1.49445	4.84E-09
chr4:115839198-11587925	Mknk1	17346	37.7	30.5	22.1	-1.10852	0.409263	-1.3572	0.000512
chr10:80665318-80676293	Mknk2	17347	96.8	114.6	43.9	1.34037	0.238988	-1.72229	0.003011
chr6:39397821-39420369:	Mkrn1	54484	69.3	57.5	29.2	-1.07505	0.374616	-1.89212	1.49E-29
chr11:87853225-87863679	Mks1	380718	18.9	11.3	7.3	-1.50056	0.015982	-2.03837	8.02E-08
chr18:6934966-7004779:-	Mkx	210719	5.3	3.9	1.4	-1.23304	0.464354	-2.85364	1.75E-07
chr15:88955884-88978553	Mlc1	170790	1.2	0.0	0.1	-7.84915	0.0001	-4.69372	0.0006736
chr5:115142981-11515817	Mlec	109154	75.2	81.7	126.4	1.22215	0.104028	2.08667	4.12E-16
chr3:67374097-67400000:	Mlf1	17349	16.3	3.2	3.9	-3.90167	3.17E-05	-2.93894	0.0001346
chr6:124931388-12493614	Mlf2	30853	131.9	136.6	205.5	1.16734	0.182441	1.93922	1.46E-15
chr9:111228228-11127160	Mlh1	17350	31.7	27.0	31.4	-1.05361	0.669799	1.23757	0.0059383
chr12:85234466-85270599	Mlh3	217716	24.8	19.5	12.5	-1.14178	0.37251	-1.56794	1.68E-05
chr17:56892611-56935388	Mllt1	64144	30.5	32.5	52.5	1.2037	0.138578	2.14126	3.42E-17
chr3:95218544-95228677:	Mllt11	56772	7.5	6.1	13.8	-1.08563	0.707913	2.24558	2.87E-10
chr4:87769925-88033407:	Mllt3	70122	32.2	26.3	8.4	-1.10127	0.50045	-3.04206	1.48E-31
chr11:97663412-97685458	Mllt6	246198	73.4	65.6	40.5	-1.00165	0.989875	-1.44727	2.73E-09
chr1:90915100-90951142:	Mlph	171531	2.9	5.0	6.1	1.84379	0.099436	2.35734	0.0023996
chr17:24473550-24479078	Mlst8	56716	10.5	12.9	20.6	1.38408	0.093599	2.40295	7.60E-10
chr11:101087290-1010922	Mlx	21428	35.6	39.5	61.1	1.24825	0.042456	2.13775	3.35E-21
chr8:79266424-79294956:	Mmaa	109136	23.8	20.4	15.4	-1.03861	0.770989	-1.23644	0.0081832
chr4:116702434-11670838	Mmachc	67096	16.7	14.5	18.4	-1.02852	0.861197	1.37556	0.0003191
chr2:50279881-50296677:	Mmadhc	109129	85.8	97.7	157.2	1.28418	0.101651	2.26044	3.30E-13
chr11:90249476-90278573	Mmd	67468	72.6	47.0	25.9	-1.38094	0.177288	-2.16873	1.11E-05
chr3:63295435-63383713:	Mme	17380	56.1	43.2	8.9	-1.16586	0.413299	-4.87473	2.21E-35
chr4:154869585-15489553	Mmel1	27390	2.1	0.2	0.3	-6.073	0.00018	-3.90143	0.0009036
chrX:56585512-56597919:	Mmgt1	236792	28.0	34.2	46.3	1.36919	0.005077	2.0495	4.84E-16
chr11:62648664-62666359	Mmgt2	216829	36.8	27.8	15.1	-1.18729	0.232076	-1.9325	2.65E-10
chr9:7502342-7510242:+	Mmp10	17384	3.9	3.2	0.3	-1.10068	0.841355	-7.98724	1.48E-11
chr10:75923224-75932463	Mmp11	17385	136.5	83.9	11.6	-1.45916	0.1219	-8.5949	3.12E-33
chr8:95352337-95374293:	Mmp15	17388	11.7	9.7	6.0	-1.08221	0.723594	-1.53255	0.0022399
chr4:17853482-18118734:	Mmp16	17389	19.3	15.6	2.6	-1.11418	0.577976	-5.68167	2.35E-41
chr10:128790910-1288008	Mmp19	58223	23.0	39.3	178.1	1.86725	0.03313	8.36365	4.72E-22
chr8:92827328-92853420:	Mmp2	17390	304.6	234.2	101.8	-1.1581	0.158577	-2.37748	8.39E-31
chr4:155650655-15565338	Mmp23	26561	80.8	62.7	40.5	-1.16306	0.409343	-1.58925	0.0003169
chr17:23629458-23645269	Mmp25	240047	1.1	1.7	3.1	1.48418	0.427588	2.77645	0.0033539
chr11:83441876-83462961	Mmp28	118453	4.3	2.5	1.2	-1.50387	0.223243	-2.69398	7.46E-05
chr9:7445822-7455974:+	Mmp3	17392	21.6	18.5	8.0	-1.05145	0.903627	-2.07412	0.0017204
chr2:164948219-16495584	Mmp9	17395	16.5	8.7	3.5	-1.6265	0.176279	-3.32786	5.97E-06
chr6:60944317-60989378:	Mmrn1	70945	77.4	71.5	44.8	1.02931	0.830635	-1.38221	3.61E-05
chr14:34375504-34404286	Mmrn2	105450	27.3	22.1	17.4	-1.11341	0.363413	-1.25764	0.0069171
chr19:41943707-41981136	Mms19	72199	52.5	39.0	32.8	-1.20969	0.093599	-1.27661	0.0049475
chr3:84087934-84155786:	Mnd1	76915	15.1	11.9	4.1	-1.13894	0.647987	-2.80111	4.71E-08
chr1:173896341-17391304	Mnda	381308	14.6	29.4	30.8	2.09854	0.012121	2.45804	0.0001326
chr1:173857220-17388018	Mndal	1E+08	93.3	102.4	44.1	1.20691	0.38615	-1.67016	0.0008398
chr9:72438529-72458576:	Mns1	17427	10.2	4.9	3.9	-1.83428	0.007949	-2.04162	0.0001095
chr11:74830924-74845725	Mnt	17428	15.7	16.8	7.2	1.2122	0.40043	-1.71135	0.000943
chr6:83326039-83340949:	Mob1a	232157	116.6	132.9	161.0	1.27652	0.058245	1.71094	2.78E-08
chr5:88720871-88758455:	Mob1b	68473	28.4	31.6	35.7	1.25956	0.236297	1.55268	0.0020853
chr7:142008553-14206103	Mob2	101513	80.7	82.8	46.9	1.15044	0.032009	-1.37421	4.65E-10

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr10:80685253-80701820	Mob3a	208228	38.6	51.2	61.9	1.49121	0.016395	1.97517	1.56E-07
chr4:34949074-35157484:	Mob3b	214944	12.2	9.5	4.3	-1.14155	0.45322	-2.23687	2.78E-11
chr4:115828092-11583618	Mob3c	100465	16.7	24.8	17.8	1.64665	0.002127	1.32085	0.0461489
chr1:55131245-55154899:	Mob4	19070	56.5	74.7	84.0	1.48554	0.013552	1.83437	1.49E-06
chr13:114818237-1148294	Mocs2	17434	52.2	46.4	64.6	-1.01247	0.927874	1.54134	8.87E-10
chr2:168230622-16823230	Mocs3	69372	5.9	7.1	9.6	1.35615	0.35675	1.94259	0.004739
chr6:83115506-83118898:	Mogs	57377	43.7	53.0	95.7	1.36483	0.013746	2.70574	6.55E-25
chr12:110807798-1108409	Mok	26448	10.0	6.6	1.5	-1.36057	0.207543	-4.94004	5.35E-17
chr9:107888129-10790313	Mon1a	72825	16.0	17.8	18.3	1.25152	0.146843	1.42398	0.0023159
chr10:122992061-1230765	Mon2	67074	48.7	49.6	47.0	1.14682	0.145095	1.20763	0.0082725
chr17:33135590-33139683	Morc2b	240069	3.9	0.3	0.6	-8.2225	1.62E-06	-4.12571	0.0002124
chr16:93832121-93876073	Morc3	338467	64.9	62.2	60.4	1.07257	0.286791	1.16287	0.0014454
chr9:90091669-90114820:	Morf4l1	21761	233.2	213.2	270.1	1.02919	0.820785	1.4439	5.02E-07
chrX:136732948-13674368	Morf4l2	56397	155.0	211.2	426.1	1.5311	0.030937	3.31608	9.48E-16
chr4:155086577-15514550	Morn1	76866	13.0	7.7	4.5	-1.49825	0.011742	-2.27063	2.28E-10
chr17:80290212-80297476	Morn2	378462	35.4	21.9	11.8	-1.43967	0.063129	-2.33707	1.79E-08
chr5:123037127-12304682	Morn3	74890	5.4	0.6	0.8	-4.8628	0.002089	-3.84164	0.0016086
chr19:42074939-42086370	Morn4	226123	11.0	7.1	5.1	-1.39547	0.052991	-1.7118	5.12E-05
chr2:36049473-36079709:	Morn5	75495	8.0	0.6	0.7	-6.81886	5.55E-05	-5.77161	1.71E-05
chrX:53344594-53370559:	Mospd1	70380	37.7	29.7	20.8	-1.14215	0.270258	-1.44708	2.18E-05
chr5:137596647-13760105	Mospd3	68929	5.2	4.0	2.2	-1.16727	0.567802	-1.8547	0.0008598
chr3:104794834-10481856	Mov10	17454	20.7	16.9	9.5	-1.0868	0.489778	-1.73032	1.99E-11
chr15:88982994-89055152	Mov10l1	83456	1.4	0.0	0.2	-10.4542	3.33E-06	-4.15849	0.0011933
chr10:24223517-24302783	Moxd1	59012	78.9	68.9	21.9	-1.02354	0.864119	-2.86654	1.56E-44
chr17:8283813-8297661:+	Mpc1	55951	62.8	63.5	72.3	1.13442	0.20507	1.4365	3.48E-07
chr7:64376541-64392236:	Mphosph10	67973	31.2	67.7	130.3	2.34957	0.003091	4.65793	3.73E-11
chr8:117791645-11780192	Mphosph6	68533	35.1	33.7	61.8	1.07341	0.561256	2.18601	1.00E-25
chr9:57544268-57552752:	Mpi	110119	21.9	21.2	34.0	1.09604	0.592818	1.9291	1.30E-09
chr17:56009201-56016783	Mpnd	68047	57.2	51.7	31.4	1.00582	0.971034	-1.44781	1.40E-05
chrX:75109733-75130949:	Mpp1	17524	64.4	53.1	41.7	-1.08563	0.287105	-1.23525	0.0001414
chr11:102057017-1020885	Mpp2	50997	3.9	3.4	1.5	-1.02774	0.925733	-2.01302	1.33E-05
chr11:101999653-1020269	Mpp3	13384	5.5	3.3	2.3	-1.48007	0.172654	-1.82138	0.0057492
chr12:78748947-78840713	Mpp5	56217	40.0	35.8	21.3	-1.00166	0.990707	-1.50184	2.23E-09
chr6:50110241-50198598:	Mpp6	56524	42.2	31.1	45.5	-1.21507	0.060296	1.34477	0.0001389
chr18:7347962-7626863:-	Mpp7	75739	24.9	21.9	13.3	-1.01468	0.950475	-1.48551	0.0014842
chr18:67225530-67245830	Mppe1	225651	25.0	19.6	11.2	-1.15209	0.577976	-1.75555	0.0008527
chr15:78406712-78414015	Mpst	246221	44.0	33.7	8.6	-1.17678	0.443111	-3.93622	8.54E-21
chr5:31140663-31154251:	Mpv17	17527	90.8	82.9	40.2	1.01917	0.879574	-1.8017	1.18E-17
chr16:13903161-13949619	Mpv17l	93734	3.2	2.0	1.3	-1.41726	0.110599	-2.00291	3.53E-05
chr1:165592181-16563454	Mpzl1	68481	52.0	37.7	29.4	-1.22222	0.177433	-1.40658	0.0021539
chr9:45055181-45075042:	Mpzl3	319742	4.8	6.3	9.2	1.44158	0.068384	2.32625	3.72E-09
chr1:155127878-15514678	Mr1	15064	47.9	32.0	11.1	-1.34505	0.075899	-3.35796	3.26E-22
chr16:90738324-90749776	Mrap	77037	9.1	6.5	1.2	-1.18717	0.818704	-3.18794	0.0095252
chr9:99385420-99436712:	Mras	17532	22.2	30.8	35.2	1.55779	0.062917	1.93082	0.0002955
chr11:105292646-1053511	Mrc2	17534	50.1	38.9	19.2	-1.15042	0.151966	-2.07074	1.96E-24
chr9:14784707-14834417:	Mre11a	17535	29.3	28.4	35.5	1.08497	0.32845	1.51443	3.20E-13
chr5:36794867-36796754:	Mrfap1	67568	189.7	215.3	333.6	1.27619	0.111418	2.16794	6.91E-12
chr2:180581304-18058563	Mrgbp	73247	37.0	31.7	37.9	-1.04286	0.750702	1.27761	0.0020374
chr17:12876034-12877842	Mrgprh	80978	1.4	0.7	0.1	-1.56478	0.297185	-6.20128	2.34E-07
chr8:84250576-84257324:	Mri1	67873	21.6	19.2	25.2	-1.00996	0.941735	1.45206	3.31E-08
chr11:84813061-84819515	Mrm1	217038	13.0	11.2	14.3	-1.05346	0.779865	1.36275	0.0054428
chr15:76380513-76453039	Mroh1	223658	20.4	16.5	9.0	-1.11175	0.373355	-1.80876	7.67E-13
chr1:88227020-88262289:	Mroh2a	1E+08	3.1	0.7	1.4	-3.56144	2.05E-06	-1.75075	0.0180673
chr15:4898737-4962201:+	Mroh2b	223825	7.4	0.4	0.9	-8.28458	1.20E-05	-4.31494	0.0005711
chr15:74606028-74636318	Mroh4	69439	9.2	0.4	1.1	-10.2171	5.84E-07	-4.53849	0.0002219
chr4:106680417-10672793	Mroh7	381538	8.4	4.7	2.1	-1.5817	0.01953	-3.09697	2.82E-13
chr2:157208548-15727954	Mroh8	629499	2.6	0.2	0.4	-6.62011	4.80E-05	-4.16788	0.0003558
chr5:96210115-96266727:	Mrpl1	94061	20.3	19.0	20.5	1.05088	0.652775	1.26603	0.0007141

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:97041586-97049213	Mrpl10	107732	58.6	56.1	65.2	1.0656	0.57348	1.38548	7.73E-06
chr19:4962306-4966995:+	Mrpl11	66419	20.6	19.8	29.0	1.07197	0.49256	1.75553	5.10E-18
chr11:120484669-1204887	Mrpl12	56282	40.9	54.5	115.2	1.49533	0.024378	3.42095	5.55E-20
chr15:55534095-55557312	Mrpl13	68537	71.4	66.1	81.8	1.03126	0.820887	1.4301	3.72E-06
chr1:4773200-4785726:-	Mrpl15	27395	20.7	21.9	31.5	1.18643	0.122237	1.89721	1.29E-15
chr19:11770415-11774946	Mrpl16	94063	27.7	34.1	63.9	1.38678	0.066618	2.82158	1.83E-15
chr7:105803782-10581108	Mrpl17	27397	14.8	20.3	33.0	1.54477	0.016529	2.72583	7.37E-13
chr17:12911355-12916091	Mrpl18	67681	64.1	59.3	88.2	1.03729	0.814283	1.71262	9.88E-10
chr6:81957842-81965949:	Mrpl19	56284	9.2	10.2	19.2	1.23782	0.057298	2.58374	5.28E-32
chr17:46646248-46650132	Mrpl2	27398	47.2	43.1	77.2	1.01659	0.900601	2.03456	9.09E-26
chr4:155803618-15580882	Mrpl20	66448	75.0	99.4	216.1	1.49171	0.033824	3.49063	7.25E-19
chr19:3283047-3292837:+	Mrpl21	353242	39.9	47.8	79.7	1.34089	0.017723	2.47124	2.01E-22
chr11:58171654-58179581	Mrpl22	216767	33.0	41.3	57.1	1.39875	0.094167	2.11104	4.73E-07
chr7:142533117-14254074	Mrpl23	19935	79.3	78.0	78.6	1.09418	0.428356	1.2356	0.0077879
chr11:94653791-94660087	Mrpl27	94064	62.6	57.2	72.0	1.01898	0.884981	1.43436	1.69E-07
chr17:26123503-26126613	Mrpl28	68611	67.5	70.5	76.2	1.17196	0.062917	1.40966	5.72E-08
chr9:105053268-10507747	Mrpl3	94062	56.1	61.1	93.2	1.22436	0.076815	2.06484	3.76E-18
chr1:37890553-37898333:	Mrpl30	107734	148.8	143.1	180.8	1.07393	0.517013	1.51379	9.03E-09
chr13:14610301-14613037	Mrpl32	75398	58.6	69.3	89.3	1.33055	0.06968	1.88432	6.41E-08
chr5:31613951-31622644:	Mrpl33	66845	136.8	122.2	182.9	-1.00272	0.986222	1.66305	6.42E-11
chr8:71464926-71465753:	Mrpl34	94065	30.1	27.8	14.3	1.02972	0.865684	-1.66565	5.26E-07
chr6:71812997-71823784:	Mrpl35	66223	15.8	17.3	22.3	1.22291	0.040663	1.7535	1.03E-14
chr13:73331009-73332178	Mrpl36	94066	40.7	41.7	58.1	1.15256	0.277638	1.77404	2.29E-10
chr4:107055874-10706686	Mrpl37	56280	41.9	42.1	60.7	1.13389	0.266527	1.80548	4.36E-14
chr11:116131817-1161388	Mrpl38	60441	43.5	48.0	66.3	1.24689	0.158917	1.89003	2.29E-08
chr16:84717580-84735302	Mrpl39	27393	45.7	41.4	50.1	1.01191	0.9294	1.36694	8.13E-06
chr9:21002737-21008837:	Mrpl4	66163	52.8	60.5	86.4	1.28862	0.087249	2.02119	1.20E-10
chr16:18872018-18876637	Mrpl40	18100	46.0	41.0	49.9	-1.00203	0.992005	1.34738	0.0016248
chr2:24972470-24975098:	Mrpl41	107733	17.0	19.2	30.2	1.26934	0.112027	2.19518	5.65E-13
chr10:95480806-95501927	Mrpl42	67270	90.6	90.7	104.0	1.11674	0.263358	1.4301	2.45E-07
chr19:45005014-45006442	Mrpl43	94067	31.7	34.6	47.4	1.22588	0.333367	1.83219	4.58E-05
chr1:79776018-79781445:	Mrpl44	69163	33.4	29.8	33.9	-1.00242	0.986222	1.26649	0.0008598
chr11:97315716-97329920	Mrpl45	67036	26.2	27.1	36.8	1.16097	0.174567	1.75147	7.95E-13
chr7:78775341-78783089:	Mrpl46	67308	32.7	42.0	55.9	1.44568	0.048851	2.09934	1.40E-07
chr3:32727497-32736755:	Mrpl47	74600	37.8	42.6	58.5	1.26316	0.103806	1.91691	5.05E-10
chr7:100549117-10060799	Mrpl48	52443	81.9	77.7	83.7	1.0614	0.459048	1.27738	6.00E-06
chr19:6053630-6057751:-	Mrpl49	18120	50.0	49.1	55.3	1.10325	0.396185	1.381	5.83E-05
chr4:49512597-49521083:	Mrpl50	28028	39.3	46.4	56.3	1.32542	0.039126	1.77864	2.41E-08
chr6:125192200-12519439	Mrpl51	66493	51.8	61.2	90.0	1.32951	0.074247	2.14169	1.14E-10
chr14:54426909-54429750	Mrpl52	68836	98.5	124.6	214.2	1.41523	0.024532	2.66597	2.99E-17
chr6:83109108-83109932:	Mrpl53	68499	50.6	57.9	72.7	1.28398	0.059398	1.78391	3.42E-09
chr10:81264722-81266926	Mrpl54	66047	56.6	65.9	161.3	1.30684	0.006487	3.5325	2.52E-67
chr11:59202486-59206135	Mrpl55	67212	35.6	36.4	44.2	1.14559	0.208786	1.54717	1.00E-08
chr14:57826239-57828745	Mrpl57	67840	15.3	15.2	23.7	1.10928	0.329812	1.93189	1.09E-20
chr3:94443336-94448708:	Mrpl9	78523	74.9	75.3	86.1	1.12739	0.250921	1.43318	1.33E-06
chr17:47368887-47378679	Mrps10	64657	37.6	37.3	66.2	1.1174	0.304305	2.19339	1.96E-27
chr7:78783131-78792988:	Mrps11	67994	24.2	27.0	43.0	1.24548	0.038679	2.20462	1.88E-25
chr7:28739641-28741781:	Mrps12	24030	47.3	55.4	86.6	1.30902	0.006557	2.27228	7.27E-28
chr1:160195260-16020118	Mrps14	64659	31.3	29.4	44.7	1.05538	0.693046	1.77756	1.58E-12
chr4:126046928-12605553	Mrps15	66407	64.6	67.3	83.9	1.17057	0.097246	1.62185	2.06E-12
chr14:20391231-20393555	Mrps16	66242	91.2	79.8	132.5	-1.025	0.876369	1.80256	2.62E-12
chr5:129715528-12971869	Mrps17	66258	73.2	76.9	89.3	1.17883	0.150794	1.51946	6.28E-07
chr17:46111004-46128908	Mrps18a	68565	77.0	80.3	114.1	1.17508	0.285905	1.83907	8.65E-09
chr17:35910385-35916369	Mrps18b	66973	34.9	44.1	108.8	1.42129	0.119488	3.72144	1.23E-15
chr5:100798759-10080446	Mrps18c	68735	70.0	79.1	110.5	1.26876	0.120472	1.95193	2.25E-09
chr2:28468066-28471177:	Mrps2	118451	30.9	37.7	62.1	1.3796	0.067146	2.46843	3.68E-12
chr9:98588730-98601679:	Mrps22	64655	30.8	40.3	77.4	1.47247	0.026963	3.06508	1.46E-17
chr11:88194106-88211507	Mrps23	64656	32.9	40.9	51.3	1.40093	0.108599	1.90845	3.94E-05

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:5703983-5707699:-	Mrps24	64660	44.7	48.3	61.4	1.21108	0.084923	1.70683	4.26E-11
chr6:92169523-92184023:	Mrps25	64658	16.6	15.3	16.8	1.03023	0.822747	1.26712	0.0022973
chr2:130563757-13056539	Mrps26	99045	47.9	50.9	81.5	1.1952	0.184644	2.10655	4.28E-15
chr13:99344786-99415561	Mrps27	218506	24.3	23.4	38.2	1.07445	0.451841	1.95964	1.24E-28
chr3:8802146-8923857:-	Mrps28	66230	25.0	29.3	62.5	1.30177	0.050133	3.07256	4.12E-32
chr13:118380110-1183872	Mrps30	59054	37.0	36.3	43.2	1.10171	0.309286	1.4597	9.43E-09
chr8:22411340-22429665:	Mrps31	57312	37.4	38.3	46.8	1.15075	0.305177	1.55361	5.10E-06
chr17:24895120-24896273	Mrps34	79044	28.6	33.2	56.9	1.30572	0.186363	2.42671	8.24E-10
chr6:147042770-14707090	Mrps35	232536	46.6	42.6	55.3	1.0164	0.922634	1.47831	7.52E-06
chr2:127587426-12760398	Mrps5	77721	61.3	56.8	81.3	1.04181	0.735359	1.65553	1.68E-12
chr11:115604151-1156076	Mrps7	50529	64.3	82.9	127.1	1.45423	0.068414	2.41139	9.59E-09
chr13:24992295-25020317	Mrs2	380836	22.8	22.1	38.4	1.09764	0.561143	2.09091	3.79E-13
chr4:139347440-13935257	Mrto4	69902	41.9	67.6	214.2	1.79047	0.029682	5.80659	2.98E-18
chr7:110868258-11098246	Mrvi1	17540	149.6	168.9	188.9	1.25474	0.086171	1.57202	5.31E-06
chr19:11169418-11196723	Ms4a13	73466	3.0	0.1	0.3	-6.97432	0.000293	-4.55165	0.0009356
chr19:11407661-11427246	Ms4a4c	64380	3.9	4.8	5.9	1.36297	0.243142	1.8432	0.0013842
chr19:11536849-11558466	Ms4a4d	66607	66.6	49.4	23.9	-1.21984	0.472955	-2.15828	5.09E-05
chr19:11273866-11283813	Ms4a5	269063	4.6	0.2	0.7	-6.64158	0.000407	-3.47405	0.006678
chr5:34915915-34923839:	Msantd1	403174	2.3	2.2	3.6	1.09408	0.753222	1.91939	9.22E-05
chr4:48539946-48561920:	Msantd3	66665	13.4	13.2	15.7	1.10247	0.451905	1.45993	1.21E-05
chr9:4383537-4386869:+	Msantd4	78100	64.2	62.8	74.9	1.09443	0.264127	1.45365	3.95E-11
chr17:87672557-87723713	Msh2	17685	49.1	39.1	13.2	-1.13308	0.548718	-2.89163	5.88E-15
chr13:92211881-92355003	Msh3	17686	28.5	22.9	11.7	-1.11761	0.441216	-1.93516	2.34E-11
chr3:153857141-15390613	Msh4	55993	1.0	1.4	3.4	1.50534	0.128147	3.88108	5.90E-13
chr17:35028605-35046745	Msh5	17687	2.6	2.0	0.8	-1.19406	0.580979	-2.50017	3.25E-05
chr17:87975050-87990892	Msh6	17688	43.1	45.2	46.0	1.17681	0.250501	1.33235	0.0058316
chrX:168653099-16867390	Msl3	17692	55.9	49.4	36.0	-1.01303	0.887651	-1.2423	1.78E-05
chr17:25748613-25754327	Msln	56047	26.8	14.4	9.5	-1.62031	0.094783	-2.14844	0.0004879
chr8:64718145-64733578:	Msmo1	66234	20.1	24.4	96.7	1.3655	0.294966	5.44701	2.28E-16
chr4:43583216-43584494:	Msmp	1E+08	1.6	1.8	0.2	1.23627	0.688696	-3.3909	0.0013696
chrX:96096045-96168553:	Msn	17698	122.1	120.6	227.3	1.10745	0.360589	2.30577	3.61E-28
chr8:39581700-39642678:	Msr1	20288	6.0	5.5	14.2	1.01445	0.980031	2.58582	0.0017818
chr14:64122621-64455903	Msra	110265	17.5	15.7	23.8	1.00369	0.978513	1.69525	1.58E-15
chr2:19371636-19394971:	Msrb2	76467	90.4	100.6	121.1	1.23682	0.060296	1.66775	1.26E-09
chr10:120781101-1208989	Msrb3	320183	138.4	129.3	142.8	1.04596	0.725703	1.28672	0.0014768
chr9:107906889-10792038	Mst1r	19882	17.4	10.1	7.6	-1.54583	0.056043	-1.79471	0.0008481
chr3:88909616-88913950:	Msto1	229524	29.3	26.6	36.2	1.01918	0.899426	1.53888	9.09E-08
chr12:113098278-1131372	Mta1	116870	52.5	48.3	77.2	1.03328	0.757134	1.83675	3.74E-23
chr19:8941920-8952300:+	Mta2	23942	93.8	110.5	144.8	1.33195	0.14575	1.8984	1.18E-05
chr17:83706163-83814905	Mta3	116871	29.8	23.1	17.5	-1.1561	0.270025	-1.3567	0.001457
chr4:89137370-89181090:	Mtap	66902	29.0	25.1	52.0	-1.04101	0.826436	2.22063	5.95E-15
chr15:55557408-55626423	Mtbp	105837	13.3	9.9	15.0	-1.20337	0.181927	1.41156	0.0006535
chr17:29332076-29347904	Mtch1	56462	184.6	194.9	228.9	1.19076	0.289959	1.53875	0.0002769
chr2:90847155-90866634:	Mtch2	56428	81.3	78.8	99.5	1.09172	0.471474	1.5253	2.77E-07
chrX:75404846-75416584:	Mtcp1	17763	43.0	35.5	21.6	-1.08509	0.460996	-1.58564	1.20E-09
chr15:34082719-34142385	Mtdh	67154	95.0	102.5	178.5	1.21257	0.070225	2.33358	1.68E-27
chr5:4192367-4197651:+	Mterf1b	208595	7.5	5.6	3.3	-1.21396	0.53266	-1.75604	0.0087155
chr10:85119433-85128027	Mterf2	74238	24.6	15.6	4.8	-1.40179	0.335691	-3.62793	2.42E-07
chr13:66912098-66933072	Mterf3	66410	61.7	72.1	83.1	1.32082	0.106741	1.67058	7.26E-05
chr4:124802549-12484980	Mtf1	17764	11.1	12.4	13.3	1.25347	0.108035	1.48759	0.0001674
chr4:134525555-13453538	Mtfr1l	76824	99.8	95.0	129.5	1.06987	0.438474	1.6193	1.16E-16
chr10:20347819-20361669	Mtfr2	71804	1.2	1.2	3.1	1.14381	0.672624	3.17219	9.37E-11
chr12:76255232-76319820	Mthfd1	108156	39.8	53.2	80.4	1.50434	0.137954	2.41485	1.64E-05
chr10:3973075-4167081:+	Mthfd1l	270685	8.5	5.2	27.2	-1.4723	0.000572	3.92628	2.17E-58
chr6:83305704-83317604:	Mthfd2	17768	4.9	8.2	68.3	1.82885	0.003493	15.8431	2.71E-68
chr9:89211190-89240225:	Mthfs	107885	21.5	19.4	8.1	1.00814	0.967812	-2.08554	1.44E-10
chr8:121097557-12110837	Mthfsd	234814	43.5	30.4	25.6	-1.28217	0.05046	-1.35343	0.0021024
chr9:88688605-88719798:	Mthfsl	1E+08	21.7	17.7	9.5	-1.10119	0.62732	-1.79967	7.94E-06

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:29526397-29545447	Mtif2	76784	30.7	27.9	32.9	1.01706	0.863205	1.34033	4.22E-08
chr5:146951573-14696379	Mtif3	76366	13.0	10.9	8.2	-1.06206	0.494106	-1.25944	0.0001315
chr19:3388857-3407823:+	Mtl5	17771	2.2	0.2	0.3	-5.74885	9.58E-05	-4.10794	0.00023
chrX:71210767-71315295:	Mtm1	17772	12.5	10.1	5.9	-1.11133	0.511925	-1.6801	2.01E-06
chrX:71364760-71419196:	Mtmr1	53332	26.8	24.5	27.5	1.02005	0.826655	1.27892	1.68E-06
chr6:113237843-11328139	Mtmr14	97287	42.0	35.3	12.8	-1.07345	0.715367	-2.57612	1.51E-15
chr9:13749181-13806481:	Mtmr2	77116	73.3	68.3	123.7	1.04382	0.587579	2.10549	2.28E-52
chr11:4480868-4594815:-	Mtmr3	74302	95.0	81.0	53.9	-1.04558	0.551042	-1.40582	2.49E-12
chr11:87592217-87616296	Mtmr4	170749	35.4	44.0	50.4	1.39978	0.011587	1.76752	5.16E-08
chr14:63523610-63543953	Mtmr9	210376	33.6	28.0	34.7	-1.07625	0.345373	1.29012	1.65E-06
chr9:78448210-78474152:	Mto1	68291	24.6	24.5	29.7	1.11443	0.284315	1.50816	4.69E-09
chr4:148448582-14855768	Mtor	56717	34.3	32.8	36.3	1.07746	0.49116	1.32309	0.0001393
chr6:35508824-35539888:	Mtpn	14489	97.1	101.4	128.7	1.16982	0.043136	1.65214	3.38E-18
chr13:12186540-12258113	Mtr	238505	44.8	40.8	24.4	1.02176	0.853682	-1.46995	4.06E-09
chr13:68560780-68582121	Mtrr	210009	16.6	18.0	25.9	1.21369	0.025188	1.95355	9.21E-26
chr15:58941234-59082026	Mtss1	211401	27.2	27.7	33.0	1.14484	0.33906	1.50969	3.76E-05
chr3:138089855-13814338	Mttp	17777	8.0	5.0	2.5	-1.42937	0.010682	-2.58049	5.28E-17
chr6:54681624-54703855:	Mturn	68235	82.1	71.1	6.4	-1.03937	0.847572	-9.83401	1.09E-91
chr8:40990912-41133726:	Mtus1	102103	43.4	35.6	20.5	-1.0882	0.293879	-1.68647	2.33E-20
chr3:89209081-89214335:	Mtx1	17827	45.2	41.0	51.9	1.01908	0.890054	1.43442	1.04E-06
chr2:74825812-74876748:	Mtx2	53375	74.5	72.8	91.9	1.09356	0.333367	1.53691	1.29E-11
chr3:89229056-89233381:	Muc1	17829	12.8	13.2	28.3	1.14089	0.571772	2.68955	2.19E-11
chr6:121838541-12188905	Mug1	17836	0.2	0.4	5.7	2.22364	0.005185	30.0849	5.69E-68
chr4:138434672-13844226	Mul1	68350	22.0	25.2	24.1	1.29268	0.039372	1.37031	0.001095
chr10:80226598-80245144	Mum1	68114	60.4	44.5	35.2	-1.21421	0.080889	-1.36463	0.0002315
chrX:139210044-13923833	Mum1l1	245631	3.8	2.2	5.4	-1.52997	0.02055	1.73897	5.43E-05
chr19:5482840-5488336:-	Mus81	71711	39.7	40.1	66.0	1.13784	0.289118	2.06732	4.53E-18
chr14:30879257-30881610	Mustn1	66175	50.0	45.1	24.2	-1.00124	0.996946	-1.63866	0.0004571
chr17:40934685-40961989	Mut	17850	54.2	48.4	28.2	-1.00555	0.971599	-1.52718	2.05E-07
chr4:116807734-11681943	Mutyh	70603	15.6	11.7	5.8	-1.18904	0.385849	-2.11051	1.39E-07
chr2:33729956-33887946:	Mvb12b	72543	16.2	14.0	15.5	-1.0274	0.795674	1.20115	0.0029703
chr8:122433596-12244342	Mvd	192156	5.6	6.8	16.5	1.36105	0.101294	3.59672	2.92E-22
chr5:114444306-11446059	Mvk	17855	17.3	14.9	24.1	-1.04669	0.862672	1.71967	0.0002274
chr7:126986860-12701459	Mvp	78388	86.0	88.7	143.8	1.15355	0.040039	2.08348	5.00E-47
chr16:97536081-97560901	Mx2	17858	13.3	15.5	4.9	1.28685	0.354751	-2.06905	0.0002052
chr6:86647045-86669159:	Mxd1	17119	15.0	13.3	4.4	-1.01436	0.959665	-2.63612	3.63E-11
chr5:34176580-34187710:	Mxd4	17122	99.7	75.7	16.5	-1.18806	0.304706	-4.69182	5.25E-38
chr19:53310506-53375810	Mxi1	17859	41.8	27.4	2.0	-1.37206	0.204199	-14.4828	9.97E-50
chr4:155839680-15584410	Mxra8	74761	172.7	128.1	23.0	-1.21452	0.185587	-5.86326	5.97E-63
chr10:21124930-21160984	Myb	17863	6.7	6.5	11.3	1.09491	0.820999	2.01165	0.0030191
chr11:72441378-72451550	Mybbp1a	18432	80.2	91.9	281.6	1.29421	0.090301	4.29923	1.16E-39
chr10:88518279-88605152	Mybpc1	109272	33.9	23.3	14.1	-1.26934	0.36527	-1.86761	0.0008417
chr7:44501699-44524669:	Mybpc2	233199	2.9	2.2	4.7	-1.16783	0.646373	1.96938	0.0014045
chr15:61985341-61990361	Myc	17869	23.3	49.7	54.2	2.294	0.000109	2.77957	2.22E-08
chr14:103113411-1033468	Mycbp2	105689	80.6	70.6	56.5	-1.02234	0.787535	-1.14149	0.0077985
chr10:5593728-5606791:+	Myct1	68632	10.5	7.1	14.1	-1.30352	0.120616	1.6693	3.78E-05
chr9:119335988-11934004	Myd88	17874	36.4	69.1	81.5	2.05688	0.001112	2.6783	7.71E-08
chr17:56176541-56183920	Mydgf	28106	79.7	93.4	191.4	1.31389	0.038215	2.95709	6.91E-29
chr2:125086271-12512366	Myef2	17876	49.0	46.8	64.3	1.07097	0.502409	1.63664	1.89E-13
chr1:92637145-92641985:	Myeov2	66915	78.6	81.2	81.3	1.15741	0.209549	1.28878	0.0031
chr15:102331709-1023381	Myg1	60315	52.8	52.7	57.1	1.12155	0.274961	1.35184	5.62E-05
chr11:68691915-68816624	Myh10	77579	99.4	86.1	114.5	-1.02987	0.77149	1.43722	1.44E-09
chr7:44605803-44670843:	Myh14	71960	10.2	11.9	16.7	1.32153	0.395448	1.96113	0.0037746
chr14:54970688-54994549	Myh7	140781	0.1	1.3	5.0	2.32413	0.178603	5.0472	0.0005025
chr15:77760585-77842175	Myh9	17886	274.7	308.2	404.1	1.27143	0.280302	1.80503	0.0002237
chr1:66924296-66945056:	Myl1	17901	3.2	1.5	0.4	-1.64855	0.368128	-3.74862	0.0010441
chr17:70993793-71002533	Myl12a	67268	201.1	215.2	396.6	1.20573	0.187798	2.43445	1.89E-18
chr17:70973963-70990516	Myl12b	67938	293.1	255.0	172.7	-1.0306	0.857326	-1.35449	0.0014647

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:104550663-1045872	Myl4	17896	8.5	9.4	18.8	1.24052	0.42967	2.64682	8.74E-08
chr10:128490861-1284938	Myl6	17904	####	4291.0	4741.8	1.20185	0.017827	1.48023	6.12E-11
chr2:156775464-15678165	Myl9	98932	####	1587.0	1926.4	1.08132	0.610439	1.46945	0.0001134
chr13:45389742-45411940	Mylip	218203	86.7	50.3	27.0	-1.54321	0.084392	-2.46679	1.75E-06
chr8:85324929-85381041:	Mylk3	213435	1.4	0.5	0.3	-2.17275	0.019588	-3.49739	3.97E-06
chr8:10153923-10633950:	Myo16	244281	1.2	1.0	0.4	-1.02862	0.940103	-2.42572	2.18E-05
chr11:84880220-84911131	Myo19	66196	8.3	11.4	22.1	1.52787	0.109323	3.13872	4.56E-09
chr1:51749758-51915978:	Myo1b	17912	44.2	39.6	27.0	1.00407	0.980021	-1.30485	0.0019773
chr11:75651509-75674634	Myo1c	17913	86.8	81.3	105.7	1.05061	0.513262	1.51959	2.00E-17
chr2:70039126-70429195:	Myo3b	329421	18.2	13.6	5.0	-1.18035	0.398631	-2.83991	1.56E-14
chr9:75232014-75305450:	Myo5c	208943	50.3	41.4	9.4	-1.08736	0.678101	-4.14252	1.15E-30
chr9:80165034-80311729:	Myo6	17920	53.6	41.1	18.6	-1.16882	0.073608	-2.28924	8.15E-38
chr7:98051054-98119493:	Myo7a	17921	17.1	12.6	7.4	-1.21732	0.099623	-1.83377	9.12E-12
chr8:71272714-71360712:	Myo9b	17925	54.9	51.0	50.7	1.04128	0.612764	1.1549	0.0061306
chr1:162639150-16264969	Myoc	17926	15.3	8.4	1.5	-1.61994	0.011122	-7.52593	1.19E-34
chr4:135759715-13581556	Myom3	242702	1.3	0.6	0.1	-1.97451	0.041361	-8.80148	6.09E-14
chr7:18991245-19001766:	Mypop	232934	7.1	5.2	3.5	-1.22163	0.293657	-1.62581	0.0004984
chr9:120304073-12047483	Myrip	245049	5.0	20.1	44.3	3.76911	0.000571	7.94334	9.65E-11
chr4:94942041-94979100:	Mysm1	320713	60.4	53.4	41.3	-1.01046	0.894424	-1.1682	0.0003631
chr14:99034544-99046136	Mzt1	76789	50.7	51.1	52.1	1.13007	0.160344	1.28278	0.0001065
chr4:42917251-42941607:	N28178	230085	1.3	2.1	3.9	1.75901	0.087718	3.45577	3.59E-07
chr5:150571643-15059452	N4bp2l1	100637	18.0	12.4	3.1	-1.29936	0.161163	-4.47789	3.13E-25
chr5:150635973-15066561	N4bp2l2	381695	65.4	70.6	65.1	1.21582	0.053411	1.24159	0.0058749
chr11:51643089-51651073	N4bp3	212706	20.8	24.9	33.8	1.34558	0.153492	1.99204	7.08E-06
chr16:87354185-87368649	N6amt1	67768	13.2	13.5	28.9	1.14753	0.24191	2.71043	5.26E-38
chr14:57549598-57571569	N6amt2	68043	30.3	30.4	35.7	1.11979	0.293475	1.46667	2.03E-07
chrX:73916870-73921944:	Naa10	56292	75.2	64.9	104.1	-1.03608	0.760826	1.7277	3.04E-16
chr3:51416016-51475985:	Naa15	74838	39.7	47.6	75.3	1.35268	0.106119	2.32515	9.81E-10
chr14:79334507-79390668	Naa16	66897	19.8	24.7	23.5	1.40845	0.030937	1.4768	0.0016962
chr2:145903241-14591642	Naa20	67877	82.5	82.2	113.4	1.11239	0.216224	1.71318	3.15E-19
chr5:121397982-12144011	Naa25	231713	49.7	64.2	103.2	1.45574	0.039179	2.54207	1.03E-11
chr14:49172227-49191031	Naa30	70646	33.4	38.6	40.5	1.30091	0.084154	1.50146	0.0004389
chr13:59585333-59634781	Naa35	78689	43.8	45.4	46.2	1.1671	0.177575	1.31613	0.0012372
chr11:69395791-69396671	Naa38	78304	52.4	44.3	67.0	-1.06057	0.698803	1.58804	2.37E-07
chr16:44139809-44163364	Naa50	72117	47.5	53.7	105.5	1.27186	0.081746	2.7373	2.29E-23
chr9:18323021-18385928:	Naalad2	72560	62.9	54.3	15.8	-1.04408	0.791118	-3.14442	3.89E-33
chr1:52455849-52500448:	Nab1	17936	35.1	32.9	52.0	1.04275	0.762673	1.84167	6.02E-14
chr10:127660918-1276667	Nab2	17937	41.6	89.4	126.5	2.30133	0.013514	3.37717	4.80E-06
chr10:128401395-1284097	Nabp2	69917	34.0	29.5	44.0	-1.02618	0.838442	1.61581	1.59E-12
chr10:128035346-1280486	Naca	17938	145.3	150.5	200.6	1.16134	0.177983	1.71585	1.75E-11
chr8:84670479-84687862:	Nacc1	66830	33.4	38.9	71.2	1.31337	0.066261	2.62582	1.00E-18
chr4:155562392-15559100	Nadk	192185	75.0	85.6	132.6	1.28345	0.007392	2.19817	1.48E-27
chr15:9071260-9110496:+	Nadk2	68646	35.1	25.9	7.2	-1.2217	0.363118	-3.73527	6.33E-18
chr7:143795594-14382284	Nadsyn1	78914	17.2	15.7	7.2	1.02625	0.879465	-1.89179	3.55E-11
chr8:104511028-10453463	Nae1	234664	94.5	91.8	94.1	1.09156	0.352299	1.24241	0.0011613
chr8:66860217-66890564:	Naf1	234344	7.0	9.8	14.5	1.5633	0.018415	2.52576	1.63E-10
chr15:82329532-82338826	Naga	17939	67.3	54.3	29.8	-1.11279	0.377597	-1.79478	3.72E-12
chr6:83795057-83802556:	Nagk	56174	53.7	38.7	21.2	-1.24979	0.135652	-2.00276	3.67E-10
chr11:101070094-1010776	Naglu	27419	26.8	18.0	10.9	-1.3412	0.07407	-1.94055	9.13E-08
chr16:5195280-5204012:-	Nagpa	27426	25.0	21.9	15.9	-1.01915	0.889035	-1.25285	0.0032425
chr13:100407770-1004528	Naip1	17940	0.3	0.1	0.0	-2.15764	0.137021	-3.14729	0.0040373
chr13:100211740-1002473	Naip5	17951	4.9	3.8	2.4	-1.13172	0.589626	-1.58474	0.0026744
chr14:123276641-1236271	Nalcn	338370	3.1	2.4	0.3	-1.16408	0.374705	-9.12329	8.33E-46
chr12:32820335-32853369	Nampt	59027	51.1	50.2	58.0	1.0936	0.456719	1.41487	2.39E-05
chr4:46489329-46503438:	Nans	94181	23.3	28.7	50.6	1.38375	0.001312	2.69601	2.21E-35
chr10:111473192-1114981	Nap1l1	53605	113.9	108.6	180.7	1.0702	0.414805	1.97746	2.08E-34
chrX:122394561-12239738	Nap1l3	54561	5.5	3.7	1.2	-1.34289	0.323174	-3.51484	8.50E-09
chr7:143513579-14354912	Nap1l4	17955	134.5	143.3	177.4	1.19838	0.100588	1.64302	1.06E-09

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr6:58905233-58907126:	Nap1l5	58243	18.3	13.0	5.3	-1.26035	0.220833	-2.69906	1.13E-12
chr7:16098643-16117975:	Napa	108124	102.3	105.2	125.6	1.16104	0.265305	1.52922	9.59E-06
chr2:148694657-14873242	Napb	17957	12.1	8.3	4.6	-1.3052	0.295813	-2.05844	8.44E-05
chr18:62977916-62999451	Napg	108123	31.0	29.9	31.1	1.08035	0.270714	1.25193	5.81E-06
chr15:75890964-75894481	Naprt	223646	21.3	19.2	11.9	-1.00423	0.986557	-1.42147	0.0077456
chr11:121237236-1212558	Narf	67608	32.2	25.5	5.5	-1.14184	0.585416	-4.49926	8.42E-22
chr18:64499647-64516557	Nars	70223	119.4	137.4	419.8	1.29806	0.097006	4.29	2.31E-37
chr7:96951527-97064757:	Nars2	244141	11.2	10.1	18.8	1.00932	0.948404	2.09721	2.55E-26
chr4:116601052-11662795	Nasp	50927	48.8	54.2	70.4	1.26063	0.369337	1.76632	0.0019046
chr2:103721259-10376125	Nat10	98956	35.1	39.1	88.0	1.25628	0.111198	3.09338	1.41E-27
chr5:33995984-34005916:	Nat8l	269642	1.5	1.3	0.3	-1.02648	0.960817	-3.25035	5.15E-05
chr11:115182832-1151873	Nat9	66176	52.3	40.2	16.7	-1.16734	0.282075	-2.46492	3.29E-18
chr11:60902246-60913792	Natd1	24083	15.1	10.5	4.6	-1.29329	0.184539	-2.58166	2.42E-11
chr1:135434580-13558535	Nav1	215690	22.7	15.4	11.6	-1.32368	0.001482	-1.55788	1.02E-09
chr10:109683439-1100002	Nav3	260315	2.1	1.8	5.5	-1.0421	0.901905	3.15045	9.40E-11
chr12:13269127-13583811	Nbas	71169	30.7	28.7	50.0	1.04692	0.594851	2.0324	4.27E-40
chr3:55625198-56183701:	Nbea	26422	48.8	41.6	27.7	-1.05226	0.783766	-1.40594	0.0023741
chr1:60180599-60334705:	Nbeal1	269198	54.0	47.4	33.8	-1.02382	0.866159	-1.27773	0.002035
chr4:139082292-13909297	Nbl1	17965	480.1	458.0	216.6	1.05992	0.659067	-1.76396	4.50E-12
chr4:15957967-15992589:	Nbn	27354	45.5	51.0	76.4	1.25809	0.008088	2.09126	2.08E-28
chr11:101552107-1015819	Nbr1	17966	137.8	124.0	50.9	1.00743	0.923231	-2.16122	6.31E-83
chr9:49502146-49799069:	Ncam1	17967	34.3	26.8	6.4	-1.13689	0.314825	-4.18745	7.19E-58
chr6:125168007-12519158	Ncapd2	68298	18.0	15.1	7.7	-1.06236	0.670199	-1.86008	3.54E-12
chr9:27030175-27095315:	Ncapd3	78658	28.1	23.8	9.8	-1.05979	0.676832	-2.28041	1.29E-21
chr15:89355719-89372850	Ncaph2	52683	91.3	93.2	98.9	1.14683	0.097604	1.35359	8.65E-07
chr4:46138511-46172402:	Ncbp1	433702	43.7	58.6	119.7	1.5129	0.083234	3.26892	2.18E-11
chr16:31948546-31958472	Ncbp2	68092	63.7	68.5	85.6	1.20979	0.112912	1.67108	6.91E-09
chr4:126743750-12675342	Ncdn	26562	21.3	20.0	30.9	1.05527	0.607039	1.81465	2.64E-20
chr3:27183004-27244911:	Nceh1	320024	39.5	26.2	12.5	-1.34835	0.056311	-2.48917	8.16E-15
chr5:134220053-13422962	Ncf1	17969	14.8	11.1	5.9	-1.18243	0.661902	-1.92125	0.0084492
chr9:100495003-10054605	Nck1	17973	77.8	76.2	84.1	1.09512	0.40094	1.34606	7.82E-05
chr2:80500512-80581182:	Nckap1	50884	137.5	132.6	168.1	1.08212	0.28976	1.52537	4.08E-16
chr1:125913636-12683063	Nckap5	210356	5.6	4.0	0.8	-1.23607	0.128404	-5.19542	2.92E-47
chr9:108808380-10881836	Nckipsd	80987	10.2	10.8	13.4	1.18424	0.145072	1.6272	4.85E-09
chr1:86344719-86359455:	Ncl	17975	133.7	140.0	373.1	1.18287	0.292326	3.42515	7.65E-29
chr10:81486459-81496363	Ncln	103425	49.2	49.1	81.2	1.11888	0.057664	2.06343	1.13E-66
chr12:4247362-4477182:-	Ncoa1	17977	36.3	32.4	23.7	1.00355	0.977442	-1.22486	0.0022569
chr1:13139105-13374083:	Ncoa2	17978	46.7	39.6	17.2	-1.05533	0.60384	-2.15189	2.59E-31
chr2:165992637-16607324	Ncoa3	17979	50.1	42.4	27.4	-1.05404	0.346805	-1.45755	2.83E-22
chr14:32159887-32179855	Ncoa4	27057	50.5	54.2	76.2	1.20465	0.11423	1.87119	4.48E-13
chr2:165000357-16503477	Ncoa5	228869	44.6	46.9	47.7	1.18545	0.194125	1.33186	0.0032216
chr7:4337724-4345164:+	Ncr1	17086	7.6	6.2	2.6	-1.10616	0.756298	-2.27477	5.53E-05
chr2:31245923-31295471:	Ncs1	14299	9.3	11.7	15.4	1.40776	0.033455	2.03822	4.69E-09
chr16:14163275-14192923	Nde1	67203	44.2	47.5	45.6	1.20554	0.02292	1.28649	8.22E-05
chr11:68821446-68853131	Ndel1	83431	74.6	96.2	95.1	1.45259	0.021649	1.57905	0.0003534
chr14:105258673-1053092	Ndfip2	76273	29.0	29.3	33.1	1.13733	0.313206	1.42285	9.85E-05
chr6:65671611-65706930:	Ndnf	68169	2.1	5.4	6.5	2.72432	3.60E-05	3.56577	7.60E-10
chr7:64871650-64873040:	Ndnl2	66647	32.4	34.9	49.4	1.21223	0.288317	1.88163	7.36E-07
chrX:16885522-16911764:	Ndp	17986	31.0	16.4	1.6	-1.58622	0.390503	-8.33907	1.31E-08
chr15:66929318-66969641	Ndrg1	17988	140.7	129.9	55.6	1.02532	0.90468	-2.00252	9.71E-10
chr14:51905271-51913488	Ndrg2	29811	269.5	245.5	60.8	1.01875	0.905719	-3.49727	2.22E-50
chr2:156927342-15699211	Ndrg3	29812	37.9	31.7	24.2	-1.07086	0.424002	-1.25273	0.0001718
chr8:95703037-95715119:	Ndrg4	234593	14.2	12.8	3.6	1.01208	0.945754	-3.1143	8.69E-31
chr3:123526166-12369085	Ndst3	83398	4.5	3.0	0.4	-1.3416	0.529167	-6.62622	1.70E-09
chrX:37187589-37191238:	Ndufa1	54405	69.0	70.0	98.1	1.13599	0.308111	1.76526	3.24E-11
chr1:92439719-92473758:	Ndufa10	67273	120.8	116.2	160.0	1.08271	0.464863	1.65372	3.55E-12
chr17:56717762-56724248	Ndufa11	69875	23.8	28.8	55.6	1.36653	0.093431	2.84863	1.53E-14
chr10:94199009-94220948	Ndufa12	66414	135.7	143.5	273.8	1.18568	0.120233	2.50672	6.96E-32

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr18:36742332-36744587	Ndufa2	17991	151.9	151.8	159.5	1.11922	0.316661	1.30826	0.0008329
chr6:11900373-11907446:	Ndufa4	17992	320.8	332.1	433.1	1.15916	0.187129	1.68005	1.14E-10
chr10:127514939-1275171	Ndufa4l2	407790	9.0	7.3	3.1	-1.10566	0.634242	-2.2384	4.21E-08
chr6:24518666-24527687:	Ndufa5	68202	111.8	109.1	133.0	1.09196	0.360773	1.48391	1.57E-09
chr15:82350139-82354291	Ndufa6	67130	255.8	228.0	133.0	-1.0061	0.961536	-1.53559	1.24E-10
chr17:33824572-33838316	Ndufa7	66416	119.0	119.6	115.4	1.12247	0.164736	1.21184	0.0019417
chr2:36036334-36049292:	Ndufa8	68375	81.0	73.2	115.6	1.00959	0.943107	1.78017	1.48E-18
chr6:126821863-12684914	Ndufa9	66108	103.7	100.9	136.2	1.09002	0.394489	1.63653	7.11E-13
chr7:122088044-12210184	Ndufab1	70316	57.5	60.9	98.6	1.19406	0.210947	2.12791	3.73E-14
chr13:108052589-1081586	Ndufaf2	75597	24.8	25.5	37.1	1.15743	0.314718	1.86111	2.40E-10
chr4:24898083-24905001:	Ndufaf4	68493	18.3	24.6	54.4	1.5024	0.049729	3.55946	1.89E-16
chr2:140170646-14020525	Ndufaf5	69487	10.2	10.2	12.8	1.11107	0.303702	1.55546	1.62E-10
chr4:11051046-11076205:	Ndufaf6	76947	18.3	14.9	20.2	-1.10095	0.602438	1.37678	0.0071273
chr17:78937135-78948052	Ndufaf7	73694	23.9	20.4	23.4	-1.05198	0.65935	1.22267	0.0056416
chr17:24722067-24724388	Ndufb10	68342	161.5	158.2	175.5	1.10015	0.291665	1.35632	1.70E-06
chr6:39592583-39599471:	Ndufb2	68198	84.4	101.8	151.2	1.34962	0.028325	2.21369	7.92E-15
chr16:37647602-37654368	Ndufb4	68194	95.6	86.9	109.5	1.01122	0.945436	1.42636	2.28E-05
chr3:32737063-32751559:	Ndufb5	66046	101.3	98.0	106.2	1.08313	0.371785	1.30695	1.56E-05
chr4:40270663-40279368:	Ndufb6	230075	81.0	92.8	163.6	1.28565	0.084572	2.49	6.33E-18
chr8:83566758-83571623:	Ndufb7	66916	117.9	123.2	195.5	1.16906	0.064389	2.06683	1.52E-33
chr19:44550254-44555415	Ndufb8	67264	200.6	203.7	255.8	1.14015	0.256036	1.5875	1.52E-08
chr15:58933810-58939489	Ndufb9	66218	225.5	206.5	298.7	1.02572	0.81845	1.65149	6.39E-16
chr3:51405479-51408955:	Ndufc1	66377	82.7	70.8	82.8	-1.04671	0.715112	1.24659	0.0036918
chr1:63143592-63176822:	Ndufs1	227197	80.4	85.9	106.6	1.20181	0.111748	1.6501	4.50E-09
chr1:171234860-17124711	Ndufs2	226646	185.8	197.4	284.9	1.19358	0.09787	1.90555	1.66E-16
chr2:90894636-90904721:	Ndufs3	68349	110.0	111.3	144.1	1.13345	0.089834	1.63468	2.40E-20
chr13:114287795-1143880	Ndufs4	17993	55.7	55.9	77.5	1.11826	0.283192	1.73037	2.47E-14
chr13:73319876-73328482	Ndufs6	407785	69.6	65.3	88.3	1.05026	0.715358	1.57748	1.00E-08
chr10:80249452-80256792	Ndufs7	75406	109.8	113.0	132.2	1.1583	0.174092	1.50192	2.05E-07
chr19:3908863-3912774:-	Ndufs8	225887	73.3	75.0	110.9	1.14496	0.169109	1.88372	8.77E-20
chr19:4007499-4012755:-	Ndufv1	17995	148.0	138.2	161.3	1.04473	0.56047	1.36209	1.34E-10
chr17:66078795-66101559	Ndufv2	72900	81.4	90.3	149.4	1.244	0.00863	2.28372	1.69E-38
chr17:31520115-31531325	Ndufv3	78330	81.9	66.6	45.9	-1.10814	0.50669	-1.41971	0.0008828
chr2:52136647-52338798:	Neb	17996	1.0	0.9	0.3	-1.07378	0.859934	-2.56258	4.47E-05
chr6:122874557-12288894	Necap1	67602	35.5	40.6	43.7	1.28495	0.024068	1.53122	6.30E-07
chr4:141066512-14107834	Necap2	66147	44.4	43.6	62.0	1.10018	0.401949	1.73665	7.04E-13
chr9:72662347-72749848:	Nedd4	17999	914.1	733.4	562.7	-1.11686	0.158084	-1.2979	6.62E-06
chr18:64887756-65217826	Nedd4l	83814	25.5	41.4	72.2	1.80419	0.066266	3.24548	1.14E-06
chr14:55662267-55671906	Nedd8	18002	185.7	204.3	248.4	1.23226	0.012774	1.66697	2.12E-15
chr3:156561794-15731646	Negr1	320840	12.3	11.2	5.0	1.01411	0.927397	-1.96856	1.54E-16
chr9:57143256-57147034:	Neil1	72774	26.2	18.1	9.3	-1.29989	0.101133	-2.21308	6.95E-11
chr14:63182445-63193525	Neil2	382913	15.8	10.4	1.4	-1.35854	0.170685	-8.32094	4.63E-32
chr8:60993193-61131346:	Nek1	18004	22.7	20.7	13.2	1.01862	0.868056	-1.37163	4.32E-07
chr8:22128283-22166435:	Nek3	23954	9.7	8.6	3.5	-1.02116	0.939749	-2.15141	2.79E-07
chr14:30951488-30987401	Nek4	23955	29.7	24.1	17.6	-1.10078	0.381768	-1.34564	0.0001293
chr8:22073616-22125053:	Nek5	330721	2.7	2.0	0.3	-1.17858	0.709476	-5.41785	9.83E-09
chr2:38511697-38587490:	Nek6	59126	16.3	18.9	38.7	1.29774	0.050632	2.93089	2.46E-28
chr1:138484714-13861969	Nek7	59125	80.9	75.3	47.2	1.03665	0.723814	-1.37025	4.23E-07
chr11:78166106-78176666	Nek8	140859	14.1	10.4	3.3	-1.20905	0.268538	-3.33236	1.93E-21
chr5:33898180-33936258:	Nelfa	24116	34.6	36.7	46.6	1.19511	0.14847	1.67792	8.58E-09
chr17:34850391-34856372	Nelfe	27632	39.6	41.9	55.4	1.19255	0.170685	1.74468	1.85E-09
chr7:49975350-50863289:	Nell1	338352	24.6	24.0	12.3	1.08673	0.736555	-1.57934	0.0030191
chr12:69311543-69357176	Nemf	66244	72.2	83.4	98.1	1.30304	0.10091	1.68184	1.71E-05
chr9:58874680-59036441:	Neo1	18007	68.2	57.6	30.0	-1.05964	0.581515	-1.8116	1.08E-18
chr3:87971093-87980451:	Nes	18008	18.2	23.8	36.9	1.46126	0.263172	2.36078	0.0004676
chr8:85636588-85691009:	Neto2	74513	65.6	41.9	14.0	-1.40413	0.205541	-3.52538	6.89E-11
chr1:87574027-87597840:	Neu2	23956	1.2	0.6	0.1	-1.78431	0.21737	-8.14826	5.36E-08
chr2:164830730-16483359	Neurl2	415115	12.0	7.2	4.4	-1.5006	0.056106	-2.15909	2.96E-06

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr1:36264602-36273425:	Neurl3	214854	14.8	10.3	5.7	-1.28601	0.228702	-2.03486	3.49E-06
chr3:152236984-15226632	Nexn	68810	58.0	50.9	70.8	-1.02033	0.924629	1.51757	0.0002263
chr11:79339892-79581609	Nf1	18015	49.4	47.2	49.6	1.07328	0.49929	1.25407	0.0015157
chr11:4765845-4849544:-	Nf2	18016	55.4	50.6	63.3	1.02439	0.766138	1.42652	6.25E-14
chr8:107293470-10737951	Nfat5	54446	48.1	39.3	22.6	-1.09631	0.535255	-1.68854	8.62E-08
chr14:55824795-55833943	Nfatc4	73181	56.1	50.5	14.9	1.01418	0.945645	-2.96678	2.55E-24
chr11:96817414-96829968	Nfe2l1	18023	88.6	122.7	151.4	1.55777	0.010689	2.09934	5.95E-08
chr4:97581943-98118876:	Nfia	18027	39.8	31.5	11.2	-1.1311	0.357344	-2.79569	6.41E-29
chr4:82290173-82505779:	Nfib	18028	66.7	49.8	28.7	-1.20416	0.281886	-1.83392	7.89E-07
chr13:52967209-52981039	Nfil3	18030	10.3	54.0	76.7	5.10851	5.44E-08	7.64257	7.27E-15
chr8:84704712-84800338:	Nfix	18032	42.4	36.7	22.2	-1.02926	0.823758	-1.51665	2.37E-08
chr19:46304737-46312090	Nfkb2	18034	38.2	48.8	91.1	1.40661	0.08299	2.89891	2.27E-13
chr12:55489409-55492647	Nfkbia	18035	108.8	194.4	179.1	1.95852	0.000364	2.00911	1.31E-05
chr7:28758251-28766524:	Nfkbib	18036	12.9	15.6	20.9	1.36058	0.052538	2.012	3.01E-09
chr2:156123637-15614418	Nfs1	18041	45.1	44.6	43.0	1.10774	0.161639	1.19197	0.0011994
chr6:87009836-87028461:	Nfu1	56748	49.3	43.3	51.8	-1.01889	0.868056	1.31151	8.68E-06
chr4:40970906-41025992:	Nfx1	74164	61.8	58.9	64.4	1.07139	0.506114	1.30195	0.0001638
chr5:72513304-72559645:	Nfxl1	100978	39.6	37.4	41.6	1.05793	0.483042	1.31119	4.22E-07
chr10:82748700-82764141	Nfyb	18045	42.2	51.0	59.4	1.35505	0.004799	1.74962	6.59E-11
chr4:120757435-12083157	Nfyc	18046	57.2	62.9	73.9	1.23954	0.074725	1.61129	1.11E-07
chr14:55015454-55024137	Ngdn	68966	73.3	97.3	148.6	1.49257	0.012992	2.48824	2.82E-13
chr1:87476829-87573870:	Ngef	53972	22.3	20.0	3.7	1.02697	0.957008	-4.17592	2.14E-08
chr11:95568821-95587698	Ngfr	18053	10.8	62.5	236.2	5.32918	5.41E-07	18.6648	1.72E-24
chrX:136270253-13627197	Ngfrap1	12070	98.6	95.7	119.1	1.08149	0.47273	1.50533	1.87E-08
chr1:74967346-75046639:	Nhej1	75570	15.1	13.3	5.6	-1.01178	0.957008	-2.10951	9.91E-10
chr13:47012557-47014850	Nhlrc1	105193	3.4	3.0	8.3	-1.02489	0.927605	2.9988	1.18E-17
chr11:51619773-51623714	Nhp2	52530	44.2	71.1	189.5	1.78555	0.016395	4.97444	4.36E-18
chr15:82041345-82047598	Nhp2l1	20826	110.4	148.7	251.1	1.51355	0.0276	2.7675	1.06E-12
chrX:161836430-16215944	Nhs	195727	6.4	5.2	11.0	-1.09396	0.702046	2.11151	1.21E-07
chrX:101849385-10209205	Nhsl2	1E+08	17.2	13.4	8.8	-1.14901	0.392268	-1.54429	0.0001394
chr9:108290457-10829649	Nicn1	66257	52.7	37.9	10.4	-1.24753	0.103806	-3.96214	3.86E-41
chr13:13437602-13512275	Nid1	18073	142.6	122.4	63.2	-1.04034	0.68847	-1.8001	8.12E-23
chr14:19751257-19811787	Nid2	18074	37.2	26.6	6.7	-1.25579	0.226402	-4.3054	2.65E-27
chr1:58447633-58462276:	Nif3l1	65102	25.2	26.1	35.1	1.16293	0.226523	1.72632	6.06E-10
chr1:118321843-11833383	Nifk	67949	55.4	79.5	147.0	1.61044	0.025126	3.18969	8.28E-13
chr13:119710094-1197558	Nim1k	245269	3.3	2.6	1.5	-1.11709	0.502807	-1.69633	5.66E-06
chr2:150934519-15100939	Ninl	78177	24.1	19.6	12.1	-1.10353	0.356607	-1.58503	7.47E-10
chr8:107056877-10706092	Nip7	66164	23.5	38.8	78.6	1.8361	0.006053	3.95319	3.58E-15
chr7:55931266-55962493:	Nipa2	93790	23.0	32.5	39.4	1.58701	0.015853	2.09671	7.69E-07
chr5:72647796-72671078:	Nipal1	70701	1.4	2.6	3.8	2.07129	0.038451	3.07878	2.92E-05
chr4:135448901-13549450	Nipal3	74552	28.7	20.0	3.0	-1.28848	0.144624	-7.3417	2.85E-53
chr11:46148155-46166359	Nipal4	214112	7.3	6.5	11.2	-1.00837	0.979019	1.87698	0.0001205
chr15:8289824-8444463:-	Nipbl	71175	83.9	74.9	58.3	1.00056	0.996288	-1.14967	0.009857
chr11:4874003-4894200:+	Nipsnap1	18082	43.9	34.3	13.5	-1.14999	0.471064	-2.54506	1.37E-12
chr4:53011924-53022059:	Nipsnap3b	66536	24.9	27.8	34.4	1.25098	0.189022	1.70562	1.67E-05
chr1:171342237-17134564	Nit1	27045	50.1	41.7	30.0	-1.07721	0.459541	-1.33064	4.01E-05
chr16:57156665-57167332	Nit2	52633	68.2	49.4	35.0	-1.24663	0.239664	-1.54502	0.0015868
chr4:130530131-13057403	Nkain1	67149	4.8	4.4	10.7	1.03381	0.902866	2.75064	6.83E-13
chr4:20118874-20778668:	Nkain3	269513	5.1	4.3	2.2	-1.04862	0.731826	-1.81203	9.56E-12
chr2:180934772-18095469	Nkain4	58237	11.0	4.9	2.8	-1.86482	0.103397	-2.8367	0.0003643
chrX:37126763-37150746:	Nkap	67050	19.5	18.5	19.6	1.061	0.511517	1.25263	0.0001799
chr13:21467047-21468501	Nkapl	66707	6.6	4.4	2.5	-1.33484	0.204722	-2.03564	3.68E-05
chr13:73819328-73847631	Nkd2	72293	63.3	36.6	19.7	-1.54523	0.132417	-2.44371	3.53E-05
chr14:18271142-18284000	Nkiras1	69721	4.6	5.2	6.3	1.28127	0.110929	1.70385	3.19E-06
chr11:100622955-1006276	Nkiras2	71966	39.8	35.1	45.9	-1.011	0.920907	1.44064	8.40E-11
chrX:36887542-36902899:	Nkrf	77286	8.1	11.6	24.9	1.61068	0.016455	3.71342	4.26E-18
chr9:121719181-12175684	Nktr	18087	74.7	92.2	120.7	1.39389	0.090687	1.98509	3.17E-06
chr11:82900768-82908395	Nle1	217011	19.5	32.1	69.2	1.83901	0.003622	4.21948	4.65E-18

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr3:25431841-26331909:	Nlgn1	192167	7.9	7.0	0.9	-1.01047	0.956889	-6.46581	2.86E-60
chrX:101299179-10132135	Nlgn3	245537	1.5	1.1	0.4	-1.17916	0.515147	-2.70786	1.45E-07
chr11:78567168-78697425	Nlk	18099	15.3	15.4	21.2	1.12615	0.194617	1.72113	2.42E-17
chr8:94472763-94527272:	Nlrc5	434341	12.6	19.6	22.1	1.7061	0.006544	2.13863	1.38E-06
chr7:107166990-10719810	Nlrp14	76858	2.0	0.1	0.3	-8.36909	1.76E-05	-3.44699	0.0039159
chr11:59542686-59566956	Nlrp3	216799	1.4	3.9	3.8	2.82225	0.000611	3.04962	1.20E-05
chr3:69722055-69749046:	Nmd3	97112	45.7	66.7	109.7	1.63455	0.022606	2.88764	1.36E-10
chr11:93958925-93968521	Nme1	18102	42.6	59.6	260.4	1.56728	0.010953	7.29033	2.32E-49
chr11:93949814-93956256	Nme2	18103	172.3	204.9	564.8	1.33169	0.026551	4.0232	2.85E-47
chr17:24896500-24897529	Nme3	79059	65.2	61.3	38.6	1.0539	0.67943	-1.34839	0.0002336
chr17:26091745-26095470	Nme4	56520	25.2	20.0	6.8	-1.13261	0.559354	-2.86252	5.38E-13
chr18:34562641-34579106	Nme5	75533	14.5	8.4	2.3	-1.52045	0.165856	-4.48748	1.44E-10
chr9:109832794-10984296	Nme6	54369	32.7	25.5	63.3	-1.14658	0.317839	2.40939	2.81E-22
chr1:164307672-16443730	Nme7	171567	17.5	14.8	6.9	-1.05805	0.700937	-2.02305	1.80E-14
chr13:19645079-19697760	Nme8	73412	2.8	0.1	0.4	-7.8387	5.13E-05	-3.92255	0.0018342
chr1:152955101-15311926	Nmnat2	226518	0.8	0.9	2.9	1.23525	0.492366	4.16818	1.17E-13
chr19:18632016-18652184	Nmrk1	225994	12.5	9.9	3.4	-1.12743	0.57361	-2.87194	4.51E-13
chr11:103028562-1030661	Nmt1	18107	86.0	88.8	144.2	1.16115	0.150024	2.08507	6.02E-23
chr2:3284212-3328877:+	Nmt2	18108	39.1	35.1	26.3	1.00711	0.934669	-1.18742	0.0002003
chr1:86386325-86388141:	Nmur1	14767	1.1	0.4	0.1	-1.95963	0.220678	-4.08359	0.0008568
chr11:56024990-56040987	Nmur2	216749	35.9	46.6	12.0	1.45569	0.20232	-2.28294	0.0001436
chr13:119334317-1194091	Nnt	18115	55.1	47.2	28.7	-1.0406	0.666122	-1.53221	1.03E-13
chr5:77294169-77310086:	Noa1	56412	9.9	9.7	21.3	1.09657	0.477365	2.65448	5.97E-34
chr8:107412489-10742503	Nob1	67619	32.9	38.3	65.8	1.3138	0.139895	2.45011	2.58E-11
chr4:156236010-15624761	Noc2l	57741	62.1	69.1	175.7	1.2552	0.135669	3.47581	5.37E-30
chr19:38788128-38819237	Noc3l	57753	23.7	31.9	60.2	1.51667	0.014121	3.1052	3.92E-18
chr5:110648419-11065338	Noc4l	100608	19.7	28.4	41.9	1.61113	0.032835	2.56952	2.85E-08
chr6:54923942-54972612:	Nod1	107607	33.9	28.1	14.5	-1.09268	0.785828	-1.8213	0.0023039
chr11:89300638-89302559	Nog	18121	1.4	3.1	4.0	2.39822	0.012415	3.25312	1.80E-05
chr12:17348493-17430095	Nol10	217431	13.6	21.4	47.2	1.75476	0.027779	4.05333	5.04E-13
chr11:107166661-1071893	Nol11	68979	44.2	55.5	93.1	1.41448	0.06369	2.57209	1.12E-11
chr15:78934933-78941910	Nol12	97961	18.6	23.0	60.0	1.39292	0.050378	3.93138	2.23E-28
chr4:41114427-41124339:	Nol6	230082	27.0	27.8	51.1	1.1622	0.320052	2.34091	4.17E-16
chr13:43398376-43402858	Nol7	70078	57.5	56.6	76.8	1.09892	0.266527	1.66291	3.52E-18
chr13:49653078-49679016	Nol8	70930	30.7	42.0	65.9	1.53768	0.003679	2.64051	1.99E-16
chr4:152039327-15206149	Nol9	74035	20.4	27.7	50.3	1.52939	0.016039	3.01052	4.08E-16
chr19:46075847-46085543	Nolc1	70769	39.8	68.1	137.8	1.9004	0.017473	4.00618	2.93E-11
chr5:29434667-29452169:	Nom1	433864	36.2	41.7	50.5	1.29974	0.086618	1.72914	1.73E-06
chr7:46033696-46084212:	Nomo1	211548	29.8	31.7	68.8	1.1971	0.135869	2.86239	2.85E-34
chrX:101429651-10144859	Nono	53610	298.2	286.6	300.1	1.07529	0.26258	1.25727	7.13E-07
chr2:112261926-11226289	Nop10	66181	107.9	131.4	131.2	1.36655	0.055627	1.50536	0.0010964
chr5:34638536-34660148:	Nop14	75416	46.4	55.1	96.1	1.34002	0.117348	2.53559	1.25E-11
chr13:54584191-54590074	Nop16	28126	27.2	40.6	71.2	1.66875	0.005507	3.16693	2.30E-15
chr6:125131883-12514475	Nop2	110109	43.7	72.0	182.3	1.83292	0.020479	4.80546	4.21E-15
chr2:130274412-13027931	Nop56	67134	113.4	224.9	483.3	2.16355	0.009942	4.74031	3.49E-11
chr1:59685006-59711510:	Nop58	55989	101.2	188.6	478.2	2.05739	0.003679	5.41133	1.58E-17
chr14:55745693-55755634	Nop9	67842	17.5	18.3	27.0	1.18586	0.439966	1.89209	2.52E-05
chr5:117867119-11795381	Nos1	18125	2.6	1.6	0.3	-1.38334	0.356852	-5.6109	4.46E-11
chr1:170317496-17058984	Nos1ap	70729	3.5	3.3	1.4	1.05304	0.819747	-1.90177	4.15E-06
chr5:24364819-24384474:	Nos3	18127	12.2	19.1	44.1	1.7484	0.067	4.11533	4.80E-10
chr2:69135800-69189329:	Nostrin	329416	4.4	4.2	8.2	1.03682	0.889979	2.25083	1.33E-09
chr3:98013538-98150367:	Notch2	18129	96.3	76.7	54.7	-1.12684	0.391981	-1.40213	0.0005831
chr17:32120893-32166852	Notch3	18131	13.2	10.4	7.1	-1.13477	0.454394	-1.47953	0.0008513
chr11:120653789-1206608	Notum	77583	16.6	13.8	4.2	-1.05794	0.868954	-2.95952	1.99E-08
chr15:54745928-54753761	Nov	18133	13.8	8.5	3.5	-1.43132	0.201085	-2.98051	1.21E-07
chr7:87246649-87398708:	Nox4	50490	4.2	2.9	1.0	-1.27891	0.37658	-3.29801	2.90E-09
chr2:25085670-25095205:	Noxa1	241275	19.4	14.2	6.4	-1.22815	0.517827	-2.28649	0.0001285
chr17:24696234-24700529	Noxo1	71893	7.0	4.6	2.6	-1.35132	0.333367	-2.08605	0.001124

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr12:87221123-87238601	Noxred1	71275	5.3	3.1	2.2	-1.50228	0.138273	-1.82683	0.0041159
chr1:39194272-39363240:	Npas2	18143	4.2	11.4	7.1	2.90774	1.33E-10	2.0499	1.94E-06
chr19:4984355-4989971:-	Npas4	225872	2.8	2.9	5.4	1.14058	0.618911	2.34747	1.83E-07
chr18:12189694-12236386	Npc1	18145	33.8	27.2	17.5	-1.10812	0.36201	-1.54054	4.10E-08
chr12:84754559-84773112	Npc2	67963	124.4	105.4	49.5	-1.06036	0.642755	-2.00485	9.85E-19
chr9:104002544-10404381	Nphp3	74025	14.4	10.1	5.8	-1.27659	0.070359	-1.95431	4.13E-11
chr11:120379798-1204377	Nploc4	217365	37.1	39.0	60.1	1.19	0.288317	2.0038	1.56E-09
chr11:33152498-33163206	Npm1	18148	780.2	730.9	1342.2	1.04942	0.728493	2.13477	5.81E-20
chr19:45747734-45749563	Npm3	18150	66.2	73.4	173.5	1.25051	0.227754	3.19445	5.11E-19
chr6:85076141-85077126:	Npm3-ps1	108176	0.8	1.1	2.5	1.43479	0.43463	3.26295	9.53E-05
chr3:132881745-13295029	Npnt	114249	20.2	14.5	8.0	-1.24409	0.121504	-1.98466	6.54E-11
chr1:86666293-86670573:	Nppc	18159	0.7	6.0	5.3	5.55822	0.000102	5.31727	1.08E-05
chr3:90450592-90465866:	Npr1	18160	70.0	57.6	17.5	-1.09096	0.587606	-3.1407	7.80E-29
chr4:43631935-43651240:	Npr2	230103	71.8	107.7	138.0	1.67263	0.106886	2.26452	0.000711
chr15:11839896-11907371	Npr3	18162	37.7	20.1	12.1	-1.6669	0.046675	-2.38288	9.73E-06
chr11:32231963-32267707	Nprl3	17168	28.3	21.3	30.2	-1.18957	0.107587	1.33372	0.0003252
chr11:119538719-1195478	Nptx1	18164	8.4	13.1	2.8	1.71667	0.043973	-2.30425	6.17E-05
chr5:144545887-14455747	Nptx2	53324	6.1	5.4	20.3	-1.01467	0.962981	3.95749	5.65E-18
chr8:66697422-66706798:	Npy1r	18166	6.5	5.9	1.3	-1.01632	0.977781	-3.24775	0.0001286
chr8:107388225-10740320	Nqo1	18104	12.1	9.7	4.5	-1.11904	0.671088	-2.09863	1.34E-05
chr13:33964659-33988465	Nqo2	18105	14.4	10.7	4.5	-1.21492	0.310057	-2.52516	1.36E-11
chr11:98767932-98775377	Nr1d1	217166	107.3	55.2	14.9	-1.70847	0.107095	-5.03962	4.67E-11
chr14:18204056-18239106	Nr1d2	353187	231.9	184.7	47.1	-1.11147	0.43266	-3.88193	4.53E-51
chr2:91184061-91195116:	Nr1h3	22259	25.5	20.7	10.4	-1.11148	0.643604	-1.92633	7.32E-06
chr10:89454234-89533622	Nr1h4	20186	2.0	1.5	0.3	-1.22073	0.731826	-3.72631	0.0003866
chr10:94147931-94197214	Nr2c1	22025	21.5	17.1	10.1	-1.12966	0.345373	-1.68831	9.40E-09
chr6:92091418-92173058:	Nr2c2	22026	58.8	49.3	36.9	-1.0714	0.395932	-1.27464	1.88E-05
chr8:70131327-70133751:	Nr2c2ap	75692	14.4	16.8	36.7	1.30909	0.115603	3.11904	7.32E-21
chr7:70351950-70366746:	Nr2f2	11819	93.0	54.3	35.3	-1.51979	0.214223	-1.99249	0.0059009
chr8:71374119-71381952:	Nr2f6	13864	22.2	28.8	35.6	1.45558	0.054535	1.96802	4.56E-06
chr18:39410545-39487245	Nr3c1	14815	112.7	82.2	52.7	-1.23318	0.119697	-1.70021	1.14E-07
chr8:76902508-77243639:	Nr3c2	110784	34.9	25.3	7.2	-1.22929	0.210446	-3.78456	5.20E-29
chr4:48051248-48083352:	Nr4a3	18124	0.6	2.7	1.8	3.735	0.001082	2.82908	0.0025064
chr1:136843584-13696044	Nr5a2	26424	3.5	2.4	5.3	-1.26107	0.230309	1.88607	1.62E-06
chr9:110621135-11062439	Nradd	67169	36.5	34.8	21.2	1.0749	0.680047	-1.36882	0.0053385
chr2:25180758-25183332:	Nrarp	67122	4.4	6.8	7.9	1.7024	0.01594	2.18582	5.55E-06
chr3:103058285-10306791	Nras	18176	54.1	65.8	69.8	1.36758	0.025626	1.60235	1.47E-05
chr10:67266689-67285281	Nrbf2	641340	14.2	13.7	15.1	1.0744	0.630889	1.32839	0.0028386
chr5:31240918-31251562:	Nrbp1	192292	144.6	161.1	174.5	1.25766	0.094904	1.50164	8.39E-05
chr15:76085594-76090013	Nrbp2	223649	93.4	74.1	52.5	-1.1219	0.445944	-1.41218	0.0010236
chr12:44328885-44601846	Nrcam	319504	2.2	1.7	0.8	-1.11084	0.613602	-2.17868	2.74E-08
chr4:109000805-10906177	Nrd1	230598	87.1	75.7	95.4	-1.02387	0.83333	1.36747	9.76E-07
chr12:100125450-1001596	Nrde2	217827	30.3	19.0	11.6	-1.43023	0.1051	-2.0327	1.92E-05
chr18:33437019-33464029	Nrep	27528	96.8	68.1	9.4	-1.28191	0.296342	-7.58398	6.58E-34
chr6:30047988-30153458:	Nrf1	18181	33.4	37.5	46.6	1.26582	0.075591	1.73588	2.50E-08
chr8:31818028-31918203:	Nrg1	211323	8.8	11.0	62.9	1.3962	0.005185	8.77608	6.82E-139
chr18:36017658-36197160	Nrg2	1E+08	12.4	20.6	43.7	1.79319	0.164592	3.69313	2.52E-05
chr9:55220222-55283625:	Nrg4	83961	7.0	5.5	1.3	-1.13808	0.77459	-3.6919	2.48E-06
chr16:76290862-76373049	Nrip1	268903	36.6	98.9	72.1	2.82377	0.00168	2.25864	0.0035083
chr6:128399766-12840893	Nrip2	60345	7.8	5.3	1.1	-1.30711	0.316149	-5.31943	3.92E-16
chr7:109758056-10978154	Nrip3	78593	0.3	0.6	1.1	1.91049	0.116353	3.497	3.46E-05
chrX:138914430-13900909	Nrk	27206	0.8	1.0	4.0	1.32017	0.283036	5.70358	1.66E-24
chr13:36725622-36734477	Nrn1	68404	36.7	24.7	6.2	-1.32676	0.070429	-4.61411	3.61E-36
chr12:87442848-87444017	Nrp	654309	7.9	10.7	13.9	1.50789	0.150297	2.11908	0.0003999
chr8:128359073-12850547	Nrp1	18186	71.6	95.1	301.5	1.49563	0.054488	5.00912	2.27E-25
chr17:56751325-56757530	Nrtn	18188	1.7	8.0	8.3	3.84658	0.002127	4.2045	7.61E-05
chr19:6418738-6533217:+	Nrxn2	18190	1.7	1.2	0.7	-1.24269	0.389075	-1.99688	0.0001449
chr11:103821783-1039540	Nsf	18195	25.8	24.3	40.7	1.05707	0.558435	1.96419	2.29E-30

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr2:151494182-15151131	Nsfl1c	386649	121.5	125.6	183.4	1.16248	0.139339	1.8791	9.42E-18
chr5:38137193-38159467:	Nsg1	18196	26.2	24.7	17.1	1.06219	0.581684	-1.22257	0.0065319
chr11:32000419-32059211	Nsg2	18197	12.1	8.1	0.5	-1.30944	0.483873	-13.1891	4.45E-21
chr4:6396208-6454271:-	Nsmaf	18201	114.3	89.6	54.9	-1.14619	0.224016	-1.66036	3.22E-10
chr7:125467640-12549154	Nsmce1	67711	76.9	81.1	99.4	1.17117	0.318093	1.60707	2.32E-05
chr2:25054379-25062881:	Nsmf	56876	105.9	90.9	62.9	-1.0411	0.586504	-1.34568	5.31E-10
chr13:69612016-69635779	Nsun2	28114	77.0	80.0	154.2	1.16933	0.199099	2.48235	5.88E-26
chr4:116031770-11605387	Nsun4	72181	12.9	12.9	16.0	1.12167	0.319241	1.54591	4.75E-08
chr5:135369953-13537679	Nsun5	100609	27.6	31.4	45.9	1.28448	0.085365	2.06692	1.15E-11
chr2:14995131-15054872:	Nsun6	74455	10.4	8.6	5.0	-1.08553	0.588668	-1.63609	8.41E-07
chr5:66259898-66298028:	Nsun7	70918	7.6	4.0	0.6	-1.68047	0.090183	-8.70394	1.17E-19
chr12:10369971-10390174	Nt5c1b	70881	10.4	0.4	1.2	-10.7465	1.46E-06	-4.33394	0.0007461
chr19:46886831-47015189	Nt5c2	76952	51.2	49.1	53.0	1.072	0.5567	1.29224	0.0010706
chr6:56882402-56923932:	Nt5c3	107569	37.9	32.9	40.5	-1.03782	0.804218	1.33097	0.0011022
chr9:88327609-88372089:	Nt5e	23959	29.3	23.3	3.3	-1.12098	0.779328	-6.04019	8.15E-14
chr16:13819277-13835451	Ntan1	18203	91.1	83.2	50.6	1.01743	0.901164	-1.439	2.30E-06
chr17:24632682-24638838	Nthl1	18207	26.8	18.4	8.9	-1.30506	0.14311	-2.34885	4.68E-10
chr9:28995964-29963129:	Ntm	235106	23.6	22.1	3.1	1.0462	0.798381	-5.86198	1.24E-51
chr2:30807977-30823014:	Ntmt1	66617	46.4	52.8	70.8	1.28395	0.117307	1.88691	6.89E-08
chr10:93641049-93745972	Ntn4	57764	44.3	31.5	15.3	-1.26954	0.333346	-2.24892	3.63E-06
chr3:109780050-11014347	Ntng1	80883	2.9	2.5	0.7	-1.03886	0.916488	-2.9488	8.61E-08
chr3:87778244-87795162:	Ntrk1	18211	2.7	2.1	1.0	-1.14647	0.657701	-2.07997	0.0003566
chr13:58806569-59133970	Ntrk2	18212	25.8	22.9	14.5	-1.00991	0.956497	-1.42421	0.00016
chr7:78192114-78577838:	Ntrk3	18213	6.1	5.2	2.3	-1.03959	0.895093	-2.02989	1.81E-05
chr10:102481756-1024904	Nts	67405	1.5	8.7	10.2	4.84386	3.79E-05	6.07112	3.81E-08
chr5:24685815-24710555:	Nub1	53312	106.5	90.4	46.0	-1.05426	0.467771	-1.84815	2.41E-36
chr16:10411938-10424425	Nubp1	26425	20.2	26.2	70.0	1.46016	0.00495	4.24549	4.72E-44
chr17:24882611-24886350	Nubp2	26426	35.3	36.2	44.0	1.15641	0.285466	1.55501	4.15E-06
chr12:52097746-52310959	Nubpl	76826	15.1	12.3	7.0	-1.10269	0.490819	-1.72365	5.46E-08
chr7:116504369-11654058	Nucb2	53322	38.8	33.0	52.1	-1.05502	0.686827	1.67299	9.49E-11
chr1:131910458-13193632	Nucks1	98415	99.6	94.7	150.1	1.06768	0.590112	1.87496	4.36E-16
chr4:133532542-13354602	Nudc	18221	133.6	143.8	206.3	1.21119	0.078691	1.92293	3.03E-16
chr15:44375227-44428307	Nudcd1	67429	18.1	20.1	35.2	1.24328	0.011813	2.42158	1.05E-42
chr11:40733661-40740046	Nudcd2	52653	22.1	23.6	45.4	1.2005	0.249999	2.52801	3.22E-17
chr11:6105692-6200451:-	Nudcd3	209586	58.3	51.2	75.2	-1.01701	0.819049	1.61297	7.98E-32
chr17:59001401-59013322	Nudt12	67993	11.8	8.6	4.2	-1.24071	0.444157	-2.15022	0.0001013
chr14:20294690-20317575	Nudt13	67725	18.3	14.1	8.4	-1.1638	0.37658	-1.71605	8.43E-06
chr12:112934733-1129421	Nudt14	66174	17.9	15.8	9.8	-1.01431	0.949542	-1.45394	0.0023283
chr14:73519864-73548242	Nudt15	214254	2.0	1.9	3.0	1.05783	0.836692	1.81539	5.14E-05
chr9:105129338-10513180	Nudt16	75686	23.3	14.0	7.2	-1.48407	0.231427	-2.42876	0.0002505
chr14:70577847-70582571	Nudt18	213484	5.5	2.6	2.7	-1.88155	0.000673	-1.60241	0.002652
chr7:35547185-35555928:	Nudt19	110959	14.3	15.1	24.8	1.17563	0.096307	2.15339	2.12E-30
chr4:41465148-41480926:	Nudt2	66401	23.3	19.5	26.7	-1.07084	0.705493	1.42497	0.0011953
chr8:94019403-94037039:	Nudt21	68219	73.1	71.8	89.2	1.09998	0.472838	1.51683	3.19E-06
chr19:6993019-6996037:-	Nudt22	68323	27.6	22.9	28.5	-1.08061	0.567781	1.29187	0.0034434
chr17:27579382-27623452	Nudt3	56409	61.8	61.9	91.0	1.12609	0.203131	1.83355	3.20E-20
chr2:5845034-5868736:+	Nudt5	53893	29.2	31.5	42.3	1.20918	0.061626	1.81034	8.96E-16
chr8:114133574-11415231	Nudt7	67528	12.3	7.7	3.6	-1.43683	0.19421	-2.56986	4.44E-06
chr19:4000580-4002102:+	Nudt8	66387	18.9	13.5	10.7	-1.24513	0.119488	-1.40827	0.001438
chr14:76110891-76137379	Nufip1	27275	14.1	19.3	24.2	1.53158	0.026698	2.10126	5.12E-07
chr11:77686139-77717966	Nufip2	68564	58.2	75.0	84.5	1.45307	0.060626	1.78713	0.0001319
chr7:101969843-10201495	Numa1	101706	196.5	161.3	62.5	-1.08945	0.356852	-2.49763	3.30E-47
chr12:83794034-83921934	Numb	18222	34.6	31.7	21.6	1.02521	0.771007	-1.2813	1.66E-06
chr10:117750643-1177927	Nup107	103468	41.2	42.4	45.0	1.15459	0.1274	1.36354	9.24E-06
chr13:46679902-46727849	Nup153	218210	73.8	88.9	94.1	1.36144	0.094904	1.57765	0.0011611
chr15:8109313-8159859:+	Nup155	170762	36.2	37.3	38.9	1.15736	0.076268	1.34266	1.86E-06
chr2:90677215-90736328:	Nup160	59015	29.7	30.8	37.5	1.17163	0.172083	1.57559	7.08E-08
chr2:30286433-30344262:	Nup188	227699	32.7	29.6	39.0	1.0172	0.889958	1.49115	1.84E-09

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr6:35177616-35247598:	Nup205	70699	51.3	49.9	80.3	1.09585	0.395816	1.95325	4.62E-20
chr6:91013067-91116826:	Nup210	54563	14.0	17.6	17.8	1.41687	0.070164	1.57712	0.0020147
chr2:80638812-80660071:	Nup35	69482	18.8	24.0	32.0	1.4375	0.011958	2.09976	3.51E-11
chr10:88146992-88178395	Nup37	69736	26.3	24.4	31.3	1.03659	0.802372	1.48651	1.20E-06
chr10:7667504-7678886:+	Nup43	69912	24.1	25.9	45.6	1.20992	0.250934	2.33606	1.88E-13
chr5:92415540-92435199:	Nup54	269113	44.5	52.0	64.9	1.31611	0.065211	1.80779	1.11E-07
chr7:44816420-44830806:	Nup62	18226	38.7	46.4	58.9	1.34905	0.019746	1.88976	1.08E-10
chr11:115564444-1155839	Nup85	445007	89.1	86.8	96.2	1.09545	0.375213	1.34994	2.87E-05
chr11:70943058-70969973	Nup88	19069	72.5	71.7	79.1	1.112	0.236799	1.36304	1.52E-06
chr8:94214601-94315066:	Nup93	71805	22.5	19.6	37.3	-1.02342	0.849079	2.06393	3.00E-29
chr7:102119400-10221016	Nup98	269966	55.0	68.8	98.6	1.41268	0.045793	2.20741	1.27E-09
chr14:60219468-60251378	Nupl1	71844	64.6	83.8	98.1	1.46314	0.060143	1.86498	5.13E-05
chr5:24164963-24184008:	Nupl2	231042	8.2	6.5	9.2	-1.129	0.383713	1.39851	0.0003732
chr5:129908540-12991128	Nupr1l	69034	7.0	3.5	1.3	-1.70149	0.169915	-3.6941	1.53E-05
chr10:52417547-52440192	Nus1	52014	27.1	31.3	41.9	1.3028	0.043289	1.92097	2.85E-11
chr8:105860634-10588040	Nutf2	68051	10.1	10.2	15.6	1.13609	0.373193	1.92001	6.34E-12
chr1:181093423-18114415	Nvl	67459	58.5	60.7	74.6	1.16808	0.097773	1.59154	1.49E-11
chr8:72646711-72714748:	Nwd1	319555	2.3	1.6	0.4	-1.28448	0.475574	-3.9141	2.32E-08
chr5:63649103-63810543:	Nwd2	319807	1.9	0.9	0.1	-1.75819	0.211324	-7.33812	2.71E-09
chr19:8757103-8770910:+	Nxf1	53319	149.8	163.2	160.6	1.23144	0.15998	1.3364	0.0097423
chrX:136072099-13608525	Nxf3	245610	1.1	0.1	0.1	-6.40562	0.000428	-4.00265	0.0019169
chr11:76257226-76399141	Nxn	18230	71.1	65.5	154.4	1.03465	0.810712	2.6932	2.13E-35
chr13:51171025-51175187	Nxnl2	75124	1.6	3.6	5.4	2.32206	0.02686	3.64014	9.06E-06
chr16:55839953-55895279	Nxpe3	385658	2.3	1.7	1.1	-1.20967	0.49748	-1.68335	0.0077571
chr6:8950019-9248578:+	Nxph1	18231	3.7	2.0	0.5	-1.59452	0.304932	-4.44091	9.51E-06
chr2:148672615-14867602	Nxt1	56488	29.0	32.7	39.3	1.26738	0.210836	1.66972	0.0002013
chr5:137730963-13773999	Nyap1	243300	6.6	5.9	2.8	-1.00404	0.990354	-1.87643	9.85E-05
chr14:55854115-55874736	Nynrin	277154	45.0	36.8	21.4	-1.07846	0.693526	-1.66549	1.75E-05
chr17:48410000-48417270	Oard1	106821	64.7	49.2	35.1	-1.18122	0.298584	-1.4651	0.0009871
chr5:120812635-12082416	Oas1b	23961	17.1	15.9	6.8	1.03308	0.903548	-1.98063	5.79E-06
chr5:120800199-12081251	Oas1c	114643	6.3	4.3	1.4	-1.32715	0.418113	-3.28539	1.68E-06
chr5:120876142-12088761	Oas1g	23960	7.5	8.6	3.1	1.27662	0.43881	-1.86542	0.0057717
chr5:120730333-12074984	Oas2	246728	11.0	13.5	3.4	1.34735	0.363377	-2.39098	0.0001937
chr5:114896934-11491224	Oasl2	23962	49.4	51.0	10.6	1.14978	0.658843	-3.45735	3.67E-10
chr9:65676548-65690300:	Oaz2	18247	111.1	91.8	74.6	-1.08573	0.297829	-1.1904	0.0023352
chr3:94433388-94436651:	Oaz3	53814	47.4	2.4	5.4	-10.7106	1.75E-08	-5.0978	1.18E-05
chr2:25700074-25703326:	Obp2a	227627	0.0	0.5	1.8	2.42977	0.155063	6.08796	8.86E-05
chr5:73292794-73314077:	Ociad1	68095	92.6	91.8	105.8	1.11136	0.140719	1.42556	1.08E-11
chr5:73322199-73338639:	Ociad2	433904	22.0	17.7	6.8	-1.12478	0.687819	-2.48465	6.20E-07
chr13:100497367-1005524	Ocln	18260	21.5	17.3	8.5	-1.11635	0.640264	-1.99729	4.35E-06
chr12:17544873-17551502	Odc1	18263	73.9	89.8	211.9	1.3686	0.044814	3.51337	2.13E-27
chr15:38219203-38226735	Odf1	18285	23.7	1.5	3.0	-7.35265	5.68E-05	-4.13879	0.0009925
chr2:29889720-29931746:	Odf2	18286	80.4	44.6	37.7	-1.58229	0.00659	-1.67752	0.0001572
chr3:145118589-14515391	Odf2l	52184	27.8	23.8	15.9	-1.04222	0.761941	-1.38899	7.77E-05
chr7:140847916-14085092	Odf3	69287	5.6	0.4	0.7	-5.63272	0.001033	-4.08613	0.0014984
chr15:89377449-89379254	Odf3b	70113	3.1	1.7	0.4	-1.54884	0.24666	-4.6335	5.52E-07
chr11:68921835-68927081	Odf4	252868	6.4	0.3	0.7	-7.30515	0.000149	-4.24239	0.0013864
chrX:166390033-16644070	Ofd1	237222	19.1	16.7	21.9	-1.0206	0.861604	1.42968	2.12E-08
chr11:6291597-6359094:+	Ogdh	18293	50.0	48.4	72.2	1.08909	0.352925	1.80275	5.75E-21
chr14:32322019-32347820	Ogdhl	239017	11.1	8.2	2.3	-1.21191	0.354876	-3.71861	1.50E-18
chr8:94037198-94067922:	Ogfod1	270086	16.3	15.8	24.3	1.08686	0.214938	1.86046	1.52E-42
chr5:124112338-12411547	Ogfod2	66627	28.6	21.4	14.3	-1.19519	0.143085	-1.59069	3.51E-07
chr2:180589407-18059583	Ogfr	72075	73.6	97.0	113.1	1.48256	0.017263	1.89553	7.22E-07
chr1:23366424-23383175:	Ogfrl1	70155	15.0	9.7	7.3	-1.39486	0.112128	-1.62704	0.0022959
chr13:49608071-49624500	Ogn	18295	277.7	314.0	398.1	1.24935	0.326535	1.74636	0.0006072
chrX:101640051-10168435	Ogt	108155	274.5	198.6	97.9	-1.23864	0.007323	-2.23395	4.46E-38
chr2:119609532-11961850	Oip5	70645	3.8	3.2	1.5	-1.06804	0.865126	-1.86723	0.0063809
chr2:73092801-73214447:	Ola1	67059	34.0	32.8	85.9	1.07969	0.504803	3.13625	1.19E-55

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr2:28193093-28230736:	Olfm1	56177	25.9	24.8	16.6	1.06197	0.635111	-1.25212	0.0068092
chr9:20667986-20728214:	Olfm2	244723	2.4	3.7	6.1	1.64261	0.298403	2.63983	0.0049305
chr7:107567433-10759136	Olfml1	244198	40.7	26.0	1.8	-1.40402	0.238904	-15.2185	2.88E-37
chr2:38931980-38960585:	Olfml2a	241327	40.6	28.2	3.8	-1.29154	0.076234	-8.27753	2.27E-75
chr1:170644532-17068278	Olfml2b	320078	14.4	8.8	2.8	-1.46092	0.110929	-3.86908	4.15E-14
chr3:103735394-10373800	Olfml3	99543	93.4	121.2	304.1	1.45722	0.005579	3.98561	7.36E-39
chr2:86020640-86044808:	Olfr1033	258571	13.1	11.8	2.9	-1.01525	0.965877	-3.44905	5.45E-11
chr2:86046444-86047466:	Olfr1034	258216	4.4	3.3	0.3	-1.1902	0.762673	-6.15793	8.90E-07
chr11:52154876-52157907	Olfr1372-ps1	257871	8.9	6.8	2.5	-1.1771	0.395633	-2.82729	3.42E-13
chr7:140345052-14034598	Olfr60	18361	0.4	2.7	3.4	2.7709	0.099176	3.62453	0.0065354
chr7:102740721-10275947	Olfr78	170639	8.3	7.1	1.1	-1.04263	0.858826	-5.86656	1.12E-33
chr4:103313846-10336642	Oma1	67013	27.0	21.4	14.2	-1.13083	0.262833	-1.51486	1.79E-07
chr13:49582747-49592609	Omd	27047	2.1	2.3	0.7	1.24253	0.480666	-2.21962	0.0007017
chr16:29579334-29654602	Opa1	74143	50.5	45.2	49.5	1.00257	0.979019	1.22383	6.97E-05
chr7:19228389-19246817:	Opa3	403187	14.5	24.1	47.4	1.84038	0.012538	3.82288	1.47E-12
chr9:27791269-28925048:	Opcml	330908	1.3	1.3	0.5	1.10055	0.749222	-2.17622	6.14E-05
chrX:98557515-98890985:	Ophn1	94190	47.6	40.6	12.7	-1.04804	0.579315	-2.99016	1.08E-84
chr15:76296603-76307245	Oplah	75475	34.9	28.0	11.3	-1.11807	0.523365	-2.42114	2.23E-14
chr6:29376671-29380513:	Opn1sw	12057	1.6	1.0	0.5	-1.46695	0.287787	-2.51101	0.0006869
chr5:123015074-12303045	Orai1	109305	10.5	12.0	15.1	1.28051	0.158441	1.76633	8.49E-06
chr4:108579454-10861483	Orc1	18392	1.2	1.1	2.0	1.03073	0.945754	2.08674	0.0012274
chr1:58462771-58505109:	Orc2	18393	29.2	38.9	63.5	1.50097	0.018729	2.66425	1.38E-13
chr4:34566781-34614942:	Orc3	50793	36.4	33.2	37.2	1.01897	0.783766	1.2764	7.47E-10
chr2:48902754-48949267:	Orc4	26428	33.4	36.9	48.1	1.24109	0.062646	1.78964	1.43E-11
chr8:85299632-85308279:	Orc6	56452	35.4	40.2	44.1	1.28099	0.162646	1.54652	0.0009664
chr4:63344566-63348162:	Orm1	18405	19.5	10.2	2.5	-1.49254	0.530359	-3.52126	0.0037314
chr10:128817457-1288216	Ormdl2	66844	17.7	22.9	24.1	1.44958	0.003171	1.68863	2.50E-07
chr19:11965844-11994114	Osbp	76303	45.5	45.9	56.4	1.13977	0.289959	1.54649	6.25E-07
chr11:3703731-3863903:-	Osbp2	74309	17.9	10.3	2.2	-1.52965	0.112912	-5.94199	6.22E-19
chr18:12755312-12941841	Osbpl1a	64291	28.6	32.3	13.5	1.27848	0.258004	-1.66571	0.0013055
chr2:180119366-18016268	Osbpl2	228983	59.3	48.7	33.0	-1.08876	0.332355	-1.43245	6.38E-09
chr7:143688762-14374196	Osbpl5	79196	67.4	58.0	41.2	-1.03299	0.742498	-1.30595	9.22E-06
chr2:76406508-76600647:	Osbpl6	99031	3.3	2.4	1.3	-1.20591	0.403427	-2.05413	5.42E-06
chr4:109061145-10920227	Osbpl9	100273	96.4	85.9	51.6	-1.00861	0.942286	-1.49265	5.09E-11
chr4:126058565-12608933	Oscp1	230751	18.5	10.1	5.5	-1.62312	0.030829	-2.59444	3.95E-08
chr2:163405822-16341947	Oser1	66680	37.5	38.8	23.0	1.16154	0.145357	-1.30353	0.0007606
chr4:15997121-16013877:	Osgin2	209212	15.3	17.9	16.6	1.31024	0.002735	1.35626	3.53E-05
chr15:6813577-6874313:-	Osmr	18414	30.2	58.2	89.0	1.99936	0.036472	3.29975	2.57E-06
chr5:30906516-30907788:	Ost4	67695	159.4	169.8	166.6	1.18976	0.010917	1.30362	7.26E-07
chr3:130695917-13070944	Ostc	66357	83.3	93.0	222.1	1.24716	0.059423	3.28983	9.84E-45
chr10:42678916-42702462	Ostm1	14628	21.6	21.6	25.2	1.11642	0.419084	1.45063	7.75E-05
chr19:7198206-7206284:-	Otub1	107260	86.0	92.9	134.8	1.21825	0.149125	1.94497	2.50E-11
chr2:19658062-19660590:	Otud1	71198	25.4	18.8	6.9	-1.21727	0.330757	-2.8524	2.57E-13
chr8:79639676-79677755:	Otud4	73945	75.6	89.3	97.9	1.33465	0.089163	1.60591	0.0002283
chrX:7841831-7876626:+	Otud5	54644	56.4	53.5	33.6	1.06173	0.312887	-1.33976	3.68E-12
chr4:14809505-14826587:	Otud6b	72201	41.5	47.5	64.9	1.28466	0.023753	1.94121	2.80E-15
chr15:27605921-27630693	Otulin	432940	42.7	42.1	53.8	1.1075	0.337089	1.57159	5.86E-10
chr11:75175943-75178808	Ovca2	246257	19.5	24.4	36.0	1.40749	0.042672	2.26854	8.77E-11
chr15:4026428-4155344:+	Oxct1	67041	185.5	168.9	75.5	1.01187	0.945108	-1.9497	3.46E-14
chr4:123116248-12311800	Oxct2b	353371	2.6	0.2	0.4	-6.91544	3.17E-05	-3.61217	0.0010905
chr11:120456604-1204580	Oxld1	66431	17.8	13.0	8.2	-1.23133	0.476317	-1.6996	0.0098904
chr15:41447482-41861047	Oxr1	170719	63.3	52.2	30.2	-1.09212	0.502257	-1.66632	5.76E-09
chr14:16238659-16249808	Oxsm	71147	7.9	4.6	4.1	-1.52495	0.032093	-1.50035	0.0088527
chr9:119238433-11932242	Oxsr1	108737	44.3	44.6	47.1	1.12626	0.07975	1.32992	1.46E-08
chr6:112473684-11248980	Oxtr	18430	21.4	114.2	216.8	5.63508	1.87E-18	11.3426	3.54E-40
chr5:110339812-11034303	P2rx2	231602	6.8	3.7	0.3	-1.57923	0.23792	-10.7389	3.62E-15
chr16:17561885-17572012	P2rx6	18440	39.8	27.5	4.2	-1.29865	0.323858	-6.96256	4.98E-25
chr5:122643911-12269143	P2rx7	18439	63.8	44.5	21.9	-1.29009	0.253358	-2.26807	2.93E-07

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr3:59216271-59262831:	P2ry12	70839	3.0	2.3	0.8	-1.1425	0.692789	-2.65036	1.09E-05
chr3:59207894-59210882:	P2ry13	74191	2.6	2.7	0.7	1.10965	0.792527	-2.89604	2.07E-05
chr3:59114623-59153492:	P2ry14	140795	19.9	59.3	119.0	2.96269	0.003859	5.80636	6.34E-09
chr16:25960323-26105784	P3h2	210530	28.6	23.2	4.6	-1.11132	0.719227	-4.63967	1.97E-17
chr6:124841095-12485768	P3h3	14789	56.9	44.4	27.4	-1.15065	0.265923	-1.65353	2.42E-08
chr10:59323296-59373304	P4ha1	18451	49.1	70.0	70.2	1.5966	0.000365	1.77266	2.30E-07
chr7:100285520-10031969	P4ha3	320452	0.8	3.1	8.1	3.6124	0.001151	9.05364	8.80E-12
chr11:120560304-1205729	P4hb	18453	412.6	398.9	792.7	1.08305	0.420891	2.38865	2.86E-39
chr9:108578826-10859760	P4htm	74443	35.1	25.0	15.2	-1.25894	0.162368	-1.82558	8.33E-07
chr10:128557766-1285659	Pa2g4	18813	91.4	103.3	223.6	1.27297	0.094175	3.01441	7.86E-26
chr15:36595658-36608973	Pabpc1	18458	272.3	239.9	301.2	-1.00863	0.95616	1.38063	5.31E-05
chr18:39773497-39776082	Pabpc2	18459	8.1	0.3	1.0	-11.6607	6.63E-08	-4.52826	0.0001539
chr4:123282911-12329883	Pabpc4	230721	45.9	49.9	127.7	1.22456	0.125126	3.43053	1.54E-38
chr3:46442197-46447941:	Pabpc4l	241989	6.1	3.9	0.5	-1.37792	0.541251	-6.36362	1.09E-07
chrX:119927196-11993016	Pabpc5	93728	3.4	2.6	0.5	-1.19463	0.778712	-3.88872	0.0004329
chr17:9666497-9669704:-	Pabpc6	67543	5.1	0.2	0.6	-13.4749	2.63E-09	-4.80895	3.24E-05
chr14:54894143-54898927	Pabpn1	54196	154.7	133.5	166.5	-1.02668	0.857795	1.34358	0.0003612
chr8:122619471-12262273	Pabpn1l	382035	1.4	0.9	0.2	-1.41857	0.579703	-4.01908	0.0013697
chr17:10403012-10840191	Pacrg	69310	6.5	2.8	1.7	-2.00089	0.039269	-2.79572	9.17E-05
chr5:48372392-48388756:	Pacrgl	66768	19.3	15.1	12.2	-1.14429	0.242347	-1.26525	0.0057749
chr19:5133685-5273119:-	Pacs1	107975	23.8	18.6	11.7	-1.14037	0.240526	-1.61688	2.61E-09
chr12:113014508-1130744	Pacs2	217893	46.7	40.0	45.6	-1.04251	0.727681	1.22119	0.0073012
chr15:83375607-83464606	Pacsin2	23970	48.3	50.2	64.5	1.16487	0.005579	1.66855	2.33E-33
chr4:140812981-14084577	Padi1	18599	10.5	83.5	192.6	3.0558	0.063475	5.41363	0.0002348
chr4:140906360-14095258	Padi2	18600	4.4	19.6	79.0	2.75497	0.074247	7.78497	1.53E-06
chr4:140745508-14077420	Padi4	18602	4.5	6.1	14.3	1.5071	0.209389	3.62793	3.64E-08
chr7:28392996-28399383:	Paf1	54624	80.9	85.6	95.1	1.19333	0.213736	1.46341	0.0002488
chr11:74673949-74724384	Pafah1b1	18472	130.8	150.2	177.1	1.29564	0.077258	1.67973	2.55E-06
chr9:45965311-45984871:	Pafah1b2	18475	73.9	83.9	113.8	1.28259	0.122321	1.90344	6.81E-08
chr3:9687482-9833679:-	Pag1	94212	5.4	5.3	5.5	1.08982	0.454807	1.27644	0.0019909
chr7:127015051-12701735	Pagr1a	67278	93.0	66.4	28.8	-1.25964	0.263661	-2.51572	3.73E-10
chr13:119428600-1194603	Paip1	218693	44.9	49.2	60.1	1.23669	0.141799	1.66109	2.04E-06
chr18:35598667-35617185	Paip2	67869	240.2	230.5	66.7	1.07146	0.42426	-2.87137	4.34E-71
chr7:97842939-97912381:	Pak1	18479	25.2	22.0	11.3	-1.0274	0.852946	-1.7768	3.29E-12
chr13:41001010-41013033	Pak1ip1	68083	68.5	89.5	134.2	1.47148	0.061152	2.38779	1.82E-08
chr16:32016290-32079342	Pak2	224105	55.7	62.2	70.3	1.25993	0.126029	1.56765	7.08E-05
chrX:143518591-14379779	Pak3	18481	4.3	7.6	45.7	1.9553	0.005313	11.8128	1.79E-39
chr7:28558819-28598184:	Pak4	70584	14.3	15.7	19.4	1.23532	0.142728	1.6904	6.37E-07
chr2:118663577-11869802	Pak6	214230	0.6	1.0	1.2	1.82227	0.113293	2.33096	0.0031446
chr7:122107262-12213294	Palb2	233826	6.1	4.2	2.5	-1.30625	0.248525	-1.88757	0.0001833
chr10:61319657-61383523	Pald1	27355	27.7	24.8	12.7	1.00855	0.959665	-1.7344	2.71E-10
chr8:61511429-61902694:	Palld	72333	59.8	72.7	66.6	1.35916	0.019627	1.3873	0.0017107
chr10:79793572-79820896	Palm	18483	56.5	41.4	21.4	-1.21678	0.019609	-2.1012	5.52E-30
chr3:116918262-11696895	Palmd	114301	16.3	11.5	19.7	-1.265	0.062949	1.50976	8.25E-06
chr1:97821094-98095632:	Pam	18484	195.5	163.3	82.8	-1.07314	0.623414	-1.87782	4.25E-12
chr16:4616466-4624946:-	Pam16	66449	41.2	38.7	54.3	1.05404	0.7519	1.63772	3.61E-07
chr2:102550021-10264304	Pamr1	210622	266.8	201.7	15.6	-1.19308	0.368313	-12.8544	9.97E-81
chr10:128303335-1283213	Pan2	103135	45.0	36.2	20.1	-1.11129	0.410055	-1.77785	7.03E-11
chr5:147430580-14754850	Pan3	72587	82.9	75.0	48.7	1.01427	0.878356	-1.3607	1.26E-09
chr19:34806936-34879455	Pank1	75735	5.2	4.4	2.3	-1.05087	0.796095	-1.81378	2.29E-07
chr11:35769495-35791285	Pank3	211347	67.3	67.6	75.0	1.13083	0.380698	1.38733	0.000943
chr9:15005785-15045478:	Panx1	55991	8.9	10.1	10.6	1.26305	0.183882	1.46193	0.0034728
chr15:89059726-89070907	Panx2	406218	1.2	1.1	0.1	1.01385	0.976569	-5.14183	1.15E-08
chr7:140125685-14013433	Paox	212503	25.4	22.1	12.1	-1.03482	0.911463	-1.65093	0.0034046
chr13:93147400-93192283	Papd4	100715	66.2	63.7	72.1	1.08061	0.350227	1.36201	7.07E-08
chr8:88199213-88259722:	Papd5	214627	28.0	25.5	29.4	1.02468	0.860458	1.31151	0.0005028
chr13:69497959-69533864	Papd7	210106	25.5	24.8	32.6	1.08823	0.268443	1.59746	3.67E-19
chr12:105784702-1058389	Papola	18789	111.7	127.4	153.5	1.28502	0.022003	1.71145	1.67E-10

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr5:142527740-14253007	Papolb	56522	11.5	2.7	1.6	-3.27439	0.001225	-4.71568	4.15E-07
chr4:65124174-65357509:	Pappa	18491	44.0	38.8	10.7	-1.02127	0.903048	-3.25904	5.97E-37
chr1:158711731-15895743	Pappa2	23850	1.4	1.0	0.4	-1.15423	0.656576	-2.53056	1.14E-05
chr3:131564768-13164367	Papss1	23971	74.5	60.5	37.5	-1.11119	0.536243	-1.58066	5.75E-05
chr17:23736186-23740330	Paqr4	76498	14.1	11.6	5.2	-1.08451	0.676949	-2.13128	9.61E-10
chr3:88364589-88368541:	Paqr6	68957	5.3	3.1	0.6	-1.51502	0.117818	-6.07425	2.12E-15
chr1:20890622-20938756:	Paqr8	74229	13.4	11.5	5.6	-1.035	0.876369	-1.8867	2.54E-07
chr8:127064056-12761228	Pard3	93742	39.5	34.8	48.7	-1.00949	0.945436	1.54266	9.55E-10
chr1:61638824-62642284:	Pard3b	72823	40.1	33.1	19.2	-1.08274	0.444592	-1.66689	4.44E-13
chr8:105701148-10570349	Pard6a	56513	9.4	7.2	4.9	-1.17839	0.460949	-1.53984	0.0061383
chr18:80046895-80119640	Pard6g	93737	26.8	19.3	16.2	-1.24215	0.093966	-1.32414	0.004577
chr14:32201971-32297549	Parg	26430	50.2	55.2	60.4	1.23536	0.049831	1.5001	6.74E-07
chr17:10840384-12063360	Park2	50873	7.5	6.2	2.8	-1.06894	0.696744	-2.08749	2.19E-11
chr4:150897133-15090992	Park7	57320	186.0	174.8	215.3	1.05108	0.451669	1.44631	2.46E-17
chr16:20279821-20302362	Parl	381038	48.3	44.7	69.2	1.04176	0.811952	1.78235	3.36E-09
chr5:91517700-91623996:	Parm1	231440	20.3	15.7	6.2	-1.15888	0.465369	-2.55983	1.48E-11
chr16:13537964-13668170	Parn	74108	53.2	40.6	28.9	-1.17829	0.189879	-1.46419	3.49E-05
chr1:180568975-18060125	Parp1	11545	62.2	55.1	62.9	-1.00929	0.929682	1.2638	2.36E-05
chr15:76232995-76243440	Parp10	671535	37.1	38.3	38.6	1.1604	0.044327	1.3022	2.35E-06
chr16:35832878-35871382	Parp14	547253	63.1	76.3	29.1	1.35656	0.057699	-1.71942	9.20E-06
chr14:50807946-50821300	Parp2	11546	55.3	52.5	51.8	1.06335	0.423264	1.17015	0.0032998
chr9:106470353-10647665	Parp3	235587	41.8	44.3	65.8	1.17306	0.4514	1.93213	5.21E-06
chr14:56575619-56659798	Parp4	328417	25.5	22.9	14.6	1.0056	0.968189	-1.39151	1.08E-05
chr9:59617284-59650290:	Parp6	67287	47.9	39.5	30.0	-1.08645	0.487215	-1.27339	0.0033696
chr13:116854824-1170255	Parp8	52552	43.7	34.3	18.1	-1.1463	0.427956	-1.90907	5.22E-08
chr16:35938470-35972621	Parp9	80285	52.7	59.2	30.0	1.2583	0.094173	-1.39864	0.0013843
chr1:93309437-93342788:	Pask	269224	4.7	3.0	2.1	-1.37462	0.210064	-1.76287	0.0026958
chr19:11912399-11945096	Patl1	225929	21.2	25.2	25.6	1.33748	0.066993	1.49881	0.0008423
chr11:3289131-3309083:+	Patz1	56218	44.3	31.4	20.1	-1.2681	0.077258	-1.75003	2.93E-08
chr19:44757394-44837869	Pax2	18504	2.7	2.5	0.9	1.07387	0.877818	-2.17943	0.0036483
chr4:44531506-44710440:	Pax5	18507	2.5	1.4	0.4	-1.46976	0.52053	-3.12909	0.0061876
chr5:27740081-27791550:	Paxip1	55982	17.6	17.6	20.1	1.12452	0.318124	1.42903	1.76E-05
chrX:105079756-10511709	Pbdc1	67683	19.3	24.7	34.6	1.43656	0.032935	2.19638	9.73E-10
chr10:63061617-63077536	Pbld1	68371	10.6	8.5	0.5	-1.09493	0.793037	-13.8949	9.59E-29
chr10:63024512-63058812	Pbld2	67307	4.4	2.7	1.7	-1.40841	0.25077	-1.92898	0.002991
chr6:135309129-13531038	Pbp2	76400	3.5	0.3	0.6	-4.8171	0.003171	-3.02876	0.0123146
chr14:31019138-31121592	Pbrm1	66923	74.4	68.1	75.2	1.02468	0.713814	1.26247	6.53E-09
chr2:34171457-34372045:	Pbx3	18516	7.4	6.8	8.8	1.0189	0.910121	1.47705	6.59E-06
chr8:69832704-69872292:	Pbx4	80720	5.5	2.5	1.0	-1.86162	0.064943	-3.97627	2.17E-07
chr3:89436704-89450952:	Pbxip1	229534	108.5	99.6	62.2	1.01683	0.931185	-1.39341	0.0014345
chr6:86524497-86526165:	Pcbp1	23983	55.6	77.1	125.1	1.55539	0.049729	2.70772	4.16E-09
chr9:106453838-10646401	Pcbp4	59092	33.6	42.4	48.4	1.42147	0.067	1.77502	8.04E-05
chr14:122534328-1228899	Pcca	110821	25.2	22.6	14.8	-1.00071	0.997875	-1.34962	0.0053011
chrX:120290327-12091061	Pcdh11x	245578	2.0	1.4	0.9	-1.30176	0.287352	-1.79067	0.0012944
chr14:84443563-84537060	Pcdh17	219228	3.5	2.3	1.8	-1.34813	0.122009	-1.51484	0.0048679
chrX:133582861-13368899	Pcdh19	279653	3.6	2.4	1.1	-1.37944	0.231007	-2.45353	4.96E-06
chr5:57718021-58132240:	Pcdh7	54216	137.4	107.1	55.4	-1.15554	0.492095	-1.94925	2.58E-06
chr14:93013700-93890669	Pcdh9	211712	18.3	14.2	2.1	-1.15584	0.595628	-6.33067	1.23E-25
chr18:37755773-37841872	Pcdhga11	93723	11.3	9.9	5.8	-1.0213	0.934865	-1.5292	0.0023134
chr18:37765580-37841872	Pcdhga12	93724	6.9	5.9	3.2	-1.04692	0.879767	-1.67443	0.0026941
chr18:37674335-37841872	Pcdhga3	93711	10.8	8.8	5.7	-1.10122	0.6144	-1.49576	0.0013835
chr18:37685400-37841870	Pcdhga4	93712	15.0	12.1	7.7	-1.10816	0.586668	-1.53422	0.0006099
chr18:37694501-37841870	Pcdhga5	93713	14.0	11.7	7.3	-1.0745	0.727681	-1.52444	0.0010236
chr18:37714834-37841872	Pcdhga7	93715	14.9	12.7	7.5	-1.04646	0.866236	-1.57027	0.0034587
chr18:37736936-37841863	Pcdhga9	93717	13.5	11.7	6.4	-1.03063	0.912903	-1.66126	0.0008433
chr18:37680458-37841870	Pcdhgb1	93699	9.9	8.4	5.2	-1.05448	0.79963	-1.49828	0.001282
chr18:37742094-37841872	Pcdhgb6	93703	16.0	14.1	8.2	-1.0161	0.950142	-1.53588	0.0016267
chr18:37751779-37841870	Pcdhgb7	93704	11.4	10.5	5.8	1.03208	0.899914	-1.54403	0.0021812

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr18:37819546-37841872	Pcdhgc5	93708	3.3	2.6	1.5	-1.13696	0.623313	-1.67452	0.0029406
chr15:97247107-97385691	Pced1b	239647	16.4	10.8	4.1	-1.35385	0.294125	-3.00826	1.09E-07
chr11:97688823-97700497	Pcgf2	22658	17.0	13.0	8.6	-1.16521	0.283598	-1.57342	1.06E-05
chr8:13077525-13105343:	Pcid2	234069	27.2	27.6	32.6	1.14565	0.284964	1.49277	8.38E-06
chr2:173153073-17315925	Pck1	18534	25.0	8.7	2.8	-1.93715	0.277881	-3.71522	0.0031048
chr14:55540266-55550017	Pck2	74551	39.4	26.1	13.5	-1.35717	0.268893	-2.23897	5.16E-05
chr10:7630236-7663584:-	Pcmt1	18537	67.0	71.5	75.4	1.19622	0.0121	1.40429	8.94E-10
chr1:7088920-7173628:+	Pcmtd1	319263	96.1	79.7	33.0	-1.08808	0.60219	-2.30583	5.26E-16
chr2:181837854-18185746	Pcmtd2	245867	109.9	85.9	9.9	-1.15222	0.36195	-8.55244	3.25E-88
chr2:132249286-13225318	Pcna	18538	127.5	171.5	277.1	1.50556	0.007785	2.66904	3.79E-16
chr16:56015508-56029717	Pcnp	76302	113.2	114.7	133.4	1.13897	0.252664	1.46839	2.37E-06
chr10:76351254-76442912	Pcnt	18541	34.6	26.9	13.4	-1.1501	0.182492	-2.04587	2.92E-21
chr19:5664635-5688908:-	Pcnxl3	104401	26.1	24.3	28.3	1.051	0.731826	1.35469	0.000683
chr16:96467606-96525793	Pcp4	18546	418.1	428.3	236.0	1.13039	0.508935	-1.41079	0.0069683
chr1:171173264-17119626	Pcp4l1	66425	76.9	182.7	397.5	2.5273	0.004238	5.5044	4.95E-11
chr19:17432832-17837632	Pcsk5	18552	8.2	9.9	17.1	1.33308	0.102143	2.55949	2.98E-13
chr7:65862136-66050386:	Pcsk6	18553	14.6	13.6	22.4	1.0554	0.844343	1.87889	5.09E-05
chr9:45906569-45929722:	Pcsk7	18554	25.4	29.4	37.3	1.30529	0.079959	1.81822	1.39E-07
chr4:106442334-10646432	Pcsk9	100102	0.8	0.9	2.6	1.18484	0.608649	3.76677	1.30E-11
chr11:89983417-90002894	Pctp	18559	25.9	16.1	9.0	-1.44727	0.133683	-2.23248	1.34E-05
chr19:4510472-4621752:+	Pcx	18563	51.7	29.5	9.4	-1.50068	0.302944	-3.76385	2.27E-06
chr6:86386006-86397150:	Pcyox1	66881	68.0	52.6	36.3	-1.16386	0.130017	-1.49708	5.49E-08
chr16:32430921-32475065	Pcyt1a	13026	41.5	41.6	44.2	1.12953	0.283036	1.33095	0.0004579
chr11:120610087-1206178	Pcyt2	68671	46.8	41.5	61.5	-1.00224	0.993758	1.63278	0.0001316
chr5:145128770-14514008	Pdap1	231887	56.5	55.4	104.1	1.10209	0.371567	2.29092	7.25E-30
chr1:94038305-94052553:	Pdcd1	18566	1.4	3.4	5.8	2.29112	0.062632	4.03	3.36E-05
chr19:47090766-47131145	Pdcd11	18572	40.3	46.0	81.8	1.2913	0.13871	2.49545	3.65E-13
chr17:15521575-15527301	Pdcd2	18567	39.5	39.0	57.6	1.10935	0.466675	1.81105	2.95E-10
chr7:34184497-34196647:	Pdcd2l	68079	30.0	30.6	46.8	1.14946	0.330852	1.93348	1.76E-11
chr19:53892231-53929861	Pdcd4	18569	153.3	120.2	66.5	-1.14293	0.048095	-1.84	1.81E-33
chr7:35641985-35647482:	Pdcd5	56330	121.5	135.4	179.2	1.25521	0.070251	1.8321	6.88E-11
chr9:113651744-11370825	Pdcd6ip	18571	49.8	50.2	70.8	1.13447	0.242028	1.7685	7.02E-14
chr5:76312146-76331111:	Pdcl2	79455	12.7	0.5	1.3	-8.69426	2.45E-05	-4.48191	0.0007955
chr1:38987814-38997236:	Pdcl3	68833	90.4	101.9	102.2	1.26773	0.059398	1.40728	0.0003814
chr7:141408184-14141412	Pddc1	213350	58.7	37.7	18.7	-1.40144	0.192935	-2.4069	3.80E-06
chr17:8526801-8986648:+	Pde10a	23984	6.5	12.3	13.2	2.07804	0.028566	2.36205	0.0010165
chr14:26664117-26669846	Pde12	211948	9.0	19.7	33.9	2.35652	0.006301	4.16914	1.13E-08
chr15:103503034-1035300	Pde1b	18574	10.2	7.1	3.3	-1.30598	0.238412	-2.43734	6.67E-08
chr6:56069804-56369634:	Pde1c	18575	2.3	1.1	0.3	-1.82249	0.018729	-6.17076	8.38E-19
chr7:101421691-10151282	Pde2a	207728	29.0	24.3	8.5	-1.06645	0.542068	-2.70825	1.36E-45
chr6:141249269-14149935	Pde3a	54611	52.3	51.1	13.1	1.08468	0.668113	-3.12638	2.83E-22
chr9:21165714-21213248:	Pde4a	18577	4.8	3.3	1.8	-1.31271	0.169471	-2.05033	1.27E-06
chr4:102254742-10260726	Pde4b	18578	8.0	15.3	13.1	2.0616	0.002026	1.97641	0.0004928
chr8:70724064-70751176:	Pde4c	110385	3.9	2.7	0.6	-1.28395	0.478927	-4.31846	4.75E-09
chr13:108654177-1099559	Pde4d	238871	17.3	13.1	6.0	-1.18398	0.249973	-2.28352	3.63E-15
chr3:122729158-12285937	Pde5a	242202	194.7	160.3	25.3	-1.09987	0.677707	-5.88878	3.06E-37
chr11:120447607-1204535	Pde6g	18588	2.3	1.7	0.7	-1.20443	0.672799	-2.39262	0.0038696
chr10:20398004-20725068	Pde7b	29863	14.6	13.4	20.0	1.02245	0.911127	1.69606	6.30E-07
chr17:31386234-31476309	Pde9a	18585	21.9	18.2	8.2	-1.07876	0.620434	-2.10373	1.09E-13
chr8:107046290-10704861	Pdf	68023	33.4	38.1	56.7	1.28172	0.06949	2.10166	1.29E-13
chr15:79995876-80014808	Pdgfb	18591	13.8	16.3	22.6	1.32987	0.259048	1.98162	0.0001714
chr3:81036416-81214031:	Pdgfc	54635	50.7	40.2	24.6	-1.13549	0.476943	-1.63558	5.66E-05
chr9:6168612-6377519:+	Pdgfd	71785	34.9	30.8	5.6	-1.01546	0.942182	-4.86698	4.09E-43
chr5:75152291-75198204:	Pdgfra	18595	330.2	284.9	125.0	-1.05	0.859643	-2.06462	2.63E-06
chr18:61045150-61085067	Pdgfrb	18596	113.5	108.0	56.4	1.07943	0.723955	-1.5907	0.0005218
chr8:40926233-40990770:	Pdgfrl	68797	16.7	12.3	2.9	-1.20607	0.419113	-4.40875	1.29E-18
chrX:160122219-16013833	Pdha1	18597	176.8	149.8	180.0	-1.05777	0.43693	1.27148	1.08E-06
chr3:141210004-14121235	Pdha2	18598	3.1	0.1	0.3	-8.3855	4.27E-05	-4.72471	0.0005519

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr2:103021057-10307351	Pdhx	27402	22.7	23.9	31.4	1.19001	0.19365	1.72312	1.38E-08
chr2:121413902-12143868	Pdia3	14827	213.4	223.2	483.5	1.17961	0.283145	2.79094	9.29E-22
chr6:47796141-47813512:	Pdia4	12304	150.0	156.3	312.5	1.16497	0.25417	2.57758	4.82E-24
chr16:35397312-35490873	Pdia5	72599	10.3	8.5	17.5	-1.08412	0.589091	2.11188	3.07E-17
chr12:17266595-17284770	Pdia6	71853	197.3	244.9	584.9	1.39296	0.021088	3.63461	1.81E-32
chr4:134275005-13428784	Pdik1l	230809	19.0	19.9	21.8	1.17492	0.094783	1.43174	5.02E-07
chr7:119486587-11952348	Pdilt	71830	3.5	0.2	0.3	-7.13288	0.000139	-5.19282	0.0001984
chr2:71873224-71903858:	Pdk1	228026	20.0	11.7	7.3	-1.52732	0.066817	-2.12064	1.79E-05
chr11:95026258-95041371	Pdk2	18604	34.4	19.8	3.2	-1.5486	0.075384	-7.83499	3.27E-28
chr14:70164218-70177672	Pdlim2	213019	20.6	16.3	9.2	-1.13105	0.540694	-1.78523	1.86E-05
chr13:55497487-55513446	Pdlim7	67399	70.4	77.6	103.5	1.23959	0.116746	1.82272	2.86E-09
chr4:11958183-11966450:	Pdp1	381511	43.0	34.1	17.4	-1.14204	0.693272	-1.91075	0.0022185
chr8:104591468-10459684	Pdp2	382051	32.5	24.8	13.5	-1.16403	0.339815	-1.90162	9.90E-09
chr17:24073680-24150922	Pdpk1	18607	43.5	45.4	48.2	1.17453	0.092406	1.38447	5.38E-06
chr8:111094745-11113514	Pdpr	319518	40.4	33.9	19.6	-1.06817	0.543213	-1.64473	3.55E-12
chr2:153008890-15301538	Pdrg1	68559	86.3	104.1	122.8	1.35987	0.10107	1.7541	6.60E-05
chr5:65615260-65697856:	Pds5a	71521	97.6	102.5	124.3	1.18289	0.135869	1.58513	2.58E-08
chr2:22895522-22940259:	Pdss1	56075	10.3	13.3	31.5	1.44811	0.012087	3.74636	1.60E-33
chr10:78436747-78464948	Pdxk	216134	66.3	82.2	121.1	1.39523	0.379086	2.12819	0.005128
chrX:100622906-10062590	Pdzd11	72621	50.1	41.9	56.3	-1.06879	0.494385	1.40565	6.00E-08
chr15:12357054-12592556	Pdzd2	68070	11.1	9.7	4.7	-1.01902	0.932943	-1.88688	7.79E-08
chrX:73793357-73824969:	Pdzd4	245469	16.2	14.8	18.4	1.01909	0.905632	1.41798	5.47E-05
chr19:59296084-59345780	Pdzd8	107368	44.0	45.8	53.5	1.17341	0.256203	1.5112	4.65E-05
chr7:120659296-12067034	Pdzd9	67983	2.8	0.3	0.6	-4.62729	0.004367	-2.84042	0.0188623
chr3:96830065-96870926:	Pdzk1	59020	3.8	0.3	0.5	-6.39345	0.000132	-4.02529	0.0008385
chr4:115088708-11509389	Pdzk1ip1	67182	19.8	23.0	8.4	1.30097	0.204647	-1.85438	8.15E-05
chr1:172196729-17220678	Pea15a	18611	187.8	159.6	88.1	-1.05754	0.606383	-1.70261	1.42E-14
chr3:87749097-87768953:	Pear1	73182	42.1	31.4	13.7	-1.20171	0.217152	-2.42157	1.21E-16
chr5:117282651-11728756	Pebp1	23980	234.7	211.1	278.6	1.0119	0.942524	1.48054	3.73E-06
chr14:69840407-70059918	Pebp4	73523	4.7	0.4	0.8	-6.74027	4.96E-05	-3.50568	0.0018041
chr4:130107556-13012813	Pef1	67898	83.9	79.3	48.5	1.05969	0.564641	-1.37889	1.31E-06
chr7:62461871-62464510:	Peg12	27412	1.9	1.6	2.9	-1.07522	0.831667	1.85412	0.0011049
chr15:72805600-72810324	Peg13	353342	51.2	47.7	29.0	1.04661	0.646026	-1.40844	4.78E-08
chr7:6705960-6730419:-	Peg3	18616	29.8	23.8	3.4	-1.11372	0.526597	-6.65693	8.93E-63
chr11:21091324-21150327	Peli1	67245	38.3	36.1	24.7	1.04852	0.686178	-1.24147	0.0036916
chr14:48120869-48260883	Peli2	93834	39.1	39.1	21.8	1.13018	0.412732	-1.42672	0.0007311
chr19:4931855-4943092:-	Peli3	240518	19.1	12.1	3.1	-1.40519	0.313126	-4.31862	1.32E-09
chr13:115088355-1150901	Pelo	105083	18.2	17.1	30.4	1.04663	0.74286	2.08088	9.03E-21
chr11:70392881-70410031	Pelp1	75273	26.4	25.9	36.3	1.10133	0.387258	1.71751	7.95E-13
chr11:59970614-60046489	Pemt	18618	5.2	5.5	11.1	1.18207	0.519716	2.584	8.14E-09
chr4:4133536-4138445:-	Penk	18619	101.0	76.0	15.1	-1.19379	0.410219	-5.09609	4.06E-28
chr7:34912407-35044708:	Pepd	18624	47.2	48.0	79.0	1.13782	0.210122	2.08174	1.99E-24
chr11:69098956-69109957	Per1	18626	29.7	26.2	10.5	-1.01738	0.959877	-2.19261	1.25E-05
chr4:151003655-15104466	Per3	18628	118.1	46.2	9.8	-2.22929	0.000513	-8.60205	1.21E-29
chr11:3963975-3980004:+	Pes1	64934	72.1	81.2	150.3	1.26748	0.043032	2.58289	6.73E-28
chr11:83294645-83298977	Pex12	103737	10.9	7.8	13.3	-1.25209	0.079216	1.51651	6.28E-06
chr4:148960535-14909981	Pex14	56273	33.7	30.3	41.7	1.00831	0.943265	1.54754	2.59E-14
chr1:172126755-17213649	Pex19	19298	78.9	67.4	53.8	-1.04646	0.600314	-1.16965	0.0063284
chr3:5560188-5576248:-	Pex2	19302	42.1	36.8	48.5	-1.02863	0.810421	1.43465	7.12E-08
chr10:13523842-13553142	Pex3	56535	36.2	33.2	35.9	1.02819	0.792355	1.24195	0.0004899
chr3:32949634-33143191:	Pex5l	58869	4.8	3.3	2.0	-1.27965	0.177093	-1.91342	2.39E-06
chr17:46711463-46725541	Pex6	224824	44.5	34.5	25.8	-1.15643	0.098568	-1.37774	1.18E-06
chr11:68985701-69008460	Pfas	237823	27.8	23.4	42.6	-1.06358	0.600439	1.91724	1.07E-18
chr18:36403679-36454495	Pfdn1	67199	74.9	69.0	83.0	1.02839	0.844823	1.38236	6.02E-05
chr1:171345699-17135817	Pfdn2	18637	47.0	48.4	68.3	1.15671	0.235035	1.80632	3.07E-12
chr2:170496428-17051907	Pfdn4	109054	25.2	34.8	53.3	1.55196	0.054507	2.558	4.15E-08
chr15:102326116-1023314	Pfdn5	56612	686.8	638.0	392.0	1.0359	0.730877	-1.40127	6.49E-08
chr17:33938909-33940343	Pfdn6	14976	88.5	93.6	136.5	1.18791	0.127222	1.91797	1.14E-15

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chrX:150589921-15064387	Pfkfb1	18639	4.6	2.5	1.8	-1.61622	0.147046	-1.97079	0.0073619
chr1:130689043-13072925	Pfkfb2	18640	25.4	17.4	13.9	-1.31434	0.102314	-1.45214	0.0034961
chr15:98092589-98132447	Pfkm	18642	44.5	28.1	9.5	-1.41419	0.00515	-3.69047	4.22E-39
chr11:70651847-70654650	Pfn1	18643	332.9	386.7	767.3	1.3036	0.030895	2.84484	5.37E-30
chr3:57841895-57847757:	Pfn2	18645	42.1	41.3	55.8	1.10099	0.42375	1.64884	7.68E-10
chr12:4769295-4778266:+	Pfn4	382562	4.2	0.6	0.8	-4.40295	0.000504	-3.33222	0.0007712
chr19:41911871-41918665	Pgam1	18648	32.4	37.3	57.3	1.29711	0.181283	2.16846	3.89E-08
chr11:5801637-5803796:-	Pgam2	56012	16.8	1.2	2.9	-8.085	2.92E-07	-3.69204	0.0002144
chr5:110259135-11026989	Pgam5	72542	42.7	50.6	79.1	1.33525	0.060866	2.28927	4.32E-13
chr1:54473000-54557684:	Pgap1	241062	10.2	8.3	4.1	-1.11276	0.668113	-1.94735	2.29E-05
chr7:102210335-10223856	Pgap2	233575	40.4	33.0	21.5	-1.09344	0.468199	-1.50058	1.53E-06
chr11:98388672-98400490	Pgap3	320655	10.8	9.8	14.8	1.01532	0.919073	1.71035	4.99E-13
chr13:21421275-21441053	Pgbd1	319207	2.7	2.0	0.8	-1.21941	0.567341	-2.4183	0.0001774
chr8:124369049-12443393	Pgbd5	209966	8.7	9.9	18.4	1.26566	0.274902	2.5639	4.02E-10
chr4:149149985-14916670	Pgd	110208	49.2	40.2	52.4	-1.08819	0.54657	1.32715	0.0024132
chr18:46239949-46280850	Pggt1b	225467	39.4	40.6	42.7	1.15713	0.238821	1.35007	0.0008863
chrX:106187100-10620369	Pgk1	18655	98.4	101.6	215.7	1.15588	0.277243	2.70685	3.62E-27
chr17:40207018-40208609	Pgk2	18663	17.1	0.8	2.3	-11.0001	1.65E-08	-4.49683	5.57E-05
chr8:71592184-71596267:	Pgls	66171	45.8	40.2	52.0	-1.02244	0.87282	1.41583	3.68E-06
chr7:18884690-18890438:	Pglyrp1	21946	8.1	7.1	18.0	-1.00745	0.980031	2.72802	3.96E-13
chr17:32412461-32424167	Pglyrp2	57757	1.5	2.1	2.6	1.48653	0.275672	2.01315	0.0080203
chr5:64092950-64128158:	Pgm1	66681	43.2	48.4	54.0	1.25122	0.018008	1.55406	1.41E-09
chr4:99929451-99987294:	Pgm2	72157	31.7	29.3	48.4	1.04176	0.844182	1.88897	4.36E-08
chr7:100227607-10027887	Pgm2l1	70974	21.6	15.5	4.7	-1.25904	0.277337	-3.51616	4.40E-17
chr9:86552476-86571842:	Pgm3	109785	14.1	13.9	21.7	1.10541	0.298403	1.92846	6.83E-24
chr19:24678261-24861842	Pgm5	226041	262.9	229.2	81.9	-1.03395	0.865776	-2.53401	8.44E-18
chr17:24470473-24471596	Pgp	67078	18.3	17.9	29.9	1.11282	0.744473	1.97802	0.0006158
chr7:68236608-68264233:	Pgpep1l	78444	10.3	7.3	1.8	-1.26457	0.405604	-4.1895	1.94E-11
chr9:8899833-8968611:+	Pgr	18667	84.2	189.0	388.3	2.45124	6.77E-05	5.31117	1.43E-18
chrX:36598225-36606079:	Pgrmc1	53328	292.8	249.6	130.2	-1.05292	0.701864	-1.79242	9.83E-13
chr11:117986857-1180240	Pgs1	74451	24.9	36.0	62.7	1.61382	0.001273	3.08176	7.62E-21
chr10:13207717-13474396	Phactr2	215789	37.3	28.2	8.7	-1.1849	0.146567	-3.39707	1.08E-46
chr11:95666957-95680773	Phb	18673	82.0	89.2	172.1	1.22139	0.102129	2.59721	4.56E-27
chr6:124712289-12471694	Phb2	12034	135.7	139.1	246.9	1.15289	0.188406	2.26252	1.48E-26
chr6:122317731-12234022	Phc1	13619	20.9	15.8	11.9	-1.18134	0.166611	-1.39591	0.000203
chr4:128654702-12875288	Phc2	54383	34.4	43.9	52.3	1.44158	0.122832	1.85601	0.0005421
chr3:30899295-30969415:	Phc3	241915	48.0	42.3	30.6	-1.01371	0.913234	-1.25068	0.0010985
chr17:14944995-14961260	Phf10	72057	66.2	76.6	98.3	1.30817	0.169035	1.82818	2.77E-05
chr14:59347407-59365490	Phf11d	219132	34.5	39.1	15.7	1.25596	0.247814	-1.73917	0.0001219
chr15:66577572-66645255	Phf20l1	239510	59.8	62.1	66.0	1.16404	0.011571	1.37875	6.50E-12
chr2:92184182-92364666:	Phf21a	192285	40.8	31.5	14.8	-1.16278	0.276253	-2.17732	1.67E-15
chr11:69995766-70000011	Phf23	78246	46.8	60.7	60.0	1.46036	0.092837	1.57763	0.0084194
chr15:81864516-81871892	Phf5a	68479	37.1	46.9	61.3	1.4232	0.012605	2.04364	7.39E-11
chrX:52912214-52956961:	Phf6	70998	24.7	26.7	31.5	1.21117	0.021529	1.58895	2.42E-13
chr14:31237696-31251218	Phf7	71838	41.3	6.9	9.2	-4.55308	2.59E-06	-3.17053	4.83E-05
chr3:98313171-98339969:	Phgdh	236539	34.6	25.8	80.7	-1.20664	0.466577	2.8054	2.29E-09
chr9:82866159-82975489:	Phip	83946	87.6	82.6	50.9	1.05353	0.449001	-1.37481	8.80E-12
chrX:102513975-10264424	Phka1	18679	21.2	18.6	12.4	-1.01616	0.89607	-1.36387	4.87E-06
chrX:160502166-16059887	Phka2	110094	33.1	26.0	9.5	-1.14202	0.394515	-2.75157	4.30E-21
chr8:85841002-86060642:	Phkb	102093	44.6	41.3	26.1	1.0344	0.65935	-1.3702	6.94E-11
chr5:129863435-12987908	Phkg1	18682	1.4	1.0	0.3	-1.17404	0.719033	-3.53321	2.89E-05
chr7:127573348-12758330	Phkg2	68961	63.2	43.9	24.6	-1.28788	0.030616	-2.03615	2.28E-15
chr10:111506286-1115086	Phlda1	21664	5.8	9.3	10.3	1.78368	0.002323	2.18396	4.15E-07
chr1:135766085-13576913	Phlda3	27280	36.3	33.7	96.1	1.04803	0.813364	3.25124	1.40E-26
chr9:44686308-44735198:	Phldb1	102693	69.2	76.2	26.0	1.25045	0.380823	-2.06435	5.11E-05
chr16:45746231-45844378	Phldb2	208177	52.9	35.5	17.8	-1.34423	0.210989	-2.31385	1.04E-06
chr1:106171869-10639424	Phlpp1	98432	24.1	19.0	7.0	-1.1347	0.357259	-2.69947	2.84E-25
chr7:141228788-14126275	Phrf1	101471	38.5	46.3	57.4	1.36077	0.09397	1.84384	8.99E-06

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr3:103968110-10400749	Phtf1	18685	36.8	31.5	23.5	-1.04894	0.673513	-1.24996	0.0020165
chr2:4918996-4938743:+	Phyh	16922	68.1	55.6	32.6	-1.10168	0.472463	-1.65921	3.51E-08
chr2:30266203-30282149:	Phyhd1	227696	23.5	18.4	7.9	-1.13972	0.397356	-2.34355	7.53E-15
chr10:70557686-70599291	Phyhipl	70911	2.7	1.5	9.2	-1.43235	0.50758	3.35696	0.0009136
chr17:29318882-29328902	Pi16	74116	23.1	17.2	10.5	-1.1894	0.50045	-1.72635	0.0020121
chr19:42090435-42122218	Pi4k2a	84095	26.5	27.7	30.5	1.17853	0.209549	1.43505	0.0001574
chr5:52741574-52769344:	Pi4k2b	67073	30.2	28.3	14.6	1.0507	0.518365	-1.65167	6.00E-22
chr3:94974731-95006937:	Pi4kb	107650	58.2	52.9	54.8	1.02016	0.803658	1.17723	0.0005333
chr6:124996720-12500309	Pianp	319352	6.1	5.3	1.8	-1.02702	0.937625	-2.63766	2.05E-07
chr9:62880077-62980879:	Pias1	56469	56.7	53.6	33.5	1.0638	0.547591	-1.3482	1.21E-05
chr18:77065208-77155708	Pias2	17344	49.3	40.7	32.0	-1.08517	0.218836	-1.23256	1.57E-05
chr7:90130232-90209447:	Picalm	233489	172.5	197.5	258.6	1.28523	0.010917	1.86284	4.66E-16
chr1:84036293-84284645:	Pid1	98496	72.3	60.4	19.3	-1.07572	0.624141	-2.95074	2.29E-30
chr7:141438515-14144335	Pidd1	57913	2.2	1.9	2.9	-1.02637	0.928974	1.65215	0.0007197
chr8:122481698-12255132	Piezo1	234839	30.8	28.5	36.2	1.04698	0.779313	1.46383	9.81E-05
chr18:63010213-63387183	Piezo2	667742	15.1	12.5	4.6	-1.07867	0.53387	-2.58619	2.78E-32
chr3:105996957-10601464	Pifo	1.01E+08	2.6	0.3	0.7	-5.16277	0.000591	-2.41619	0.0268881
chrX:164419787-16443391	Piga	18700	9.9	11.3	11.9	1.29378	0.068968	1.49884	0.0001549
chr17:86997259-87025401	Pigf	18701	24.5	22.8	26.5	1.03571	0.828841	1.34261	0.0014874
chr1:172376531-17238409	Pigm	67556	21.8	22.4	24.0	1.15843	0.16345	1.37321	4.62E-05
chr16:94358763-94371015	Pigp	56176	54.7	40.9	23.0	-1.20607	0.364956	-1.87645	1.57E-05
chr17:25926420-25941989	Pigq	14755	39.1	34.8	41.7	1.00102	0.994268	1.33285	7.26E-06
chr2:155278252-15535742	Pigu	228812	40.4	38.0	51.1	1.04917	0.632908	1.57658	1.05E-13
chr4:133661425-13367264	Pigv	230801	19.6	15.2	8.7	-1.16129	0.471975	-1.77955	5.67E-05
chr11:84876313-84880285	Pigw	70325	3.3	4.9	11.2	1.66594	0.015185	4.11046	3.08E-19
chr16:31933851-31946046	Pigz	239827	4.1	2.3	0.4	-1.59466	0.113404	-6.39857	4.61E-14
chr1:133046012-13310868	Pik3c2b	240752	11.7	8.0	6.5	-1.29445	0.047905	-1.42785	0.0003961
chr18:30272896-30348120	Pik3c3	225326	55.4	46.8	22.7	-1.06327	0.700726	-1.9341	1.44E-11
chr3:32436151-32468486:	Pik3ca	18706	64.8	61.3	31.8	1.05839	0.361728	-1.62828	5.18E-30
chr11:3330731-3342971:+	Pik3ip1	216505	141.4	68.9	3.3	-1.67941	0.352413	-13.6534	1.42E-11
chr8:70768181-70776712:	Pik3r2	18709	41.9	32.0	15.2	-1.17529	0.236449	-2.18711	1.32E-15
chr4:116221914-11630305	Pik3r3	18710	13.1	10.6	23.5	-1.09796	0.471474	2.21588	3.11E-21
chr9:105642995-10568765	Pik3r4	75669	40.6	31.4	19.2	-1.15613	0.094046	-1.6833	5.30E-16
chr11:68503019-68552695	Pik3r6	104709	4.5	3.6	2.3	-1.10717	0.696666	-1.54301	0.0095353
chr1:65186685-65278696:	Pikfyve	18711	26.5	25.5	24.8	1.08263	0.335691	1.16778	0.0092918
chr17:29491045-29495459	Pim1	18712	77.2	135.5	86.6	1.93784	0.000283	1.38895	0.0413882
chr15:88862194-88865726	Pim3	223775	34.4	78.6	40.2	2.47545	0.000465	1.42852	0.124004
chr9:20652130-20666584:	Pin1	23988	21.8	26.5	33.9	1.37268	0.044782	1.92712	3.58E-08
chrX:102119465-10212767	Pin4	69713	57.8	51.4	79.7	1.00267	0.990707	1.71032	4.73E-07
chr4:138313410-13832629	Pink1	68943	199.9	154.0	53.1	-1.16343	0.111341	-2.98987	1.11E-55
chr14:63860312-63919859	Pinx1	72400	13.9	20.0	44.4	1.61303	0.031828	3.81456	8.67E-16
chr2:18842256-18998121:	Pip4k2a	18718	37.8	36.3	45.9	1.07451	0.518628	1.51462	1.38E-08
chr11:97715157-97744704	Pip4k2b	108083	34.5	28.1	34.1	-1.10407	0.378897	1.23373	0.0086135
chr19:24294796-24555827	Pip5k1b	18719	6.6	6.4	11.9	1.09388	0.747493	2.21198	1.54E-06
chr10:81292963-81319974	Pip5k1c	18717	46.4	40.2	23.2	-1.03093	0.797936	-1.59271	2.16E-11
chr11:77880615-77893872	Pipox	19193	1.2	0.7	0.1	-1.50048	0.489388	-5.303	7.14E-05
chrX:164269431-16437301	Pir	69656	11.2	9.9	2.2	-1.01801	0.937383	-3.93276	5.50E-24
chr5:32736314-32785626:	Pisd	320951	51.2	58.0	74.6	1.27459	0.047122	1.81014	9.10E-11
chr17:3064318-3084183:-	Pisd-ps2	328734	5.4	4.5	2.8	-1.07345	0.785869	-1.52977	0.0091922
chrUn_JH584304:52674-59	Pisd-ps3	66776	277.3	229.3	110.4	-1.09743	0.751869	-1.96207	0.0001662
chr4:135975602-13598724	Pithd1	66193	38.1	35.1	42.6	1.03387	0.803163	1.39672	1.43E-05
chr11:75588108-75628778	Pitpna	18738	60.1	79.2	118.5	1.48326	0.107191	2.37503	2.15E-06
chr5:111330697-11138835	Pitpnb	56305	41.1	45.0	64.6	1.23386	0.151149	1.94637	4.43E-10
chr11:107207892-1074707	Pitpnc1	71795	20.1	16.2	10.0	-1.11295	0.226997	-1.61257	8.07E-14
chr5:128736246-12875547	Piwil1	57749	3.8	0.2	0.4	-8.50181	9.20E-06	-4.56205	0.0003147
chr17:64281006-64331883	Pja2	224938	138.9	121.0	145.2	-1.02594	0.816342	1.30427	3.41E-05
chr5:104459457-10450581	Pkd2	18764	121.7	105.0	71.1	-1.03988	0.695575	-1.36867	3.26E-07
chr18:34409423-34442788	Pkd2l2	53871	1.3	0.3	0.1	-3.08493	0.038184	-5.19666	0.0001079

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr17:83215283-83225069	Pkdcc	106522	53.6	42.0	81.5	-1.14251	0.269733	1.88701	3.67E-14
chr15:85814676-85821733	Pkdrej	18766	2.6	1.4	1.2	-1.67699	0.005301	-1.74126	0.0002334
chr1:20057779-20618057:	Pkhd1	241035	4.9	4.6	2.4	1.04447	0.880354	-1.57023	0.0059448
chr15:44457553-44597135	Pkhd1l1	192190	15.0	8.0	3.6	-1.6473	0.012772	-3.19675	1.12E-13
chr10:57631981-57741112	Pkib	18768	2.1	1.6	2.7	-1.19519	0.452869	1.55515	0.0061116
chr2:163658386-16372615	Pkig	18769	64.7	55.2	34.0	-1.0503	0.582169	-1.51815	8.74E-13
chr9:59656368-59679375:	Pkm	18746	334.4	307.9	446.4	1.02997	0.682338	1.6665	6.14E-32
chr3:142790902-14288200	Pkn2	109333	71.1	74.1	76.1	1.17274	0.138273	1.33435	0.0003394
chr17:31564773-31607693	Pknox1	18771	38.8	52.9	56.3	1.53832	0.033768	1.78699	0.0002237
chr9:36890979-37147322:	Pknox2	208076	28.9	30.1	46.7	1.17731	0.430572	1.99241	1.20E-06
chr16:16213345-16272712	Pkp2	67451	16.7	14.5	19.2	-1.03464	0.880762	1.4204	0.0056613
chr7:141078229-14109051	Pkp3	56460	7.9	7.5	11.1	1.06341	0.820785	1.71448	0.0006074
chr2:59160850-59355205:	Pkp4	227937	62.3	58.0	59.6	1.03927	0.713814	1.19561	0.0065405
chr16:38396117-38433145	Pla1a	85031	5.6	6.1	13.9	1.17904	0.667602	2.84756	1.11E-05
chr16:13715057-13730983	Pla2g10	26565	7.2	4.1	0.3	-1.48387	0.380823	-10.5138	1.63E-12
chr16:13729836-13739471	Pla2g10os	76684	8.9	3.6	0.3	-1.81494	0.340641	-6.40402	4.04E-05
chr3:129878606-12989582	Pla2g12a	66350	23.1	18.7	24.7	-1.10484	0.479698	1.33221	0.0026946
chr8:106150399-10616471	Pla2g15	192654	33.8	25.1	18.8	-1.2115	0.166091	-1.43804	0.0004429
chr19:7557459-7588545:+	Pla2g16	225845	29.7	22.8	10.6	-1.17371	0.47893	-2.19966	2.90E-07
chr1:149829622-14996128	Pla2g4a	18783	60.0	44.5	23.9	-1.20396	0.453169	-1.97206	6.79E-05
chr4:138799247-13886346	Pla2g5	18784	13.0	10.8	2.2	-1.07581	0.830091	-4.40182	1.61E-13
chr17:43568451-43612201	Pla2g7	27226	125.9	101.8	35.5	-1.10297	0.634269	-2.79253	2.12E-15
chr2:60417543-60553308:	Pla2r1	18779	53.0	41.0	9.8	-1.16494	0.413299	-4.21207	9.37E-30
chr4:94565139-94603247:	Plaa	18786	26.8	30.8	57.8	1.29533	0.11171	2.64936	2.71E-16
chr5:100553733-10057220	Plac8	231507	360.2	501.0	634.7	1.51298	0.112728	2.11991	0.0001333
chr4:3901158-3938405:-	Plag1	56711	9.6	7.3	1.3	-1.17903	0.509053	-5.33924	1.50E-22
chr10:13090788-13131695	Plagl1	22634	26.7	22.3	10.1	-1.07328	0.700297	-2.08361	6.67E-11
chr2:153227769-15324135	Plagl2	54711	9.0	11.1	11.0	1.37629	0.028875	1.51945	0.0002279
chr14:20836662-20843388	Plau	18792	21.0	39.1	52.0	2.04129	0.004791	2.90572	1.57E-07
chr7:24462500-24475873:	Plaur	18793	10.9	28.2	36.4	2.72837	0.000336	3.75167	1.83E-08
chr5:32232708-32364356:	Plb1	665270	4.2	2.5	1.1	-1.47822	0.189985	-2.74023	5.37E-06
chr5:120483893-12050362	Plbd2	71772	25.9	23.6	28.4	1.027	0.874229	1.37049	0.0007822
chr19:6953713-6969814:-	Plcb3	18797	42.1	37.0	38.7	-1.01712	0.825679	1.14961	0.0017714
chr2:135741830-13601306	Plcb4	18798	55.4	50.8	26.6	1.02538	0.887987	-1.65141	2.91E-07
chr9:119071528-11909350	Plcd1	18799	31.8	35.2	42.4	1.25216	0.244482	1.64731	0.0003752
chr11:103070296-1031016	Plcd3	72469	28.1	24.2	11.7	-1.03035	0.876369	-1.91291	1.05E-09
chr1:74542889-74565977:	Plcd4	18802	2.3	0.3	0.4	-5.10289	0.000207	-3.88414	0.0002767
chr19:38524197-38785100	Plce1	74055	39.5	33.9	13.1	-1.04119	0.805063	-2.38626	2.12E-20
chr2:160731310-16077576	Plcg1	18803	107.0	84.4	43.6	-1.13529	0.249805	-1.94675	1.38E-17
chr1:55405946-55754285:	Plcl1	227120	9.4	7.5	1.9	-1.11039	0.417434	-3.83799	4.22E-46
chr16:45959261-46010413	Plcxd2	433022	2.0	1.8	6.3	-1.01604	0.968506	3.70258	3.95E-10
chr15:4375491-4575579:+	Plcxd3	239318	1.3	0.9	0.2	-1.27292	0.68241	-3.48654	0.0012946
chr6:139989722-14004141	Plcz1	114875	11.3	4.6	2.7	-2.09259	0.014172	-3.09078	2.33E-06
chr3:27938680-28133362:	Pld1	18805	26.2	32.5	7.9	1.40367	0.113111	-2.57638	3.28E-09
chr11:70540272-70558110	Pld2	18806	18.6	16.9	8.7	1.02185	0.85829	-1.71054	2.80E-15
chr7:27532018-27553112:	Pld3	18807	60.8	54.4	32.2	1.00044	0.998624	-1.50793	4.66E-05
chr1:175962306-17627531	Pld5	319455	1.3	0.9	0.1	-1.23751	0.543035	-8.67572	1.60E-13
chr11:59783893-59787657	Pld6	194908	1.8	0.7	0.5	-2.13069	0.08209	-2.39454	0.0094973
chr15:76170974-76231378	Plec	18810	59.8	59.5	70.0	1.11899	0.398093	1.45508	5.42E-05
chr2:76675315-76697335:	Plekha3	83435	34.0	39.5	46.9	1.30469	0.012778	1.71362	8.05E-11
chr7:45526330-45554229:	Plekha4	69217	13.1	12.7	6.7	1.07914	0.672303	-1.53965	0.0001937
chr1:133246097-13330343	Plekha6	240753	39.2	22.7	7.0	-1.53902	0.051202	-4.25084	2.37E-18
chr6:54595111-54645822:	Plekha8	231999	15.0	25.5	31.4	1.88979	0.012538	2.49849	5.52E-06
chr7:100643896-10066239	Plekhb1	27276	4.9	3.5	1.7	-1.24994	0.303845	-2.30207	2.57E-07
chr1:34849959-34879585:	Plekhb2	226971	29.8	32.2	34.6	1.21426	0.144193	1.44363	0.0002137
chr10:3740377-3967302:+	Plekhg1	213783	23.4	18.7	5.4	-1.1273	0.583784	-3.36434	6.78E-18
chr4:152086863-15211540	Plekhg5	269608	15.6	11.7	7.4	-1.18847	0.112027	-1.68476	1.65E-10
chr17:84511895-84622142	Plekhh2	213556	48.6	33.9	20.7	-1.2906	0.111011	-1.85668	2.15E-07

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:101162680-1011713	Plekhh3	217198	29.3	25.8	53.0	-1.01317	0.932681	2.24457	4.72E-25
chr10:80796099-80798626	Plekhj1	78670	39.2	43.6	59.1	1.25336	0.102572	1.87551	5.35E-10
chr11:103365092-1034126	Plekhm1	353047	17.9	15.3	11.0	-1.0372	0.723507	-1.29707	4.65E-05
chr1:64789121-64956824:	Plekhm3	241075	16.4	13.7	5.9	-1.07488	0.597926	-2.224	1.19E-19
chr4:156221456-15622854	Plekhn1	231002	13.2	9.9	5.0	-1.18582	0.315405	-2.10093	1.60E-09
chr9:65552577-65580087:	Plekho2	102595	35.1	36.2	53.1	1.15282	0.212738	1.87818	7.00E-15
chr19:56461637-56486729	Plekhs1	226245	198.9	122.6	14.4	-1.44136	0.263061	-9.31289	2.55E-22
chr9:50494525-50505639:	Plet1	76509	76.4	207.4	305.2	2.47069	0.070164	3.55592	0.0008957
chr19:29348677-29361871	Plgrkt	67759	78.6	67.1	35.8	-1.05397	0.738099	-1.74857	6.77E-09
chr4:86656565-86670059:	Plin2	11520	130.1	107.8	138.1	-1.08728	0.562759	1.31786	0.004159
chr17:56278962-56290511	Plin3	66905	115.7	88.8	31.2	-1.17682	0.34105	-2.90912	2.75E-19
chr17:56100591-56109802	Plin4	57435	52.3	30.0	15.0	-1.50722	0.186179	-2.61302	2.53E-05
chr13:110395044-1104008	Plk2	20620	36.8	120.6	236.4	3.31	0.000411	6.45371	4.45E-11
chr4:117128655-11713395	Plk3	12795	3.7	11.1	16.6	3.08809	0.000313	4.83502	1.79E-09
chr8:94674895-94696242:	Pllp	67801	6.5	5.8	2.4	1.00085	0.998624	-2.11856	0.0001897
chr10:53337686-53345999	Pln	18821	53.1	29.6	14.7	-1.58887	0.151966	-2.67839	4.30E-05
chr4:147909753-14793677	Plod1	18822	48.9	99.8	152.9	2.18025	0.03139	3.41238	1.12E-05
chr9:92542223-92608427:	Plod2	26432	66.3	103.7	181.6	1.71372	0.002706	3.30953	1.04E-16
chr5:136987019-13699664	Plod3	26433	45.4	44.6	56.1	1.10519	0.362385	1.54172	1.10E-08
chrX:136822746-13683858	Plp1	18823	9.7	7.2	2.5	-1.20136	0.368466	-3.03459	2.79E-14
chr3:83055538-83072291:	Plrg1	53317	92.6	109.8	122.2	1.33522	0.056133	1.63692	1.79E-05
chrX:75785654-75875170:	Pls3	102866	175.8	143.7	99.7	-1.10123	0.444011	-1.40839	8.28E-05
chr9:92275602-92297752:	Plscr2	18828	11.0	10.0	3.7	1.00022	0.99998	-2.32134	9.93E-08
chr9:92457378-92492516:	Plscr4	235527	53.2	42.8	20.4	-1.11448	0.377457	-2.07416	8.72E-18
chr2:164839518-16485770	Pltp	18830	155.4	115.8	58.3	-1.20017	0.14637	-2.11387	3.90E-16
chr8:71497753-71511769:	Plvap	84094	10.3	9.4	16.2	1.00522	0.984129	1.91827	8.66E-07
chr11:97923237-97986446	Plxdc1	72324	7.0	4.7	2.7	-1.32036	0.150157	-2.01157	1.73E-06
chr2:16356304-16755839:	Plxdc2	67448	57.7	48.1	9.6	-1.07767	0.479714	-4.76478	1.72E-106
chr1:194619829-19481686	Plxna2	18845	26.3	19.6	14.9	-1.19736	0.257133	-1.40051	0.0038103
chr6:32144557-32588192:	Plxna4	243743	12.2	12.0	14.2	1.10371	0.511872	1.45283	0.0002275
chr9:109095436-10911991	Plxnb1	235611	30.1	19.6	7.8	-1.37313	0.044814	-3.00276	2.00E-20
chr15:89155546-89180788	Plxnb2	140570	107.1	81.6	50.5	-1.17261	0.00085	-1.69307	1.87E-41
chr1:131797395-13181811	Pm20d1	212933	1.4	1.1	0.6	-1.15485	0.667434	-1.85511	0.0055647
chr4:33170406-33189737:	Pm20d2	242377	3.0	2.6	4.9	-1.03244	0.902942	1.97106	1.05E-06
chr8:109494027-10954264	Pmfbp1	56523	8.0	1.2	0.7	-4.55577	0.000645	-5.89374	2.12E-06
chr7:30670722-30671605:	Pmis2	74927	1.7	0.2	0.1	-2.76516	0.08935	-3.27586	0.009978
chr9:58217180-58249786:	Pml	18854	21.4	17.8	13.1	-1.075	0.579603	-1.30466	0.0021871
chr15:81951106-81960930	Pmm1	29858	78.3	59.4	44.7	-1.18035	0.023369	-1.39981	2.82E-09
chr16:8637707-8657524:+	Pmm2	54128	43.7	40.9	59.3	1.04872	0.669799	1.69202	4.87E-15
chr11:63128982-63159547	Pmp22	18858	134.3	99.4	39.6	-1.22254	0.419113	-2.62072	1.81E-08
chr2:26389348-26397121:	Pmpca	66865	61.7	69.4	97.7	1.27082	0.143085	1.95708	2.26E-08
chr5:21737160-21757152:	Pmpcb	73078	95.8	100.1	145.7	1.1784	0.272187	1.88568	1.80E-09
chr1:53189189-53296996:	Pms1	227099	13.2	10.8	7.1	-1.09559	0.577976	-1.47048	0.0004054
chr3:89459118-89469009:	Pmvk	68603	28.6	24.1	35.4	-1.06515	0.788718	1.53788	0.0021896
chrX:73655992-73660070:	Pnck	93843	52.9	41.2	16.3	-1.15289	0.45615	-2.54592	7.07E-13
chr4:21847583-21876475:	Pnisr	66625	232.9	188.8	120.1	-1.10175	0.283036	-1.54616	6.84E-12
chr1:74285034-74353692:	Pnkd	56695	15.1	12.6	7.3	-1.07162	0.567487	-1.65314	3.61E-10
chr7:44857146-44862929:	Pnkp	59047	28.3	26.1	40.2	1.03258	0.750702	1.7699	1.96E-23
chr7:16944682-16948828:	Pnmal2	434128	6.1	3.6	1.9	-1.49014	0.106587	-2.44202	1.82E-06
chr12:59066919-59074017	Pnn	18949	105.2	106.3	129.0	1.14284	0.437053	1.52289	0.0004198
chr11:17203200-17211589	Pno1	66249	23.9	42.7	142.7	1.97553	0.005033	6.79512	9.94E-24
chr14:50944303-50953412	Pnp	18950	51.5	103.6	144.9	2.17583	0.014228	3.18089	3.60E-06
chr7:141455188-14146074	Pnpla2	66853	49.0	44.2	20.4	1.01984	0.959587	-1.85701	0.0024388
chr15:84167816-84189521	Pnpla3	116939	6.8	4.9	0.8	-1.15643	0.851057	-3.26542	0.0083069
chr8:3515384-3544267:+	Pnpla6	50767	34.5	27.6	15.3	-1.12078	0.382333	-1.78439	1.63E-10
chr2:24976033-25054072:	Pnpla7	241274	43.2	29.4	7.7	-1.32284	0.085107	-4.37369	2.27E-34
chr12:44269154-44313435	Pnpla8	67452	81.1	75.5	40.0	1.03796	0.633466	-1.62043	8.60E-23
chr11:96937816-96944019	Pnpo	103711	20.3	16.2	27.2	-1.12466	0.314302	1.6584	1.33E-10

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:29130751-29161828	Pnpt1	71701	49.5	51.8	60.6	1.16421	0.123805	1.52326	6.69E-09
chr4:33245423-33248787:	Pnrc1	108767	186.9	159.8	64.5	-1.05293	0.744504	-2.29262	1.51E-18
chr10:99107171-99197988	Poc1b	382406	20.1	15.1	12.4	-1.19217	0.075315	-1.28919	0.0007622
chr4:108014793-10803209	Podn	242608	13.5	6.7	3.3	-1.79039	0.000113	-3.15669	9.74E-19
chr8:84125989-84132517:	Podnl1	244550	3.3	6.1	11.3	1.78491	0.217874	3.40416	0.0003635
chr6:31519493-31563937:	Podxl	27205	43.7	33.0	80.3	-1.17944	0.00649	2.29242	2.14E-73
chr6:88842558-88874044:	Podxl2	319655	35.0	31.6	9.9	1.01025	0.958004	-2.77359	9.78E-24
chr10:77259300-77269586	Pofut2	80294	55.2	62.2	78.4	1.26917	0.068267	1.76324	5.75E-09
chr1:166393612-16640982	Pogk	71592	35.7	35.7	50.2	1.12457	0.142134	1.75504	1.29E-22
chr19:5940543-5964206:-	Pola2	18969	22.2	19.4	12.1	-1.02646	0.886083	-1.45901	0.0002078
chr8:22628119-22653437:	Polb	18970	52.4	70.2	77.3	1.51026	0.024378	1.81957	2.58E-05
chr7:44532744-44548815:	Pold1	18971	23.9	20.2	13.0	-1.06406	0.710888	-1.45858	0.0002976
chr11:5872180-5878256:-	Pold2	18972	30.5	32.5	49.5	1.19661	0.139674	2.0234	4.85E-16
chr19:4231899-4233634:+	Pold4	69745	49.9	34.1	21.5	-1.3177	0.142826	-1.82961	1.81E-05
chr11:78512296-78522736	Poldip2	67811	76.3	67.5	95.8	-1.01043	0.917543	1.56846	1.81E-18
chr15:83125978-83149336	Poldip3	73826	95.5	105.4	110.5	1.24681	0.190779	1.43815	0.0038476
chr4:62523801-62525014:	Pole3	59001	77.1	69.1	86.3	1.00641	0.968464	1.39583	9.00E-05
chr6:82646712-82652865:	Pole4	66979	40.1	55.9	93.8	1.56516	1.49E-05	2.89618	1.23E-34
chr11:106768204-1067795	Polg2	50776	23.7	16.0	10.3	-1.32334	0.192366	-1.7978	0.0002334
chr17:46171993-46202625	Polh	80905	25.1	28.5	35.4	1.27657	0.075315	1.75179	3.91E-08
chr18:70508680-70530321	Poli	26447	17.4	10.5	4.9	-1.48182	0.103382	-2.70422	3.78E-08
chr19:45552276-45560543	Poll	56626	17.4	12.6	8.7	-1.24283	0.359523	-1.57424	0.0079661
chr11:5827860-5838016:-	Polm	54125	13.4	9.7	7.1	-1.22369	0.105229	-1.50519	1.43E-05
chr5:34007179-34169526:	Poln	272158	1.3	0.5	0.3	-2.15974	0.028878	-2.78976	0.0002435
chr16:37011786-37095417	Polq	77782	4.4	3.8	2.0	-1.03915	0.865776	-1.69475	4.68E-05
chr6:71909053-71979360:	Polr1a	20019	30.3	33.2	73.6	1.23375	0.07849	3.00539	6.72E-37
chr2:129100996-12912659	Polr1b	20017	25.4	31.2	58.1	1.38713	0.017326	2.82917	2.66E-23
chr17:46243920-46248045	Polr1c	20016	72.4	88.2	91.6	1.37071	0.030119	1.57158	5.88E-05
chr5:147077346-14711136	Polr1d	20018	68.9	87.2	113.1	1.42363	0.032835	2.02207	2.32E-08
chr4:45018609-45034279:	Polr1e	64424	7.1	10.0	30.2	1.58415	0.002263	5.16945	3.10E-44
chr5:77310484-77349328:	Polr2b	231329	89.2	96.7	108.4	1.22008	0.097555	1.51381	3.80E-06
chr8:94857450-94864240:	Polr2c	20021	63.4	74.1	107.5	1.31785	0.065448	2.09766	2.69E-11
chr18:31789159-31796701	Polr2d	69241	40.9	49.1	66.4	1.35107	0.147744	1.98553	7.98E-06
chr10:80035953-80039659	Polr2e	66420	103.9	111.0	125.3	1.20651	0.271179	1.49708	0.0010883
chr15:79141367-79151767	Polr2f	69833	121.6	136.4	164.0	1.26147	0.167722	1.67059	3.43E-05
chr19:8793129-8798557:-	Polr2g	67710	90.6	88.4	115.4	1.0953	0.387373	1.58574	1.02E-10
chr16:20717826-20722265	Polr2h	245841	58.2	73.4	146.7	1.41265	0.030084	3.08355	2.62E-21
chr7:30232074-30233387:	Polr2i	69920	61.3	64.3	78.4	1.17812	0.176415	1.59269	9.17E-08
chr5:136116691-13612294	Polr2j	20022	98.2	112.8	111.2	1.28668	0.017512	1.41169	3.23E-05
chr15:36174010-36177012	Polr2k	17749	51.3	60.5	66.2	1.3272	0.090007	1.60087	0.0001787
chr7:141471860-14147515	Polr2l	66491	16.1	23.6	54.4	1.63864	0.014203	4.04574	1.03E-19
chr9:71478437-71485983:	Polr2m	28015	121.7	136.3	206.9	1.2594	0.058884	2.10839	1.64E-16
chr14:24448694-24487046	Polr3a	218832	33.5	31.1	40.5	1.04735	0.684522	1.51112	2.68E-09
chr10:84622437-84727178	Polr3b	70428	28.8	26.2	34.8	1.01944	0.874296	1.51035	3.95E-10
chr14:70438748-70443471	Polr3d	67065	27.4	55.8	86.5	2.22985	0.00398	3.62674	9.02E-09
chr7:120917744-12094743	Polr3e	26939	27.2	32.3	62.2	1.33677	0.049208	2.81058	3.24E-21
chr2:144527745-14454177	Polr3f	70408	35.1	36.8	41.0	1.18032	0.214096	1.45342	0.0001222
chr13:81673837-81711013	Polr3g	67486	5.8	5.0	8.1	-1.04553	0.864121	1.72451	0.0001386
chr3:96577872-96594181:	Polr3gl	69870	63.6	48.2	16.3	-1.18861	0.303365	-3.0653	6.37E-21
chr15:81915030-81926213	Polr3h	78929	20.2	17.4	30.2	-1.04218	0.726894	1.86381	3.85E-20
chr2:181864360-18187082	Polr3k	67005	23.0	22.1	25.8	1.06529	0.627734	1.39412	6.03E-05
chr10:79736125-79746581	Polrmt	216151	18.4	19.6	22.9	1.19776	0.211944	1.54626	3.24E-05
chr5:135376140-13539454	Pom121	107939	12.9	15.5	16.9	1.36012	0.167971	1.614	0.0042543
chr11:14599240-14600316	Pom121l12	432536	1.1	0.0	0.2	-6.37066	0.000792	-2.6547	0.0427361
chr13:21981181-21988734	Pom121l2	195236	1.8	0.2	0.4	-6.06989	3.05E-05	-3.1495	0.0020264
chr12:3954945-3960643:+	Pomc	18976	1.0	1.1	1.8	1.23181	0.626732	2.18185	0.0031403
chr4:116150518-11615984	Pomgnt1	68273	57.9	58.4	98.1	1.13505	0.210425	2.11022	7.63E-26
chr8:25980604-25994121:	Pomk	74653	14.0	10.9	9.1	-1.14934	0.156341	-1.23133	0.0050069

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr5:147860628-14787577	Pomp	66537	141.2	149.3	221.5	1.18286	0.102521	1.94857	3.36E-19
chr12:87106866-87147902	Pomt2	217734	28.0	29.3	36.1	1.17867	0.188233	1.60811	1.54E-07
chr6:5264624-5298373:-	Pon2	330260	58.1	50.5	27.7	-1.0366	0.821165	-1.67423	2.44E-08
chr6:5220852-5256233:-	Pon3	269823	22.7	20.2	12.9	-1.00362	0.987299	-1.40027	0.0049366
chr15:34495311-34530653	Pop1	67724	10.5	14.1	35.2	1.50468	0.0001	4.135	4.81E-63
chr5:115235851-11524097	Pop5	117109	31.4	34.4	40.1	1.22688	0.127879	1.58564	2.91E-06
chr5:137501439-13750242	Pop7	74097	16.7	20.4	47.8	1.36236	0.147879	3.44234	3.79E-16
chr16:38362173-38378216	Popdc2	64082	18.3	21.0	28.5	1.29192	0.264803	1.90621	9.14E-05
chr5:135689214-13573532	Por	18984	87.6	63.1	49.9	-1.24079	0.024985	-1.40062	6.56E-06
chrX:8193850-8206525:-	Porcn	53627	33.5	23.8	12.3	-1.25161	0.033891	-2.16018	7.13E-21
chr6:25743735-25809226:	Pot1a	101185	36.4	27.4	9.5	-1.20143	0.398425	-2.97923	3.65E-13
chr17:55652025-55712628	Pot1b	72836	30.5	23.6	8.4	-1.16041	0.263811	-2.87902	1.89E-28
chr8:27447670-27495172:	Poteg	70952	2.1	0.2	0.2	-4.75921	0.006219	-3.66342	0.0055433
chr1:165865154-16600263	Pou2f1	18986	20.6	15.0	9.9	-1.23605	0.195082	-1.65009	2.98E-05
chr15:100575318-1005863	Pou6f1	19009	27.6	20.3	12.3	-1.21522	0.187931	-1.77829	1.05E-07
chr10:61648621-61674165	Ppa1	67895	24.3	30.9	148.9	1.42579	0.007492	7.48904	4.39E-91
chr3:133310110-13337823	Ppa2	74776	42.9	35.5	25.5	-1.08808	0.565807	-1.33952	0.0029743
chr9:20888175-20892179:	Ppan	235036	49.4	86.2	180.1	1.9355	0.01217	4.21333	2.28E-12
chr13:112800777-1128678	Ppap2a	19012	56.3	59.5	74.5	1.1813	0.112197	1.64523	9.03E-11
chr4:105157347-10523276	Ppap2b	67916	152.3	158.2	288.5	1.1482	0.391005	2.3377	1.15E-14
chr10:79526424-79533787	Ppap2c	50784	22.1	21.1	40.0	1.07572	0.808407	2.19098	6.58E-06
chr8:25720048-25724887:	Ppapdc1b	71910	40.0	38.5	73.0	1.07667	0.369686	2.27401	2.65E-54
chr15:85735564-85806851	Ppara	19013	3.5	4.1	1.2	1.3091	0.264472	-2.29119	3.07E-06
chr5:51454249-51553921:	Ppargc1a	19017	13.2	6.9	2.0	-1.67583	0.165763	-4.52037	3.58E-08
chr5:76913249-76951578:	Ppat	231327	20.2	20.5	35.2	1.1366	0.345373	2.16102	8.68E-17
chr9:57412660-57440114:	Ppcdc	66812	23.9	18.3	8.6	-1.17825	0.318093	-2.19645	1.74E-11
chr4:119418533-11942242	Ppcs	106564	12.6	12.2	14.9	1.08109	0.636005	1.46871	0.0001805
chr7:144476755-14455372	Ppfia1	233977	44.1	50.2	58.0	1.29156	0.189488	1.62965	0.000715
chr6:146888494-14703202	Ppfibp1	67533	103.4	128.3	236.6	1.39674	0.18499	2.73649	3.85E-08
chr7:107595051-10774858	Ppfibp2	19024	34.3	18.8	5.0	-1.62526	0.044814	-5.10097	4.19E-19
chr15:93398350-93491912	Pphln1	223828	20.9	21.5	35.6	1.15812	0.176553	2.11471	1.72E-22
chr11:6415870-6419810:+	Ppia	268373	####	1166.3	1934.6	1.13848	0.182311	2.09767	1.08E-26
chr9:66060169-66066629:	Ppib	19035	479.0	477.2	521.2	1.11171	0.263579	1.35635	6.98E-06
chr18:53406341-53418007	Ppic	19038	127.4	102.6	64.6	-1.1203	0.435227	-1.57136	7.02E-06
chr3:79591389-79603650:	Ppid	67738	111.2	140.4	220.4	1.42181	0.059049	2.42427	2.05E-10
chr4:123127125-12313994	Ppie	56031	69.4	72.1	94.6	1.15991	0.127173	1.6943	5.94E-14
chr14:25694170-25700466	Ppif	105675	23.1	32.1	38.7	1.56096	0.070285	2.03277	0.0001444
chr2:69723088-69754059:	Ppig	228005	42.8	48.3	52.6	1.2723	0.113729	1.52693	0.00023
chr4:119300010-11932052	Ppih	66101	18.9	19.0	20.6	1.13294	0.313278	1.3644	0.0004109
chr17:29250835-29263971	Ppil1	68816	35.0	33.9	49.6	1.07861	0.601066	1.76093	4.36E-10
chr16:17086556-17111252	Ppil2	66053	112.9	101.7	73.0	1.00887	0.902659	-1.23553	9.36E-08
chr1:58430993-58445486:	Ppil3	70225	27.3	24.5	31.5	-1.00044	0.998519	1.43372	2.21E-05
chr10:7792894-7822563:+	Ppil4	67418	69.7	80.6	79.6	1.3055	0.113017	1.41714	0.0067874
chr10:41490439-41514288	Ppil6	73075	8.3	6.0	1.2	-1.21941	0.458405	-4.84899	4.00E-14
chr1:97706043-97770092:	Ppip5k2	227399	38.6	31.8	41.7	-1.0886	0.406331	1.34838	2.38E-05
chr16:5086291-5132481:-	Ppl	19041	18.0	13.7	6.3	-1.16229	0.610777	-2.20674	3.78E-05
chr17:84956741-85023992	Ppm1b	19043	50.5	46.1	32.8	1.02274	0.754594	-1.22884	2.18E-06
chr11:85311254-85347071	Ppm1d	53892	37.6	30.9	16.2	-1.0883	0.506114	-1.84439	6.96E-13
chr11:87226906-87358994	Ppm1e	320472	14.4	9.5	3.9	-1.35737	0.112013	-2.89214	1.18E-13
chr16:16896469-16927375	Ppm1f	68606	41.4	42.1	50.3	1.13884	0.033843	1.5178	5.47E-20
chr5:31202668-31220545:	Ppm1g	14208	73.5	83.8	176.4	1.29087	0.25417	2.9071	1.58E-11
chr6:57506502-57535426:	Ppm1k	243382	30.6	21.6	6.5	-1.27234	0.454839	-3.49085	1.18E-08
chr3:69316918-69555396:	Ppm1l	242083	47.9	41.1	16.5	-1.03345	0.853425	-2.29283	5.86E-17
chr9:106194953-10619923	Ppm1m	67905	45.3	37.8	24.2	-1.07194	0.576403	-1.49201	8.99E-07
chr7:100326737-10037189	Ppme1	72590	38.6	45.6	56.5	1.32983	0.048877	1.81187	5.06E-08
chr1:171276992-17128118	Ppox	19044	79.0	64.2	35.6	-1.09903	0.415064	-1.76473	1.20E-12
chr19:4192174-4195419:+	Ppp1ca	19045	276.6	276.0	409.4	1.11938	0.283036	1.84217	6.86E-17
chr5:32458970-32493712:	Ppp1cb	19046	274.9	251.1	276.4	1.01979	0.795125	1.25562	2.60E-07

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr5:122158279-12217526	Ppp1cc	19047	121.5	140.8	177.1	1.3068	0.081503	1.80447	2.78E-07
chr17:35917196-35932283	Ppp1r10	52040	50.4	49.8	72.3	1.11381	0.366078	1.78865	1.15E-12
chr17:36948355-36951792	Ppp1r11	76497	62.0	65.0	78.8	1.18327	0.25874	1.58132	1.75E-05
chr1:134765943-13495594	Ppp1r12b	329251	86.1	60.3	43.4	-1.27762	0.218046	-1.56627	0.0022493
chr7:4481521-4501680:-	Ppp1r12c	232807	116.2	126.6	162.3	1.22396	0.079093	1.73435	1.11E-10
chr19:6975048-6977324:+	Ppp1r14b	18938	53.3	60.0	185.7	1.26117	0.049812	4.29853	1.72E-66
chr7:45522917-45526268:	Ppp1r15a	17872	31.4	76.1	42.3	2.61804	0.000359	1.62989	0.0399472
chr1:133131166-13313980	Ppp1r15b	108954	45.6	66.5	98.0	1.6375	0.039144	2.58258	1.85E-07
chr17:35865595-35875596	Ppp1r18	76448	24.3	28.0	44.6	1.27736	0.127897	2.25309	4.46E-12
chr15:103530279-1035379	Ppp1r1a	58200	6.1	3.1	0.9	-1.67108	0.196518	-4.21203	1.79E-06
chr16:31251541-31275277	Ppp1r2	66849	77.3	83.7	91.2	1.21436	0.060983	1.47182	7.43E-07
chr17:88530124-88588367	Ppp1r21	73825	41.7	36.8	27.9	-1.0176	0.874528	-1.19648	0.0042392
chr2:28447941-28455508:	Ppp1r26	241289	12.2	9.7	6.8	-1.12976	0.413299	-1.41913	0.0008838
chr19:10474257-10482897	Ppp1r32	67752	5.1	0.8	1.9	-4.18224	0.000479	-1.95038	0.0567969
chr5:137778918-13778010	Ppp1r35	69871	14.3	15.5	16.0	1.20935	0.224199	1.3921	0.0036278
chr12:76417599-76439491	Ppp1r36	210762	8.3	3.3	1.3	-2.136	0.008402	-4.34243	6.31E-10
chr7:19530967-19562398:	Ppp1r37	232947	52.7	58.7	57.9	1.25659	0.098248	1.3695	0.0028017
chr8:35375741-35388137:	Ppp1r3b	244416	6.4	5.4	2.9	-1.07009	0.722119	-1.77603	1.49E-06
chr1:9968622-10009136:-	Ppp1r42	69312	2.3	0.3	0.3	-4.19833	0.002562	-4.60459	0.000103
chr1:93343645-93367618:	Ppp1r7	66385	27.8	25.8	28.2	1.04571	0.713651	1.26593	0.001733
chr4:132826924-13284316	Ppp1r8	100336	46.8	55.4	69.2	1.33425	0.08384	1.82993	1.27E-06
chr6:4903320-5165661:+	Ppp1r9a	243725	45.3	34.3	13.7	-1.17375	0.202006	-2.6093	1.13E-26
chr11:94991212-95006898	Ppp1r9b	217124	58.4	53.0	65.5	1.01405	0.904276	1.39843	9.55E-08
chr11:52098824-52122749	Ppp2ca	19052	225.3	280.7	389.2	1.4035	0.064389	2.11948	4.66E-08
chr8:33599621-33619804:	Ppp2cb	19053	83.3	101.2	124.2	1.36866	0.077976	1.83633	5.66E-06
chr17:20945454-20965905	Ppp2r1a	51792	202.5	215.2	298.9	1.19485	0.078778	1.83872	3.16E-16
chr14:67014056-67072471	Ppp2r2a	71978	22.8	27.2	28.4	1.34164	0.040749	1.54316	8.29E-05
chr5:36868570-36955078:	Ppp2r2c	269643	2.6	15.2	34.1	3.21574	0.042983	5.90662	6.03E-05
chr9:101104989-10125183	Ppp2r3a	235542	45.2	37.7	22.8	-1.07688	0.577976	-1.57688	1.36E-07
chr12:55280814-55303000	Ppp2r3c	59032	24.2	25.6	26.1	1.18968	0.083234	1.3477	7.11E-05
chr2:30416050-30447807:	Ppp2r4	110854	94.2	87.9	123.6	1.04603	0.443797	1.64024	4.87E-38
chr1:191351981-19139704	Ppp2r5a	226849	152.5	155.8	89.5	1.15598	0.36246	-1.35627	0.0077402
chr17:46682991-46705002	Ppp2r5d	21770	53.3	51.6	51.0	1.08764	0.322721	1.19859	0.0030062
chr14:20499314-20546573	Ppp3cb	19056	64.8	65.0	89.8	1.12283	0.040261	1.72874	4.59E-40
chr14:70217898-70289449	Ppp3cc	19057	36.5	31.9	22.9	-1.02522	0.869917	-1.27388	0.0054876
chr11:17159298-17200380	Ppp3r1	19058	69.7	71.0	85.9	1.14439	0.119066	1.5368	1.13E-11
chr4:49678747-49681983:	Ppp3r2	19059	4.8	0.1	0.5	-11.6517	6.61E-07	-4.56867	0.0004531
chr7:126785868-12679247	Ppp4c	56420	97.2	123.2	190.2	1.42853	0.044782	2.40222	5.15E-11
chr17:65783355-65841926	Ppp4r1	70351	41.2	52.7	71.1	1.44481	0.072382	2.11634	1.11E-06
chr2:173579320-17365953	Ppp4r1l-ps	1E+08	16.3	12.2	4.7	-1.19068	0.232627	-2.70283	9.74E-21
chr6:100833638-10086871	Ppp4r2	232314	68.7	80.2	92.4	1.31426	0.077005	1.66574	1.18E-05
chr12:103532565-1036138	Ppp4r4	74521	6.2	5.1	2.0	-1.0907	0.727681	-2.47127	7.43E-09
chr7:17004641-17027914:	Ppp5c	19060	42.1	47.1	61.0	1.26055	0.086147	1.79704	4.36E-09
chr2:39196798-39226338:	Ppp6c	67857	85.8	102.0	127.7	1.34024	0.061613	1.84193	2.11E-07
chr19:3454929-3575749:-	Ppp6r3	52036	115.7	124.9	118.6	1.21528	0.043231	1.28044	0.0009121
chr19:46056539-46072909	Pprc1	226169	13.3	34.6	64.5	2.78474	0.000136	5.40478	8.43E-14
chr4:122836227-12285917	Ppt1	19063	118.8	91.7	46.4	-1.16306	0.13892	-2.04258	1.02E-21
chr5:122284398-12232428	Pptc7	320717	22.7	32.7	31.6	1.6166	0.053411	1.7004	0.00598
chrX:7894519-7899269:-	Pqbp1	54633	57.7	60.0	81.0	1.16755	0.137652	1.74866	1.01E-13
chr18:80255245-80292724	Pqlc1	66943	11.7	13.5	13.6	1.29366	0.073416	1.44306	0.0008046
chr17:33638056-33645706	Pram1	378460	11.4	7.7	4.9	-1.31847	0.300191	-1.8063	0.0023551
chr7:92875253-92934581:	Prcp	72461	43.5	38.3	22.6	-1.02261	0.896782	-1.53638	6.37E-06
chr9:31315107-31378543:	Prdm10	382066	12.5	10.5	7.3	-1.06574	0.723181	-1.34769	0.0084388
chr16:97791467-97851227	Prdm15	114604	17.6	16.7	18.3	1.06761	0.543097	1.29772	0.0002481
chr4:154316125-15463687	Prdm16	70673	4.0	2.9	1.6	-1.24041	0.161748	-2.01484	1.17E-09
chr10:85891968-85916986	Prdm4	72843	28.7	33.3	33.0	1.30813	0.04864	1.43346	0.0005934
chr17:15543079-15563323	Prdm9	213389	3.0	1.9	1.2	-1.39299	0.068197	-2.05358	4.64E-07
chr4:116685599-11670000	Prdx1	18477	408.8	404.6	663.2	1.10753	0.587407	1.99442	1.19E-08

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr19:60864066-60874538	Prdx3	11757	91.8	84.0	128.7	1.02133	0.846424	1.74655	6.35E-21
chrX:155323920-15533845	Prdx4	53381	152.3	142.7	99.6	1.04553	0.652419	-1.22203	0.001638
chr19:6906819-6909645:-	Prdx5	54683	174.8	155.0	202.2	-1.00774	0.95781	1.44054	8.65E-07
chr2:80292470-80295358:	Prdx6b	320769	4.0	0.2	0.7	-7.9762	1.92E-05	-3.29019	0.0050742
chr5:30951667-30960327:	Preb	50907	41.3	40.5	65.7	1.10262	0.404391	1.97939	7.06E-18
chr13:55322055-55325272	Prelid1	66494	137.3	147.3	195.0	1.20256	0.055117	1.76791	1.07E-15
chr18:41875696-41951194	Prelid2	77619	23.0	16.1	5.6	-1.28192	0.330088	-3.106	1.30E-09
chr1:133910304-13392140	Prelp	116847	93.8	68.3	11.7	-1.23229	0.189549	-6.21058	3.93E-57
chr10:45067214-45158995	Prep	19072	31.0	32.6	66.2	1.18006	0.116336	2.65096	1.68E-38
chr1:10993465-11303682:	Prex2	109294	55.5	44.9	8.7	-1.10225	0.338999	-5.06622	9.20E-117
chrX:7657379-7668186:+	Prickle3	54630	8.5	6.3	4.1	-1.20759	0.238773	-1.62511	4.06E-05
chr17:47688474-47694736	Prickle4	381104	5.7	5.2	1.8	1.01455	0.967187	-2.4262	8.16E-06
chr8:46575594-46617200:	Primpol	408022	17.6	11.6	5.6	-1.36455	0.097706	-2.45658	1.56E-10
chr5:116013590-11602442	Prkab1	19079	45.0	45.6	56.1	1.14902	0.524379	1.54513	0.0032674
chr3:146729579-14681294	Prkacb	18749	76.2	73.0	70.4	1.07096	0.331735	1.15347	0.0050416
chr15:98812797-98831508	Prkag1	19082	91.7	90.7	93.1	1.11234	0.311307	1.26676	0.0017944
chr11:109650949-1096696	Prkar1a	19084	178.1	181.0	216.0	1.14129	0.09518	1.51274	1.21E-12
chr9:108692143-10874951	Prkar2a	19087	40.6	42.0	96.9	1.16563	0.160267	2.96033	9.01E-45
chr12:31958479-32061279	Prkar2b	19088	16.6	9.9	2.8	-1.46673	0.240526	-4.23646	8.87E-10
chr7:122289125-12263440	Prkcb	18751	16.7	14.0	63.2	-1.05239	0.813016	4.60489	1.56E-36
chr17:86167785-86657919	Prkce	18754	18.2	21.4	34.8	1.32958	0.122853	2.35545	2.75E-10
chr2:11172382-11301226:	Prkcq	18761	7.0	5.5	3.5	-1.1312	0.533171	-1.57941	0.0007024
chr9:22002988-22014245:	Prkcsh	19089	78.0	75.8	93.8	1.09	0.315405	1.5019	8.19E-12
chr4:155260118-15536142	Prkcz	18762	9.0	8.2	3.5	1.03128	0.91139	-2.03639	2.96E-06
chr12:50341232-50649223	Prkd1	18760	18.1	15.3	4.9	-1.06013	0.67353	-2.94744	7.19E-34
chr7:16842902-16870461:	Prkd2	101540	20.8	19.9	11.2	1.07354	0.501829	-1.4828	4.36E-08
chr17:78949405-79020816	Prkd3	75292	98.4	96.8	95.5	1.10199	0.294381	1.2121	0.0042233
chr16:15637866-15842239	Prkdc	19090	14.3	12.3	8.9	-1.03791	0.671164	-1.28376	5.80E-06
chr19:30564487-31765033	Prkg1	19091	65.1	58.2	36.6	-1.00057	0.997767	-1.41688	1.95E-05
chr2:76629937-76647994:	Prkra	23992	54.3	47.0	23.4	-1.03939	0.814172	-1.84158	1.73E-10
chr5:136180357-13619895	Prkrip1	66801	21.2	26.6	32.7	1.41495	0.088746	1.89458	2.95E-05
chr7:98703363-98718061:	Prkrir	72981	75.4	88.3	161.8	1.32006	0.046503	2.64762	6.10E-21
chrX:77762030-77795960:	Prkx	19108	19.7	24.3	33.0	1.38354	0.056506	2.05568	1.58E-08
chr15:10177238-10349180	Prlr	19116	3.2	2.7	6.8	-1.07374	0.79491	2.56931	2.33E-09
chr16:10796332-10796823	Prm1	19118	111.7	3.9	12.9	-13.5879	2.63E-09	-4.96243	3.53E-05
chr16:10791381-10792097	Prm2	19119	254.6	13.5	28.1	-10.757	6.47E-09	-5.33811	3.90E-06
chr16:10790508-10790914	Prm3	19120	9.4	0.2	1.1	-9.829	1.44E-05	-4.10646	0.0021437
chr7:44976755-44986420:	Prmt1	15469	73.0	84.8	209.8	1.30823	0.044327	3.53759	6.30E-38
chr8:77549397-77581338:	Prmt10	102182	26.3	26.9	26.1	1.14646	0.184879	1.23567	0.0058267
chr7:49778358-49858265:	Prmt3	71974	36.4	37.2	81.4	1.14376	0.077773	2.7861	3.88E-82
chr14:54507182-54517470	Prmt5	27374	51.3	52.8	98.3	1.1574	0.198026	2.37827	2.21E-27
chr3:110246104-11025099	Prmt6	99890	13.6	17.1	23.0	1.41283	0.033879	2.0863	2.54E-09
chr8:106211054-10625169	Prmt7	214572	34.3	35.7	64.2	1.17009	0.14493	2.33113	1.77E-28
chr2:131909928-13193843	Prnp	19122	129.2	110.6	75.9	-1.04694	0.672303	-1.36242	5.25E-06
chr18:35650351-35655199	Prob1	381148	4.7	3.5	1.8	-1.22682	0.361577	-2.01071	1.30E-05
chr11:78193392-78205763	Proca1	216974	7.4	5.5	1.7	-1.15506	0.750684	-2.99446	0.0001041
chr2:155751217-15575547	Procr	19124	15.1	20.2	40.2	1.49502	0.166372	3.10558	8.48E-08
chr5:43993622-44101736:	Prom1	19126	53.9	65.4	59.9	1.34277	0.043081	1.3813	0.0044239
chr11:29511757-29515033	Prorsd1	67939	14.2	15.1	18.8	1.18753	0.182602	1.63634	8.82E-08
chr16:62854334-62929340	Pros1	19128	134.4	125.1	56.1	1.03129	0.870583	-1.90445	6.76E-10
chr8:27042555-27056132:	Prosc	114863	38.9	35.3	44.6	1.01984	0.856741	1.43059	1.91E-09
chr7:30539134-30552272:	Proser3	333193	11.7	7.7	1.8	-1.34593	0.26244	-4.7487	1.45E-15
chr1:190121777-19017068	Prox1	19130	6.6	4.3	2.7	-1.37789	0.060626	-1.93931	4.22E-07
chr12:85086814-85106431	Prox2	73422	3.5	1.8	1.0	-1.73241	0.036219	-2.57761	4.72E-06
chr2:4622167-4652086:-	Prpf18	67229	53.3	51.9	35.5	1.09209	0.178866	-1.19968	0.0001968
chr19:10895231-10909559	Prpf19	28000	62.7	63.8	80.8	1.13834	0.171718	1.60482	4.90E-12
chr3:95830622-95855753:	Prpf3	70767	35.3	39.8	50.9	1.27514	0.228737	1.77577	9.35E-05
chr7:3629985-3642484:+	Prpf31	68988	39.9	38.8	71.1	1.09334	0.335224	2.22208	1.74E-37

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr4:108564867-10857933	Prpf38a	230596	72.9	100.9	112.5	1.55496	0.044791	1.88663	0.0001731
chr3:108902807-10891170	Prpf38b	66921	89.5	94.8	96.9	1.19468	0.208105	1.34788	0.0044227
chr4:62408783-62426990:	Prpf4	70052	20.2	22.2	26.2	1.23489	0.18416	1.60569	4.77E-05
chr2:53138476-53191187:	Prpf40a	56194	94.8	98.7	135.2	1.17235	0.133055	1.7766	8.97E-14
chr2:181601319-18165566	Prpf6	68879	117.3	121.2	141.8	1.16636	0.290659	1.50494	8.80E-05
chr11:75486777-75509447	Prpf8	192159	156.9	149.5	206.1	1.07466	0.550254	1.63966	2.72E-10
chrX:140456603-14047614	Prps1	19139	35.4	39.7	49.5	1.25616	0.033917	1.7446	5.27E-12
chr12:34984761-34986436	Prps1l1	75456	3.4	0.2	0.5	-7.40626	8.22E-05	-3.87157	0.0019638
chr12:57230412-57242168	Prps1l3	328099	49.0	56.0	66.9	1.28565	0.050019	1.69563	4.86E-08
chr5:32789207-32854230:	Prr14l	215476	30.3	29.5	29.3	1.09688	0.314567	1.20973	0.0041905
chr18:51117898-51304641	Prr16	71373	8.1	5.5	1.3	-1.29931	0.398631	-4.6084	9.04E-12
chr5:87825697-87846386:	Prr27	73779	1.1	0.2	0.1	-2.79995	0.097211	-3.47546	0.0088961
chr17:35972539-35979825	Prr3	75210	14.2	13.3	15.8	1.05944	0.75058	1.38981	0.0028697
chr14:101197690-1012000	Prr30	76627	2.1	0.2	0.2	-5.56698	0.001003	-4.59056	0.0004924
chr2:101714285-10183898	Prr5l	72446	7.7	7.6	2.3	1.08793	0.710368	-2.56699	3.73E-11
chr18:57354733-57392719	Prrc1	73137	18.4	15.5	23.3	-1.06554	0.628056	1.57809	2.47E-08
chr17:35149086-35164877	Prrc2a	53761	70.2	80.1	88.5	1.28937	0.176216	1.56576	0.0013603
chrX:78449610-78583897:	Prrg1	546336	21.3	18.0	8.6	-1.06334	0.70051	-1.95937	8.19E-12
chrX:71962625-71972722:	Prrg3	208748	13.5	9.5	3.1	-1.26942	0.203558	-3.39383	3.84E-19
chr7:127017542-12702121	Prrt2	69017	51.0	31.0	5.1	-1.46638	0.136198	-7.18795	2.21E-25
chr3:123446913-12350660	Prss12	19142	2.6	1.7	1.1	-1.38189	0.218966	-1.86191	0.0017215
chr17:23868072-23873113	Prss21	57256	1.9	0.1	0.2	-4.92367	0.005142	-3.82181	0.0041966
chr7:89507785-89517586:	Prss23	76453	153.1	171.0	228.4	1.23402	0.143211	1.84332	6.49E-09
chr7:127932638-12794672	Prss36	77613	6.0	4.6	2.4	-1.19329	0.405752	-1.99964	4.96E-06
chr6:40514824-40519508:	Prss37	67690	6.9	0.3	0.8	-8.79915	7.89E-06	-4.48396	0.0003642
chr1:34498430-34503062:	Prss39	21755	8.2	0.4	1.1	-8.37777	2.43E-05	-3.84107	0.002153
chr1:34552331-34560943:	Prss40	21756	1.4	0.0	0.1	-6.17555	0.001045	-4.0334	0.0031328
chr9:110844506-11085652	Prss46	74306	1.5	0.1	0.3	-5.16002	0.002448	-3.13854	0.0106264
chr14:64093696-64097672	Prss51	1.01E+08	1.3	0.1	0.1	-4.10197	0.017347	-4.19609	0.0024526
chr14:64104323-64113751	Prss52	73382	1.8	0.1	0.2	-4.64471	0.008255	-3.1527	0.0164447
chr7:127885444-12789097	Prss53	330657	5.0	3.2	1.0	-1.39063	0.38828	-3.57231	3.22E-06
chr8:95559292-95575197:	Prss54	70993	2.8	0.2	0.5	-5.38023	0.002755	-2.99756	0.020113
chr14:64075443-64085389	Prss55	71037	3.9	0.3	0.5	-4.85067	0.005186	-3.3425	0.0097038
chr6:40895262-40900387:	Prss58	232717	2.2	0.1	0.1	-6.21814	0.000871	-7.16502	1.95E-05
chr9:72807274-72917307:	Prtg	235472	12.1	7.4	1.8	-1.45425	0.209646	-4.74999	5.01E-13
chr10:79879667-79883172	Prtn3	19152	3.7	2.0	1.0	-1.57063	0.258755	-2.56012	0.0017955
chr19:15905123-15925059	Psat1	107272	23.4	21.4	85.1	1.01607	0.960435	4.31595	7.51E-19
chr19:46312087-46327156	Psd	73728	68.9	57.8	23.9	-1.07291	0.727681	-2.26511	2.18E-11
chr8:67689082-67974574:	Psd3	234353	21.4	20.3	11.2	1.05635	0.581304	-1.52769	4.67E-11
chr12:83688563-83735199	Psen1	19164	55.1	55.4	58.9	1.13371	0.271762	1.33474	0.000454
chr4:83455681-83486448:	Psip1	101739	95.7	82.9	59.4	-1.03631	0.736736	-1.28774	0.0001026
chr8:105900474-10593180	Pskh1	244631	48.8	37.9	28.7	-1.15909	0.307553	-1.3552	0.0038632
chr7:114264550-11427611	Psma1	26440	163.1	174.4	253.7	1.20113	0.097347	1.9333	3.37E-16
chr13:14613242-14625673	Psma2	19166	188.1	219.0	353.3	1.30514	0.02686	2.32469	1.28E-20
chr12:70974623-70994923	Psma3	19167	193.4	215.6	388.0	1.25442	0.057795	2.48539	4.46E-25
chr9:54950859-54958030:	Psma4	26441	152.3	163.0	283.8	1.20087	0.155743	2.30597	2.20E-19
chr3:108256926-10827995	Psma5	26442	125.0	135.2	203.7	1.21512	0.102314	2.02356	5.70E-16
chr12:55398825-55418459	Psma6	26443	186.7	191.4	331.7	1.15169	0.236462	2.20458	3.77E-21
chr2:180036367-18004246	Psma7	26444	112.2	126.4	199.6	1.26276	0.068382	2.20278	5.72E-17
chr17:15475721-15498276	Psmb1	19170	213.5	226.9	305.9	1.19032	0.110426	1.78086	5.40E-13
chr8:105935728-10593839	Psmb10	19171	58.1	72.4	71.8	1.39782	0.046569	1.53016	0.0010621
chr4:126677643-12670971	Psmb2	26445	145.5	162.1	298.4	1.25367	0.089904	2.53571	9.85E-22
chr11:97703434-97713500	Psmb3	26446	134.6	163.1	348.4	1.35876	0.027246	3.18346	6.86E-29
chr3:94884324-94886958:	Psmb4	19172	202.2	228.1	423.9	1.26705	0.103434	2.58279	3.78E-19
chr14:54614120-54617995	Psmb5	19173	62.1	69.4	159.5	1.25262	0.139156	3.15092	4.55E-26
chr11:70525357-70527858	Psmb6	19175	193.4	220.5	427.0	1.28137	0.03665	2.73242	4.57E-30
chr2:38588046-38643906:	Psmb7	19177	172.6	195.5	343.2	1.27286	0.034786	2.4654	3.00E-26
chr17:34198195-34201454	Psmb8	16913	68.6	83.5	96.7	1.34809	0.107074	1.73514	7.34E-05

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr12:100112331-1001233	Psmc1	19179	159.7	165.1	260.3	1.16144	0.172726	2.02669	2.39E-19
chr5:21785283-21803784:	Psmc2	19181	90.0	97.4	205.2	1.2214	0.238669	2.79713	7.83E-18
chr2:91054016-91059438:	Psmc3	19182	180.4	179.4	282.1	1.11464	0.157218	1.94916	2.64E-34
chr11:101092141-1010954	Psmc3ip	19183	22.4	22.4	24.7	1.12334	0.485412	1.37811	0.0047278
chr7:28041702-28050092:	Psmc4	23996	110.6	133.6	298.3	1.3629	0.043779	3.31192	6.44E-26
chr11:106256185-1062631	Psmc5	19184	85.6	103.5	274.1	1.36322	0.06953	3.89579	1.32E-27
chr14:45329824-45349071	Psmc6	67089	177.2	203.1	289.3	1.28824	0.066817	2.01898	7.54E-12
chr1:86064619-86139295:	Psmd1	70247	91.3	99.5	236.3	1.22653	0.073767	3.20389	1.22E-44
chr11:80428615-80472133	Psmd11	69077	59.7	68.7	109.5	1.29641	0.060878	2.27102	1.07E-15
chr11:107479528-1074980	Psmd12	66997	85.0	98.9	202.9	1.31167	0.091729	2.92874	6.35E-20
chr7:140882394-14089864	Psmd13	23997	80.7	88.3	156.0	1.22931	0.070588	2.39729	9.17E-26
chr2:61711694-61800376:	Psmd14	59029	68.5	71.6	182.9	1.16904	0.147849	3.30626	1.64E-55
chr16:20651652-20663414	Psmd2	21762	143.2	155.8	300.9	1.22799	0.212358	2.5846	5.54E-16
chr11:98682554-98695978	Psmd3	22123	89.4	89.6	139.4	1.13089	0.509952	1.92399	1.31E-07
chr3:95032691-95042614:	Psmd4	19185	144.8	156.2	273.8	1.21458	0.081987	2.34812	1.13E-25
chr2:34852089-34870962:	Psmd5	66998	61.6	67.1	87.3	1.22476	0.079442	1.76242	3.14E-11
chr14:14112185-14120904	Psmd6	66413	100.8	128.4	234.9	1.43433	0.024817	2.85648	6.34E-18
chr8:107580380-10758848	Psmd7	17463	90.6	97.5	163.2	1.2133	0.148844	2.23107	1.19E-16
chr7:29174187-29180673:	Psmd8	57296	121.9	134.2	195.6	1.24169	0.157849	1.98395	8.53E-10
chr14:55578494-55581527	Psme1	19186	198.7	212.7	230.8	1.1974	0.034767	1.44979	9.54E-09
chr14:55587440-55591101	Psme2	19188	140.4	148.8	219.0	1.18328	0.102179	1.93931	8.42E-19
chr11:101316251-1013235	Psme3	19192	38.9	56.8	125.3	1.6415	0.024718	3.847	8.85E-16
chr11:30771775-30880361	Psme4	103554	79.6	80.1	98.4	1.13418	0.307044	1.53975	7.74E-07
chr16:95979935-95990903	Psmg1	56088	32.9	31.1	53.8	1.05694	0.626756	2.04008	1.83E-26
chr18:67641599-67654162	Psmg2	107047	48.2	50.6	63.1	1.17251	0.112678	1.63226	1.48E-11
chr5:139823594-13982684	Psmg3	66506	24.9	24.7	42.8	1.10232	0.520998	2.12445	2.74E-15
chr13:34162964-34178172	Psmg4	69666	40.4	37.2	57.0	1.02973	0.844375	1.75831	8.46E-13
chr14:56722449-56778316	Pspc1	66645	62.1	79.1	83.4	1.43629	0.031375	1.66189	9.75E-05
chr5:129765558-12978725	Psph	100678	8.9	8.4	17.2	1.05289	0.783293	2.38256	1.78E-17
chr10:79854432-79864435	Ptbp1	19205	141.8	189.7	283.8	1.50803	0.084215	2.41812	7.26E-07
chr13:99319649-99344678	Ptcd2	68927	36.1	31.6	37.7	-1.03143	0.858487	1.30051	0.0076443
chr6:71880638-71908762:	Ptcd3	69956	80.1	87.0	99.7	1.22206	0.050162	1.55264	1.14E-08
chr13:63511533-63565520	Ptch1	19206	115.9	46.4	33.1	-2.10948	0.046258	-2.5102	0.0015128
chr11:121830218-1218434	Ptchd3	74675	1.1	0.1	0.2	-4.38684	0.008327	-2.84052	0.0230363
chr13:66932830-66998401	Ptdss1	19210	55.4	54.6	57.1	1.10362	0.295439	1.2853	0.0001932
chr19:32757577-32826160	Pten	19211	72.0	73.3	81.4	1.14516	0.183666	1.41003	3.96E-06
chr2:12924041-13003453:	Pter	19212	18.1	12.4	6.1	-1.31246	0.168704	-2.31005	8.93E-09
chr2:25466712-25469749:	Ptgds	19215	12.3	6.0	4.6	-1.7665	0.083233	-2.01067	0.0057867
chr3:157566892-15764475	Ptger3	19218	20.6	20.6	60.7	1.07551	0.881121	3.25923	1.03E-05
chr2:32395890-32402740:	Ptges2	96979	17.6	23.3	39.9	1.48789	0.117395	2.71584	1.02E-07
chr10:128058982-1280772	Ptges3	56351	193.7	239.6	461.8	1.39304	0.019235	2.93493	1.77E-23
chr11:101418814-1014253	Ptges3l	73635	6.0	3.9	7.4	-1.36504	0.153987	1.51646	0.0075809
chr3:101040236-10111016	Ptgfrn	19221	81.6	75.1	47.8	1.02188	0.886059	-1.36339	0.000209
chr2:167203196-16724053	Ptgis	19223	73.1	87.0	125.6	1.32804	0.125985	2.09832	6.35E-08
chr4:58965590-58987078:	Ptgr1	67103	12.3	10.5	4.9	-1.04336	0.80472	-2.00642	2.54E-11
chr12:84285296-84315832	Ptgr2	77219	40.3	30.4	24.0	-1.19031	0.093511	-1.345	0.000161
chr2:36230426-36252271:	Ptgs1	19224	34.6	32.6	14.8	1.03851	0.902942	-1.83495	0.0004405
chr9:110722085-11074714	Pth1r	19228	30.0	29.4	12.8	1.10987	0.634123	-1.84173	1.46E-05
chr15:73205105-73423191	Ptk2	14083	53.2	51.4	88.0	1.0801	0.294023	2.06323	1.51E-47
chr17:46564451-46629504	Ptk7	71461	160.7	112.0	71.5	-1.28629	0.010762	-1.78826	4.77E-14
chr1:86526736-86530698:	Ptma	19231	####	1692.7	1895.1	1.21478	0.212706	1.49958	0.0004086
chr6:124913675-12491794	Ptms	69202	225.3	184.6	129.5	-1.09708	0.459806	-1.38649	0.0001556
chr6:36715663-36811361:	Ptn	19242	106.8	103.4	62.0	1.07403	0.636577	-1.37844	0.0010133
chr7:44863068-44869788:	Ptov1	84113	128.5	112.9	71.2	-1.01575	0.905083	-1.43652	4.67E-07
chr1:30940303-30949755:	Ptp4a1	19243	6.2	6.4	13.7	1.16752	0.382038	2.74497	1.24E-17
chr4:129820479-12985000	Ptp4a2	19244	170.8	150.4	163.7	-1.01704	0.860765	1.19566	0.0010558
chr13:48577869-48625672	Ptpdc1	218232	25.5	17.6	13.2	-1.29988	0.131509	-1.5324	0.0011482
chr2:14026831-14056035:	Ptpla	30963	35.8	38.7	60.0	1.20826	0.132246	2.07596	3.38E-16

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr9:64986983-65021717:	Ptplad1	57874	80.1	76.6	100.5	1.07128	0.434553	1.56485	3.47E-14
chr4:88412930-88438926:	Ptplad2	66775	27.9	20.5	5.3	-1.22134	0.251642	-4.07925	4.97E-28
chr16:35022421-35109175	Ptplb	70757	16.4	17.2	21.9	1.18051	0.292498	1.65871	5.61E-06
chr2:90910713-90918050:	Ptpmt1	66461	29.3	31.9	58.4	1.22316	0.188558	2.45587	9.26E-17
chr2:167932327-16797938	Ptpn1	19246	25.2	52.0	50.0	2.24243	0.002755	2.34379	0.0001304
chr5:121130533-12119139	Ptpn11	19247	73.1	71.0	119.0	1.08801	0.208986	2.02813	1.80E-51
chr5:103425192-10359836	Ptpn13	19249	90.8	64.8	14.6	-1.25703	0.108599	-4.84641	3.57E-52
chr1:189728268-18987669	Ptpn14	19250	40.2	32.4	13.6	-1.11213	0.441514	-2.34127	6.65E-20
chr18:67665501-67724621	Ptpn2	19255	11.8	18.0	27.3	1.70668	0.001026	2.8234	6.51E-15
chr14:33589270-33640754	Ptpn20	19256	1.8	0.1	0.2	-6.95068	0.000113	-5.17296	0.0001317
chr4:57190841-57301837:	Ptpn3	545622	21.9	13.6	7.5	-1.44996	0.030119	-2.29582	2.41E-10
chr7:47077800-47133684:	Ptpn5	19259	1.5	22.5	126.0	14.006	2.78E-35	79.4378	1.68E-102
chr1:135132725-13514532	Ptpn7	320139	6.2	7.4	11.5	1.29042	0.496818	2.16477	0.0025858
chr9:56994968-57062807:	Ptpn9	56294	34.4	35.1	51.5	1.14303	0.106119	1.86645	9.41E-26
chr2:130450278-13055430	Ptpra	19262	94.8	83.4	66.7	-1.01627	0.839665	-1.13666	0.005949
chr10:116301374-1163895	Ptprb	19263	29.5	24.1	15.9	-1.09042	0.391061	-1.47726	2.37E-08
chr4:75941237-78211895:	Ptprd	19266	40.5	33.5	10.0	-1.0822	0.586825	-3.19123	6.02E-36
chr10:28074820-28597397	Ptprk	19272	33.4	29.3	19.4	-1.01799	0.856073	-1.37133	8.88E-09
chr17:66666848-67354459	Ptprm	19274	31.8	28.1	19.4	-1.00685	0.962808	-1.30274	0.0008744
chr10:116018363-1162749	Ptprr	19279	19.1	12.6	3.0	-1.30286	0.562343	-4.15313	2.04E-06
chr17:56412426-56476480	Ptprs	19280	66.3	73.1	100.9	1.24809	0.206153	1.88175	6.52E-07
chr1:135108498-13513257	Ptprv	13924	1.6	2.9	2.8	1.99048	0.005923	2.08683	0.000292
chr11:100956736-1009706	Ptrf	19285	279.9	224.3	174.5	-1.11582	0.111162	-1.28333	1.20E-06
chr2:32775821-32777593:	Ptrh1	329384	4.6	9.8	29.6	2.24645	0.026661	6.53779	9.82E-12
chr11:86683983-86692457	Ptrh2	217057	23.4	23.7	33.5	1.13485	0.264803	1.78445	2.04E-13
chr12:4234027-4240123:+	Ptrhd1	69709	3.8	3.6	5.2	1.05968	0.702147	1.72348	3.43E-10
chr9:50521617-50528641:	Pts	19286	81.5	59.6	34.8	-1.2241	0.051075	-1.86502	2.59E-15
chr11:43420248-43426248	Pttg1	30939	49.8	47.6	24.0	1.06757	0.535255	-1.65276	1.13E-12
chr10:77581767-77598732	Pttg1ip	108705	227.5	209.2	131.1	1.02928	0.733081	-1.38786	1.49E-10
chr15:76070182-76080946	Puf60	67959	136.2	149.1	199.1	1.23311	0.049972	1.82041	6.02E-14
chr18:36281162-36288244	Pura	19290	37.6	42.2	40.6	1.26149	0.079559	1.34569	0.003399
chr11:6467599-6476076:-	Purb	19291	69.1	83.8	110.5	1.36727	0.061235	1.96991	6.77E-08
chr8:33386325-33417469:	Purg	75029	21.5	18.3	10.8	-1.04757	0.738944	-1.58519	9.36E-08
chr5:110773667-11078061	Pus1	56361	17.6	26.5	61.1	1.68066	0.004368	4.17665	1.47E-23
chr9:35559466-35567400:	Pus3	67049	36.6	40.0	50.4	1.23129	0.144193	1.7075	3.09E-07
chr5:23740165-23783711:	Pus7	78697	28.4	29.4	70.8	1.17017	0.295868	3.07723	1.84E-27
chr15:94522640-94543507	Pus7l	78895	5.3	5.4	14.2	1.13845	0.441118	3.32448	1.05E-29
chr4:155888860-15589176	Pusl1	433813	29.7	36.0	67.8	1.35895	0.053953	2.79978	1.09E-18
chr7:19903578-19921143:	Pvr	52118	14.3	21.5	32.3	1.67976	0.014081	2.73403	8.76E-10
chr16:46394858-46496967	Pvrl3	58998	47.4	38.9	89.1	-1.09442	0.548151	2.33175	1.38E-18
chr15:62037987-62250975	Pvt1	19296	27.3	23.1	36.6	-1.06481	0.771293	1.65938	9.20E-05
chr10:85871831-85889103	Pwp1	103136	43.7	47.9	82.4	1.23204	0.093997	2.33664	7.03E-21
chr10:78170910-78185149	Pwp2	110816	30.3	40.6	84.4	1.50848	0.018448	3.39063	4.45E-20
chr14:8098213-8165111:+	Pxk	218699	44.7	46.6	48.1	1.1708	0.059904	1.34461	2.60E-06
chr5:110274286-11028616	Pxmp2	19301	11.5	10.4	3.3	1.03375	0.93472	-2.63177	1.44E-05
chr2:154587044-15460367	Pxmp4	59038	23.2	17.9	7.1	-1.16277	0.292187	-2.56988	4.70E-19
chr5:115506676-11555598	Pxn	19303	47.5	58.2	53.9	1.37826	0.048608	1.40847	0.0069357
chr17:28933986-28942262	Pxt1	69307	1.1	0.1	0.1	-4.59489	0.007843	-4.22621	0.0019887
chr9:96823343-96889474:	Pxylp1	235534	29.9	22.2	6.8	-1.21525	0.295823	-3.42248	1.43E-20
chr11:120635712-1206436	Pycr1	209027	1.5	1.2	2.7	-1.08881	0.771007	2.25895	2.85E-07
chr1:180904274-18090808	Pycr2	69051	35.3	39.1	71.0	1.24512	0.123049	2.48189	7.68E-19
chr15:75916463-75921560	Pycrl	66194	33.3	34.2	70.1	1.15621	0.167841	2.62465	1.78E-40
chr1:173673680-17369839	Pydc3	1E+08	0.7	1.2	1.8	1.7314	0.185587	2.89965	0.0004279
chr2:150786796-15083174	Pygb	110078	168.5	122.4	65.5	-1.23947	0.159147	-2.035	1.74E-10
chr12:70190815-70227683	Pygl	110095	59.2	40.8	9.4	-1.30135	0.060866	-4.91362	8.48E-51
chr19:6384429-6398459:+	Pygm	19309	23.1	20.1	10.4	-1.02793	0.889737	-1.75129	3.46E-07
chr3:89430214-89435130:	Pygo2	68911	35.1	35.4	38.0	1.13369	0.161663	1.35491	3.71E-06
chr19:42725858-42752775	Pyroxd2	74580	11.3	9.0	3.2	-1.12799	0.507319	-2.76755	4.23E-16

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr6:57684739-57692078:	Pyurf	66459	17.2	15.4	19.0	1.00724	0.960166	1.37797	2.15E-05
chr5:45434032-45450229:	Qdpr	110391	51.7	42.4	31.0	-1.09263	0.463783	-1.331	0.000651
chr17:10206471-10319361	Qk	19317	65.5	71.0	89.3	1.22106	0.081772	1.69562	5.91E-10
chr17:79051906-79090243	Qpct	70536	18.3	18.8	23.4	1.14377	0.390458	1.58871	1.72E-05
chr7:19140217-19149196:	Qpctl	67369	11.6	11.4	14.4	1.10086	0.442145	1.54976	1.06E-07
chr7:127107770-12712202	Qprt	67375	2.3	2.7	6.3	1.25786	0.456977	3.17247	3.31E-09
chr9:108517087-10856016	Qrich1	69232	110.7	118.7	143.7	1.20924	0.144193	1.61459	5.95E-07
chr11:116441325-1164543	Qrich2	217341	10.1	1.1	1.3	-6.36102	9.24E-07	-4.76284	2.06E-06
chr10:43874190-43901736	Qrsl1	76563	9.7	12.0	25.9	1.38413	0.012332	3.2941	1.29E-35
chr1:155778155-15581289	Qsox1	104009	50.9	45.8	71.2	1.00308	0.98087	1.7415	1.84E-17
chr2:26209124-26237399:	Qsox2	227638	15.3	15.0	28.0	1.09471	0.323174	2.27799	3.74E-42
chr9:21411837-21420279:	Qtrt1	60507	31.4	38.6	62.6	1.38153	0.007608	2.47258	2.65E-22
chr16:43861413-43889676	Qtrtd1	106248	41.0	47.4	68.7	1.30576	0.119251	2.06941	8.51E-09
chr14:69697304-69714809	R3hcc1	71843	33.7	28.6	34.1	-1.05068	0.589091	1.26474	5.61E-05
chr19:42518805-42592256	R3hcc1l	52013	42.0	38.2	24.0	1.02054	0.870436	-1.39651	1.69E-06
chr7:143021784-14305368	R74862	97423	8.0	7.2	2.6	1.00734	0.978103	-2.36557	1.42E-09
chr11:20201602-20226856	Rab1	19324	117.0	125.4	171.9	1.20742	0.106205	1.82574	2.12E-12
chr12:3247428-3309969:-	Rab10	19325	77.8	83.0	120.1	1.19998	0.039737	1.92292	3.32E-23
chr9:64715300-64737756:	Rab11a	53869	85.6	102.7	102.3	1.35098	0.044392	1.48324	0.0006397
chr11:79591212-79694012	Rab11fip4	268451	8.7	6.9	3.8	-1.12584	0.538847	-1.83394	3.30E-06
chr6:85334962-85374634:	Rab11fip5	52055	41.1	25.0	22.0	-1.47488	0.002307	-1.48334	0.0001904
chr3:90213715-90226387:	Rab13	68328	27.3	20.1	6.7	-1.22307	0.212765	-3.18092	7.02E-22
chr1:90958133-90969620:	Rab17	19329	5.2	2.6	0.2	-1.66092	0.222695	-13.5672	4.20E-15
chr18:6765167-6791606:+	Rab18	19330	66.5	68.2	73.3	1.14906	0.146577	1.37355	7.46E-06
chr19:5099207-5106996:-	Rab1b	76308	91.5	87.7	102.2	1.07189	0.372896	1.39484	4.05E-10
chr8:11453977-11478499:	Rab20	19332	44.1	84.1	54.2	2.07707	0.00717	1.49615	0.078746
chr10:115289862-1153155	Rab21	216344	50.3	53.7	59.0	1.1975	0.071274	1.46021	3.81E-07
chr13:55319223-55321980	Rab24	19336	71.6	60.4	41.3	-1.05997	0.532029	-1.38462	1.56E-07
chr17:24528251-24528744	Rab26os	75614	34.8	49.3	186.7	1.57517	0.135988	5.97295	3.21E-16
chr9:73044810-73097614:	Rab27a	11891	16.1	20.7	23.8	1.42308	0.004736	1.82528	1.40E-09
chr5:41624976-41708155:	Rab28	100972	53.8	51.0	54.9	1.05957	0.573175	1.27383	0.0002944
chr1:131867277-13187288	Rab29	226422	23.3	18.5	10.6	-1.13181	0.422041	-1.74874	2.98E-07
chr7:92741714-92837117:	Rab30	75985	18.3	11.3	6.3	-1.4486	0.218899	-2.19556	0.0004026
chr17:65651726-65772752	Rab31	106572	45.1	52.1	55.7	1.29618	0.192218	1.52113	0.0046982
chrX:48519285-48530240:	Rab33a	19337	1.3	2.2	2.8	1.74298	0.150722	2.37431	0.0025502
chr3:51483966-51496212:	Rab33b	19338	30.4	30.9	36.1	1.13828	0.103168	1.48153	1.09E-11
chr5:115631987-11564715	Rab35	77407	51.0	60.7	65.0	1.33691	0.011726	1.58446	3.67E-07
chr10:75037089-75054100	Rab36	76877	11.0	6.3	1.4	-1.5492	0.063367	-5.70828	6.77E-21
chrX:75572045-75578231:	Rab39b	67790	4.6	5.7	8.5	1.39116	0.011095	2.30383	1.01E-17
chr8:70754679-70758686:	Rab3a	19339	17.8	10.1	6.3	-1.56243	0.162458	-2.14455	0.0014984
chr4:108879070-10894332	Rab3b	69908	1.1	0.6	0.3	-1.57393	0.16417	-2.94413	3.01E-05
chr9:21907511-21918121:	Rab3d	19340	22.2	14.5	5.9	-1.37187	0.048792	-2.95822	5.79E-19
chr1:185204168-18528674	Rab3gap2	98732	35.8	31.7	36.6	-1.00477	0.959877	1.27988	4.13E-07
chr19:10018228-10035586	Rab3il1	74760	51.0	36.4	18.7	-1.25798	0.281662	-2.13882	5.83E-07
chr10:116905784-1169503	Rab3ip	216363	21.1	21.3	26.9	1.12975	0.307363	1.58689	2.89E-08
chr11:121356121-1213882	Rab40b	217371	6.7	5.9	2.6	-1.02856	0.907368	-2.04421	3.50E-07
chr6:87788853-87812164:	Rab43	69834	40.0	57.4	29.3	1.61413	0.003696	-1.08825	0.578251
chr7:27168433-27178883:	Rab4b	19342	31.0	32.5	34.0	1.17181	0.143558	1.3676	8.50E-05
chr17:53479234-53507678	Rab5a	271457	48.9	56.4	55.4	1.29713	0.081121	1.40427	0.0029406
chr10:128677183-1286962	Rab5b	19344	112.9	105.8	74.9	1.04807	0.546719	-1.20465	0.0003463
chr11:100715266-1007381	Rab5c	19345	148.4	153.2	217.2	1.15848	0.099106	1.82354	2.06E-20
chr7:100607586-10064126	Rab6a	19346	58.7	68.7	91.0	1.31506	0.043588	1.91813	1.71E-10
chr9:103112074-10318527	Rab6b	270192	25.9	24.1	10.9	1.0447	0.830635	-1.87058	1.13E-07
chr6:87999106-88045270:	Rab7	19349	122.1	117.9	145.6	1.0853	0.461028	1.4851	1.41E-07
chr8:72161200-72181366:	Rab8a	17274	77.5	77.5	91.5	1.12188	0.214297	1.4728	4.81E-09
chr9:66843664-66919705:	Rab8b	235442	43.3	45.6	46.9	1.17514	0.226997	1.34447	0.0026397
chr7:24969750-24972728:	Rabac1	14470	286.7	278.4	164.1	1.08653	0.350227	-1.39806	8.37E-08
chr11:70844761-70943105	Rabep1	54189	52.4	63.0	71.2	1.3546	0.046385	1.6818	7.65E-06

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr7:126428767-12644590	Rabep2	70314	25.8	21.4	14.2	-1.07861	0.391887	-1.44903	2.31E-09
chr2:34778666-34799912:	Rabepk	227746	19.5	15.8	20.7	-1.09957	0.470473	1.32568	0.001449
chr1:160219174-16079293	Rabgap1l	29809	38.3	31.9	19.3	-1.0807	0.619553	-1.57655	6.04E-06
chr14:55715877-55722176	Rabggta	56187	19.5	17.8	22.2	1.01636	0.89911	1.42202	2.35E-07
chr3:153907289-15391296	Rabggtb	19352	85.9	110.9	241.7	1.45212	0.032282	3.4216	5.12E-21
chr1:134494660-13450788	Rabif	98710	29.5	27.4	35.8	1.03606	0.76134	1.50989	1.11E-09
chr15:89582527-89591923	Rabl2	68708	23.3	18.8	9.9	-1.10629	0.442648	-1.85598	1.95E-11
chr2:25583018-25608446:	Rabl6	227624	66.5	66.1	110.0	1.124	0.499573	2.04629	4.31E-10
chr5:143505481-14352799	Rac1	19353	206.0	192.8	212.6	1.04876	0.577448	1.28802	4.96E-06
chr11:120721468-1207239	Rac3	170758	20.0	17.1	9.6	-1.03843	0.906894	-1.63346	0.0070866
chr13:100617164-1006510	Rad17	19356	28.0	33.6	39.5	1.35032	0.041497	1.74805	5.83E-07
chr6:112619851-11269667	Rad18	58186	17.3	33.2	78.2	2.13322	8.80E-06	5.41704	1.07E-31
chr15:51962604-51991760	Rad21	19357	125.5	114.4	78.5	1.01765	0.866909	-1.2766	3.08E-05
chr8:84834652-84840665:	Rad23a	19358	54.1	47.5	81.6	-1.02061	0.837409	1.88311	4.55E-32
chr4:55350042-55392237:	Rad23b	19359	94.3	97.5	181.5	1.16431	0.244532	2.38444	2.92E-21
chr11:53649519-53707319	Rad50	19360	35.7	27.7	20.6	-1.16122	0.260851	-1.38282	0.0008046
chr12:79297282-79814690	Rad51b	19363	43.3	36.5	4.7	-1.0656	0.760455	-7.02884	4.41E-53
chr11:82871961-82890624	Rad51d	19364	19.2	12.5	8.0	-1.37606	0.141222	-1.87106	0.0001128
chr9:106688080-10678921	Rad54l2	81000	21.7	20.8	23.8	1.07634	0.391921	1.37042	9.37E-08
chr5:122325508-12235419	Rad9b	231724	11.1	7.1	3.8	-1.39535	0.059077	-2.28613	1.83E-09
chr5:142484839-14255109	Radil	231858	18.0	14.4	2.6	-1.12669	0.567341	-5.25283	1.07E-32
chr2:173000117-17301573	Rae1	66679	67.6	71.3	114.6	1.18515	0.047766	2.11364	6.38E-33
chr6:115618573-11567663	Raf1	110157	130.3	134.2	147.5	1.1596	0.125418	1.41418	1.38E-06
chr11:60105013-60199195	Rai1	19377	24.4	35.0	38.2	1.60545	0.106416	1.88182	0.0047352
chrX:161717036-16177949	Rai2	24004	27.9	20.8	13.9	-1.20651	0.35852	-1.57961	0.0017571
chr13:17880575-17944217	Rala	56044	44.6	44.6	70.1	1.12077	0.101009	1.95971	1.40E-42
chr1:119470305-11950478	Ralb	64143	49.4	63.1	81.9	1.4373	0.046962	2.03533	2.81E-07
chr17:65848428-65885755	Ralbp1	19765	72.7	65.6	33.8	1.00351	0.984192	-1.70768	5.38E-09
chr12:55602890-55821516	Ralgapa1	56784	70.2	68.2	71.5	1.09205	0.361723	1.27294	0.0004069
chr2:146241299-14651200	Ralgapa2	241694	21.7	17.1	12.7	-1.13235	0.281204	-1.35722	0.0002381
chr2:158409853-15849925	Ralgapb	228850	40.9	41.0	47.0	1.1269	0.121951	1.43649	1.68E-10
chr2:28513167-28553082:	Ralgds	19730	49.8	57.4	23.9	1.2625	0.378769	-1.63338	0.009773
chr2:33133419-33371494:	Ralgps1	241308	7.6	6.4	3.6	-1.07155	0.663461	-1.67439	3.54E-07
chr1:156804166-15693962	Ralgps2	78255	24.6	20.1	12.0	-1.09906	0.348357	-1.6413	1.99E-12
chr2:154791110-15486726	Raly	19383	168.7	374.9	1084.7	2.43751	0.000124	7.27152	1.73E-24
chr1:91179822-91225196:	Ramp1	51801	23.5	21.4	7.5	1.01534	0.95724	-2.44112	1.46E-09
chr11:101246334-1012482	Ramp2	54409	87.9	77.7	106.7	-1.0178	0.918391	1.50908	5.54E-06
chr5:129020156-12902432	Ran	19384	99.0	142.7	415.8	1.61586	0.024187	4.96932	2.51E-23
chr16:18239979-18248694	Ranbp1	19385	114.3	151.4	393.1	1.48901	0.025201	4.16224	1.69E-26
chr11:33211794-33513746	Ranbp17	66011	8.9	6.2	3.9	-1.27711	0.096796	-1.81527	7.88E-08
chr10:58446852-58494154	Ranbp2	19386	165.3	214.3	259.6	1.4617	0.034148	1.93322	1.65E-06
chr17:56673225-56711769	Ranbp3	71810	67.9	74.8	96.5	1.24546	0.161748	1.76315	8.42E-07
chr13:43402673-43480973	Ranbp9	56705	91.8	81.5	52.4	-1.01344	0.928961	-1.3972	2.74E-05
chr15:81704248-81729919	Rangap1	19387	34.8	47.9	105.9	1.54971	0.046517	3.6454	3.57E-15
chr11:68972484-68975185	Rangrf	57785	26.0	23.7	52.6	1.02763	0.899039	2.49715	2.66E-16
chr3:105727260-10580138	Rap1a	109905	71.8	74.7	90.6	1.16194	0.015084	1.57284	4.24E-22
chr10:117814597-1178459	Rap1b	215449	164.0	177.3	194.9	1.21083	0.064196	1.47847	4.81E-07
chr11:74383483-74590158	Rap1gap2	380711	22.9	54.4	14.0	2.51534	0.007884	-1.271	0.435383
chr3:138925897-13907520	Rap1gds1	229877	35.4	33.8	47.9	1.06474	0.442648	1.68562	2.49E-22
chrX:51003914-51018018:	Rap2c	72065	25.3	25.6	31.8	1.12965	0.186349	1.55974	1.29E-11
chr2:29619720-29740363:	Rapgef1	107746	42.3	43.2	75.9	1.15063	0.195165	2.23217	1.19E-25
chr3:79062529-79145875:	Rapgef2	76089	33.5	27.8	21.1	-1.07957	0.349628	-1.27017	3.66E-05
chr11:54522845-54699286	Rapgef6	192786	42.2	39.1	24.5	1.03548	0.650693	-1.37628	3.29E-11
chr1:60483185-60566765:	Raph1	77300	10.9	9.8	6.2	1.00588	0.971247	-1.4032	9.66E-05
chr11:98937696-98974942	Rara	19401	21.0	35.0	36.5	1.85228	0.005435	2.1062	3.40E-05
chr14:16430840-17082331	Rarb	218772	5.4	3.6	0.8	-1.32063	0.454821	-4.47703	7.56E-09
chr15:102234938-1022575	Rarg	19411	54.9	42.0	17.5	-1.16958	0.180131	-2.4873	5.82E-27
chr6:48569698-48572670:	Rarres2	71660	961.7	780.7	212.2	-1.11274	0.511517	-3.56615	7.65E-33

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:35808381-35834528	Rars	104458	80.4	101.0	201.2	1.41269	0.01217	3.07709	2.56E-26
chr4:34614958-34660167:	Rars2	109093	40.0	37.9	51.1	1.06254	0.509817	1.59992	1.61E-15
chr9:96539300-96631503:	Rasa2	114713	31.8	32.1	31.3	1.13355	0.21472	1.22815	0.0060537
chr8:13567218-13677587:	Rasa3	19414	78.3	65.4	32.1	-1.06447	0.525917	-1.9416	1.02E-24
chr5:136083916-13611186	Rasa4	54153	15.2	12.9	6.6	-1.04889	0.841257	-1.82014	1.42E-05
chr11:59963181-59964942	Rasd1	19416	16.4	52.8	47.0	3.06085	0.011	2.91192	0.0026341
chr8:75213944-75224113:	Rasd2	75141	64.8	40.8	15.6	-1.41866	0.156997	-3.14249	2.61E-10
chr6:118066385-11809154	Rasgef1a	70727	12.1	7.5	1.8	-1.41607	0.379706	-4.4208	8.62E-08
chr5:99217420-99252927:	Rasgef1b	320292	21.6	23.3	10.6	1.18375	0.48989	-1.6049	0.0053166
chr9:89909775-90026979:	Rasgrf1	19417	11.4	9.2	5.3	-1.11284	0.584761	-1.71507	2.85E-05
chr13:91880407-91988042	Rasgrf2	19418	4.6	3.0	2.0	-1.35157	0.059398	-1.77102	3.11E-06
chr2:117279993-11734287	Rasgrp1	19419	4.8	7.9	8.1	1.71916	0.11278	1.97415	0.0094633
chr19:6400583-6415216:+	Rasgrp2	19395	17.8	13.5	8.4	-1.1792	0.185107	-1.69358	1.12E-08
chr11:83410072-83421038	Rasl10b	276952	0.3	0.2	1.1	-1.21998	0.700726	4.36111	1.07E-07
chr5:146845071-14684772	Rasl11a	68895	15.1	27.5	17.9	2.01997	0.000135	1.46134	0.0206625
chr5:74195326-74199477:	Rasl11b	68939	25.2	20.4	29.8	-1.10783	0.646466	1.46516	0.0077011
chr7:5124942-5125950:-	Rasl2-9	19428	3.2	0.2	0.8	-5.31257	0.00106	-2.32801	0.0501132
chr9:107551555-10756226	Rassf1	56289	49.7	70.8	87.3	1.59708	0.034472	2.13452	8.43E-06
chr7:112953962-11295745	Rassf10	78748	12.9	5.9	4.4	-1.92212	0.010132	-2.26301	5.92E-05
chr2:131992850-13202998	Rassf2	215653	84.5	64.2	21.0	-1.19077	0.548913	-3.05866	4.28E-09
chr10:121410351-1214762	Rassf3	192678	58.4	56.4	56.9	1.077	0.422226	1.21564	0.0025801
chr6:116633008-11667383	Rassf4	213391	16.8	14.4	6.5	-1.04036	0.895123	-2.01719	2.48E-05
chr7:141215860-14121865	Rassf7	66985	22.2	18.1	11.3	-1.09686	0.677836	-1.5537	0.0019706
chr10:102512222-1025465	Rassf9	237504	21.4	13.5	7.1	-1.42005	0.168005	-2.33245	7.32E-06
chr9:21074164-21091988:	Raver1	71766	6.8	7.3	10.9	1.21616	0.110684	2.00067	1.44E-15
chr4:101069038-10115237	Raver2	242570	16.5	11.4	2.4	-1.30311	0.188233	-5.22653	1.88E-28
chr14:73195502-73325791	Rb1	19645	38.2	37.1	22.5	1.08925	0.257641	-1.35971	1.61E-08
chr1:6214662-6276104:+	Rb1cc1	12421	77.8	78.8	30.8	1.13631	0.027246	-2.01732	3.12E-57
chr5:143164779-14316575	Rbakdn	1E+08	13.4	0.6	1.4	-9.32348	3.45E-06	-4.97864	0.0001225
chr4:129307100-12933537	Rbbp4	19646	105.0	107.1	117.9	1.14514	0.184851	1.39983	6.80E-06
chr1:132477367-13250566	Rbbp5	213464	44.8	44.8	45.9	1.12402	0.14847	1.27963	3.89E-05
chrX:162760372-16277909	Rbbp7	245688	255.6	277.9	480.3	1.2247	0.130578	2.32605	5.01E-18
chr18:11633276-11743207	Rbbp8	225182	29.0	34.4	41.4	1.33008	0.037623	1.77001	4.20E-08
chr2:144542265-14455085	Rbbp9	26450	77.6	64.6	25.6	-1.08427	0.676781	-2.38685	4.31E-13
chr2:152316334-15233263	Rbck1	24105	69.6	67.2	72.5	1.08338	0.263612	1.30266	1.77E-07
chr18:80192264-80200619	Rbfa	68731	32.0	27.0	34.8	-1.05685	0.66342	1.35748	9.47E-05
chr15:77078990-77307053	Rbfox2	93686	66.0	61.2	67.5	1.04701	0.759909	1.2781	0.008003
chr8:91070057-91123844:	Rbl2	19651	61.7	49.2	21.9	-1.12889	0.440839	-2.22966	5.31E-14
chrX:20617503-20650905:	Rbm10	236732	43.5	48.5	64.5	1.2511	0.017723	1.84781	1.54E-17
chr16:75592891-75602825	Rbm11	224344	4.4	2.8	0.8	-1.3758	0.388348	-3.90498	3.12E-07
chr2:156094882-15611196	Rbm12	75710	45.6	63.3	63.9	1.56396	0.044023	1.7198	0.0016216
chr19:4800566-4811634:-	Rbm14	56275	34.2	35.0	37.2	1.14979	0.177996	1.35828	5.57E-05
chr9:106883985-10688700	Rbm15b	109095	35.1	47.9	61.1	1.53648	0.024836	2.1337	2.78E-07
chr2:11585439-11603199:	Rbm17	76938	128.0	139.3	205.0	1.22555	0.077258	1.99209	3.99E-16
chr2:36116079-36136704:	Rbm18	67889	47.4	57.8	54.7	1.37302	0.045862	1.43339	0.0035295
chr5:120116513-12019897	Rbm19	74111	23.7	27.3	53.1	1.29626	0.057159	2.7671	2.77E-24
chr19:53677306-53867080	Rbm20	73713	3.7	3.0	8.3	-1.09882	0.433807	2.74614	2.90E-43
chr18:60560786-60572729	Rbm22	66810	56.3	63.8	82.4	1.27861	0.091228	1.81559	3.33E-08
chr13:46418300-46431099	Rbm24	666794	103.7	57.7	24.8	-1.58915	0.139267	-3.07242	1.33E-06
chr12:83632234-83683123	Rbm25	67039	137.7	130.7	160.1	1.06782	0.518813	1.45206	2.99E-08
chr14:105114519-1051773	Rbm26	74213	74.2	76.2	101.8	1.15905	0.220519	1.70999	4.95E-10
chr18:42275353-42341540	Rbm27	225432	35.4	40.7	48.1	1.2938	0.039634	1.69208	2.98E-08
chr6:29123573-29164724:	Rbm28	68272	38.2	39.3	64.5	1.15414	0.141314	2.10075	2.00E-26
chrX:8138975-8145880:-	Rbm3	19652	81.2	95.7	304.6	1.32214	0.110929	4.53689	1.29E-32
chr5:28317189-28419242:	Rbm33	381626	41.3	31.8	20.4	-1.16588	0.270819	-1.60827	1.90E-06
chr8:126947173-12697107	Rbm34	52202	17.4	17.7	29.6	1.1427	0.331572	2.11255	1.72E-15
chr2:173021902-17303473	Rbm38	56190	8.8	8.9	12.4	1.13677	0.568566	1.73915	0.0001404
chr7:30640995-30650228:	Rbm42	68035	61.4	67.7	100.3	1.24406	0.118933	2.02518	5.72E-12

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr1:91145103-91170795:	Rbm44	329207	1.7	0.3	0.2	-3.79226	0.001504	-4.92605	6.02E-06
chr2:76369984-76383767:	Rbm45	241490	42.3	41.3	63.7	1.09478	0.301545	1.87954	1.61E-26
chr5:66016549-66151954:	Rbm47	245945	7.2	6.7	9.5	1.06583	0.787231	1.64243	0.0003932
chr9:107740495-10777100	Rbm5	83486	262.5	249.0	172.2	1.06661	0.530929	-1.21669	0.0050421
chr9:48488697-48495330:	Rbm7	67010	128.5	150.9	153.7	1.32245	0.048201	1.48609	0.0002684
chr3:96629928-96633791:	Rbm8a	60365	36.9	42.7	69.9	1.3047	0.122165	2.32717	2.14E-11
chr10:128129470-1281802	Rbms2	56516	50.8	39.0	24.2	-1.17032	0.17106	-1.6727	8.49E-10
chr9:116572747-11762991	Rbms3	207181	91.0	82.6	36.8	1.01201	0.932423	-1.9678	1.72E-20
chrX:48695004-48710719:	Rbmx2	209003	12.0	12.5	14.1	1.17208	0.379809	1.4629	0.0026949
chr8:78505269-78508928:	Rbmxl1	19656	41.4	51.0	70.9	1.387	0.066817	2.10509	2.26E-08
chr9:98422961-98446550:	Rbp1	19659	38.9	33.3	20.0	-1.04698	0.741425	-1.55354	2.06E-07
chr4:149449702-14945496	Rbp7	63954	5.6	4.0	9.6	-1.24427	0.582445	2.00343	0.0058099
chr6:92186712-92214811:	Rbsn	78287	37.3	41.3	48.9	1.24972	0.099639	1.63328	1.16E-06
chr15:81466316-81476369	Rbx1	56438	85.8	85.8	100.6	1.12175	0.220112	1.46286	1.32E-08
chr1:160906411-16097497	Rc3h1	381305	50.3	50.3	27.5	1.1239	0.14402	-1.4587	1.32E-10
chr2:37370071-37422903:	Rc3h2	319817	54.5	62.0	60.4	1.28206	0.050162	1.37955	0.0010211
chr16:92391951-92466169	Rcan1	54720	19.3	32.8	47.7	1.87499	0.003171	2.95715	2.62E-10
chr17:43801851-44039516	Rcan2	53901	12.5	8.2	1.8	-1.36175	0.048201	-5.34974	2.19E-40
chr4:135412309-13543380	Rcan3	53902	17.1	12.2	6.1	-1.25724	0.273174	-2.18305	1.84E-07
chr4:132331919-13234575	Rcc1	100088	14.3	15.6	37.9	1.23928	0.280466	3.23802	9.69E-18
chr4:140701473-14072322	Rcc2	108911	45.6	44.0	84.5	1.08072	0.414982	2.31065	4.53E-40
chr7:80316616-80324454:	Rccd1	269955	19.3	21.1	30.5	1.2285	0.224372	1.94974	3.30E-08
chr19:4622551-4625617:-	Rce1	19671	39.6	43.9	57.5	1.24447	0.113638	1.79841	7.81E-09
chr5:91948842-91963068:	Rchy1	68098	45.0	40.7	45.5	1.01181	0.879712	1.26279	1.73E-08
chr19:29101375-29143843	Rcl1	59028	43.9	55.0	77.9	1.40231	0.012006	2.19603	3.99E-14
chr2:105385948-10539931	Rcn1	19672	87.9	102.8	115.2	1.31708	0.111515	1.62037	0.000217
chr12:111039798-1111133	Rcor1	217864	30.2	36.1	35.2	1.34863	0.045656	1.45135	0.0012779
chr1:192098546-19213804	Rcor3	214742	26.6	18.7	14.5	-1.27472	0.003552	-1.46485	1.54E-08
chr1:165648945-16570809	Rcsd1	226594	24.9	18.8	9.5	-1.19381	0.412557	-2.06125	1.62E-06
chr1:16105882-16132550:	Rdh10	98711	69.0	61.1	109.7	-1.02275	0.952885	1.93603	0.0009281
chr7:4425665-4445657:-	Rdh13	108841	20.7	24.3	36.6	1.31788	0.050463	2.18831	7.86E-14
chr10:128913591-1289192	Rdh5	19682	21.7	14.0	5.1	-1.38794	0.165856	-3.23518	3.69E-11
chr11:101627949-1016360	Rdm1	66599	59.9	51.7	19.2	-1.04279	0.795389	-2.46853	8.91E-21
chr9:52047150-52088738:	Rdx	19684	145.9	162.3	181.9	1.25405	0.112912	1.54864	4.55E-05
chr14:55618166-55625395	Rec8	56739	15.6	10.0	1.8	-1.3802	0.202409	-6.39601	3.99E-22
chr4:43875530-43944806:	Reck	53614	44.1	34.2	13.9	-1.15676	0.109791	-2.52099	1.53E-42
chr6:142350342-14238708	Recql	19691	12.7	10.8	13.5	-1.04687	0.667279	1.32922	1.28E-05
chr18:34840589-34847463	Reep2	225362	10.7	9.6	14.4	1.00397	0.986595	1.66931	1.24E-05
chr18:34344886-34373415	Reep5	13476	61.5	50.9	63.0	-1.0847	0.425111	1.27636	0.0005604
chr10:80330145-80336441	Reep6	70335	7.0	1.9	4.2	-2.76459	0.003286	-1.27501	0.426865
chr6:78466268-78468874:	Reg3g	19695	0.0	0.4	4.2	2.32619	0.16036	14.0332	4.49E-10
chr11:23741729-23770970	Rel	19696	4.7	9.9	8.0	2.27851	0.001364	2.02591	0.0011534
chr19:5637490-5648130:+	Rela	19697	53.2	66.5	64.6	1.40616	0.007401	1.51051	5.69E-05
chr7:19606222-19629438:	Relb	19698	21.0	30.9	54.7	1.59894	0.059904	3.09307	1.35E-09
chr5:63908898-63968897:	Rell1	100532	31.3	30.0	19.5	1.07434	0.577976	-1.28409	0.0037002
chr5:21884454-22344705:	Reln	19699	26.4	23.3	13.2	-1.01254	0.92844	-1.60101	1.09E-10
chr7:100845848-10086341	Relt	320100	2.7	7.3	6.3	2.75879	0.005167	2.58411	0.0014366
chr2:152627008-15263519	Rem1	19700	38.8	23.7	13.9	-1.46872	0.127854	-2.15186	5.35E-05
chr10:18055940-18125155	Reps1	19707	53.8	53.8	60.9	1.12722	0.276165	1.41223	1.04E-05
chrX:162411952-16264365	Reps2	194590	15.9	15.0	9.9	1.05623	0.62367	-1.27647	0.0008129
chr4:155074112-15508629	Rer1	67830	137.5	148.6	212.0	1.21355	0.109171	1.9138	2.20E-13
chr4:150281916-15062196	Rere	68703	78.4	62.9	29.6	-1.11701	0.587579	-2.07977	2.73E-08
chr6:137054825-13717049	Rerg	232441	10.6	9.7	27.4	1.02806	0.881188	3.19009	6.43E-35
chr6:139493182-13950190	Rergl	632971	6.9	4.1	0.1	-1.43095	0.525759	-10.4414	5.81E-09
chr5:77265494-77283697:	Rest	19712	38.4	38.2	40.0	1.12105	0.270025	1.30024	0.00044
chr6:118151748-11819774	Ret	19713	1.3	2.6	4.0	2.13912	0.086349	3.22483	0.0005019
chr16:48842552-48844461	Retnla	57262	96.4	31.2	11.4	-2.58947	0.000269	-5.99821	5.62E-16
chr16:48872608-48874498	Retnlg	245195	18.2	8.3	3.3	-1.71767	0.303565	-3.19314	0.0024406

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr6:72598628-72607488:	Retsat	67442	23.7	18.8	8.5	-1.13212	0.425089	-2.20716	3.90E-13
chr10:39732160-39875205	Rev3l	19714	164.2	135.8	66.4	-1.09739	0.762036	-1.92112	0.0004686
chr10:80540926-80561560	Rexo1	66932	18.9	21.1	23.7	1.26358	0.181202	1.55688	0.0006288
chr9:48468514-48480611:	Rexo2	104444	96.8	105.1	191.4	1.21354	0.000735	2.46165	3.36E-90
chr2:26953563-26964386:	Rexo4	227656	57.0	65.1	74.7	1.28405	0.018727	1.63245	2.22E-09
chr16:23113948-23127730	Rfc4	106344	26.8	27.7	27.0	1.15386	0.218051	1.25664	0.0075175
chr11:82803819-82871210	Rffl	67338	20.7	16.8	12.5	-1.1053	0.264993	-1.32493	1.46E-05
chr19:17394043-17401349	Rfk	54391	49.4	48.7	69.5	1.1031	0.180601	1.75361	5.71E-28
chr11:120780745-1207842	Rfng	19719	26.5	24.2	27.3	1.02395	0.843027	1.287	0.0001729
chr9:55962589-55980932:	Rfpl3s	75258	1.7	0.1	0.1	-4.89989	0.0058	-4.06919	0.0030902
chr17:49993307-50190497	Rftn1	76438	36.2	28.9	21.3	-1.11676	0.468719	-1.35473	0.0042717
chr1:55170160-55226782:	Rftn2	74013	21.5	15.1	1.9	-1.28671	0.147872	-8.66387	7.13E-57
chr1:159232326-15934758	Rfwd2	26374	54.4	56.9	70.0	1.17643	0.078816	1.60298	4.85E-12
chr8:84066836-84096992:	Rfx1	19724	17.7	15.9	6.3	1.01603	0.945406	-2.19303	1.06E-10
chr19:27761721-28011166	Rfx3	19726	20.0	14.5	4.3	-1.245	0.245216	-3.5865	1.75E-21
chr3:94955015-94961561:	Rfx5	53970	26.2	19.2	14.9	-1.22707	0.119488	-1.40324	0.0006596
chr1:39665301-39720989:	Rfx8	619289	1.8	0.2	0.2	-4.70262	0.003565	-3.82444	0.0021442
chr8:70130806-70139197:	Rfxank	19727	23.2	22.5	7.8	1.09007	0.453616	-2.37133	4.20E-27
chr1:152517530-15262511	Rgl1	19731	52.6	44.8	14.1	-1.05224	0.71908	-2.95042	2.17E-36
chr17:33929894-33937687	Rgl2	19732	55.5	48.5	28.8	-1.02158	0.818342	-1.53539	1.43E-15
chr9:21971527-21989453:	Rgl3	71746	14.4	12.0	6.0	-1.06916	0.782377	-1.89109	1.31E-05
chr17:15806253-15826586	Rgmb	68799	57.2	44.3	24.0	-1.16618	0.641226	-1.84114	0.0042834
chr1:144244669-14424910	Rgs1	50778	32.6	20.6	10.8	-1.39681	0.281161	-2.31035	0.0001869
chr17:26202962-26211324	Rgs11	50782	19.1	13.3	4.0	-1.27667	0.125126	-3.68432	6.22E-26
chr5:34949448-35033593:	Rgs12	71729	24.4	19.9	9.7	-1.0923	0.548718	-1.98421	1.22E-12
chr1:153740353-15374546	Rgs16	19734	4.4	12.5	13.8	2.87616	0.001149	3.45951	4.60E-06
chr10:5825664-5922400:-	Rgs17	56533	1.5	0.9	0.3	-1.44846	0.304764	-3.46298	2.59E-06
chr2:181688419-18169397	Rgs19	56470	19.8	21.9	44.1	1.24517	0.196722	2.73062	5.25E-17
chr1:4909576-5070285:-	Rgs20	58175	1.3	1.7	0.1	1.43984	0.334944	-8.02691	7.82E-10
chr15:36009477-36140400	Rgs22	626596	23.8	12.5	2.9	-1.69256	0.002673	-6.17528	2.26E-36
chr1:169655501-16969352	Rgs5	19737	163.9	152.3	44.6	1.02793	0.894272	-2.89631	2.74E-21
chr1:175059076-17549254	Rgs7	24012	0.8	0.5	2.7	-1.30816	0.544439	3.95791	2.55E-07
chr13:104947153-1050549	Rgs7bp	52882	9.0	5.9	1.8	-1.36376	0.076862	-3.94356	2.02E-24
chr1:153779387-15384414	Rgsl1	240816	2.1	0.9	0.2	-1.89008	0.083654	-5.85003	2.08E-09
chr1:82316579-82445367:	Rhbdd1	76867	22.2	18.0	29.8	-1.10913	0.303565	1.66922	8.38E-14
chr11:32209585-32222293	Rhbdf1	13650	51.6	49.6	64.9	1.07687	0.454394	1.56618	1.16E-11
chr11:116598166-1166270	Rhbdf2	217344	18.4	29.4	44.3	1.78327	0.01702	2.8769	1.99E-08
chr4:123787875-12382990	Rhbdl2	230726	3.6	3.9	7.1	1.19995	0.485994	2.34736	3.12E-07
chr5:24802823-24842361:	Rheb	19744	106.5	130.5	146.8	1.38185	0.09787	1.69781	0.0003355
chr15:98877760-98881414	Rhebl1	69159	48.0	29.1	1.7	-1.46762	0.282507	-16.2921	9.42E-27
chr6:115931927-11593883	Rho	212541	1.7	1.2	0.6	-1.20068	0.619183	-2.0785	0.0033114
chr9:108306205-10833793	Rhoa	11848	221.2	232.9	337.8	1.18324	0.128307	1.89557	2.27E-15
chr12:8497759-8499985:-	Rhob	11852	74.8	106.0	103.8	1.57981	0.007278	1.71243	9.13E-05
chr14:69784990-69805545	Rhobtb2	246710	24.1	18.9	10.9	-1.14691	0.502409	-1.74137	6.22E-05
chr3:104789034-10479445	Rhoc	11853	132.2	218.8	366.6	1.83047	0.028209	3.22516	2.89E-08
chr19:4425457-4439424:-	Rhod	11854	13.2	12.5	19.5	1.061	0.684248	1.84039	3.19E-13
chr17:86963111-87000069	Rhoq	104215	79.8	64.0	22.7	-1.11894	0.238821	-2.80281	3.84E-52
chr11:80209055-80267907	Rhot1	59040	51.4	55.7	58.9	1.22389	0.113777	1.42821	0.0002165
chr8:123653929-12366388	Rhou	69581	39.0	73.9	79.3	2.05484	0.031375	2.35203	0.0010706
chr15:75704288-75714419	Rhpn1	14787	5.3	4.6	1.8	-1.03043	0.923047	-2.32056	1.17E-06
chr7:35334237-35392287:	Rhpn2	52428	17.3	12.0	6.4	-1.27775	0.342951	-2.07752	7.19E-05
chr12:109603945-1096617	Rian	75745	52.4	45.9	55.8	-1.01465	0.937274	1.32297	0.0044075
chr15:85132099-85144569	Ribc2	67747	1.3	0.1	0.2	-3.89523	0.016855	-3.27427	0.0091621
chr7:140857397-14086373	Ric8	101489	75.2	64.9	51.0	-1.03971	0.632117	-1.17967	0.0017365
chr15:6708381-6800400:+	Rictor	78757	62.0	55.4	34.4	1.00098	0.993941	-1.43829	2.08E-10
chr2:52072837-52122381:	Rif1	51869	68.7	66.3	71.4	1.08244	0.4056	1.29852	8.44E-05
chr3:94464985-94473591:	Riiad1	66353	10.4	5.0	4.0	-1.81055	0.029186	-2.00524	0.0011326
chr5:124493080-12453139	Rilpl1	75695	32.5	29.1	19.4	1.00738	0.959921	-1.33447	0.0002235

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr5:124463265-12447823	Rilpl2	80291	30.8	26.8	15.3	-1.03039	0.869967	-1.5998	6.34E-06
chr16:17208135-17213982	Rimbp3	239731	4.3	0.2	0.5	-11.0147	2.34E-08	-4.91201	2.36E-05
chr6:122453609-12248630	Rimklb	108653	4.7	2.2	0.8	-1.89449	0.005125	-4.27074	2.72E-14
chr1:22288422-22432843:	Rims1	116837	8.9	5.7	2.4	-1.40328	0.207543	-2.83853	1.75E-07
chr1:22468191-22805724:	Rims1	116837	2.9	2.8	0.9	1.05349	0.916655	-2.26866	0.0036834
chr15:39198286-39684372	Rims2	116838	2.6	1.8	0.7	-1.29773	0.445944	-2.63169	5.20E-05
chr19:5050808-5057071:+	Rin1	225870	4.4	4.0	12.0	1.04848	0.899241	3.23054	5.60E-09
chr2:145786116-14588761	Rin2	74030	125.8	91.9	18.8	-1.23018	0.082422	-5.27323	4.93E-80
chr7:28788969-28798966:	Rinl	320435	7.6	9.4	12.6	1.33284	0.393898	1.95836	0.0048794
chr5:23787744-23820369:	Rint1	72772	35.1	31.5	42.9	1.00527	0.959326	1.52902	7.68E-17
chr13:38036989-38061433	Riok1	71340	47.7	60.1	74.5	1.42211	0.023826	1.93164	3.97E-08
chr17:17374332-17394899	Riok2	67045	35.3	42.1	71.0	1.34168	0.030129	2.48219	4.24E-19
chr18:12128850-12157367	Riok3	66878	81.5	92.6	115.2	1.2786	0.032945	1.75767	1.09E-10
chr13:34002874-34035170	Ripk1	19766	31.0	53.7	36.5	1.90099	0.001354	1.45318	0.0307166
chr14:55784995-55788857	Ripk3	56532	5.6	7.7	13.7	1.52198	0.166767	2.82421	2.80E-06
chr3:88716854-88731048:	Rit1	19769	49.0	46.9	31.4	1.06617	0.483042	-1.249	0.0004208
chr18:30974314-31317128	Rit2	19762	2.9	3.2	0.3	1.2022	0.631009	-6.32792	1.46E-10
chrX:103957167-10398128	Rlim	19820	84.4	96.5	100.1	1.28663	0.07923	1.47315	0.000387
chr8:84043067-84044979:	Rln3	212108	0.6	0.9	2.9	1.4455	0.582169	3.7776	0.0020893
chr4:19575066-19606932:	Rmdn1	66302	28.2	22.7	14.5	-1.11828	0.49787	-1.5477	0.0001063
chr17:79614900-79682152	Rmdn2	381110	20.3	18.9	20.5	1.03815	0.779055	1.26049	0.003536
chr2:119136998-11915703	Rmdn3	67809	26.8	30.6	42.2	1.28127	0.051359	1.95339	1.26E-12
chr6:71388634-71440637:	Rmnd5a	68477	106.4	96.8	34.1	1.01807	0.769978	-2.49372	1.41E-139
chr11:51623673-51635896	Rmnd5b	66089	38.9	40.6	89.0	1.17191	0.189308	2.83144	6.90E-35
chr4:43492785-43493059:	Rmrp	19782	####	38660.1	24705.8	1.47266	0.007019	1.04852	0.722663
chr10:92081746-92165178	Rmst	110333	65.2	40.1	23.7	-1.45825	0.086592	-2.1538	3.65E-06
chr6:47744058-47744231:	Rn4.5s	19799	0.7	1.8	4.2	1.7985	0.36603	3.63363	0.0045892
chr17:39842997-39848829	Rn45s	1.01E+08	####	1655.4	2152.6	1.48763	0.067693	2.10889	5.47E-06
chr14:51049451-51050163	Rnase11	497113	0.0	0.2	1.6	1.70413	0.427578	6.70258	4.47E-05
chr14:51091077-51106151	Rnase4	58809	381.0	313.6	110.1	-1.0925	0.459806	-2.75034	7.39E-37
chr12:28649602-28659591	Rnaseh1	19819	27.6	27.0	33.6	1.09356	0.352479	1.51743	1.08E-10
chr8:84956610-84966011:	Rnaseh2a	69724	36.0	25.9	14.1	-1.24863	0.219099	-2.00961	1.10E-07
chr11:70238123-70239852	Rnasek	52898	57.9	59.7	71.0	1.15601	0.191056	1.52524	8.80E-08
chr1:153749426-15376422	Rnasel	24014	58.4	44.2	6.0	-1.18656	0.426552	-7.3255	4.06E-42
chr15:98669205-98677461	Rnd1	223881	1.8	24.3	13.6	11.9411	4.50E-20	7.69394	1.40E-15
chr11:101468338-1014713	Rnd2	11858	10.7	7.3	4.5	-1.29418	0.233811	-1.85765	0.0001613
chr2:51130439-51149111:	Rnd3	74194	60.7	64.7	113.8	1.19441	0.195302	2.31464	8.21E-18
chr5:115241770-11527289	Rnf10	50849	80.5	84.2	87.8	1.17749	0.155857	1.36085	0.0003313
chr6:71493894-71510881:	Rnf103	22644	40.0	36.9	24.1	1.03008	0.747826	-1.32726	4.68E-07
chr4:109452857-10947650	Rnf11	29864	111.0	119.6	157.4	1.20832	0.060847	1.76259	3.50E-14
chr9:70425429-70503725:	Rnf111	93836	31.3	36.0	36.7	1.2965	0.07356	1.45892	0.0006359
chrX:37191343-37192465:	Rnf113a1	69942	8.4	8.5	11.3	1.14273	0.610101	1.65117	0.0029451
chr3:96727611-96791155:	Rnf115	67845	37.7	40.8	42.8	1.2142	0.067348	1.41521	1.34E-05
chr7:102019872-10206513	Rnf121	75212	35.7	35.5	53.6	1.11395	0.25417	1.86733	2.71E-22
chr8:31111846-31131473:	Rnf122	68867	9.6	9.4	3.8	1.07071	0.86071	-1.92785	0.0033851
chr18:20944625-20983848	Rnf125	67664	23.3	17.4	7.4	-1.20861	0.621066	-2.3507	0.000656
chr10:79758515-79766952	Rnf126	70294	22.9	27.7	45.5	1.36374	0.258179	2.38425	9.63E-06
chr3:57736062-57835425:	Rnf13	24017	64.5	58.4	34.9	1.00749	0.942286	-1.47638	1.92E-13
chr6:23648869-23650305:	Rnf133	386611	6.3	0.9	1.2	-5.06128	9.79E-06	-3.62285	4.11E-05
chr11:80183872-80199753	Rnf135	71956	14.3	12.0	6.3	-1.07477	0.746328	-1.78538	2.66E-05
chr18:21001300-21028224	Rnf138	56515	24.3	22.0	30.6	1.02267	0.910115	1.5615	3.28E-05
chrX:163760139-16376133	Rnf138rt1	74264	1.3	0.7	0.1	-1.48043	0.54979	-3.74129	0.0034003
chr15:58889229-58902390	Rnf139	75841	46.1	42.9	49.0	1.04698	0.742498	1.3231	0.0010843
chr18:38296635-38317849	Rnf14	56736	63.6	55.4	62.5	-1.0302	0.783672	1.22765	0.0015795
chr7:110816535-11084438	Rnf141	67150	57.4	68.4	56.6	1.33361	0.000364	1.23087	0.0028963
chr12:26306794-26415262	Rnf144a	108089	15.6	13.2	5.5	-1.06807	0.727849	-2.22472	4.93E-12
chr13:47122720-47247991	Rnf144b	218215	26.6	15.6	7.2	-1.53352	0.016855	-2.8807	2.70E-14
chr6:23653895-23655136:	Rnf148	71300	3.2	1.0	0.6	-2.35091	0.087132	-3.12361	0.0031433

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr1:39551296-39577347:	Rnf149	67702	46.4	41.9	57.6	1.00637	0.972912	1.54044	9.48E-06
chr8:82863356-83091271:	Rnf150	330812	20.3	17.6	5.4	-1.0318	0.748913	-2.98653	5.23E-75
chr17:24715840-24718057	Rnf151	67504	8.7	1.1	2.9	-5.35159	5.64E-06	-2.18477	0.0149513
chr1:105276917-10535671	Rnf152	320311	1.7	1.0	0.3	-1.59973	0.172385	-3.97988	9.75E-08
chr11:116336345-1164130	Rnf157	217340	7.7	5.4	2.5	-1.29085	0.295439	-2.38426	7.39E-07
chr8:122466147-12247606	Rnf166	68718	55.7	54.1	70.0	1.08875	0.218836	1.56846	4.54E-21
chr11:70647589-70651414	Rnf167	70510	182.1	144.6	53.4	-1.13226	0.325356	-2.69799	2.05E-29
chr16:32277461-32301439	Rnf168	70238	24.1	25.5	27.5	1.17969	0.113017	1.42274	5.57E-06
chr7:99920254-99980458:	Rnf169	108937	33.0	30.4	31.5	1.03262	0.743609	1.19477	0.0031995
chr14:56402697-56525031	Rnf17	30054	3.8	1.1	1.0	-2.62206	0.007401	-2.78256	0.0004519
chr13:43615797-43670944	Rnf182	328234	2.0	0.9	0.2	-1.83849	0.07347	-6.41333	4.20E-11
chr4:62427542-62434726:	Rnf183	76072	0.5	0.6	1.1	1.28717	0.620717	2.46372	0.0042854
chr11:3415973-3452956:-	Rnf185	193670	29.7	31.6	31.6	1.19432	0.029322	1.32691	6.10E-06
chr11:58932288-58938906	Rnf187	108660	114.9	112.1	144.5	1.09364	0.243221	1.57147	3.75E-17
chr15:36239934-36283147	Rnf19a	30945	68.6	89.3	104.1	1.46742	0.064647	1.85997	8.39E-05
chr4:129058271-12908452	Rnf19b	75234	37.4	87.5	39.4	2.49457	0.001929	1.29066	0.336019
chr4:49632060-49656886:	Rnf20	109331	81.2	82.8	82.1	1.1475	0.202836	1.26157	0.0037702
chr14:104477534-1045226	Rnf219	72486	15.5	16.9	19.4	1.22556	0.080981	1.56314	2.32E-07
chr4:117271464-11749691	Rnf220	66743	41.2	37.7	53.9	1.02654	0.770925	1.63431	1.26E-21
chr5:29195993-29225524:	Rnf32	56874	11.2	3.9	1.9	-2.40508	0.01279	-3.98645	8.75E-07
chr4:44126212-44168283:	Rnf38	73469	52.3	43.4	17.6	-1.07964	0.519631	-2.35486	8.29E-28
chr5:34336250-34353445:	Rnf4	19822	101.7	131.1	161.7	1.45332	0.06949	1.94868	1.83E-05
chr7:127588698-12760360	Rnf40	233900	60.0	59.2	65.9	1.11467	0.405947	1.37044	0.0005819
chr5:146209194-14622145	Rnf6	74132	50.8	57.2	55.8	1.2705	0.030616	1.37211	0.0002348
chr9:96470957-96478595:	Rnf7	19823	130.9	136.8	162.6	1.17588	0.310133	1.54035	0.0001553
chr4:33310311-33502610:	Rngtt	24018	21.5	22.4	32.1	1.16814	0.102537	1.8642	1.17E-19
chr7:141160326-14117285	Rnh1	107702	123.0	108.1	130.0	-1.01871	0.871062	1.31797	1.28E-05
chr19:33137745-33392295	Rnls	67795	3.8	1.5	1.4	-2.08987	0.022401	-2.05885	0.0045917
chr11:76243736-76250622	Rnmtl1	67390	16.6	27.3	54.0	1.83097	0.010226	3.83383	2.14E-13
chr17:24414675-24425897	Rnps1	19826	69.2	80.0	132.0	1.30557	0.093707	2.35341	2.35E-13
chr4:132270079-13227018	Rnu11	353373	80.0	128.8	379.7	1.78507	0.028351	5.44619	6.93E-18
chr15:83149645-83149794	Rnu12	104307	49.6	57.4	139.5	1.2926	0.151315	3.44505	6.80E-25
chr3:86140617-86140687:	Rnu73b	19871	68.2	100.0	175.1	1.61805	0.093068	3.01008	1.34E-07
chr16:72663149-73046100	Robo1	19876	20.0	16.4	3.2	-1.08678	0.479375	-4.96437	6.97E-85
chr16:73892306-74410912	Robo2	268902	18.4	15.6	3.7	-1.05461	0.641623	-3.89874	2.21E-75
chr12:16894978-16988274	Rock2	19878	73.6	101.7	103.6	1.55527	0.035322	1.72656	0.0008261
chr16:5008729-5013553:-	Rogdi	66049	28.2	20.6	14.4	-1.21906	0.051057	-1.55692	1.36E-08
chr2:156144153-15614579	Romo1	67067	46.1	56.7	82.9	1.38046	0.003128	2.23381	2.93E-21
chr16:34651211-34678610	Ropn1	76378	11.8	0.7	1.6	-7.78616	2.33E-05	-4.03962	0.0008844
chr15:31441210-31453689	Ropn1l	252967	24.2	2.4	3.2	-6.17702	1.51E-05	-4.422	4.82E-05
chr13:53109317-53286109	Ror2	26564	20.9	25.2	39.6	1.36261	0.128859	2.32123	1.99E-08
chr9:68653786-69388246:	Rora	19883	34.2	29.6	7.7	-1.03041	0.803888	-3.53088	7.07E-74
chr19:18930609-19111196	Rorb	225998	16.5	12.7	5.0	-1.1734	0.496961	-2.5343	3.77E-09
chrX:20364481-20405653:	Rp2h	19889	29.0	25.0	16.8	-1.04067	0.778057	-1.37675	0.0001708
chr9:22448312-22468356:	Rp9	55934	74.1	59.4	42.7	-1.11978	0.308471	-1.38667	4.23E-05
chr6:8255936-8259141:-	Rpa3	68240	46.2	40.3	26.3	-1.0337	0.879431	-1.39602	0.0075187
chr11:70970200-70977933	Rpain	69723	49.4	66.9	35.6	1.51391	0.003297	-1.10694	0.427873
chr15:97675105-97705822	Rpap3	71919	29.3	25.5	29.6	-1.02487	0.849284	1.26523	0.0012587
chr1:66700893-66719805:	Rpe	66646	40.4	39.4	46.2	1.09019	0.30104	1.42885	7.33E-10
chr3:146506346-14652142	Rpf1	70285	35.9	42.6	49.9	1.33297	0.049729	1.7238	9.03E-07
chr10:40223246-40247039	Rpf2	67239	24.2	33.2	78.0	1.53795	0.016855	3.89806	2.76E-23
chrX:10158216-10216795:	Rpgr	19893	6.4	4.9	3.1	-1.1675	0.296342	-1.65431	2.49E-06
chr14:52110903-52161339	Rpgrip1	77945	4.1	1.6	0.6	-2.22033	0.005104	-4.7205	3.10E-11
chr8:91217030-91313222:	Rpgrip1l	244585	11.3	9.9	2.5	-1.03054	0.858487	-3.54233	6.53E-39
chr11:75830992-75925891	Rph3al	380714	7.5	6.2	1.4	-1.0934	0.740718	-4.00496	4.11E-16
chr6:70765720-70792175:	Rpia	19895	40.8	41.9	58.9	1.14879	0.188604	1.79784	3.69E-15
chrX:74270816-74273135:	Rpl10	110954	####	2725.3	2999.1	1.05736	0.654562	1.29834	0.0010538
chr17:28328471-28331033	Rpl10a	19896	####	1367.8	1513.1	1.12354	0.103434	1.38795	5.59E-10

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr12:66283379-66284401	Rpl10l	238217	5.0	0.2	0.5	-8.31862	3.74E-05	-4.89029	0.0003305
chr4:136049948-13605337	Rpl11	67025	####	1660.4	1898.3	1.03167	0.826767	1.31511	0.0010161
chr9:120571517-12057465	Rpl14	67115	####	1500.8	1566.1	1.03558	0.751888	1.20737	0.0057613
chr14:18267823-18270986	Rpl15	66480	398.3	463.8	581.1	1.30943	0.068359	1.80616	9.85E-08
chr7:45718071-45720835:	Rpl18	19899	####	1629.6	2049.6	1.11624	0.240526	1.56493	1.74E-11
chr11:98026710-98030493	Rpl19	19921	####	2464.8	2609.7	1.09314	0.303652	1.29251	3.28E-05
chr16:55966275-55971437	Rpl24	68193	####	1106.8	1449.5	1.083	0.472838	1.57888	9.15E-10
chr11:101442245-1014455	Rpl27	19942	691.2	678.9	998.6	1.0985	0.467665	1.79412	1.55E-11
chr7:4792965-4794547:+	Rpl28	19943	####	1605.8	1839.8	1.00985	0.928106	1.29218	8.20E-06
chr9:106429539-10643156	Rpl29	19944	806.4	784.4	931.9	1.08723	0.247913	1.44265	7.37E-13
chr15:80077781-80083406	Rpl3	27367	####	2039.7	2178.2	1.03352	0.756793	1.23362	0.001255
chr6:115805514-11580874	Rpl32	19951	####	2280.2	2465.0	1.05701	0.646026	1.2759	0.0016804
chr3:130726827-13073039	Rpl34	68436	1.7	3.7	8.6	2.25355	0.021529	5.42909	9.79E-11
chr2:39001581-39005131:	Rpl35	66489	####	1159.3	1334.0	1.11213	0.314231	1.42585	2.07E-06
chr17:56613395-56614246	Rpl36	54217	####	1269.1	1419.2	1.04903	0.727849	1.31068	0.0014999
chr12:69182734-69184067	Rpl36al	66483	211.2	253.0	547.6	1.34443	0.064425	3.16931	9.93E-23
chr16:10170228-10174911	Rpl39l	68172	6.1	0.2	1.0	-6.85537	0.000345	-3.13583	0.0138885
chr10:128548110-1285491	Rpl41	67945	####	2268.1	3536.5	1.19973	0.041361	2.07821	2.73E-28
chr5:121204501-12120924	Rpl6	19988	####	1330.7	1485.9	1.06417	0.55967	1.32761	5.29E-05
chr2:26910807-26913311:	Rpl7a	27176	####	1925.4	2918.5	1.13743	0.070359	1.92652	2.47E-36
chr17:46773907-46782656	Rpl7l1	66229	95.0	129.2	219.9	1.53028	0.01502	2.82609	1.41E-14
chr15:76904071-76906318	Rpl8	26961	####	2027.2	2556.6	1.08425	0.389075	1.52402	6.38E-11
chr5:115559467-11556372	Rplp0	11837	####	2151.0	2534.4	1.09443	0.309286	1.43915	5.77E-09
chr9:61913283-61914510:	Rplp1	56040	####	3939.8	4022.2	1.10278	0.35675	1.25657	0.0025738
chr7:141447650-14145134	Rplp2	67186	####	1498.0	1797.3	1.03722	0.786838	1.39005	4.04E-05
chr6:88084473-88105304:	Rpn1	103963	99.3	107.4	248.1	1.21606	0.138726	3.08176	2.48E-32
chr2:157279098-15732631	Rpn2	20014	138.6	128.8	226.0	1.04133	0.645745	2.03477	4.31E-40
chr14:8080313-8091846:+	Rpp14	67053	33.1	33.8	39.5	1.14625	0.067701	1.49157	2.06E-13
chr4:41712033-41713517:	Rpp25l	69961	53.0	62.2	64.4	1.3221	0.105001	1.50751	0.0016559
chr19:36083716-36104773	Rpp30	54364	34.2	35.3	40.8	1.15855	0.292402	1.48466	6.43E-05
chr2:3328949-3332628:-	Rpp38	227522	23.3	39.1	69.1	1.87518	0.000361	3.58946	1.17E-18
chr13:35895104-35906347	Rpp40	208366	10.5	8.1	11.7	-1.16389	0.382694	1.39252	0.0063798
chr14:50807447-50807771	Rpph1	85029	####	75695.2	50982.8	1.3944	4.80E-05	1.04675	0.566233
chr2:158028497-15807820	Rprd1b	70470	22.4	23.8	24.8	1.19857	0.169829	1.37883	0.0010649
chr3:95759873-95818953:	Rprd2	75137	31.9	27.3	20.3	-1.04139	0.707731	-1.25441	0.0007685
chr7:45122388-45124389:	Rps11	27207	####	1628.7	2071.6	1.0899	0.394541	1.54749	3.21E-10
chr7:116331507-11633419	Rps13	68052	####	1099.4	1340.6	1.06265	0.614132	1.44341	2.10E-06
chr7:118104376-11811614	Rps15a	267019	258.6	247.0	278.2	1.0663	0.626039	1.33937	0.000603
chr17:33951999-33955641	Rps18	20084	####	3409.8	3922.7	1.08585	0.437726	1.3947	5.03E-06
chr15:80260614-80264306	Rps19bp1	66538	30.5	40.3	77.8	1.48369	0.048608	3.08957	2.62E-14
chr17:24720063-24721927	Rps2	16898	####	1545.9	2619.8	1.11653	0.164736	2.11111	8.75E-40
chr2:180257379-18025844	Rps21	66481	####	2043.1	1426.8	-1.03168	0.865432	-1.31504	0.009485
chr10:128624529-1286265	Rps26	27370	####	1467.6	1818.2	1.11199	0.245669	1.53641	3.59E-11
chr3:90212667-90213648:	Rps27	57294	10.5	13.5	21.6	1.42141	0.268538	2.4247	8.51E-05
chr11:29545842-29548040	Rps27a	78294	####	1348.8	1566.2	1.0384	0.801823	1.34187	0.0009573
chr9:66946118-66949509:	Rps27l	67941	207.8	237.3	511.3	1.28338	0.159597	3.0021	6.84E-18
chr6:148354656-14835559	Rps4l	66184	17.0	18.1	25.3	1.19676	0.47356	1.81687	0.0004517
chr4:86854099-86857367:	Rps6	20104	####	1164.7	1345.4	1.08404	0.413436	1.39807	8.84E-07
chr17:7170115-7303316:+	Rps6ka2	20112	11.5	11.3	5.0	1.10778	0.492055	-1.81778	4.40E-09
chr19:6829084-6840627:-	Rps6ka4	56613	26.2	23.2	33.6	-1.00571	0.965255	1.60146	1.37E-12
chr12:100549778-1007250	Rps6ka5	73086	19.8	19.0	3.9	1.07614	0.487749	-4.0429	5.21E-74
chr11:86499011-86544807	Rps6kb1	72508	39.1	42.1	44.2	1.21524	0.110753	1.4089	0.0001961
chr1:190772879-19091177	Rps6kc1	320119	35.3	33.1	42.3	1.04922	0.534276	1.49825	2.74E-16
chr7:3704041-3706897:+	Rps9	76846	####	2413.5	2597.3	1.01687	0.887987	1.22448	0.0022568
chr9:120127766-12013236	Rpsa	16785	####	1902.8	2177.8	1.10602	0.282075	1.41368	1.87E-07
chr11:119602995-1198995	Rptor	74370	27.3	25.3	28.9	1.03936	0.754196	1.32387	0.0001659
chr17:25727751-25731456	Rpusd1	106707	21.5	16.8	11.0	-1.13997	0.273546	-1.55132	4.46E-07
chr2:119034790-11904219	Rpusd2	271842	4.0	4.6	6.5	1.28985	0.028771	2.02051	1.24E-16

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr9:35267881-35275957:	Rpusd4	71989	28.2	24.2	28.6	-1.04464	0.680986	1.2648	0.0002965
chr1:74506060-74530842:	Rqcd1	58184	36.6	31.1	42.6	-1.0539	0.700937	1.45301	7.53E-06
chr4:86575673-86577283:	Rraga	68441	44.4	51.1	90.9	1.29785	0.143988	2.50889	1.18E-12
chrX:153139958-15317194	Rragb	245670	14.7	11.9	7.9	-1.09957	0.427299	-1.48366	2.86E-06
chr4:123917433-12393699	Rragc	54170	59.2	62.2	75.3	1.18407	0.194617	1.58154	1.24E-06
chr4:32982998-33022180:	Rragd	52187	8.8	5.9	1.6	-1.33726	0.21115	-4.22181	4.11E-17
chr7:114046782-11411778	Rras2	66922	33.3	42.3	65.1	1.42174	0.071274	2.38692	2.09E-09
chr2:143947395-14401126	Rrbp1	81910	129.5	141.8	192.1	1.23916	0.200076	1.83766	5.48E-07
chr12:24708254-24714146	Rrm2	20135	4.3	6.0	9.0	1.54436	0.047909	2.54156	1.05E-08
chr15:37923953-37961055	Rrm2b	382985	30.1	27.3	17.2	1.00969	0.931273	-1.39506	2.29E-08
chr16:13780699-13814841	Rrn3	106298	50.0	64.3	120.2	1.44759	0.055064	2.92338	7.91E-14
chr3:87922601-87930195:	Rrnad1	229503	36.3	33.1	20.7	1.02082	0.865708	-1.39961	9.97E-07
chr10:78400362-78413043	Rrp1	18114	157.7	164.7	268.4	1.18181	0.338243	2.10158	1.00E-09
chr19:41862851-41896153	Rrp12	107094	10.4	22.5	100.1	2.34915	0.004498	10.1047	2.15E-22
chr1:186721087-18674935	Rrp15	67223	46.3	62.4	164.2	1.5187	0.02789	4.27754	1.85E-24
chr17:32036162-32062862	Rrp1b	72462	18.0	28.6	44.4	1.76646	0.063655	2.8743	5.27E-06
chr17:46667453-46674255	Rrp36	224823	44.6	46.9	68.3	1.18075	0.134914	1.90546	4.58E-16
chr15:83115846-83122801	Rrp7a	74778	70.7	82.3	103.4	1.31066	0.028351	1.81734	1.93E-10
chr7:105731730-10573738	Rrp8	101867	25.6	35.3	67.1	1.54437	0.049133	3.14348	4.36E-12
chr9:106477309-10648541	Rrp9	27966	30.3	50.3	118.7	1.85315	0.001921	4.66134	5.37E-22
chr1:9545408-9547455:+	Rrs1	59014	20.6	42.3	116.9	2.23835	0.003514	6.29805	6.41E-17
chr12:26442743-26456452	Rsad2	58185	14.1	13.0	3.4	1.01308	0.96991	-3.13816	5.48E-10
chr3:103914120-10396662	Rsbn1	229675	47.8	46.7	28.6	1.0984	0.500003	-1.33601	0.0023893
chr5:20893024-20951822:	Rsbn1l	242860	31.7	24.6	14.8	-1.15967	0.191815	-1.70459	9.79E-11
chr7:97579896-97692782:	Rsf1	233532	33.0	29.0	19.2	-1.01556	0.877489	-1.37756	5.48E-09
chr4:141213956-14122011	Rsg1	76166	6.0	4.7	1.8	-1.13405	0.73387	-2.48531	0.0001504
chr16:11193037-11203292	Rsl1d1	66409	123.0	170.3	320.6	1.55669	0.033772	3.14207	3.74E-13
chr9:73113469-73123333:	Rsl24d1	225215	52.4	61.0	96.2	1.30903	0.044857	2.27144	1.83E-16
chr13:67096613-67114028	Rslcan18	432770	7.6	5.9	3.3	-1.16148	0.561581	-1.80181	0.000669
chr17:31255020-31277356	Rsph1	22092	20.5	2.4	2.8	-5.541	1.99E-05	-4.45099	1.78E-05
chr17:6904716-6948356:-	Rsph3b	1E+08	15.3	11.9	7.8	-1.15323	0.288176	-1.57283	3.70E-06
chr7:19054687-19074447:	Rsph6a	83434	2.9	0.5	0.6	-3.77608	0.001744	-3.10956	0.0012879
chr17:46129277-46144198	Rsph9	75564	35.8	28.2	8.7	-1.13432	0.347294	-3.23915	8.06E-31
chr4:124986430-12500909	Rspo1	192199	44.3	31.4	12.2	-1.26934	0.277736	-2.82716	3.25E-11
chr10:29453107-29535867	Rspo3	72780	265.1	141.2	46.8	-1.62182	0.273174	-3.70592	3.61E-05
chr5:123728426-12374941	Rsrc2	208606	209.2	191.0	126.0	1.02283	0.788367	-1.32544	1.30E-08
chr4:134923625-13492737	Rsrp1	27981	497.1	426.7	206.6	-1.04284	0.743015	-1.91862	1.30E-17
chr2:13076967-13271415:	Rsu1	20163	156.0	140.2	85.6	-1.00034	0.998624	-1.45512	2.43E-06
chr3:116488964-11650817	Rtca	66368	34.2	36.9	56.8	1.21569	0.189879	2.05492	1.23E-11
chr10:85938637-85957793	Rtcb	28088	218.9	217.8	254.6	1.11515	0.180062	1.45181	2.11E-10
chr12:72211749-72409054	Rtn1	104001	1.5	0.9	0.5	-1.44915	0.260006	-2.29101	0.0007644
chr10:43901807-43947862	Rtn4ip1	170728	5.4	4.6	7.9	-1.04578	0.775734	1.81886	2.64E-12
chr16:18127706-18152408	Rtn4r	65079	2.3	1.1	0.3	-1.67987	0.204199	-5.24985	2.84E-07
chr11:75193993-75267762	Rtn4rl1	237847	4.8	4.0	1.1	-1.07509	0.762036	-3.33365	9.07E-15
chr16:23609919-23614222	Rtp4	67775	36.6	46.1	12.7	1.39541	0.214932	-2.19697	7.07E-05
chr18:88971790-89131014	Rttn	246102	20.1	18.5	9.3	1.03076	0.783293	-1.72331	7.23E-17
chr11:50389303-50431111	Rufy1	216724	43.2	42.4	52.0	1.10872	0.478004	1.49984	3.98E-05
chr10:62980223-63018742	Rufy2	70432	19.5	14.7	9.0	-1.18448	0.193153	-1.71785	1.08E-08
chr11:102393403-1024029	Rundc3a	51799	2.0	1.7	0.8	-1.0309	0.932943	-1.84743	0.0026065
chr16:92601466-92826074	Runx1	12394	5.8	8.1	9.1	1.5183	0.138931	1.87953	0.0030637
chr17:44495987-44814797	Runx2	12393	3.1	2.2	0.9	-1.25472	0.504456	-2.65487	2.57E-05
chr4:43381982-43427092:	Rusc2	100213	47.9	33.6	18.9	-1.2755	0.32967	-1.96837	0.0001433
chr6:88465423-88497566:	Ruvbl1	56505	56.8	63.4	97.2	1.26054	0.122866	2.1212	7.36E-12
chr7:45421898-45434464:	Ruvbl2	20174	58.1	56.6	100.2	1.09267	0.355868	2.15229	5.77E-33
chr10:33996555-34019616	Rwdd1	66521	65.8	69.7	121.0	1.18913	0.130437	2.28102	7.04E-24
chr9:86571988-86574899:	Rwdd2a	69519	4.3	2.7	1.2	-1.42915	0.302295	-2.59508	0.0002138
chr3:121155402-12117169	Rwdd3	66568	11.4	6.3	3.7	-1.59879	0.033904	-2.3879	4.62E-07
chr8:47533645-47552837:	Rwdd4a	192174	18.5	22.7	32.5	1.38357	0.066688	2.16685	4.28E-09

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr3:79644716-79737794:	Rxfp1	381489	158.8	160.5	220.0	1.12483	0.479698	1.71253	1.76E-06
chr5:150018675-15008218	Rxfp2	140498	2.6	4.1	42.5	1.73981	0.034695	17.6995	3.11E-51
chr2:27677201-27763319:	Rxra	20181	51.7	38.5	25.5	-1.20589	0.122787	-1.61482	1.07E-07
chr1:167598362-16763962	Rxrg	20183	0.6	0.5	1.2	1.04906	0.929375	2.42961	0.0010579
chr6:100228565-10028735	Rybp	56353	24.0	42.5	56.3	1.97624	9.20E-05	2.84725	1.20E-12
chr9:102834920-10290830	Ryk	20187	103.0	94.7	97.4	1.02719	0.767606	1.18025	0.0026888
chr3:90511034-90514330:	S100a1	20193	83.7	73.5	45.2	-1.02086	0.898442	-1.48	1.39E-05
chr3:90541223-90543151:	S100a16	67860	109.5	102.3	121.3	1.04057	0.783489	1.37712	0.0001983
chr3:90603770-90606045:	S100a4	20198	72.0	85.1	142.8	1.26629	0.555104	2.26749	0.0021273
chr3:90654302-90658130:	S100a7a	381493	21.3	14.6	2.5	-1.30161	0.543493	-5.59217	5.11E-09
chr4:129150825-12918948	S100pbp	74648	76.8	72.9	39.3	1.06215	0.436909	-1.55829	1.50E-16
chr3:115710433-11571505	S1pr1	13609	32.1	46.9	61.8	1.62544	0.000583	2.37197	1.29E-13
chr7:46740499-46742980:	Saa1	20208	1.1	1.4	6.7	1.27944	0.628755	5.83102	2.02E-09
chr19:6116004-6118586:-	Sac3d1	66406	10.2	10.0	17.5	1.09276	0.619553	2.12295	2.52E-12
chr9:123529882-12359259	Sacm1l	83493	77.2	82.1	94.9	1.19307	0.033782	1.53369	9.76E-12
chr14:61138457-61240693	Sacs	50720	10.7	9.0	18.1	-1.07554	0.747989	2.08221	4.21E-08
chr7:16320236-16387896:	Sae1	56459	54.6	52.8	76.6	1.08761	0.535498	1.74941	2.30E-10
chr14:52311177-52328670	Sall2	50524	20.5	14.7	11.6	-1.25439	0.051588	-1.40649	0.0001345
chr15:53461801-53902436	Samd12	320679	11.3	9.2	3.8	-1.10275	0.718408	-2.28871	2.28E-06
chr11:95009879-95026087	Samd14	217125	18.0	16.0	9.5	-1.01033	0.964309	-1.50433	0.0010484
chr12:87200543-87213538	Samd15	238333	1.8	0.8	0.6	-1.8325	0.100578	-2.10123	0.0091041
chr14:46882965-47105817	Samd4	74480	40.2	38.0	22.6	1.06114	0.708877	-1.41608	0.000435
chr7:28399522-28436191:	Samd4b	233033	21.1	25.3	24.9	1.35204	0.098248	1.46222	0.0065087
chr10:9627259-9675208:-	Samd5	320825	2.3	2.8	5.2	1.34117	0.20473	2.73115	3.07E-10
chr14:21750531-21798725	Samd8	67630	15.4	16.0	21.5	1.17716	0.383188	1.7286	2.71E-05
chr6:3372258-3399571:-	Samd9l	209086	80.5	77.1	37.3	1.06105	0.761198	-1.71395	4.35E-06
chr2:157097529-15713522	Samhd1	56045	42.0	36.6	20.0	-1.02939	0.876369	-1.67452	5.45E-07
chr15:84192233-84214303	Samm50	68653	85.9	74.8	108.6	-1.02705	0.811917	1.57853	5.46E-13
chr11:115933659-1159655	Sap30bp	57230	56.7	58.4	65.7	1.15446	0.089818	1.44488	3.63E-09
chr11:57801637-57810615	Sap30l	50724	35.9	35.5	18.8	1.10979	0.399359	-1.52241	1.67E-06
chr17:35025973-35028016	Sapcd1	78376	1.1	0.7	0.1	-1.38545	0.557691	-3.62373	0.0013949
chr2:25372035-25378213:	Sapcd2	72080	0.8	0.8	1.3	1.18909	0.626745	2.02949	0.0013774
chr10:61680321-61693297	Sar1a	20224	173.1	204.3	286.9	1.32741	0.02601	2.05288	1.07E-13
chr11:51763663-51791953	Sar1b	66397	58.9	67.0	88.7	1.28142	0.117552	1.86149	1.13E-07
chr8:34154563-34170847:	Saraf	67887	171.6	194.1	226.5	1.27545	0.119066	1.6361	2.50E-05
chr2:27188393-27247303:	Sardh	192166	15.4	13.8	18.7	-1.00094	0.994268	1.51527	1.78E-11
chr11:78472330-78497754	Sarm1	237868	1.9	1.6	0.8	-1.04907	0.878604	-1.92141	0.0003252
chr10:128821771-1288776	Sarnp	66118	88.7	106.9	145.8	1.35532	0.02556	2.03381	6.92E-12
chr3:108424864-10844525	Sars	20226	59.4	55.2	110.4	1.04	0.671635	2.31456	2.63E-52
chr7:28741968-28753879:	Sars2	71984	6.0	5.8	10.2	1.07349	0.711796	2.10112	1.14E-11
chr19:5377523-5388703:-	Sart1	20227	36.8	36.9	48.1	1.13192	0.359632	1.62849	2.14E-07
chr5:113742446-11377164	Sart3	53890	37.4	38.3	43.1	1.15763	0.329666	1.43496	0.0007618
chr10:8722219-8886070:-	Sash1	70097	66.0	51.7	19.7	-1.14939	0.41487	-2.6403	7.73E-17
chr3:116594958-11663098	Sass6	72776	9.8	7.8	6.3	-1.12077	0.325523	-1.24839	0.0086276
chr11:69622109-69623869	Sat2	69215	30.9	14.9	10.4	-1.84587	0.001476	-2.30273	2.02E-07
chr17:51736187-51833290	Satb1	20230	14.4	10.2	3.3	-1.26726	0.291665	-3.35352	2.88E-14
chr12:69965013-69987002	Sav1	64010	51.7	53.6	51.6	1.16188	0.056074	1.24854	0.0002037
chr15:89288236-89315311	Sbf1	77980	50.4	53.5	60.8	1.19915	0.189879	1.50366	6.07E-05
chr10:80057014-80102702	Sbno2	216161	26.5	99.6	78.9	3.60683	0.000103	3.23875	3.74E-05
chr7:30751471-30756134:	Sbsn	282619	11.3	7.0	3.7	-1.42937	0.25874	-2.31922	0.0002682
chr1:15853862-15892722:	Sbspon	226866	18.6	19.6	6.6	1.14985	0.65935	-2.16314	0.0001433
chr9:42254177-42264300:	Sc5d	235293	30.4	32.6	45.8	1.21224	0.416714	1.84455	0.000208
chr7:45002950-45016249:	Scaf1	233208	29.4	30.3	31.5	1.15919	0.257896	1.33797	0.0021822
chr15:96411698-96460843	Scaf11	72193	88.1	75.6	79.0	-1.04014	0.533838	1.12127	0.0075445
chr17:3114972-3198859:+	Scaf8	106583	66.3	73.6	74.8	1.25315	0.120616	1.40493	0.0020602
chr2:39066215-39190730:	Scai	320271	32.8	27.5	15.5	-1.06872	0.578055	-1.688	1.07E-11
chr9:57560944-57588798:	Scamp2	24044	57.1	54.7	68.8	1.07346	0.456298	1.50353	1.35E-10
chr3:89177485-89182770:	Scamp3	24045	36.4	36.9	46.4	1.13721	0.377106	1.58241	5.08E-06

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr10:80602882-80615783	Scamp4	56214	26.0	28.1	42.7	1.21549	0.0796	2.04239	5.86E-19
chr9:110333288-11038494	Scap	235623	31.0	29.2	38.3	1.0541	0.533207	1.54407	1.05E-15
chr9:55549883-55938115:	Scaper	244891	45.6	38.6	16.5	-1.05693	0.542878	-2.20294	3.48E-40
chr14:65919395-65953744	Scara3	219151	41.1	29.3	15.9	-1.26435	0.213233	-2.03649	2.00E-07
chr14:65666403-65764826	Scara5	71145	21.4	15.4	2.7	-1.25158	0.465102	-5.65964	6.93E-17
chr5:125277087-12534109	Scarb1	20778	36.1	34.1	17.4	1.05943	0.572156	-1.65027	7.11E-14
chr16:17797282-17808287	Scarf2	224024	29.5	53.0	58.3	1.94154	0.082549	2.24875	0.0058217
chr6:125186361-12518643	Scarna10	1E+08	####	6393.7	3954.6	1.05928	0.741383	-1.36475	0.0040277
chr12:105031075-1050313	Scarna13	1E+08	####	1281.2	823.1	1.04638	0.799743	-1.33043	0.0079872
chr9:15326289-15326330:	Scarna9	1E+08	459.8	423.0	259.8	1.03021	0.890054	-1.41252	0.0053016
chr19:44394450-44407709	Scd1	20249	520.2	337.5	83.0	-1.28346	0.712072	-3.14115	0.0070305
chr14:103513341-1036133	Scel	64929	2.3	2.2	0.3	1.0269	0.967213	-4.74392	1.08E-05
chr12:51377580-51450096	Scfd1	76983	79.6	85.2	145.0	1.20093	0.015682	2.26746	6.53E-47
chr5:74204816-74531742:	Scfd2	212986	8.4	7.5	8.3	1.00037	0.998371	1.22827	0.0018565
chr11:49663595-49665118	Scgb3a1	68662	0.1	0.4	1.3	1.72045	0.389133	4.38768	0.0005018
chr3:41626705-41742514:	Sclt1	67161	32.3	25.3	12.6	-1.14324	0.144522	-2.04497	1.28E-25
chr1:91298338-91321080:	Scly	50880	16.5	16.1	18.5	1.0939	0.469578	1.3996	5.49E-05
chrX:161162750-16125821	Scml2	107815	5.9	4.2	1.5	-1.25149	0.196303	-3.06496	1.62E-17
chr10:42860512-42960782	Scml4	268297	3.7	6.6	26.9	1.94422	0.029763	7.76812	4.60E-19
chr7:31116524-31126945:	Scn1b	20266	15.4	12.6	7.8	-1.10402	0.700726	-1.56374	0.0063617
chr2:65670445-65767447:	Scn2a1	110876	8.6	6.5	1.6	-1.18395	0.44502	-4.11319	1.54E-20
chr9:45117876-45130070:	Scn2b	72821	5.6	5.0	2.6	-1.01469	0.966532	-1.68673	0.0056631
chr9:45139042-45154061:	Scn4b	399548	1.2	1.2	1.6	1.08576	0.779176	1.57667	0.0083065
chr2:66673426-66784910:	Scn7a	20272	32.0	25.6	6.3	-1.12306	0.489627	-3.99496	3.58E-35
chr3:95129719-95134012:	Scnm1	69269	98.1	81.4	50.1	-1.07959	0.483873	-1.55838	2.40E-09
chr11:67052670-67067440	Sco1	52892	11.4	13.6	19.6	1.33718	0.064915	2.11463	1.32E-10
chr15:89371637-89373818	Sco2	1E+08	3.1	4.7	10.4	1.66621	0.020955	4.03513	1.40E-18
chr8:83434492-83458396:	Scoc	56367	34.9	40.1	49.1	1.28836	0.037201	1.74632	1.18E-09
chr4:108043830-10811854	Scp2	20280	102.7	84.6	56.9	-1.08929	0.531365	-1.44029	6.60E-05
chr2:144823666-14482441	Scp2d1	66328	8.5	0.4	0.8	-7.9621	4.80E-05	-5.04726	0.0002292
chr11:88924020-88955442	Scpep1	74617	155.9	121.4	71.2	-1.15127	0.093997	-1.74748	2.50E-19
chr15:76047186-76069730	Scrib	105782	30.8	30.4	37.7	1.11546	0.410447	1.52922	3.60E-06
chr6:54508816-54566382:	Scrn1	69938	26.8	18.9	13.3	-1.27688	0.188797	-1.60088	0.0006699
chr11:97029952-97033960	Scrn2	217140	15.8	11.7	6.6	-1.22308	0.30465	-1.89633	7.15E-06
chr15:83602583-83725039	Scube1	64706	17.1	30.9	170.1	1.97851	0.045068	10.1428	7.65E-20
chr7:109798691-10986567	Scube2	56788	8.8	9.1	2.5	1.17223	0.381302	-2.72017	2.83E-14
chr15:76457438-76459468	Scx	20289	14.3	8.1	3.0	-1.57601	0.094783	-3.56193	1.38E-09
chr10:89640107-89686285	Scyl2	213326	40.3	49.2	47.3	1.37461	0.043923	1.45793	0.0020657
chr5:92284010-92310024:	Sdad1	231452	30.8	41.7	77.8	1.51956	0.051851	3.039	5.13E-12
chr12:8771396-8793687:+	Sdc1	20969	62.8	75.8	106.1	1.35962	0.213233	2.05135	6.64E-05
chr15:32920723-33034721	Sdc2	15529	103.8	82.7	34.0	-1.12787	0.194617	-2.42952	1.57E-40
chr2:164424247-16444318	Sdc4	20971	220.4	299.6	405.8	1.51172	0.140334	2.1948	0.0001755
chr2:26382800-26389316:	Sdccag3	68112	90.5	113.5	130.6	1.41674	0.049729	1.78301	1.96E-05
chr1:176814660-17702043	Sdccag8	76816	31.9	26.5	11.8	-1.08266	0.418113	-2.16722	2.95E-29
chr16:17130138-17132383	Sdf2l1	64136	12.0	16.3	58.0	1.50302	0.026719	5.76067	3.16E-39
chr4:155992843-15601361	Sdf4	20318	84.0	77.5	79.0	1.03102	0.592617	1.17466	1.30E-05
chr7:30321409-30322375:	Sdhaf1	68332	19.2	16.9	30.5	-1.00637	0.975981	1.97757	7.57E-11
chr19:10500512-10525209	Sdhaf2	66072	28.2	30.6	39.6	1.21644	0.011776	1.75303	2.33E-21
chr4:140961271-14097919	Sdhb	67680	124.1	131.2	218.3	1.18614	0.107561	2.18499	1.92E-24
chr1:171129157-17115060	Sdhc	66052	141.8	132.1	160.7	1.04176	0.607465	1.41652	3.45E-12
chr9:50596340-50603849:	Sdhd	66925	132.0	128.3	145.0	1.08922	0.489388	1.36901	0.00018
chr5:141241534-14221379	Sdk1	330222	9.3	8.4	18.5	1.01892	0.934896	2.45489	2.56E-14
chr11:113780790-1140659	Sdk2	237979	8.2	7.4	3.9	1.01594	0.952617	-1.66944	0.0002636
chr1:51289126-51302960:	Sdpr	20324	177.1	110.5	37.1	-1.43899	0.188854	-3.57469	2.08E-10
chr14:55897285-55900232	Sdr39u1	654795	37.4	28.1	42.6	-1.20021	0.269345	1.41526	0.0034391
chr7:80915379-80947550:	Sec11a	56529	131.0	145.5	171.6	1.24897	0.113514	1.62603	3.53E-06
chr18:65800578-65817657	Sec11c	66286	55.8	55.2	119.2	1.10019	0.442115	2.64399	5.40E-34
chr6:113728052-11374068	Sec13	110379	118.2	149.4	366.3	1.42312	0.028953	3.77862	5.17E-28

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:117115172-1171592	Sec14l1	74136	37.3	29.9	19.8	-1.12258	0.32344	-1.50243	9.50E-07
chr2:26409431-26445216:	Sec16a	227648	46.1	49.9	62.6	1.22537	0.185831	1.68754	3.13E-06
chr1:157506796-15756842	Sec16b	89867	9.6	6.0	2.5	-1.43405	0.141568	-2.89113	6.21E-09
chr3:97901227-97922318:	Sec22b	20333	60.0	67.3	100.0	1.26084	0.076824	2.06357	5.74E-14
chr12:58958384-59012017	Sec23a	20334	68.3	73.6	68.5	1.20969	0.029415	1.25203	0.0010038
chr2:144556229-14459075	Sec23b	27054	100.1	108.2	189.0	1.20514	0.1775	2.33692	1.17E-17
chr7:128744870-12878483	Sec23ip	207352	33.2	36.9	58.6	1.25228	0.154231	2.17893	1.16E-11
chr11:51692263-51756834	Sec24a	77371	13.2	16.5	19.9	1.40821	0.106505	1.84579	0.0001205
chr14:20674321-20694850	Sec24c	218811	66.5	70.2	89.0	1.19131	0.144193	1.66682	5.99E-09
chr3:123267496-12336563	Sec24d	69608	65.0	66.2	132.2	1.13833	0.051108	2.53387	1.59E-83
chr5:100361649-10041623	Sec31a	69162	107.1	106.9	171.1	1.1237	0.269879	1.98968	1.07E-20
chr19:44516957-44545848	Sec31b	240667	7.2	5.7	2.7	-1.13392	0.373038	-2.07924	7.20E-13
chr6:88503607-88518800:	Sec61a1	53421	137.0	149.8	432.7	1.23319	0.131605	3.88254	6.61E-42
chr4:47474661-47483233:	Sec61b	66212	73.7	92.7	307.0	1.40768	0.001929	5.12321	7.36E-82
chr11:16501638-16508484	Sec61g	20335	102.2	108.3	236.3	1.18627	0.236069	2.84409	2.41E-25
chr10:42761496-42832514	Sec63	140740	52.9	52.6	70.3	1.12016	0.338932	1.65411	1.11E-09
chr13:51651714-51683646	Secisbp2	75420	30.3	32.9	48.0	1.2236	0.183679	1.96383	6.37E-10
chr11:121067403-1210811	Sectm1a	209588	0.4	0.6	5.2	1.48687	0.379888	11.6065	1.88E-18
chr11:121053423-1210635	Sectm1b	58210	0.1	1.1	8.7	6.38371	1.23E-05	42.7407	2.27E-26
chr18:67774876-67795487	Seh1l	72124	57.2	60.7	94.2	1.19138	0.077743	2.047	5.69E-23
chr12:91806043-91849157	Sel1l	20338	58.2	56.1	64.4	1.08033	0.302944	1.38139	7.61E-10
chr2:140229858-14038971	Sel1l2	228684	1.4	0.1	0.2	-5.29473	0.002722	-3.0728	0.0157744
chr5:53107083-53213452:	Sel1l3	231238	12.3	11.7	18.6	1.0716	0.756884	1.8729	2.56E-06
chr1:164048234-16405767	Sele	20339	0.5	4.7	6.4	6.19406	3.70E-05	8.72036	1.04E-08
chr3:94933083-94944758:	Selenbp1	20341	130.9	93.7	11.5	-1.25273	0.219719	-8.59639	4.25E-59
chr3:94693573-94704406:	Selenbp2	20342	1.9	1.6	0.7	-1.06854	0.863804	-2.08727	0.0019558
chr14:29968380-29975074	Selk	80795	147.5	161.5	182.3	1.22914	0.039546	1.53895	1.24E-08
chr11:3514702-3517351:+	Selm	114679	278.0	243.3	107.3	-1.03219	0.890141	-2.04418	1.31E-08
chr1:164115264-16415002	Selp	20344	2.9	12.5	6.9	3.50418	0.00633	2.3848	0.0229836
chr3:58576658-58593546:	Selt	69227	69.2	80.7	119.9	1.31162	0.016199	2.14907	9.02E-19
chr5:13396784-13603485:	Sema3a	20346	28.5	24.3	45.3	-1.05715	0.795825	1.9598	8.12E-08
chr5:14025276-14256689:	Sema3e	20349	8.7	5.9	2.0	-1.27057	0.467797	-3.23923	1.84E-07
chr3:88435962-88461182:	Sema4a	20351	11.4	12.4	15.0	1.22094	0.337646	1.6243	0.0010674
chr1:36548639-36558381:	Sema4c	20353	51.9	48.7	17.6	1.04055	0.861525	-2.32072	3.19E-11
chr6:82911885-82939750:	Sema4f	20355	0.4	0.7	1.0	1.63544	0.233621	2.58567	0.0014798
chr19:44989344-45003395	Sema4g	26456	2.9	2.8	1.1	1.08236	0.773091	-1.99402	6.32E-05
chr15:32244813-32696341	Sema5a	20356	150.7	125.4	20.4	-1.07195	0.659221	-5.75875	5.93E-74
chr16:35541362-35664258	Sema5b	20357	1.7	2.4	7.9	1.58276	0.288479	4.78016	2.85E-07
chr3:95160420-95174050:	Sema6c	20360	15.8	9.9	0.9	-1.42098	0.198026	-11.8801	1.20E-33
chr9:57940135-57962865:	Sema7a	20361	13.0	13.4	16.1	1.15954	0.38646	1.5389	0.0002995
chr15:98038744-98093569	Senp1	223870	20.0	20.1	28.3	1.13312	0.34579	1.76202	6.57E-10
chr16:22009484-22049269	Senp2	75826	41.2	45.4	51.4	1.24501	0.131502	1.55265	4.88E-05
chr16:31959670-32003287	Senp5	320213	24.4	30.5	46.2	1.40965	0.046062	2.32886	6.28E-11
chr9:80066903-80144780:	Senp6	215351	108.3	125.8	137.6	1.31235	0.07891	1.57796	9.87E-05
chr16:56075404-56190031	Senp7	66315	23.0	17.8	8.7	-1.15951	0.262686	-2.10367	2.21E-15
chr9:59734259-59750649:	Senp8	71599	8.1	7.0	3.8	-1.0493	0.885581	-1.6749	0.0063775
chr3:144570427-14459767	15-Sep	93684	253.4	252.8	315.3	1.11494	0.296357	1.54776	2.44E-09
chr7:127271879-12727405	Sephs2	20768	34.8	39.4	56.9	1.28177	0.219719	2.01274	1.66E-06
chr15:3270767-3280508:+	Sepp1	20363	####	868.2	213.2	-1.08839	0.623307	-3.86434	2.94E-36
chr5:52643407-52669701:	Sepsecs	211006	28.6	30.4	35.5	1.19678	0.26244	1.53845	0.0001832
chr10:59141627-59221847	10-Sep	103080	39.2	31.2	21.6	-1.13045	0.471474	-1.44044	0.0020016
chr5:93093457-93174958:	11-Sep	52398	43.6	43.6	48.5	1.11441	0.186093	1.38437	3.91E-08
chr16:4986858-4997852:-	12-Sep	71089	3.8	0.3	0.4	-6.83502	6.37E-05	-5.08713	8.31E-05
chr1:93478993-93509732:	2-Sep	18000	221.2	237.8	283.4	1.20757	0.090238	1.59274	1.91E-08
chr11:87578389-87590539	4-Sep	18952	27.0	16.0	2.9	-1.51396	0.029883	-6.93263	2.99E-36
chrX:36911272-36989695:	6-Sep	56526	12.9	11.7	7.1	1.00038	0.999289	-1.44995	0.0028301
chr9:25252439-25308571:	7-Sep	235072	219.8	238.8	342.3	1.21631	0.048877	1.93445	4.74E-19
chr11:117199661-1173623	9-Sep	53860	62.2	75.2	119.7	1.36336	0.119488	2.34749	6.63E-09

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr17:6040571-6079739:-	Serac1	321007	13.3	9.3	4.8	-1.28865	0.068458	-2.20039	5.91E-14
chr6:67266979-67289302:	Serbp1	66870	133.1	164.0	275.7	1.38773	0.044583	2.54349	2.19E-14
chr13:100108019-1001142	Serf1	20365	52.0	35.3	11.3	-1.31495	0.101394	-3.57946	2.16E-22
chr7:46443159-46639807:	Sergef	27414	16.1	14.7	19.2	1.02163	0.889766	1.49461	7.08E-07
chr15:83100205-83116671	Serhl	68607	39.4	30.2	14.1	-1.17384	0.303245	-2.21298	1.10E-12
chr10:57515775-57532529	Serinc1	56442	318.2	317.6	327.9	1.1144	0.097246	1.28512	2.42E-07
chr4:130253497-13027558	Serinc2	230779	7.8	7.1	12.1	1.01051	0.962879	1.91895	1.09E-08
chr2:163623273-16364514	Serinc3	26943	404.9	377.4	184.5	1.03912	0.736736	-1.75376	1.83E-16
chr3:58521971-58525884:	Serp1	28146	117.7	150.9	467.2	1.44104	0.039179	4.78495	1.33E-32
chr14:76532812-76556889	Serp2	72661	4.1	3.5	1.8	-1.04436	0.903471	-1.79874	0.0057083
chr12:103946932-1039568	Serpina1e	20704	9.8	6.9	1.9	-1.22089	0.736736	-3.02205	0.0028348
chr12:104146907-1041538	Serpina3c	16625	6.1	3.7	0.6	-1.32396	0.690579	-3.62778	0.0038505
chr12:104101113-1041061	Serpina5	268591	2.0	0.1	0.2	-7.0457	0.000359	-3.68006	0.0058195
chr1:107529003-10754927	Serpinb10	241197	1.0	1.0	3.1	1.10146	0.891244	2.84138	0.0086825
chr1:106861180-10688334	Serpinb5	20724	0.5	0.4	2.8	-1.06528	0.933557	4.56649	0.0001201
chr1:107422689-10745268	Serpinb7	116872	12.8	11.8	36.5	1.01972	0.974057	3.04931	0.0004482
chr13:33004541-33017955	Serpinb9	20723	33.9	44.0	53.8	1.45682	0.01953	1.95429	7.90E-08
chr5:137061506-13707227	Serpine1	18787	8.9	11.3	25.1	1.40531	0.215268	3.29394	1.18E-09
chr11:75410029-75422623	Serpinf1	20317	169.0	141.4	90.4	-1.0706	0.646856	-1.49343	2.30E-05
chr2:84765360-84775429:	Serping1	12258	534.3	481.9	204.0	-1.00052	0.998614	-2.07877	1.40E-11
chr7:99345375-99353239:	Serpinh1	12406	484.6	607.2	1412.9	1.4078	0.04703	3.5488	5.21E-23
chr3:75557533-75642523:	Serpini1	20713	6.4	5.0	1.7	-1.1601	0.398425	-2.97551	7.24E-17
chr7:27486953-27490314:	Sertad1	55942	30.9	65.2	89.8	2.27184	0.009845	3.27393	2.63E-06
chr7:27473840-27477364:	Sertad3	170742	22.2	21.6	12.4	1.08311	0.53036	-1.43176	4.59E-05
chr10:41810574-41908436	Sesn1	140742	95.3	60.6	13.7	-1.40249	0.362477	-4.77806	1.33E-09
chr4:132492807-13251045	Sesn2	230784	4.8	6.7	23.8	1.55962	0.073081	5.80721	1.07E-22
chr9:14276301-14326134:	Sesn3	75747	91.4	61.8	19.7	-1.32847	0.240541	-3.51932	3.21E-13
chr2:77180340-77280592:	Sestd1	228071	52.5	38.5	25.1	-1.22637	0.190394	-1.66121	8.82E-06
chr2:30061996-30072577:	Set	56086	174.6	200.0	424.0	1.29026	0.095789	2.98553	1.29E-22
chr6:113077639-11315342	Setd5	72895	75.8	73.4	74.7	1.08938	0.40938	1.23149	0.0045788
chr8:95715913-95719004:	Setd6	66083	18.4	22.6	32.5	1.37502	0.005006	2.1841	5.88E-19
chr3:51515318-51560823:	Setd7	73251	74.1	59.0	24.7	-1.12415	0.385356	-2.37491	6.41E-21
chr5:124439930-12446230	Setd8	67956	32.8	39.4	75.6	1.35322	0.093328	2.81748	4.23E-15
chr14:59402011-59440877	Setdb2	239122	11.2	11.5	14.1	1.15075	0.166611	1.56799	3.80E-10
chr2:29124992-29182471:	Setx	269254	74.9	64.0	38.2	-1.04542	0.707387	-1.55951	6.51E-10
chr19:6363690-6378038:+	Sf1	22668	76.2	83.9	98.5	1.24617	0.206324	1.60409	0.0002165
chr11:4160354-4182541:+	Sf3a1	67465	28.7	29.5	68.5	1.15693	0.146974	2.96561	1.24E-52
chr10:80798735-80804922	Sf3a2	20222	33.1	38.8	62.6	1.32079	0.069506	2.33968	4.55E-14
chr4:124714861-12473242	Sf3a3	75062	97.7	110.0	165.6	1.26732	0.054488	2.10258	4.00E-16
chr19:5273921-5295455:-	Sf3b2	319322	210.5	189.4	197.3	1.00888	0.928217	1.17295	0.0025071
chr8:110810492-11084680	Sf3b3	101943	116.9	140.0	232.7	1.35369	0.105968	2.43875	1.11E-10
chr3:96172550-96177564:	Sf3b4	107701	27.5	34.7	57.4	1.42055	0.044208	2.56194	4.47E-13
chr10:13008450-13009183	Sf3b5	66125	61.8	70.3	75.0	1.27373	0.062981	1.50853	2.75E-05
chr12:4817608-4827659:+	Sf3b6	66055	69.9	85.8	109.6	1.37833	0.059571	1.93297	2.61E-07
chr11:3131850-3193463:-	Sfi1	78887	75.2	47.0	14.5	-1.43459	0.003434	-4.07937	7.16E-46
chr2:10370451-10595253:	Sfmbt2	353282	2.8	1.5	0.8	-1.65687	0.00988	-2.57522	1.77E-09
chr4:133600556-13360216	Sfn	55948	9.5	15.9	35.2	1.73501	0.234368	3.62817	0.0001313
chr4:127021301-12703701	Sfpq	71514	199.8	241.5	214.4	1.36142	0.024378	1.33633	0.0078089
chr19:47731756-47735588	Sfr1	67788	160.8	153.2	107.7	1.06608	0.306054	-1.19489	7.72E-05
chr8:23411502-23449632:	Sfrp1	20377	26.5	20.6	6.0	-1.15093	0.652382	-3.34617	6.91E-10
chr3:83766321-83774314:	Sfrp2	20319	98.9	75.5	7.0	-1.17037	0.355668	-10.6882	1.24E-84
chr13:19623175-19632823	Sfrp4	20379	86.4	72.8	39.0	-1.07911	0.806835	-1.74267	0.0027166
chr17:8311103-8327442:+	Sft2d1	106489	42.7	50.2	56.6	1.32068	0.044318	1.64598	1.87E-06
chr1:165174341-16519443	Sft2d2	108735	72.9	57.0	24.2	-1.15265	0.37564	-2.37382	4.66E-15
chr13:54071845-54108345	Sfxn1	14057	34.9	26.7	47.0	-1.16942	0.159825	1.67973	7.50E-11
chr19:60837277-60861430	Sfxn4	94281	23.9	16.9	3.3	-1.26944	0.251739	-5.50549	4.00E-29
chr6:85213051-85333422:	Sfxn5	94282	10.2	8.4	3.8	-1.08579	0.459776	-2.1178	4.94E-21
chr11:94962777-94976327	Sgca	20391	1.8	1.1	0.4	-1.47172	0.237439	-3.24619	7.44E-06

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:46978783-47379302	Sgcd	24052	24.1	22.9	4.1	1.05516	0.768167	-4.57006	2.61E-36
chr6:4674350-4747204:-	Sgce	20392	105.1	82.3	37.3	-1.14595	0.124177	-2.25008	3.81E-35
chr4:102760135-10297268	Sgip1	73094	4.6	2.7	0.3	-1.55727	0.017826	-10.4752	1.55E-41
chr10:21882184-21999902	Sgk1	20393	16.2	43.1	49.7	2.79964	0.000352	3.45384	3.40E-07
chr1:9798130-9902568:+	Sgk3	170755	19.2	17.4	11.5	1.0083	0.951887	-1.33296	6.54E-05
chr3:131318986-13134492	Sgms2	74442	15.7	42.9	36.4	2.75838	0.005772	2.54783	0.0019272
chr12:75714248-75735729	Sgpp1	81535	47.7	41.4	50.0	-1.03427	0.823082	1.30533	0.0025345
chr1:78310346-78420286:	Sgpp2	433323	4.4	3.0	0.8	-1.30738	0.292326	-3.82735	1.36E-12
chr11:74849264-74897080	Sgsm2	97761	12.2	9.8	6.6	-1.11114	0.2608	-1.47933	7.77E-09
chr15:80977765-81012290	Sgsm3	105835	14.5	15.0	17.1	1.16291	0.136115	1.47933	9.29E-08
chr10:81044073-81060154	Sgta	52551	80.3	77.2	88.4	1.08082	0.396617	1.3764	3.98E-07
chr13:104109790-1041414	Sgtb	218544	9.3	6.3	2.5	-1.32384	0.350254	-2.83254	1.20E-06
chr5:121817215-12183680	Sh2b3	16923	25.1	26.3	29.3	1.18207	0.319423	1.4499	0.0021037
chr2:32721055-32755007:	Sh2d3c	27387	11.4	11.3	5.9	1.10824	0.400239	-1.53336	1.00E-06
chr4:138250411-13826096	Sh2d5	230863	0.5	1.7	10.5	2.85426	0.009453	15.9389	4.74E-19
chr16:96200470-96228933	Sh3bgr	50795	53.6	41.5	21.1	-1.16308	0.443572	-1.99785	3.53E-07
chr9:83548338-83600291:	Sh3bgrl2	212531	20.9	19.8	26.0	1.06825	0.756884	1.54057	0.0008544
chr5:34525784-34563639:	Sh3bp2	24055	13.2	11.6	14.3	-1.01041	0.958929	1.3458	0.0045768
chr1:89070462-89153793:	Sh3bp4	98402	30.4	26.2	12.3	-1.02777	0.873353	-1.9634	1.47E-12
chr14:31373964-31436033	Sh3bp5	24056	40.4	34.5	21.6	-1.04693	0.594096	-1.49671	6.37E-13
chr11:58330718-58347728	Sh3bp5l	79566	32.6	30.8	19.4	1.04992	0.694129	-1.34035	0.000165
chr3:86084434-86130521:	Sh3d19	27059	78.5	57.5	21.1	-1.22912	0.275672	-2.90609	1.10E-15
chr4:126150602-12616334	Sh3d21	66938	29.9	18.3	6.3	-1.42345	0.110719	-3.62991	6.36E-15
chr17:56016750-56036637	Sh3gl1	20405	54.3	58.0	64.7	1.20557	0.155914	1.48779	4.62E-05
chr4:85205456-85389379:	Sh3gl2	20404	7.7	6.4	10.6	-1.0758	0.703612	1.70821	2.69E-06
chr2:30344777-30359316:	Sh3glb2	227700	59.4	46.2	37.1	-1.15371	0.236431	-1.27497	0.0065738
chrX:159627272-15997592	Sh3kbp1	58194	26.9	23.5	13.0	-1.03032	0.84948	-1.65119	1.64E-08
chr11:32347811-32428183	Sh3pxd2b	268396	42.7	49.2	47.8	1.29143	0.026222	1.39429	0.0002138
chr8:61224171-61396072:	Sh3rf1	59009	20.1	19.0	11.7	1.05528	0.771519	-1.36892	0.0059446
chr18:42053710-42158695	Sh3rf2	269016	4.2	1.2	1.7	-2.82644	0.001921	-1.81366	0.0362407
chr10:58813359-59138916	Sh3rf3	237353	3.2	2.9	1.1	1.0139	0.947823	-2.30413	1.43E-12
chr12:30911669-30960160	Sh3yl1	24057	11.0	9.8	4.2	-1.01155	0.965618	-2.04427	9.50E-07
chr7:144175520-14442267	Shank2	210274	5.2	3.9	1.4	-1.17356	0.184549	-2.80696	3.20E-28
chr13:51431042-51567084	Shc3	20418	6.6	4.4	2.9	-1.34832	0.274364	-1.79354	0.0038418
chr1:153425209-15345257	Shcbp1l	71836	4.8	0.7	0.8	-4.5642	0.000327	-3.87035	0.0001593
chr17:55970482-55976619	Shd	20420	6.1	4.4	0.5	-1.22697	0.575733	-7.20509	1.03E-13
chr3:89831370-89858846:	She	214547	11.5	11.7	14.3	1.14324	0.396085	1.54119	8.01E-05
chr6:6558275-6578658:-	Shfm1	20422	293.8	296.9	378.5	1.13171	0.449136	1.59465	3.10E-05
chr14:59625281-59631660	Shisa2	219134	3.4	3.0	12.8	1.00748	0.984808	4.42632	3.30E-14
chr5:67607883-67613987:	Shisa3	330096	4.2	1.5	0.6	-2.38727	0.027396	-4.77964	4.04E-07
chr1:135371456-13537506	Shisa4	77552	13.3	13.4	19.2	1.12094	0.586668	1.77576	1.75E-05
chr16:11984113-12270904	Shisa9	72555	0.7	0.5	1.5	-1.14756	0.696722	2.6608	8.42E-07
chr7:27342133-27356008:	Shkbp1	192192	8.5	10.0	21.1	1.3287	0.045063	3.06745	2.76E-28
chr11:60788897-60811265	Shmt1	20425	18.2	16.6	31.1	1.01871	0.946688	2.09249	2.22E-07
chr10:127517123-1275224	Shmt2	108037	30.6	28.0	66.9	1.02358	0.865776	2.72389	1.93E-43
chr19:53944306-54033278	Shoc2	56392	55.2	63.5	62.3	1.29564	0.049902	1.40549	0.0008352
chr6:100573082-10067115	Shq1	72171	12.6	13.9	17.2	1.23406	0.046503	1.69576	6.70E-12
chrX:152609509-15276948	Shroom2	110380	15.0	11.0	7.5	-1.2275	0.155827	-1.58506	1.79E-05
chr9:37613847-37648318:	Siae	22619	35.0	28.3	7.8	-1.11659	0.504535	-3.51378	8.19E-30
chr8:86723938-86746006:	Siah1a	20437	76.7	69.5	45.3	1.00644	0.96814	-1.35221	0.0004801
chrX:164070703-16407604	Siah1b	20438	5.2	6.1	7.9	1.31311	0.289367	1.86427	0.0006519
chr3:58674949-58692388:	Siah2	20439	5.9	9.4	14.9	1.7581	0.051439	2.95032	7.40E-07
chr9:45937857-45955249:	Sidt2	214597	105.8	94.2	49.8	1.00215	0.987936	-1.69062	2.69E-13
chr7:43351341-43359470:	Siglecf	233186	2.1	0.7	0.4	-2.4174	0.01702	-3.55611	2.06E-05
chr7:43408280-43418349:	Siglecg	243958	4.2	2.7	1.1	-1.31587	0.561143	-2.55865	0.0032199
chr4:41738493-41741359:	Sigmar1	18391	28.0	31.3	50.0	1.26015	0.157414	2.20064	2.34E-11
chr17:31844250-31855792	Sik1	17691	11.5	28.3	20.4	2.617	0.002181	2.08047	0.0055993
chr9:50892801-51009073:	Sik2	235344	42.5	39.3	24.6	1.03605	0.805774	-1.37763	0.0001718

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr3:102995740-10300391	Sike1	66641	41.7	36.9	37.8	-1.01163	0.891325	1.13129	0.0090485
chr18:35266396-35498925	Sil1	81500	42.5	35.6	22.1	-1.06572	0.537054	-1.53603	4.66E-10
chr13:54503805-54551290	Simc1	319719	20.8	23.4	27.0	1.27367	0.157104	1.61466	0.0001626
chr9:57072040-57128368:	Sin3a	20466	53.8	45.7	29.7	-1.05368	0.492095	-1.44767	3.71E-13
chr8:72723270-72758203:	Sin3b	20467	69.9	72.9	72.8	1.17932	0.230309	1.30131	0.009955
chr12:82170016-82451784	Sipa1l1	217692	30.5	28.5	29.7	1.04618	0.611804	1.2167	0.0006876
chr8:125418063-12549271	Sipa1l2	244668	24.1	42.9	59.0	1.96752	0.018086	2.86549	2.54E-06
chr7:28766752-28788665:	Sirt2	64383	89.5	71.7	53.5	-1.11567	0.166777	-1.33426	7.75E-07
chr7:140863663-14088230	Sirt3	64384	26.0	19.1	7.6	-1.22624	0.270714	-2.67645	2.31E-13
chr5:115478010-11548448	Sirt4	75387	19.6	13.9	8.7	-1.26583	0.280353	-1.77345	0.0002995
chr13:43370716-43395203	Sirt5	68346	24.6	18.2	8.5	-1.21744	0.430123	-2.22539	4.51E-06
chr10:81621786-81627608	Sirt6	50721	15.3	13.9	16.7	1.01845	0.896635	1.36434	3.52E-05
chr4:43482083-43483709:	Sit1	54390	1.1	3.4	5.9	2.27987	0.145151	3.84729	0.0015234
chr7:19094544-19098345:	Six5	20475	34.2	25.2	10.8	-1.22284	0.495611	-2.41412	1.05E-05
chr11:87109261-87122974	Ska2	66140	36.5	35.4	36.9	1.08564	0.437131	1.26182	0.0013978
chr6:51859165-52012549:	Skap2	54353	30.8	30.0	36.6	1.08113	0.726354	1.46313	0.0059356
chr13:112867780-1129273	Skiv2l2	72198	80.3	88.6	104.1	1.24259	0.084603	1.61112	4.07E-07
chr11:52231995-52246858	Skp1a	21402	337.3	343.8	443.1	1.14584	0.297891	1.63228	1.15E-07
chr15:9111982-9155425:-	Skp2	27401	8.4	7.4	9.0	-1.01239	0.946688	1.33605	0.002506
chr2:156872922-15688707	Sla2	77799	1.3	2.1	2.8	1.63639	0.217704	2.43271	0.0023353
chr5:72914362-72978841:	Slain2	75991	52.3	52.3	67.0	1.12639	0.29377	1.59627	4.29E-09
chrX:74369219-74373349:	Slc10a3	214601	11.2	11.5	33.2	1.15321	0.424002	3.60287	2.71E-28
chr15:100387900-1004230	Slc11a2	18174	14.6	21.5	35.8	1.63722	0.001003	2.99864	2.23E-19
chr2:112266314-11236316	Slc12a6	107723	68.2	53.1	11.4	-1.15578	0.32375	-4.68093	6.62E-52
chr13:73763697-73816742	Slc12a7	20499	28.1	22.6	15.0	-1.10952	0.334822	-1.49673	1.19E-07
chr11:72241994-72266604	Slc13a5	237831	2.7	1.3	0.2	-1.61525	0.431861	-6.07848	2.43E-05
chr14:121459621-1215052	Slc15a1	56643	1.1	0.9	0.2	-1.10633	0.848342	-3.25106	0.0002502
chr16:36750164-36784962	Slc15a2	57738	95.9	35.8	13.2	-2.29017	0.001113	-5.26882	1.70E-15
chr19:10842544-10857915	Slc15a3	65221	5.2	10.1	30.7	2.06724	0.022704	6.3541	2.23E-14
chr5:127595666-12761739	Slc15a4	100561	26.8	30.6	28.7	1.28452	0.054488	1.3359	0.0040108
chr3:104638664-10465846	Slc16a1	20501	30.0	82.4	84.2	2.81256	0.004369	3.03765	0.0001802
chr11:70213910-70216414	Slc16a11	216867	5.7	3.3	0.9	-1.5293	0.216584	-4.30414	2.14E-08
chr11:70216792-70220994	Slc16a13	69309	12.9	9.4	6.7	-1.22898	0.190782	-1.52731	0.0003039
chr3:107291292-10731211	Slc16a4	229699	5.5	5.0	1.6	1.01547	0.960185	-2.68904	1.18E-08
chr11:109450856-1094735	Slc16a6	104681	6.7	10.3	19.5	1.66927	0.155857	3.24057	1.05E-05
chr10:125227485-1253285	Slc16a7	20503	22.8	13.9	10.5	-1.46641	0.07117	-1.70223	0.0010685
chr10:70245276-70285951	Slc16a9	66859	22.1	27.2	5.9	1.37479	0.001077	-2.96197	7.87E-38
chr9:78536487-78588045:	Slc17a5	235504	26.6	17.9	5.3	-1.33913	0.17008	-3.82429	8.68E-18
chr10:23796986-23827968	Slc18b1	76306	17.6	12.8	5.2	-1.23479	0.188683	-2.64058	2.89E-16
chr10:77032739-77050432	Slc19a1	20509	19.4	13.7	24.7	-1.27143	0.271273	1.57112	0.0042015
chr1:164249046-16426538	Slc19a2	116914	19.3	17.1	29.3	-1.01323	0.949307	1.88164	2.03E-09
chr1:83012523-83038448:	Slc19a3	80721	2.8	2.4	0.2	-1.05482	0.890378	-10.1458	3.07E-18
chr15:8634124-8710807:-	Slc1a3	20512	15.7	10.6	2.7	-1.31916	0.136115	-4.47831	7.30E-27
chr11:20302180-20332713	Slc1a4	55963	7.1	5.6	21.4	-1.14689	0.578094	3.60514	8.19E-17
chr7:16781346-16798274:	Slc1a5	20514	118.4	101.1	147.4	-1.04468	0.720261	1.55688	1.79E-09
chr10:78780496-78814825	Slc1a6	20513	1.4	1.1	0.3	-1.12352	0.771007	-3.05689	3.92E-05
chr2:129198773-12921161	Slc20a1	20515	24.5	40.5	60.2	1.83708	0.017674	2.90649	8.65E-08
chr17:12648875-12675838	Slc22a1	20517	2.6	1.8	0.5	-1.2967	0.426563	-4.06735	2.57E-08
chr9:119169456-11919039	Slc22a14	382113	4.3	0.5	0.7	-4.75736	0.001951	-3.38869	0.0037724
chr10:40570362-40604132	Slc22a16	70840	3.8	0.3	0.5	-6.67676	8.52E-05	-4.2046	0.0005349
chr14:54906727-54913132	Slc22a17	59049	44.1	28.5	10.6	-1.38717	0.090325	-3.20821	6.13E-16
chr7:143473755-14349933	Slc22a18	18400	5.1	3.4	1.9	-1.29645	0.426552	-2.06817	0.0019202
chr11:53950824-53980027	Slc22a21	56517	21.9	18.6	11.9	-1.05584	0.638115	-1.46205	3.43E-07
chr13:34179158-34345182	Slc22a23	73102	13.6	13.1	2.9	1.07581	0.567341	-3.74097	6.82E-52
chr17:12419974-12507704	Slc22a3	20519	22.5	17.5	3.8	-1.13674	0.500968	-4.60517	6.02E-32
chr11:53983126-54028090	Slc22a4	30805	15.5	13.0	3.5	-1.06245	0.700575	-3.45204	3.35E-32
chr18:35614604-35627227	Slc23a1	20522	6.4	4.1	1.3	-1.38154	0.240985	-3.64627	2.44E-10
chr2:132052496-13214510	Slc23a2	54338	31.1	29.2	33.6	1.05153	0.508472	1.35043	1.73E-09

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr2:145242611-14564193	Slc24a3	94249	105.1	88.1	28.3	-1.05982	0.700015	-2.92753	4.01E-32
chr11:120491837-1205011	Slc25a10	27376	25.0	15.6	11.1	-1.4292	0.075985	-1.76523	0.0002081
chr2:71274295-71367554:	Slc25a12	78830	46.7	44.6	51.4	1.0714	0.417019	1.37454	3.72E-08
chrX:48623578-48662298:	Slc25a14	20523	11.5	9.6	6.4	-1.06623	0.661902	-1.41792	0.0002497
chr8:22375550-22398621:	Slc25a15	18408	9.4	8.3	15.7	-1.01357	0.928857	2.07407	4.38E-23
chr10:62920633-62946494	Slc25a16	73132	18.2	14.5	21.0	-1.1247	0.303946	1.44159	4.07E-06
chr15:81318921-81360765	Slc25a17	20524	69.3	67.8	75.8	1.09253	0.187946	1.36556	6.79E-11
chr11:115614181-1156282	Slc25a19	67283	22.8	22.3	12.1	1.10032	0.432474	-1.49631	2.38E-06
chr9:108662098-10868464	Slc25a20	57279	34.6	34.3	46.6	1.10583	0.282849	1.67399	7.43E-16
chr7:141429749-14143787	Slc25a22	68267	13.8	15.2	25.6	1.24476	0.188604	2.29691	2.27E-12
chr17:57043711-57059863	Slc25a23	66972	28.6	22.1	10.7	-1.15786	0.324714	-2.11107	1.28E-12
chr2:32414487-32451470:	Slc25a25	227731	9.7	15.7	27.0	1.78693	0.056074	3.20478	3.68E-07
chr17:43641900-43667015	Slc25a27	74011	63.1	40.1	3.5	-1.40759	0.102881	-13.0464	3.45E-59
chr19:43663801-43674881	Slc25a28	246696	52.3	53.0	55.9	1.13803	0.117878	1.33362	2.35E-06
chr10:91116578-91123963	Slc25a3	18674	238.8	250.7	432.7	1.18094	0.12272	2.25261	2.63E-25
chr3:40708871-40726094:	Slc25a31	73333	1.2	0.2	0.1	-3.48588	0.017215	-4.47421	0.0003427
chr15:39094191-39112716	Slc25a32	69906	25.2	22.7	25.5	1.00439	0.97799	1.26361	0.0052847
chr4:149744036-14977426	Slc25a33	70556	13.8	17.2	19.0	1.38267	0.145072	1.69214	0.0016234
chr9:97077011-97111041:	Slc25a36	192287	97.8	99.9	52.9	1.15226	0.300223	-1.47137	8.50E-05
chr9:120110399-12012431	Slc25a38	208638	30.0	32.9	32.0	1.23528	0.101859	1.3326	0.0034242
chr11:102402976-1024075	Slc25a39	68066	89.7	108.2	211.1	1.36383	0.144977	2.85366	1.50E-11
chr8:46207341-46211009:	Slc25a4	11739	398.3	376.6	562.4	1.05695	0.561727	1.75865	1.54E-20
chr8:70184340-70212281:	Slc25a42	73095	6.0	5.7	2.6	1.07504	0.734288	-1.84475	6.04E-06
chr3:88410494-88425141:	Slc25a44	229517	26.1	28.5	31.3	1.23166	0.110209	1.49689	3.53E-05
chr19:5878466-5885768:+	Slc25a45	107375	17.1	13.0	6.5	-1.18248	0.419343	-2.06928	6.32E-07
chr18:31580168-31609902	Slc25a46	67453	37.1	35.1	40.9	1.05709	0.445112	1.37884	3.79E-11
chrX:36795652-36798806:	Slc25a5	11740	150.5	226.2	838.9	1.68063	0.021511	6.47645	9.74E-28
chr4:45395924-45408766:	Slc25a51	230125	56.0	51.8	38.2	1.03443	0.50115	-1.1731	2.75E-06
chr11:119355557-1193810	Slc26a11	268512	18.5	13.9	5.5	-1.19688	0.227164	-2.67543	3.07E-19
chr18:61196854-61211596	Slc26a2	13521	16.1	17.1	18.5	1.19843	0.196539	1.43708	0.0004198
chr4:14505197-14621778:	Slc26a7	208890	49.1	50.6	4.4	1.11746	0.782377	-7.52844	1.58E-17
chr17:28637779-28689987	Slc26a8	224661	4.0	1.7	1.2	-2.06173	0.018509	-2.4447	0.0002386
chr1:131744022-13177040	Slc26a9	320718	0.5	0.5	1.0	1.06521	0.907394	2.29533	0.0042952
chr8:71568927-71586708:	Slc27a1	26457	76.9	53.5	15.2	-1.27693	0.103418	-3.95343	2.80E-35
chr3:90385233-90389927:	Slc27a3	26568	14.2	10.3	6.1	-1.22647	0.325523	-1.8426	4.37E-05
chr7:12988346-12998192:	Slc27a5	26459	1.3	0.4	0.3	-2.33158	0.041361	-3.33729	0.0002447
chr17:45585200-45599603	Slc29a1	63959	129.3	103.9	53.0	-1.11453	0.29708	-1.9393	1.10E-19
chr19:5024006-5031972:+	Slc29a2	13340	5.9	6.7	11.3	1.26817	0.211661	2.34977	1.38E-10
chr10:60712072-60752782	Slc29a3	71279	12.6	8.8	7.0	-1.28298	0.045626	-1.43812	0.0001532
chr4:119108745-11913732	Slc2a1	20525	21.8	25.3	32.9	1.30289	0.120396	1.86146	8.40E-07
chr2:165503897-16551991	Slc2a10	170441	4.8	4.4	6.4	1.03278	0.867981	1.65868	1.07E-06
chr15:91267691-91573261	Slc2a13	239606	6.0	4.7	2.5	-1.12918	0.446423	-1.8952	8.58E-09
chr6:122727809-12274274	Slc2a3	20527	31.0	28.3	12.4	1.04399	0.902064	-1.93784	0.0006998
chr11:69942286-69948190	Slc2a4	20528	20.6	12.1	4.1	-1.51602	0.127623	-3.74172	8.82E-11
chr2:181384250-18138759	Slc2a4rg-ps	329584	22.8	17.3	13.1	-1.18504	0.268893	-1.38422	0.0038153
chr4:150119344-15014416	Slc2a5	56485	6.4	1.0	0.8	-4.64149	9.58E-05	-4.9596	2.11E-06
chr2:32972989-32982056:	Slc2a8	56017	19.1	16.5	5.3	-1.02344	0.921977	-2.8142	7.01E-16
chr5:38349273-38502152:	Slc2a9	117591	4.1	2.2	0.9	-1.66349	0.056491	-3.36487	4.95E-09
chr1:191906781-19191324	Slc30a1	22782	27.3	31.0	35.4	1.27624	0.091181	1.60771	1.16E-05
chr5:31086106-31093527:	Slc30a3	22784	2.0	0.2	0.2	-5.3404	0.001133	-4.18624	0.0008951
chr2:122681233-12270266	Slc30a4	22785	45.6	51.1	74.0	1.26283	0.103291	2.00717	4.04E-11
chr13:100802648-1008334	Slc30a5	69048	62.3	69.2	113.0	1.25277	0.098394	2.2453	5.39E-16
chr17:74395608-74424229	Slc30a6	210148	18.5	18.4	22.2	1.1118	0.306807	1.49618	1.66E-08
chr3:115938973-11600740	Slc30a7	66500	25.6	24.1	24.2	1.05181	0.493366	1.1786	0.0010538
chr5:67306957-67356145:	Slc30a9	109108	61.4	64.3	66.1	1.17484	0.094821	1.34374	4.47E-05
chr4:62360701-62391769:	Slc31a1	20529	23.5	28.3	34.2	1.35446	0.089284	1.79233	1.32E-05
chr4:62286429-62298412:	Slc31a2	20530	63.4	49.4	17.0	-1.15963	0.486443	-2.9072	8.20E-14
chr3:63942324-63964733:	Slc33a1	11416	31.3	28.0	65.0	-1.00421	0.979507	2.57858	1.16E-31

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr4:34663257-34687438:	Slc35a1	24060	31.2	28.3	33.9	1.00902	0.947066	1.35378	1.29E-05
chr3:116670798-11671228	Slc35a3	229782	37.3	37.8	47.3	1.14091	0.207265	1.58127	8.79E-10
chr18:36679215-36683862	Slc35a4	67843	39.0	41.9	73.3	1.20861	0.072086	2.33308	1.68E-28
chr16:45139573-45158673	Slc35a5	74102	27.3	21.8	14.1	-1.12887	0.463826	-1.53706	0.000165
chr11:95384922-95391652	Slc35b1	110172	57.6	81.8	303.9	1.59434	0.028789	6.21217	2.67E-30
chr17:45564152-45567669	Slc35b2	73836	48.5	48.4	69.8	1.11944	0.20106	1.79243	3.67E-21
chr2:92452765-92460518:	Slc35c1	228368	8.2	7.3	11.0	-1.00663	0.971146	1.66354	3.45E-08
chr2:165276522-16528783	Slc35c2	228875	26.4	25.0	39.6	1.05466	0.680085	1.86957	3.96E-16
chr13:64096310-64129330	Slc35d2	70484	13.0	8.7	3.3	-1.34265	0.367302	-2.93734	3.26E-06
chr8:72477995-72492614:	Slc35e1	270066	18.5	27.3	37.5	1.6583	0.00552	2.47071	4.84E-10
chr10:117733678-1177463	Slc35e3	215436	14.4	11.9	18.5	-1.08783	0.528237	1.59607	5.51E-08
chr11:3907022-3914664:-	Slc35e4	103710	11.0	14.5	14.9	1.47758	0.12104	1.65003	0.0093297
chr8:126298579-12639597	Slc35f3	210027	1.5	1.7	0.1	1.29172	0.600566	-5.67089	6.44E-07
chr5:30647939-30659729:	Slc35f6	74919	26.1	24.1	34.1	1.03133	0.783975	1.62539	3.74E-14
chr19:38395980-38405607	Slc35g1	240660	8.9	9.4	14.5	1.19355	0.470473	1.99631	3.21E-05
chr11:69759886-69761844	Slc35g3	56293	1.4	0.1	0.1	-4.69046	0.007808	-3.88691	0.004268
chr11:55204340-55236330	Slc36a1	215335	10.9	7.5	3.7	-1.30212	0.149036	-2.31544	6.78E-10
chr11:55158468-55185077	Slc36a2	246049	10.0	6.6	1.1	-1.32103	0.607222	-5.19046	3.25E-06
chr6:39334771-39377707:	Slc37a3	72144	37.8	39.7	21.3	1.18112	0.057755	-1.41798	1.87E-07
chr15:96571418-96642913	Slc38a1	105727	43.4	54.2	77.6	1.40049	0.007369	2.21105	9.42E-16
chr2:65316633-65364026:	Slc38a11	320106	6.6	5.7	0.4	-1.0417	0.927309	-9.5642	6.71E-17
chr12:73286848-73354045	Slc38a6	625098	23.1	16.7	7.5	-1.24823	0.383372	-2.3946	9.53E-07
chr8:95835923-95853491:	Slc38a7	234595	21.7	15.6	7.1	-1.24544	0.204199	-2.40326	3.41E-12
chr13:112660766-1127387	Slc38a9	268706	14.6	11.4	3.9	-1.15339	0.293879	-2.95649	2.66E-29
chr3:90248192-90253612:	Slc39a1	30791	97.4	104.6	197.2	1.19437	0.253966	2.49205	6.55E-17
chr11:113244855-1135658	Slc39a11	69806	9.6	7.6	16.5	-1.13719	0.335698	2.1216	6.12E-18
chr14:70303467-70351424	Slc39a14	213053	28.0	34.9	37.7	1.37986	0.129505	1.65641	0.0016674
chr15:76612383-76616852	Slc39a4	72027	94.2	74.9	43.7	-1.13724	0.617016	-1.69409	0.0017209
chr18:24579881-24603817	Slc39a6	106957	22.5	24.6	43.9	1.22841	0.019746	2.43376	5.93E-42
chr17:34028266-34031690	Slc39a7	14977	105.3	122.3	283.8	1.31027	0.117034	3.28944	2.72E-21
chr12:80644215-80683342	Slc39a9	328133	30.4	29.4	34.7	1.08844	0.549632	1.42121	0.0001752
chr17:85028347-85064241	Slc3a1	20532	2.3	1.4	0.8	-1.4016	0.227048	-2.11014	0.0004511
chr19:8706882-8723369:-	Slc3a2	17254	77.0	86.4	177.3	1.26214	0.08615	2.83948	5.81E-26
chr1:45908070-45925594:	Slc40a1	53945	59.0	40.3	23.1	-1.30694	0.458821	-1.92496	0.0097737
chr1:131828012-13184886	Slc41a1	98396	27.7	52.4	29.5	2.09372	0.001208	1.31443	0.178945
chr10:83231139-83337817	Slc41a2	338365	6.9	12.4	14.6	1.9841	0.015113	2.49693	3.91E-05
chr6:90604880-90646412:	Slc41a3	71699	7.1	6.0	2.7	-1.06272	0.759423	-2.05029	8.75E-09
chr2:84839408-84863586:	Slc43a1	72401	31.6	29.2	6.7	1.01954	0.949412	-3.60922	6.95E-16
chr4:53440413-53622478:	Slc44a1	100434	55.8	48.1	32.0	-1.04285	0.680986	-1.39376	1.77E-07
chr9:21320719-21355028:	Slc44a2	68682	89.8	63.6	34.2	-1.26635	0.015816	-2.09166	1.70E-22
chr1:131962915-13198297	Slc45a3	212980	10.5	6.9	3.2	-1.35947	0.110015	-2.546	1.21E-10
chr15:73580291-73624744	Slc45a4	106068	17.1	13.8	9.7	-1.10397	0.342351	-1.39833	6.00E-06
chr5:147878441-14789480	Slc46a3	71706	12.7	8.5	5.2	-1.33219	0.149432	-1.91668	1.35E-05
chr11:61301631-61342860	Slc47a2	380701	2.2	0.7	0.2	-2.53262	0.042483	-5.75287	1.48E-06
chr15:97784365-97792692	Slc48a1	67739	77.5	54.5	31.5	-1.27298	0.007808	-1.96023	6.45E-21
chr5:31526995-31554038:	Slc4a1ap	20534	50.0	52.0	52.0	1.17059	0.16057	1.30078	0.0017215
chr1:75546266-75559431:	Slc4a3	20536	27.0	21.7	13.6	-1.12367	0.566291	-1.56922	0.0008433
chr3:89268246-89270570:	Slc50a1	19729	90.5	68.8	45.5	-1.1847	0.31471	-1.57986	0.0001586
chr15:76538943-76542130	Slc52a2	52710	12.9	12.4	24.4	1.07897	0.515509	2.35956	1.73E-32
chr7:123214866-12327325	Slc5a11	233836	9.4	8.1	0.3	-1.05029	0.953897	-8.08943	1.97E-06
chr16:92058322-92087473	Slc5a3	53881	39.8	43.5	16.5	1.23583	0.293129	-1.89187	9.22E-06
chr8:70882889-70892757:	Slc5a5	114479	0.5	1.3	2.4	2.28403	0.089602	4.05583	0.000127
chr5:31036036-31048924:	Slc5a6	330064	13.2	9.5	14.3	-1.2548	0.056237	1.34466	0.0008792
chr10:103367808-1034193	Slc6a15	103098	8.1	5.0	0.6	-1.43502	0.244266	-9.23475	1.99E-21
chr6:91684067-91759063:	Slc6a6	21366	177.7	82.8	32.0	-1.91724	7.82E-10	-4.36387	1.23E-57
chr5:148327410-14839990	Slc7a1	11987	11.3	16.4	48.2	1.63375	0.052245	4.97278	1.43E-17
chr7:35186385-35201111:	Slc7a10	53896	5.7	2.2	0.5	-1.852	0.309248	-4.2993	0.00089
chr8:40862367-40922070:	Slc7a2	11988	25.1	16.8	11.7	-1.34283	0.08299	-1.70436	3.32E-05

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr16:17572018-17576671	Slc7a4	224022	8.8	5.1	3.5	-1.5136	0.05637	-1.96857	4.79E-05
chr8:121881146-12190768	Slc7a5	20539	15.5	59.7	71.5	3.22478	0.017723	3.89673	0.0005058
chr8:106168875-10619870	Slc7a6	330836	17.6	30.4	30.1	1.90628	0.028973	2.03063	0.0022829
chr8:106200438-10621093	Slc7a6os	66432	40.8	54.2	60.1	1.49394	0.02853	1.81442	2.64E-05
chr14:54722215-54781886	Slc7a8	50934	42.2	35.1	19.9	-1.07832	0.690579	-1.67558	1.13E-05
chr7:16130300-16160511:	Slc8a2	110891	3.6	4.2	5.1	1.30929	0.135396	1.76873	1.57E-05
chr5:120511192-12053402	Slc8b1	170756	41.1	34.1	11.1	-1.07352	0.477365	-2.94327	7.86E-55
chr11:115163341-1151811	Slc9a3r1	26941	33.0	52.8	51.3	1.77963	0.000294	1.90893	1.61E-06
chr17:24639282-24650305	Slc9a3r2	65962	65.4	51.0	69.1	-1.14399	0.099201	1.31964	3.97E-06
chr8:105348258-10536988	Slc9a5	277973	1.4	1.0	0.6	-1.30439	0.293237	-1.9103	0.0005588
chrX:20105755-20291764:	Slc9a7	236727	6.0	5.3	3.3	-1.02084	0.930759	-1.45558	0.0042665
chr3:135348037-13539782	Slc9b1	74446	2.9	0.2	0.4	-6.06224	0.000371	-3.78002	0.0020469
chr3:135307700-13534276	Slc9b2	97086	2.9	2.2	0.1	-1.19949	0.509817	-12.2267	2.97E-20
chr16:45535266-45607001	Slc9c1	208169	1.8	0.1	0.2	-7.9174	2.66E-05	-4.3579	0.0005169
chr6:141805440-14185617	Slco1a4	28250	1.6	0.8	0.0	-1.76515	0.144513	-16.1421	1.78E-15
chr9:103008489-10308784	Slco2a1	24059	9.2	17.2	32.3	2.00778	0.060983	3.77323	2.30E-06
chr7:99657804-99711340:	Slco2b1	101488	32.1	32.4	9.2	1.13329	0.200606	-2.77021	8.38E-46
chr1:12866550-12991135:	Slco5a1	240726	3.7	5.3	26.4	1.62989	0.001085	8.69161	1.04E-74
chr1:97059449-97128303:	Slco6c1	74441	2.5	0.1	0.4	-7.76233	0.000104	-3.39779	0.0078144
chr11:83116845-83122659	Slfn1	20555	1.8	3.9	3.7	2.23186	0.023551	2.35458	0.002172
chr11:83028126-83040533	Slfn10-ps	237887	2.2	2.3	2.9	1.13966	0.632908	1.62277	0.0055234
chr11:83065112-83070678	Slfn2	20556	37.1	56.5	42.6	1.68132	0.001691	1.42187	0.0125633
chr11:82952102-82964850	Slfn5	327978	41.1	44.9	20.7	1.20684	0.406237	-1.56842	0.0051882
chr4:120532231-12053666	Slfnl1	194219	8.9	2.6	2.4	-2.72501	0.00411	-2.61855	0.0007797
chr12:87443896-87449924	Slirp	380773	104.5	116.9	182.8	1.25075	0.126675	2.15909	3.89E-13
chr5:47983155-48306282:	Slit2	20563	20.1	15.5	7.7	-1.16564	0.226339	-2.08109	7.87E-16
chr11:35121456-35708507	Slit3	20564	40.4	33.1	23.5	-1.08619	0.594944	-1.36676	0.0023691
chr3:73048125-73056943:	Slitrk3	386750	14.1	8.5	31.7	-1.48697	0.218836	2.61577	3.88E-05
chr19:47580019-47645246	Slk	20874	104.2	103.7	109.7	1.11795	0.202836	1.31389	1.92E-05
chr2:174465091-17447294	Slmo2	66390	35.4	58.7	131.8	1.84074	0.013348	4.33224	1.46E-14
chr9:70542778-70592232:	Sltm	66660	77.0	71.4	93.6	1.04256	0.738048	1.5149	2.96E-08
chr11:43433731-43447981	Slu7	193116	73.0	69.2	43.0	1.05912	0.417141	-1.35706	4.29E-10
chr7:126688927-12669578	Slx1b	75764	14.8	9.0	4.8	-1.4714	0.112728	-2.35052	3.07E-06
chr16:3979106-4001678:-	Slx4	52864	15.9	16.3	22.2	1.15955	0.300694	1.745	2.87E-08
chr8:79338398-79399468:	Smad1	17125	63.3	68.8	68.7	1.21605	0.102455	1.35423	0.0008261
chr18:76241701-76311747	Smad2	17126	29.4	26.8	29.8	1.02294	0.823082	1.2671	5.43E-05
chr9:63646767-63757994:	Smad3	17127	48.0	46.0	25.3	1.07725	0.532302	-1.51412	1.58E-07
chr3:54755582-54801269:	Smad9	55994	6.3	2.4	0.6	-2.28113	0.013767	-7.10593	1.83E-13
chr1:23844825-23922381:	Smap1	98366	40.5	36.6	43.2	1.01444	0.898625	1.33286	2.35E-06
chr4:120968317-12101724	Smap2	69780	14.4	13.2	15.4	1.02417	0.859336	1.33491	9.73E-05
chrX:47809370-47892552:	Smarca1	93761	22.9	21.8	12.2	1.06478	0.604155	-1.49301	3.97E-07
chr19:26605160-26778321	Smarca2	67155	139.9	102.1	23.9	-1.22698	0.10873	-4.58458	1.59E-60
chr9:21616169-21704230:	Smarca4	20586	44.6	46.6	73.4	1.17941	0.164053	2.04784	4.42E-17
chr8:80699943-80739459:	Smarca5	93762	96.5	117.4	168.0	1.373	0.075384	2.14139	1.07E-08
chr6:65042667-65116049:	Smarcad1	13990	50.6	49.4	51.5	1.09883	0.434704	1.27014	0.0047199
chr10:75896769-75921614	Smarcb1	20587	65.5	58.0	91.2	-1.01332	0.920237	1.73888	3.48E-16
chr10:128459236-1284901	Smarcc2	68094	107.9	94.0	70.2	-1.02328	0.82988	-1.22726	0.0010831
chr15:99702287-99713995	Smarcd1	83797	27.0	25.7	27.7	1.07152	0.625775	1.28277	0.006918
chr11:99209048-99231017	Smarce1	57376	94.0	100.2	115.2	1.20267	0.157104	1.52515	1.19E-05
chrX:152016428-15206197	Smc1a	24061	153.1	149.5	169.8	1.09158	0.13764	1.38475	3.12E-14
chr15:85064689-85131957	Smc1b	140557	3.5	0.4	0.4	-5.72373	5.12E-05	-5.39372	5.43E-06
chr3:69004972-69034623:	Smc4	70099	64.3	62.1	41.6	1.08386	0.460996	-1.23247	0.0062872
chr17:71344493-71475343	Smchd1	74355	71.3	78.9	78.1	1.24795	0.087489	1.36487	0.0016682
chr6:146850110-14687140	Smco2	69371	2.7	0.2	0.5	-4.99502	0.002824	-2.8521	0.0194619
chr3:92583866-92589024:	Smcp	17235	12.5	0.8	1.5	-8.53485	2.16E-06	-4.8801	5.30E-05
chr15:82346046-82349062	Smdt1	69029	96.3	104.0	196.7	1.21172	0.075592	2.5372	2.33E-33
chr12:101039409-1010837	Smek1	68734	72.7	83.2	92.0	1.29387	0.129682	1.56974	0.0004198
chr11:29172907-29220797	Smek2	104570	88.6	97.0	93.8	1.23148	0.090283	1.31998	0.003143

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr3:88336260-88362337:	Smg5	229512	51.2	59.5	108.2	1.31226	0.098004	2.59934	2.12E-15
chr1:152836995-15290264	Smg7	226517	53.8	58.5	68.2	1.22666	0.165724	1.57514	2.96E-05
chr11:87077732-87086777	Smg8	74133	19.1	24.7	27.4	1.45663	0.024985	1.77782	9.45E-06
chr4:154020470-15402604	Smim1	68859	21.1	19.2	9.1	1.02375	0.901905	-1.84619	5.74E-09
chr4:127243784-12724780	Smim12	80284	42.5	44.6	52.8	1.18119	0.151072	1.54742	2.22E-07
chr5:65448755-65492835:	Smim14	68552	97.6	76.7	47.3	-1.14571	0.35199	-1.64086	1.45E-06
chr13:108044474-1080491	Smim15	75616	89.3	93.7	85.4	1.17204	0.06146	1.19156	0.0076404
chr8:22462614-22476879:	Smim19	102032	28.6	21.9	15.6	-1.17416	0.226617	-1.4608	0.0001054
chr11:32820376-32824594	Smim23	69351	4.7	0.3	0.4	-4.37525	0.011937	-3.47313	0.0091162
chr10:81393064-81395079	Smim24	72273	39.4	11.1	9.1	-2.88939	0.000291	-3.14547	4.02E-06
chr11:115900139-1159062	Smim5	66528	5.8	8.4	0.9	1.55423	0.412834	-3.5588	0.0010807
chr11:115912017-1159139	Smim6	68528	10.6	6.0	4.5	-1.56477	0.114681	-1.81911	0.0061213
chr8:72565198-72571048:	Smim7	66818	67.3	75.8	102.0	1.26647	0.111011	1.87507	9.81E-09
chr13:100123205-1001376	Smn1	20595	16.9	18.5	31.1	1.23816	0.293895	2.25542	9.20E-09
chr19:53379214-53390573	Smndc1	76479	32.6	42.6	53.7	1.47264	0.073855	2.01009	1.90E-05
chr6:29735497-29761366:	Smo	319757	102.3	85.3	68.2	-1.07428	0.410421	-1.19723	0.0034729
chr12:81026808-81186414	Smoc1	64075	38.9	50.3	75.4	1.45611	0.163425	2.33379	2.07E-05
chr17:14279506-14404790	Smoc2	64074	143.4	156.0	249.9	1.22902	0.298877	2.1483	4.88E-08
chr10:41487172-41490340	Smpd2	20598	69.8	48.6	32.6	-1.29251	0.067436	-1.7024	5.10E-07
chr10:57794544-57811830	Smpdl3a	57319	100.9	86.8	29.6	-1.04735	0.823348	-2.69299	6.73E-17
chr4:132732966-13275717	Smpdl3b	100340	10.6	6.2	14.8	-1.50917	0.005702	1.73149	1.04E-06
chrX:157443954-15749204	Sms	20603	22.2	19.8	24.9	-1.00324	0.980045	1.39965	3.98E-07
chr11:3517522-3539292:-	Smtn	29856	224.6	191.1	73.6	-1.06411	0.820785	-2.37891	4.01E-08
chr4:40735649-40757885:	Smu1	74255	85.2	93.5	120.4	1.23627	0.136115	1.75176	8.82E-08
chr1:189880492-18992228	Smyd2	226830	62.3	56.3	102.4	1.01071	0.891244	2.05231	2.58E-75
chr1:178955039-17951800	Smyd3	69726	17.9	14.3	5.8	-1.11849	0.228872	-2.432	5.37E-37
chr6:85431976-85446429:	Smyd5	232187	32.0	33.6	86.7	1.17593	0.033171	3.37335	5.87E-112
chr16:14705859-14709382	Snai2	20583	13.4	16.5	34.9	1.36114	0.112726	3.16636	2.52E-16
chr8:122454206-12246069	Snai3	30927	0.8	0.9	2.3	1.1944	0.726677	2.99241	0.0002392
chr2:120567671-12060072	Snap23	20619	69.7	68.1	68.4	1.09497	0.284809	1.22488	0.0008714
chr12:73964530-73984820	Snapc1	75627	25.5	33.2	45.0	1.46244	0.008263	2.17633	5.22E-12
chr8:4253102-4256220:+	Snapc2	102209	47.2	50.1	63.1	1.19428	0.14575	1.66486	9.93E-09
chr3:90488026-90491013:	Snapin	20615	89.1	70.2	47.9	-1.14117	0.342708	-1.48195	6.99E-05
chr14:34370274-34374669	Sncg	20618	21.9	12.1	8.6	-1.58377	0.107808	-1.96167	0.0020345
chr6:28480348-28888832:	Snd1	56463	94.4	85.2	176.9	1.0082	0.932968	2.33918	1.13E-67
chr1:93235897-93296448:	Sned1	208777	232.5	169.1	33.9	-1.21741	0.279023	-5.2751	1.50E-39
chr11:96034917-96047405	Snf8	27681	47.1	43.8	72.4	1.0479	0.767658	1.91179	1.37E-12
chr19:8723487-8726326:+	Snhg1	83673	257.5	371.3	906.2	1.61387	0.037201	4.15643	1.53E-16
chr2:158375638-15838614	Snhg11	319317	2.6	1.8	0.4	-1.26765	0.434	-4.66596	2.52E-12
chr4:132308678-13231102	Snhg12	1E+08	104.6	127.9	312.6	1.37625	0.108383	3.60808	7.27E-19
chr7:59969577-59974431:	Snhg14	52480	10.3	8.4	3.1	-1.10977	0.576391	-2.62779	3.36E-14
chr15:32240568-32244662	Snhg18	1.01E+08	93.5	65.7	31.1	-1.28367	0.378426	-2.30627	2.65E-05
chr4:132351933-13235368	Snhg3	399101	57.8	51.9	186.4	1.00427	0.977781	3.99363	1.83E-88
chr18:35553410-35558316	Snhg4	1.01E+08	16.7	17.7	65.7	1.18416	0.249606	4.82766	3.88E-60
chr9:88521053-88522897:	Snhg5	72655	102.2	96.7	274.2	1.05907	0.477467	3.33651	1.96E-125
chr1:9942025-9944118:-	Snhg6	73824	65.9	87.3	222.5	1.48419	0.024378	4.09111	3.60E-27
chr2:26637176-26640244:	Snhg7	72091	59.4	61.1	92.1	1.15562	0.218899	1.9293	9.84E-16
chr3:123507552-12350833	Snhg8	69895	85.3	84.8	143.1	1.11496	0.46673	2.0752	1.60E-13
chr4:125066693-12507404	Snip1	76793	30.2	37.1	38.0	1.38395	0.10091	1.55442	0.0034757
chr16:11066298-11074986	Snn	20621	41.6	44.6	14.8	1.21597	0.425038	-2.1817	4.68E-06
chr4:132309465-13230960	Snora16a	1E+08	50.6	72.4	171.0	1.59643	0.070417	3.98274	1.61E-13
chr2:26639190-26639321:	Snora17	1E+08	63.0	63.7	114.6	1.13914	0.595832	2.23429	1.27E-07
chr11:97781639-97781766	Snora21	1E+08	37.3	48.4	75.9	1.44244	0.258696	2.3933	0.0001522
chr15:98526348-98526459	Snora2b	1E+08	25.8	32.7	42.7	1.40522	0.214932	2.01002	0.0003198
chr7:109520132-10952025	Snora3	1E+08	56.3	100.7	178.3	1.96706	0.014463	3.67334	1.00E-09
chr14:75847923-75848034	Snora31	1E+08	52.1	68.2	94.0	1.46523	0.15966	2.18433	8.01E-05
chr10:23785347-23785451	Snora33	1.01E+08	48.9	93.8	228.3	2.09257	0.005761	5.31131	8.85E-16
chr1:63179023-63179135:	Snora41	1E+08	32.4	48.1	86.7	1.62741	0.144623	3.06464	3.91E-06

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr2:26637847-26637985:	Snora43	1E+08	48.7	48.5	81.6	1.11433	0.634371	2.06285	9.51E-08
chr4:132309953-13231006	Snora44	1E+08	87.0	101.9	128.7	1.30876	0.249973	1.8195	0.00035
chr7:141448803-14144893	Snora52	1E+08	33.9	64.6	103.4	2.04544	0.033004	3.4197	1.47E-06
chr4:132310307-13231036	Snora61	1E+08	83.0	144.5	385.8	1.91906	0.008217	5.3928	2.81E-19
chr9:120130434-12013056	Snora62	104433	22.1	40.1	84.7	1.96575	0.021088	4.37758	1.44E-11
chr17:24720789-24720905	Snora64	104366	37.6	59.5	102.1	1.74191	0.034062	3.20385	2.08E-09
chr2:32963301-32963418:	Snora65	104367	129.3	216.5	454.5	1.84566	0.044857	3.98958	1.63E-09
chr8:70895759-70895856:	Snora68	104370	87.1	91.1	111.7	1.17178	0.544357	1.57649	0.0088585
chrX:37082912-37083033:	Snora69	104369	18.9	28.9	68.6	1.66684	0.103434	4.16261	1.28E-10
chrX:74272492-74272620:	Snora70	104368	37.4	68.9	122.7	2.00239	0.015455	3.7615	1.64E-09
chr1:86351170-86351285:	Snora75	1E+08	39.8	44.7	77.5	1.25802	0.486609	2.30945	0.0001313
chr6:115807975-11580810	Snora7a	1E+08	67.7	68.0	119.0	1.13727	0.693046	2.12072	0.0001526
chr16:23110770-23110933	Snora81	1E+08	219.6	260.3	320.3	1.3365	0.181465	1.78906	0.0002735
chr10:23785754-23785821	Snord100	1.01E+08	62.5	117.7	312.6	2.02795	0.033826	5.42094	1.10E-11
chr11:106500991-1065010	Snord104	1E+08	205.8	289.9	580.2	1.57798	0.056491	3.36419	6.55E-12
chr1:59704808-59704870:	Snord11	1E+08	10.2	24.4	40.6	2.18882	0.127222	3.56982	0.0008869
chr2:130275515-13027557	Snord110	1E+08	4.7	19.7	27.3	3.08037	0.034911	4.27559	0.0003991
chr8:110838535-11083859	Snord111	1E+08	37.7	59.9	62.1	1.7216	0.109095	1.94646	0.0097423
chr2:167065293-16706535	Snord12	1E+08	39.6	70.2	331.9	1.89985	0.039458	9.00623	8.76E-23
chr2:32777988-32778009:	Snord14a	1E+08	8.6	34.7	116.6	2.51275	0.110929	6.72719	7.48E-06
chr7:99482785-99482932:	Snord15a	449630	34.9	38.3	52.4	1.23346	0.452274	1.83463	0.0012937
chr9:64175432-64175522:	Snord16a	1E+08	22.6	38.6	72.7	1.8355	0.084572	3.58408	6.82E-07
chr14:31016219-31016272	Snord19	1E+08	93.2	151.9	203.4	1.76473	0.137489	2.46738	0.0016321
chr11:116674147-1166742	Snord1b	1E+08	11.5	22.0	31.6	1.95373	0.128469	2.91788	0.0010181
chr11:116672505-1166725	Snord1c	1E+08	10.1	16.6	30.8	1.70424	0.221864	3.24442	0.0001187
chr16:23108953-23109020	Snord2	1E+08	222.6	309.7	448.4	1.55699	0.119632	2.3974	3.74E-05
chr19:8725866-8725991:+	Snord22	1E+08	149.8	197.9	349.8	1.48159	0.053725	2.84081	3.93E-12
chr7:45127383-45127463:	Snord32a	27209	24.1	36.6	60.3	1.65045	0.160992	2.86914	4.20E-05
chr7:45126864-45126945:	Snord33	27208	3.7	15.4	23.3	3.27948	0.010291	5.11038	6.13E-06
chr7:45126603-45126668:	Snord34	27210	10.6	18.3	29.5	1.7639	0.213694	2.94987	0.0008673
chr7:45126347-45126435:	Snord35a	27211	11.2	12.4	32.4	1.22674	0.715112	3.04332	0.0008417
chr7:45123026-45123111:	Snord35b	27212	6.7	16.2	32.6	2.23901	0.096948	4.4439	2.84E-05
chr10:81178961-81179013	Snord37	1E+08	32.7	46.1	98.0	1.54208	0.222548	3.44478	4.25E-07
chr11:78183059-78183113	Snord42b	1.01E+08	48.1	54.2	80.1	1.25118	0.567341	1.97993	0.0074769
chr15:80082859-80082906	Snord43	1E+08	54.7	139.4	435.4	2.50155	0.023635	7.35586	8.76E-11
chr3:153910567-15391061	Snord45b	1E+08	86.7	103.7	264.7	1.34393	0.296678	3.62466	9.27E-12
chr1:161038092-16103815	Snord47	1E+08	48.8	85.5	294.8	1.90139	0.031627	6.69826	2.83E-18
chr11:62603460-62603521	Snord49a	1E+08	60.2	106.2	401.1	1.90286	0.058272	7.07848	2.59E-15
chr11:62603086-62603148	Snord49b	1E+08	15.6	30.3	92.8	1.96928	0.10091	5.91917	1.39E-09
chr11:78181687-78181756	Snord4a	1E+08	29.7	60.1	85.8	2.16814	0.011	3.33227	3.09E-07
chr17:34950950-34951008	Snord52	1E+08	52.7	103.5	373.7	2.03331	0.082488	6.82456	1.48E-10
chr17:71640889-71640956	Snord53	1E+08	92.4	135.7	208.8	1.62826	0.098248	2.66346	7.03E-06
chr17:71641639-71641658	Snord53	1E+08	116.2	164.8	240.8	1.54452	0.303227	2.35194	0.0046879
chr7:110848296-11084831	Snord53	1E+08	1.4	4.7	33.6	1.3999	0.645966	5.01392	0.0005894
chr2:130278026-13027808	Snord57	1E+08	7.7	24.4	34.4	2.64008	0.062209	3.74948	0.0008285
chr18:75001068-75001122	Snord58b	1E+08	46.0	55.3	119.7	1.33847	0.347294	3.0985	2.93E-08
chr7:59978811-59978856:	Snord64	1E+08	43.7	30.6	10.0	-1.26449	0.601742	-2.90603	0.00089
chr11:62604530-62604586	Snord65	1E+08	12.9	30.3	94.4	2.34127	0.02853	7.32619	1.19E-12
chr8:123103058-12310310	Snord68	1E+08	16.5	26.3	56.0	1.63726	0.329812	3.40188	0.0005006
chr14:31014293-31014351	Snord69	1E+08	27.2	85.3	104.0	3.0308	0.005293	3.87406	2.39E-05
chr1:59691958-59692010:	Snord70	1E+08	61.0	98.3	111.5	1.77178	0.023583	2.21161	4.01E-05
chr15:5118421-5118480:+	Snord72	1E+08	71.4	156.9	236.5	2.33635	0.00633	3.70708	1.06E-07
chr3:86138791-86138858:	Snord73a	19870	32.0	45.4	87.6	1.53032	0.262931	3.07078	2.40E-05
chr1:86356260-86356327:	Snord82	80828	10.7	19.5	32.5	1.78826	0.260339	2.98574	0.0031516
chr15:80078503-80078579	Snord83b	1E+08	24.5	46.0	162.6	2.0001	0.049729	7.01659	2.32E-14
chr1:9942470-9942543:-	Snord87	266793	18.5	24.6	82.2	1.43328	0.391617	4.70168	1.88E-08
chr7:44249855-44249938:	Snord88c	1E+08	28.2	59.6	48.9	2.2254	0.016453	2.02002	0.0088885
chr11:74905446-74905505	Snord91a	1E+08	26.2	41.5	86.6	1.69282	0.202426	3.56424	1.50E-05

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr17:71631279-71631361	Snord92	1E+08	12.0	24.1	33.3	2.00458	0.135592	2.86129	0.0024648
chr5:23852233-23852277:	Snord93	1E+08	12.0	25.2	64.2	1.96705	0.189879	4.63368	3.23E-05
chr11:48803139-48803206	Snord95	1E+08	83.0	114.6	207.0	1.53625	0.080187	2.98827	6.60E-10
chr11:48802033-48802109	Snord96a	1E+08	248.3	368.7	629.2	1.66066	0.026551	3.03906	1.44E-10
chr4:132310703-13231075	Snord99	1E+08	85.5	151.6	372.4	1.9111	0.065314	4.7149	2.33E-09
chr2:151590549-15163259	Snph	241727	2.5	2.0	1.1	-1.11416	0.656262	-1.74769	0.0004673
chr2:127208404-12724045	Snrnp200	320632	148.2	131.1	164.3	-1.0065	0.959762	1.38512	9.35E-07
chr11:32205415-32208995	Snrnp25	78372	14.2	13.7	6.7	1.06974	0.76868	-1.65386	0.000542
chr6:86675169-86684491:	Snrnp27	66618	93.3	102.7	117.2	1.23897	0.064981	1.56373	2.57E-07
chr5:124483155-12449112	Snrnp35	76167	18.3	17.7	22.0	1.09289	0.550549	1.50335	1.89E-05
chr4:130360132-13039003	Snrnp40	66585	49.7	64.2	99.9	1.45345	0.033949	2.46497	1.30E-11
chr13:38204939-38227663	Snrnp48	67797	51.2	53.4	53.3	1.17069	0.111492	1.29999	0.0004284
chr7:27187006-27196271:	Snrpa	53607	49.5	55.6	102.4	1.26632	0.096678	2.55675	9.18E-20
chr7:66060336-66074587:	Snrpa1	68981	49.5	57.3	101.2	1.303	0.08286	2.52003	1.12E-16
chr2:130171636-13017936	Snrpb	20638	222.5	269.3	456.6	1.36206	0.041675	2.52749	3.02E-16
chr2:143063069-14307205	Snrpb2	20639	84.3	90.8	113.5	1.21336	0.194112	1.66987	2.11E-06
chr17:27840087-27851967	Snrpc	20630	56.2	65.0	103.6	1.29658	0.007185	2.29388	1.13E-29
chr18:10617796-10628230	Snrpd1	20641	82.4	113.8	248.7	1.54675	0.023234	3.63916	6.88E-19
chr7:19149838-19152726:	Snrpd2	107686	223.8	230.3	342.1	1.15296	0.247164	1.8987	1.13E-13
chr10:75518042-75535440	Snrpd3	67332	81.5	91.9	197.7	1.26624	0.102143	2.98208	6.20E-26
chr1:133603871-13361028	Snrpe	20643	186.1	190.6	297.8	1.14985	0.417849	1.97434	7.23E-09
chr10:93583029-93589658	Snrpf	69878	60.5	67.1	135.4	1.24382	0.172907	2.74664	6.34E-19
chr6:86371540-86378902:	Snrpg	68011	176.5	194.3	225.6	1.23207	0.109766	1.58782	1.76E-06
chr15:55639154-55906949	Sntb1	20649	19.3	14.2	5.7	-1.21466	0.421399	-2.60887	1.32E-08
chr9:56950924-56983199:	Snupn	66069	20.2	21.2	26.2	1.17627	0.119671	1.61698	1.08E-10
chr12:87449910-87472299	Snw1	66354	146.3	144.1	157.6	1.10857	0.460141	1.34268	0.0023349
chr11:96767549-96777555	Snx11	74479	25.6	27.1	39.4	1.19695	0.270025	1.9055	2.02E-08
chrX:101097786-10122256	Snx12	55988	27.0	26.3	28.5	1.08775	0.233701	1.31569	3.34E-08
chr9:88376747-88438951:	Snx14	244962	57.4	52.7	22.6	1.02181	0.840006	-2.03097	2.08E-31
chr5:31193304-31198900:	Snx17	266781	114.4	109.8	148.3	1.08028	0.511602	1.61379	6.85E-10
chr9:30427329-30466726:	Snx19	102607	37.0	34.6	56.1	1.05321	0.654918	1.88991	3.14E-19
chr2:164786021-16479277	Snx21	101113	52.7	41.8	18.2	-1.13426	0.443328	-2.29062	2.00E-13
chr9:66065176-66069731:	Snx22	382083	3.4	2.6	1.5	-1.16933	0.606487	-1.75388	0.0061492
chr18:53245662-53390825	Snx24	69226	23.5	14.9	11.3	-1.41914	0.053411	-1.65251	0.0003111
chr16:11322904-11755473	Snx29	74478	37.1	29.3	11.0	-1.13244	0.256459	-2.67779	2.19E-35
chr10:42502054-42535369	Snx3	54198	82.1	89.4	135.1	1.22414	0.069672	2.04407	2.08E-18
chr4:59805650-59904740:	Snx30	209131	16.2	11.5	8.3	-1.27208	0.047201	-1.56289	1.41E-06
chr19:5495278-5510489:-	Snx32	225861	29.8	15.4	7.3	-1.70225	0.075599	-3.03386	9.71E-07
chr9:56917200-56928371:	Snx33	235406	56.4	38.7	15.7	-1.30685	0.006176	-2.84343	2.03E-41
chr16:33251456-33299562	Snx4	69150	84.9	83.8	89.7	1.10741	0.209455	1.31792	2.61E-06
chr2:144250124-14427090	Snx5	69178	194.5	273.4	271.0	1.57653	0.034453	1.70702	0.001465
chr3:117781497-11786893	Snx7	76561	12.4	10.0	17.4	-1.12362	0.638377	1.72812	0.0004838
chr1:156428108-15647432	Soat1	20652	53.7	51.0	61.9	1.07004	0.675663	1.43429	0.0003957
chr16:10783809-10785536	Socs1	12703	4.9	29.7	31.5	4.98312	9.68E-05	5.511	1.36E-06
chr10:95411490-95416857	Socs2	216233	31.3	79.8	94.9	2.70839	1.91E-05	3.53483	2.79E-10
chr11:117966087-1179693	Socs3	12702	22.7	187.4	117.3	7.62953	1.16E-11	5.37201	5.69E-10
chr14:47277143-47291591	Socs4	67296	26.8	34.2	31.4	1.43281	0.007468	1.45444	0.0005802
chr18:88867880-88894207	Socs6	54607	41.6	44.5	45.7	1.20404	0.110929	1.37049	0.0003275
chr16:90220742-90226324	Sod1	20655	431.0	388.9	429.3	1.0079	0.945645	1.24245	0.0003585
chr17:13007839-13018119	Sod2	20656	37.3	41.8	68.0	1.25072	0.08616	2.25431	1.72E-17
chr8:45507788-45827906:	Sorbs2	234214	41.8	33.3	20.4	-1.12959	0.437474	-1.62279	7.65E-06
chr8:45723325-45819297:	Sorbs2os	319940	3.5	2.6	0.5	-1.1642	0.760826	-4.72057	7.47E-07
chr14:70180468-70207671	Sorbs3	20410	55.0	44.1	24.4	-1.11116	0.415616	-1.79074	6.44E-11
chr2:122234839-12226533	Sord	20322	101.0	48.0	11.8	-1.8619	0.001573	-6.42089	5.08E-31
chr9:41968489-42124289:	Sorl1	20660	22.4	20.3	11.5	1.01552	0.928961	-1.5476	2.05E-06
chr3:108284064-10836151	Sort1	20661	57.1	45.0	19.4	-1.14126	0.37658	-2.32243	2.38E-16
chr12:69583761-69681852	Sos2	20663	29.7	24.6	16.6	-1.07975	0.19925	-1.42837	1.99E-16
chr10:59221922-59226433	Sowahc	268301	20.6	24.4	25.5	1.33277	0.044129	1.5353	8.67E-05

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr2:152393612-15239804	Sox12	20667	12.9	12.2	5.2	1.0794	0.845738	-1.91935	0.0043356
chr1:4490928-4497354:-	Sox17	20671	46.6	42.7	21.4	1.01042	0.978408	-1.70391	0.0092437
chr2:181669837-18167164	Sox18	20672	15.8	17.1	24.7	1.21173	0.11253	1.93607	1.73E-14
chr13:28950730-28953682	Sox4	20677	123.5	56.5	40.5	-1.89402	0.065531	-2.25849	0.0022524
chr6:143828425-14420956	Sox5	20678	12.1	9.8	38.1	-1.10647	0.477065	3.86098	4.09E-49
chr7:115470872-11603874	Sox6	20679	3.9	2.4	1.5	-1.44186	0.032945	-2.07348	4.04E-08
chr11:112782210-1127877	Sox9	20682	1.4	3.1	5.5	2.44863	0.003978	4.42299	2.13E-09
chr1:85650050-85709448:	Sp100	20684	71.8	58.4	20.2	-1.10344	0.619877	-2.79586	3.89E-16
chr2:72936432-72980446:	Sp3	20687	152.8	181.2	213.2	1.33678	0.030603	1.73226	9.10E-08
chr2:72979432-72989249:	Sp3os	1.01E+08	12.2	8.5	4.4	-1.29233	0.277736	-2.16429	9.08E-06
chr12:118231686-1183014	Sp4	20688	33.6	28.7	14.9	-1.05427	0.74955	-1.79415	4.13E-09
chr9:37603294-37613720:	Spa17	20686	30.7	7.3	5.6	-3.35606	8.99E-05	-3.84827	3.73E-07
chr4:34024872-34050067:	Spaca1	67652	3.5	0.4	0.4	-4.04063	0.014463	-3.50172	0.0063542
chr11:80858389-80867814	Spaca3	75622	4.0	0.2	0.6	-5.47978	0.002336	-3.1673	0.0141355
chr7:45725107-45725816:	Spaca4	69363	3.2	0.1	0.4	-4.68552	0.007608	-2.87785	0.0282542
chr8:12573049-12600738:	Spaca7	78634	3.7	0.2	0.5	-5.02855	0.004014	-3.43726	0.0078629
chr1:69826970-70725132:	Spag16	66722	1.4	0.0	0.1	-11.0146	2.53E-06	-5.28176	0.0001802
chr3:99885417-100143322	Spag17	74362	2.9	0.1	0.3	-10.315	7.10E-07	-4.63292	0.0002116
chr16:16753016-16829363	Spag6	50525	4.5	0.6	0.7	-5.04133	7.25E-05	-3.9402	8.70E-05
chr11:70663769-70669416	Spag7	216873	66.3	70.6	91.5	1.19363	0.074375	1.71781	8.67E-14
chr4:43651330-43653552:	Spag8	433700	5.0	2.3	1.0	-1.93735	0.009663	-3.88995	3.49E-10
chr6:24791188-24801048:	Spam1	20690	1.1	0.1	0.1	-5.61548	0.001756	-4.62492	0.0008748
chr5:104079109-10411408	Sparcl1	13602	####	2451.5	823.4	-1.03232	0.840052	-2.70819	5.35E-30
chr3:146457203-14649975	Spata1	70951	14.5	8.1	5.2	-1.57725	0.028799	-2.15013	2.43E-06
chr3:26637631-26983212:	Spata16	70862	5.7	0.3	0.6	-6.90877	0.000179	-4.61514	0.0005669
chr1:187048407-18721544	Spata17	74717	2.5	1.2	0.6	-1.69053	0.225695	-2.87074	0.0012728
chr5:73651380-73679484:	Spata18	73472	9.7	0.5	0.9	-9.40116	7.10E-07	-5.74967	9.24E-06
chr9:27396821-27401710:	Spata19	75469	17.0	0.8	1.9	-8.70969	1.50E-05	-4.53237	0.0005255
chr2:167481136-16749287	Spata2	263876	9.4	12.0	12.7	1.44878	0.075384	1.66709	0.0013231
chr11:94478904-94485310	Spata20	217116	18.2	1.3	2.5	-8.91469	1.10E-08	-4.62855	5.65E-06
chr4:141088345-14111275	Spata21	329972	14.2	0.7	1.5	-11.5979	5.90E-09	-5.65743	2.63E-06
chr18:35656689-35662186	Spata24	71242	32.3	14.4	8.0	-1.96955	0.001082	-3.07399	1.01E-10
chr2:164827382-16482853	Spata25	75642	5.4	1.9	1.4	-2.28907	0.056631	-2.6054	0.0045578
chr8:123232258-12323620	Spata2l	78779	5.3	4.8	1.8	1.00524	0.980435	-2.36285	3.93E-12
chr1:86021942-86029958:	Spata3	70060	4.4	0.3	0.5	-6.19265	0.000445	-4.24709	0.001067
chr13:59712284-59719289	Spata31d1b	238662	2.2	0.1	0.2	-5.80918	0.001217	-3.88762	0.0032116
chr11:103208127-1032184	Spata32	328019	2.0	0.4	0.2	-3.05695	0.045969	-4.44352	0.0006474
chr8:123212858-12322204	Spata33	320869	25.0	4.6	4.2	-4.04898	0.0001	-4.00591	6.64E-06
chr8:54600781-54610098:	Spata4	69281	22.5	1.7	3.0	-7.00261	4.35E-05	-4.10084	0.0006494
chr1:191036822-19104294	Spata45	75558	4.7	0.3	0.3	-6.2345	0.000688	-5.88044	9.67E-05
chr3:37420280-37579095:	Spata5	57815	36.3	47.4	96.5	1.47109	0.013732	3.25512	8.98E-23
chr2:122630625-12263270	Spata5l1	214616	6.2	8.3	12.0	1.50031	0.086762	2.36138	8.31E-07
chr4:111720010-11182914	Spata6	67946	47.2	27.9	12.1	-1.51402	0.011893	-3.03749	8.80E-18
chr12:98628142-98669819	Spata7	104871	21.2	9.8	4.8	-1.89684	0.003622	-3.36727	1.24E-11
chr13:75967739-75998968	Spata9	75571	2.1	0.2	0.5	-5.08897	0.000383	-2.96975	0.0037098
chr15:76268089-76292572	Spatc1	74281	3.5	0.2	0.4	-6.82274	0.000296	-3.89546	0.0027794
chr10:76562272-76570200	Spatc1l	76573	3.0	0.4	0.5	-4.14342	0.00819	-3.16585	0.008447
chr15:99126845-99212466	Spats2	72572	20.0	16.8	22.2	-1.06091	0.537001	1.39043	4.11E-08
chr1:57774861-57948397:	Spats2l	67198	24.2	22.2	8.4	1.02118	0.879016	-2.30241	2.00E-27
chr14:30999826-31001666	Spcs1	69019	137.8	146.9	213.7	1.19896	0.20801	1.91967	2.58E-10
chr7:99837569-99858883:	Spcs2	66624	79.2	85.1	153.0	1.20516	0.04954	2.40094	3.89E-36
chr8:54520433-54529998:	Spcs3	76687	58.7	60.3	124.4	1.14699	0.094537	2.63309	2.82E-61
chr17:71552061-71589533	Spdya	70891	5.4	2.8	0.6	-1.66771	0.074321	-6.05778	1.40E-14
chr11:61956763-62223013	Specc1	432572	5.6	4.8	7.2	-1.04234	0.779127	1.59273	4.07E-08
chr5:11340408-11346273:	Speer1-ps1	70896	1.1	0.1	0.1	-4.06042	0.018448	-3.49579	0.0087865
chr5:15680710-15714596:	Speer7-ps1	75858	11.7	6.1	0.3	-1.61565	0.346949	-14.0997	1.80E-12
chr5:14945294-14978541:	Speer8-ps1	74062	6.5	2.4	0.2	-2.18381	0.103397	-11.2382	2.16E-10
chr7:3128146-3144992:+	Speer9-ps1	73949	2.1	1.3	0.6	-1.36616	0.521743	-2.52586	0.0083741

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr2:131170261-13117481	Spef1	70997	23.8	19.2	25.2	-1.10801	0.379898	1.31891	0.0005957
chr15:9662736-9748806:-	Spef2	320277	1.4	0.6	0.4	-2.03256	0.034795	-2.36024	0.0011425
chr11:69820871-69822165	Spem1	74288	14.0	2.2	2.3	-4.27447	0.001155	-3.69727	0.0005025
chr14:75582834-75593116	Spert	67926	9.6	0.5	0.9	-8.81038	9.73E-06	-5.2735	0.0001082
chr9:62270729-62282179:	Spesp1	66712	3.1	0.2	0.5	-5.70484	0.001435	-3.1541	0.0135354
chr11:116531911-1165366	Sphk1	20698	17.1	37.3	52.0	2.35132	0.000508	3.53727	7.23E-10
chr1:83255781-83408200:	Sphkap	77629	5.6	4.7	2.3	-1.07117	0.761941	-1.90963	3.04E-06
chr16:44347401-44388492	Spice1	212514	30.1	24.1	7.4	-1.12363	0.459224	-3.19828	1.84E-27
chr13:51100880-51152562	Spin1	20729	124.3	112.2	78.8	1.00974	0.89394	-1.26111	5.45E-09
chr18:44104523-44108543	Spink12	78242	1.0	3.3	5.3	2.29452	0.136352	3.67745	0.0019013
chr5:77205106-77211471:	Spink2	69982	10.2	0.6	1.4	-6.13321	0.000591	-3.52394	0.0052626
chr7:29256330-29281977:	Spint2	20733	125.0	95.7	64.2	-1.16633	0.2289	-1.55133	2.26E-06
chr18:67488209-67552721	Spire1	68166	16.1	15.1	21.6	1.05487	0.589091	1.67503	5.42E-17
chr8:123332713-12336951	Spire2	234857	4.0	3.0	1.2	-1.20316	0.409728	-2.65994	5.80E-09
chr7:127132232-12713782	Spn	20737	5.5	8.0	15.3	1.51006	0.324296	2.98757	0.0002448
chr15:90891396-90898476	Spn-ps	20738	2.7	0.1	0.4	-5.4267	0.00293	-3.10459	0.0184154
chr7:126370060-12637793	Spns1	73658	38.7	31.9	23.0	-1.08478	0.345014	-1.34368	1.27E-06
chr11:72451638-72489920	Spns2	216892	18.4	23.2	23.1	1.41218	0.103382	1.53932	0.007875
chr2:172979842-17299357	Spo11	26972	3.8	1.5	0.4	-2.15731	0.028351	-6.55321	1.58E-10
chr10:60106257-60133913	Spock2	94214	100.5	78.2	25.1	-1.15255	0.343349	-3.14318	2.09E-28
chr7:113765998-11404337	Spon1	233744	16.6	22.7	179.5	1.53029	0.113017	11.8918	4.98E-37
chr5:33213518-33218238:	Spon2	100689	60.7	81.1	317.8	1.4702	0.041218	6.22554	3.22E-39
chr2:23510054-23572104:	Spopl	76857	38.7	35.8	38.1	1.03422	0.72368	1.22895	0.0003861
chr11:104186327-1041911	Sppl2c	237958	4.4	0.1	0.4	-12.2967	4.01E-07	-5.0824	0.0001644
chr11:19924442-20022597	Spred2	114716	16.6	15.5	8.5	1.04796	0.715463	-1.55731	3.85E-08
chr7:140150628-14015465	Sprn	212518	4.9	3.7	0.8	-1.20989	0.610954	-4.34412	4.10E-09
chr3:92483954-92485881:	Sprr1a	20753	0.5	2.7	9.3	3.30817	0.006534	10.2856	9.73E-12
chr3:92316705-92318085:	Sprr2b	20756	0.1	0.3	1.1	1.49289	0.564418	3.71109	0.0039401
chr3:92365187-92366442:	Sprr2f	20760	2.9	6.7	89.1	2.20443	0.030036	25.902	1.29E-34
chr3:92373915-92375229:	Sprr2g	20761	4.1	6.8	21.9	1.73181	0.147033	5.51964	3.17E-10
chr3:37639950-37644599:	Spry1	24063	64.6	45.4	25.8	-1.28301	0.405445	-1.93237	0.001865
chr14:105891947-1058968	Spry2	24064	49.6	57.7	89.7	1.31656	0.271326	2.19472	1.11E-05
chr18:38586265-38601268	Spry4	24066	4.7	13.9	23.0	2.96006	0.005104	4.88747	3.58E-07
chr15:102116528-1021362	Spryd3	223918	35.3	31.6	47.8	-1.00031	0.998371	1.6888	1.25E-23
chr10:128209910-1282117	Spryd4	66701	21.5	27.2	45.4	1.42453	0.017971	2.60662	2.51E-17
chr14:61534305-61556886	Spryd7	66674	25.1	25.1	45.8	1.13002	0.37143	2.26609	3.32E-19
chr4:149896284-14995500	Spsb1	74646	19.0	71.6	22.7	3.86253	6.05E-06	1.44112	0.193091
chr17:24886674-24892147	Spsb3	79043	31.5	34.3	34.1	1.22828	0.137829	1.34968	0.0041548
chr12:76580488-76710547	Sptb	20741	4.1	2.7	0.7	-1.36791	0.123124	-4.68701	3.43E-23
chr11:30099395-30219772	Sptbn1	20742	276.9	227.7	119.4	-1.08886	0.203583	-1.85178	1.40E-38
chr19:4711223-4752352:+	Sptbn2	20743	8.4	5.0	2.9	-1.48978	0.039836	-2.23881	5.59E-08
chr13:53332748-53377361	Sptlc1	268656	54.5	57.3	73.9	1.18273	0.094547	1.69124	8.74E-13
chr12:87307889-87388230	Sptlc2	20773	39.0	46.2	55.3	1.32562	0.029838	1.75559	1.31E-08
chr2:139493920-13963767	Sptlc3	228677	7.9	6.1	0.7	-1.15049	0.534813	-8.20426	3.11E-33
chr3:69819539-69859894:	Sptssb	66183	1.2	0.5	0.0	-1.78893	0.334338	-5.84993	6.47E-05
chr7:46990396-47008414:	Spty2d1	101685	30.1	70.1	63.9	2.53244	0.00022	2.50916	1.88E-05
chr13:92574632-92576232	Spz1	79401	24.7	1.2	3.1	-10.6598	1.01E-07	-4.61424	9.86E-05
chr15:59315092-59331193	Sqle	20775	11.8	17.3	92.2	1.62828	0.109769	8.43408	6.84E-22
chr2:122765359-12280955	Sqrdl	59010	77.3	56.9	29.8	-1.22374	0.138726	-2.06144	5.61E-13
chr11:50200152-50210820	Sqstm1	18412	572.7	512.4	346.9	-1.00093	0.993858	-1.31942	2.35E-07
chr18:36667187-36670311	Sra1	24068	61.0	68.6	90.0	1.26711	0.137791	1.82486	2.86E-07
chr17:85984665-86145175	Srbd1	78586	31.5	27.9	18.6	-1.00957	0.924886	-1.35342	1.81E-08
chr2:157424293-15747183	Src	20779	34.3	31.8	35.0	1.03708	0.593992	1.27217	2.50E-08
chr13:69573449-69611463	Srd5a1	78925	9.6	6.9	2.4	-1.24763	0.339132	-2.99578	5.42E-11
chr15:82147269-82204960	Srebf2	20788	25.2	30.0	60.6	1.34127	0.081626	2.95693	1.84E-18
chr17:46546839-46556162	Srf	20807	50.7	76.2	152.0	1.68344	0.045495	3.52544	1.31E-10
chr18:52465693-52490738	Srfbp1	67222	43.3	61.8	94.8	1.60044	0.018509	2.65684	2.13E-10
chr10:121780991-1220473	Srgap1	117600	8.3	8.4	9.8	1.1312	0.381923	1.47949	6.52E-05

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr1:131285251-13152736	Srgap2	14270	25.3	20.8	11.0	-1.09112	0.48537	-1.83497	4.47E-13
chr6:112717972-11294726	Srgap3	259302	12.4	12.8	6.8	1.16043	0.257311	-1.45432	9.09E-05
chr10:62494428-62507755	Srgn	19073	162.0	216.6	258.9	1.49179	0.027512	1.95814	1.54E-06
chr5:8046078-8069314:+	Sri	109552	87.1	77.7	49.1	-1.00716	0.956393	-1.41872	1.53E-07
chr4:148591513-14859461	Srm	20810	27.3	53.2	230.3	2.15056	0.000479	9.57793	1.73E-36
chr2:118475843-11847969	Srp14	20813	153.0	152.6	150.6	1.11808	0.173528	1.22824	0.0006981
chr18:34331145-34336599	Srp19	66384	64.9	70.5	109.1	1.22659	0.304148	2.06322	2.32E-07
chr12:55080496-55115367	Srp54a	24067	2.8	3.2	4.4	1.27448	0.141314	1.9286	2.33E-08
chr11:116245166-1162742	Srp68	217337	73.5	69.2	109.1	1.06097	0.646	1.84844	1.08E-14
chr5:76974701-76999935:	Srp72	66661	86.3	86.7	158.5	1.13129	0.167596	2.2888	6.29E-39
chr1:182124737-18213241	Srp9	27058	68.3	72.1	113.1	1.18672	0.226126	2.04818	8.38E-13
chr17:28589592-28622454	Srpk1	20815	82.1	95.2	133.2	1.30901	0.057683	2.01122	4.06E-11
chr5:23503356-23616571:	Srpk2	20817	54.7	42.6	18.1	-1.15196	0.142274	-2.40549	7.55E-36
chrX:73774422-73778924:	Srpk3	56504	3.1	2.4	1.3	-1.13981	0.695013	-1.84748	0.0047278
chr9:35211203-35217003:	Srpr	67398	95.5	112.0	209.6	1.32197	0.065473	2.7006	6.58E-19
chr9:103188033-10320206	Srprb	20818	36.3	52.5	102.4	1.62852	0.020192	3.39582	2.81E-14
chrX:10037977-10117661:	Srpx	51795	23.7	21.0	7.1	-1.02164	0.934669	-2.61109	4.01E-12
chrX:133908425-13393244	Srpx2	68792	1.3	1.1	0.2	-1.10665	0.833233	-3.65098	1.67E-05
chr11:74906359-74925798	Srr	27364	31.4	24.5	16.9	-1.14897	0.199655	-1.4758	8.73E-07
chr5:112337391-11234304	Srrd	70118	22.8	28.1	30.6	1.3914	0.08651	1.66293	0.000481
chr5:137295704-13730767	Srrt	83701	106.9	114.7	168.2	1.21027	0.121552	1.95703	9.93E-14
chr11:88047373-88053757	Srsf1	110809	196.2	207.8	259.3	1.19494	0.206457	1.6422	1.25E-06
chr4:135856071-13586989	Srsf10	14105	74.1	95.7	128.2	1.45417	0.023583	2.12871	2.74E-09
chr3:158010493-15803663	Srsf11	69207	103.1	113.6	115.3	1.24489	0.183706	1.39031	0.0076296
chr4:33208991-33233340:	Srsf12	272009	3.8	3.9	6.8	1.14658	0.468659	2.2064	6.67E-11
chr11:116849897-1168530	Srsf2	20382	208.5	274.7	484.0	1.48365	0.029634	2.83	3.79E-14
chr17:29032660-29043372	Srsf3	20383	252.8	371.9	407.9	1.65189	0.016855	1.97222	4.03E-05
chr4:131873639-13190172	Srsf4	57317	51.3	52.3	66.8	1.15386	0.458405	1.61274	0.0003179
chr2:162931508-16293712	Srsf6	67996	188.1	204.2	264.8	1.22548	0.14493	1.7486	5.20E-08
chr5:115327177-11533308	Srsf9	108014	54.4	59.2	94.2	1.22761	0.260296	2.1317	4.00E-09
chr2:152105524-15211137	Srxn1	76650	27.1	28.0	77.7	1.1572	0.543737	3.43307	1.72E-15
chr2:69861562-69871846:	Ssb	20823	179.7	211.6	336.3	1.32779	0.130578	2.29201	1.81E-09
chr6:40471415-40481823:	Ssbp1	381760	37.7	33.2	41.6	-1.01509	0.877818	1.37922	5.67E-10
chr13:91461097-91706175	Ssbp2	66970	45.0	37.1	17.2	-1.09235	0.618701	-2.06414	1.41E-10
chr4:106911470-10704969	Ssbp3	72475	60.9	64.4	28.2	1.20025	0.417834	-1.6978	0.0008367
chr8:70597490-70608314:	Ssbp4	76900	39.5	46.1	52.7	1.29951	0.106119	1.64757	3.77E-05
chr7:4925844-4944797:+	Ssc5d	269855	13.8	14.5	8.3	1.17743	0.271876	-1.33567	0.0086671
chr11:77216425-77460219	Ssh2	237860	28.1	21.5	9.5	-1.17964	0.64441	-2.23482	0.0004502
chr6:30509849-30520253:	Ssmem1	75647	5.6	1.0	1.3	-4.0254	0.000376	-2.83992	0.0016576
chr6:145934147-14596522	Sspn	16651	42.5	25.6	6.6	-1.48093	0.142211	-4.73932	1.99E-15
chr13:37971401-37994190	Ssr1	107513	52.1	51.1	103.8	1.1044	0.322369	2.47819	8.39E-40
chr3:88579671-88588413:	Ssr2	66256	125.9	142.6	348.2	1.27003	0.007785	3.43036	2.70E-72
chr3:65379657-65392553:	Ssr3	67437	213.3	248.9	486.5	1.31306	0.069701	2.80156	1.35E-20
chrX:73787028-73790828:	Ssr4	20832	118.6	121.0	235.6	1.14108	0.136855	2.4678	1.25E-47
chr2:85037120-85047114:	Ssrp1	20833	162.8	158.1	274.7	1.0921	0.423735	2.10058	1.21E-23
chr19:5730306-5731732:-	Sssca1	56390	36.9	41.9	72.7	1.27307	0.008415	2.45769	4.55E-41
chr12:58211804-58216036	Sstr1	20605	0.4	0.4	2.3	-1.03814	0.959762	4.43387	9.31E-05
chr4:155704815-15573387	Ssu72	68991	60.6	59.5	103.7	1.10173	0.471171	2.12364	1.79E-17
chr3:146404642-14644013	Ssx2ip	99167	24.3	18.8	27.4	-1.15279	0.343303	1.40647	0.0013452
chr15:81365044-81399694	St13	70356	288.6	317.5	378.0	1.23521	0.067633	1.63013	1.56E-08
chr15:67102875-67176882	St3gal1	20442	14.9	18.7	30.5	1.38594	0.10325	2.47858	8.05E-10
chr8:110919865-11097249	St3gal2	20444	29.2	22.3	16.5	-1.17597	0.289295	-1.40443	0.0022185
chr4:117932153-11813494	St3gal3	20441	18.3	19.7	31.1	1.20978	0.2536	2.10737	1.96E-10
chr6:72097608-72154570:	St3gal5	20454	10.6	15.4	22.8	1.61504	0.01857	2.6018	9.86E-10
chr16:58470541-58523312	St3gal6	54613	47.0	38.3	23.0	-1.10824	0.620105	-1.61934	0.0003629
chr16:23224740-23360350	St6gal1	20440	33.4	26.4	11.5	-1.1362	0.550549	-2.26844	5.17E-09
chr17:55445717-55499226	St6gal2	240119	1.6	0.8	0.5	-1.64274	0.171789	-2.47038	0.0012154
chr11:116676705-1166946	St6galnac2	20446	44.5	36.9	10.6	-1.07463	0.723955	-3.26802	2.05E-21

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr3:153202509-15372513	St6galnac3	20447	7.9	8.7	4.0	1.2253	0.181992	-1.55214	0.0001443
chr2:32587078-32599696:	St6galnac4	20448	12.9	25.7	26.7	2.11314	0.054928	2.3202	0.0053769
chr3:152820710-15298220	St6galnac5	26938	7.4	5.8	11.4	-1.10882	0.774112	1.861	0.0041107
chr6:17693994-17943023:	St7	64213	19.8	16.9	26.7	-1.0445	0.735828	1.68182	4.60E-12
chr3:104864506-10493006	St7l	229681	21.1	23.7	30.4	1.26536	0.035983	1.79313	4.77E-12
chr7:73939120-74013682:	St8sia2	20450	2.1	1.6	0.5	-1.144	0.707999	-3.06036	1.20E-06
chr10:86841210-87007942	Stab2	192188	2.5	1.3	0.5	-1.6073	0.126324	-3.40363	1.92E-07
chr9:111561434-11169021	Stac	20840	3.1	2.7	0.4	-1.03863	0.947823	-4.65924	1.19E-06
chr9:100643623-10095854	Stag1	20842	105.7	99.2	101.2	1.04979	0.387088	1.19668	4.02E-06
chrX:42149412-42277186:	Stag2	20843	153.3	147.7	89.5	1.07387	0.356852	-1.37108	4.58E-09
chr5:138280509-13831239	Stag3	50878	8.5	2.7	2.8	-2.63611	0.000784	-2.29613	0.0006623
chr2:52692206-52742149:	Stam2	56324	36.2	33.2	34.0	1.02786	0.720527	1.17488	0.0006157
chr19:34192270-34240328	Stambpl1	76630	12.7	10.5	17.4	-1.08037	0.536748	1.7031	4.06E-12
chr5:86071828-86103993:	Stap1	56792	10.4	10.4	22.4	1.09735	0.808905	2.5134	3.18E-05
chr13:19357676-19395752	Stard3nl	76205	72.5	62.9	43.2	-1.03886	0.824787	-1.33929	0.0041178
chr18:33201421-33213816	Stard4	170459	15.6	10.2	19.3	-1.35885	0.066261	1.53194	0.0006637
chr18:70472454-70501065	Stard6	170461	12.3	3.8	2.4	-2.69098	0.00094	-3.6548	2.44E-07
chr2:127270229-12729893	Stard7	99138	67.9	63.8	85.2	1.05349	0.528237	1.56709	3.41E-17
chrX:99042581-99074728:	Stard8	236920	13.1	8.2	4.8	-1.4208	0.014465	-2.16968	7.01E-12
chr11:100886810-1009395	Stat3	20848	111.3	204.8	276.3	2.00038	0.005104	2.93324	6.19E-08
chr11:100859351-1008851	Stat5a	20850	12.6	38.0	31.5	3.00621	0.003669	2.70055	0.0015331
chr10:127642986-1276609	Stat6	20852	90.0	85.0	63.1	1.05679	0.292326	-1.14012	0.0005472
chr14:69029289-69041401	Stc1	20855	20.9	9.0	5.2	-2.02658	0.010386	-2.9966	5.27E-07
chr11:31359441-31370061	Stc2	20856	15.0	14.1	23.8	1.04888	0.860368	1.94883	8.54E-06
chr5:5736322-5749317:-	Steap1	70358	2.2	3.6	9.0	1.77403	0.013005	4.8629	1.32E-21
chr1:120226416-12027108	Steap3	68428	68.5	56.7	17.5	-1.07996	0.519935	-3.1012	2.86E-46
chr7:102267824-10243685	Stim1	20866	38.7	31.8	15.3	-1.08771	0.410421	-2.00662	5.83E-23
chr19:7020696-7040026:-	Stip1	20867	89.7	176.2	315.2	2.17412	0.000345	4.13792	3.57E-15
chr1:75521529-75537335:	Stk11ip	71728	22.5	16.1	8.2	-1.25542	0.113404	-2.15732	7.06E-13
chr1:75210829-75215606:	Stk16	20872	48.1	51.4	58.0	1.20774	0.227044	1.50056	0.0003805
chr17:34823993-34836903	Stk19	54402	32.2	33.5	36.9	1.15943	0.223393	1.4252	4.87E-05
chrX:50841436-50891850:	Stk26	70415	17.7	12.8	8.2	-1.23284	0.45203	-1.68004	0.0081053
chr15:34875499-35155806	Stk3	56274	66.1	65.0	71.3	1.10182	0.132344	1.34863	1.70E-10
chr6:49395604-49469502:	Stk31	77485	1.7	0.1	0.2	-5.19327	0.002946	-4.22772	0.0016975
chr7:109279216-10943905	Stk33	117229	8.7	3.7	1.4	-2.00449	0.014356	-4.50396	3.98E-11
chr1:74601455-74636893:	Stk36	269209	5.7	3.5	1.0	-1.44727	0.101012	-4.04968	6.33E-16
chr17:28970885-29007937	Stk38	106504	62.9	53.3	40.3	-1.05162	0.681887	-1.24568	0.0049617
chr2:68210447-68471981:	Stk39	53416	25.0	20.1	28.2	-1.11462	0.350556	1.408	2.22E-05
chr4:126103957-12614102	Stk40	74178	26.7	33.5	61.2	1.41497	0.038105	2.81061	1.62E-16
chr2:26934069-26953496:	Stkld1	279029	2.9	0.3	0.5	-6.36469	3.16E-06	-4.11031	2.95E-05
chr4:134468320-13447384	Stmn1	16765	87.7	81.1	28.0	1.02501	0.929871	-2.42786	2.59E-09
chr13:46273721-46300115	Stmnd1	380842	30.2	26.4	2.4	-1.03613	0.926091	-8.8716	2.09E-25
chr2:35313990-35337009:	Stom	13830	139.4	105.6	66.7	-1.19046	0.364834	-1.65622	0.0002053
chr9:58253164-58262524:	Stoml1	69106	41.8	31.7	19.1	-1.1898	0.403427	-1.7252	0.0001931
chr4:43027690-43031384:	Stoml2	66592	63.9	65.6	121.6	1.15008	0.174388	2.36539	1.15E-32
chr17:88626555-88645724	Ston1	77057	22.8	15.5	9.9	-1.31637	0.303885	-1.78486	0.0028633
chr10:62659422-62726099	Stox1	216021	2.0	1.3	0.7	-1.41482	0.37251	-2.15986	0.0064686
chr8:47180048-47352348:	Stox2	71069	11.0	8.0	6.5	-1.23683	0.117505	-1.36232	0.0027861
chr4:135495987-13553780	Stpg1	78806	2.7	0.8	0.1	-2.57497	0.037204	-10.0411	4.68E-10
chr11:120710941-1207137	Stra13	20892	48.3	46.7	28.2	1.08263	0.558435	-1.36272	0.0007976
chr9:58129088-58153997:	Stra6	20897	12.6	10.8	3.8	-1.0468	0.81768	-2.61569	2.57E-16
chr1:58973571-58995121:	Stradb	227154	19.9	14.0	7.8	-1.26913	0.05348	-2.01137	1.55E-13
chr6:137735082-13775193	Strap	20901	67.8	84.8	168.3	1.41001	0.057303	3.02799	1.42E-16
chr2:37569868-37647285:	Strbp	20744	20.2	16.3	9.4	-1.10702	0.380823	-1.71486	1.64E-11
chr3:107612532-10763171	Strip1	229707	39.3	42.3	57.0	1.2147	0.124835	1.80346	2.22E-10
chr6:29917013-29959680:	Strip2	320609	2.3	1.5	0.8	-1.35312	0.215704	-2.27794	6.93E-06
chr17:78653964-78736560	Strn	268980	37.6	30.7	23.6	-1.09805	0.34402	-1.27067	0.0006996
chr12:51608541-51691914	Strn3	94186	103.6	111.0	126.3	1.205	0.093149	1.51674	4.85E-07

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr7:16815889-16840931:	Strn4	97387	65.1	68.2	100.2	1.18061	0.159083	1.91404	2.50E-14
chr9:36732413-36767578:	Stt3a	16430	153.5	157.1	347.8	1.14717	0.083233	2.81759	1.35E-73
chr9:115242582-11531042	Stt3b	68292	102.2	98.0	129.7	1.07428	0.376945	1.58341	8.66E-17
chr17:25830636-25833361	Stub1	56424	103.1	104.0	167.7	1.13767	0.303799	2.0221	6.10E-16
chr10:12939983-12964259	Stx11	74732	8.2	13.5	15.1	1.69631	0.134205	2.12976	0.0046666
chr4:132854064-13288445	Stx12	100226	85.4	90.6	92.1	1.19359	0.089531	1.34521	0.0001644
chr2:174077051-17409977	Stx16	228960	72.9	63.6	45.7	-1.01934	0.892158	-1.27064	0.0026213
chr4:48124919-48186506:	Stx17	67727	29.9	21.4	13.9	-1.2569	0.105001	-1.70385	4.28E-07
chr5:38039230-38137769:	Stx18	71116	43.0	48.2	83.4	1.24676	0.101294	2.3965	4.43E-19
chr5:128984558-12900857	Stx2	13852	29.7	21.7	13.7	-1.23455	0.20413	-1.71973	8.21E-06
chr19:11775118-11819403	Stx3	20908	20.8	17.9	11.2	-1.03274	0.689438	-1.4845	3.21E-15
chr19:8741424-8755642:+	Stx5a	56389	136.2	134.4	86.5	1.10729	0.146974	-1.25846	1.21E-05
chr1:155158703-15520351	Stx6	58244	45.8	47.5	52.5	1.16505	0.081071	1.43166	3.13E-08
chr11:90476493-90638108	Stxbp4	20913	17.8	13.8	4.5	-1.15696	0.353497	-3.07979	1.80E-24
chr12:44852486-45074483	Stxbp6	217517	10.7	10.0	4.3	1.04216	0.818263	-1.99355	7.84E-11
chr6:131299144-13131382	Styk1	243659	5.9	4.5	1.8	-1.167	0.619183	-2.48656	8.09E-06
chr14:45351186-45376884	Styx	56291	12.8	12.7	13.3	1.11214	0.327646	1.29902	0.0006776
chr5:135747220-13577838	Styxl1	76571	2.9	1.0	0.6	-2.34933	0.017233	-3.42899	2.05E-05
chr15:11981339-11996007	Sub1	20024	59.8	63.9	74.1	1.19818	0.141107	1.53877	2.02E-06
chr14:73552786-73596142	Sucla2	20916	103.9	97.3	128.4	1.05039	0.597383	1.54215	1.70E-13
chr6:73248505-73276907:	Suclg1	56451	80.8	76.1	99.3	1.05093	0.653027	1.53	4.13E-10
chr1:161816112-16187666	Suco	226551	50.9	53.2	58.9	1.16991	0.021247	1.44415	1.65E-12
chr19:46396896-46488804	Sufu	24069	17.1	13.9	9.8	-1.09661	0.302226	-1.38416	3.84E-07
chr13:16857475-17694765	Sugct	192136	5.4	4.5	1.7	-1.0604	0.817423	-2.3863	5.60E-08
chr8:70234226-70263105:	Sugp2	234373	28.3	27.0	37.4	1.07897	0.587579	1.65238	2.20E-08
chr14:79587691-79629755	Sugt1	67955	90.2	90.6	86.2	1.12532	0.167052	1.1928	0.0060124
chr1:12692430-12860372:	Sulf1	240725	80.2	67.7	41.5	-1.06727	0.668398	-1.53999	6.15E-06
chr2:166073899-16615568	Sulf2	72043	47.3	51.6	70.3	1.2297	0.201602	1.83724	2.07E-07
chr7:126672870-12667635	Sult1a1	20887	28.0	23.9	2.7	-1.05929	0.887873	-7.16281	7.84E-18
chr17:53829637-53845958	Sult1c2	69083	5.3	4.2	1.3	-1.13648	0.814274	-2.66954	0.0027153
chr5:87554650-87569006:	Sult1d1	53315	65.5	70.1	14.8	1.17023	0.596353	-3.36204	2.25E-10
chr15:84076097-84105754	Sult4a1	29859	0.3	0.5	1.4	1.61162	0.281538	4.80486	8.74E-08
chr8:123142847-12315828	Sult5a1	57429	6.0	5.9	2.0	1.10402	0.744652	-2.30269	2.92E-05
chr1:59639434-59670834:	Sumo1	22218	129.9	142.0	141.0	1.22936	0.173442	1.34931	0.008689
chr11:115523109-1155362	Sumo2	170930	110.3	128.9	181.8	1.31095	0.059271	2.03674	2.74E-11
chr10:77606097-77618331	Sumo3	20610	81.3	77.8	116.7	1.07097	0.422226	1.78971	2.17E-24
chr15:79724068-79742536	Sun2	223697	134.1	114.6	32.2	-1.04688	0.697549	-3.29662	3.62E-63
chr11:9016054-9048991:-	Sun3	194974	2.1	0.1	0.2	-4.77022	0.006942	-3.69424	0.0059091
chr2:153856190-15387108	Sun5	76407	2.4	0.1	0.3	-6.26921	0.000978	-3.46501	0.0093585
chr14:52160419-52197239	Supt16	114741	121.1	128.3	167.6	1.19264	0.193003	1.71873	3.27E-08
chr17:44777171-45119284	Supt3	109115	15.1	11.4	7.7	-1.17707	0.262001	-1.56742	2.50E-05
chr11:87737565-87743617	Supt4a	20922	120.0	106.7	47.8	-1.00912	0.949715	-2.00159	7.52E-20
chr7:28314896-28338719:	Supt5	20924	125.1	116.4	140.7	1.04712	0.667177	1.40568	3.25E-07
chr11:78206749-78245703	Supt6	20926	80.3	85.9	108.1	1.21287	0.298936	1.66871	0.0001195
chr10:62429378-62449693	Supv3l1	338359	29.0	31.7	52.3	1.22545	0.060983	2.23892	1.61E-24
chr2:26916421-26920170:	Surf2	20931	66.5	79.2	153.2	1.34077	0.042909	2.83641	2.11E-22
chr2:26920041-26933511:	Surf4	20932	122.1	141.6	333.1	1.3071	0.089403	3.34123	1.14E-25
chr2:26890772-26902813:	Surf6	20935	31.5	41.0	67.8	1.46398	0.04602	2.62377	1.63E-11
chr4:59314683-59438633:	Susd1	634731	25.0	18.8	11.7	-1.18442	0.361388	-1.69689	5.53E-05
chr1:182764906-18289565	Susd4	96935	6.1	5.6	3.0	1.03026	0.917554	-1.58218	0.004473
chr9:114057354-11409873	Susd5	382111	3.7	2.6	0.7	-1.26982	0.347387	-3.95372	5.80E-13
chr12:80790532-80880833	Susd6	217684	39.3	47.0	49.5	1.32276	0.061473	1.56427	8.41E-05
chr2:3455815-3474986:-	Suv39h2	64707	1.8	2.3	7.3	1.44978	0.043828	4.9526	1.13E-35
chr7:4740127-4747514:+	Suv420h2	232811	30.6	24.7	9.1	-1.10838	0.44502	-2.66896	1.51E-25
chr11:79993106-80034123	Suz12	52615	45.1	54.7	55.9	1.36815	0.094821	1.53425	0.00278
chr3:96181227-96195180:	Sv2a	64051	6.6	3.0	2.5	-1.96841	0.000306	-2.03722	7.63E-06
chr4:58042796-58206596:	Svep1	64817	24.2	16.9	10.2	-1.28944	0.206433	-1.86411	2.29E-05
chr18:5046589-5119293:+	Svil	225115	161.3	158.0	75.4	1.09656	0.454819	-1.6988	2.11E-10

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr7:51997161-52006018:	Svip	75744	24.4	17.6	8.3	-1.24313	0.088101	-2.32683	1.45E-18
chr2:164289268-16429150	Svs3a	64335	5.2	1.7	1.1	-2.32007	0.086592	-2.95598	0.004194
chr2:32278805-32288069:	Swi5	72931	237.5	260.8	436.8	1.2395	0.148162	2.27348	2.63E-14
chr9:21955753-21958270:	Swsap1	66962	10.5	8.8	15.5	-1.06938	0.616979	1.83786	6.95E-15
chrX:162856843-16288846	Syap1	67043	62.5	64.6	79.0	1.16077	0.141107	1.57363	8.09E-10
chr7:140777229-14078785	Syce1	74075	8.1	0.4	1.0	-8.01766	2.45E-05	-4.12591	0.0009482
chr3:102818499-10293610	Sycp1	20957	3.2	0.2	0.4	-8.01514	1.43E-05	-4.62598	0.000228
chr2:178345296-17840765	Sycp2	320558	4.9	1.3	1.0	-2.92695	0.00633	-3.32059	0.0001718
chr10:88459587-88473236	Sycp3	20962	5.6	0.7	0.7	-4.7875	0.001033	-4.21232	0.0003231
chr4:134930980-13493753	Syf2	68592	163.8	160.8	86.6	1.09792	0.283036	-1.51082	2.65E-11
chr10:86048746-86498896	Syn3	27204	1.4	1.0	0.2	-1.25252	0.245933	-4.35329	4.20E-21
chr4:129287621-12930855	Sync	68828	15.5	13.0	31.8	-1.08321	0.817834	2.44513	7.48E-06
chr9:88449364-88482397:	Syncrip	56403	72.3	95.0	169.5	1.48022	0.030172	2.85908	1.81E-14
chr2:149830783-15000439	Syndig1	433485	80.7	76.5	29.1	1.04754	0.875204	-2.15195	2.97E-06
chr10:5336949-5550692:-	Syne1	64009	12.6	9.5	4.6	-1.17888	0.317327	-2.18545	2.06E-11
chr10:5020196-5194707:-	Syne1	64009	57.8	53.3	40.5	1.03164	0.854595	-1.13902	0.202654
chr12:75818318-76110928	Syne2	319565	97.4	83.5	23.6	-1.04022	0.762673	-3.27141	1.38E-54
chr15:80091334-80119501	Syngr1	20972	4.4	3.2	1.5	-1.24217	0.417745	-2.1926	3.44E-05
chr11:117809667-1178142	Syngr2	20973	82.0	82.6	97.4	1.12656	0.303769	1.47918	1.72E-06
chr7:45886845-45896711:	Syngr4	58867	6.1	0.5	0.8	-6.12988	0.000138	-4.06999	0.0005343
chr17:5941280-6044290:+	Synj2	20975	43.6	31.2	23.3	-1.25214	0.080174	-1.49034	4.04E-05
chr7:67730161-67759742:	Synm	233335	46.9	38.5	18.2	-1.09674	0.646658	-2.03154	2.22E-08
chr18:60593990-60624305	Synpo	104027	8.0	27.4	35.7	2.93128	0.034494	3.78428	0.0007821
chr14:13284780-13615469	Synpr	72003	2.4	2.2	0.4	1.0125	0.974417	-4.49177	9.84E-11
chrX:7638580-7653256:+	Syp	20977	2.7	2.0	0.6	-1.18799	0.654147	-3.2699	4.32E-06
chr2:164460971-16446551	Sys1	66460	38.7	38.7	42.2	1.12081	0.219228	1.35997	3.60E-06
chr10:108497650-1090109	Syt1	20979	2.8	2.6	0.4	1.03724	0.908391	-4.90476	1.91E-16
chr19:4445908-4477143:-	Syt12	171180	0.7	0.5	1.1	-1.2406	0.587993	1.98965	0.0049183
chr14:34220046-34230421	Syt15	319508	14.5	11.3	1.2	-1.1544	0.652788	-8.24357	5.85E-25
chr7:118381856-11844355	Syt17	110058	1.9	1.5	0.3	-1.14552	0.818231	-3.55681	0.0005062
chr7:44384126-44400030:	Syt3	20981	1.0	0.7	0.1	-1.25819	0.578363	-5.69596	8.06E-08
chr3:103575282-10364556	Syt6	54524	0.0	0.7	2.8	5.16639	0.002588	14.9136	9.07E-10
chr7:142434977-14244039	Syt8	55925	0.7	1.2	2.2	1.67809	0.146028	3.37585	1.19E-06
chr7:107370790-10754865	Syt9	60510	5.0	3.8	0.9	-1.17263	0.404474	-4.26497	7.46E-23
chr7:90302355-90410719:	Sytl2	83671	10.2	9.9	21.8	1.0729	0.78501	2.61264	1.39E-10
chrX:133936385-13398181	Sytl4	27359	5.6	4.9	1.8	-1.0456	0.82074	-2.42852	6.53E-14
chrX:9885621-9998864:+	Sytl5	236643	4.1	5.3	23.4	1.4481	0.049092	6.8021	8.88E-45
chr19:6046576-6053718:+	Syvn1	74126	17.9	25.5	41.8	1.6034	0.034148	2.82515	8.18E-10
chr4:141112978-14113979	Szrd1	213491	76.1	81.2	118.1	1.20037	0.093431	1.93157	1.40E-16
chr4:118362740-11840926	Szt2	230676	18.0	13.7	8.1	-1.17265	0.307026	-1.7482	4.74E-07
chr10:7905648-7956123:-	Tab2	68652	60.3	59.8	63.1	1.11486	0.251169	1.30555	9.65E-05
chr8:25154552-25201542:	Tacc1	320165	73.2	99.3	120.1	1.52777	0.019895	2.01632	7.40E-07
chr11:106066107-1060736	Taco1	70207	13.7	12.0	17.2	-1.02501	0.878957	1.5673	8.51E-08
chr6:82402475-82560104:	Tacr1	21336	0.6	0.7	1.7	1.26878	0.507718	3.10279	9.25E-07
chr5:36473670-36484285:	Tada2b	231151	15.3	21.9	32.3	1.61185	0.054488	2.53598	6.88E-07
chr6:113366657-11337752	Tada3	101206	30.1	29.0	31.3	1.0857	0.479297	1.30367	0.0007811
chrX:101532735-10160178	Taf1	270627	56.8	58.1	62.5	1.15232	0.222035	1.37104	0.0001997
chr7:105742894-10574433	Taf10	24075	67.4	91.5	183.5	1.52639	0.015095	3.31575	2.08E-19
chr17:27901128-27907724	Taf11	68776	39.2	39.2	41.2	1.11931	0.288031	1.30919	0.0003483
chr4:132274375-13229333	Taf12	66464	31.9	40.2	58.5	1.41729	0.00293	2.27387	7.22E-19
chr3:108571699-10858206	Taf13	99730	19.9	20.7	31.8	1.16738	0.298584	1.9858	1.65E-11
chr11:83473108-83506740	Taf15	70439	47.4	47.4	54.1	1.12423	0.44244	1.42228	0.0008385
chr8:119597974-11960524	Taf1c	21341	15.9	17.0	17.5	1.19867	0.107481	1.36867	0.0001913
chr9:15306214-15316997:	Taf1d	75316	82.2	106.2	247.4	1.45427	0.073715	3.61514	8.53E-17
chr15:55015129-55072152	Taf2	319944	38.7	36.1	43.5	1.04295	0.464964	1.40518	1.51E-19
chr2:9914552-10048609:-	Taf3	209361	11.0	9.8	11.2	-1.00232	0.987927	1.27491	0.0018895
chr18:14783245-14900359	Taf4b	72504	5.9	8.4	19.0	1.60832	0.006859	3.92156	1.11E-23
chr8:123996313-12402130	Taf5l	102162	28.1	37.5	58.1	1.49968	0.036774	2.52059	3.02E-10

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr5:138178617-13818718	Taf6	21343	45.5	42.0	46.9	1.03722	0.746008	1.29215	0.0001687
chr18:37640491-37644204	Taf7	24074	22.9	32.7	29.2	1.6077	0.032652	1.57318	0.0098591
chr17:47488050-47502287	Taf8	63856	41.8	37.6	22.5	1.00101	0.994565	-1.48279	4.08E-08
chr13:100651343-1006560	Taf9	108143	60.9	60.2	96.0	1.11681	0.536942	1.95033	1.05E-08
chrX:106206874-10622115	Taf9b	407786	17.6	17.5	32.0	1.108	0.375217	2.26253	1.00E-26
chr17:7926000-7934897:+	Tagap	72536	86.5	110.4	110.7	1.40773	0.013621	1.5856	2.62E-05
chr9:45929628-45936058:	Tagln	21345	####	1696.8	2868.1	1.09867	0.651563	2.05608	3.24E-08
chr1:172500246-17250737	Tagln2	21346	110.7	109.5	199.8	1.1008	0.448559	2.23428	1.24E-21
chr7:141392160-14140297	Taldo1	21351	111.5	98.4	141.0	-1.01484	0.907394	1.57522	1.63E-11
chr6:115004381-11503787	Tamm41	68971	23.4	28.8	35.6	1.38155	0.107468	1.87148	2.79E-05
chr2:59612042-59846213:	Tanc1	66860	43.0	38.0	16.7	-1.00728	0.956159	-2.04978	1.51E-27
chr16:18300825-18343932	Tango2	27883	17.2	13.8	9.8	-1.10446	0.545152	-1.39476	0.002857
chr2:61578586-61654169:	Tank	21353	30.5	34.7	58.3	1.27114	0.0316	2.36434	2.37E-25
chr11:77529162-77607815	Taok1	216965	86.6	86.2	88.3	1.11855	0.146577	1.27325	2.55E-05
chr5:117120129-11727509	Taok3	330177	20.5	18.1	13.9	-1.01235	0.899161	-1.18043	0.0023495
chr6:125224212-12523186	Tapbpl	213233	22.9	25.3	25.1	1.24309	0.102537	1.36351	0.0021408
chr5:44175162-44226606:	Tapt1	231225	61.4	65.9	70.8	1.20953	0.203533	1.43229	0.0011382
chr15:102518192-1025236	Tarbp2	21357	27.7	27.0	31.2	1.09164	0.282921	1.40812	8.85E-10
chr15:11383663-11399658	Tars	110960	63.9	75.5	254.7	1.32745	0.013621	4.90222	5.23E-75
chr3:95739974-95754977:	Tars2	71807	23.8	21.9	26.7	1.02526	0.810979	1.39768	1.69E-08
chr4:155859270-15586335	Tas1r3	83771	4.5	2.6	1.1	-1.5231	0.311546	-2.92505	0.0003775
chr15:58890153-58933730	Tatdn1	69694	19.3	18.4	23.8	1.0593	0.654562	1.53655	3.06E-08
chr6:113697499-11371106	Tatdn2	381801	51.8	69.5	119.0	1.51123	0.078828	2.76154	6.43E-09
chr1:191045830-19106293	Tatdn3	68972	47.6	39.7	12.0	-1.07538	0.658724	-3.10523	1.20E-26
chr6:52713729-52766779:	Tax1bp1	52440	179.0	196.1	251.3	1.23268	0.056977	1.74481	1.17E-11
chr11:73177083-73182046	Tax1bp3	76281	42.8	45.0	59.2	1.1855	0.392833	1.70637	0.0001208
chrX:74282718-74290151:	Taz	66826	122.3	92.6	69.4	-1.18355	0.04062	-1.40685	5.10E-08
chr10:61171964-61188841	Tbata	65971	4.1	0.5	0.5	-5.34995	0.000336	-4.68161	9.94E-05
chr5:64160260-64351486:	Tbc1d1	57915	71.9	80.9	88.3	1.26543	0.101294	1.52468	9.65E-05
chr11:4186833-4215505:+	Tbc1d10a	103724	28.8	34.5	38.1	1.34626	0.081765	1.63306	0.0001445
chr7:127197459-12720846	Tbc1d10b	68449	31.5	41.7	42.2	1.49245	0.094357	1.64314	0.0068219
chr10:115197871-1152514	Tbc1d15	66687	37.2	33.7	17.7	1.01059	0.956393	-1.66775	2.27E-07
chr11:119143043-1192284	Tbc1d16	207592	28.9	22.1	11.0	-1.16869	0.025292	-2.10115	1.75E-43
chr7:44840776-44849079:	Tbc1d17	233204	116.4	85.5	14.5	-1.22539	0.357751	-6.05541	2.77E-32
chr5:53809627-53904380:	Tbc1d19	67249	44.1	38.4	22.3	-1.03267	0.798897	-1.57736	8.14E-10
chr9:58359804-58370369:	Tbc1d21	74286	4.4	0.2	0.6	-6.33192	0.000709	-3.5752	0.0061831
chr17:29549802-29606808	Tbc1d22b	381085	13.1	13.3	14.6	1.14671	0.216272	1.3974	2.58E-05
chr16:57168864-57231466	Tbc1d23	67581	65.2	53.8	29.8	-1.08936	0.432474	-1.74731	6.11E-14
chr9:90202049-90270769:	Tbc1d2b	67016	51.7	43.9	19.8	-1.05762	0.496436	-2.07752	1.10E-40
chr15:57912199-57970068	Tbc1d31	210544	8.6	6.6	3.8	-1.1724	0.338473	-1.78895	1.03E-06
chr10:56014294-56228689	Tbc1d32	544696	18.0	15.3	3.8	-1.05261	0.653902	-3.7489	4.73E-71
chr14:101442360-1016091	Tbc1d4	210789	17.0	12.1	6.7	-1.25785	0.00679	-2.02187	3.10E-25
chr17:50733127-51179352	Tbc1d5	72238	21.0	16.6	11.4	-1.13463	0.072456	-1.47696	1.54E-13
chr1:39371496-39478747:	Tbc1d8	54610	31.7	25.9	8.6	-1.09855	0.333698	-2.91855	1.26E-53
chr11:50131360-50172785	Tbc1d9b	76795	66.5	53.6	36.6	-1.11562	0.311994	-1.4499	1.36E-06
chr13:94788943-94842899	Tbca	21371	200.5	202.7	239.6	1.13259	0.375076	1.4854	5.42E-05
chr7:30224131-30232029:	Tbcb	66411	42.9	52.8	117.3	1.38278	0.013966	3.3678	2.98E-34
chr17:46890621-46892463	Tbcc	72726	24.4	26.4	29.1	1.2169	0.13964	1.48291	6.07E-05
chr11:121451949-1216171	Tbcd	108903	38.4	32.0	42.0	-1.07419	0.458524	1.36744	1.49E-06
chr9:42412317-42472226:	Tbcel	272589	24.6	20.3	14.0	-1.08565	0.391165	-1.40679	3.37E-07
chr11:97136171-97149712	Tbkbp1	73174	11.9	10.4	6.2	-1.02203	0.909494	-1.50655	0.0001219
chr3:22076652-22216594:	Tbl1xr1	81004	57.9	41.7	20.0	-1.25293	0.244893	-2.26756	3.43E-09
chr5:135149711-13516266	Tbl2	27368	17.7	16.7	23.6	1.06046	0.635927	1.66016	3.54E-11
chr17:24700653-24707653	Tbl3	213773	25.6	35.7	102.2	1.56682	0.028444	4.76055	3.46E-24
chr9:37649182-37657312:	Tbrg1	21376	131.1	142.4	266.7	1.21897	0.041991	2.52769	2.59E-38
chr11:6615598-6626067:-	Tbrg4	21379	22.0	29.0	54.4	1.48649	0.044	3.00365	7.19E-14
chr9:87702800-87731260:	Tbx18	76365	2.1	1.1	0.6	-1.60067	0.124042	-2.50696	8.90E-05
chr11:85832615-85841948	Tbx2	21385	6.6	4.6	2.4	-1.30285	0.098375	-2.21158	1.08E-10

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr7:126781483-12678554	Tbx6	21389	14.1	8.4	0.6	-1.46662	0.318124	-13.735	1.03E-19
chr6:42672547-42693059:	Tcaf1	77574	89.5	76.4	44.8	-1.04753	0.625775	-1.59516	8.45E-15
chr6:42623043-42645041:	Tcaf2	232748	8.6	8.0	4.2	1.0267	0.901905	-1.62059	5.72E-05
chr11:98383811-98384953	Tcap	21393	6.8	2.7	0.8	-2.15945	0.005405	-5.60228	4.10E-12
chr1:4857694-4897909:+	Tcea1	21399	91.0	99.8	175.5	1.23332	0.058884	2.39183	1.19E-26
chr2:181680310-18168805	Tcea2	21400	57.9	38.5	24.8	-1.34258	0.112036	-1.83072	1.50E-05
chr4:136247957-13627489	Tcea3	21401	18.3	10.9	3.5	-1.49723	0.068622	-3.92456	2.99E-15
chrX:136666375-13666837	Tceal3	594844	29.2	26.7	33.8	1.02793	0.894244	1.43953	0.0013913
chrX:136168984-13617225	Tceal8	66684	54.8	54.7	77.6	1.12196	0.392718	1.75636	9.78E-10
chrX:166499815-16651047	Tceanc	245695	11.1	7.5	5.0	-1.3292	0.258609	-1.73369	0.0028794
chr4:107134162-10717836	Tceanc2	66526	14.1	11.5	6.8	-1.09768	0.406635	-1.6553	1.16E-10
chr1:16642765-16656865:	Tceb1	67923	79.2	96.2	158.6	1.36696	0.026118	2.4702	1.30E-17
chr17:23824740-23829109	Tceb2	67673	322.5	344.6	535.5	1.20016	0.075599	2.06425	4.72E-22
chr4:136003370-13602164	Tceb3	27224	52.1	55.6	66.9	1.20381	0.139949	1.60029	3.84E-07
chr18:42511487-42575785	Tcerg1	56070	43.5	50.9	79.3	1.32102	0.065853	2.25072	4.94E-13
chr9:71844252-72111819:	Tcf12	21406	101.1	90.4	95.3	1.00425	0.965484	1.17832	0.0018116
chr10:22817275-22820128	Tcf21	21412	85.2	68.7	114.4	-1.11049	0.302295	1.67409	1.43E-13
chr5:30968677-30977018:	Tcf23	69852	22.1	27.5	34.9	1.38148	0.02602	1.9549	1.45E-09
chr1:9960163-9967485:-	Tcf24	1E+08	5.2	4.3	2.5	-1.07793	0.730767	-1.65614	0.0002419
chr8:123373711-12340417	Tcf25	66855	188.5	170.8	199.1	1.01747	0.842883	1.31978	1.62E-08
chr10:80409165-80433653	Tcf3	21423	44.1	38.2	42.6	-1.02806	0.754666	1.21012	0.0003433
chr6:72626371-72789045:	Tcf7l1	21415	7.5	7.0	2.4	1.04757	0.88031	-2.47003	2.54E-07
chr19:55741810-55933655	Tcf7l2	21416	9.1	7.3	2.6	-1.12	0.515941	-2.7611	1.88E-17
chr2:180621957-18064269	Tcfl5	277353	5.1	0.3	0.8	-8.81854	1.46E-06	-3.83298	0.0006256
chr19:3896050-3907133:-	Tcirg1	27060	51.9	47.8	27.9	1.03409	0.833025	-1.48752	1.60E-05
chr11:3917078-3932078:-	Tcn2	21452	70.5	52.8	16.4	-1.19794	0.070493	-3.40005	2.05E-58
chr18:60813756-60848964	Tcof1	21453	21.9	21.5	34.3	1.10533	0.389032	1.95816	9.11E-18
chr17:12916329-12925067	Tcp1	21454	267.8	290.9	510.1	1.22511	0.147744	2.35534	4.06E-17
chr17:7324660-7345860:+	Tcp10a	21461	5.0	0.2	0.4	-11.6909	9.26E-08	-6.08451	5.81E-06
chr17:13061111-13082226	Tcp10b	21462	5.5	1.0	1.6	-4.00313	0.000434	-2.34627	0.0113394
chr17:13354572-13377223	Tcp10c	1E+08	6.5	0.3	0.7	-11.016	1.22E-08	-5.36757	4.21E-06
chr17:28066747-28080639	Tcp11	21463	28.8	2.0	3.2	-8.61358	6.74E-08	-5.40235	1.58E-06
chr10:84576947-84614355	Tcp11l2	216198	88.2	76.1	6.0	-1.04987	0.886059	-10.5786	1.89E-37
chr17:13716436-13761394	Tcte2	21646	7.7	3.7	1.6	-1.78573	0.019445	-3.66849	1.63E-10
chr4:102986379-10300559	Tctex1d1	67344	2.0	0.1	0.2	-7.1584	5.13E-05	-4.4231	0.0003335
chr16:32419702-32428892	Tctex1d2	66061	32.2	20.3	19.5	-1.41648	0.005845	-1.31408	0.0077389
chr5:122239495-12226446	Tctn1	654470	26.1	17.8	7.8	-1.31099	0.164835	-2.6086	1.92E-11
chr5:124598749-12462773	Tctn2	67978	15.1	11.4	6.3	-1.18552	0.214178	-1.90172	1.80E-10
chr19:40596446-40612215	Tctn3	67590	20.6	20.0	11.4	1.09305	0.543716	-1.43599	0.0002569
chr19:56826209-56870012	Tdrd1	83561	2.4	0.3	0.5	-5.36906	4.73E-06	-3.49182	8.58E-05
chr1:156255296-15630360	Tdrd5	214575	1.5	0.2	0.3	-5.35346	0.000105	-3.65639	0.0003999
chr17:43615335-43630299	Tdrd6	210510	7.1	0.6	0.8	-7.12045	2.05E-06	-5.02801	8.43E-06
chr7:45215753-45233619:	Tead2	21677	85.4	76.7	28.0	1.01458	0.946393	-2.39869	4.67E-15
chr17:28331673-28350805	Tead3	21678	39.9	49.0	47.9	1.36616	0.051559	1.49029	0.0012455
chr6:128227143-12830081	Tead4	21679	2.4	5.0	6.7	2.23282	0.013603	3.116	9.06E-06
chr5:72755718-72868448:	Tec	21682	33.3	31.4	14.1	1.0588	0.781088	-1.86683	3.87E-07
chr8:83571698-83594491:	Tecr	106529	212.7	170.2	92.5	-1.11782	0.285298	-1.82646	2.33E-16
chr1:153849542-15385119	Teddm2	240817	1.1	0.8	0.1	-1.14382	0.839366	-4.28792	0.0003759
chr15:81802673-81826863	Tef	21685	217.3	130.4	39.1	-1.47982	4.53E-05	-4.38671	4.88E-75
chr11:80136678-80142153	Tefm	68550	19.1	19.3	24.5	1.13146	0.300895	1.59515	9.90E-09
chr4:94739289-94874976:	Tek	21687	36.4	32.1	15.0	-1.01932	0.902659	-1.92286	1.69E-14
chr11:72344717-72362442	Tekt1	21689	7.3	0.7	0.8	-5.70583	0.000229	-5.02357	6.23E-05
chr4:126322121-12632519	Tekt2	24084	8.3	3.9	2.6	-1.84305	0.019829	-2.45677	1.57E-05
chr11:63061659-63094960	Tekt3	71062	3.4	0.4	0.3	-5.09809	0.001252	-4.82508	0.0001964
chr17:25471590-25476594	Tekt4	71840	5.0	0.7	0.7	-4.07921	0.007325	-3.73659	0.0019994
chr16:10357952-10395465	Tekt5	70426	2.3	0.3	0.7	-4.18776	0.001476	-2.25468	0.03033
chr17:25099569-25115967	Telo2	71718	31.1	23.9	40.4	-1.16486	0.269098	1.61942	7.63E-07
chr15:102102988-1021164	Tenc1	209039	80.4	59.6	23.3	-1.21009	0.327993	-2.69909	3.09E-13

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chrX:42532393-43274784:	Tenm1	23963	3.6	3.4	1.2	1.05397	0.87181	-2.36523	3.03E-06
chr8:48225665-48674690:	Tenm3	23965	26.7	20.6	2.4	-1.158	0.211142	-8.77196	1.08E-137
chr7:96210637-96908554:	Tenm4	23966	21.5	17.4	11.3	-1.10582	0.649735	-1.49861	0.0046724
chr14:50824061-50870554	Tep1	21745	24.0	19.1	11.7	-1.12817	0.208844	-1.63758	1.06E-12
chr8:95311598-95321329:	Tepp	73407	3.3	0.9	0.2	-2.64233	0.056207	-6.81128	2.35E-06
chr1:15805646-15844052:	Terf1	21749	28.9	23.3	14.1	-1.11326	0.479375	-1.62553	2.89E-06
chr13:73627001-73649041	Tert	21752	8.2	5.6	2.7	-1.31844	0.229475	-2.38601	2.71E-07
chr5:118027824-11806187	Tesc	57816	3.2	3.8	5.5	1.30659	0.475247	2.01263	0.0060535
chr7:24333080-24333965:	Tescl	69301	2.6	0.2	0.2	-4.19307	0.013504	-4.06971	0.0025591
chr4:43442277-43448075:	Tesk1	21754	31.6	29.9	50.7	1.08234	0.803644	1.95536	0.0003497
chr4:116720955-11680424	Tesk2	230661	9.8	6.7	3.0	-1.31332	0.112912	-2.53131	1.52E-12
chr10:62804570-62880014	Tet1	52463	14.7	7.6	1.7	-1.69937	0.095392	-6.1434	1.15E-14
chr3:133463677-13354439	Tet2	214133	40.9	36.8	19.5	1.01261	0.925733	-1.66903	2.56E-13
chr6:83362374-83441678:	Tet3	194388	23.3	18.0	12.7	-1.15637	0.171196	-1.45684	1.44E-06
chr7:24668012-24672050:	Tex101	56746	6.6	0.5	0.9	-6.25461	0.000208	-4.04381	0.0009261
chrX:138208165-13820958	Tex13a	67944	1.3	0.0	0.2	-5.36287	0.003171	-3.37469	0.0109731
chr8:33570544-33585585:	Tex15	104271	15.3	10.8	4.3	-1.26242	0.04368	-2.85122	8.64E-33
chr11:106502139-1066129	Tex2	21763	39.6	72.4	116.2	1.96128	0.087221	3.17179	0.0001068
chr12:76198690-76246746	Tex21	80384	2.6	0.2	0.5	-4.96809	0.00425	-2.92206	0.0218213
chr5:149439706-14947062	Tex26	75860	3.0	1.0	0.4	-2.40122	0.036306	-4.106	2.58E-05
chr6:83770414-83775812:	Tex261	21766	67.4	61.6	80.6	1.01979	0.845208	1.49084	3.26E-13
chr9:106658746-10668595	Tex264	21767	52.8	43.6	35.2	-1.08715	0.378466	-1.20023	0.0071273
chr1:44086617-44102388:	Tex30	75623	14.1	18.2	19.0	1.45448	0.143733	1.64987	0.0099788
chr15:78378400-78395912	Tex33	73376	11.2	0.8	1.3	-6.8487	9.08E-05	-4.44963	0.0004309
chr1:157099148-15710864	Tex35	73435	6.0	0.3	0.8	-8.10427	9.56E-06	-4.36073	0.0002672
chr7:133587024-13360211	Tex36	73808	4.3	0.2	0.4	-7.22357	0.000222	-4.52778	0.0010033
chr6:70913089-70918922:	Tex37	74221	5.3	0.2	0.6	-8.78516	2.46E-05	-4.55743	0.0006326
chr19:6922426-6925380:-	Tex40	67077	12.8	2.0	2.3	-4.59856	1.02E-05	-3.73064	9.68E-06
chr18:56588348-56594779	Tex43	67343	5.9	2.1	1.4	-2.16118	0.082607	-2.77345	0.0030203
chr9:72458055-72491959:	Tex9	21778	15.8	10.7	5.8	-1.32563	0.094311	-2.12425	2.42E-09
chr2:172549593-17255862	Tfap2c	21420	3.4	1.6	0.6	-1.86491	0.050464	-4.07837	2.20E-08
chr16:4544661-4559720:-	Tfap4	83383	32.1	17.1	10.6	-1.63634	0.193003	-2.2184	0.0048138
chr8:13338751-13378448:	Tfdp1	21781	62.4	72.1	164.5	1.30228	0.055328	3.24839	2.54E-31
chr9:96196275-96323646:	Tfdp2	211586	32.9	23.9	3.8	-1.23575	0.167685	-6.67852	2.68E-64
chrX:7762661-7775202:+	Tfe3	209446	23.4	21.2	34.0	1.01353	0.90685	1.81448	1.18E-23
chr17:47737037-47792416	Tfeb	21425	15.2	11.8	9.1	-1.1496	0.171673	-1.34064	0.0001154
chr16:56690329-56717450	Tfg	21787	64.6	67.6	107.9	1.17557	0.11253	2.07682	3.33E-23
chr7:3620324-3629929:-	Tfpt	69714	26.8	28.0	27.9	1.17612	0.197148	1.29995	0.0047178
chr16:32608896-32632794	Tfrc	22042	19.4	28.4	115.6	1.62648	0.078875	6.70026	8.32E-21
chr7:128246812-12825569	Tgfb1i1	21804	67.8	71.5	106.9	1.18635	0.184006	1.96015	3.14E-13
chr1:186623186-18670599	Tgfb2	21808	14.2	18.2	30.5	1.44317	0.230375	2.53439	2.81E-05
chr12:86056743-86079041	Tgfb3	21809	48.4	43.0	24.1	1.00202	0.994176	-1.59935	0.0001528
chr13:56609603-56639339	Tgfbi	21810	593.5	379.8	128.0	-1.37358	0.176667	-3.55106	7.92E-14
chr9:116087695-11617536	Tgfbr2	21813	141.2	124.8	180.3	-1.01865	0.90822	1.58873	9.42E-08
chr5:107106570-10728959	Tgfbr3	21814	125.2	139.7	127.2	1.25253	0.009647	1.26985	0.0006535
chr8:4248214-4251423:+	Tgfbr3l	1E+08	15.8	12.4	7.5	-1.1426	0.584586	-1.66176	0.0019284
chr17:70844205-70853532	Tgif1	21815	63.7	45.2	20.9	-1.27112	0.448317	-2.30935	0.0001299
chr14:55700009-55713492	Tgm1	21816	2.1	3.9	15.5	1.7065	0.322607	5.69945	5.24E-06
chr2:158116405-15814639	Tgm2	21817	296.3	330.2	591.2	1.23874	0.030937	2.47741	2.53E-34
chr4:3574879-3616623:+	Tgs1	116940	27.1	29.9	40.4	1.24523	0.142261	1.84379	2.31E-08
chr11:49057196-49064212	Tgtp2	1E+08	18.5	30.7	11.4	1.82006	0.002298	-1.29014	0.140442
chr17:84190056-84466208	Thada	240174	39.5	36.5	40.1	1.03701	0.754907	1.26905	0.0007707
chr8:26158169-26164151:	Thap1	73754	11.0	13.8	16.8	1.40524	0.05872	1.88398	2.73E-06
chr4:151982638-15198898	Thap3	69876	82.1	51.3	33.4	-1.43753	0.021723	-1.94081	6.89E-08
chr5:91962882-91972137:	Thap6	381650	7.3	4.9	3.6	-1.34473	0.160344	-1.63153	0.0020783
chr16:17527982-17531052	Thap7	69009	38.3	43.4	63.1	1.27434	0.08299	2.03965	3.20E-12
chr2:118111922-11812713	Thbs1	21825	185.2	216.6	354.9	1.27843	0.298308	2.32566	4.62E-07
chr3:89215187-89226837:	Thbs3	21827	69.8	59.4	30.2	-1.05779	0.752997	-1.83838	1.36E-08

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr13:92751586-92794818	Thbs4	21828	1.9	3.4	7.4	1.8955	0.046722	4.25272	1.61E-09
chr10:79576477-79587136	Theg	21830	3.1	0.2	0.5	-6.03415	0.000775	-3.2847	0.0087849
chr3:94342099-94347352:	Them5	66198	4.5	3.6	0.3	-1.10836	0.872449	-5.8757	1.89E-06
chr11:45945306-45955503	Thg1l	66628	5.2	6.4	17.0	1.36902	0.007487	4.0075	3.90E-58
chr2:21205724-21215009:	Thnsl1	208967	12.3	8.1	5.6	-1.36693	0.120583	-1.72701	0.0003368
chr6:71128166-71144380:	Thnsl2	232078	21.6	15.0	3.4	-1.29745	0.255828	-4.78492	1.01E-20
chr18:9958180-9995484:+	Thoc1	225160	50.8	59.2	91.3	1.31409	0.065158	2.21921	4.00E-13
chrX:41794994-41911901:	Thoc2	331401	75.9	76.3	73.1	1.12821	0.051967	1.20363	9.29E-05
chr13:54458837-54468840	Thoc3	73666	28.5	30.9	42.3	1.22139	0.14493	1.84677	7.72E-10
chr11:4895343-4928865:+	Thoc5	107829	42.2	42.9	74.5	1.14373	0.273926	2.1951	1.92E-20
chr17:23668619-23673770	Thoc6	386612	16.5	21.2	45.3	1.44702	0.012917	3.37058	1.52E-27
chr10:81070083-81082360	Thop1	50492	25.1	23.0	44.6	1.02944	0.856251	2.21091	2.42E-20
chr11:98741873-98765111	Thra	21833	118.3	89.0	19.7	-1.19588	0.302915	-4.65447	1.17E-36
chr4:126164083-12620271	Thrap3	230753	141.2	139.3	158.3	1.11171	0.374562	1.39834	6.09E-05
chr14:17660960-18038088	Thrb	21834	23.8	22.7	6.9	1.07056	0.664823	-2.73036	1.68E-24
chr7:97412957-97417510:	Thrsp	21835	89.5	75.0	13.2	-1.07711	0.901879	-4.14971	1.81E-05
chr6:12311608-12749253:	Thsd7a	330267	8.3	7.2	1.9	-1.03394	0.729974	-3.48455	6.63E-85
chr1:129273304-13021927	Thsd7b	210417	1.3	1.1	0.3	-1.07621	0.835746	-3.18466	1.09E-07
chr7:119715094-11972079	Thumpd1	233802	57.6	63.2	97.2	1.23479	0.113049	2.0912	3.78E-14
chr6:113046327-11306827	Thumpd3	14911	39.9	47.9	83.6	1.35035	0.057303	2.57662	5.40E-16
chr9:26999677-27007334:	Thyn1	77862	46.2	45.7	106.0	1.10312	0.366494	2.85103	5.07E-50
chr17:3326573-3519397:+	Tiam2	24001	19.9	19.9	7.3	1.12208	0.391887	-2.15442	1.99E-16
chr17:56269462-56276767	Ticam1	106759	10.7	11.2	17.7	1.17055	0.248816	2.04946	2.37E-14
chr4:118471191-11848984	Tie1	21846	39.7	36.1	23.7	1.01845	0.839501	-1.33729	1.83E-08
chr3:127789913-12779838	Tifa	211550	25.3	21.8	6.9	-1.05424	0.894695	-2.7466	4.97E-06
chr6:59208870-59212033:	Tigd2	68140	37.3	27.7	16.7	-1.21541	0.408976	-1.74845	0.0007891
chr2:84827021-84830213:	Timm10	30059	30.1	54.4	106.7	2.00532	0.000861	4.19523	3.41E-17
chr7:105640540-10564184	Timm10b	14356	42.7	41.6	48.5	1.08951	0.413751	1.41171	1.16E-06
chr10:80899450-80900969	Timm13	30055	42.4	47.5	72.2	1.25413	0.018265	2.11815	8.64E-26
chr1:135301535-13531373	Timm17a	21854	81.4	102.1	173.6	1.41221	0.061235	2.60526	2.69E-12
chrX:7899398-7907652:+	Timm17b	21855	23.8	24.2	28.6	1.13693	0.187946	1.4978	4.40E-09
chr11:76406925-76416313	Timm22	56322	16.9	18.2	26.8	1.21192	0.20473	1.96593	3.88E-10
chr14:32180166-32201891	Timm23	53600	47.0	70.8	151.6	1.68489	0.032919	3.80015	4.84E-13
chr8:4259731-4275905:-	Timm44	21856	75.8	72.8	77.0	1.07578	0.307026	1.26963	2.02E-06
chr7:28305826-28312046:	Timm50	66525	42.4	50.6	86.6	1.34056	0.018717	2.52745	4.65E-23
chrX:134537258-13454162	Timm8a1	30058	6.6	11.2	24.8	1.86719	0.022388	4.30071	1.68E-12
chr9:50603901-50605320:	Timm8b	30057	93.9	100.5	121.9	1.20129	0.176718	1.61163	1.24E-06
chr12:71123172-71136675	Timm9	30056	42.0	50.1	92.2	1.34111	0.060866	2.69828	5.43E-18
chr16:38497843-38522663	Timmdc1	76916	22.9	22.1	30.3	1.07893	0.498391	1.65044	4.61E-12
chrX:20870166-20874737:	Timp1	21857	14.8	24.7	50.1	1.67218	0.251642	3.41405	0.0001528
chr11:118301061-1183554	Timp2	21858	231.0	185.5	93.4	-1.11591	0.104659	-1.97497	2.77E-43
chr10:86300412-86349505	Timp3	21859	377.5	362.0	477.6	1.08517	0.645842	1.57153	6.34E-05
chr4:130165600-13017512	Tinagl1	94242	30.3	54.4	89.4	1.95908	0.046385	3.31585	3.11E-06
chr14:55679080-55681817	Tinf2	28113	40.3	41.2	41.5	1.14847	0.225056	1.28689	0.002601
chr3:65528447-65555518:	Tiparp	99929	35.1	147.5	46.8	4.16773	1.47E-05	1.57656	0.134435
chr9:64281607-64304792:	Tipin	66131	42.1	45.8	77.7	1.22369	0.245506	2.2744	1.89E-11
chr1:165212286-16523695	Tiprl	226591	23.3	23.6	25.4	1.1367	0.135935	1.36395	8.25E-07
chr9:35184391-35200291:	Tirap	117149	12.6	14.1	15.1	1.24303	0.13871	1.48267	0.0003267
chr17:46257851-46283026	Tjap1	74094	22.1	25.1	27.2	1.27684	0.06642	1.53292	2.03E-05
chr7:65296165-65371244:	Tjp1	21872	121.6	97.2	57.9	-1.12071	0.2289	-1.67534	2.28E-14
chr19:24094502-24225026	Tjp2	21873	77.0	65.3	39.0	-1.06209	0.788965	-1.56089	0.0009888
chr14:30549131-30574726	Tkt	21881	159.0	129.1	183.3	-1.10246	0.563793	1.43606	0.0012373
chr11:78178149-78180819	Tlcd1	68385	18.5	22.6	6.0	1.37884	0.330234	-2.31548	0.0004376
chr11:75468050-75470899	Tlcd2	380712	14.3	13.8	7.6	1.07765	0.640493	-1.4894	0.0001795
chr8:119760587-11977841	Tldc1	74347	15.7	11.2	6.3	-1.26278	0.243337	-1.95472	4.23E-06
chr10:81575287-81590845	Tle2	21886	19.6	14.6	4.0	-1.19816	0.487125	-3.66884	1.68E-13
chr9:61372366-61418497:	Tle3	21887	36.4	49.9	64.8	1.54364	0.042516	2.17075	1.99E-06
chr2:70712408-70825480:	Tlk1	228012	52.1	45.8	47.3	-1.01672	0.770667	1.13441	0.0001891

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:105178807-1052839	Tlk2	24086	42.8	42.4	48.2	1.11699	0.302918	1.40808	7.18E-06
chr8:64014770-64205993:	Tll1	21892	5.1	4.2	2.0	-1.08359	0.649144	-2.07186	2.66E-10
chr4:43531513-43562583:	Tln1	21894	159.1	150.1	192.6	1.05673	0.567144	1.50915	3.35E-11
chr9:67217085-67559703:	Tln2	70549	49.7	45.9	10.3	1.03262	0.844375	-3.78594	9.93E-49
chr5:64924680-64933558:	Tlr1	21897	6.1	5.9	8.9	1.07941	0.791402	1.76929	0.0008263
chr8:45395665-45410539:	Tlr3	142980	10.6	9.4	4.9	-1.01292	0.95724	-1.71735	1.76E-05
chr4:66827811-66842796:	Tlr4	21898	85.1	66.3	30.0	-1.16589	0.623937	-2.18421	0.0001113
chr1:182954788-18297604	Tlr5	53791	2.4	1.7	0.9	-1.2253	0.404731	-2.14669	2.07E-05
chr5:64953095-64960034:	Tlr6	21899	3.8	3.0	1.6	-1.15047	0.587579	-1.85863	0.0004103
chr4:98355370-98383265:	Tm2d1	94043	39.7	40.2	49.5	1.13326	0.259275	1.55628	9.54E-09
chr7:65693417-65701913:	Tm2d3	68634	62.7	57.8	63.4	1.02498	0.869967	1.25828	0.0070006
chr3:57287064-57301919:	Tm4sf1	17112	102.3	127.0	148.3	1.38985	0.074865	1.78176	3.56E-05
chr3:57425410-57441675:	Tm4sf4	229302	0.8	0.5	0.1	-1.22431	0.74811	-3.11558	0.0059588
chr19:6062821-6067850:-	Tm7sf2	73166	16.5	10.9	6.0	-1.35482	0.106064	-2.14386	9.17E-08
chr6:146602276-14663459	Tm7sf3	67623	58.4	44.2	22.3	-1.18796	0.167052	-2.07357	9.77E-16
chr14:55635966-55643806	Tm9sf1	74140	52.8	49.4	69.8	1.05133	0.565036	1.65295	3.72E-20
chr14:122107082-1221596	Tm9sf2	68059	146.3	143.7	172.5	1.10345	0.317327	1.4701	2.52E-08
chr19:41210842-41264004	Tm9sf3	107358	146.5	145.2	193.7	1.11011	0.203485	1.64728	1.44E-17
chr2:153161301-15321046	Tm9sf4	99237	48.5	44.8	59.9	1.03907	0.733369	1.54279	1.09E-10
chr8:66476346-66486507:	Tma16	66282	17.4	24.5	49.1	1.57725	0.000933	3.46304	4.65E-30
chr9:109077988-10908238	Tma7	66167	112.3	125.8	162.4	1.25709	0.048491	1.79841	1.03E-11
chr1:74288247-74304336:	Tmbim1	69660	73.2	64.1	106.6	-1.01759	0.866159	1.81564	4.24E-27
chr10:120208826-1202248	Tmbim4	68212	78.0	80.2	83.1	1.15646	0.230638	1.32612	0.0014548
chr5:3657004-3679544:+	Tmbim7	75010	4.7	0.2	0.8	-6.39348	0.000661	-2.95071	0.0214488
chr7:3665754-3677553:-	Tmc4	353499	34.1	28.5	18.7	-1.06195	0.792355	-1.44442	0.007916
chr7:118597297-11867508	Tmc5	74424	1.1	0.2	0.2	-3.848	0.003371	-3.93004	0.0002888
chr11:117765985-1177806	Tmc6	217353	15.3	12.0	7.8	-1.14238	0.231938	-1.56781	3.40E-08
chr7:118535844-11858468	Tmc7	209760	2.4	0.9	0.8	-2.16978	0.033826	-2.25008	0.0046373
chr1:132356315-13239128	Tmcc2	68875	17.7	15.2	18.5	-1.04309	0.792541	1.30785	0.0049983
chr4:121105651-12110922	Tmco2	69469	9.5	0.4	0.6	-8.62741	1.50E-05	-6.85899	7.67E-06
chr8:13288013-13322924:	Tmco3	234076	22.6	23.2	21.9	1.14938	0.080381	1.21122	0.0015474
chr2:116878691-11689250	Tmco5	67356	7.5	0.5	1.1	-6.47577	0.000426	-3.55222	0.0054086
chr2:113285732-11329719	Tmco5b	75275	1.0	0.1	0.0	-3.30001	0.048388	-4.05996	0.0027729
chr18:36735070-36742391	Tmco6	71983	30.5	24.2	6.2	-1.14616	0.719227	-3.57019	4.84E-08
chr9:21507380-21510186:	Tmed1	17083	40.8	41.4	57.7	1.13734	0.103937	1.76156	4.46E-24
chr12:85340614-85374717	Tmed10	68581	70.1	64.8	110.7	1.0371	0.72442	1.96563	1.31E-28
chr5:124540791-12455050	Tmed2	56334	120.1	143.0	305.7	1.34099	0.046675	3.12567	2.11E-25
chr11:6270714-6274837:-	Tmed4	103694	109.4	92.3	71.0	-1.06206	0.550254	-1.23101	0.0021121
chr5:108121647-10813259	Tmed5	73130	28.8	37.3	79.9	1.45432	0.03482	3.36734	6.78E-20
chr18:46585928-46597535	Tmed7	66676	100.9	110.5	178.1	1.23033	0.066854	2.1901	4.57E-21
chr12:87166242-87200229	Tmed8	382620	17.8	15.8	17.1	-1.00571	0.958351	1.20126	0.0011554
chr13:55593135-55597694	Tmed9	67511	112.8	116.4	287.3	1.1611	0.267979	3.14225	1.00E-34
chr4:48585193-48663131:	Tmeff1	230157	17.6	15.8	10.0	1.00497	0.981791	-1.39747	0.0043087
chr1:50927523-51187270:	Tmeff2	56363	5.0	3.5	2.3	-1.28619	0.226638	-1.76311	0.0002447
chr6:13069759-13089269:	Tmem106b	71900	110.9	84.2	34.6	-1.1894	0.30837	-2.53219	6.56E-15
chr15:97964229-97970286	Tmem106c	380967	44.5	34.1	9.8	-1.17154	0.240225	-3.59373	1.17E-37
chr11:69070809-69073293	Tmem107	66910	22.5	17.4	7.2	-1.16345	0.400069	-2.45986	2.58E-12
chr9:103482936-10376183	Tmem108	81907	3.2	3.0	1.1	1.0417	0.892029	-2.19155	7.61E-06
chr11:60864452-60879038	Tmem11	216821	33.4	42.7	56.1	1.44095	0.023583	2.07802	3.04E-09
chr9:107533945-10753865	Tmem115	56395	54.1	63.5	68.1	1.32247	0.087257	1.56212	0.0003166
chr12:113185903-1131895	Tmem121	69195	1.2	1.3	2.9	1.1548	0.724738	2.71466	2.15E-05
chr4:118540941-11854372	Tmem125	230678	3.9	4.5	10.5	1.31117	0.330916	3.21163	7.55E-10
chr7:90450712-90457208:	Tmem126a	66271	41.9	45.0	72.5	1.20257	0.106851	2.14793	3.21E-21
chr5:38260375-38269618:	Tmem128	66309	47.5	56.8	64.7	1.34312	0.12562	1.67717	0.0003512
chr19:10857829-10869779	Tmem132a	98170	22.4	27.7	21.5	1.3864	2.79E-05	1.19754	0.0095544
chr5:127241826-12756579	Tmem132c	208213	29.1	25.4	5.9	-1.01962	0.887987	-3.89131	3.17E-69
chr9:43108653-43116570:	Tmem136	235300	9.3	6.0	2.6	-1.39255	0.177996	-2.74987	2.83E-08
chr6:42261970-42264555:	Tmem139	109218	2.5	1.8	0.6	-1.24784	0.548678	-3.06515	4.02E-05

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr6:34863146-34874946:	Tmem140	68487	34.3	25.5	3.7	-1.21215	0.679027	-5.89213	7.60E-10
chr7:45897069-45917413:	Tmem143	70209	17.4	11.2	4.6	-1.38146	0.127879	-2.88964	2.97E-11
chr7:30727701-30729534:	Tmem147	69804	105.3	102.5	165.8	1.09233	0.198215	1.96535	1.63E-47
chr1:21218575-21230167:	Tmem14a	75712	15.4	11.1	2.8	-1.23963	0.377604	-4.16009	1.36E-15
chr13:41016250-41022582	Tmem14c	66154	68.2	70.5	91.8	1.15889	0.204471	1.6752	4.24E-10
chr17:45541940-45549677	Tmem151b	210573	1.1	1.1	0.4	1.14929	0.658552	-1.96203	0.0017944
chr7:120102426-12012098	Tmem159	233806	59.4	46.5	15.5	-1.15181	0.390328	-3.0098	8.40E-22
chr8:70172408-70183681:	Tmem161a	234371	33.8	32.1	34.4	1.06433	0.404351	1.27352	2.21E-06
chr13:84222296-84295966	Tmem161b	72745	20.3	20.4	23.3	1.12308	0.161316	1.43193	1.23E-09
chr5:76183880-76209244:	Tmem165	21982	94.1	95.4	97.3	1.13557	0.158598	1.28836	0.0001502
chr13:90089667-90114921	Tmem167	66074	16.0	17.2	25.8	1.20246	0.120729	1.99189	1.81E-15
chr3:108556425-10856246	Tmem167b	67495	80.2	78.2	97.7	1.09217	0.338999	1.51749	6.55E-11
chr6:13580689-13608063:	Tmem168	101118	43.9	46.5	46.8	1.18404	0.031455	1.32971	2.21E-06
chr1:72284373-72302995:	Tmem169	271711	1.2	0.8	0.3	-1.32541	0.503208	-2.57142	0.0016559
chr11:22512283-22519231	Tmem17	103765	8.2	7.5	10.4	1.00811	0.97389	1.56837	0.0003344
chr18:35733678-35740554	Tmem173	72512	27.3	45.4	48.5	1.81146	0.007297	2.1454	1.78E-05
chr5:108629810-10864777	Tmem175	72392	38.0	26.2	12.0	-1.30339	0.19421	-2.46227	1.25E-09
chr6:48833811-48841374:	Tmem176b	65963	299.9	262.2	148.6	-1.03342	0.884604	-1.59962	0.00018
chr1:119907899-11991316	Tmem177	66343	10.8	9.0	4.8	-1.0802	0.728521	-1.78069	3.03E-05
chr6:40110253-40248353:	Tmem178b	434008	1.3	1.0	0.1	-1.15216	0.748913	-5.97212	8.01E-09
chr12:30584443-30591219	Tmem18	211986	39.6	33.6	42.3	-1.06318	0.674866	1.33288	0.0017917
chr17:6439002-6450994:-	Tmem181b-ps	547127	35.7	34.2	19.9	1.07204	0.597499	-1.43131	3.12E-05
chr1:40805601-40855267:	Tmem182	381339	1.8	1.0	0.1	-1.42222	0.590025	-4.13566	0.0013343
chr1:134346097-13436199	Tmem183a	57439	54.1	66.2	83.8	1.38155	0.054021	1.91545	2.82E-07
chr8:77595978-77610653:	Tmem184c	234463	31.4	26.9	33.6	-1.05011	0.746154	1.33419	0.0017297
chr1:119526154-11952898	Tmem185b	226351	15.8	26.7	43.8	1.88735	0.00088	3.33413	1.40E-14
chr16:8633731-8637701:-	Tmem186	66690	27.2	24.8	31.9	1.02097	0.845594	1.46703	4.78E-11
chr16:17276300-17278661	Tmem191c	224019	9.6	6.9	2.3	-1.23214	0.324635	-3.25076	3.42E-13
chr8:64947185-64969037:	Tmem192	73067	23.1	16.6	11.5	-1.24684	0.236062	-1.58688	0.0007792
chr10:127677065-1277010	Tmem194	210035	13.2	10.2	4.2	-1.16171	0.477467	-2.45745	3.34E-10
chr1:52630705-52651919:	Tmem194b	227094	19.0	12.3	4.6	-1.37966	0.332355	-3.05479	2.18E-06
chr12:119945962-1200212	Tmem196	217951	10.6	6.8	0.9	-1.36421	0.554834	-6.52143	6.01E-08
chr11:78507055-78512168	Tmem199	195040	27.3	25.1	41.4	1.03065	0.788497	1.8959	1.33E-25
chr4:131921771-13192314	Tmem200b	623230	85.3	84.9	44.0	1.12524	0.62802	-1.53215	0.0076383
chr9:59518685-59525501:	Tmem202	73893	2.2	0.7	0.6	-2.4158	0.018415	-2.7289	0.000759
chr17:25057702-25081114	Tmem204	407831	54.1	41.1	16.3	-1.18942	0.450732	-2.57266	1.78E-09
chr9:21921009-21927535:	Tmem205	235043	54.3	41.0	18.3	-1.18761	0.160892	-2.34957	1.19E-20
chr1:191325965-19135292	Tmem206	66950	12.1	8.0	4.2	-1.34989	0.015054	-2.25637	8.99E-17
chr8:105326364-10532905	Tmem208	66320	84.3	90.7	111.7	1.20704	0.051955	1.64917	2.59E-12
chr6:38109353-38115806:	Tmem213	77522	7.7	14.9	106.8	2.11632	0.001077	15.5622	4.37E-54
chr5:30869647-30877467:	Tmem214	68796	57.9	62.6	109.3	1.22084	0.141314	2.33986	4.39E-18
chr17:29526018-29549593	Tmem217	71138	1.1	0.0	0.3	-4.91043	0.005561	-2.35253	0.0776296
chr9:37208333-37223211:	Tmem218	66279	33.3	22.4	8.7	-1.33603	0.165763	-2.95436	3.98E-12
chr11:67025154-67035312	Tmem220	338369	5.6	2.7	2.0	-1.8024	0.094079	-2.14254	0.0048295
chr4:133266045-13327779	Tmem222	52174	66.2	68.6	104.0	1.16281	0.079011	1.9597	1.41E-27
chr6:24951141-24956125:	Tmem229a	319832	2.6	3.1	12.1	1.31886	0.278866	5.41732	3.14E-22
chr12:78961795-79007277	Tmem229b	268567	11.3	15.7	14.2	1.55503	0.010978	1.54852	0.0017624
chr8:111912018-11193379	Tmem231	234740	16.2	11.9	3.9	-1.22391	0.29958	-3.21481	9.48E-17
chr17:65256005-65540782	Tmem232	381107	2.3	0.4	0.4	-4.23122	0.001397	-3.64273	0.0005943
chr4:129600707-12960787	Tmem234	76799	137.3	117.5	125.5	-1.04637	0.547996	1.14157	0.0081525
chr7:4784785-4789560:-	Tmem238	664968	7.5	6.2	17.3	-1.06077	0.830635	2.8094	1.63E-12
chr2:130406522-13040779	Tmem239	66766	2.2	0.1	0.2	-7.53754	0.000193	-4.41532	0.0014943
chr4:155734804-15574056	Tmem240	381582	2.6	1.9	0.8	-1.20156	0.622987	-2.49537	0.0004321
chr5:9100737-9118983:+	Tmem243	652925	34.0	30.0	17.4	-1.01448	0.943107	-1.55197	3.87E-05
chr4:56876013-56947429:	Tmem245	242474	30.7	25.8	17.7	-1.06315	0.610447	-1.3823	3.42E-05
chr4:49584506-49597870:	Tmem246	67063	13.1	10.2	5.3	-1.1474	0.455721	-1.94687	1.80E-07
chr17:86917348-86922367	Tmem247	78469	6.9	0.4	1.0	-8.16293	1.83E-05	-4.06769	0.0008353
chr5:130219744-13024376	Tmem248	71667	35.6	44.0	90.3	1.39881	0.102477	3.07516	9.76E-14

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr12:102743760-1027453	Tmem251	320351	16.4	24.4	36.7	1.64528	0.096796	2.61304	1.84E-05
chrX:38196573-38252481:	Tmem255a	245386	10.4	7.2	4.5	-1.28761	0.097341	-1.84315	1.05E-07
chr8:13435459-13461451:	Tmem255b	272465	11.9	10.4	2.0	-1.03681	0.918948	-4.27705	6.86E-13
chr19:10204202-10207824	Tmem258	69038	136.2	138.4	198.0	1.13409	0.19421	1.80846	2.65E-18
chr10:79977120-79984330	Tmem259	216157	70.4	76.8	110.6	1.22875	0.096625	1.95017	1.99E-13
chr10:68723746-68782654	Tmem26	327766	12.3	8.3	4.3	-1.33723	0.378844	-2.19087	0.000803
chr14:48446352-48515159	Tmem260	218989	26.5	23.1	15.5	-1.02834	0.837405	-1.35877	9.83E-05
chr4:75277354-75278286:	Tmem261	66928	53.9	49.0	53.0	1.01628	0.901564	1.2297	0.0037804
chr10:85102627-85117747	Tmem263	103266	31.9	30.6	32.2	1.07394	0.513391	1.25613	0.0020296
chrX:150397773-15045915	Tmem29	382245	13.1	12.5	8.0	1.06176	0.638115	-1.30164	0.0016701
chr9:79768941-79793430:	Tmem30a	69981	103.1	115.6	157.2	1.2617	0.06949	1.89028	2.21E-11
chr12:73543114-73546395	Tmem30b	238257	7.5	6.6	8.9	-1.01023	0.969439	1.4628	0.0079384
chr16:57266139-57292851	Tmem30c	71027	1.2	0.1	0.3	-4.40026	0.0069	-2.59657	0.0324951
chr5:67260565-67291461:	Tmem33	67878	33.1	42.6	49.8	1.45045	0.029763	1.85281	2.88E-06
chrX:134295225-13430596	Tmem35	67564	7.5	7.2	2.1	1.07214	0.794248	-2.79681	7.85E-10
chr8:72572103-72587284:	Tmem38a	74166	25.6	21.9	12.7	-1.04738	0.698199	-1.6117	1.60E-10
chr4:53826045-53862018:	Tmem38b	52076	8.0	6.9	11.2	-1.04046	0.865288	1.7231	2.09E-05
chr16:38558698-38592162	Tmem39a	67846	32.8	39.4	59.7	1.35567	0.017304	2.25931	6.79E-17
chr4:129676355-12969683	Tmem39b	230770	13.0	12.5	13.6	1.08272	0.564547	1.30941	0.0027112
chr7:109972187-10998623	Tmem41b	233724	26.9	29.9	38.4	1.25176	0.196781	1.7621	7.72E-06
chr6:91473751-91488458:	Tmem43	74122	100.3	79.4	52.7	-1.13514	0.301509	-1.51986	1.64E-06
chr16:30511855-30550578	Tmem44	224090	9.5	7.0	2.0	-1.21966	0.186968	-3.72114	7.36E-30
chr9:31426196-31464238:	Tmem45b	235135	37.2	30.4	17.7	-1.09276	0.739677	-1.65584	0.0023635
chrX:81070644-81097875:	Tmem47	192216	75.9	64.3	39.3	-1.06375	0.637683	-1.54208	1.87E-07
chr10:122081260-1220971	Tmem5	216395	59.9	56.0	103.3	1.04542	0.637704	2.14689	2.91E-42
chr4:134897849-13491491	Tmem50a	71817	189.1	170.8	53.7	1.00158	0.993941	-2.79416	9.52E-29
chr4:117251951-11726858	Tmem53	68777	16.8	7.2	3.4	-2.00857	0.01357	-3.5661	1.67E-08
chr14:50926070-50930849	Tmem55b	219024	47.3	44.2	25.8	1.04899	0.700559	-1.45883	9.50E-07
chr3:121202010-12126331	Tmem56	99887	5.2	5.3	10.5	1.13043	0.529747	2.46207	6.91E-13
chr4:107178630-10720099	Tmem59	56374	267.2	227.9	115.0	-1.05217	0.606723	-1.85427	8.23E-23
chr8:70483867-70487358:	Tmem59l	67937	9.2	10.5	13.3	1.26967	0.383372	1.76306	0.0033074
chr2:120977062-12100784	Tmem62	96957	11.8	12.1	12.0	1.14455	0.263441	1.27525	0.0054645
chr17:45660177-45686218	Tmem63b	224807	19.6	19.5	19.8	1.1159	0.23566	1.26451	0.0004441
chr15:58782269-58823427	Tmem65	74868	66.8	63.6	88.2	1.06733	0.588514	1.64461	1.01E-10
chr4:12039356-12088007:	Tmem67	329795	16.5	12.9	4.9	-1.1552	0.273058	-2.68881	7.22E-25
chr4:3549041-3574768:-	Tmem68	72098	23.1	27.7	36.3	1.34934	0.004791	1.95373	9.62E-16
chr4:116551528-11655594	Tmem69	230657	12.2	12.9	13.7	1.18029	0.11856	1.40223	1.44E-05
chr1:16665191-16678275:	Tmem70	70397	41.8	41.0	92.5	1.09697	0.303227	2.75343	4.18E-65
chr3:88328653-88334433:	Tmem79	71913	4.9	4.2	7.4	-1.03689	0.886059	1.84228	4.08E-06
chr7:141328130-14133715	Tmem80	71448	23.4	14.8	11.8	-1.41728	0.076268	-1.56185	0.0031897
chr7:47050640-47054776:	Tmem86a	67893	34.7	31.4	38.0	1.01121	0.937099	1.36736	1.69E-05
chr2:120355309-12040411	Tmem87a	211499	99.6	101.4	97.4	1.14225	0.087694	1.2198	0.000783
chr1:136008219-13603503	Tmem9	66241	59.0	46.2	23.7	-1.14471	0.177983	-1.97891	1.85E-20
chr11:78541817-78550735	Tmem97	69071	24.1	17.1	54.8	-1.24556	0.303479	2.77137	3.24E-12
chr11:80810415-80822033	Tmem98	103743	57.4	67.5	22.2	1.33272	0.270819	-1.99735	0.0002636
chr7:109735836-10975226	Tmem9b	56786	33.5	37.8	58.9	1.26679	0.039454	2.17767	3.65E-20
chr6:97151950-97179124:	Tmf1	232286	42.2	43.6	48.6	1.16377	0.187272	1.4364	1.70E-05
chr9:110866046-11088008	Tmie	20776	7.4	5.3	1.2	-1.2046	0.667408	-4.22653	2.03E-07
chr11:76904545-76916586	Tmigd1	66601	1.9	1.7	0.2	-1.00187	0.997767	-4.5793	1.27E-06
chr3:105870858-10592404	Tmigd3	69296	1.9	0.2	0.2	-5.83427	0.000484	-4.22941	0.0007392
chr4:46039222-46116032:	Tmod1	21916	11.3	28.0	26.8	2.55708	0.013732	2.61443	0.0016517
chr9:75565622-75611325:	Tmod2	50876	28.1	22.4	8.0	-1.13586	0.511143	-2.76228	2.08E-15
chr9:75497784-75559657:	Tmod3	50875	102.7	105.4	108.1	1.14889	0.269269	1.31063	0.0031322
chr5:86410410-86468990:	Tmprss11a	194597	0.0	0.0	1.7	-1.02727	0.974151	25.4669	3.72E-20
chr5:86302854-86373387:	Tmprss11d	231382	0.0	0.0	0.5	1.09784	0.906894	6.01134	2.40E-06
chr5:86705186-86745807:	Tmprss11e	243084	0.1	0.1	0.3	1.03155	0.967389	3.36159	0.0010842
chr5:86485877-86518600:	Tmprss11g	320454	0.1	0.2	5.7	2.08624	0.136089	36.699	1.43E-27
chr9:45319100-45347580:	Tmprss13	214531	3.5	2.4	0.3	-1.27465	0.488835	-7.02167	4.43E-14

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr9:45172726-45204075:	Tmprss4	214523	2.9	3.5	8.3	1.34199	0.334581	3.38826	4.82E-09
chrX:167207094-16720921	Tmsb4x	19241	####	2710.3	3346.5	1.14049	0.486552	1.57014	0.000476
chr10:100443902-1004873	Tmtc3	237500	24.8	25.6	24.4	1.15948	0.021511	1.22874	3.92E-05
chr5:24445463-24447846:	Tmub1	64295	14.6	14.8	16.8	1.13461	0.365513	1.43085	0.0001934
chr11:102284820-1022894	Tmub2	72053	42.7	35.4	23.3	-1.0781	0.323764	-1.45996	2.40E-12
chr12:70453154-70467624	Tmx1	72736	75.1	78.5	99.1	1.17231	0.160239	1.64032	1.79E-09
chr2:84671311-84678828:	Tmx2	66958	46.1	43.1	59.3	1.03785	0.794189	1.6032	9.77E-09
chr18:90510154-90543267	Tmx3	67988	67.0	66.4	63.8	1.10746	0.227044	1.1874	0.0060154
chr4:63959785-64047015:	Tnc	21923	32.7	29.9	108.3	1.01114	0.969334	3.95702	3.99E-20
chr17:35199367-35202007	Tnf	21926	3.7	6.7	11.8	1.82706	0.119488	3.37469	2.44E-05
chr11:78522850-78536260	Tnfaip1	21927	50.3	53.0	77.9	1.18761	0.122161	1.93005	4.72E-16
chr12:111442661-1114550	Tnfaip2	21928	16.2	43.9	38.3	2.61297	0.012434	2.55771	0.0023914
chr2:52038113-52056681:	Tnfaip6	21930	10.5	15.8	44.0	1.57595	0.202128	4.5485	3.27E-09
chr9:54025606-54068411:	Tnfaip8l3	244882	18.1	50.0	128.8	2.96327	7.10E-07	8.04488	1.16E-28
chr14:69767472-69784411	Tnfrsf10b	21933	7.9	13.7	15.6	1.91452	0.009942	2.34483	2.15E-05
chr17:23675445-23677449	Tnfrsf12a	27279	12.5	63.0	196.4	3.79091	0.005978	9.91672	2.96E-09
chr4:154922210-15492807	Tnfrsf14	230979	35.8	32.0	18.9	-1.01345	0.961536	-1.5003	0.0073147
chr14:60963834-61046855	Tnfrsf19	29820	80.6	54.9	22.3	-1.3211	0.224218	-2.78132	5.21E-10
chr6:125349723-12536248	Tnfrsf1a	21937	80.6	133.1	192.8	1.82008	0.00932	2.85841	7.56E-09
chr7:143665807-14368587	Tnfrsf23	79201	1.1	1.0	1.6	1.00219	0.995945	1.67884	0.0054645
chr4:150920155-15094610	Tnfrsf9	21942	1.8	2.3	3.8	1.40052	0.379898	2.42515	0.000905
chr3:27317077-27339665:	Tnfsf10	22035	29.6	22.9	11.5	-1.15109	0.411804	-2.0371	1.82E-09
chr11:69686240-69696098	Tnfsf12	21944	28.0	19.0	6.7	-1.32418	0.145866	-3.21515	6.83E-16
chr11:69682577-69685554	Tnfsf13	69583	9.7	5.1	2.0	-1.66798	0.006179	-3.65385	3.60E-16
chr8:10006633-10035999:	Tnfsf13b	24099	11.4	9.1	4.8	-1.12992	0.5567	-1.87297	7.68E-06
chr3:28263214-28670585:	Tnik	665113	13.1	11.9	6.2	1.00756	0.959877	-1.67643	5.09E-11
chr2:85050460-85073048:	Tnks1bp1	228140	73.7	63.9	94.4	-1.02668	0.756755	1.60011	2.81E-21
chr14:31208312-31211711	Tnnc1	21924	0.4	0.5	1.5	1.25063	0.743854	3.0755	0.0055345
chr7:142442468-14244440	Tnni2	21953	16.1	17.2	30.6	1.20356	0.468656	2.32027	7.12E-07
chr7:4518308-4522443:-	Tnni3	21954	7.5	4.6	2.6	-1.42004	0.220629	-2.21956	0.0002437
chr1:73015075-73015899:	Tnp1	21958	122.4	4.8	12.0	-11.4331	1.70E-07	-5.30089	5.07E-05
chr16:10787935-10788655	Tnp2	21959	111.7	4.9	10.6	-11.9253	9.09E-09	-5.85324	3.29E-06
chr8:85036915-85057582:	Tnpo2	212999	53.9	47.8	66.5	-1.00615	0.950843	1.54303	6.63E-18
chr6:29540827-29609607:	Tnpo3	320938	87.0	91.3	108.4	1.18062	0.072915	1.55378	1.47E-10
chr5:142724605-14281738	Tnrc18	231861	34.0	32.4	19.3	1.07264	0.68847	-1.39796	0.0023709
chr7:123123885-12319529	Tnrc6a	233833	79.1	64.8	47.5	-1.09195	0.32449	-1.33073	6.51E-06
chr15:80711313-80941086	Tnrc6b	213988	43.8	35.1	10.3	-1.11603	0.371326	-3.34044	4.10E-47
chr11:117654289-1177634	Tnrc6c	217351	53.9	51.2	30.4	1.0737	0.65128	-1.41063	0.000625
chr11:99065678-99089306	Tns4	217169	8.2	5.9	13.2	-1.24375	0.456558	1.95534	0.0008612
chr17:34670535-34719815	Tnxb	81877	116.8	108.5	36.7	1.04375	0.816254	-2.51883	1.23E-18
chr4:116804003-11680755	Toe1	68276	42.8	49.2	48.3	1.29396	0.063497	1.40398	0.0014296
chr7:141881585-14190240	Tollip	54473	41.7	42.5	50.3	1.15159	0.340831	1.5023	0.0001048
chr8:75033686-75070121:	Tom1	21968	18.0	15.1	20.4	-1.05739	0.653537	1.41691	4.63E-06
chr11:60226714-60352905	Tom1l2	216810	48.6	45.0	28.7	1.04059	0.755566	-1.34883	0.0001177
chr8:126930664-12694592	Tomm20	67952	51.5	48.8	73.6	1.0665	0.594739	1.78045	5.70E-14
chr12:71111428-71123222	Tomm20l	75266	1.8	0.1	0.2	-5.10055	0.004384	-3.3477	0.0114051
chr15:79670868-79672862	Tomm22	223696	119.3	129.3	188.5	1.21864	0.187931	1.95292	6.11E-10
chr7:19701313-19715429:	Tomm40	53333	33.7	40.6	110.0	1.35529	0.044031	3.99639	4.31E-36
chr1:171217803-17122251	Tomm40l	641376	21.6	21.0	30.1	1.08467	0.470425	1.73291	9.61E-14
chr4:45105210-45108113:	Tomm5	68512	73.2	77.1	94.7	1.1752	0.165856	1.60978	1.38E-08
chr17:47686645-47688386	Tomm6	66119	60.1	68.9	110.8	1.28705	0.032903	2.28396	4.82E-21
chr16:57121714-57154530	Tomm70a	28185	75.7	88.6	169.2	1.31925	0.077976	2.74563	2.52E-18
chr15:76626237-76639929	Tonsl	72749	6.0	5.2	2.2	-1.03768	0.889958	-2.17461	2.50E-07
chr2:160645897-16072276	Top1	21969	68.5	107.8	128.2	1.76103	0.010573	2.26849	3.06E-06
chr15:75657033-75678790	Top1mt	72960	15.1	13.0	19.5	-1.03961	0.780733	1.6107	1.17E-09
chr14:16365206-16430787	Top2b	21974	129.5	120.7	117.1	1.03974	0.547244	1.12953	0.0051296
chr9:122747346-12280207	Topaz1	671232	1.6	0.6	0.0	-2.09969	0.06949	-14.5072	1.42E-14
chr4:40259606-40269841:	Topors	106021	61.6	63.2	62.8	1.15311	0.132842	1.27272	0.0007017

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr4:52596274-52612163:	Toporsl	68274	2.3	0.1	0.3	-5.79909	0.00167	-3.18777	0.0147217
chr4:40269579-40270221:	Toporsos	1.01E+08	51.6	49.4	23.3	1.06529	0.700559	-1.75816	1.65E-07
chr2:30960561-30967918:	Tor1a	30931	45.3	49.6	53.5	1.23241	0.100606	1.46812	5.48E-05
chr1:156035664-15606885	Tor1aip2	240832	47.3	52.3	56.7	1.24764	0.202128	1.4859	0.0020499
chr2:30953001-30959015:	Tor1b	30934	61.6	65.1	82.1	1.18624	0.112912	1.65882	1.70E-10
chr2:32757234-32762244:	Tor2a	30933	33.9	40.4	59.1	1.3408	0.081746	2.14257	9.33E-10
chr1:156653617-15667433	Tor3a	30935	22.5	19.8	10.7	-1.02043	0.903091	-1.67682	1.94E-08
chr2:25192720-25196813:	Tor4a	227612	34.2	28.2	19.6	-1.09164	0.554847	-1.39681	0.0007371
chr4:6687386-6990723:-	Tox	252838	7.1	5.5	2.0	-1.15677	0.536243	-2.69277	8.43E-10
chr8:90247112-90348252:	Tox3	244579	6.6	3.2	0.5	-1.765	0.099964	-7.66605	2.43E-14
chr14:52279146-52295509	Tox4	268741	55.8	60.2	64.3	1.2185	0.196421	1.43382	0.0014611
chr9:85842380-85847055:	Tpbg	21983	14.4	12.8	6.8	-1.00787	0.975957	-1.68669	0.0001702
chr5:120534157-12058861	Tpcn1	252972	32.5	29.9	8.1	1.04328	0.854044	-3.13542	5.45E-19
chr3:8929436-9004515:-	Tpd52	21985	42.2	43.1	55.1	1.14657	0.392718	1.61589	1.59E-05
chr10:79669410-79676126	Tpgs1	110012	14.2	16.8	16.5	1.31653	0.123124	1.43022	0.0082715
chr6:124810592-12481429	Tpi1	21991	246.3	219.4	254.6	-1.00822	0.958594	1.28851	0.0021291
chr6:43345007-43666175:	Tpk1	29807	14.8	11.4	5.6	-1.16427	0.253637	-2.10054	3.37E-14
chr9:67022593-67049213:	Tpm1	22003	605.6	560.7	643.8	1.02857	0.880315	1.32202	0.0083551
chr4:43513726-43523554:	Tpm2	22004	317.6	320.7	493.6	1.12419	0.348111	1.92855	2.53E-14
chr3:90072651-90100902:	Tpm3	59069	104.2	113.2	187.3	1.21912	0.194617	2.21629	3.75E-13
chr8:72135292-72153129:	Tpm4	326618	298.1	330.9	766.9	1.24689	0.101602	3.16402	6.41E-32
chr13:47023543-47043217	Tpmt	22017	7.5	6.2	2.4	-1.08972	0.700367	-2.41212	6.75E-10
chr7:105744847-10575220	Tpp1	12751	54.1	42.1	24.2	-1.15255	0.109171	-1.7861	9.10E-19
chr1:43934007-44002971:	Tpp2	22019	65.1	75.0	94.3	1.29789	0.055955	1.79616	1.06E-08
chr13:74009419-74035753	Tppp	72948	38.4	24.0	8.6	-1.43651	0.111418	-3.41392	3.03E-13
chr14:51918761-51920700	Tppp2	219038	5.8	0.9	0.9	-3.53873	0.026403	-3.24738	0.0089555
chr1:150392838-15044993	Tpr	108989	113.3	114.0	141.6	1.1304	0.098087	1.56055	2.43E-16
chr6:88902251-88912240:	Tpra1	24100	66.4	53.3	25.8	-1.11556	0.245287	-2.053	2.85E-26
chr4:154157485-15416068	Tprgl	67808	171.0	156.3	69.4	1.01807	0.882563	-1.96251	1.24E-24
chr5:112276707-11231535	Tpst2	22022	26.9	31.8	33.5	1.32668	0.011257	1.55342	4.66E-07
chr14:75845256-75848303	Tpt1	22070	####	4422.3	2573.5	1.00448	0.963941	-1.52765	2.28E-16
chr8:22283441-22371418:	Tpte	234129	1.6	0.7	0.4	-1.92795	0.104774	-2.80877	0.0009882
chr2:152847964-15289532	Tpx2	72119	6.8	9.9	6.6	1.63015	0.006879	1.21197	0.219253
chr16:22245741-22265929	Tra2b	20462	128.8	201.4	229.8	1.75084	0.003648	2.17763	6.48E-07
chr15:89076064-89087075	Trabd	67976	48.4	61.7	98.0	1.43765	0.051744	2.47675	8.74E-11
chr4:114406724-11461509	Trabd2b	666048	3.7	10.6	56.6	2.92193	0.001415	14.2882	1.64E-22
chr2:25517982-25546940:	Traf2	22030	30.2	30.8	31.7	1.13974	0.039179	1.30843	1.43E-08
chr12:111166370-1112671	Traf3	22031	14.9	15.6	29.9	1.16877	0.02822	2.49915	7.15E-71
chr1:91494668-91529307:	Traf3ip1	74019	12.2	19.8	19.7	1.80033	0.044814	1.93257	0.0038516
chr1:191997203-19209259	Traf5	22033	34.1	24.1	15.1	-1.26452	0.009027	-1.79549	3.45E-16
chr17:24508850-24527938	Traf7	224619	89.2	89.2	125.5	1.12553	0.213007	1.7553	5.79E-17
chr5:121371725-12138561	Trafd1	231712	80.3	74.5	31.7	1.0437	0.751869	-2.01373	5.45E-18
chr1:58900450-58973482:	Trak2	70827	28.2	34.6	47.9	1.37729	0.003361	2.10713	9.68E-18
chr1:13564693-13589910:	Tram1	72265	149.1	136.9	219.2	1.02489	0.788154	1.8328	5.34E-31
chr16:4039977-4077810:-	Trap1	68015	108.2	104.3	129.9	1.07886	0.235871	1.50035	1.27E-19
chr10:78186726-78244642	Trappc10	216131	37.1	43.3	60.5	1.32001	0.082627	2.01553	3.72E-09
chr12:28690628-28750453	Trappc12	217449	43.7	36.8	26.7	-1.06067	0.373193	-1.30675	6.46E-09
chr13:104142153-1041784	Trappc13	66975	32.1	35.6	42.9	1.24631	0.046873	1.66443	9.30E-10
chrX:166440825-16645254	Trappc2	66226	23.5	22.4	35.3	1.06972	0.671635	1.86959	2.13E-11
chr4:126262405-12627588	Trappc3	27096	81.4	94.6	96.1	1.31042	0.136089	1.46175	0.0057695
chr9:44403759-44407548:	Trappc4	60409	47.5	56.4	79.1	1.32959	0.004682	2.07014	1.83E-20
chr8:3676477-3680921:+	Trappc5	66682	33.1	31.2	37.8	1.05178	0.67131	1.42513	1.24E-06
chr7:19508729-19516145:	Trappc6a	67091	50.4	38.6	19.4	-1.17298	0.184662	-2.0677	8.24E-16
chr12:59043092-59061461	Trappc6b	78232	65.7	69.0	82.6	1.1808	0.130738	1.56481	2.61E-08
chr18:20817224-20896078	Trappc8	75964	58.4	58.7	64.4	1.13081	0.190841	1.37604	3.14E-06
chr2:13510161-13544664:	Trdmt1	13434	14.9	12.3	15.7	-1.08422	0.582169	1.32083	0.0036292
chr17:47140942-47359458	Trerf1	224829	16.9	13.8	4.4	-1.08784	0.656427	-2.97572	9.42E-20
chr9:109057932-10905972	Trex1	22040	54.4	56.5	51.9	1.16228	0.045874	1.19158	0.0025195

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr9:103208876-10323028	Trf	22041	180.2	119.6	57.6	-1.333	0.355868	-2.37712	8.21E-05
chr10:114398821-1148013	Trhde	237553	31.1	26.8	2.7	-1.03839	0.844993	-8.84384	1.37E-84
chr5:115341247-11534355	Triap1	69076	32.5	31.4	38.4	1.08185	0.620987	1.46549	0.0001629
chr15:59648654-59657099	Trib1	211770	9.7	14.2	19.4	1.62442	0.078954	2.39143	2.80E-05
chr2:152337425-15234406	Trib3	228775	5.1	4.0	7.4	-1.11674	0.651139	1.8055	6.63E-05
chr6:53815468-53820825:	Tril	66873	13.9	7.8	1.5	-1.5665	0.238821	-6.00715	6.12E-11
chr11:58978093-58991462	Trim11	94091	35.2	34.4	33.9	1.09617	0.356852	1.20257	0.0096303
chr7:104299897-10431549	Trim12a	76681	58.3	51.7	13.7	-1.01447	0.945908	-3.34256	4.09E-27
chr7:104338754-10435335	Trim12c	319236	37.5	35.0	10.5	1.02969	0.901905	-2.78528	2.40E-15
chr14:61598226-61605945	Trim13	66597	14.2	12.7	18.5	-1.00632	0.972822	1.61139	2.61E-07
chr4:46505072-46536141:	Trim14	74735	13.2	11.9	4.7	1.00119	0.996987	-2.20957	1.41E-08
chr11:62820253-62842948	Trim16	94092	15.4	14.8	19.6	1.08501	0.736555	1.56811	0.0026188
chr11:58963781-58971729	Trim17	56631	6.8	1.0	0.7	-4.35833	0.000906	-5.6029	3.81E-06
chr7:102557920-10256548	Trim21	20821	39.4	37.8	24.7	1.07128	0.522675	-1.27207	0.0010479
chr13:104179098-1042020	Trim23	81003	43.7	33.2	18.6	-1.18647	0.361651	-1.85412	2.67E-06
chr17:36837146-36859398	Trim26	22670	37.3	34.0	35.3	1.02512	0.802859	1.18516	0.0038281
chr13:21179931-21194723	Trim27	19720	27.1	31.4	45.6	1.30738	0.111258	2.07966	3.84E-09
chr7:13024152-13031032:	Trim28	21849	136.0	141.5	237.5	1.17271	0.144193	2.17432	6.19E-23
chr7:104409026-10446519	Trim30a	20128	31.7	40.2	18.2	1.40871	0.017233	-1.38763	0.0047369
chr7:104244457-10426223	Trim34a	94094	29.1	26.9	7.8	1.02947	0.889958	-2.93161	2.13E-20
chr14:66297025-66311424	Trim35	66854	91.7	79.2	96.5	-1.03647	0.638293	1.31495	8.43E-09
chr18:46165300-46212607	Trim36	28105	5.1	2.1	1.7	-2.08386	0.006487	-2.26228	0.00019
chr11:87127075-87220686	Trim37	68729	37.1	28.2	20.9	-1.17583	0.135869	-1.40887	2.29E-05
chr17:36258873-36272004	Trim39	79263	35.5	38.7	42.7	1.23226	0.194393	1.49586	0.0006932
chr2:102300119-10240090	Trim44	80985	93.5	89.5	136.8	1.07663	0.42875	1.82534	7.90E-22
chr4:134315120-13432962	Trim63	433766	3.1	2.0	0.6	-1.38891	0.391547	-3.79744	2.68E-06
chr11:116124708-1161311	Trim65	338364	12.3	9.1	5.6	-1.21289	0.28944	-1.72462	3.49E-05
chr7:102677580-10268732	Trim68	101700	31.8	23.3	14.9	-1.23035	0.410104	-1.67066	0.0040522
chr2:122160700-12217902	Trim69	70928	3.2	0.7	0.7	-3.52299	0.002348	-3.1469	0.0007822
chr11:48826138-48850195	Trim7	94089	10.8	9.0	2.9	-1.06153	0.851117	-2.89381	1.50E-08
chr19:46501648-46516455	Trim8	93679	30.2	23.4	18.7	-1.1583	0.224199	-1.28499	0.0051944
chr11:115440545-1154482	Trim80	432613	3.8	0.3	0.4	-6.51583	2.32E-05	-5.04858	1.98E-05
chr15:27730649-28025848	Trio	223435	104.1	86.5	51.9	-1.08098	0.699102	-1.58555	0.0002275
chr15:78947724-79005869	Triobp	110253	19.1	39.3	40.6	2.23686	0.010917	2.46866	0.0003636
chr17:57249451-57263697	Trip10	106628	71.6	69.6	43.2	1.08865	0.536243	-1.31878	0.0029501
chr12:101837372-1019131	Trip11	109181	47.3	54.6	69.9	1.30422	0.053932	1.83421	4.56E-09
chr9:65828926-65908794:	Trip4	56404	21.3	18.3	22.1	-1.04262	0.617354	1.29482	9.71E-07
chr5:137309899-13731424	Trip6	22051	83.2	86.3	144.4	1.17399	0.353932	2.14215	1.87E-10
chr4:12906837-12981485:	Triqk	208820	18.2	13.4	3.5	-1.22763	0.378898	-3.9944	1.93E-16
chr8:84689247-84699808:	Trmt1	212528	84.6	74.3	93.4	-1.01798	0.858309	1.3792	4.15E-09
chr3:138143538-13815982	Trmt10a	108943	8.6	7.9	15.3	1.02901	0.877096	2.21006	3.09E-16
chr16:56033720-56037774	Trmt10c	52575	41.4	65.0	85.9	1.75359	0.015701	2.49558	4.90E-07
chr10:30534225-30600749	Trmt11	73681	22.8	19.9	32.0	-1.01923	0.890054	1.75129	8.43E-15
chr19:6909698-6911026:+	Trmt112	67674	39.7	44.7	60.6	1.2569	0.016855	1.89786	3.48E-19
chr3:116581336-11661458	Trmt13	229780	18.4	18.6	18.9	1.13774	0.130535	1.28729	6.06E-05
chr16:18248883-18254772	Trmt2a	15547	45.2	43.9	56.4	1.09162	0.303515	1.55947	4.75E-14
chrX:134222955-13427698	Trmt2b	215201	27.5	22.6	9.8	-1.09385	0.525499	-2.21081	3.24E-17
chr12:73280410-73286711	Trmt5	76357	30.6	26.9	36.1	-1.02862	0.877149	1.46395	0.0001378
chr2:132804215-13281605	Trmt6	66926	22.1	26.5	57.8	1.34874	0.034861	3.22011	7.71E-29
chr12:111678105-1116839	Trmt61a	328162	14.4	25.3	111.9	1.9623	0.000732	9.03714	2.39E-42
chr17:71557027-71598761	Trmt61b	68789	4.2	4.8	10.2	1.27072	0.22415	2.922	2.73E-15
chr4:132311763-13232953	Trnau1ap	71787	63.7	72.8	116.8	1.28429	0.032722	2.27258	4.26E-21
chr6:106769138-10678247	Trnt1	70047	42.0	43.6	46.3	1.1671	0.185965	1.37266	0.0002295
chr11:69580359-69591873	Trp53	22059	55.8	53.6	99.1	1.0752	0.455513	2.21309	2.54E-36
chr1:182409167-18246243	Trp53bp2	209456	33.9	27.8	20.8	-1.09166	0.225971	-1.29949	6.35E-07
chr17:29057474-29079126	Trp53cor1	1.01E+08	1.7	0.9	0.4	-1.63297	0.240526	-3.1089	0.0002978
chr11:77508099-77513273	Trp53i13	216964	20.7	19.1	11.7	1.02611	0.859574	-1.41841	3.57E-05
chr4:11156441-11174377:	Trp53inp1	60599	108.5	94.5	22.2	-1.04147	0.891868	-3.73509	4.74E-16

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr2:155381856-15538984	Trp53inp2	68728	6.7	8.2	9.8	1.37112	0.169716	1.78757	0.0006551
chr2:166793767-16679949	Trp53rk	76367	5.1	5.7	7.9	1.25648	0.16887	1.92373	4.01E-08
chr2:164470304-16447372	Trp53tg5	73603	2.1	0.1	0.2	-6.53015	0.00064	-3.98906	0.0031516
chr9:95706629-95750358:	Trpc1	22063	21.3	17.9	9.5	-1.0627	0.638854	-1.77593	4.69E-12
chr3:54156057-54318471:	Trpc4	22066	16.7	19.3	6.4	1.29172	0.103964	-2.0486	1.47E-09
chr2:155634277-15569238	Trpc4ap	56407	98.4	92.5	90.1	1.05561	0.444276	1.14568	0.0059776
chrX:144381671-14468818	Trpc5	22067	0.0	0.1	1.2	1.99367	0.230896	24.8047	3.67E-18
chr9:8544142-8680741:+	Trpc6	22068	7.3	6.4	11.7	-1.01836	0.912685	1.98041	8.54E-16
chr19:22139117-22989884	Trpm3	226025	3.5	2.5	0.3	-1.27451	0.343698	-7.8486	1.82E-27
chr7:45303155-45333780:	Trpm4	68667	30.6	24.2	6.5	-1.13512	0.389075	-3.71443	1.61E-37
chr7:143071529-14309464	Trpm5	56843	1.4	1.0	0.2	-1.24914	0.56429	-4.64995	2.54E-08
chr19:18749983-18892511	Trpm6	225997	7.9	4.1	2.8	-1.7198	0.02217	-2.20172	2.11E-05
chr2:126791558-12687626	Trpm7	58800	91.0	78.2	59.5	-1.04147	0.529091	-1.22318	2.71E-06
chr19:6996131-6999046:+	Trpt1	107328	23.7	14.8	10.6	-1.42522	0.119373	-1.74645	0.0012764
chr11:62574486-62600305	Trpv2	22368	17.4	22.1	23.7	1.41793	0.053827	1.67786	0.0001813
chr5:114622154-11465842	Trpv4	63873	7.0	9.5	14.6	1.50382	0.304182	2.35453	0.0029012
chr5:144768792-14485977	Trrap	100683	52.2	43.9	31.9	-1.057	0.716146	-1.30386	0.0054789
chr2:29774684-29787671:	Trub2	227682	19.3	17.5	23.7	1.01674	0.858136	1.5365	1.96E-18
chr2:28641233-28691172:	Tsc1	64930	38.9	31.7	20.0	-1.09907	0.424909	-1.54609	9.22E-08
chr14:76415821-76507766	Tsc22d1	21807	154.7	142.5	74.4	1.02342	0.878604	-1.65496	1.14E-09
chrX:140539529-14060052	Tsc22d3	14605	120.5	116.5	25.5	1.05917	0.867165	-3.55477	2.64E-11
chr1:152370736-15238668	Tsen15	66637	33.3	35.1	42.3	1.17459	0.176041	1.57876	8.49E-08
chr6:115544704-11557833	Tsen2	381802	26.0	23.9	30.6	1.02138	0.868954	1.46909	2.47E-08
chr10:127022332-1270308	Tsfm	66399	15.6	20.1	47.0	1.43991	0.003623	3.69731	2.55E-43
chr7:46889027-46919930:	Tsg101	22088	63.4	71.2	101.0	1.26712	0.116492	1.97074	1.01E-09
chr1:37754572-37865298:	Tsga10	211484	14.9	11.2	6.9	-1.18923	0.284989	-1.71732	3.43E-06
chrX:83486676-83487924:	Tsga8	1.01E+08	4.0	0.2	0.4	-7.31273	0.000131	-4.77685	0.0004469
chr12:91400993-91540509	Tshr	22095	4.2	3.6	7.3	-1.03115	0.934669	2.11884	0.0001232
chr2:169633646-16988850	Tshz2	228911	62.9	51.3	26.6	-1.0985	0.337566	-1.8797	1.99E-20
chr7:44943240-44958037:	Tsks	22116	8.6	0.6	1.1	-8.06826	2.80E-06	-4.62326	8.32E-05
chr18:32815383-32819799	Tslp	53603	4.1	2.1	1.0	-1.71063	0.153393	-3.05773	0.0001128
chr1:118298518-11831113	Tsn	22099	85.2	79.4	89.7	1.0444	0.708025	1.31451	0.0001304
chr8:125012997-12503419	Tsnax	53424	105.0	99.3	127.6	1.06338	0.673748	1.51206	5.41E-06
chr8:105827744-10584467	Tsnaxip1	72236	5.1	0.3	0.5	-8.07713	3.54E-06	-5.68121	9.15E-06
chr6:127887622-12795303	Tspan11	68498	15.2	12.1	2.9	-1.12374	0.53387	-4.06166	2.15E-28
chr12:36014555-36042478	Tspan13	66109	124.4	136.3	217.8	1.20466	0.327646	2.14323	1.07E-08
chr13:54789405-54796775	Tspan17	74257	12.8	8.5	4.5	-1.34174	0.065182	-2.27458	3.91E-11
chr2:93201760-93334487:	Tspan18	241556	25.1	22.9	6.7	1.02826	0.888249	-2.92778	8.96E-23
chr3:102734770-10277231	Tspan2	70747	70.2	54.7	33.2	-1.15223	0.38646	-1.67723	5.93E-06
chr10:127067290-1270702	Tspan31	67125	101.5	111.2	155.9	1.22903	0.064389	1.90601	4.53E-15
chr6:29694214-29718558:	Tspan33	232670	5.1	4.7	8.1	1.03497	0.898795	1.97608	1.60E-06
chr3:138742208-13890443	Tspan5	56224	39.1	34.5	19.5	-1.00622	0.959008	-1.59513	7.64E-14
chrX:133891070-13389842	Tspan6	56496	27.8	24.2	15.8	-1.03591	0.846424	-1.40087	0.0014564
chr10:115817284-1158498	Tspan8	216350	90.5	71.5	29.8	-1.13593	0.628671	-2.3602	3.34E-07
chr17:48448435-48451501	Tspo2	70026	0.1	0.4	2.0	1.75303	0.402699	4.88113	0.0007786
chr10:34282190-34284885	Tspyl1	22110	107.2	97.9	58.3	1.02107	0.83008	-1.46898	4.60E-12
chrX:152336852-15234248	Tspyl2	52808	62.4	55.0	93.4	-1.00955	0.951605	1.8653	3.55E-15
chr2:153222370-15322544	Tspyl3	241732	9.5	7.1	3.8	-1.211	0.381673	-1.94452	1.84E-05
chr15:33683875-33687883	Tspyl5	239364	11.7	7.6	4.5	-1.3793	0.306807	-2.00321	0.0023708
chr11:74898080-74909340	Tsr1	104662	43.7	85.0	209.9	2.14282	0.002181	5.48011	2.15E-17
chrX:151087094-15109654	Tsr2	69499	29.7	29.8	47.6	1.12956	0.245933	1.99817	2.51E-21
chr17:25240170-25242799	Tsr3	68327	39.2	46.1	62.7	1.32629	0.081339	1.97857	1.27E-08
chr12:28751828-28867491	Tssc1	380752	14.7	16.9	17.1	1.28698	0.059221	1.45362	0.0002165
chr7:143069368-14307108	Tssc4	56844	47.0	47.4	71.5	1.12865	0.316661	1.89052	1.65E-14
chr16:17894203-17895653	Tssk1	22114	6.9	0.5	1.1	-6.93126	2.39E-05	-3.65781	0.001049
chr16:17898637-17900024	Tssk2	22115	11.1	0.5	1.1	-10.3092	9.24E-07	-5.29917	6.00E-05
chr4:129489008-12949077	Tssk3	58864	5.5	0.3	0.5	-6.70626	0.000305	-4.7443	0.0005253
chr8:69902215-69903518:	Tssk6	83984	3.8	0.5	0.9	-4.55228	0.000545	-2.71654	0.0066232

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr15:75924683-75929730	Tsta3	22122	39.9	40.8	52.3	1.15079	0.196421	1.63646	1.56E-10
chr1:171419033-17142035	Tstd1	226654	13.7	9.8	5.4	-1.23951	0.406635	-1.95137	0.0003897
chr4:46114746-46138475:	Tstd2	272027	28.1	32.2	38.1	1.28898	0.060427	1.68267	2.94E-07
chr17:46442448-46487675	Ttbk1	106763	1.3	0.4	0.6	-2.45757	0.006086	-1.71439	0.0454882
chr2:120732817-12085058	Ttbk2	140810	26.6	24.4	18.0	1.02568	0.803292	-1.18037	0.0065774
chr11:43730006-43747973	Ttc1	66827	62.7	67.2	67.8	1.20352	0.076031	1.34807	0.0001543
chr9:49436961-49486225:	Ttc12	235330	9.4	6.5	1.9	-1.29154	0.023753	-4.00438	5.10E-45
chr8:124671327-12472197	Ttc13	234875	25.3	25.0	36.9	1.10903	0.377608	1.81394	5.94E-14
chr3:33800183-33814860:	Ttc14	67120	84.9	69.9	53.9	-1.08564	0.211142	-1.25878	1.41E-06
chr2:94300766-94406689:	Ttc17	74569	33.8	32.9	32.5	1.09541	0.364925	1.20594	0.00928
chr11:62281473-62316441	Ttc19	72795	21.6	27.5	33.2	1.43587	0.015242	1.90536	2.69E-08
chr9:119937606-11996779	Ttc21a	74052	2.3	0.3	0.3	-5.43371	4.69E-05	-4.23992	5.02E-05
chr2:66184327-66256617:	Ttc21b	73668	38.5	38.3	19.7	1.12586	0.516218	-1.54386	0.0004575
chr7:67647410-67726576:	Ttc23	67009	19.6	13.1	8.0	-1.34421	0.214297	-1.92118	0.0001883
chr15:10503947-10558668	Ttc23l	75777	2.6	0.1	0.4	-5.84583	0.001469	-2.94214	0.0228781
chr11:100545632-1005725	Ttc25	74407	3.9	1.0	0.4	-2.67818	0.046873	-4.67502	5.72E-05
chr6:38381524-38427647:	Ttc26	264134	11.7	9.6	5.2	-1.08729	0.606463	-1.76849	7.95E-08
chr17:74717750-74863570	Ttc27	74196	31.3	32.1	54.1	1.15172	0.150042	2.15386	2.85E-28
chr5:110879803-11128977	Ttc28	209683	24.5	22.2	7.6	1.01494	0.94163	-2.5463	1.45E-19
chr8:78213342-78394326:	Ttc29	73301	3.0	0.7	0.5	-3.26809	0.005698	-3.61821	0.0002287
chr16:94370739-94469221	Ttc3	22129	191.8	165.2	105.3	-1.03812	0.695332	-1.4544	1.26E-10
chr2:75976172-75978179:	Ttc30a2	620631	2.8	0.3	0.5	-5.16107	0.000343	-3.62945	0.0008634
chr2:75935850-75938462:	Ttc30b	72421	31.0	20.6	4.9	-1.35113	0.331611	-4.5615	3.68E-12
chr15:5185560-5218332:+	Ttc33	67515	61.0	49.5	21.1	-1.10989	0.427884	-2.29338	5.12E-20
chr13:76098734-76187983	Ttc37	218343	42.6	42.2	59.9	1.10958	0.123094	1.75328	3.47E-31
chr15:85832304-85858822	Ttc38	239570	24.4	22.3	10.5	1.03145	0.890817	-1.83544	1.22E-06
chr4:109407100-10944474	Ttc39a	230603	6.7	3.5	8.6	-1.69129	0.00659	1.58739	0.0021278
chr4:83220301-83324189:	Ttc39b	69863	20.1	15.7	12.6	-1.14531	0.209998	-1.2775	0.0022439
chr17:80215914-80217936	Ttc39d	67737	3.2	0.3	0.4	-5.73895	0.000504	-4.44709	0.00045
chr14:50765409-50785520	Ttc5	219022	52.2	39.1	28.2	-1.19912	0.050378	-1.47413	3.55E-08
chr12:98920574-98983238	Ttc8	76260	36.8	32.8	10.1	-1.00697	0.96001	-2.89101	3.69E-45
chr12:81631369-81664941	Ttc9	69480	5.8	5.5	17.4	1.06076	0.863909	3.52123	1.00E-11
chr19:8809075-8819294:-	Ttc9c	70387	33.1	35.0	45.6	1.18322	0.087848	1.7123	9.00E-14
chr2:29060263-29087650:	Ttf1	22130	32.2	29.5	20.6	1.02485	0.778719	-1.24872	2.36E-05
chr2:157981803-15800936	Tti1	75425	32.1	28.1	21.0	-1.02031	0.849079	-1.22217	0.0009689
chr8:31150316-31164703:	Tti2	234138	19.5	18.7	22.8	1.07894	0.293237	1.46588	1.01E-14
chr15:83483769-83510907	Ttll1	319953	16.0	13.4	8.7	-1.06611	0.646323	-1.46591	2.28E-05
chr4:156034837-15605081	Ttll10	330010	8.1	2.8	1.1	-2.48875	0.00022	-5.10993	3.65E-14
chr15:83575094-83595157	Ttll12	223723	15.2	17.2	40.8	1.28442	0.209574	3.27183	4.68E-17
chr7:80246376-80260821:	Ttll13	269954	6.0	0.7	0.9	-5.58058	4.61E-05	-3.90413	0.0001846
chr17:7350904-7352696:-	Ttll2	1E+08	1.2	0.3	0.0	-2.76422	0.06395	-6.70722	1.14E-05
chr1:74661754-74697973:	Ttll4	67534	38.2	39.8	44.5	1.17502	0.223293	1.45279	0.000108
chr12:85824950-86053760	Ttll5	320244	21.7	16.4	9.7	-1.17883	0.1207	-1.76854	4.99E-13
chr11:96133786-96165452	Ttll6	237930	2.6	0.5	0.3	-3.62429	0.005324	-4.69519	4.10E-05
chr3:146852367-14698400	Ttll7	70892	12.1	12.6	6.3	1.16472	0.077638	-1.52406	1.73E-10
chr15:88913898-88954418	Ttll8	239591	1.6	0.2	0.3	-5.14373	0.001074	-3.37172	0.0038144
chr2:152962485-15300848	Ttll9	74711	1.8	0.2	0.6	-4.86661	0.000102	-2.05198	0.0385393
chr2:76703984-76982547:	Ttn	22138	2.5	2.0	0.6	-1.11901	0.606019	-3.37791	1.76E-18
chr2:163602314-16361901	Ttpal	76080	23.0	32.3	41.6	1.57923	0.002587	2.22867	6.08E-11
chr5:140620578-14064903	Ttyh3	78339	15.1	12.1	6.6	-1.11465	0.466675	-1.81174	5.69E-09
chr7:109010880-10903445	Tub	22141	3.8	3.1	1.0	-1.0964	0.73555	-2.90226	4.44E-10
chr15:98931431-98934390	Tuba1b	22143	379.6	357.0	487.5	1.04728	0.719227	1.60111	1.38E-09
chr15:99029891-99038105	Tuba1c	22146	31.8	48.3	130.9	1.69628	0.029835	4.7983	1.21E-17
chr6:125278274-12528604	Tuba3a	22144	20.9	1.0	2.3	-9.87497	7.10E-07	-4.94754	8.39E-05
chr6:145615963-14562147	Tuba3b	22147	26.0	1.1	3.5	-10.4657	3.65E-07	-4.21596	0.0004143
chr1:75214974-75219253:	Tuba4a	22145	33.2	44.1	98.2	1.49169	0.031589	3.59335	4.79E-20
chr6:121210770-12122609	Tuba8	53857	7.0	1.4	3.2	-3.35686	0.006672	-1.61428	0.206339
chr13:34074280-34078008	Tubb2a	22151	47.8	59.6	89.2	1.39406	0.099262	2.26897	4.13E-08

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr8:123411564-12342201	Tubb3	22152	0.9	0.5	3.1	-1.518	0.335568	3.83015	7.89E-07
chr2:25222158-25224702:	Tubb4b	227613	200.3	217.6	444.0	1.22735	0.220855	2.72793	3.04E-17
chr17:35833920-35838301	Tubb5	22154	459.5	409.3	766.3	-1.00547	0.962771	2.0798	6.41E-34
chr18:67390731-67402749	Tubb6	67951	143.1	184.0	640.7	1.4458	0.015455	5.43645	1.56E-48
chr10:39134023-39151058	Tube1	71924	6.9	4.6	3.0	-1.34702	0.181202	-1.82874	0.0002902
chr11:101120131-1011264	Tubg1	103733	17.4	15.5	45.3	-1.01228	0.953264	3.20837	3.11E-31
chr7:55794148-55831447:	Tubgcp5	233276	51.3	42.3	50.1	-1.08585	0.299484	1.22206	0.0003854
chr7:126487355-12649073	Tufm	233870	65.9	68.3	107.0	1.16886	0.267696	2.01649	1.13E-12
chr17:28351519-28365143	Tulp1	22157	4.6	3.1	1.6	-1.33408	0.233118	-2.30399	5.00E-06
chr7:45486263-45522603:	Tulp2	56734	11.1	0.7	1.6	-8.14789	1.26E-06	-3.99083	0.0002745
chr6:128321161-12835585	Tulp3	22158	15.1	12.9	16.0	-1.04896	0.783672	1.32523	0.0070385
chr8:39005867-39130817:	Tusc3	80286	83.3	74.5	50.0	-1.00295	0.979507	-1.33224	1.71E-06
chr11:76679873-76698664	Tusc5	237858	7.3	2.7	0.5	-2.05171	0.148865	-6.62202	3.66E-07
chr19:8953850-8966210:+	Tut1	70044	36.4	40.4	54.6	1.25285	0.136446	1.86087	2.20E-08
chr16:10420559-10447350	Tvp23a	383103	7.2	5.6	2.9	-1.15867	0.581956	-1.93562	0.0002107
chr11:62879490-62895184	Tvp23b	67510	48.3	45.7	51.3	1.05888	0.494037	1.32804	2.69E-07
chr15:94577948-94589824	Twf1	19230	53.0	64.6	99.6	1.36756	0.040558	2.31182	2.70E-13
chr12:33429624-33439380	Twistnb	28071	34.0	40.7	51.8	1.34423	0.041497	1.88458	6.81E-09
chr17:65923065-65951187	Twsg1	65960	126.9	118.6	73.2	1.03944	0.732848	-1.38569	2.40E-06
chr4:129626077-12964106	Txlna	109658	50.9	54.9	69.9	1.2103	0.035826	1.71221	3.32E-15
chr10:17796219-17845663	Txlnb	378431	8.5	5.2	0.6	-1.45917	0.167841	-9.45237	1.96E-26
chr4:57943373-57956411:	Txn1	22166	162.7	162.5	219.6	1.1173	0.318124	1.6774	2.28E-11
chr15:77915051-77928994	Txn2	56551	84.2	86.9	166.5	1.16329	0.227044	2.45407	1.29E-24
chr16:11074911-11134532	Txndc11	106200	23.3	29.7	59.1	1.43787	0.024817	3.10767	1.38E-20
chr14:45134448-45219394	Txndc16	70561	64.9	51.9	9.2	-1.12199	0.303565	-5.54421	1.63E-101
chr11:72207554-72210487	Txndc17	52700	75.1	96.8	104.4	1.4495	0.103937	1.70028	0.0022463
chr17:65637505-65642204	Txndc2	213272	9.4	0.7	1.3	-8.07947	5.84E-07	-4.47222	3.85E-05
chr13:38500271-38528824	Txndc5	105245	125.1	119.9	217.1	1.07146	0.351363	2.1622	7.21E-54
chr1:37983867-37997208:	Txndc9	98258	41.7	48.4	55.3	1.30569	0.055158	1.64501	2.23E-06
chr3:96557957-96561857:	Txnip	56338	####	998.5	400.2	-1.17163	0.714628	-2.37376	0.0013401
chr18:63662801-63692359	Txnl1	53382	58.7	71.8	116.9	1.37765	0.059221	2.44563	1.47E-12
chr18:80206798-80225851	Txnl4a	27366	49.1	54.1	64.4	1.24159	0.073081	1.63361	5.35E-08
chr10:82833951-82897724	Txnrd1	50493	48.3	65.5	128.1	1.51038	0.0525	3.1879	2.90E-13
chr9:21104068-21131275:	Tyk2	54721	29.2	23.6	10.8	-1.11402	0.381978	-2.1469	4.42E-19
chr2:119797740-11981810	Tyro3	22174	17.0	12.8	7.1	-1.19521	0.410267	-1.88407	2.90E-05
chr10:61695514-61702773	Tysnd1	71767	14.0	11.9	14.1	-1.05488	0.702474	1.25657	0.0079024
chr5:130255619-13034156	Tyw1	100929	12.4	10.3	7.8	-1.08521	0.413822	-1.26493	0.0008725
chr3:154576520-15459709	Tyw3	209584	8.3	7.8	8.7	1.0381	0.814283	1.29753	0.0051172
chr17:31647082-31658754	U2af1	108121	141.8	178.4	280.9	1.41785	0.085531	2.41426	5.26E-09
chr7:5062143-5079945:+	U2af2	22185	133.6	146.2	300.9	1.2354	0.134755	2.78346	1.19E-23
chr9:95456894-95511996:	U2surp	67958	70.7	69.8	71.5	1.11036	0.401556	1.26043	0.0092823
chr1:170142003-17017494	Uap1	107652	44.2	58.9	92.0	1.49164	0.000283	2.5739	1.71E-25
chr2:25361492-25365626:	Uap1l1	227620	63.9	44.6	29.0	-1.28548	0.012087	-1.75396	9.18E-13
chrX:20658302-20683179:	Uba1	22201	140.8	135.0	228.2	1.07821	0.415411	2.02038	1.15E-29
chr7:34140697-34168529:	Uba2	50995	112.1	121.4	155.7	1.21812	0.084094	1.72854	9.71E-11
chr6:97183632-97205647:	Uba3	22200	59.0	66.9	90.4	1.27408	0.012401	1.90551	5.50E-18
chr9:104046588-10406312	Uba5	66663	49.0	61.0	103.3	1.40092	0.008388	2.60831	4.98E-22
chr5:86110730-86172743:	Uba6	231380	33.8	38.2	42.7	1.2669	0.000453	1.57752	2.31E-16
chr9:107975567-10798405	Uba7	74153	60.6	48.5	21.1	-1.11673	0.218526	-2.28408	2.31E-37
chr2:25996958-26021760:	Ubac1	98766	26.6	27.1	27.6	1.14352	0.111886	1.29787	3.30E-05
chr14:121878606-1220210	Ubac2	68889	32.6	28.6	38.4	-1.02146	0.857326	1.47112	1.38E-09
chr16:4874779-4879851:-	Ubald1	207740	64.2	59.4	26.2	1.03916	0.815499	-1.93701	5.52E-12
chr11:62551504-62553212	Ubb	22187	144.6	128.3	149.7	-1.00722	0.945251	1.29056	2.26E-06
chr5:125385965-12539001	Ubc	22190	130.0	165.1	148.2	1.43117	0.03313	1.41516	0.0089387
chrX:36874366-36884220:	Ube2a	22209	22.5	30.6	29.6	1.52623	0.075495	1.61132	0.009466
chr11:51985146-52000466	Ube2b	22210	142.9	145.3	71.8	1.13876	0.120567	-1.58996	7.57E-14
chr2:164769929-16477290	Ube2c	68612	8.0	10.7	11.1	1.47559	0.067731	1.7069	0.0008981
chr18:35771559-35807172	Ube2d2a	56550	65.1	82.5	102.9	1.43063	0.067693	1.94379	7.00E-06

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr5:107830162-10783177	Ube2d2b	73318	6.0	0.5	0.8	-6.21521	0.000178	-4.1416	0.0006691
chr3:135438759-13546717	Ube2d3	66105	224.6	272.3	403.9	1.36525	0.050133	2.214	2.78E-11
chr14:18282729-18331844	Ube2e1	22194	62.2	111.8	116.1	1.94125	0.079011	2.13537	0.0092953
chr1:91250319-91286025:	Ube2f	67921	37.0	62.1	87.9	1.86234	0.016455	2.8075	3.37E-07
chr10:77622321-77645990	Ube2g2	22213	40.1	54.8	91.4	1.53681	0.012751	2.78294	1.73E-14
chr6:30211290-30304539:	Ube2h	22214	50.6	46.9	27.9	1.04221	0.700937	-1.4494	2.06E-08
chr17:25260511-25274310	Ube2i	22196	96.9	100.9	122.3	1.17074	0.099131	1.57397	1.22E-10
chr4:33031425-33052364:	Ube2j1	56228	60.0	77.3	104.5	1.45005	0.043973	2.13458	5.53E-08
chr4:155943813-15595960	Ube2j2	140499	1.9	2.8	3.5	1.60126	0.163106	2.13179	0.002644
chr5:65537261-65598989:	Ube2k	53323	35.4	37.5	46.8	1.19465	0.176973	1.64344	2.21E-07
chr16:17152015-17201492	Ube2l3	22195	68.2	70.2	103.4	1.15949	0.23544	1.88505	7.01E-13
chr2:84798828-84810003:	Ube2l6	56791	40.1	41.7	20.6	1.14851	0.453775	-1.54611	0.0007649
chr7:13035120-13038275:	Ube2m	22192	72.9	78.2	149.3	1.21118	0.208844	2.52708	9.14E-18
chr10:95515162-95545658	Ube2n	93765	33.2	38.0	57.5	1.29067	0.11455	2.13465	2.01E-10
chr3:89773609-89783997:	Ube2q1	70093	46.2	49.8	59.4	1.21601	0.158543	1.59816	4.37E-06
chr9:55149369-55207529:	Ube2q2	109161	59.2	66.3	79.9	1.26469	0.184539	1.66857	8.30E-05
chr13:69702832-69739897	Ube2ql1	76980	1.6	4.6	2.7	2.84646	0.003669	1.8883	0.037822
chr4:41136021-41193370:	Ube2r2	67615	61.5	64.7	69.9	1.18197	0.08487	1.41667	1.58E-06
chr7:4808014-4812340:-	Ube2s	77891	63.3	91.6	150.7	1.62378	0.027592	2.87029	3.18E-10
chr2:167607639-16763200	Ube2v1	66589	22.9	25.0	37.7	1.23453	0.21987	2.03648	6.16E-09
chr16:15550986-15594518	Ube2v2	70620	12.2	12.3	18.2	1.1341	0.065314	1.87119	8.93E-39
chr1:16540788-16619338:	Ube2w	66799	34.4	33.8	34.6	1.10505	0.35512	1.25305	0.0033961
chr11:96047431-96065364	Ube2z	268470	54.1	60.8	74.1	1.26601	0.049729	1.70415	3.77E-09
chr7:59228750-59306727:	Ube3a	22215	81.3	84.3	97.3	1.16396	0.07416	1.4917	2.44E-10
chr5:29569242-29676077:	Ube3c	100763	65.7	65.4	87.8	1.11646	0.11432	1.6678	5.23E-24
chr4:149328416-14942663	Ube4b	63958	46.6	38.3	21.9	-1.09273	0.448095	-1.6965	2.85E-11
chr7:122067198-12208219	Ubfd1	28018	40.6	48.4	57.6	1.3416	0.009944	1.76527	2.03E-10
chr4:148434497-14844475	Ubiad1	71707	13.6	14.9	28.2	1.23098	0.097133	2.57045	3.65E-26
chrX:74365718-74368548:	Ubl4	27643	21.1	23.5	32.6	1.24857	0.082202	1.91397	3.64E-12
chr3:107553698-10755507	Ubl4b	67591	5.0	0.4	0.7	-5.37128	0.002318	-3.37995	0.0085789
chr9:20643318-20646789:	Ubl5	66177	43.7	44.8	52.4	1.15082	0.269724	1.49131	1.03E-05
chr9:57910986-57929968:	Ubl7	69459	50.8	37.7	22.9	-1.20802	0.091381	-1.76293	1.61E-11
chr11:44454571-44470548	Ublcp1	79560	47.6	43.9	66.2	1.03061	0.712984	1.7349	2.11E-31
chr16:5050068-5086285:+	Ubn1	170644	49.8	48.3	32.1	1.09159	0.317673	-1.23925	0.0006964
chr6:38433925-38512763:	Ubn2	320538	29.8	27.3	16.1	1.02859	0.78977	-1.47374	4.10E-10
chr2:130589996-13063003	Ubox5	140629	11.4	10.3	11.2	1.0071	0.958092	1.22405	0.0036224
chr13:58176156-58215653	Ubqln1	56085	60.8	73.3	112.4	1.36113	0.090826	2.26932	1.34E-09
chrX:153498232-15350155	Ubqln2	54609	23.1	21.5	14.9	1.04475	0.731826	-1.232	0.0096746
chr7:104140623-10414327	Ubqln3	244178	7.0	0.3	0.7	-9.0855	6.85E-06	-4.75604	0.0002866
chr3:88553716-88569725:	Ubqln4	94232	48.3	56.6	86.3	1.32491	0.069612	2.21057	5.29E-12
chr7:104148259-10415055	Ubqlnl	244179	3.9	0.2	0.6	-7.84486	6.77E-05	-3.62997	0.0041901
chr2:120860276-12097071	Ubr1	22222	56.6	56.1	56.6	1.11261	0.224372	1.24819	0.0005706
chr17:46928291-47010532	Ubr2	224826	64.4	57.5	36.9	1.0046	0.976763	-1.39035	6.63E-05
chr2:69897246-70024010:	Ubr3	68795	66.5	62.6	65.9	1.06045	0.608436	1.23724	0.0048233
chr15:37967328-38078854	Ubr5	70790	106.6	102.6	115.5	1.08429	0.505832	1.35141	0.0002528
chr12:102757975-1027777	Ubr7	66622	50.2	52.1	51.6	1.16657	0.164971	1.28251	0.0027309
chr11:32455372-32518709	Ubtd2	327900	34.1	41.2	39.2	1.36102	0.02556	1.43219	0.0009068
chr19:8871559-8875656:+	Ubxn1	225896	169.7	170.1	185.7	1.12825	0.317948	1.36458	0.0003184
chr4:138709837-13873843	Ubxn10	212190	4.4	1.2	0.8	-2.89197	0.005303	-3.83497	1.43E-05
chr4:134102583-13412678	Ubxn11	67586	16.4	10.5	5.1	-1.38546	0.098244	-2.48583	1.31E-09
chr12:4879032-4907520:-	Ubxn2a	217379	43.4	53.1	67.2	1.3775	0.021416	1.91834	1.10E-09
chr1:128244181-12827937	Ubxn4	67812	72.6	82.1	127.6	1.27466	0.096507	2.17138	5.20E-13
chr17:56068253-56074989	Ubxn6	66530	82.4	70.9	34.3	-1.04222	0.69433	-1.91157	1.60E-23
chr16:32332252-32393747	Ubxn7	224111	60.2	50.9	28.5	-1.0573	0.468345	-1.68645	2.56E-24
chr8:33619586-33641976:	Ubxn8	108159	12.9	12.7	19.0	1.10536	0.37152	1.84016	1.91E-16
chr14:101653967-1016961	Uchl3	50933	26.6	30.9	90.4	1.30921	0.14978	4.12647	9.96E-27
chr1:143777278-14380746	Uchl5	56207	24.7	22.6	33.7	1.02242	0.899426	1.69484	2.03E-08
chr2:32255002-32260105:	Uck1	22245	42.3	64.3	70.0	1.6981	0.041149	1.99842	0.0005478

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr1:167226084-16728512	Uck2	80914	29.4	30.0	79.8	1.14557	0.37075	3.34944	2.81E-33
chr7:100472991-10048643	Ucp3	22229	1.2	0.4	0.1	-1.96755	0.248164	-4.91212	0.0002504
chr7:46923216-46958518:	Uevld	54122	21.0	17.5	7.3	-1.07221	0.484262	-2.30245	4.13E-34
chr1:171288564-17129498	Ufc1	66155	92.6	87.6	145.3	1.05535	0.656718	1.94947	1.04E-19
chr16:18812294-18835261	Ufd1l	22230	79.8	76.5	99.2	1.08057	0.500318	1.55162	7.69E-09
chr4:25248586-25281821:	Ufl1	67490	37.2	30.5	42.7	-1.09577	0.394018	1.43346	1.05E-06
chr3:53853376-53863807:	Ufm1	67890	24.6	27.4	45.9	1.25568	0.095549	2.30993	4.42E-17
chr5:137294669-13729566	Ufsp1	70240	4.4	5.1	12.2	1.30446	0.392833	3.25798	1.15E-08
chr4:59189550-59222833:	Ugcg	22234	43.1	72.6	52.2	1.85636	0.00314	1.48669	0.0251025
chr1:36140028-36244302:	Uggt1	320011	48.2	47.4	73.4	1.10408	0.153593	1.90035	1.78E-38
chr11:21321126-21371267	Ugp2	216558	70.7	86.2	85.5	1.36404	0.013621	1.50075	4.60E-05
chr1:88134809-88220002:	Ugt1a6a	94284	10.8	8.1	3.1	-1.20895	0.198342	-2.78106	4.15E-20
chr1:88103257-88218998:	Ugt1a6b	394435	1.5	0.7	0.5	-1.77082	0.118019	-2.24081	0.0043486
chr1:170199256-17021539	Uhmk1	16589	38.1	37.8	39.5	1.10904	0.228072	1.29407	2.95E-05
chr17:56303337-56323486	Uhrf1	18140	10.4	10.4	15.0	1.11372	0.727681	1.76717	0.0029148
chr17:27856507-27900040	Uhrf1bp1	224648	10.5	9.1	12.9	-1.01978	0.871062	1.53602	3.77E-11
chr10:89744991-89819869	Uhrf1bp1l	75089	34.2	31.9	39.7	1.04012	0.705465	1.44606	4.52E-09
chr19:30030513-30093724	Uhrf2	109113	114.8	113.0	65.9	1.10048	0.262723	-1.38879	7.93E-08
chr5:110784489-11081008	Ulk1	22241	29.1	26.8	6.5	1.03462	0.861354	-3.52651	4.48E-31
chr11:61775598-61855092	Ulk2	29869	46.1	39.5	21.9	-1.04808	0.664618	-1.68265	1.12E-14
chr9:57589452-57596233:	Ulk3	71742	13.5	9.6	7.8	-1.25877	0.080215	-1.38707	0.0011375
chr9:120964454-12127717	Ulk4	209012	11.5	7.6	2.8	-1.34777	0.154945	-3.11879	3.41E-13
chr16:33955012-33967003	Umps	22247	26.4	44.4	70.2	1.87233	0.015029	3.13623	1.28E-08
chr10:60762595-60831581	Unc5b	107449	6.7	6.7	3.3	1.13346	0.583614	-1.61322	0.0017707
chr17:48454901-48468684	Unc5cl	76589	0.4	3.0	13.4	3.98626	0.006297	13.0742	1.53E-10
chr17:25188400-25234443	Unkl	74154	19.9	17.9	8.2	1.0099	0.94966	-1.91797	1.61E-15
chr3:146597149-14663148	Uox	22262	0.1	0.6	5.4	2.94716	0.04062	19.2193	2.34E-14
chr10:75406911-75441679	Upb1	103149	2.2	1.8	0.5	-1.05957	0.911885	-2.94918	0.0002662
chr8:70331522-70353273:	Upf1	19704	39.8	56.0	71.6	1.58137	0.063722	2.17344	3.50E-05
chr8:13785615-13798537:	Upf3a	67031	38.0	42.2	67.9	1.24729	0.054802	2.21943	1.83E-21
chrX:37091834-37110322:	Upf3b	68134	49.7	42.1	31.0	-1.05675	0.640194	-1.28234	0.001111
chr5:136038496-13604499	Upk3b	100647	48.1	27.0	16.9	-1.56392	0.109747	-2.1895	0.0002054
chr5:136057267-13606432	Upk3bl	69665	6.4	4.6	1.3	-1.20412	0.69751	-3.3595	8.04E-05
chr11:9118008-9136170:+	Upp1	22271	4.6	7.2	13.8	1.70835	9.32E-05	3.6302	3.59E-33
chrX:104482782-10450626	Uprt	331487	15.8	14.3	16.9	1.00782	0.968765	1.33202	0.0067639
chr2:155846886-15593031	Uqcc1	56046	39.1	38.6	47.7	1.1047	0.218046	1.52541	9.88E-14
chr17:27122665-27133891	Uqcc2	67267	67.8	65.5	146.0	1.08363	0.595832	2.66756	2.21E-26
chr19:8880014-8880933:-	Uqcc3	107197	62.6	55.0	36.2	-1.02098	0.879613	-1.38115	2.79E-05
chr11:4701968-4704344:-	Uqcr10	66152	175.2	181.3	214.3	1.15707	0.113467	1.52362	3.94E-10
chr10:80402997-80406821	Uqcr11	66594	236.7	236.2	324.2	1.11758	0.286096	1.70602	1.34E-13
chr13:66900621-66905350	Uqcrb	67530	259.3	279.1	452.1	1.21051	0.233146	2.14974	1.78E-11
chr9:108936648-10894964	Uqcrc1	22273	129.7	126.6	216.5	1.09534	0.196518	2.08477	8.36E-51
chr7:120635189-12065952	Uqcrc2	67003	183.2	183.1	255.5	1.1219	0.324633	1.73386	1.35E-11
chr13:30540312-30545316	Uqcrfs1	66694	96.0	111.3	134.8	1.30671	0.084392	1.74	1.82E-06
chr11:53428948-53430831	Uqcrq	22272	59.3	62.4	164.4	1.18832	0.371388	3.38576	4.11E-21
chr7:140835496-14083796	Urah	76974	13.3	12.4	24.0	1.04266	0.902942	2.1862	1.97E-05
chr16:90751527-90810413	Urb1	207932	16.0	20.8	41.2	1.46871	0.067674	3.10969	3.38E-13
chr8:124023473-12404850	Urb2	382038	18.5	23.1	44.8	1.40779	0.095882	2.93658	9.76E-13
chr2:29827389-29844996:	Urm1	68205	36.9	36.8	38.8	1.11808	0.297763	1.31545	0.0003358
chr4:116990217-11699437	Urod	22275	77.3	61.2	30.3	-1.13481	0.28976	-2.0292	9.32E-17
chr8:71366848-71369732:	Use1	67023	266.7	246.5	150.5	1.03122	0.716538	-1.41736	1.35E-11
chr1:171411681-17141874	Usf1	22278	71.2	59.6	37.2	-1.07275	0.561173	-1.52609	9.51E-08
chr8:71384274-71395801:	Ushbp1	234395	24.0	18.7	4.8	-1.15016	0.175922	-3.93653	8.40E-66
chr19:47083471-47090625	Usmg5	66477	255.6	304.0	440.7	1.33579	0.084572	2.1229	1.42E-09
chr5:92137938-92202795:	Uso1	56041	26.8	32.3	62.9	1.36058	0.084392	2.86949	8.91E-16
chr4:98923810-98935542:	Usp1	230484	78.3	71.4	122.2	1.02119	0.808939	1.94628	3.44E-43
chr8:119910852-11995755	Usp10	22224	34.9	42.7	74.6	1.38016	0.06967	2.61833	2.42E-13
chrX:20703909-20720539:	Usp11	236733	49.6	38.2	22.8	-1.15744	0.249321	-1.72559	1.92E-09

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr18:9993615-10030149:	Usp14	59025	46.3	48.2	82.9	1.17158	0.106693	2.22954	1.07E-29
chr10:123105006-1231970	Usp15	14479	29.3	30.2	33.3	1.15839	0.083884	1.41707	3.62E-08
chr16:87454985-87483513	Usp16	74112	64.3	87.2	101.9	1.52774	0.037185	1.94315	2.16E-05
chr9:108490676-10850233	Usp19	71472	86.8	85.2	53.6	1.10818	0.442648	-1.29086	0.0066445
chr9:44067021-44095627:	Usp2	53376	26.2	16.6	7.7	-1.37425	0.109931	-2.64259	4.95E-11
chr2:30982279-31022655:	Usp20	74270	16.5	11.1	9.4	-1.33514	0.064835	-1.40092	0.0052945
chr4:106316213-10644132	Usp24	329908	45.7	55.1	70.0	1.36458	0.145879	1.87953	7.59E-05
chr16:77014069-77116780	Usp25	30940	71.4	67.4	72.4	1.05668	0.487215	1.26674	9.80E-06
chr9:48985385-49042517:	Usp28	235323	22.5	18.4	13.1	-1.09008	0.483869	-1.3697	0.0001964
chr11:84984488-85139955	Usp32	237898	33.3	29.4	23.1	-1.01023	0.914492	-1.15418	0.0060665
chr11:23306895-23490560	Usp34	17847	66.2	64.3	72.9	1.09082	0.337566	1.37493	5.68E-07
chr7:97309380-97325964:	Usp35	244144	15.4	11.0	4.0	-1.25492	0.296564	-3.00943	1.25E-12
chr11:118259653-1182902	Usp36	72344	23.0	36.4	49.6	1.76343	0.045709	2.55435	1.54E-05
chr1:74435510-74544286:	Usp37	319651	29.6	35.1	35.1	1.33488	0.064425	1.47298	0.0012156
chr8:80980733-81014906:	Usp38	74841	31.8	39.9	39.8	1.41707	0.06369	1.55022	0.0024302
chr6:72318676-72345175:	Usp39	28035	26.0	39.9	66.0	1.71305	0.045284	2.99578	6.96E-08
chr9:108347831-10839252	Usp4	22258	87.6	103.5	142.8	1.33434	0.075335	2.01324	7.34E-09
chr5:143710326-14373228	Usp42	76800	17.9	22.2	24.5	1.40061	0.089531	1.69093	0.0004788
chr10:93831555-93858087	Usp44	327799	2.5	0.2	0.4	-7.27088	1.01E-05	-3.6908	0.0007822
chr4:21776270-21837872:	Usp45	77593	28.4	23.1	15.6	-1.10846	0.462663	-1.45111	0.0001153
chr5:74000038-74068411:	Usp46	69727	22.1	19.4	27.7	-1.02821	0.872865	1.55767	3.24E-06
chr7:112023506-11211138	Usp47	74996	127.2	126.2	142.9	1.11582	0.25417	1.40093	9.38E-07
chr6:124815019-12482944	Usp5	22225	67.7	57.4	110.1	-1.05168	0.515272	2.03073	5.01E-47
chr2:126761050-12678346	Usp50	75083	2.2	0.3	0.1	-4.13618	0.009577	-6.30667	3.08E-05
chr16:8688722-8738342:-	Usp7	252870	109.0	121.1	148.6	1.25514	0.144118	1.69084	5.14E-06
chr5:149184560-14921543	Uspl1	231915	40.3	67.9	76.9	1.8712	0.02027	2.27417	0.0001069
chr10:8204753-8518825:-	Ust	338362	9.5	8.8	3.2	1.04297	0.775824	-2.34182	2.33E-20
chr4:124678764-12469355	Utp11l	67205	75.0	79.3	120.3	1.19081	0.218045	1.98703	8.20E-12
chrX:48256934-48282449:	Utp14a	72554	47.4	50.5	101.1	1.19695	0.109747	2.64591	2.01E-33
chr1:78657825-78667601:	Utp14b	195434	15.6	16.9	21.0	1.22429	0.321376	1.66818	0.000448
chr13:98246845-98262992	Utp15	105372	30.9	40.5	56.0	1.47565	0.031433	2.22376	6.67E-09
chr11:93859243-93885766	Utp18	217109	24.0	39.0	76.1	1.80822	0.022267	3.70139	4.46E-11
chr10:88746607-88826814	Utp20	70683	31.9	33.6	94.8	1.18437	0.09787	3.68358	1.13E-70
chr15:51877441-51884622	Utp23	78581	11.6	13.3	14.1	1.28573	0.075136	1.51711	8.74E-05
chr5:88554483-88556083:	Utp3	65961	60.0	73.1	80.6	1.37273	0.137028	1.65065	0.0018002
chr11:79933956-79962387	Utp6	216987	50.2	77.1	101.2	1.71465	0.044353	2.40441	1.88E-05
chr4:150997097-15100181	Uts2	24111	0.0	0.0	1.6	0	1	5.87945	0.000109
chr5:33378696-33419754:	Uvssa	71101	25.1	17.0	13.9	-1.32501	0.056631	-1.43363	0.0015454
chr1:43750231-43827708:	Uxs1	67883	59.4	56.7	73.6	1.05734	0.777641	1.53918	0.000249
chrX:20951665-20961978:	Uxt	22294	27.7	30.4	39.7	1.23272	0.151721	1.77441	5.06E-08
chr8:110618638-11072039	Vac14	234729	23.2	20.7	34.4	-1.00016	0.999471	1.85542	3.39E-26
chr6:125215581-12522230	Vamp1	22317	13.5	8.0	6.6	-1.51518	0.004822	-1.62956	4.60E-05
chr4:151047305-15105795	Vamp3	22319	72.7	74.7	85.9	1.1578	0.336743	1.46846	0.0004016
chr1:162570828-16259907	Vamp4	53330	98.2	65.8	26.5	-1.34119	0.166482	-2.86201	1.05E-11
chr6:72368049-72380468:	Vamp5	53620	13.2	11.1	4.9	-1.06208	0.798752	-2.14406	9.77E-08
chr3:102155900-10220469	Vangl1	229658	18.5	13.2	10.5	-1.2649	0.14057	-1.39443	0.0060167
chr1:172004371-17202726	Vangl2	93840	11.6	7.2	6.6	-1.43709	0.000664	-1.39762	0.0001724
chr17:65580053-65613555	Vapa	30960	121.2	168.5	271.7	1.56188	0.058165	2.692	2.13E-08
chr2:173737571-17378433	Vapb	56491	29.9	25.6	27.9	-1.04737	0.568429	1.16508	0.0044357
chr17:35000907-35016329	Vars	22321	46.3	41.2	87.4	-1.00388	0.974417	2.35217	2.86E-45
chr1:190947646-19097929	Vash2	226841	6.3	3.9	1.2	-1.4513	0.119066	-3.91119	8.48E-14
chr7:19256930-19271854:	Vasp	22323	95.5	119.3	160.7	1.4072	0.047171	2.06863	2.29E-08
chr11:101458748-1014661	Vat1	26949	124.7	98.2	56.7	-1.13941	0.198295	-1.75575	1.29E-14
chr3:109340683-10968569	Vav3	57257	29.6	23.4	17.7	-1.13802	0.310057	-1.3326	0.0018576
chrX:75514297-75534946:	Vbp1	22327	75.0	82.3	99.6	1.23156	0.101859	1.64876	1.15E-07
chr14:20929433-21033673	Vcl	22330	181.9	197.7	266.8	1.22449	0.158188	1.819	1.22E-08
chr4:42979964-43000507:	Vcp	269523	218.4	215.6	446.5	1.10997	0.303702	2.5405	1.17E-40
chr12:69577628-69583028	Vcpkmt	207965	13.6	11.9	17.8	-1.0248	0.889651	1.62926	5.01E-08

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:52361115-52389396	Vdac1	22333	137.1	136.4	148.9	1.11987	0.369686	1.35375	0.0006798
chr14:21831561-21845879	Vdac2	22334	188.8	188.9	300.8	1.12745	0.441373	1.97342	1.10E-10
chr8:22577075-22593813:	Vdac3	22335	137.3	139.9	194.2	1.14131	0.172645	1.76133	3.43E-16
chr15:97854427-97908296	Vdr	22337	3.7	3.4	1.2	1.03698	0.926564	-2.35867	6.38E-05
chr17:46016993-46032377	Vegfa	22339	66.5	194.7	211.8	2.65036	0.052163	2.96823	0.0053035
chr19:6982472-6987651:-	Vegfb	22340	30.1	22.8	14.2	-1.18093	0.372965	-1.66739	0.0001152
chr8:54077532-54186454:	Vegfc	22341	19.4	12.7	4.8	-1.3727	0.203018	-3.07306	8.35E-10
chr3:66053558-66296837:	Veph1	72789	2.7	1.9	0.2	-1.23964	0.461454	-8.03356	3.35E-21
chr10:93961522-94035799	Vezt	215008	15.7	13.1	8.9	-1.07219	0.49031	-1.39966	8.49E-07
chr6:114862092-11492175	Vgll4	232334	93.6	71.0	38.6	-1.18658	0.177433	-1.92464	1.55E-12
chr6:113624021-11363163	Vhl	22346	34.1	30.9	38.1	1.01375	0.889716	1.3916	2.24E-10
chr7:66079649-66089405:	Vimp	109815	48.6	57.4	152.7	1.32674	0.048241	3.85791	3.17E-38
chr12:87238875-87266286	Vipas39	104799	64.3	55.4	39.8	-1.03417	0.712056	-1.28873	6.27E-06
chr12:116077726-1161462	Vipr2	22355	5.5	4.2	0.5	-1.16362	0.59683	-7.57582	9.37E-23
chr17:78508063-78627409	Vit	74199	6.1	4.3	2.9	-1.27546	0.157849	-1.65464	0.0001109
chr7:127893063-12789561	Vkorc1	27973	84.2	74.1	31.4	-1.019	0.897964	-2.12769	3.42E-20
chr5:129942109-12998669	Vkorc1l1	69568	25.3	25.8	31.1	1.1456	0.178034	1.533	4.40E-09
chr19:27217020-27254231	Vldlr	22359	93.9	89.1	52.4	1.05726	0.777614	-1.42277	0.0031765
chrX:71816080-71824706:	Vma21	67048	13.5	13.2	19.4	1.0953	0.407646	1.7841	3.15E-15
chr17:56713932-56717699	Vmac	106639	38.7	27.9	13.4	-1.24514	0.10539	-2.29226	2.26E-16
chr7:41399732-41448641:	Vmn2r57	269902	1.4	0.9	0.2	-1.42226	0.408209	-3.89903	1.97E-05
chr11:86583865-86683822	Vmp1	75909	64.1	125.2	189.3	2.11916	0.000348	3.49662	8.74E-13
chr10:23894688-23905343	Vnn1	22361	8.1	8.5	1.0	1.17093	0.480666	-5.84348	8.95E-25
chr6:57752264-57825125:	Vopp1	232023	38.5	35.6	41.1	1.02688	0.889958	1.331	0.0078186
chr9:106821976-10688099	Vprbp	321006	44.2	49.2	52.2	1.25885	0.114031	1.47276	0.0004412
chr9:44348105-44361670:	Vps11	71732	75.2	65.1	50.5	-1.03214	0.68847	-1.18939	0.0004513
chr19:16615366-16780933	Vps13a	271564	37.6	30.7	25.3	-1.09906	0.274961	-1.18973	0.0060579
chr15:35371546-35931229	Vps13b	666173	100.7	85.2	40.6	-1.05743	0.46411	-1.976	2.99E-41
chr9:67840396-67995634:	Vps13c	320528	62.4	42.8	18.5	-1.30723	0.025203	-2.67169	2.52E-27
chr11:101253707-1012595	Vps25	28084	67.5	55.4	73.6	-1.09048	0.287409	1.36249	3.59E-08
chr5:122354413-12236328	Vps29	56433	78.1	80.9	100.9	1.15866	0.195302	1.60551	5.97E-09
chr7:80269655-80291579:	Vps33b	233405	27.7	24.9	28.4	1.01445	0.918195	1.28149	0.0008532
chr8:85260392-85299497:	Vps35	65114	162.8	165.2	178.0	1.13744	0.146807	1.36293	2.40E-06
chr8:22192860-22218597:	Vps36	70160	40.8	47.3	71.6	1.30117	0.013427	2.18027	4.10E-22
chr8:40511783-40551134:	Vps37a	52348	29.0	34.3	43.1	1.33586	0.062344	1.84041	1.73E-07
chr5:124004641-12403226	Vps37b	330192	13.0	24.1	23.4	2.01247	0.04674	2.08619	0.0074525
chr19:10688815-10714419	Vps37c	107305	25.5	23.2	32.6	1.01646	0.885506	1.59443	2.47E-15
chr5:135072900-13507826	Vps37d	194309	13.9	10.2	5.4	-1.22211	0.223293	-2.0431	6.17E-09
chr2:120316461-12035313	Vps39	269338	53.0	43.2	27.7	-1.09945	0.248724	-1.52675	5.28E-13
chr13:18717292-18866811	Vps41	218035	97.1	82.9	37.1	-1.04904	0.492055	-2.09291	1.30E-56
chr8:107031326-10704575	Vps4a	116733	70.7	76.6	94.2	1.22354	0.155063	1.6571	1.32E-06
chr19:6067842-6077187:-	Vps51	68505	47.5	44.0	32.5	1.03955	0.618351	-1.16637	0.0026945
chr11:76046226-76179630	Vps53	68299	33.9	28.1	39.1	-1.07625	0.476144	1.44127	8.93E-08
chr7:44748629-44777514:	Vrk3	101568	31.8	30.8	18.3	1.08122	0.465175	-1.38735	1.14E-05
chr5:117319266-11735500	Vsig10	231668	45.6	40.3	10.4	-1.00589	0.976536	-3.42905	9.70E-33
chr9:37539255-37544205:	Vsig2	57276	17.2	13.8	8.9	-1.11032	0.517724	-1.53045	0.0001355
chr14:32856756-32939489	Vstm4	320736	19.1	17.8	5.9	1.02187	0.957008	-2.4693	1.60E-05
chr10:14655333-14705489	Vta1	66201	53.9	57.2	64.9	1.19409	0.175487	1.50068	2.25E-05
chr19:55316057-55627461	Vti1a	53611	18.3	15.1	19.2	-1.07642	0.458282	1.3149	4.20E-05
chr12:79156017-79172458	Vti1b	53612	92.0	104.4	132.8	1.27536	0.033171	1.79211	1.29E-11
chr11:78499120-78502325	Vtn	22370	10.0	8.5	3.7	-1.04986	0.859336	-2.10059	3.12E-06
chr4:155768495-15577456	Vwa1	246228	20.3	26.2	24.9	1.45388	0.019993	1.52153	0.0009646
chr19:56874416-56912078	Vwa2	240675	21.9	17.0	9.7	-1.14316	0.419079	-1.7837	4.98E-07
chr7:120739557-12080554	Vwa3a	233813	1.6	1.1	0.4	-1.27949	0.573013	-3.07577	0.000151
chr9:38718268-38743337:	Vwa5a	67776	128.2	121.9	65.0	1.05515	0.729406	-1.57378	1.72E-06
chr16:20589582-20605377	Vwa5b2	328643	2.2	1.2	0.1	-1.53688	0.208712	-13.1846	1.41E-18
chr14:78849178-79202310	Vwa8	219189	40.9	33.1	17.8	-1.10332	0.308227	-1.82424	7.08E-19
chr9:64960832-64986981:	Vwa9	69882	32.1	34.7	41.6	1.21418	0.076824	1.61402	3.87E-09

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr11:11114016-11263526	Vwc2	319922	2.8	1.8	0.2	-1.39361	0.436764	-9.07642	2.96E-12
chr6:125552948-12568667	Vwf	22371	13.0	11.5	4.7	-1.00932	0.962343	-2.17951	5.32E-14
chr14:34673928-34747983	Wapal	218914	83.6	91.8	108.9	1.23918	0.132025	1.61791	5.38E-06
chr12:108860030-1088941	Wars	22375	43.7	45.5	75.4	1.16841	0.087967	2.15239	2.13E-31
chr4:133130633-13319833	Wasf2	242687	49.8	42.0	32.2	-1.06209	0.600314	-1.23478	0.005597
chr5:146385006-14647112	Wasf3	245880	11.4	11.1	13.6	1.09012	0.577976	1.48321	7.80E-05
chr6:83119044-83121461:	Wbp1	22377	68.1	56.3	28.4	-1.08856	0.599123	-1.90044	8.28E-10
chr6:136813654-13682821	Wbp11	60321	46.5	42.4	52.4	1.02875	0.850995	1.40717	5.88E-05
chr11:116078573-1160869	Wbp2	22378	72.8	60.7	34.9	-1.06816	0.55967	-1.65957	6.82E-12
chr15:82298984-82314558	Wbp2nl	74716	2.4	0.2	0.3	-5.08012	0.001289	-4.55639	0.0003197
chr14:79459937-79481268	Wbp4	22380	31.2	35.6	38.6	1.28677	0.06968	1.54135	3.82E-05
chr5:134148058-13417676	Wbscr16	94254	19.9	21.0	40.6	1.19759	0.325523	2.51864	2.82E-13
chr5:135052957-13506466	Wbscr22	66138	32.0	42.8	70.8	1.50349	0.036648	2.69121	1.65E-11
chr5:134987433-13500135	Wbscr25	71304	5.0	0.5	0.6	-6.32887	4.43E-05	-4.48235	0.0001115
chr5:134932373-13494263	Wbscr27	79565	42.9	25.5	2.0	-1.50111	0.161557	-14.5308	1.43E-35
chr5:134901593-13490673	Wbscr28	76629	1.6	0.1	0.1	-5.54944	0.002184	-5.14343	0.0004254
chr1:79702262-79761769:	Wdfy1	69368	48.9	45.9	52.4	1.0521	0.69751	1.33366	0.0003797
chr11:21572281-21898686	Wdpcp	216560	30.2	25.7	10.2	-1.05331	0.690579	-2.35734	1.25E-25
chr5:38526813-38561595:	Wdr1	22388	249.1	302.7	557.2	1.36889	0.089818	2.72856	2.01E-13
chr1:60076868-60098500:	Wdr12	57750	23.1	25.8	63.3	1.25827	0.052362	3.39615	5.76E-46
chrX:8123301-8132858:-	Wdr13	73447	56.3	45.7	37.7	-1.10566	0.218899	-1.19569	0.0031004
chr8:54629616-54724368:	Wdr17	244484	1.3	0.8	0.2	-1.42947	0.369036	-4.55799	3.76E-07
chr10:79960152-79969246	Wdr18	216156	37.3	39.9	68.4	1.20552	0.074183	2.28086	1.88E-27
chr5:65199696-65260415:	Wdr19	213081	25.4	16.9	1.8	-1.34999	0.056133	-10.7377	1.44E-79
chr12:65225517-65228454	Wdr20rt	70948	2.2	0.3	0.4	-5.0603	0.000253	-3.71794	0.0004299
chr17:14818672-14943124	Wdr27	71682	1.4	0.7	0.4	-1.67999	0.216515	-2.73816	0.0015298
chr3:100138180-10016240	Wdr3	269470	51.6	59.7	74.2	1.30603	0.069545	1.78253	1.56E-07
chr4:62452632-62470895:	Wdr31	71354	13.2	8.5	3.6	-1.38806	0.169379	-2.84214	3.87E-09
chr2:30031558-30048879:	Wdr34	71820	32.1	23.8	12.2	-1.2121	0.282075	-2.0655	1.49E-08
chr12:8974001-9028847:+	Wdr35	74682	31.9	23.9	13.9	-1.19663	0.059077	-1.83187	2.53E-17
chr18:32837225-32866420	Wdr36	225348	46.0	51.2	95.9	1.25195	0.049853	2.58257	2.64E-29
chr2:38998309-39001584:	Wdr38	76646	1.2	0.2	0.1	-2.90074	0.069677	-3.7182	0.003864
chr17:31494322-31512487	Wdr4	57773	22.7	26.9	56.0	1.33367	0.019098	3.04969	1.48E-33
chr13:94976344-95023316	Wdr41	218460	25.8	21.4	28.8	-1.07802	0.330948	1.39655	1.47E-10
chr17:71616215-71659031	Wdr43	72515	70.3	112.5	244.7	1.78496	0.01457	4.08705	1.66E-14
chrX:7722220-7728201:+	Wdr45	54636	102.1	78.9	8.6	-1.16709	0.375881	-9.11015	1.88E-71
chr11:121327203-1213544	Wdr45b	66840	59.8	70.5	75.8	1.32905	0.075136	1.5702	0.0001999
chr17:33940723-33949695	Wdr46	57315	21.8	28.5	90.6	1.46961	0.044458	4.98131	4.95E-30
chr9:119894895-11992657	Wdr48	67561	75.9	73.0	37.4	1.07796	0.383372	-1.61969	5.33E-16
chr2:27515147-27536538:	Wdr5	140858	47.7	62.0	87.6	1.46509	0.042261	2.25269	1.10E-08
chr6:83152710-83156379:	Wdr54	75659	7.5	6.0	1.9	-1.11603	0.694107	-2.95378	5.94E-09
chr18:36760239-36763708	Wdr55	67936	34.6	40.1	56.8	1.30039	0.019209	2.03637	4.30E-17
chr8:111448784-11152210	Wdr59	319481	22.5	17.4	9.5	-1.1666	0.422711	-1.87653	2.35E-06
chr12:116207050-1162630	Wdr60	217935	27.2	19.5	9.5	-1.26007	0.136137	-2.25774	1.21E-12
chr9:54717153-54734549:	Wdr61	66317	68.8	82.7	87.3	1.35118	0.010558	1.57922	8.55E-07
chr7:30240138-30280421:	Wdr62	233064	5.0	1.6	1.2	-2.67905	0.000504	-3.01563	4.01E-06
chr3:146040526-14610803	Wdr63	242253	1.7	0.2	0.2	-5.14339	0.000323	-4.20848	0.0001843
chr1:175698593-17581573	Wdr64	75820	2.2	0.1	0.1	-8.89536	6.02E-06	-6.93118	3.85E-06
chr15:7873055-8099209:-	Wdr70	545085	21.4	20.3	31.8	1.06349	0.642969	1.84873	2.21E-14
chr19:8735839-8740624:+	Wdr74	107071	52.1	69.7	160.2	1.50408	0.028044	3.72085	4.76E-21
chr1:45795501-45823613:	Wdr75	73674	57.3	79.0	167.2	1.54936	0.023664	3.52028	1.09E-17
chr3:105959498-10596976	Wdr77	70465	67.8	76.8	139.0	1.27472	0.087187	2.53314	4.19E-19
chr4:103038065-10311429	Wdr78	242584	10.9	8.0	2.3	-1.21523	0.279382	-3.62293	2.53E-22
chr4:154142372-15415681	Wdr8	59002	20.8	19.4	24.9	1.03704	0.786681	1.49297	1.72E-07
chr11:75440943-75454717	Wdr81	192652	19.2	13.4	3.7	-1.29142	0.174567	-4.03012	3.14E-24
chr8:85080963-85082339:	Wdr83os	414077	61.6	57.0	89.1	1.03615	0.759842	1.80502	1.90E-19
chr5:24712269-24730680:	Wdr86	269633	12.6	5.5	0.6	-1.97792	0.037201	-13.0178	1.30E-21
chr12:75630594-75669537	Wdr89	72338	3.3	2.9	4.3	-1.01614	0.961324	1.62182	0.0051491

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr17:25844734-25861515	Wdr90	106618	14.5	11.4	5.8	-1.13028	0.42375	-1.95932	2.10E-10
chr11:17211893-17235200	Wdr92	103784	13.9	12.6	15.2	1.00597	0.967321	1.361	4.69E-05
chr7:79743163-79785950:	Wdr93	626359	2.9	1.3	0.3	-1.81033	0.112728	-6.20572	1.53E-09
chr2:59852365-59882606:	Wdsub1	72137	57.6	39.3	12.4	-1.31752	0.135396	-3.59659	4.70E-21
chr4:133292466-13333931	Wdtc1	230796	26.9	21.6	8.6	-1.11315	0.331572	-2.46457	1.14E-30
chr7:110122059-11014329	Wee1	22390	26.1	22.9	13.1	-1.00276	0.992	-1.57038	0.0004513
chr8:119666365-11968802	Wfdc1	67866	77.7	83.4	41.3	1.19535	0.076234	-1.49794	1.49E-07
chr2:164656046-16465736	Wfdc10	629756	7.2	5.5	1.9	-1.16413	0.789832	-2.54787	0.0086023
chr2:164562716-16456850	Wfdc2	67701	469.2	384.9	165.0	-1.08165	0.848342	-2.1544	0.0011262
chr11:94235952-94242579	Wfikkn2	278507	29.7	23.4	8.1	-1.11119	0.658083	-2.82777	3.58E-12
chr10:128747879-1287665	Wibg	78428	26.0	31.9	47.5	1.37582	0.063661	2.24061	2.44E-10
chr6:54452883-54503768:	Wipf3	330319	3.7	2.7	1.0	-1.25991	0.489509	-2.84827	6.28E-06
chr11:109573521-1096113	Wipi1	52639	50.2	37.6	15.3	-1.20089	0.216625	-2.57928	1.13E-18
chr5:142629584-14266937	Wipi2	74781	78.7	71.7	41.6	1.02225	0.840052	-1.508	2.95E-11
chr15:66891393-66923199	Wisp1	22402	11.1	9.8	38.8	-1.03547	0.940427	3.91704	1.08E-08
chr17:32354050-32389439	Wiz	22404	17.0	16.6	18.3	1.101	0.55711	1.3439	0.0069155
chr3:159839695-15993517	Wls	68151	255.9	197.5	93.2	-1.16413	0.224218	-2.1857	1.63E-18
chrX:151198078-15132019	Wnk3	279561	2.6	2.2	4.2	-1.04164	0.812352	2.03887	3.68E-14
chr7:98835112-98854747:	Wnt11	22411	4.2	3.7	0.6	-1.01758	0.978844	-4.30544	2.75E-05
chr6:22288227-22298522:	Wnt16	93735	46.9	43.1	16.3	1.02712	0.922172	-2.25463	2.23E-08
chr6:17988940-18030445:	Wnt2	22413	3.7	2.8	0.9	-1.1819	0.595628	-3.22265	1.01E-07
chr3:104944805-10496170	Wnt2b	22414	5.0	2.7	1.7	-1.63005	0.026493	-2.35165	7.51E-07
chr14:28505473-28525515	Wnt5a	22418	52.4	39.5	71.3	-1.19231	0.162524	1.69122	9.25E-09
chr6:119432531-11954434	Wnt5b	22419	17.5	24.4	29.8	1.55612	0.052836	2.07051	2.79E-05
chr1:74771892-74785319:	Wnt6	22420	8.8	4.7	0.4	-1.60621	0.224802	-12.994	1.88E-17
chr15:85535437-85581821	Wnt7b	22422	1.1	4.1	2.6	3.26611	0.007213	2.31625	0.0214817
chr11:59306930-59333552	Wnt9a	216795	15.6	28.7	32.9	2.00331	0.04186	2.43475	0.000753
chr8:33234373-33385527:	Wrn	22427	37.1	32.5	11.2	-1.02371	0.820999	-2.62733	1.29E-58
chr11:79239382-79254695	Wsb1	78889	90.6	155.7	129.3	1.90899	0.013794	1.73059	0.0099187
chr5:117357305-11737858	Wsb2	59043	50.0	64.6	82.0	1.4568	0.084132	2.00308	2.29E-05
chr11:71750703-71789646	Wscd1	216881	7.2	5.5	2.9	-1.1791	0.418786	-1.94732	4.22E-06
chr5:113550420-11358972	Wscd2	320916	11.9	12.7	26.5	1.19134	0.219586	2.74126	2.37E-24
chr2:105126529-10517361	Wt1	22431	100.4	112.7	42.7	1.26894	0.206433	-1.85431	7.34E-06
chr17:12966799-12992539	Wtap	60532	43.3	46.5	52.2	1.20883	0.069354	1.50149	2.04E-07
chr7:34109550-34133268:	Wtip	101543	36.5	36.5	47.1	1.12107	0.214984	1.60963	1.69E-13
chr11:35839178-35980089	Wwc1	211652	24.5	20.1	12.0	-1.08484	0.644136	-1.61697	1.99E-05
chr8:114439652-11535271	Wwox	80707	13.4	11.1	7.8	-1.07989	0.625825	-1.37541	0.0021122
chr4:19608300-19709004:	Wwp1	107568	56.8	56.0	80.1	1.10197	0.344492	1.75087	2.39E-15
chr11:72301629-72313733	Xaf1	327959	28.2	28.4	9.5	1.11646	0.676394	-2.31304	4.15E-07
chr11:5520641-5525993:+	Xbp1	22433	181.2	278.0	399.9	1.71994	0.000207	2.70831	3.60E-16
chrX:42067836-42109664:	Xiap	11798	63.9	59.7	44.7	1.04028	0.600285	-1.14525	0.0066308
chrX:9272784-9313245:+	Xk	22439	5.8	5.7	2.9	1.10615	0.603149	-1.58043	0.0004085
chr1:3214482-3671498:-	Xkr4	497097	1.4	0.9	0.5	-1.40203	0.287409	-2.01302	0.0030824
chr8:18932729-18950975:	Xkr5	319581	0.5	0.5	0.2	1.14674	0.730675	-2.20538	0.0046134
chr4:132724904-13273254	Xkr8	381560	10.1	6.5	4.3	-1.39293	0.138777	-1.83304	0.0003229
chrX:73086293-73097095:	Xlr3a	22445	2.4	0.9	0.8	-2.17359	0.041152	-2.27731	0.0054899
chrX:73192179-73202930:	Xlr3b	574437	11.4	4.1	0.2	-2.16902	0.121926	-15.3789	8.33E-13
chr7:102065491-10208376	Xndc1	1.02E+08	10.1	8.5	4.3	-1.07901	0.715358	-1.85642	2.04E-06
chr4:46175222-46196311:	Xpa	22590	45.0	33.2	17.8	-1.22237	0.308941	-1.99349	1.15E-06
chr6:91489307-91515888:	Xpc	22591	65.4	42.4	20.2	-1.3851	0.015501	-2.55726	2.16E-19
chr19:52991180-53038654	Xpnpep1	170750	38.6	38.8	76.5	1.12899	0.309216	2.46322	2.01E-28
chrX:48108725-48136981:	Xpnpep2	170745	10.7	6.4	2.4	-1.4623	0.248465	-3.19811	1.11E-06
chr11:23256041-23297597	Xpo1	103573	99.5	96.8	120.4	1.08348	0.283168	1.51133	2.16E-15
chr14:57582271-57664956	Xpo4	57258	40.8	46.8	66.7	1.29627	0.145072	2.01527	8.77E-08
chr17:46202855-46242299	Xpo5	72322	58.3	63.7	111.7	1.23325	0.163789	2.36908	1.93E-15
chr7:126101719-12620040	Xpo6	74204	51.8	47.4	56.7	1.02959	0.783672	1.36676	5.47E-07
chr10:121587380-1216263	Xpot	73192	39.1	41.0	95.1	1.18442	0.219721	3.00347	8.84E-30
chr1:155275657-15541744	Xpr1	19775	28.2	24.1	19.5	-1.04703	0.458862	-1.15785	0.0006424

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr12:111803193-1118138	Xrcc3	74335	3.1	2.8	1.4	1.02007	0.947823	-1.73425	0.0011403
chr15:82016369-82040084	Xrcc6	14375	49.2	49.5	60.8	1.12376	0.303769	1.53957	5.82E-08
chr9:95954760-96053029:	Xrn1	24127	56.3	51.7	34.5	1.03131	0.74364	-1.30476	3.54E-06
chr2:147013060-14707799	Xrn2	24128	114.1	117.0	157.6	1.15297	0.189873	1.71954	3.72E-12
chr7:99859218-99917824:	Xrra1	446101	5.3	0.2	0.6	-9.52034	1.90E-06	-4.46141	0.0002994
chr16:30955503-31081432	Xxylt1	268880	13.3	12.1	22.4	1.00818	0.962629	2.08675	5.08E-17
chr9:119357381-11939379	Xylb	102448	2.7	1.9	1.3	-1.27872	0.296342	-1.63804	0.0044362
chr7:117380979-11766763	Xylt1	233781	6.4	6.5	2.9	1.13415	0.684248	-1.70114	0.0079024
chr13:17986640-17993351	Yae1d1	67008	25.3	26.1	41.9	1.1551	0.113241	2.05762	1.42E-28
chr15:93283833-93336935	Yaf2	67057	23.6	22.4	29.0	1.07023	0.641771	1.53295	2.73E-06
chr9:7932001-8004596:-	Yap1	22601	101.7	98.6	93.5	1.0849	0.097246	1.14922	0.0001665
chr4:129189795-12921960	Yars	107271	38.9	37.0	164.3	1.06753	0.565775	5.22197	1.14E-123
chr16:16302965-16309640	Yars2	70120	19.9	28.6	52.4	1.61095	0.001774	3.21754	8.97E-22
chr4:119277327-11929451	Ybx1	22608	320.9	308.3	410.6	1.07595	0.568988	1.5923	2.24E-08
chr11:69935899-69941599	Ybx2	53422	19.0	2.9	2.5	-4.67014	3.32E-05	-4.74569	1.15E-06
chr6:131364858-13138845	Ybx3	56449	115.7	95.5	218.1	-1.07856	0.560704	2.3451	3.72E-25
chr16:17146967-17148857	Ydjc	69101	3.1	2.6	8.7	-1.05618	0.867424	3.3572	8.85E-14
chr10:117215141-1172245	Yeats4	64050	30.2	31.1	38.2	1.14993	0.204199	1.57804	4.56E-09
chr19:5088538-5092879:+	Yif1a	68090	55.3	56.5	89.7	1.1473	0.211309	2.01814	7.89E-20
chr7:29238323-29247532:	Yif1b	77254	50.7	46.5	74.8	1.02497	0.824949	1.83858	6.53E-24
chr4:107314363-10735982	Yipf1	230584	66.6	53.6	37.1	-1.1156	0.304932	-1.43383	2.41E-06
chr9:21588682-21592831:	Yipf2	74766	40.0	29.1	22.1	-1.23523	0.105072	-1.44029	0.0002138
chr17:74489493-74500277	Yipf4	67864	58.0	58.3	56.3	1.12655	0.172907	1.21071	0.0033602
chr18:40204865-40219399	Yipf5	67180	42.2	46.6	72.2	1.24527	0.111162	2.11962	8.18E-14
chrX:98937781-98949020:	Yipf6	77929	35.3	33.5	41.5	1.06399	0.510252	1.4665	6.04E-10
chr11:5955758-5967781:+	Ykt6	56418	51.2	68.4	127.6	1.50106	0.080627	2.98399	2.36E-10
chr2:23156505-23199260:	Yme1l1	27377	136.5	142.6	167.2	1.17347	0.12143	1.52536	3.28E-08
chr1:130717327-13072205	Yod1	226418	25.0	25.8	29.3	1.16001	0.210737	1.458	1.12E-05
chr16:17070139-17086736	Ypel1	106369	19.0	11.3	0.9	-1.49405	0.113667	-13.7505	4.31E-39
chr11:86936425-86993762	Ypel2	77864	48.2	37.7	12.7	-1.14646	0.401038	-2.96111	2.33E-22
chr7:126776975-12678051	Ypel3	66090	154.6	116.6	9.0	-1.19415	0.291567	-13.0258	5.82E-94
chr2:84734204-84737877:	Ypel4	241525	57.5	46.9	1.3	-1.10896	0.844823	-20.4819	1.51E-22
chr17:72836704-72851195	Ypel5	383295	42.6	33.5	9.8	-1.14652	0.426573	-3.4128	3.05E-25
chr4:124850759-12485524	Yrdc	230734	21.6	41.9	74.5	2.12974	0.007475	3.94568	8.40E-10
chr5:86804490-86836657:	Ythdc1	231386	144.6	141.4	93.3	1.09668	0.292208	-1.23681	0.0007946
chr18:44828665-44889720	Ythdc2	240255	16.2	16.9	21.3	1.173	0.055955	1.6371	8.64E-16
chr2:180904377-18092093	Ythdf1	228994	46.7	60.8	69.4	1.4673	0.051851	1.82744	6.26E-05
chr4:132184916-13221225	Ythdf2	213541	45.8	62.2	77.6	1.52778	0.046852	2.06572	8.22E-06
chr3:16183183-16217037:	Ythdf3	229096	95.6	104.7	113.7	1.23425	0.068197	1.48135	6.43E-06
chr2:163995197-16401858	Ywhab	54401	119.1	118.8	170.3	1.12108	0.236885	1.78143	2.27E-17
chr11:75732887-75765841	Ywhae	22627	132.6	145.6	255.8	1.23871	0.140298	2.38449	1.56E-16
chr5:135908379-13593464	Ywhag	22628	52.0	59.9	91.4	1.29803	0.1207	2.16335	4.60E-10
chr12:21390329-21417436	Ywhaq	22630	237.6	252.5	298.6	1.19055	0.085469	1.56392	2.96E-09
chr15:36770262-36796929	Ywhaz	22631	129.5	140.8	186.1	1.22697	0.191034	1.77839	4.26E-07
chrX:157566119-15756898	Yy2	1E+08	7.9	8.5	8.8	1.19586	0.120135	1.3889	0.0001084
chr1:36761798-36782820:	Zap70	22637	2.4	4.6	6.4	1.87367	0.171693	2.74664	0.003265
chr3:75037907-75143723:	Zbbx	213234	5.6	0.3	0.7	-10.0293	5.84E-07	-4.75013	0.0001025
chr15:88751711-88784516	Zbed4	223773	7.8	9.4	9.3	1.36286	0.04864	1.48431	0.0010893
chr5:129895723-12990362	Zbed5	71970	12.9	8.6	2.2	-1.33529	0.457195	-3.96845	2.76E-07
chr9:48654297-48835945:	Zbtb16	235320	10.8	31.2	2.6	2.74861	0.01349	-2.78537	0.0018851
chr4:141444673-14146793	Zbtb17	22642	24.5	26.8	30.4	1.22986	0.07507	1.54663	4.92E-07
chr16:42907645-43619123	Zbtb20	56490	151.6	128.0	34.5	-1.05775	0.719227	-3.45869	4.31E-40
chr17:33916176-33919325	Zbtb22	81630	36.9	31.6	37.1	-1.04545	0.600354	1.25784	2.07E-05
chr9:96685423-96731675:	Zbtb38	245007	80.0	52.0	35.2	-1.38159	0.141799	-1.78047	0.0004739
chr11:69765912-69784026	Zbtb4	75580	71.1	54.5	29.8	-1.17085	0.16417	-1.8943	8.03E-15
chr4:136979732-13704869	Zbtb40	230848	16.2	14.0	9.1	-1.0392	0.814283	-1.42048	0.0002684
chr1:139422383-13945300	Zbtb41	226470	31.7	31.6	35.3	1.11912	0.18418	1.38986	8.12E-08
chr9:31030644-31075885:	Zbtb44	235132	48.4	38.6	23.6	-1.12532	0.324635	-1.62951	7.16E-09

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr4:152019776-15202767	Zbtb48	100090	16.2	18.6	21.3	1.29997	0.154251	1.63384	0.0003339
chr4:44991243-45012412:	Zbtb5	230119	17.1	12.4	8.6	-1.2328	0.127222	-1.57617	9.59E-06
chr2:37425500-37430919:	Zbtb6	241322	31.4	33.1	36.3	1.18391	0.165856	1.44176	4.65E-05
chr3:89377646-89393203:	Zbtb7b	22724	22.2	21.7	29.9	1.09859	0.479442	1.67716	4.99E-09
chr18:75820178-76148564	Zbtb7c	207259	9.3	6.5	2.9	-1.27992	0.409728	-2.46322	1.76E-05
chr17:26973179-26976203	Zbtb9	474156	27.3	28.7	31.4	1.1853	0.144842	1.43323	2.96E-05
chr3:7503426-7553848:+	Zc2hc1a	67306	44.0	35.5	20.8	-1.12081	0.541672	-1.67777	3.13E-05
chr10:128543565-1285477	Zc3h10	103284	25.1	28.9	32.9	1.29812	0.130228	1.62283	0.0001701
chr2:83644578-83664616:	Zc3h15	69082	99.2	125.4	156.2	1.42326	0.037338	1.94084	2.94E-07
chr8:122376616-12241736	Zc3h18	76014	43.1	50.2	60.1	1.31538	0.118215	1.7243	3.37E-05
chr2:128967402-12901856	Zc3h6	78751	19.0	8.2	3.9	-2.01164	0.034517	-3.44661	1.14E-06
chr16:11136594-11176393	Zc3h7a	106205	70.9	80.3	87.3	1.27232	0.03924	1.53031	1.81E-06
chr2:128926268-12894402	Zc3h8	57432	12.7	10.5	18.0	-1.0792	0.713579	1.76437	4.02E-06
chr6:38287394-38299259:	Zc3hav1l	209032	14.0	8.4	5.6	-1.48987	0.188233	-1.91714	0.0040652
chr6:30366388-30391010:	Zc3hc1	232679	32.2	35.4	43.9	1.23311	0.107359	1.69426	3.58E-08
chrX:95639194-95658509:	Zc4h2	245522	14.6	11.5	5.1	-1.15338	0.543035	-2.23259	3.25E-07
chr11:53324689-53333301	Zcchc10	67966	7.6	9.0	12.9	1.3302	0.146211	2.07584	2.27E-07
chr4:108459426-10855941	Zcchc11	230594	46.5	39.9	27.7	-1.04255	0.644359	-1.33999	2.91E-07
chrX:103630586-10363166	Zcchc13	75064	2.1	0.4	0.2	-2.91512	0.073967	-4.0368	0.002484
chr4:130316085-13035994	Zcchc17	619605	51.1	55.0	61.3	1.20621	0.004087	1.50013	1.83E-15
chrX:136993155-13699692	Zcchc18	66995	8.0	6.4	2.1	-1.12656	0.484699	-2.92412	1.24E-18
chr14:25711640-25768856	Zcchc24	71918	104.7	98.1	114.1	1.04736	0.599172	1.36124	4.47E-08
chr13:59771879-59823147	Zcchc6	214290	80.6	71.7	54.1	-1.0027	0.973695	-1.19253	4.49E-05
chr13:91796533-91807696	Zcchc9	69085	40.2	40.6	56.1	1.14187	0.473681	1.7284	1.26E-05
chr15:93386113-93398290	Zcrb1	67197	67.6	73.3	100.7	1.22281	0.229392	1.84156	3.55E-07
chr5:137787802-13782262	Zcwpw1	381678	7.3	7.1	3.6	1.07859	0.703912	-1.60436	0.0002329
chr8:105472425-10549687	Zdhhc1	70796	95.1	72.9	29.5	-1.17168	0.332355	-2.53246	4.28E-16
chr2:30090944-30093635:	Zdhhc12	66220	10.8	7.4	12.0	-1.30687	0.078527	1.37852	0.0030691
chr7:48789003-48827437:	Zdhhc13	243983	32.6	38.6	49.8	1.33369	0.04652	1.89435	4.18E-09
chr17:5492600-5753891:+	Zdhhc14	224454	7.6	6.8	4.4	1.00058	0.998371	-1.37056	0.0029392
chr19:41933472-41944103	Zdhhc16	74168	41.0	45.1	56.5	1.23936	0.103661	1.71338	3.10E-08
chr4:133606992-13363342	Zdhhc18	503610	21.0	24.4	28.7	1.30742	0.0712	1.68984	2.48E-06
chr16:32496281-32507214	Zdhhc19	245308	1.8	0.0	0.1	-6.92902	0.000383	-4.62117	0.0010292
chr4:82798738-82859661:	Zdhhc21	68268	13.6	13.0	17.6	1.06931	0.587453	1.61822	9.33E-10
chr16:43969146-43979050	Zdhhc23	332175	2.3	3.5	3.7	1.61932	0.076268	1.88556	0.0019911
chr15:88600302-88601669	Zdhhc25	70073	1.2	0.0	0.2	-4.92385	0.005328	-2.54704	0.0541733
chr9:123072310-12311320	Zdhhc3	69035	24.3	22.9	32.1	1.05639	0.549892	1.65148	9.33E-18
chr2:84687920-84715164:	Zdhhc5	228136	53.1	59.7	96.8	1.2723	0.19469	2.23966	1.76E-09
chr19:55298296-55316032	Zdhhc6	66980	56.5	56.2	55.5	1.11415	0.096815	1.22922	2.03E-05
chr8:120081095-12010147	Zdhhc7	102193	28.8	30.6	32.6	1.19672	0.144193	1.40932	0.0001768
chr18:5591860-5775468:+	Zeb1	21417	64.4	60.3	85.7	1.04874	0.522968	1.6626	3.36E-26
chr2:44983512-45113279:	Zeb2	24136	72.2	54.4	114.2	-1.19109	0.166318	1.96267	1.52E-13
chr2:30097283-30124611:	Zer1	227693	42.5	29.2	10.1	-1.30186	0.094821	-3.2975	1.84E-24
chr3:10339956-10351301:	Zfand1	66361	33.7	22.5	13.1	-1.34844	0.077506	-2.02809	3.28E-08
chr5:139471216-13948449	Zfand2a	100494	20.6	27.1	33.0	1.48126	0.017165	1.98074	9.25E-08
chr17:30005087-30210020	Zfand3	21769	52.9	44.8	53.5	-1.05884	0.43266	1.26359	1.98E-06
chr6:116264219-11633030	Zfand4	67492	6.7	3.0	1.9	-1.9503	0.003396	-2.64828	1.94E-07
chr19:21272278-21286840	Zfand5	22682	60.6	59.0	69.2	1.08995	0.380823	1.42482	1.93E-07
chr7:84615054-84679351:	Zfand6	65098	128.1	124.0	64.7	1.08194	0.154506	-1.58223	4.34E-29
chr8:108714644-10896163	Zfhx3	11906	14.9	13.9	6.6	1.04696	0.771256	-1.80056	4.08E-10
chr17:33380179-33394637	Zfp101	22643	36.5	28.8	14.6	-1.13996	0.374246	-1.97492	3.55E-11
chr9:122923078-12293102	Zfp105	22646	29.1	24.9	36.3	-1.04214	0.644407	1.55936	4.18E-17
chr2:120506830-12056383	Zfp106	20402	72.4	68.2	87.5	1.05881	0.557522	1.50832	6.12E-11
chr7:24254794-24262444:	Zfp108	54678	17.7	12.3	5.4	-1.29021	0.381923	-2.4713	1.04E-05
chr7:24112320-24127952:	Zfp112	57745	14.2	10.4	6.9	-1.2287	0.374705	-1.61795	0.0037314
chr5:138139702-13815574	Zfp113	56314	21.2	15.4	8.8	-1.23852	0.206248	-1.89168	2.26E-07
chr7:24175045-24182318:	Zfp114	232966	2.3	2.1	0.6	1.00543	0.992359	-2.67136	0.0003806
chr5:143235163-14324883	Zfp12	231866	39.2	35.1	26.9	-1.00205	0.984192	-1.16312	0.0064589

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr2:150114407-15013667	Zfp120	104348	22.0	18.3	10.7	-1.09156	0.70781	-1.63011	0.0008113
chr7:12881178-12893422:	Zfp128	243833	14.2	10.2	6.1	-1.25682	0.324455	-1.80944	0.0003811
chr13:119765186-1197911	Zfp131	72465	34.3	55.2	77.7	1.79082	0.021088	2.6921	4.40E-07
chr2:144459280-14446779	Zfp133-ps	668917	3.6	2.9	0.8	-1.10693	0.802318	-3.20332	1.03E-05
chr7:30036359-30051396:	Zfp14	243906	16.7	13.4	5.2	-1.12342	0.603847	-2.51191	2.50E-10
chr1:74565128-74588028:	Zfp142	77264	17.5	16.5	17.6	1.05779	0.673092	1.25623	0.0071702
chr7:110061702-11009539	Zfp143	20841	38.0	34.9	47.2	1.02884	0.805063	1.55125	1.95E-11
chr7:30161268-30169727:	Zfp146	26465	120.0	138.4	148.5	1.30024	0.038421	1.53975	8.89E-06
chr5:138441476-13846069	Zfp157	72154	28.0	23.0	14.4	-1.10323	0.598273	-1.54414	0.0003819
chr16:3847223-3858880:+	Zfp174	385674	7.7	4.9	2.1	-1.39998	0.293025	-2.76625	9.43E-06
chr7:24081897-24107708:	Zfp180	210135	32.2	35.3	35.9	1.23375	0.093599	1.39038	0.0005003
chrX:21026184-21062038:	Zfp182	319535	22.7	18.5	7.6	-1.09899	0.315283	-2.36781	6.85E-38
chr13:21945094-21960485	Zfp184	193452	21.3	16.9	8.1	-1.12021	0.444221	-2.08298	8.85E-13
chrX:72987339-73031543:	Zfp185	22673	12.0	8.5	4.3	-1.24918	0.437053	-2.13114	0.0001514
chr4:49521176-49531558:	Zfp189	230162	19.2	17.6	10.7	1.02209	0.848342	-1.4403	3.02E-08
chr18:24012267-24020771	Zfp191	59057	48.8	54.6	54.7	1.25864	0.116492	1.39211	0.0030062
chr11:50898712-50916176	Zfp2	22678	19.9	14.1	6.3	-1.26488	0.146843	-2.48463	4.21E-14
chr9:40192316-40213604:	Zfp202	80902	12.8	12.5	23.3	1.08904	0.409351	2.26177	4.28E-34
chr11:80383279-80405873	Zfp207	22680	208.8	216.1	222.9	1.16588	0.135917	1.33253	0.0001905
chr6:47920568-47932637:	Zfp212	232784	29.7	25.8	15.0	-1.02727	0.764222	-1.58298	4.48E-17
chr17:23556767-23564226	Zfp213	449521	19.6	18.8	23.5	1.07367	0.443247	1.49621	3.77E-11
chr2:170108643-17014267	Zfp217	228913	34.4	22.4	18.8	-1.37944	0.076062	-1.45214	0.0077337
chr17:21733724-21748969	Zfp229	381067	23.2	18.3	10.6	-1.14704	0.504005	-1.71891	0.0001013
chr7:24134163-24143241:	Zfp235	56525	18.7	16.0	10.9	-1.05088	0.779446	-1.36616	0.0039221
chr18:82593597-82692734	Zfp236	329002	28.7	27.0	26.6	1.05617	0.489627	1.16281	0.005586
chr7:30095076-30107614:	Zfp260	26466	87.4	90.2	46.7	1.15729	0.038935	-1.49498	7.75E-14
chr16:3744099-3750788:+	Zfp263	74120	57.0	61.7	61.7	1.21994	0.089242	1.35071	0.0007062
chr7:29893337-29906532:	Zfp27	22689	17.1	15.5	16.0	1.01135	0.916116	1.16871	0.0069155
chr13:67813816-67827000	Zfp273	212569	12.7	8.0	5.0	-1.41952	0.283192	-1.9379	0.0056235
chr12:40315046-40445790	Zfp277	246196	36.3	31.2	22.5	-1.0484	0.755903	-1.28846	0.0070466
chr7:6383318-6396637:+	Zfp28	22690	13.7	8.9	5.7	-1.38242	0.06733	-1.88492	2.35E-06
chr10:76032612-76042969	Zfp280b	64453	11.5	12.1	14.4	1.17693	0.161372	1.56307	1.17E-07
chrX:48541626-48594452:	Zfp280c	208968	22.6	20.7	27.9	1.02721	0.804376	1.53947	1.90E-12
chr9:72274899-72363771:	Zfp280d	235469	68.8	66.4	63.8	1.08304	0.280515	1.16003	0.0057717
chr1:136624901-13663039	Zfp281	226442	33.0	38.6	46.5	1.3127	0.013303	1.74995	5.45E-11
chr11:62778387-62789417	Zfp286	192651	24.4	19.9	14.9	-1.09617	0.417141	-1.30786	0.0007663
chr11:62711486-62729093	Zfp287	170740	17.7	12.9	9.0	-1.23157	0.248724	-1.55292	0.0008543
chr4:34803110-34882948:	Zfp292	30046	67.0	55.0	30.3	-1.09885	0.480864	-1.76175	2.81E-10
chr7:29784790-29794540:	Zfp30	22693	16.6	11.8	4.0	-1.25926	0.103397	-3.22672	1.39E-26
chrX:21079150-21089229:	Zfp300	245368	5.6	4.2	1.9	-1.21251	0.371326	-2.26761	9.58E-08
chr9:19622091-19649731:	Zfp317	244713	66.5	69.2	65.5	1.16827	0.057484	1.23052	0.0009537
chr8:82763620-82774126:	Zfp330	30932	80.1	79.8	96.2	1.11804	0.292972	1.4974	5.92E-08
chr2:164891892-16491175	Zfp335	329559	32.2	34.3	38.6	1.20274	0.211861	1.4923	0.0002144
chr18:23989634-24005371	Zfp35	22694	19.4	20.5	21.5	1.19062	0.271717	1.37572	0.0058427
chr11:51059257-51072799	Zfp354a	21408	11.1	8.7	4.3	-1.15238	0.366158	-2.03744	1.51E-10
chr11:50921786-50931635	Zfp354b	27274	8.0	5.8	3.2	-1.23292	0.382441	-1.9628	8.14E-05
chr11:50811085-50827731	Zfp354c	30944	27.2	22.0	10.8	-1.10721	0.259557	-2.00062	6.51E-27
chr8:3493138-3497208:+	Zfp358	140482	39.8	34.7	24.4	-1.02586	0.83333	-1.3001	0.0002148
chr7:28376784-28379228:	Zfp36	22695	39.0	93.4	59.6	2.5895	7.93E-06	1.85504	0.0010893
chr4:128773085-12880611	Zfp362	230761	18.7	14.5	10.9	-1.14907	0.391083	-1.36463	0.0072871
chr13:64133057-64153199	Zfp367	238673	15.2	13.7	8.1	-1.00321	0.990642	-1.49797	0.002353
chr13:65278854-65297795	Zfp369	170936	52.2	44.1	17.7	-1.06368	0.646466	-2.34146	9.26E-24
chr7:29908517-29916813:	Zfp383	73729	25.6	21.9	13.6	-1.03982	0.816254	-1.4958	4.71E-05
chr6:125009238-12503787	Zfp384	269800	32.3	36.0	35.8	1.2597	0.119494	1.38037	0.0042936
chr2:77410627-77816816:	Zfp385b	241494	2.4	2.8	4.0	1.25954	0.361651	2.03564	4.55E-05
chr12:116047724-1160632	Zfp386	56220	54.0	39.7	26.3	-1.22733	0.305884	-1.62133	0.0008198
chr14:65358676-65398930	Zfp395	380912	19.6	11.5	2.4	-1.5115	0.185982	-5.64952	2.77E-14
chr17:23173869-23193228	Zfp40	22700	20.9	14.6	9.1	-1.29264	0.311119	-1.80312	0.0013034

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr18:84207702-84589504	Zfp407	240476	27.5	26.7	37.2	1.09347	0.322369	1.69085	3.13E-17
chr7:24507087-24515682:	Zfp428	232969	4.5	4.1	8.9	1.00462	0.989875	2.3718	1.21E-07
chr2:150407137-15045149	Zfp442	668923	20.4	16.2	8.7	-1.14144	0.680846	-1.81986	0.0034739
chr7:6172513-6193104:+	Zfp444	72667	11.4	9.8	4.4	-1.04467	0.803291	-2.05031	5.16E-12
chr11:50872723-50887443	Zfp454	237758	6.3	4.5	1.4	-1.24308	0.575051	-3.19641	7.84E-06
chr13:67194506-67209298	Zfp455	218311	9.2	7.8	3.9	-1.07448	0.824787	-1.85686	0.0012838
chr13:67254918-67269068	Zfp458	238690	7.6	5.3	3.7	-1.30067	0.220833	-1.62554	0.0023159
chr13:67405713-67421418	Zfp459	328274	2.6	2.1	1.3	-1.10672	0.699086	-1.5671	0.0080803
chr4:136286069-13629394	Zfp46	22704	24.0	20.2	15.2	-1.06608	0.632043	-1.25683	0.0090046
chr4:54947945-55083563:	Zfp462	242466	10.0	10.7	5.5	1.21357	0.194896	-1.44885	0.0008656
chr6:48427692-48445825:	Zfp467	68910	19.3	12.8	4.9	-1.3575	0.091592	-3.04995	2.13E-16
chr18:52615915-52639830	Zfp474	66758	2.2	0.2	0.3	-5.76249	0.00096	-3.96538	0.0020396
chr7:35772346-35802989:	Zfp507	668501	31.4	26.9	29.9	-1.04778	0.636214	1.18889	0.0066722
chr7:140036391-14004060	Zfp511	69752	35.5	37.6	36.8	1.18856	0.063722	1.29856	0.000196
chr5:31452436-31481753:	Zfp512	269639	59.8	50.1	34.5	-1.0678	0.519702	-1.38341	1.99E-06
chr5:31198981-31202303:	Zfp513	101023	12.6	15.2	20.6	1.36305	0.177872	2.00166	3.80E-05
chr18:82910879-83005314	Zfp516	329003	50.5	46.9	23.2	1.03946	0.654363	-1.735	1.14E-24
chr19:40894705-40917947	Zfp518a	72672	26.0	25.3	27.3	1.08896	0.245271	1.30897	2.44E-07
chr5:38668484-38684826:	Zfp518b	100515	8.4	7.6	11.0	1.01638	0.898625	1.62756	3.09E-13
chr18:13687014-13972733	Zfp521	225207	45.7	33.6	8.4	-1.22184	0.337248	-4.16316	7.89E-23
chr18:65580230-65689436	Zfp532	328977	47.8	36.4	29.8	-1.17868	0.174567	-1.27788	0.0070909
chr7:16071942-16096328:	Zfp541	666528	2.2	0.1	0.3	-7.57886	3.60E-05	-4.48093	0.000393
chr7:12415149-12422491:	Zfp551	619331	17.0	12.1	4.3	-1.26459	0.38053	-2.99983	5.21E-09
chr7:127233443-12723786	Zfp553	233887	30.6	34.4	35.0	1.26502	0.071901	1.424	0.0003683
chr9:18454054-18473559:	Zfp558	72230	6.6	4.5	3.1	-1.30377	0.199845	-1.648	0.0011846
chr9:20345136-20385158:	Zfp560	434377	13.3	10.7	6.4	-1.12213	0.567341	-1.64667	0.0001883
chr7:30077337-30090510:	Zfp566	72556	9.9	7.8	11.4	-1.13628	0.467763	1.42535	0.0025324
chr7:29983955-30028282:	Zfp568	243905	15.5	18.3	21.8	1.33589	0.056491	1.74645	1.14E-06
chr7:4992852-4996101:-	Zfp579	68490	7.6	6.4	3.9	-1.0594	0.771007	-1.54087	0.0004654
chr4:134243306-13424559	Zfp593	68040	9.1	18.3	32.8	2.20017	0.001071	4.1706	4.28E-13
chr17:24669752-24682016	Zfp598	213753	42.0	54.5	71.8	1.46508	0.075354	2.09164	5.04E-06
chr7:27731409-27751689:	Zfp60	22718	30.6	25.7	16.8	-1.07191	0.597324	-1.4537	1.28E-05
chr7:12478305-12496235:	Zfp606	67370	29.9	23.5	16.0	-1.14277	0.295439	-1.49175	1.15E-05
chr7:27860585-27880825:	Zfp607	545938	21.1	15.4	9.6	-1.23575	0.339946	-1.72773	0.0005801
chr18:54888045-54990180	Zfp608	269023	28.4	15.5	10.0	-1.61865	0.136115	-2.12944	0.0019597
chr9:65691583-65827564:	Zfp609	214812	18.4	13.2	9.8	-1.25215	0.108383	-1.49688	0.0001333
chr7:24291046-24299549:	Zfp61	22719	23.7	16.8	11.2	-1.27119	0.193003	-1.67921	0.0001438
chr8:110079734-11009275	Zfp612	234725	18.4	15.2	10.8	-1.07627	0.633093	-1.35604	0.0023573
chr15:75940952-75949400	Zfp623	78834	27.6	31.5	33.3	1.28673	0.092771	1.49844	0.0003512
chr6:117841242-11784595	Zfp637	232337	70.8	62.7	44.8	-1.01016	0.937769	-1.26123	0.0008086
chr15:98286122-98296083	Zfp641	239652	9.6	6.9	4.3	-1.23662	0.24191	-1.74227	2.89E-05
chr7:127877701-12788599	Zfp646	233905	48.2	39.1	31.2	-1.10395	0.269733	-1.23118	0.0014155
chr7:43562370-43575461:	Zfp658	210104	12.0	9.8	5.2	-1.1053	0.627398	-1.80667	9.86E-06
chr7:6286580-6307883:+	Zfp667	384763	11.0	8.6	2.2	-1.16111	0.49094	-3.91257	1.01E-19
chr11:58315114-58330339	Zfp672	319475	35.3	41.6	37.5	1.32395	0.001952	1.32549	0.0001827
chr17:21383748-21399265	Zfp677	210503	19.2	15.1	8.5	-1.15168	0.56186	-1.78335	0.000355
chr7:127418966-12742203	Zfp688	69234	24.0	15.0	10.0	-1.43028	0.162756	-1.86217	0.0012665
chr7:127442136-12744915	Zfp689	71131	6.5	5.8	7.6	1.0027	0.987505	1.46117	7.59E-06
chr3:98382481-98431949:	Zfp697	242109	4.0	2.5	1.0	-1.41232	0.306959	-2.80089	2.57E-05
chr15:76879276-76892394	Zfp7	223669	33.0	27.7	20.1	-1.06126	0.704995	-1.31231	0.0060496
chr8:26977336-26981462:	Zfp703	353310	7.9	7.4	15.2	1.03966	0.887217	2.34709	5.59E-09
chr3:9427010-9610085:-	Zfp704	170753	56.3	45.0	16.9	-1.11775	0.265772	-2.64173	7.08E-44
chr15:36997027-37007402	Zfp706	68036	44.8	44.3	50.5	1.11735	0.425111	1.40466	0.000459
chr15:75969185-75975865	Zfp707	69020	22.8	17.1	10.2	-1.18968	0.419079	-1.75919	0.0001882
chr13:67038594-67061170	Zfp712	78251	13.2	11.0	5.0	-1.08897	0.738048	-2.0532	4.42E-06
chr7:43296523-43313261:	Zfp715	69930	37.6	41.9	39.1	1.25125	0.00409	1.297	4.24E-05
chr7:43579586-43593710:	Zfp719	210105	22.5	25.9	27.3	1.29615	0.039815	1.50834	2.08E-05
chr13:67667441-67683512	Zfp738	408068	30.8	30.2	20.0	1.09431	0.269345	-1.23178	0.0004683

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr15:102203645-1022156	Zfp740	68744	100.3	83.4	50.3	-1.07802	0.38135	-1.59058	3.78E-15
chr6:48062395-48086593:	Zfp746	69228	25.0	28.7	33.0	1.29878	0.094173	1.63972	2.38E-05
chr13:67128228-67141787	Zfp759	268670	14.0	9.2	4.4	-1.36389	0.264993	-2.42655	1.06E-05
chr17:21707741-21725636	Zfp760	240034	28.9	22.1	11.0	-1.17864	0.338231	-2.08591	1.12E-09
chr17:33016864-33033381	Zfp763	73451	29.4	21.0	9.9	-1.26785	0.361486	-2.30779	4.82E-06
chr2:114193461-11420143	Zfp770	228491	19.4	15.8	20.9	-1.10408	0.496367	1.34467	0.0027309
chr7:7130678-7136755:-	Zfp773	76373	2.6	2.0	0.6	-1.17859	0.615866	-3.23274	1.96E-07
chr6:48613180-48623227:	Zfp775	243372	8.9	5.4	2.4	-1.45093	0.314731	-2.6937	0.0002015
chr6:48024188-48048114:	Zfp777	72306	27.3	27.3	31.7	1.12552	0.296229	1.44741	3.65E-06
chr7:6363308-6382605:+	Zfp78	330463	2.8	2.2	1.2	-1.14788	0.581727	-1.86894	0.0002083
chr7:27959800-27979157:	Zfp780b	338354	23.3	21.7	14.2	1.04447	0.55469	-1.30613	4.28E-08
chr10:81901911-81930480	Zfp781	331188	1.8	1.4	0.8	-1.19112	0.489627	-1.86592	0.0005227
chr10:81742821-81771142	Zfp781	331188	3.6	2.9	1.8	-1.12186	0.568475	-1.61612	0.0004417
chr7:5034446-5038446:-	Zfp784	654801	12.8	8.3	5.0	-1.3836	0.217512	-1.97353	0.0004744
chr7:6131489-6155971:-	Zfp787	67109	25.3	28.0	26.9	1.24533	0.122832	1.32503	0.0094973
chr7:41633531-41651532:	Zfp788	67607	36.5	29.6	19.2	-1.10975	0.511594	-1.51225	0.0001175
chr8:85109167-85123095:	Zfp791	244556	7.9	5.3	2.1	-1.33079	0.290212	-2.8157	1.50E-07
chr17:32815453-32830261	Zfp799	240064	22.1	15.5	6.9	-1.28873	0.285905	-2.4962	6.15E-08
chr6:28239931-28261601:	Zfp800	627049	27.1	38.2	40.8	1.58475	0.035544	1.84131	0.0003248
chr13:62129890-62173936	Zfp808	630579	14.1	10.9	2.6	-1.16372	0.47046	-4.12541	4.51E-22
chr9:22225703-22243354:	Zfp809	235047	44.1	44.2	49.8	1.12654	0.32845	1.40722	7.46E-05
chr9:22276748-22307638:	Zfp810	235050	18.6	11.3	8.1	-1.47617	0.067468	-1.80458	0.0002837
chr17:32795676-32809931	Zfp811	240063	7.0	5.3	1.3	-1.18828	0.57515	-4.05018	9.66E-12
chr17:21816876-21845759	Zfp820	75424	8.6	6.7	2.0	-1.16027	0.6063	-3.22802	5.63E-10
chr13:74480057-74493950	Zfp825	235956	28.8	27.2	14.4	1.04454	0.832188	-1.58312	0.0001492
chr11:82764345-82767622	Zfp830	66983	25.2	30.8	28.0	1.37476	0.02588	1.38324	0.0040414
chr13:67747800-67755134	Zfp85	22746	18.6	13.3	8.6	-1.26287	0.268538	-1.69994	0.0005517
chr6:48504339-48534832:	Zfp862-ps	58894	15.5	10.5	8.3	-1.32102	0.107643	-1.48254	0.0028117
chr7:5020376-5033223:+	Zfp865	319748	10.6	10.7	12.1	1.13221	0.323298	1.4195	7.47E-05
chr11:59461197-59472474	Zfp867	237775	25.0	22.1	12.9	-1.01605	0.912903	-1.55029	3.23E-08
chr13:67515782-67526231	Zfp87	170763	26.8	24.5	17.9	1.0226	0.81917	-1.19717	0.0020065
chr17:32765497-32788287	Zfp871	208292	60.6	55.6	32.4	1.02739	0.741853	-1.49493	2.42E-16
chr10:82048127-82061586	Zfp873	408062	21.1	14.9	8.4	-1.27334	0.183837	-1.97276	3.99E-07
chr13:67440431-67451624	Zfp874a	238692	35.7	30.1	8.0	-1.07492	0.793037	-3.42074	2.57E-14
chr13:67471513-67484253	Zfp874b	408067	45.9	40.5	5.9	-1.02953	0.93485	-5.71564	5.93E-21
chr11:50832031-50841552	Zfp879	214779	6.2	4.2	1.7	-1.31946	0.386877	-2.7021	1.40E-05
chr8:71908606-71918851:	Zfp882	382019	19.9	17.0	10.1	-1.05902	0.74363	-1.57343	2.36E-05
chr6:118461950-11847927	Zfp9	22750	19.2	15.8	22.5	-1.09718	0.515883	1.46079	6.33E-05
chr8:106415339-10642588	Zfp90	22751	32.8	25.1	15.1	-1.1798	0.357868	-1.72162	1.91E-05
chr19:12766939-12796123	Zfp91	109910	45.6	42.8	52.5	1.05387	0.567421	1.43886	6.68E-10
chr7:24270418-24277794:	Zfp93	22755	20.5	14.8	8.1	-1.25544	0.32967	-1.9895	3.61E-05
chr2:178066878-17807842	Zfp931	353208	29.3	24.5	15.1	-1.07976	0.693205	-1.54132	0.0004026
chr5:109996527-11001041	Zfp932	69504	38.8	32.1	22.7	-1.08515	0.467797	-1.36591	5.85E-05
chr13:62516797-62558599	Zfp934	77117	12.3	10.3	2.9	-1.0802	0.620982	-3.37539	5.87E-29
chr13:62453016-62466812	Zfp935	71508	37.3	29.7	19.0	-1.12948	0.432551	-1.55921	3.81E-05
chr2:150218099-15024487	Zfp937	245174	11.9	8.7	4.6	-1.23269	0.439986	-2.02376	0.0001794
chr10:82224856-82241275	Zfp938	237411	34.2	27.7	16.3	-1.11571	0.659261	-1.64934	0.0017241
chr7:29843936-29853648:	Zfp940	233057	7.7	6.4	4.3	-1.07674	0.655616	-1.40079	0.001816
chr17:21962559-21994366	Zfp943	74670	43.3	38.7	26.6	-1.00729	0.963697	-1.29905	0.002611
chr17:22337989-22361400	Zfp944	319615	29.4	26.2	18.4	-1.00699	0.958138	-1.27623	0.0004847
chr17:22846697-22867134	Zfp945	240041	47.7	37.9	8.7	-1.13901	0.581734	-4.2152	1.94E-21
chr17:22144359-22165977	Zfp947	210853	9.3	7.3	3.6	-1.15917	0.584587	-2.04523	6.67E-05
chr17:21567046-21588682	Zfp948	381066	25.6	43.3	44.1	1.88072	0.007242	2.07834	0.0001172
chr9:88548020-88571086:	Zfp949	71640	32.3	24.6	7.6	-1.18595	0.471474	-3.29234	9.94E-14
chr13:67339309-67360572	Zfp953	629016	11.6	8.6	4.2	-1.22286	0.400673	-2.1467	5.42E-06
chr17:33239507-33255145	Zfp955a	77652	30.7	26.7	20.4	-1.03083	0.756661	-1.20687	0.001789
chr17:33289544-33304689	Zfp955b	1E+08	40.3	35.1	24.8	-1.0294	0.823758	-1.29725	0.0006672
chr6:47953390-47965299:	Zfp956	101197	26.9	18.5	14.1	-1.30594	0.046385	-1.51604	5.27E-05

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr8:69654556-69664453:	Zfp964	636741	14.2	12.3	5.9	-1.04434	0.885553	-1.86429	0.0002364
chr17:17121383-17146878	Zfp97	22759	16.9	15.3	10.4	1.003	0.98665	-1.30221	0.0051801
chr15:12117851-12185449	Zfr	22763	118.2	132.8	137.7	1.26556	0.074375	1.44919	0.0002159
chr10:81233163-81252123	Zfr2	103406	20.4	17.9	11.3	-1.01612	0.934669	-1.43979	0.0004972
chr12:83546941-83597147	Zfyve1	217695	52.6	42.2	17.3	-1.12002	0.353685	-2.41189	3.08E-25
chr13:92487749-92530810	Zfyve16	218441	39.3	38.4	43.7	1.09524	0.090035	1.39009	2.65E-17
chr12:111814170-1118283	Zfyve21	68520	94.9	65.9	28.0	-1.29815	0.226551	-2.62596	5.58E-10
chr12:79232347-79296282	Zfyve26	211978	23.4	17.1	6.9	-1.22835	0.134738	-2.68258	1.10E-22
chr19:42170567-42194592	Zfyve27	319740	25.9	20.3	16.1	-1.14312	0.113017	-1.28091	0.0001006
chr9:21062393-21067093:	Zglp1	1E+08	1.3	2.3	4.8	1.89684	0.122571	3.935	5.53E-06
chr7:10487224-10495381:	Zik1	22775	9.7	8.9	5.8	1.0175	0.926672	-1.32964	0.0056666
chr5:145194946-14520188	Zkscan14	67235	22.9	16.6	3.3	-1.2418	0.502229	-4.96953	2.10E-13
chr4:58943628-58958355:	Zkscan16	1E+08	4.0	2.9	0.4	-1.22313	0.675936	-6.10996	7.54E-09
chr11:59485521-59506640	Zkscan17	268417	37.9	34.7	38.7	1.03174	0.835401	1.27379	0.0057535
chr13:21478849-21485505	Zkscan4	544922	9.8	6.0	3.0	-1.44311	0.312329	-2.44218	0.0006898
chr5:145204559-14522175	Zkscan5	22757	23.8	17.9	14.2	-1.19622	0.07347	-1.33653	0.000139
chr9:122888471-12289612	Zkscan7	382118	36.1	23.0	9.0	-1.40647	0.148479	-3.0753	1.25E-10
chrX:134971373-13500920	Zmat1	215693	13.1	8.6	4.1	-1.36033	0.154264	-2.49695	1.22E-08
chr18:36793923-36799660	Zmat2	66492	66.2	64.3	67.7	1.08614	0.367537	1.27351	0.0001698
chr3:32334794-32365665:	Zmat3	22401	6.5	8.3	21.5	1.42453	0.010418	4.03242	2.86E-40
chr11:4704678-4737666:+	Zmat5	67178	42.0	38.8	26.2	1.03128	0.840971	-1.27748	0.0070948
chr4:121059238-12109824	Zmpste24	230709	57.8	59.9	71.4	1.15356	0.374432	1.53038	0.0001658
chr4:127047094-12706113	Zmym1	68310	25.4	26.9	16.4	1.17943	0.084784	-1.23516	0.0044874
chr14:56887795-56962579	Zmym2	76007	82.2	80.2	52.7	1.09722	0.307553	-1.24694	0.0007822
chrX:101404384-10142068	Zmym3	56364	26.1	16.6	13.2	-1.41239	0.015029	-1.56742	6.29E-05
chr4:126861820-12696792	Zmym4	67785	55.5	50.8	63.7	1.02772	0.779803	1.43429	2.88E-10
chr14:56790585-56811716	Zmym5	219105	50.6	48.4	26.4	1.07631	0.562676	-1.52903	3.30E-07
chr4:127077383-12712437	Zmym6	100177	58.1	48.2	19.9	-1.0807	0.480079	-2.32141	1.80E-30
chr9:107547310-10755131	Zmynd10	114602	7.3	1.1	1.2	-4.66623	1.92E-05	-3.95754	9.48E-06
chr13:9684836-9765314:-	Zmynd11	66505	138.8	125.4	135.6	1.01332	0.881026	1.22125	4.16E-05
chr4:119422684-11945389	Zmynd12	332934	2.1	0.8	0.4	-2.13666	0.044217	-3.39197	5.26E-05
chr2:24949802-24959413:	Zmynd19	67187	24.8	40.1	70.9	1.80076	0.015758	3.38028	1.00E-10
chr2:165784152-16588483	Zmynd8	228880	26.0	21.5	13.5	-1.08138	0.361728	-1.53924	4.53E-13
chr4:145789515-14583197	Znf41-ps	70005	4.1	3.2	1.9	-1.14953	0.353667	-1.73101	4.92E-07
chr2:181582103-18159246	Znf512b	269401	57.0	40.6	61.6	-1.25337	0.012064	1.34953	2.35E-05
chr5:136982201-13698788	Znhit1	70103	35.5	33.0	37.5	1.04706	0.782316	1.31651	0.0058045
chr19:6061207-6062468:+	Znhit2	29805	18.1	15.4	21.2	-1.03465	0.879947	1.45613	0.0024301
chr3:145576208-14560524	Znhit6	229937	17.4	22.9	52.8	1.47486	0.057664	3.65267	9.69E-18
chr17:36954358-36958428	Znrd1	66136	71.5	89.5	103.5	1.40997	0.034517	1.78942	2.84E-06
chr8:111536640-11162603	Znrf1	170737	22.3	23.1	23.9	1.1594	0.070251	1.34187	1.49E-06
chr11:5276329-5444847:-	Znrf3	407821	18.8	12.0	13.3	-1.40647	0.00659	-1.13336	0.247147
chr17:56511248-56512483	Znrf4	20834	3.0	0.2	0.4	-4.73194	0.007216	-3.1931	0.0149092
chr1:130576706-13062960	Zp3r	22789	2.3	0.2	0.3	-5.59341	0.000845	-3.82629	0.0019991
chr11:11280040-11462419	Zpbp	53604	4.0	1.5	0.9	-2.23891	0.011	-3.02663	1.31E-05
chr11:98551097-98558665	Zpbp2	69376	5.4	0.7	0.6	-4.73255	0.00064	-4.78654	4.52E-05
chr9:46273064-46282642:	Zpr1	22687	43.4	51.0	86.4	1.32494	0.081352	2.45008	4.93E-14
chr3:157534397-15754833	Zranb2	53861	168.1	149.4	203.1	-1.00468	0.96665	1.50718	9.68E-13
chr1:127954179-12810304	Zranb3	226409	15.4	13.6	3.1	-1.00553	0.967389	-3.94442	2.90E-68
chr11:22972005-22976496	Zrsr1	22183	41.7	36.5	18.2	-1.01673	0.901564	-1.82598	1.47E-16
chrX:163935443-16395866	Zrsr2	22184	14.9	17.0	19.2	1.28424	0.143733	1.5969	0.000244
chr7:80862108-80876513:	Zscan2	22691	19.3	12.3	4.4	-1.41085	0.026493	-3.40099	2.22E-23
chr5:145283343-14529146	Zscan25	666311	26.2	26.2	27.0	1.12586	0.318534	1.28515	0.0032783
chr13:21442175-21453727	Zscan26	432731	130.4	126.2	76.2	1.08742	0.28855	-1.36501	2.84E-08
chr2:164822686-16482686	Zswim1	71971	7.4	7.4	10.9	1.10878	0.416213	1.8155	4.58E-13
chr2:83915079-83941226:	Zswim2	71861	1.9	0.1	0.3	-4.87878	0.005404	-3.14272	0.0152651
chr8:84210942-84237042:	Zswim4	212168	26.5	26.9	11.5	1.14343	0.246391	-1.82562	5.71E-13
chr13:107724617-1078900	Zswim6	67263	18.3	19.1	11.5	1.17514	0.137471	-1.27015	0.0039872
chr10:33926936-33951212	Zufsp	72580	50.5	49.4	32.7	1.09249	0.195302	-1.2336	3.55E-05

mm10 coordinates	Gene Symbol	Gene ID	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
chr10:72654846-72674964	Zwint	52696	62.3	66.1	71.3	1.19385	0.076031	1.42737	2.06E-06
chrX:94724569-94730191:	Zxdb	668166	9.8	9.2	9.9	1.05502	0.68264	1.2708	0.0035192
chr6:90369494-90403486:	Zxdc	80292	25.0	35.8	51.4	1.60359	0.109242	2.4318	5.97E-05
chr4:108227755-10830109	Zyg11b	414872	38.4	36.0	34.7	1.05146	0.429791	1.12852	0.0069016
chr6:42349828-42360213:	Zyx	22793	95.0	103.0	112.0	1.21904	0.167862	1.46608	0.0003365
chr3:152396003-15246282	Zzz3	108946	64.7	64.1	74.0	1.11338	0.189879	1.42714	1.80E-09

Genes in SE or other end of loop	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	Average TPM	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
1600027J07Rik	0.4	0.5	3.5	1.5	1.27	0.7347	6.13	9.81E-06
2310015A10Rik	18.0	10.4	6.9	11.7	-1.55	0.089602	-2.02	0.0003276
2510039O18Rik	33.1	40.6	43.3	39.0	1.38	0.04488	1.62	9.31E-05
2700046A07Rik	13.6	6.2	0.5	6.8	-1.80	0.251169	-11.59	4.78E-11
4732471J01Rik	5.2	3.1	1.5	3.3	-1.49	0.049474	-2.72	1.55E-10
4930556M19Rik	1.7	1.2	0.6	1.2	-1.25	0.445867	-2.07	0.0005881
4932414N04Rik	2.7	0.3	0.4	1.1	-5.42	0.000119	-3.83	0.0003585
4933417E11Rik	2.5	1.8	0.6	1.6	-1.28	0.60395	-2.96	0.0011478
4933427D14Rik	31.7	29.6	18.7	26.7	1.05	0.761941	-1.35	0.0052204
5330417C22Rik	20.5	12.5	3.0	12.0	-1.37	0.454106	-4.54	1.70E-07
6430548M08Rik	13.2	11.4	13.8	12.8	-1.04	0.779055	1.31	0.0008481
A230028O05Rik	0.5	0.5	1.2	0.7	-1.04	0.939148	2.49	0.0013872
A330074K22Rik	3.2	2.2	0.5	2.0	-1.31	0.38828	-4.34	5.76E-10
A530013C23Rik	3.9	8.2	4.7	5.6	2.25	0.004852	1.47	0.122972
Abca1	153.8	106.7	34.3	98.3	-1.29	0.096475	-3.51	1.73E-28
Abcb1a	63.9	55.3	9.5	42.9	-1.03	0.756755	-5.30	1.08E-137
Acacb	9.6	7.4	2.8	6.6	-1.15	0.49094	-2.62	1.01E-12
Acads	37.9	30.0	17.2	28.4	-1.14	0.369417	-1.76	2.14E-08
Aco2	173.6	168.1	204.2	181.9	1.09	0.50758	1.47	1.56E-05
Actn1	155.7	174.2	296.3	208.7	1.26	0.06981	2.36	4.42E-20
Adam12	14.8	14.0	27.2	18.7	1.06	0.761941	2.26	4.66E-14
Adamts2	18.9	42.4	102.0	54.4	2.36	0.015084	5.58	4.06E-10
Adamts4	4.1	99.8	122.3	75.4	10.60	4.75E-07	13.00	3.15E-10
Adamtsl2	0.4	6.7	10.0	5.7	5.33	0.00211	7.36	8.76E-06
Adcy5	38.7	82.0	82.6	67.8	2.24	0.03756	2.39	0.0041086
Adcy6	69.2	54.3	24.4	49.3	-1.14	0.090035	-2.25	7.22E-48
Adcy7	39.5	30.0	17.2	28.9	-1.18	0.461454	-1.81	0.0001001
Adh1	202.1	359.9	1205.0	589.0	1.99	5.62E-07	7.21	1.26E-64
Adprhl2	52.2	58.7	74.9	61.9	1.27	0.066836	1.79	1.43E-09
Agbl5	17.4	9.5	5.8	10.9	-1.64	0.004357	-2.34	1.11E-09
Akap7	52.6	42.7	15.7	37.0	-1.10	0.411379	-2.64	5.04E-32
Aknad1	2.4	1.1	0.6	1.3	-1.89	0.035009	-3.07	3.70E-06
Ank1	0.4	0.9	1.1	0.8	2.14	0.085609	2.60	0.0049266
Ankrd50	27.4	21.9	13.9	21.1	-1.12	0.276998	-1.57	5.71E-10
Ano1	103.6	74.7	37.4	71.9	-1.22	0.205504	-2.18	1.16E-11
Anxa6	345.6	382.5	419.5	382.5	1.25	0.108205	1.51	6.53E-05
Arhgap28	21.0	20.6	6.6	16.1	1.10	0.343271	-2.55	1.74E-40
Arhgap42	45.8	47.5	69.2	54.2	1.17	0.362105	1.86	2.31E-07
Arhgef28	26.1	18.6	7.9	17.5	-1.25	0.019288	-2.63	3.55E-38
Arhgef3	74.5	46.2	22.7	47.8	-1.45	0.087848	-2.54	8.01E-09
Arl4c	87.9	97.6	141.9	109.2	1.25	0.375213	1.96	0.0001823
Arl5b	29.6	31.1	30.1	30.2	1.19	0.144914	1.27	0.0069893
Arl6ip4	54.6	54.3	71.7	60.2	1.12	0.191034	1.64	2.41E-17
Armc2	3.5	2.6	0.3	2.1	-1.21	0.505832	-7.72	2.45E-21
Arrb1	78.2	69.9	26.6	58.2	1.00	0.984057	-2.33	4.59E-41
Arsi	14.4	21.7	28.2	21.4	1.69	0.022688	2.37	1.14E-06
Asb6	26.3	35.5	39.4	33.7	1.52	0.109883	1.82	0.0024538
Aspg	27.6	25.6	4.2	19.1	1.04	0.911442	-4.95	3.69E-18
Atf1	34.4	40.8	60.3	45.1	1.34	0.089531	2.16	1.30E-09
Atf5	59.2	70.3	253.7	127.7	1.34	0.127779	5.15	5.23E-32
Atp12a	5.8	7.4	15.1	9.4	1.42	0.291715	3.00	2.88E-06
Atp1a1	248.2	539.0	557.0	448.1	2.36	0.002542	2.61	4.04E-05
Atp1a2	75.7	44.1	4.2	41.4	-1.52	0.10655	-12.50	3.62E-40
Atp2a3	70.8	56.8	30.0	52.5	-1.11	0.524379	-1.86	1.29E-08
Atp5g1	114.7	133.8	334.7	194.4	1.31	0.009005	3.62	4.10E-60
Atp5o	230.7	254.6	357.7	281.0	1.24	0.036602	1.93	9.39E-18
Atp6v0a1	41.2	33.8	23.2	32.7	-1.09	0.397482	-1.42	4.56E-07
Atpaf2	27.8	26.0	29.0	27.6	1.05	0.636711	1.30	2.95E-05

Genes in SE or other end of loop	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	Average TPM	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
AU015791	0.4	0.7	4.4	1.9	1.58	0.355844	9.20	8.27E-13
B230312C02Rik	13.8	11.1	4.3	9.7	-1.11	0.722639	-2.44	1.51E-06
B3gntl1	20.4	13.9	8.0	14.1	-1.32	0.29157	-1.97	0.0004184
B4galt5	20.1	137.3	140.7	99.4	5.38	6.69E-05	5.77	1.34E-06
Bag1	149.3	153.9	208.2	170.5	1.16	0.169305	1.74	9.86E-13
Bdkrb1	2.6	5.8	28.1	12.1	2.39	0.002281	11.69	3.36E-28
Bean1	1.3	1.2	3.6	2.0	1.05	0.91975	3.13	1.95E-05
Bhlhe40	55.1	83.0	83.2	73.8	1.67	0.037183	1.84	0.0016216
Bmp4	35.6	27.3	14.7	25.9	-1.17	0.490925	-1.90	4.29E-05
Bri3	36.8	28.5	18.4	27.9	-1.15	0.269269	-1.60	5.86E-07
Btbd10	22.8	35.6	57.7	38.7	1.74	0.074804	2.94	3.94E-06
Btbd3	28.3	24.7	30.0	27.7	-1.03	0.853387	1.32	0.0013411
C1qtnf1	12.4	14.6	5.8	10.9	1.33	0.183376	-1.70	0.0011616
Camk2d	34.5	32.8	20.5	29.3	1.06	0.453758	-1.35	6.27E-08
Car13	7.3	12.3	17.6	12.4	1.85	0.004736	2.89	8.18E-10
Cbs	13.9	16.3	35.9	22.0	1.33	0.358726	3.04	1.97E-07
Cbx7	115.3	93.2	27.4	78.7	-1.10	0.354178	-3.32	1.54E-58
Ccdc117	43.9	82.8	41.3	56.0	2.08	0.007116	1.16	0.535951
Ccdc42	2.2	0.3	0.7	1.1	-4.66	0.001191	-2.19	0.0471535
Ccdc63	3.0	0.4	0.7	1.4	-5.02	0.000112	-2.95	0.0023545
Ccdc93	36.7	29.9	14.7	27.1	-1.10	0.198026	-1.99	1.50E-40
Ccl11	18.1	27.0	112.9	52.7	1.59	0.141296	6.79	3.59E-17
Cd81	577.3	623.0	619.4	606.6	1.21	0.119632	1.34	0.0020494
Cdc27	51.5	57.4	75.6	61.5	1.25	0.083296	1.82	6.13E-10
Cdkl3	13.3	5.9	6.3	8.5	-1.98	0.000106	-1.65	0.0009969
Cebpb	10.3	61.1	29.0	33.5	5.19	1.30E-05	2.89	0.0014959
Cep44	41.9	35.9	17.0	31.6	-1.05	0.798752	-1.95	7.70E-09
Ces1a	0.3	0.8	2.0	1.0	1.85	0.342708	3.59	0.005934
Cfh	835.7	704.9	238.9	593.2	-1.07	0.694329	-2.77	2.32E-24
Chchd10	70.0	53.8	33.1	52.3	-1.16	0.254135	-1.68	6.37E-08
Chmp1a	96.8	89.3	97.5	94.5	1.03	0.733147	1.26	0.0001111
Chmp4b	141.4	179.6	225.3	182.1	1.43	0.004473	1.97	1.03E-11
Chrdl2	12.8	18.2	32.0	21.0	1.57	0.236799	2.83	0.0001749
Chst11	15.3	40.7	74.8	43.6	2.79	0.001323	5.19	3.65E-10
Cldn22	1.7	0.6	0.1	0.8	-1.96	0.230329	-4.65	0.0003225
Cluh	36.2	45.8	91.4	57.8	1.43	0.09271	3.06	1.26E-12
Cmklr1	14.7	47.9	122.1	61.6	3.21	0.001626	7.80	1.13E-11
Cmpk2	16.1	15.5	4.0	11.9	1.07	0.829198	-3.07	1.11E-10
Cnn2	267.8	323.5	644.8	412.0	1.36	0.092303	2.94	1.66E-15
Coil	19.8	16.5	21.3	19.2	-1.07	0.549676	1.35	1.72E-05
Col5a1	69.7	117.9	226.4	138.0	1.87	0.015825	3.77	4.71E-11
Col6a1	560.2	557.0	1189.8	769.0	1.11	0.123408	2.65	4.53E-85
Col6a2	247.6	294.0	966.2	502.6	1.33	0.064835	4.74	1.50E-42
Col6a3	156.0	238.3	657.4	350.5	1.71	0.036367	4.87	1.72E-16
Col6a5	4.7	2.1	12.4	6.4	-1.75	0.23339	2.75	0.0034094
Coro2b	3.1	4.5	4.9	4.2	1.60	0.109154	1.90	0.0039944
Cpne5	15.3	12.1	3.1	10.2	-1.11	0.716916	-3.71	2.54E-14
Crebl2	51.6	39.6	6.8	32.7	-1.17	0.427763	-5.82	3.59E-36
Csnk2a2	20.8	21.9	25.9	22.9	1.19	0.238473	1.55	3.68E-05
Csrp1	1207.9	1271.0	1636.8	1371.9	1.17	0.268538	1.68	4.82E-07
Csrp2	94.3	62.7	41.4	66.1	-1.35	0.006324	-1.82	1.42E-11
Ctnna1	238.6	231.6	267.8	246.0	1.09	0.49094	1.40	0.0001412
Ctsb	348.3	397.3	704.5	483.4	1.28	0.281204	2.45	5.08E-08
Cuedc1	36.4	28.2	22.8	29.2	-1.15	0.177367	-1.27	0.0019794
Cxcl12	158.2	120.8	72.5	117.2	-1.17	0.401988	-1.72	4.70E-05
Cygb	113.8	113.6	56.5	94.6	1.13	0.494385	-1.60	9.85E-05
D930048N14Rik	11.5	6.4	4.4	7.4	-1.61	0.012071	-2.04	2.07E-06
Dab2ip	32.1	53.8	57.5	47.8	1.84	0.078521	2.09	0.0057922

Genes in SE or other end of loop	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	Average TPM	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
Dazap1	46.0	47.5	64.7	52.7	1.16	0.296903	1.75	5.31E-08
Dbnl	59.8	61.7	96.4	72.7	1.16	0.25027	2.00	7.04E-14
Dbp	207.1	69.0	17.1	97.7	-2.54	0.003182	-7.97	3.31E-16
Ddah1	2.2	1.9	6.3	3.5	-1.02	0.952617	3.49	2.96E-19
Ddit3	81.5	68.1	125.4	91.7	-1.07	0.499573	1.92	2.51E-25
Dhrs13	6.8	7.9	13.6	9.4	1.31	0.152278	2.46	1.62E-11
Dhrs9	1.9	3.4	7.3	4.2	1.86	0.124566	3.93	5.47E-06
Dhx32	31.5	33.4	38.8	34.6	1.20	0.271876	1.53	0.0002931
Dio2	72.2	111.9	378.3	187.5	1.64	0.101859	5.80	2.34E-15
Dio3os	28.9	25.8	7.5	20.7	-1.02	0.963697	-2.81	4.87E-05
Dnajc17	25.9	24.2	27.4	25.8	1.05	0.741425	1.32	0.0005562
Dnmbp	35.0	37.9	18.6	30.5	1.23	0.297628	-1.48	0.0064629
Doc2b	6.0	5.2	0.9	4.0	-1.03	0.929375	-5.06	4.56E-24
Dock6	42.4	36.6	22.6	33.9	-1.03	0.864597	-1.49	2.90E-05
Dpysl5	2.4	1.4	0.2	1.3	-1.47	0.342173	-6.28	7.12E-10
Dyrk2	86.1	89.5	116.5	97.3	1.16	0.244823	1.68	1.08E-08
E2f6	31.3	57.8	50.3	46.5	2.03	0.015242	1.92	0.005522
Ebf4	25.3	22.5	15.4	21.1	1.00	0.991756	-1.31	0.0069308
Ecsit	26.7	29.0	60.4	38.7	1.22	0.147728	2.79	2.97E-25
Edem1	27.0	31.1	50.0	36.0	1.29	0.070916	2.29	2.69E-15
Ednra	36.9	33.5	46.7	39.0	1.00	0.986678	1.57	0.0005255
Eefsec	29.8	26.9	30.3	29.0	1.01	0.959587	1.27	0.002548
Egr1	14.7	30.0	53.4	32.7	2.24	0.002642	4.18	3.87E-11
Ehbp1l1	53.3	57.6	67.2	59.4	1.22	0.153669	1.57	9.90E-06
Eif4a2	583.8	634.7	647.2	621.9	1.22	0.119488	1.38	0.0010522
Eif4g2	253.0	319.3	454.5	342.3	1.42	0.01952	2.22	7.30E-12
Elmo1	15.4	13.9	8.4	12.5	1.01	0.913834	-1.46	2.24E-08
Eng	27.9	38.4	71.5	45.9	1.55	0.113777	3.02	6.25E-08
Eps8l2	21.8	17.8	5.8	15.2	-1.09	0.524379	-2.96	6.35E-32
Eral1	34.9	35.0	37.3	35.7	1.12	0.155701	1.34	1.36E-06
Etohd2	6.5	3.9	1.6	4.0	-1.49	0.089325	-3.13	3.25E-10
Ets2	88.5	121.1	126.3	112.0	1.54	0.017718	1.76	8.15E-05
Etv6	19.9	21.4	28.8	23.4	1.20	0.190696	1.80	7.92E-09
Eva1a	8.3	20.6	17.3	15.4	2.54	0.017876	2.31	0.0082719
Evc	52.0	46.3	13.8	37.4	1.00	0.996254	-2.97	5.80E-28
Exoc2	44.2	41.8	62.9	49.6	1.06	0.470791	1.78	5.69E-28
Extl3	60.2	59.8	58.1	59.4	1.11	0.164736	1.21	0.0011269
Ezh1	122.8	96.6	28.6	82.7	-1.15	0.452138	-3.36	1.25E-23
F630111L10Rik	0.6	1.0	1.6	1.0	1.80	0.131699	2.99	0.0001517
Fahd2a	27.0	21.1	12.6	20.2	-1.15	0.298787	-1.70	6.02E-08
Fam110b	25.9	19.1	6.5	17.2	-1.22	0.659221	-2.83	0.0002891
Fam151a	0.7	3.4	3.3	2.5	3.44	0.018772	3.52	0.0026539
Fam181a	1.7	0.1	0.3	0.7	-5.32	0.001968	-3.13	0.0112573
Fam83e	1.7	1.5	4.0	2.4	1.02	0.972822	2.61	0.0013343
Fam89b	64.9	49.5	34.1	49.5	-1.18	0.046794	-1.52	1.65E-11
Fank1	3.9	0.5	0.8	1.7	-4.76	0.000445	-3.19	0.0020445
Fbxl13	9.4	7.1	1.5	6.0	-1.18	0.5822	-4.62	3.87E-14
Fbxl7	10.7	9.9	3.9	8.2	1.03	0.921545	-2.15	4.11E-08
Fbxo6	26.9	23.3	16.7	22.3	-1.03	0.764081	-1.29	1.71E-05
Fbxo8	23.8	21.4	13.7	19.6	1.00	0.997301	-1.39	2.90E-06
Fcna	2.9	1.7	0.4	1.7	-1.43	0.374468	-4.03	5.25E-06
Fgd4	40.9	35.2	22.5	32.9	-1.05	0.74955	-1.45	1.19E-05
Fgf2	18.1	17.6	33.7	23.1	1.08	0.661974	2.30	6.80E-15
Fgf9	5.4	4.0	1.7	3.7	-1.16	0.661345	-2.34	0.0001346
Fkbp14	20.0	43.9	40.7	34.9	2.32	0.019445	2.31	0.0035301
Flrt1	9.7	24.9	5.7	13.4	2.75	0.000678	-1.32	0.303006
Fnip2	19.0	17.6	22.4	19.6	1.04	0.84948	1.47	0.0002411
Fos	7.2	94.5	48.3	50.0	8.57	6.36E-07	5.18	1.61E-05

Genes in SE or other end of loop	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	Average TPM	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
Fosl2	42.5	129.9	161.3	111.2	3.25	5.76E-07	4.37	5.04E-13
Foxk1	19.4	17.5	9.6	15.5	1.01	0.954881	-1.60	6.05E-09
Frzb	10.8	11.3	33.3	18.5	1.17	0.304343	3.78	7.13E-37
Fxyd6	161.7	139.6	54.4	118.6	-1.04	0.730531	-2.37	2.31E-35
Fyb2	2.8	23.0	20.7	15.5	6.64	8.37E-07	6.41	3.26E-08
G3bp2	89.8	97.5	96.1	94.4	1.22	0.097036	1.33	0.0018001
Gadd45g	13.3	399.8	505.8	306.3	13.87	2.74E-09	17.72	1.41E-13
Gal	0.0	1.2	5.1	2.1	2.54	0.136964	6.28	8.67E-05
Galnt10	14.5	14.7	16.5	15.2	1.15	0.202128	1.42	5.04E-06
Gamt	13.8	9.9	2.8	8.8	-1.26	0.405947	-3.59	2.36E-10
Gapdh	393.7	500.0	982.2	625.3	1.43	0.084473	3.02	7.18E-13
Gbp11	3.0	1.6	0.6	1.7	-1.59	0.300296	-3.49	0.0001462
Gid4	45.4	37.7	25.1	36.1	-1.08	0.448322	-1.44	5.83E-08
Gli3	16.5	13.1	10.2	13.3	-1.13	0.360417	-1.29	0.0083798
Gm10400	10.4	6.3	2.4	6.4	-1.45	0.380574	-3.04	0.000226
Gm10790	1.8	0.8	0.5	1.0	-1.94	0.097307	-2.73	0.001202
Gm13446	2.2	3.3	6.4	4.0	1.59	0.312196	3.00	0.0008038
Gm14005	0.6	0.7	4.1	1.8	1.35	0.396376	7.34	1.54E-18
Gm32014	1.2	2.2	15.3	6.2	1.98	0.004802	14.24	5.49E-48
Gna14	22.2	18.8	10.2	17.1	-1.06	0.756298	-1.73	6.66E-07
Gne	13.8	10.4	18.2	14.1	-1.19	0.159776	1.65	1.53E-08
Gng12	94.3	128.9	482.2	235.1	1.54	0.078285	5.93	3.59E-23
Golph3	98.0	138.3	139.6	125.3	1.58	0.085383	1.73	0.0075444
Got1	13.7	30.1	69.4	37.7	2.37	0.005121	5.50	3.05E-12
Gpr157	5.3	4.2	1.8	3.7	-1.13	0.516512	-2.25	1.18E-09
Gpr68	3.7	4.7	6.5	5.0	1.38	0.285494	2.08	0.0006913
Gprin3	18.1	11.7	5.1	11.6	-1.37	0.416099	-2.56	0.0006274
Gpsm2	69.7	52.4	25.4	49.2	-1.20	0.303515	-2.16	3.49E-10
Greb1	10.9	85.6	44.9	47.1	5.88	4.80E-05	3.63	0.0007289
Grhpr	20.1	15.8	11.8	15.9	-1.14	0.345637	-1.35	0.0024109
Gria1	3.5	5.0	9.5	6.0	1.58	0.027396	3.24	3.66E-14
Grik4	2.8	2.4	1.1	2.1	-1.05	0.854044	-1.97	5.59E-06
Gsk3a	53.3	57.5	64.1	58.3	1.22	0.147278	1.50	6.33E-05
Hbp1	137.5	107.9	24.7	90.0	-1.15	0.56637	-4.25	2.07E-19
Hdac7	34.2	27.4	16.5	26.0	-1.11	0.389435	-1.64	1.42E-08
Hdhd3	8.0	6.2	13.2	9.1	-1.14	0.51644	2.03	2.76E-08
Hey2	8.5	6.0	4.2	6.2	-1.26	0.229511	-1.59	0.0010872
Heyl	6.1	8.2	16.9	10.4	1.50	0.322133	3.05	0.0001312
Hif1a	102.9	162.3	286.2	183.8	1.76	0.002678	3.35	1.50E-15
Hivep2	35.4	41.9	43.4	40.2	1.33	0.020654	1.53	1.28E-05
Hmgb1	320.3	381.2	402.6	368.0	1.34	0.093997	1.56	0.0008806
Hnrnph3	106.1	103.4	61.7	90.4	1.10	0.587579	-1.37	0.0095927
Hoxd10	98.7	73.1	47.3	73.0	-1.22	0.310449	-1.65	0.0003295
Hoxd9	45.7	35.6	24.6	35.3	-1.15	0.33906	-1.48	0.0002364
Hrk	1.1	1.9	0.2	1.1	1.86	0.072037	-4.02	9.79E-07
Hs1bp3	28.5	17.5	5.7	17.3	-1.46	0.110209	-3.79	3.78E-14
Hsd11b2	8.9	10.0	18.8	12.6	1.22	0.466873	2.52	5.94E-07
Hsp90ab1	956.1	1082.0	1805.5	1281.2	1.28	0.066993	2.34	5.26E-18
Hspa2	66.1	58.4	29.2	51.2	-1.01	0.96384	-1.79	1.71E-10
Hspb9	18.4	1.7	2.6	7.6	-6.92	6.18E-07	-4.45	8.49E-06
Htra1	94.9	97.8	177.6	123.4	1.17	0.395448	2.30	1.52E-11
Htra3	56.3	78.7	19.5	51.5	1.57	0.064539	-2.23	1.74E-05
Hvcn1	27.8	22.6	7.9	19.5	-1.11	0.74694	-2.70	1.47E-07
Ifng	0.2	0.8	1.1	0.7	2.80	0.059104	4.12	0.0006031
Ift81	101.1	75.3	34.1	70.2	-1.20	0.157218	-2.35	5.06E-19
Igdcc4	17.4	18.0	7.2	14.2	1.17	0.414656	-1.90	9.77E-07
Igf1	47.1	67.2	433.1	182.5	1.60	0.008081	10.84	3.45E-68
Igfbp4	328.3	274.2	175.7	259.4	-1.08	0.625247	-1.49	3.98E-05

Genes in SE or other end of loop	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	Average TPM	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
Igsf8	53.0	39.3	19.0	37.1	-1.21	0.226335	-2.20	9.37E-12
Ikzf4	2.6	7.7	5.7	5.4	2.94	0.001498	2.49	0.0014502
Il16	31.9	33.2	40.3	35.1	1.15	0.319241	1.57	8.69E-06
Inhbb	13.5	217.3	322.1	184.3	13.00	1.90E-15	19.58	1.35E-23
Inmt	348.5	295.7	80.5	241.6	-1.05	0.805063	-3.38	5.78E-24
Insysn1	9.2	19.5	32.0	20.2	2.21	0.040039	3.65	1.19E-05
Iqcd	4.9	2.4	0.6	2.6	-1.81	0.030875	-5.41	5.46E-13
Irak3	18.8	60.5	29.2	36.1	3.13	0.006186	1.76	0.111803
Irf1	64.2	100.4	48.9	71.2	1.72	0.001135	-1.05	0.764565
Irf2bp2	113.6	93.2	56.8	87.9	-1.09	0.350285	-1.59	3.79E-13
Iscu	104.0	112.8	143.2	120.0	1.22	0.113838	1.71	7.09E-09
Isyna1	96.8	198.6	233.2	176.2	2.21	0.022162	2.73	0.0002211
Itga9	29.2	28.8	48.0	35.4	1.10	0.40778	2.04	2.98E-19
Itgb3	17.7	32.5	61.5	37.2	2.00	0.036639	3.87	9.94E-08
Itm2b	1333.0	1126.9	473.1	977.7	-1.06	0.514537	-2.25	9.75E-44
Jarid2	31.0	24.9	19.5	25.1	-1.10	0.333795	-1.27	0.0012072
Jmjd1c	120.6	101.1	66.8	96.2	-1.08	0.70915	-1.44	0.0030456
Jund	25.5	74.1	45.0	48.2	2.93	0.003581	2.00	0.0260751
Kalrn	16.3	17.4	24.9	19.5	1.20	0.308247	1.89	9.00E-07
Kcnip3	9.1	8.2	5.1	7.5	1.00	0.984813	-1.42	0.0036295
Kcnk2	9.2	8.8	1.9	6.6	1.06	0.844343	-3.65	2.93E-14
Kcnk5	8.5	25.8	32.8	22.3	3.27	8.61E-07	4.44	8.89E-13
Kdelr3	25.4	28.2	36.2	29.9	1.24	0.085211	1.76	4.56E-10
Khk	66.9	54.1	14.1	45.0	-1.11	0.481947	-3.71	1.46E-38
Kit	7.2	11.2	17.1	11.8	1.74	0.03346	2.82	1.75E-07
Klf13	23.6	24.6	13.5	20.6	1.17	0.140334	-1.39	3.11E-05
Klhdc4	21.9	27.4	71.2	40.2	1.41	0.014144	3.99	7.83E-40
Klhl32	8.0	8.7	17.2	11.3	1.22	0.287827	2.64	1.17E-14
Klhl38	19.9	12.5	0.6	11.0	-1.41	0.301565	-20.10	5.21E-32
Kpna3	37.0	50.5	69.9	52.5	1.53	0.033639	2.30	5.84E-08
Ksr1	19.4	51.2	70.7	47.1	2.70	0.009672	3.81	1.28E-05
Ktn1	124.5	110.8	86.4	107.2	-1.00	0.979797	-1.15	0.0064634
Lama2	86.5	68.3	47.1	67.3	-1.13	0.169305	-1.47	1.15E-08
Larp4b	61.0	55.4	64.2	60.2	1.02	0.889496	1.31	0.0007733
Lats1	46.0	52.3	72.0	56.8	1.28	0.113453	1.94	1.72E-08
Ldb1	166.5	155.7	84.9	135.7	1.06	0.702147	-1.56	2.33E-07
Ldhc	75.2	3.0	8.0	28.7	-12.89	2.63E-09	-5.33	1.13E-05
Lekr1	5.0	4.4	1.5	3.6	-1.02	0.945436	-2.64	1.92E-10
Lgr6	3.6	22.3	33.3	19.7	5.84	6.52E-08	8.98	1.12E-14
Lhfpl2	62.0	51.3	105.4	72.9	-1.07	0.785548	2.08	7.53E-07
Lif	0.9	4.5	24.2	9.9	4.25	0.000158	19.42	1.70E-20
Lin7c	76.7	85.7	104.0	88.8	1.26	0.091146	1.68	3.13E-07
Litaf	92.8	198.6	173.6	155.0	2.34	0.000461	2.24	9.64E-05
Loxl1	20.2	20.1	31.5	23.9	1.12	0.735557	1.88	0.0016791
Lpl	175.3	96.6	54.3	108.7	-1.55	0.228811	-2.38	0.0013018
Lrch1	38.6	36.0	15.5	30.0	1.05	0.64228	-1.98	6.65E-27
Lrg1	3.9	10.9	11.4	8.7	2.56	0.032378	2.94	0.0016645
Lrig3	45.7	34.8	24.0	34.8	-1.18	0.426998	-1.50	0.0063964
Lrrc71	3.3	1.6	1.1	2.0	-1.65	0.175744	-2.24	0.0040468
Lrtm2	0.4	12.2	5.4	6.0	20.52	1.68E-16	10.72	4.60E-12
Ltbr	61.6	100.8	142.6	101.6	1.82	0.007224	2.78	9.17E-09
Mafk	24.3	30.8	24.4	26.5	1.43	0.001077	1.25	0.0155551
Map2	20.3	19.7	6.9	15.6	1.09	0.539929	-2.32	3.06E-18
Map2k1	55.5	106.8	124.6	95.7	2.09	0.02174	2.59	0.0001688
Map2k6	34.3	20.3	5.9	20.2	-1.51	0.096175	-4.32	1.78E-15
Map2k7	56.0	57.4	56.7	56.7	1.16	0.212378	1.27	0.0061918
Mapk1ip1	56.2	45.8	15.3	39.1	-1.10	0.443756	-2.90	5.85E-36
Mapkapk2	116.2	244.7	234.8	198.5	2.24	0.02814	2.29	0.0041802

Genes in SE or other end of loop	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	Average TPM	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
Mau2	91.6	89.8	57.9	79.8	1.10	0.356419	-1.26	0.0026613
Mb21d2	14.3	13.4	17.3	15.0	1.04	0.810974	1.51	5.86E-05
Mcc	15.2	14.3	7.0	12.2	1.05	0.710314	-1.72	9.87E-12
Mcee	55.5	47.5	12.2	38.4	-1.05	0.798039	-3.55	1.91E-28
Mdm1	16.5	12.6	6.1	11.7	-1.18	0.323298	-2.14	8.93E-11
Me3	10.5	13.4	25.5	16.4	1.43	0.173302	2.89	2.06E-08
Med16	23.6	22.1	26.8	24.2	1.06	0.62635	1.42	4.44E-07
Meiob	1.7	1.0	0.5	1.1	-1.39	0.477967	-2.38	0.009071
Mesd	76.7	97.1	125.3	99.7	1.43	0.010693	2.02	1.01E-10
Mettl2	31.1	35.6	59.8	42.1	1.29	0.057463	2.38	1.60E-18
Mettl24	32.4	24.2	14.6	23.7	-1.20	0.453446	-1.73	0.0015254
Mettl7a1	256.3	412.7	150.4	273.2	1.80	0.000541	-1.35	0.0429429
Mex3b	59.5	39.2	10.3	36.4	-1.36	0.419969	-4.03	9.52E-08
Minos1	31.1	31.1	37.7	33.3	1.12	0.355845	1.51	2.71E-06
Mir339	16.9	8.1	3.7	9.6	-1.73	0.21668	-2.92	0.0019625
Mknk2	96.8	114.6	43.9	85.1	1.34	0.238988	-1.72	0.003011
Mmp11	136.5	83.9	11.6	77.3	-1.46	0.1219	-8.59	3.12E-33
Mphosph10	31.2	67.7	130.3	76.4	2.35	0.003091	4.66	3.73E-11
Mras	22.2	30.8	35.2	29.4	1.56	0.062917	1.93	0.0002955
Mri1	21.6	19.2	25.2	22.0	-1.01	0.941735	1.45	3.31E-08
Mroh7	8.4	4.7	2.1	5.1	-1.58	0.01953	-3.10	2.82E-13
Mrpl1	20.3	19.0	20.5	19.9	1.05	0.652775	1.27	0.0007141
Mrpl43	31.7	34.6	47.4	37.9	1.23	0.333367	1.83	4.58E-05
Mrvi1	149.6	168.9	188.9	169.1	1.25	0.086171	1.57	5.31E-06
Mst1r	17.4	10.1	7.6	11.7	-1.55	0.056043	-1.79	0.0008481
Mthfd1	39.8	53.2	80.4	57.8	1.50	0.137954	2.41	1.64E-05
Mvb12b	16.2	14.0	15.5	15.2	-1.03	0.795674	1.20	0.0029703
Mybpc1	33.9	23.3	14.1	23.8	-1.27	0.36527	-1.87	0.0008417
Myh9	274.7	308.2	404.1	329.0	1.27	0.280302	1.81	0.0002237
Myl4	8.5	9.4	18.8	12.2	1.24	0.42967	2.65	8.74E-08
Myrip	5.0	20.1	44.3	23.1	3.77	0.000571	7.94	9.65E-11
N4bp3	20.8	24.9	33.8	26.5	1.35	0.153492	1.99	7.08E-06
Naa20	82.5	82.2	113.4	92.7	1.11	0.216224	1.71	3.15E-19
Nab2	41.6	89.4	126.5	85.8	2.30	0.013514	3.38	4.80E-06
Nars	119.4	137.4	419.8	225.5	1.30	0.097006	4.29	2.31E-37
Ndrg2	269.5	245.5	60.8	191.9	1.02	0.905719	-3.50	2.22E-50
Ndufs2	185.8	197.4	284.9	222.7	1.19	0.09787	1.91	1.66E-16
Nedd4l	25.5	41.4	72.2	46.4	1.80	0.066266	3.25	1.14E-06
Neil2	15.8	10.4	1.4	9.2	-1.36	0.170685	-8.32	4.63E-32
Nek8	14.1	10.4	3.3	9.3	-1.21	0.268538	-3.33	1.93E-21
Ngfr	10.8	62.5	236.2	103.2	5.33	5.41E-07	18.66	1.72E-24
Nhp2	44.2	71.1	189.5	101.6	1.79	0.016395	4.97	4.36E-18
Noa1	9.9	9.7	21.3	13.6	1.10	0.477365	2.65	5.97E-34
Nog	1.4	3.1	4.0	2.8	2.40	0.012415	3.25	1.80E-05
Npas2	4.2	11.4	7.1	7.6	2.91	1.33E-10	2.05	1.94E-06
Nr1d1	107.3	55.2	14.9	59.1	-1.71	0.107095	-5.04	4.67E-11
Nrg1	8.8	11.0	62.9	27.6	1.40	0.005185	8.78	6.82E-139
Nrg2	12.4	20.6	43.7	25.5	1.79	0.164592	3.69	2.52E-05
Nrip1	36.6	98.9	72.1	69.2	2.82	0.00168	2.26	0.0035083
Nrp1	71.6	95.1	301.5	156.0	1.50	0.054488	5.01	2.27E-25
Nsun6	10.4	8.6	5.0	8.0	-1.09	0.588668	-1.64	8.41E-07
Nt5c2	51.2	49.1	53.0	51.1	1.07	0.5567	1.29	0.0010706
Nufip2	58.2	75.0	84.5	72.6	1.45	0.060626	1.79	0.0001319
Nup210	14.0	17.6	17.8	16.5	1.42	0.070164	1.58	0.0020147
Nup62	38.7	46.4	58.9	48.0	1.35	0.019746	1.89	1.08E-10
Nynrin	45.0	36.8	21.4	34.4	-1.08	0.693526	-1.67	1.75E-05
Omd	2.1	2.3	0.7	1.7	1.24	0.480666	-2.22	0.0007017
Ost4	159.4	169.8	166.6	165.3	1.19	0.010917	1.30	7.26E-07

Genes in SE or other end of loop	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	Average TPM	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
Oxr1	63.3	52.2	30.2	48.6	-1.09	0.502257	-1.67	5.76E-09
P2ry14	19.9	59.3	119.0	66.1	2.96	0.003859	5.81	6.34E-09
Pacsin2	48.3	50.2	64.5	54.4	1.16	0.005579	1.67	2.33E-33
Palld	59.8	72.7	66.6	66.4	1.36	0.019627	1.39	0.0017107
Palm	56.5	41.4	21.4	39.8	-1.22	0.019609	-2.10	5.52E-30
Pask	4.7	3.0	2.1	3.3	-1.37	0.210064	-1.76	0.0026958
Pbld1	10.6	8.5	0.5	6.5	-1.09	0.793037	-13.89	9.59E-29
Pbld2	4.4	2.7	1.7	3.0	-1.41	0.25077	-1.93	0.002991
Pcp4l1	76.9	182.7	397.5	219.1	2.53	0.004238	5.50	4.95E-11
Pctp	25.9	16.1	9.0	17.0	-1.45	0.133683	-2.23	1.34E-05
Pde10a	6.5	12.3	13.2	10.6	2.08	0.028566	2.36	0.0010165
Pdgfrb	113.5	108.0	56.4	92.6	1.08	0.723955	-1.59	0.0005218
Pdp2	32.5	24.8	13.5	23.6	-1.16	0.339815	-1.90	9.90E-09
Pdzd2	11.1	9.7	4.7	8.5	-1.02	0.932943	-1.89	7.79E-08
Pemt	5.2	5.5	11.1	7.2	1.18	0.519716	2.58	8.14E-09
Per1	29.7	26.2	10.5	22.1	-1.02	0.959877	-2.19	1.25E-05
Pgs1	24.9	36.0	62.7	41.2	1.61	0.001273	3.08	7.62E-21
Pheta1	26.2	22.9	9.6	19.6	-1.02	0.87275	-2.17	3.45E-23
Phf21a	40.8	31.5	14.8	29.0	-1.16	0.276253	-2.18	1.67E-15
Phf5a	37.1	46.9	61.3	48.4	1.42	0.012605	2.04	7.39E-11
Phldb1	69.2	76.2	26.0	57.2	1.25	0.380823	-2.06	5.11E-05
Pigz	4.1	2.3	0.4	2.3	-1.59	0.113404	-6.40	4.61E-14
Pim1	77.2	135.5	86.6	99.7	1.94	0.000283	1.39	0.0413882
Pim3	34.4	78.6	40.2	51.1	2.48	0.000465	1.43	0.124004
Pknox2	28.9	30.1	46.7	35.3	1.18	0.430572	1.99	1.20E-06
Plekha8	15.0	25.5	31.4	23.9	1.89	0.012538	2.50	5.52E-06
Plekhj1	39.2	43.6	59.1	47.3	1.25	0.102572	1.88	5.35E-10
Plk2	36.8	120.6	236.4	131.3	3.31	0.000411	6.45	4.45E-11
Plod1	48.9	99.8	152.9	100.5	2.18	0.03139	3.41	1.12E-05
Plscr4	53.2	42.8	20.4	38.8	-1.11	0.377457	-2.07	8.72E-18
Pltp	155.4	115.8	58.3	109.8	-1.20	0.14637	-2.11	3.90E-16
Pnpla2	49.0	44.2	20.4	37.8	1.02	0.959587	-1.86	0.0024388
Pold4	49.9	34.1	21.5	35.2	-1.32	0.142826	-1.83	1.81E-05
Polr2b	89.2	96.7	108.4	98.1	1.22	0.097555	1.51	3.80E-06
Polr2e	103.9	111.0	125.3	113.4	1.21	0.271179	1.50	0.0010883
Popdc2	18.3	21.0	28.5	22.6	1.29	0.264803	1.91	9.14E-05
Ppcdc	23.9	18.3	8.6	16.9	-1.18	0.318093	-2.20	1.74E-11
Ppp1cb	274.9	251.1	276.4	267.4	1.02	0.795125	1.26	2.60E-07
Ppp1cc	121.5	140.8	177.1	146.5	1.31	0.081503	1.80	2.78E-07
Ppp1r12b	86.1	60.3	43.4	63.3	-1.28	0.218046	-1.57	0.0022493
Ppp1r3b	6.4	5.4	2.9	4.9	-1.07	0.722119	-1.78	1.49E-06
Ppp1r7	27.8	25.8	28.2	27.3	1.05	0.713651	1.27	0.001733
Prkce	18.2	21.4	34.8	24.8	1.33	0.122853	2.36	2.75E-10
Prpf19	62.7	63.8	80.8	69.1	1.14	0.171718	1.60	4.90E-12
Psmc3	180.4	179.4	282.1	214.0	1.11	0.157218	1.95	2.64E-34
Ptbp1	141.8	189.7	283.8	205.1	1.51	0.084215	2.42	7.26E-07
Ptpn1	25.2	52.0	50.0	42.4	2.24	0.002755	2.34	0.0001304
Ptprr	19.1	12.6	3.0	11.6	-1.30	0.562343	-4.15	2.04E-06
Ptprs	66.3	73.1	100.9	80.1	1.25	0.206153	1.88	6.52E-07
Ptrh1	4.6	9.8	29.6	14.7	2.25	0.026661	6.54	9.82E-12
Pum3	48.5	59.1	130.5	79.4	1.37	0.030023	3.30	1.01E-27
Pyroxd2	11.3	9.0	3.2	7.8	-1.13	0.507319	-2.77	4.23E-16
Pyurf	17.2	15.4	19.0	17.2	1.01	0.960166	1.38	2.15E-05
Qprt	2.3	2.7	6.3	3.8	1.26	0.456977	3.17	3.31E-09
R74862	8.0	7.2	2.6	5.9	1.01	0.978103	-2.37	1.42E-09
Rab5c	148.4	153.2	217.2	173.0	1.16	0.099106	1.82	2.06E-20
Radil	18.0	14.4	2.6	11.7	-1.13	0.567341	-5.25	1.07E-32
Rai1	24.4	35.0	38.2	32.5	1.61	0.106416	1.88	0.0047352

Genes in SE or other end of loop	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	Average TPM	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
Raly	168.7	374.9	1084.7	542.7	2.44	0.000124	7.27	1.73E-24
Rara	21.0	35.0	36.5	30.9	1.85	0.005435	2.11	3.40E-05
Rasd1	16.4	52.8	47.0	38.7	3.06	0.011	2.91	0.0026341
Rasd2	64.8	40.8	15.6	40.4	-1.42	0.156997	-3.14	2.61E-10
Rasgef1a	12.1	7.5	1.8	7.2	-1.42	0.379706	-4.42	8.62E-08
Rbp1	38.9	33.3	20.0	30.7	-1.05	0.741425	-1.55	2.06E-07
Rem1	38.8	23.7	13.9	25.4	-1.47	0.127854	-2.15	5.35E-05
Rere	78.4	62.9	29.6	56.9	-1.12	0.587579	-2.08	2.73E-08
Rest	38.4	38.2	40.0	38.9	1.12	0.270025	1.30	0.00044
Rfx1	17.7	15.9	6.3	13.3	1.02	0.945406	-2.19	1.06E-10
Rgl1	52.6	44.8	14.1	37.2	-1.05	0.71908	-2.95	2.17E-36
Rhbdl2	3.6	3.9	7.1	4.9	1.20	0.485994	2.35	3.12E-07
Rhoc	132.2	218.8	366.6	239.2	1.83	0.028209	3.23	2.89E-08
Rhou	39.0	73.9	79.3	64.1	2.05	0.031375	2.35	0.0010706
Rilpl1	32.5	29.1	19.4	27.0	1.01	0.959921	-1.33	0.0002235
Rmnd5b	38.9	40.6	89.0	56.2	1.17	0.189308	2.83	6.90E-35
Rnase11	0.0	0.2	1.6	0.6	1.70	0.427578	6.70	4.47E-05
Rnd3	60.7	64.7	113.8	79.7	1.19	0.195302	2.31	8.21E-18
Rpf1	35.9	42.6	49.9	42.8	1.33	0.049729	1.72	9.03E-07
Rpl18	1632.1	1629.6	2049.6	1770.4	1.12	0.240526	1.56	1.74E-11
Rrbp1	129.5	141.8	192.1	154.5	1.24	0.200076	1.84	5.48E-07
Rufy1	43.2	42.4	52.0	45.9	1.11	0.478004	1.50	3.98E-05
Rusc2	47.9	33.6	18.9	33.5	-1.28	0.32967	-1.97	0.0001433
Rxfp2	2.6	4.1	42.5	16.4	1.74	0.034695	17.70	3.11E-51
Saa1	1.1	1.4	6.7	3.1	1.28	0.628755	5.83	2.02E-09
Samd4	40.2	38.0	22.6	33.6	1.06	0.708877	-1.42	0.000435
Sar1b	58.9	67.0	88.7	71.6	1.28	0.117552	1.86	1.13E-07
Sart3	37.4	38.3	43.1	39.6	1.16	0.329666	1.43	0.0007618
Scgb3a1	0.1	0.4	1.3	0.6	1.72	0.389133	4.39	0.0005018
Scpep1	155.9	121.4	71.2	116.1	-1.15	0.093997	-1.75	2.50E-19
Scube1	17.1	30.9	170.1	72.7	1.98	0.045068	10.14	7.65E-20
Sdc1	62.8	75.8	106.1	81.6	1.36	0.213233	2.05	6.64E-05
Sdk1	9.3	8.4	18.5	12.1	1.02	0.934896	2.45	2.56E-14
Sec24a	13.2	16.5	19.9	16.5	1.41	0.106505	1.85	0.0001205
Sec31b	7.2	5.7	2.7	5.2	-1.13	0.373038	-2.08	7.20E-13
Selenbp1	130.9	93.7	11.5	78.7	-1.25	0.219719	-8.60	4.25E-59
Sema4a	11.4	12.4	15.0	12.9	1.22	0.337646	1.62	0.0010674
Sema4g	2.9	2.8	1.1	2.3	1.08	0.773091	-1.99	6.32E-05
Sep9	62.2	75.2	119.7	85.7	1.36	0.119488	2.35	6.63E-09
Sesn3	91.4	61.8	19.7	57.6	-1.33	0.240541	-3.52	3.21E-13
Sf3a2	33.1	38.8	62.6	44.8	1.32	0.069506	2.34	4.55E-14
Sfrp2	98.9	75.5	7.0	60.5	-1.17	0.355668	-10.69	1.24E-84
Sgk1	16.2	43.1	49.7	36.3	2.80	0.000352	3.45	3.40E-07
Sh2d3c	11.4	11.3	5.9	9.5	1.11	0.400239	-1.53	1.00E-06
Sh3bp5	40.4	34.5	21.6	32.2	-1.05	0.594096	-1.50	6.37E-13
Sh3d19	78.5	57.5	21.1	52.4	-1.23	0.275672	-2.91	1.10E-15
Sh3d21	29.9	18.3	6.3	18.1	-1.42	0.110719	-3.63	6.36E-15
Shank2	5.2	3.9	1.4	3.5	-1.17	0.184549	-2.81	3.20E-28
Sin3a	53.8	45.7	29.7	43.1	-1.05	0.492095	-1.45	3.71E-13
Slc15a3	5.2	10.1	30.7	15.3	2.07	0.022704	6.35	2.23E-14
Slc16a1	30.0	82.4	84.2	65.5	2.81	0.004369	3.04	0.0001802
Slc22a23	13.6	13.1	2.9	9.9	1.08	0.567341	-3.74	6.82E-52
Slc22a3	22.5	17.5	3.8	14.6	-1.14	0.500968	-4.61	6.02E-32
Slc25a12	46.7	44.6	51.4	47.6	1.07	0.417019	1.37	3.72E-08
Slc25a28	52.3	53.0	55.9	53.7	1.14	0.117878	1.33	2.35E-06
Slc25a39	89.7	108.2	211.1	136.3	1.36	0.144977	2.85	1.50E-11
Slc29a1	129.3	103.9	53.0	95.4	-1.11	0.29708	-1.94	1.10E-19
Slc29a3	12.6	8.8	7.0	9.4	-1.28	0.045626	-1.44	0.0001532

Genes in SE or other end of loop	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	Average TPM	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
Slc2a8	19.1	16.5	5.3	13.6	-1.02	0.921977	-2.81	7.01E-16
Slc35b1	57.6	81.8	303.9	147.8	1.59	0.028789	6.21	2.67E-30
Slc35b2	48.5	48.4	69.8	55.6	1.12	0.20106	1.79	3.67E-21
Slc41a3	7.1	6.0	2.7	5.3	-1.06	0.759423	-2.05	8.75E-09
Slc43a1	31.6	29.2	6.7	22.5	1.02	0.949412	-3.61	6.95E-16
Slc8b1	41.1	34.1	11.1	28.8	-1.07	0.477365	-2.94	7.86E-55
Slco2a1	9.2	17.2	32.3	19.6	2.01	0.060983	3.77	2.30E-06
Slco2b1	32.1	32.4	9.2	24.6	1.13	0.200606	-2.77	8.38E-46
Smad3	48.0	46.0	25.3	39.8	1.08	0.532302	-1.51	1.58E-07
Smco2	2.7	0.2	0.5	1.2	-5.00	0.002824	-2.85	0.0194619
Smoc1	38.9	50.3	75.4	54.9	1.46	0.163425	2.33	2.07E-05
Smoc2	143.4	156.0	249.9	183.1	1.23	0.298877	2.15	4.88E-08
Sned1	232.5	169.1	33.9	145.2	-1.22	0.279023	-5.28	1.50E-39
Snn	41.6	44.6	14.8	33.7	1.22	0.425038	-2.18	4.68E-06
Snord104	205.8	289.9	580.2	358.6	1.58	0.056491	3.36	6.55E-12
Snord42b	48.1	54.2	80.1	60.8	1.25	0.567341	1.98	0.0074769
Snord52	52.7	103.5	373.7	176.6	2.03	0.082488	6.82	1.48E-10
Snord57	7.7	24.4	34.4	22.2	2.64	0.062209	3.75	0.0008285
Snx5	194.5	273.4	271.0	246.3	1.58	0.034453	1.71	0.001465
Socs2	31.3	79.8	94.9	68.7	2.71	1.91E-05	3.53	2.79E-10
Socs3	22.7	187.4	117.3	109.1	7.63	1.16E-11	5.37	5.69E-10
Sorbs3	55.0	44.1	24.4	41.1	-1.11	0.415616	-1.79	6.44E-11
Sox12	12.9	12.2	5.2	10.1	1.08	0.845738	-1.92	0.0043356
Sp3	152.8	181.2	213.2	182.4	1.34	0.030603	1.73	9.10E-08
Spata33	25.0	4.6	4.2	11.2	-4.05	0.0001	-4.01	6.64E-06
Sphk1	17.1	37.3	52.0	35.5	2.35	0.000508	3.54	7.23E-10
Spred2	16.6	15.5	8.5	13.5	1.05	0.715463	-1.56	3.85E-08
Spsb1	19.0	71.6	22.7	37.8	3.86	6.05E-06	1.44	0.193091
Ssc5d	13.8	14.5	8.3	12.2	1.18	0.271876	-1.34	0.0086671
St3gal5	10.6	15.4	22.8	16.3	1.62	0.01857	2.60	9.86E-10
St6galnac2	44.5	36.9	10.6	30.7	-1.07	0.723955	-3.27	2.05E-21
Stag3	8.5	2.7	2.8	4.6	-2.64	0.000784	-2.30	0.0006623
Stat5a	12.6	38.0	31.5	27.3	3.01	0.003669	2.70	0.0015331
Steap3	68.5	56.7	17.5	47.6	-1.08	0.519935	-3.10	2.86E-46
Stox2	11.0	8.0	6.5	8.5	-1.24	0.117505	-1.36	0.0027861
Stx16	72.9	63.6	45.7	60.7	-1.02	0.892158	-1.27	0.0026213
Sulf2	47.3	51.6	70.3	56.4	1.23	0.201602	1.84	2.07E-07
Supt6	80.3	85.9	108.1	91.4	1.21	0.298936	1.67	0.0001195
Synj2	43.6	31.2	23.3	32.7	-1.25	0.080174	-1.49	4.04E-05
Synpo	8.0	27.4	35.7	23.7	2.93	0.034494	3.78	0.0007821
Sytl5	4.1	5.3	23.4	10.9	1.45	0.049092	6.80	8.88E-45
Tacc1	73.2	99.3	120.1	97.6	1.53	0.019895	2.02	7.40E-07
Tbc1d1	71.9	80.9	88.3	80.4	1.27	0.101294	1.52	9.65E-05
Tbc1d2b	51.7	43.9	19.8	38.5	-1.06	0.496436	-2.08	1.10E-40
Tcerg1	43.5	50.9	79.3	57.9	1.32	0.065853	2.25	4.94E-13
Tef	217.3	130.4	39.1	128.9	-1.48	4.53E-05	-4.39	4.88E-75
Tet2	40.9	36.8	19.5	32.4	1.01	0.925733	-1.67	2.56E-13
Tet3	23.3	18.0	12.7	18.0	-1.16	0.171196	-1.46	1.44E-06
Tex2	39.6	72.4	116.2	76.1	1.96	0.087221	3.17	0.0001068
Tgfb2	14.2	18.2	30.5	20.9	1.44	0.230375	2.53	2.81E-05
Tgfbr3	125.2	139.7	127.2	130.7	1.25	0.009647	1.27	0.0006535
Thrb	23.8	22.7	6.9	17.8	1.07	0.664823	-2.73	1.68E-24
Timp3	377.5	362.0	477.6	405.7	1.09	0.645842	1.57	6.34E-05
Tinagl1	30.3	54.4	89.4	58.0	1.96	0.046385	3.32	3.11E-06
Tiparp	35.1	147.5	46.8	76.5	4.17	1.47E-05	1.58	0.134435
Tlcd1	18.5	22.6	6.0	15.7	1.38	0.330234	-2.32	0.0004376
Tlnrd1	21.9	74.3	76.5	57.6	3.57	1.21E-06	3.97	1.72E-09
Tmbim4	78.0	80.2	83.1	80.4	1.16	0.230638	1.33	0.0014548

Genes in SE or other end of loop	V TPM (avg)	E2h TPM (avg)	E6h TPM (avg)	Average TPM	fold change: E2h-vs-V	adj p-value: E2h-vs-V	fold change: E6h-vs-V	adj p-value: E6h-vs-V
Tmed2	120.1	143.0	305.7	189.6	1.34	0.046675	3.13	2.11E-25
Tmem106b	110.9	84.2	34.6	76.6	-1.19	0.30837	-2.53	6.56E-15
Tmem14a	15.4	11.1	2.8	9.8	-1.24	0.377604	-4.16	1.36E-15
Tmem206	12.1	8.0	4.2	8.1	-1.35	0.015054	-2.26	8.99E-17
Tmem214	57.9	62.6	109.3	76.6	1.22	0.141314	2.34	4.39E-18
Tnfaip2	16.2	43.9	38.3	32.8	2.61	0.012434	2.56	0.0023914
Tnfsf10	29.6	22.9	11.5	21.3	-1.15	0.411804	-2.04	1.82E-09
Tnnc1	0.4	0.5	1.5	0.8	1.25	0.743854	3.08	0.0055345
Tns4	8.2	5.9	13.2	9.1	-1.24	0.456558	1.96	0.0008612
Tpd52	42.2	43.1	55.1	46.8	1.15	0.392718	1.62	1.59E-05
Tppp2	5.8	0.9	0.9	2.5	-3.54	0.026403	-3.25	0.0089555
Tpx2	6.8	9.9	6.6	7.8	1.63	0.006879	1.21	0.219253
Trabd	48.4	61.7	98.0	69.4	1.44	0.051744	2.48	8.74E-11
Trabd2b	3.7	10.6	56.6	23.6	2.92	0.001415	14.29	1.64E-22
Trappc6a	50.4	38.6	19.4	36.1	-1.17	0.184662	-2.07	8.24E-16
Trio	104.1	86.5	51.9	80.8	-1.08	0.699102	-1.59	0.0002275
Triobp	19.1	39.3	40.6	33.0	2.24	0.010917	2.47	0.0003636
Trmt61a	14.4	25.3	111.9	50.5	1.96	0.000732	9.04	2.39E-42
Trmt9b	10.2	7.1	1.4	6.2	-1.28	0.36596	-5.19	7.87E-16
U2af2	133.6	146.2	300.9	193.6	1.24	0.134755	2.78	1.19E-23
Uba7	60.6	48.5	21.1	43.4	-1.12	0.218526	-2.28	2.31E-37
Ubc	130.0	165.1	148.2	147.8	1.43	0.03313	1.42	0.0089387
Ube2b	142.9	145.3	71.8	120.0	1.14	0.120567	-1.59	7.57E-14
Ube2d-ps	13.2	13.5	19.7	15.5	1.15	0.328072	1.85	1.15E-10
Ubxn1	169.7	170.1	185.7	175.2	1.13	0.317948	1.36	0.0003184
Ugp2	70.7	86.2	85.5	80.8	1.36	0.013621	1.50	4.60E-05
Umps	26.4	44.4	70.2	47.0	1.87	0.015029	3.14	1.28E-08
Uprt	15.8	14.3	16.9	15.7	1.01	0.968765	1.33	0.0067639
Usp2	26.2	16.6	7.7	16.9	-1.37	0.109931	-2.64	4.95E-11
Usp36	23.0	36.4	49.6	36.3	1.76	0.045709	2.55	1.54E-05
Uspl1	40.3	67.9	76.9	61.7	1.87	0.02027	2.27	0.0001069
Vapa	121.2	168.5	271.7	187.2	1.56	0.058165	2.69	2.13E-08
Vegfa	66.5	194.7	211.8	157.7	2.65	0.052163	2.97	0.0053035
Vldlr	93.9	89.1	52.4	78.5	1.06	0.777614	-1.42	0.0031765
Vps37c	25.5	23.2	32.6	27.1	1.02	0.885506	1.59	2.47E-15
Wt1	100.4	112.7	42.7	85.2	1.27	0.206433	-1.85	7.34E-06
Ypel2	48.2	37.7	12.7	32.9	-1.15	0.401038	-2.96	2.33E-22
Zbtb20	151.6	128.0	34.5	104.7	-1.06	0.719227	-3.46	4.31E-40
Zcchc10	7.6	9.0	12.9	9.8	1.33	0.146211	2.08	2.27E-07
Zcchc24	104.7	98.1	114.1	105.6	1.05	0.599172	1.36	4.47E-08
Zdhhc1	95.1	72.9	29.5	65.8	-1.17	0.332355	-2.53	4.28E-16
Zdhhc7	28.8	30.6	32.6	30.7	1.20	0.144193	1.41	0.0001768
Zeb1	64.4	60.3	85.7	70.1	1.05	0.522968	1.66	3.36E-26
Zfp317	66.5	69.2	65.5	67.0	1.17	0.057484	1.23	0.0009537
Zfp395	19.6	11.5	2.4	11.2	-1.51	0.185982	-5.65	2.77E-14
Zfp462	10.0	10.7	5.5	8.7	1.21	0.194896	-1.45	0.0008656
Zmynd8	26.0	21.5	13.5	20.3	-1.08	0.361728	-1.54	4.53E-13

Column #	Probeset ID	gene_assignment	Gene Symbol	RefSeq	seqname	Mean(Ex3aERKO-E2 2h)	Mean(Ex3aERKO-Saline)	Mean(WT-E2 2h)	Mean(WT-Saline)	Mean(ppKO E2 2h)	Mean(ppKO Saline)	Mean(ppWT E2 2h)	Mean(ppWT Saline)	p-value(Ex3aERKO-E2 2h vs. Ex3aERKO-Saline)	Ratio(Ex3aERKO-E2 2h vs. Ex3aERKO-Saline)	Fold-Change(Ex3aERKO-E2 2h vs. Ex3aERKO-Saline)	p-value(WT-E2 2h vs. WT-Saline)	Ratio(WT-E2 2h vs. WT-Saline)	Fold-Change(WT-E2 2h vs. WT-Saline)	p-value(ppKO E2 2h vs. ppKO Saline)	Ratio(ppKO E2 2h vs. ppKO Saline)	Fold-Change(ppKO E2 2h vs. ppKO Saline)	p-value(ppWT E2 2h vs. ppWT Saline)	Ratio(ppWT E2 2h vs. ppWT Saline)	Fold-Change(ppWT E2 2h vs. ppWT Saline)
20350	TC0400001090.mm.1	NM_001162980 // 1700024P1	1700024P16Rik	NM_001162980	chr4	7.36525	6.64633	10.8707	6.62508	7.49038	6.82878	9.89436	7.36155	0.026918	1.64594	1.64594	1.05E-34	18.9696	18.9696	0.041212	1.58183	1.58183	1.58E-11	5.78697	5.78697
70283	TC1800001445.mm.1	NR_037693 // 2700046A07Rik	2700046A07Rik	NR_037693	chr18	8.83148	9.3438	7.41062	9.22838	8.77242	9.39002	7.33269	8.49423	0.085287	0.701094	-1.42634	4.01E-16	0.283662	-3.52533	0.038906	0.651754	-1.53432	0.000174098	0.447036	-2.23695
36001	TC0800000626.mm.1	ENSMUST00000181638 // 503	5033428I22Rik	ENSMUST00000181638	chr8	7.94082	8.15007	6.68814	7.92743	7.74552	8.04823	6.86981	7.68757	0.22761	0.864984	-1.15609	3.17E-19	0.42358	-2.36083	0.082541	0.810728	-1.23346	9.56E-06	0.567322	-1.76267
39330	TC0900000735.mm.1	NM_176921 // 6030419C18Rik	6030419C18Rik	NM_176921	chr9	6.5209	6.38772	7.28986	6.25948	6.90657	6.28482	7.19259	6.73888	0.476525	1.09671	1.09671	4.48E-14	2.04256	2.04256	0.001313	1.53874	1.53874	0.0171857	1.36956	1.36956
21916	TC0400002665.mm.1	NM_013454 // Abca1 // ATP-b	Abca1	NM_013454	chr4	11.3126	10.6914	10.1921	11.5506	10.5456	11.0321	9.48645	10.4332	0.053097	1.5382	1.5382	3.77E-10	0.389988	-2.56418	0.127958	0.713728	-1.40109	0.00372417	0.518786	-1.92758
49647	TC1100000547.mm.1	NM_001277305 // Adamts2 //	Adamts2	NM_001277305	chr11	8.10724	7.77464	10.7368	7.88788	8.88226	8.23458	9.68029	8.50052	0.20436	1.25928	1.25928	2.24E-29	7.20479	7.20479	0.014878	1.56665	1.56665	2.12E-05	2.2654	2.2654
8307	TC0100001581.mm.1	NM_172845 // Adamts4 // a d	Adamts4	NM_172845	chr1	6.03696	5.74082	11.3447	5.59909	6.3976	6.24918	8.9867	6.4381	0.535028	1.22786	1.22786	5.35E-32	53.6528	53.6528	0.75564	1.10836	1.10836	8.94E-07	5.85066	5.85066
64390	TC1600000491.mm.1	NM_001012765 // Adcy5 // ad	Adcy5	NM_001012765	chr16	8.13569	8.0296	10.8007	8.28663	8.74439	8.55989	9.93725	8.5124	0.718197	1.07631	1.07631	3.37E-23	5.71242	5.71242	0.530642	1.13642	1.13642	6.27E-06	2.68486	2.68486
17448	TC0300001409.mm.1	NM_007409 // Adh1 // alcohol	Adh1	NM_007409	chr3	12.6678	11.2309	14.1007	12.2691	12.6005	11.9058	13.2408	12.5084	0.002777	2.70749	2.70749	4.79E-09	3.55927	3.55927	0.138805	1.61859	1.61859	0.118891	1.66152	1.66152
13753	TC0200003195.mm.1	NM_026212 // Agpat2 // 1-acy	Agpat2	NM_026212	chr2	8.77138	8.42405	9.91417	8.28381	8.56141	8.71422	8.85259	8.81887	0.237474	1.2722	1.2722	3.01E-14	3.09591	3.09591	0.601873	0.899499	-1.11173	0.908246	1.02365	1.02365
23416	TC0400004177.mm.1	NM_001035532 // Akap2 // A	Akap2	NM_001035532	chr4	8.27194	8.08822	10.3078	8.48953	8.62135	8.52035	9.39894	8.50338	0.380978	1.1358	1.1358	1.40E-23	3.52653	3.52653	0.629445	1.07251	1.07251	5.21E-05	1.86033	1.86033
40355	TC0900001771.mm.1	NM_001081395 // Amotl1 // a	Amotl1	NM_001081395	chr9	9.31637	8.94543	10.809	9.33286	9.5376	9.33998	10.1573	9.51029	0.086604	1.2932	1.2932	2.42E-18	2.78207	2.78207	0.357843	1.14681	1.14681	0.00337738	1.56588	1.56588
11181	TC0200000603.mm.1	NM_011923 // Angptl2 // angi	Angptl2	NM_011923	chr2	9.05285	9.49765	11.5108	9.66392	9.49552	9.59375	10.4655	9.91733	0.10782	0.734686	-1.36112	7.02E-18	3.59724	3.59724	0.720249	0.934176	-1.07046	0.0485159	1.4622	1.4622
8306	TC0100001580.mm.1	NM_013474 // Apoa2 // apoli	Apoa2	NM_013474	chr1	7.16505	7.33032	6.9053	9.00784	7.5973	7.35602	7.08184	6.77049	0.87334	0.891759	-1.12138	0.0010235	0.232848	-4.29464	0.815992	1.18204	1.18204	0.763984	1.24087	1.24087
59018	TC1400000271.mm.1	NM_001289686 // Arhgef3 //	Arhgef3	NM_001289686	chr14	9.82263	9.61192	8.13453	9.45874	9.28921	9.48978	8.24139	9.11046	0.344095	1.15726	1.15726	1.74E-15	0.399368	-2.50396	0.367688	0.870209	-1.14915	0.000191064	0.5475	-1.82649
62608	TC1500001038.mm.1	NM_007497 // Atf1 // activatir	Atf1	NM_007497	chr15	10.6599	10.8809	12.0237	10.9163	11.1992	10.9726	11.7484	11.0936	0.06856	0.857929	-1.1656	4.94E-25	2.15458	2.15458	0.062029	1.1701	1.1701	5.73E-07	1.57443	1.57443
18627	TC0300002605.mm.1	NM_144900 // Atp1a1 // ATPa	Atp1a1	NM_144900	chr3	15.145	14.1514	16.4611	13.8454	14.3184	14.179	15.9037	14.6963	0.000131	1.99116	1.99116	1.53E-28	6.1291	6.1291	0.572875	1.10145	1.10145	5.38E-06	2.30916	2.30916
50911	TC1100001820.mm.1	NM_015732 // Axin2 // axin2 /	Axin2	NM_015732	chr11	9.01305	9.19222	11.0092	9.25206	9.20785	9.20018	10.3803	9.02282	0.367899	0.883215	-1.13223	5.02E-24	3.38026	3.38026	0.969152	1.00533	1.00533	1.76E-09	2.5624	2.5624
15727	TC0200005186.mm.1	NM_019835 // B4galt5 // UDP	B4galt5	NM_019835	chr2	9.06927	8.35569	14.9029	8.81656	9.7936	9.32986	13.7023	9.87436	0.115375	1.63986	1.63986	3.07E-35	67.9458	67.9458	0.303847	1.37912	1.37912	1.20E-12	14.2016	14.2016
17287	TC0300001247.mm.1	NM_013867 // Bcar3 // breast	Bcar3	NM_013867	chr3	6.91235	6.63515	8.42923	6.76612	7.02564	6.83028	7.34899	7.08702	0.203255	1.21184	1.21184	1.09E-20	3.167	3.167	0.368545	1.14501	1.14501	0.228917	1.19912	1.19912
28365	TC0600001203.mm.1	NM_011498 // Bhlhe40 // basi	Bhlhe40	NM_011498	chr6	8.63513	8.46332	10.8368	8.73456	8.78236	9.25603	9.90569	9.1966	0.493232	1.12647	1.12647	9.35E-23	4.29367	4.29367	0.061533	0.720127	-1.38864	0.00578949	1.63477	1.63477
56555	TC1300000562.mm.1	NM_001039179 // Bicd2 // bic	Bicd2	NM_001039179	chr13	8.51694	8.22502	9.97091	8.34653	8.48609	8.36192	9.70328	8.56911	0.049001	1.22427	1.22427	8.84E-30	3.08308	3.08308	0.397313	1.08988	1.08988	3.43E-11	2.19492	2.19492
63585	TC1500002030.mm.1	NM_001033274 // Brd1 // bro	Brd1	NM_001033274	chr15	8.57577	8.37208	9.61807	8.53279	8.65402	8.65786	9.29324	8.61938	0.09705	1.15164	1.15164	3.25E-24	2.12179	2.12179	0.974808	0.997342	-1.00267	4.07E-07	1.59534	1.59534
34845	TC0700004126.mm.1	NM_133700 // Btbd10 // BTB	Btbd10	NM_133700	chr7	8.14595	7.9624	9.61685	7.83166	8.28746	8.09863	9.49772	8.16764	0.238206	1.13567	1.13567	8.65E-31	3.44664	3.44664	0.225077	1.13984	1.13984	8.81E-13	2.51417	2.51417
37927	TC0800002570.mm.1	NM_145970 // Cc2d1a // coile	Cc2d1a	NM_145970	chr8	7.72087	7.66647	9.62488	7.464	7.78868	7.84523	8.57953	7.69368	0.794372	1.03842	1.03842	5.85E-28	4.47188	4.47188	0.786428	0.961563	-1.03997	5.93E-05	1.84785	1.84785
51228	TC1100002142.mm.1	NM_134033 // Ccdc117 // coil	Ccdc117	NM_134033	chr11	8.9522	8.92415	10.5669	8.86513	9.14906	9.03579	9.98233	9.10546	0.868307	1.01964	1.01964	3.34E-27	3.25304	3.25304	0.503856	1.08168	1.08168	1.71E-06	1.83638	1.83638
10633	TC0200000048.mm.1	NM_028804 // Ccdc3 // coiled	Ccdc3	NM_028804	chr2	8.60353	7.68074	9.32555	8.0474	8.13584	8.03611	8.80732	8.32639	0.001697	1.89578	1.89578	7.97E-11	2.42527	2.42527	0.725807	1.07157	1.07157	0.0937562	1.39564	1.39564
62228	TC1500000654.mm.1	NM_027219 // Cdc42ep1 // CD	Cdc42ep1	NM_027219	chr15	8.87087	8.86056	11.625	8.87198	9.32239	9.20941	10.4093	9.36986	0.963205	1.00718	1.00718	1.39E-32	6.74143	6.74143	0.613683	1.08146	1.08146	1.34E-05	2.05543	2.05543
13159	TC0200002594.mm.1	NM_001287738 // Cebpb // C	Cebpb	NM_001287738	chr2	8.14469	8.39313	9.68833	8.07457	8.37225	8.18742	8.62076	8.43078	0.472391	0.841804	-1.18793	2.15E-11	3.06048	3.06048	0.592646	1.13668	1.13668	0.582385	1.14075	1.14075
32147	TC0700001399.mm.1	NM_133709 // Chrdl2 // chord	Chrdl2	NM_133709	chr7	7.65904	7.2289	9.54531	8.34891	8.56431	8.29538	9.35298	8.72675	0.201984	1.34737	1.34737	6.27E-08	2.29168	2.29168	0.423478	1.20491	1.20491	0.0648491	1.54353	1.54353
46829	TC1000000937.mm.1	NM_021439 // Chst11 // carb	Chst11	NM_021439	chr10	7.7092	7.65852	11.4944	7.71893	8.26169	7.87357	10.311	8.7028	0.856543	1.03575	1.03575	4.37E-35	13.6937	13.6937	0.168873	1.30869	1.30869	1.83E-07	3.04873	3.04873
35118	TC0700004404.mm.1	NM_029935 // Chst15 // carb	Chst15	NM_029935	chr7	7.91596	7.33512	8.73638	7.14394	7.36389	7.34765	7.89573	7.49091	0.005444	1.49572	1.49572	4.02E-21	3.01559	3.01559	0.936424	1.01132	1.01132	0.0496226	1.32392	1.32392
46735	TC1000000843.mm.1	NM_007705 // Cirbp // cold in	Cirbp	NM_007705	chr10	9.23098	10.0423	8.70141	10.0204	9.24721	9.65427	8.95723	9.35268	1.13E-05	0.569851	-1.75484	1.48E-20	0.400823	-2.49487	0.020759	0.754159	-1.32598	0.024538	0.760256	-1.31535
26482	TC0500003043.mm.1	NM_008153 // Cmklr1 // chem	Cmklr1	NM_008153	chr5	7.51449	7.03598	10.1788	7.05644	7.56947	7.5908	8.30841	7.66608	0.040717	1.3933	1.3933	3.04E-35	8.70803	8.70803	0.926265	0.985322	-1.0149	0.00658806	1.56085	1.56085
46727	TC1000000834.mm.1	NM_007725 // Cnn2 // calponi	Cnn2	NM_007725	chr10	9.94195	9.41768	11.2598	9.97966	10.8343	10.5358	11.2879	10.5455	0.073301	1.43821	1.43821	1.39E-10	2.42866	2.42866	0.304274	1.22989	1.22989	0.012096	1.67295	1.67295
48285	TC1000002405.mm.1	NM_146007 // Col6a2 // collag	Col6a2	NM_146007	chr10	9.05156	8.79185	10.0038	8.914	9.79859	9.32486	10.7015	10.2026	0.483279	1.19724	1.19724	4.23E-06	2.12847	2.12847	0.202733	1.3887	1.3887	0.180012	1.41315	1.41315
9499	TC0100002789.mm.1	NM_001243008 // Col6a3 // cc	Col6a3	NM_001243008	chr1	9.78846	9.68516	12.7838	10.4204	11.1865	10.6275	12.3392	11.3327	0.80396	1.07423	1.07423	1.36E-14	5.14578	5.14578	0.181753	1.47325	1.47325	0.0176411	2.00912	2.00912
36797	TC0800001432.mm.1	NM_030209 // Crispld2 // cyst	Crispld2	NM_030209	chr8	8.71412	8.33075	12.1591	8.621	9.18972	8.92466	10.8103	8.90524	0.267757	1.30439	1.30439	9.62E-28	11.6167	11.6167	0.442543	1.20169	1.20169	4.25E-07	3.74522	3.74522
14694	TC0200004140.mm.1	NM_001113333 // Cry2 // cryp	Cry2	NM_001113333	chr2	9.04526	9.28098	10.5409	8.83765	9.10882	9.23904	9.1572	9.00844	0.327417	0.84926	-1.1775	5.56E-19	3.25642	3.25642	0.587662	0.913694	-1.09446	0.535759	1.10861	1.10861
11119	TC0200000538.mm.1	NM_030137 // Cstad // CSA-cc	Cstad	NM_030137	chr2	7.62462	8.47871	6.82821	8.26719	8.13599	8.50823	6.80984	8.22537	0.000571	0.553213	-1.80762	9.58E-16	0.368827	-2.7113	0.120819	0.77258	-1.29436	7.67E-08	0.374871	-2.66758
59625	TC1400000895.mm.1	NM_007798 // Ctsb // catheps	Ctsb	NM_007798	chr14	14.4732	13.6507	15.1552	14.0909	14.1399	14.1309	14.6692	14.473	0.033469	1.7685	1.7685	1.13E-05	2.09113	2.09113	0.981078	1.00628	1.00628	0.606923	1.14562	1.14562
69167	TC1800000319.mm.1	NM_133687 // Cxxc5 // CXXC f	Cxxc5	NM_133687	chr18	7.18293	7.35546	9.18876	7.23471	7.61551	7.4689	7.98858	7.75751	0.366837	0.887289	-1.12703	1.09E-27	3.87461	3.87461	0.442823	1.10696	1.10696	0.227826	1.1737	1.1737
33385	TC0700002646.mm.1	NM_028775 // Cyp2s1 // cytoc	Cyp2s1	NM_028775	chr7	7.10741	7.32298	7.98098	6.94818	7.0953	7.21578	7.24159	7.11079	0.363915	0.861207	-1.16116	2.13E-10	2.046	2.046	0.611153	0.919879	-1.0871	0.581023	1.0949	1.0949
19102	TC0300003087.mm.1	NM_010516 // Cyr61 // cysteir	Cyr61	NM_010516	chr3	8.75035	9.5223	14.4668	8.40988	9.41509	9.48791	13.8844	9.04906	0.195941	0.585626	-1.70757	1.41E-27	66.5762	66.5762	0.902359	0.950778	-1.05177	6.07E-12	28.5488	28.5488
53226	TC1100004152.mm.1	NM_001112699 // Cyth1 // cyt	Cyth1	NM_001112699	chr11	8.82755	8.73398	9.84968	8.64458	8.8844	8.85221	9.2224	8.81422	0.576781	1.067	1.067	2.86E-19	2.30553	2.30553	0.847577	1.02257	1.02257	0.0168397	1.32701	1.32701
71896	TC1900001313.mm.1	NM_177474 // D19Bwg1357e	D19Bwg1357e	NM_177474	chr19	10.3375	10.2422	11.2588	10.2264	10.3182	10.259	11.6741	10.8424	0.605765	1.06834	1.06834	2.59E-14	2.04548	2.04548	0.748882	1.04183	1.04183	2.30E-05	1.77978	1.77978
54429	TC1200001064.mm.1	NM_001252508 // D430019H1	D430019H16Rik	NM_001252508	chr12	6.5224	6.79814	8.75458	6.89083	7.20335	6.9357	7.95689	6.8656	0.228278	0.826027	-1.21061	3.75E-22	3.63954	3.63954	0.242089	1.20384	1.20384	7.80E-06	2.13065	2.13065
11219	TC0200000641.mm.1	NM_001001602 // Dab2ip // d	Dab2ip	NM_001001602	chr2	8.72011	8.69309	10.2122	8.46366	8.77985	8.77303	9.6603	8.78006	0.859164	1.0189	1.0189	1.08E-30	3.36014	3.36014	0.964269	1.00474	1.00474	1.52E-07	1.84068	1.84068
31612	TC0700000861.mm.1	NM_016974 // Dbp // D site al	Dbp	NM_016974	chr7	10.2077	11.2166	8.75381	11.2958	11.0003	11.26	9.04852	11.3409	0.000595	0.496924	-2.01238	1.90E-24	0.171704	-5.82399	0.358737	0.835281	-1.1972	6.65E-12	0.204133	-4.89877
29279	TC0600002124.mm.1	NM_172477 // Dennd2a // DE	Dennd2a	NM_172477	chr6	8.07859	8.24829	12.8351	8.09318	8.60846	8.67393	10.704	8.58374	0.549898	0.889024	-1.12483	2.49E-41	26.7574	26.7574	0.817397	0.955636	-1.04642	1.11E-10	4.34775	4.34775
53507	TC1200000132.mm.1	NM_033270 // E2f6 // E2F trar	E2f6	NM_033270	chr12	8.53983	8.52731	10.2972	8.6588	8.82333	8.74756	9.82449	9.0278	0.934322	1.00872	1.00872	5.17E-29	3.11324	3.11324	0.618332	1.05392	1.05392	1.34E-06	1.73712	1.73712
71445	TC1900000859.mm.1	NR_026942 // E330013P04Rik	E330013P04Rik	NR_026942	chr19	11.3153	11.6151	10.9181	12.2389	10.8077	11.0509	11.8275	11.3405	0.373845	0.812363	-1.23098	4.91E-09	0.400319	-2.49801	0.4702	0.84485	-1.18364	0.15038	1.40149	1.40149
69149	TC1800000301.mm.1	NM_007913 // Egr1 // early gr	Egr1	NM_007913	chr18	7.89198	7.54778	10.7379	7.90219	8.66335	8.33902	10.0342	8.60063	0.464085	1.26945	1.26945	9.83E-16	7.13912	7.13912	0.490186	1.25208	1.25208	0.00303582	2.70109	2.70109
16011	TC0200005472.mm.1	NM_001146348 // Eng // endc	Eng	NM_001146348	chr2	10.3648	9.68779	11.8189	9.80503	10.0986	10.0723	11.936	10.7253	0.011338	1.59883	1.59883	9.32E-21	4.03862	4.03862	0.919792	1.01843	1.01843	1.45E-05	2.31439	2.31439
21228	TC0400001974.mm.1	NM_023119 // Eno1 // enolase	Eno1	NM_023119	chr4	10.729	9.86188	11.3405	9.81178	10.479	10.1054	11.0643	10.7435	0.000325	1.82407	1.82407	1.53E-17	2.8853	2.8853	0.108454	1.2956	1.2956	0.167207	1.24899	1.24899
69343	TC1800000498.mm.1	NM_001025388 // Eno1b // er	Eno1b	NM_001025388	chr18	8.02272	6.84557	8.45758	7.06406	7.61421	7.50622	8.36585	8.10239	0.000903	2.2613	2.2613	1.64E-09	2.62718	2.62718	0.751901	1.07772	1.07772	0.441305	1.20035	1.20035
23463	TC0400004224.mm.1	NM_010142 // Ephb2 // Eph re	Ephb2	NM_010142	chr4	8.16027	8.12923	10.2947	8.13474	8.88097	8.50605	9.69348	8.7479	0.906078	1.02175	1.02175	3.16E-22	4.46908	4.46908	0.15697	1.29676	1.29676	0.000561092	1.92596	1.92596
64964	TC1600001071.mm.1	NM_011809 // Ets2 // E26 avia	Ets2	NM_011809	chr16	9.42072	8.8399	10.6029	9.22243	9.46087	9.44543	9.94283	9.5508	0.013322	1.4957	1.4957	1.27E-15	2.60353	2.60353	0.946444	1.01076	1.01076	0.0911396	1.31224	1.31224
28066	TC0600000902.mm.1	NM_145570 // Eva1a // eva-1	Eva1a	NM_145570	chr6	5.53711	5.71588	6.88122	5.68694	5.79521	5.81676	6.40925	5.97101	0.24413	0.883457	-1.13192	4.23E-21	2.28831	2.28831	0.887802	0.985169	-1.01505	0.00522488	1.35496	1.35496
52874	TC1100003797.mm.1	NM_007970 // Ezh1 // enhanc	Ezh1	NM_007970	chr11	11.3697	11.2303	10.1976	11.4591	10.6942	11.2308	9.99851	10.7111	0.561614	1.10146	1.10146	3.00E-13	0.417138	-2.39729	0.027823	0.68941	-1.45052	0.00389557	0.610219	-1.63875
17276	TC0300001236.mm.1	NM_010171 // F3 // coagulatic	F3	NM_010171	chr3	11.6046	11.3836	14.1039	12.4752	10.9351	11.4927	13.3088	12.8017	0.513415	1.16556	1.16556	7.31E-12	3.09235	3.09235	0.101824	0.679447	-1.47179	0.136195	1.42112	1.42112
71399	TC1900000813.mm.1	NM_145505 // Fam160b1 // fa	Fam160b1	NM_145505	chr19	9.42815	9.32262	11.6428	9.33717	9.56698	9.36472	10.6377	9.47272	0.428805	1.07589	1.07589	2.29E-42	4.94384	4.94384	0.131548	1.1505	1.1505	4.28E-13	2.24223	2.24223
8267	TC0100001541.mm.1	NM_001160261 // Fam78b //	Fam78b	NM_001160261	chr1	6.07292	5.93092	7.74985	5.85638	6.13438	5.98425	7.65312	6.04743	0.505622	1.10343	1.10343	4.04E-24	3.71526	3.71526	0.481641	1.10967	1.10967	8.61E-11	3.0434	3.0434
63738	TC1500002186.mm.1	NM_024169 // Fkbp11 // FK50	Fkbp11	NM_024169	chr15	6.57769	6.71208	9.60776	6.41533	7.33382	6.52462	8.76528	7.5743	0.698968	0.91105	-1.09763	6.20E-25	9.14147	9.14147	0.022124	1.75224	1.75224	0.000958498	2.28309	2.28309
29469	TC0600002315.mm.1	NM_153573 // Fkbp14 // FK50	Fkbp14	NM_153573	chr6	7.98848	7.81544	9.65389	7.65704	8.3985	7.76961	9.53055	8.3144	0.470551	1.12744	1.12744	1.34E-22	3.99127	3.99127	0.010218	1.54638	1.54638	2.56E-06	2.32325	2.32325
71618	TC1900001033.mm.1	NM_201411 // Flrt1 // fibrone	Flrt1	NM_201411	chr19	8.81129	8.42063	11.8865	8.81375	9.22317	9.28071	11.2415	8.76558	0.195156	1.31099	1.31099	1.10E-27	8.41376	8.41376	0.847846	0.960903	-1.04069	3.73E-12	5.56339	5.56339
54200	TC1200000833.mm.1	NM_010234 // Fos // FBJ oste	Fos	NM_010234	chr12	6.18672	6.00278	10.3977	5.58076	6.43501	6.36137	8.07261	6.32377	0.68301	1.13598	1.13598	8.24E-29	28.1865	28.1865	0.870078	1.05237	1.05237	0.000211298	3.36087	3.36087
23798	TC0500000334.mm.1	NM_008037 // Fosl2 // fos-like	Fosl2	NM_008037	chr5	9.05751	8.66816	11.159	7.92735	8.33535	8.41034	10.2527	8.15634	0.173716	1.30981	1.30981	2.10E-30	9.39371	9.39371	0.792109	0.949353	-1.05335	1.79E-10	4.27643	4.27643
56600	TC1300000607.mm.1	NM_011817 // Gadd45g // gro	Gadd45g	NM_011817	chr13	6.87547	6.71557	12.9283	6.37435	7.18252	7.07406	10.955	7.44974	0.709597	1.11721	1.11721	1.14E-38	93.9599	93.9599	0.800524	1.07808	1.07808	5.54E-12	11.355	11.355
49627	TC1100000526.mm.1	NM_013529 // Gfpt2 // glutan	Gfpt2	NM_013529	chr11	8.52537	7.61852	8.94456	7.70674	8.52317	7.97832	8.3097	7.83844	0.001233	1.87495	1.87495	4.62E-11	2.35842	2.35842	0.047107	1.45888	1.45888	0.0849091	1.38632	1.38632
13921	TC0200003365.mm.1	NM_001145821 // Ggta1 // gly	Ggta1	NM_001145821	chr2	8.77131	8.54039	9.63115	8.62032	8.76567	8.66152	9.18917	8.5724	0.127383	1.17359	1.17359	7.52E-18	2.01507	2.01507	0.488995	1.07486	1.07486	9.84E-05	1.53344	1.53344
28825	TC0600001667.mm.1	NR_033555 // Gm10400 // pre	Gm10400	NR_033555	chr6	8.22776	8.57559	6.63085	9.03044	7.81648	8.61705	7.27077	7.83931	0.291077	0.785765	-1.27264	1.30E-19	0.189518	-5.27653	0.016761	0.574126	-1.74178	0.0863492	0.674296	-1.48303
15493	TC0200004948.mm.1	ENSMUST00000136046 // Gm	Gm14216	ENSMUST00000136046	chr2	5.15871	5.33221	7.22373	5.23405	5.30968	5.23355	6.67202	5.26944	0.345969	0.886693	-1.12779	3.73E-29	3.97148	3.97148	0.678494	1.05418	1.05418	5.49E-11	2.64373	2.64373
24669	TC0500001208.mm.1	ENSMUST00000141710 // Gm	Gm15736	ENSMUST00000141710	chr5	6.22492	6.208	7.53177	6.27357	6.28251	6.84189	6.4618	6.47906	0.941878	1.01179	1.01179	8.94E-14	2.39198	2.39198	0.018018	0.678592	-1.47364	0.940678	0.988103	-1.01204
27940	TC0600000775.mm.1	NM_001177556 // Gng12 // g	Gng12	NM_001177556	chr6	11.7572	11.745	14.098	12.2256	12.269	11.8986	13.8696	13.0575	0.968752	1.00846	1.00846	1.03E-15	3.66139	3.66139	0.234591	1.29277	1.29277	0.0104627	1.75581	1.75581
61683	TC1500000104.mm.1	NM_025673 // Golph3 // golgi	Golph3	NM_025673	chr15	10.5145	10.3649	11.7433	10.2671	10.7429	10.2456	11.343	10.5334	0.347322	1.10924	1.10924	3.09E-25	2.78218	2.78218	0.002394	1.41157	1.41157	2.34E-06	1.75273	1.75273
72122	TC1900001541.mm.1	NM_010324 // Got1 // glutam	Got1	NM_010324	chr19	8.06219	7.93026	10.3098	7.77252	8.3076	7.79207	10.0702	8.42715	0.596574	1.09576	1.09576	1.54E-27	5.80497	5.80497	0.041247	1.42951	1.42951	4.97E-09	3.12316	3.12316
29539	TC0600002385.mm.1	NM_183183 // Gprin3 // GPRI	Gprin3	NM_183183	chr6	8.62684	9.14852	7.79955	9.11767	8.51695	8.63228	8.05332	8.88928	0.025919	0.696558	-1.43563	9.90E-15	0.401056	-2.49342	0.616774	0.923169	-1.08323	0.000497955	0.560209	-1.78505
49737	TC1100000638.mm.1	NM_008161 // Gpx3 // glutath	Gpx3	NM_008161	chr11	11.0545	10.0051	11.9514	10.7527	11.5301	11.1323	10.4793	10.0518	0.022417	2.06968	2.06968	2.70E-05	2.29532	2.29532	0.379548	1.31749	1.31749	0.345173	1.34491	1.34491
54822	TC1200001461.mm.1	NM_001252071 // Greb1 // ge	Greb1	NM_001252071	chr12	5.99147	6.20968	11.4734	6.54015	6.74555	6.67919	9.09644	7.41081	0.518877	0.859632	-1.16329	2.19E-37	30.5537	30.5537	0.84426	1.04708	1.04708	3.63E-06	3.21679	3.21679
36802	TC0800001437.mm.1	NM_001145896 // Gse1 // gen	Gse1	NM_001145896	chr8	7.59876	7.58686	9.2333	7.48912	7.84171	7.69843	8.24956	7.84028	0.943967	1.00828	1.00828	7.90E-28	3.35004	3.35004	0.398419	1.10441	1.10441	0.0176917	1.32802	1.32802

Column #	Probeset ID	gene_assignment	Gene Symbol	RefSeq	seqname	Mean(Ex3aERKO-E2 2h)	Mean(Ex3aERKO-Saline)	Mean(WT-E2 2h)	Mean(WT-Saline)	Mean(ppKO E2 2h)	Mean(ppKO Saline)	Mean(ppWT E2 2h)	Mean(ppWT Saline)	p-value(Ex3aERKO-E2 2h vs. Ex3aERKO-Saline)	Ratio(Ex3aERKO-E2 2h vs. Ex3aERKO-Saline)	Fold-Change(Ex3aERKO-E2 2h vs. Ex3aERKO-Saline)	p-value(WT-E2 2h vs. WT-Saline)	Ratio(WT-E2 2h vs. WT-Saline)	Fold-Change(WT-E2 2h vs. WT-Saline)	p-value(ppKO E2 2h vs. ppKO Saline)	Ratio(ppKO E2 2h vs. ppKO Saline)	Fold-Change(ppKO E2 2h vs. ppKO Saline)	p-value(ppWT E2 2h vs. ppWT Saline)	Ratio(ppWT E2 2h vs. ppWT Saline)	Fold-Change(ppWT E2 2h vs. ppWT Saline)
66415	TC1700000354.mm.1	NM_001159626 // Hagh // hyc	Hagh	NM_001159626	chr17	8.1022	7.84872	9.27928	7.98043	8.11927	8.03361	8.72916	8.10153	0.108667	1.19208	1.19208	1.84E-22	2.46032	2.46032	0.584849	1.06117	1.06117	0.000138387	1.54502	1.54502
36000	TC0800000625.mm.1	NM_010402 // Hand2 // heart	Hand2	NM_010402	chr8	9.07716	8.95299	7.52459	8.66425	8.93131	8.83154	7.84877	8.8056	0.596222	1.08988	1.08988	5.26E-12	0.453868	-2.20329	0.670194	1.0716	1.0716	0.000104568	0.515188	-1.94104
54959	TC1200001601.mm.1	NM_153198 // Hbp1 // high m	Hbp1	NM_153198	chr12	11.7243	11.8211	10.433	12.0106	11.2118	11.4587	10.539	11.3166	0.611587	0.935136	-1.06936	1.90E-22	0.335027	-2.98483	0.197101	0.842686	-1.18668	0.000105262	0.583327	-1.7143
36475	TC0800001106.mm.1	NM_022331 // Herpud1 // hor	Herpud1	NM_022331	chr8	10.6579	10.495	11.6264	10.5449	10.4436	10.6102	11.3127	10.6177	0.533659	1.11948	1.11948	1.07E-09	2.11622	2.11622	0.524092	0.890899	-1.12246	0.0093411	1.61887	1.61887
64291	TC1600000392.mm.1	NM_008235 // Hes1 // hairy ar	Hes1	NM_008235	chr16	8.64585	8.77984	9.77944	8.48924	8.74645	8.83165	9.20698	8.93489	0.522684	0.911312	-1.09732	4.11E-16	2.44562	2.44562	0.684155	0.942656	-1.06083	0.196165	1.20756	1.20756
20650	TC0400001393.mm.1	NM_013905 // Heyl // hairy/er	Heyl	NM_013905	chr4	6.41921	6.21768	8.09776	6.57807	7.04385	6.85365	7.62484	7.05882	0.305034	1.14991	1.14991	6.10E-21	2.86729	2.86729	0.332822	1.14092	1.14092	0.00489668	1.48043	1.48043
54020	TC1200000652.mm.1	NM_010431 // Hif1a // hypoxi	Hif1a	NM_010431	chr12	12.8879	12.4067	13.6339	12.225	12.9477	12.559	13.4243	12.5016	0.008108	1.39588	1.39588	1.86E-21	2.65537	2.65537	0.0311	1.30915	1.30915	1.59E-06	1.89566	1.89566
32656	TC0700001913.mm.1	NM_019564 // Htra1 // HtrA s	Htra1	NM_019564	chr7	8.76054	8.49669	10.1246	9.02057	9.09024	8.69453	9.90968	9.55565	0.323196	1.20068	1.20068	1.01E-09	2.1496	2.1496	0.140063	1.31559	1.31559	0.186144	1.27813	1.27813
25702	TC0500002252.mm.1	NM_001042615 // Htra3 // Htr	Htra3	NM_001042615	chr5	10.2863	9.17619	11.7282	10.0275	9.89504	10.1183	9.85709	9.50303	0.00356	2.15859	2.15859	3.82E-11	3.25057	3.25057	0.546735	0.856657	-1.16733	0.339995	1.27815	1.27815
12865	TC0200002298.mm.1	NM_010495 // Id1 // inhibitor	Id1	NM_010495	chr2	10.6659	10.051	11.6403	10.0315	10.3424	10.4017	11.6441	10.8567	0.058612	1.53147	1.53147	1.87E-12	3.04998	3.04998	0.853553	0.959729	-1.04196	0.0162428	1.726	1.726
46955	TC1000001066.mm.1	NM_001111274 // Igf1 // insul	Igf1	NM_001111274	chr10	10.2804	10.2432	13.3276	10.9746	11.457	11.0644	12.6906	11.3606	0.911942	1.02614	1.02614	1.19E-18	5.1089	5.1089	0.245685	1.31276	1.31276	0.000168282	2.51403	2.51403
9652	TC0100002945.mm.1	NM_008381 // Inhbb // inhibir	Inhbb	NM_008381	chr1	7.19487	7.22432	10.4468	7.01423	7.31342	7.46025	8.7659	7.59483	0.943238	0.979794	-1.02062	1.77E-22	10.7968	10.7968	0.722719	0.903237	-1.10713	0.00580723	2.25179	2.25179
16358	TC0300000305.mm.1	NM_175515 // Intu // inturnec	Intu	NM_175515	chr3	6.81696	6.94012	8.09215	6.97921	7.01371	7.00144	7.47251	7.15532	0.300905	0.918174	-1.08912	1.91E-25	2.16286	2.16286	0.917575	1.00855	1.00855	0.00899421	1.24591	1.24591
48897	TC1000003019.mm.1	NM_028679 // Irak3 // interleu	Irak3	NM_028679	chr10	8.34157	7.69045	12.1162	8.12577	8.34465	8.23252	9.94699	8.20316	0.083153	1.57038	1.57038	7.03E-29	15.8947	15.8947	0.763136	1.08082	1.08082	1.16E-05	3.34924	3.34924
36130	TC0800000756.mm.1	NM_023627 // Isyna1 // myo-i	Isyna1	NM_023627	chr8	8.68471	8.20612	10.237	8.18151	8.88801	8.70593	10.035	8.68154	0.082426	1.39338	1.39338	2.80E-20	4.15675	4.15675	0.50504	1.13452	1.13452	4.05E-06	2.55522	2.55522
50821	TC1100001730.mm.1	NM_016780 // Itgb3 // integrir	Itgb3	NM_016780	chr11	6.82937	6.83094	9.85788	7.21866	7.01937	7.07528	9.14933	7.75034	0.995476	0.998917	-1.00108	6.14E-26	6.22998	6.22998	0.839413	0.961994	-1.03951	2.64E-06	2.63717	2.63717
36134	TC0800000760.mm.1	NM_001286944 // Jund // jun	Jund	NM_001286944	chr8	7.37557	7.54617	8.67788	7.14494	7.7378	7.62677	7.87637	7.75293	0.546539	0.88847	-1.12553	8.83E-14	2.89376	2.89376	0.69457	1.07999	1.07999	0.662467	1.08933	1.08933
60253	TC1400001528.mm.1	NM_021542 // Kcnk5 // potass	Kcnk5	NM_021542	chr14	7.1414	6.86748	9.31632	6.66581	7.13097	7.15751	8.60509	7.66166	0.262856	1.20909	1.20909	2.99E-29	6.2789	6.2789	0.91327	0.981777	-1.01856	0.000220189	1.9231	1.9231
54777	TC1200001416.mm.1	NM_001168564 // Kcns3 // po	Kcns3	NM_001168564	chr12	6.13669	6.07916	8.12395	6.2771	6.30655	6.34991	6.9601	6.40869	0.782984	1.04068	1.04068	5.35E-24	3.59714	3.59714	0.83549	0.970388	-1.03052	0.0098416	1.46552	1.46552
24173	TC0500000710.mm.1	NM_001122733 // Kit // kit on	Kit	NM_001122733	chr5	7.37092	7.18373	8.91392	7.29363	7.31432	7.37976	8.14552	7.46367	0.263379	1.13855	1.13855	2.44E-26	3.07437	3.07437	0.694737	0.955656	-1.0464	0.000102948	1.60419	1.60419
63130	TC1500001571.mm.1	NM_177755 // Klhl38 // kelch-	Klhl38	NM_177755	chr15	6.36295	6.32114	6.12775	7.53323	6.14435	6.26099	6.12182	6.63661	0.899626	1.0294	1.0294	5.16E-10	0.377493	-2.64906	0.724986	0.922329	-1.08421	0.123385	0.699898	-1.42878
61988	TC1500000413.mm.1	ENSMUST00000147638 // Klhl	Klhl38	ENSMUST00000147638	chr15	7.14153	6.42534	6.10313	7.38478	6.80756	6.89373	5.85221	6.4279	0.01023	1.64284	1.64284	1.80E-11	0.411323	-2.43118	0.752085	0.942025	-1.06154	0.0374958	0.670967	-1.49039
60905	TC1400002189.mm.1	NM_008466 // Kpna3 // karyo	Kpna3	NM_008466	chr14	11.0014	10.6999	12.0318	10.7878	11.2314	11.0228	11.9166	11.2638	0.046984	1.23239	1.23239	1.66E-22	2.36852	2.36852	0.166379	1.15554	1.15554	3.92E-05	1.57225	1.57225
63810	TC1500002259.mm.1	NM_001003668 // Krt83 // ker	Krt83	NM_001003668	chr15	5.838	6.09751	8.14894	5.84718	6.07481	6.0472	7.96801	6.35358	0.258299	0.835372	-1.19707	3.10E-27	4.93061	4.93061	0.903871	1.01932	1.01932	6.76E-10	3.06191	3.06191
52395	TC1100003315.mm.1	NM_013571 // Ksr1 // kinase s	Ksr1	NM_013571	chr11	7.42837	7.03123	10.0092	7.15336	7.4359	7.51643	8.8261	7.40139	0.141415	1.31689	1.31689	1.08E-28	7.23915	7.23915	0.763967	0.945715	-1.0574	1.01E-06	2.68459	2.68459
48913	TC1000003035.mm.1	NM_001081193 // Lemd3 // LE	Lemd3	NM_001081193	chr10	9.81229	10.142	11.0371	10.0015	10.1252	10.1183	10.7597	9.91037	0.008272	0.795676	-1.25679	5.00E-23	2.05002	2.05002	0.954717	1.00481	1.00481	1.03E-09	1.80165	1.80165
9826	TC0100003119.mm.1	NM_001033409 // Lgr6 // leuc	Lgr6	NM_001033409	chr1	6.12977	6.11824	9.06312	6.19088	6.52839	6.43211	8.01894	6.55531	0.957196	1.00802	1.00802	6.90E-35	7.32197	7.32197	0.654142	1.06901	1.06901	1.96E-09	2.75801	2.75801
49146	TC1100000041.mm.1	NM_001039537 // Lif // leuker	Lif	NM_001039537	chr11	5.81082	5.83113	7.20707	5.71405	6.04474	5.93793	6.50397	6.05847	0.90318	0.986018	-1.01418	2.93E-24	2.81476	2.81476	0.522955	1.07685	1.07685	0.00914435	1.36179	1.36179
66061	TC1600002178.mm.1	NM_019980 // Litaf // LPS-indu	Litaf	NM_019980	chr16	8.49891	8.18226	10.6222	8.49338	8.70298	8.48597	9.83331	8.51177	0.128552	1.24544	1.24544	8.20E-28	4.3736	4.3736	0.29559	1.16233	1.16233	1.19E-08	2.49932	2.49932
30294	TC0600003145.mm.1	NM_010736 // Ltbr // lymphot	Ltbr	NM_010736	chr6	8.97569	8.83215	9.77084	8.71027	9.185	8.86496	9.43611	9.0995	0.363083	1.10461	1.10461	6.88E-18	2.08575	2.08575	0.044878	1.24836	1.24836	0.0351447	1.26279	1.26279
71250	TC1900000662.mm.1	NM_001130525 // Lzts2 // leu	Lzts2	NM_001130525	chr19	8.89225	8.68392	10.1915	8.67	8.68479	8.95446	9.49293	9.03453	0.248988	1.15535	1.15535	6.35E-23	2.87084	2.87084	0.136827	0.82951	-1.20553	0.0126187	1.37401	1.37401
27937	TC0600000772.mm.1	NM_019499 // Mad2l1 // MAD	Mad2l1	NM_019499	chr6	8.68071	8.81	15.3905	8.8008	9.24569	8.79421	13.7333	8.99295	0.793794	0.914279	-1.09376	8.80E-35	96.3137	96.3137	0.362622	1.36745	1.36745	1.14E-14	26.7298	26.7298
21179	TC0400001925.mm.1	NM_027985 // Mad2l2 // MAD	Mad2l2	NM_027985	chr4	7.42116	7.24673	8.57467	7.10841	7.42645	7.37671	7.99808	7.47514	0.348206	1.12852	1.12852	2.29E-21	2.76304	2.76304	0.788533	1.03508	1.03508	0.00598355	1.43688	1.43688
41071	TC0900002491.mm.1	NM_008927 // Map2k1 // mitc	Map2k1	NM_008927	chr9	9.62263	9.57287	11.4695	9.15968	9.68507	9.57504	10.7087	9.56135	0.780542	1.0351	1.0351	5.95E-34	4.95826	4.95826	0.538307	1.07925	1.07925	1.04E-08	2.21505	2.21505
50932	TC1100001841.mm.1	NM_011943 // Map2k6 // mitc	Map2k6	NM_011943	chr11	9.92134	10.3815	8.22847	9.96058	9.60573	9.86647	8.3852	9.84804	0.08684	0.72692	-1.37567	3.46E-17	0.301011	-3.32214	0.328645	0.834664	-1.19809	4.84E-07	0.36278	-2.75649
9758	TC0100003051.mm.1	NM_008551 // Mapkapk2 // M	Mapkapk2	NM_008551	chr1	11.8098	11.1004	14.2197	11.1813	12.034	11.5392	13.1157	11.6813	0.012285	1.63502	1.63502	1.94E-29	8.21565	8.21565	0.077456	1.40913	1.40913	1.77E-06	2.7027	2.7027
32018	TC0700001269.mm.1	NM_181407 // Me3 // malic er	Me3	NM_181407	chr7	7.26069	7.29446	8.50094	7.46491	7.32529	7.43182	7.37251	7.29651	0.829762	0.976862	-1.02369	1.88E-17	2.05058	2.05058	0.498273	0.928822	-1.07663	0.628745	1.05409	1.05409
14935	TC0200004383.mm.1	NM_001136072 // Meis2 // M	Meis2	NM_001136072	chr2	12.9146	12.7626	11.3284	13.2804	12.6611	12.9157	11.6236	12.7623	0.490198	1.11109	1.11109	4.39E-24	0.258468	-3.86895	0.24921	0.838258	-1.19295	1.74E-06	0.454169	-2.20183
34372	TC0700003647.mm.1	NM_030705 // Mesdc1 // mes	Mesdc1	NM_030705	chr7	6.51062	6.55965	9.03972	6.67734	6.82658	6.9365	7.87043	6.99573	0.817721	0.966586	-1.03457	8.49E-30	5.14219	5.14219	0.605629	0.926642	-1.07917	9.55E-05	1.83363	1.83363
62610	TC1500001040.mm.1	NM_027334 // Mettl7a1 // me	Mettl7a1	NM_027334	chr15	10.8771	10.5813	13.3791	11.6078	10.595	10.7728	12.699	11.3187	0.388519	1.22756	1.22756	5.43E-13	3.41357	3.41357	0.603651	0.88405	-1.13116	0.000125995	2.60312	2.60312
31941	TC0700001192.mm.1	NM_175366 // Mex3b // mex3	Mex3b	NM_175366	chr7	8.67906	9.70228	7.52308	10.2686	9.16278	9.35027	7.28558	9.05201	0.000235	0.492018	-2.03245	6.44E-28	0.149117	-6.70616	0.48085	0.878132	-1.13878	3.94E-09	0.293934	-3.40213
30200	TC0600003050.mm.1	NM_001270475 // Mical3 // m	Mical3	NM_001270475	chr6	9.33082	9.17756	11.7614	10.0379	9.65785	9.69177	11.3612	9.74564	0.496635	1.11208	1.11208	1.24E-20	3.30236	3.30236	0.880245	0.976765	-1.02379	4.14E-10	3.06428	3.06428
62239	TC1500000666.mm.1	NM_177461 // Micall1 // micr	Micall1	NM_177461	chr15	7.87029	7.7024	9.33671	7.77881	8.65728	8.18023	8.68033	8.19943	0.396034	1.12341	1.12341	2.52E-21	2.94426	2.94426	0.017717	1.3919	1.3919	0.0168549	1.39561	1.39561
70264	TC1800001426.mm.1	NR_029601 // Mir143 // micro	Mir143	NR_029601	chr18	10.0679	9.43807	12.2843	9.83744	9.49775	10.5944	11.1945	10.2713	0.282831	1.54742	1.54742	7.53E-10	5.45222	5.45222	0.063549	0.467602	-2.13857	0.117078	1.89631	1.89631
70263	TC1800001425.mm.1	NR_029557 // Mir145a // micr	Mir145a	NR_029557	chr18	11.9994	11.8719	14.4583	12.2501	12.6466	12.6569	13.7375	12.4352	0.765569	1.09242	1.09242	5.93E-13	4.62105	4.62105	0.980781	0.992886	-1.00716	0.00311698	2.46622	2.46622
50283	TC1100001187.mm.1	NR_029579 // Mir193a // micr	Mir193a	NR_029579	chr11	5.16799	4.92151	6.58911	4.89426	5.18629	5.33417	5.25291	5.20861	0.543421	1.18631	1.18631	7.82E-10	3.23742	3.23742	0.71521	0.902572	-1.10795	0.91295	1.03118	1.03118
39514	TC0900000919.mm.1	NR_037296 // Mir3109 // micr	Mir3109	NR_037296	chr9	7.24359	7.60493	8.59888	7.36357	7.43738	7.93997	8.39265	7.51493	0.167199	0.778446	-1.28461	1.22E-11	2.35432	2.35432	0.056155	0.705842	-1.41675	0.00112887	1.83748	1.83748
50415	TC1100001320.mm.1	NR_106195 // Mir8115 // micr	Mir8115	NR_106195	chr11	7.24832	8.80569	7.04178	8.24225	7.31698	8.90084	6.26406	9.27951	0.009718	0.339768	-2.94318	0.0009647	0.435134	-2.29814	0.008597	0.333586	-2.99772	2.17E-06	0.123669	-8.08612
48272	TC1000002392.mm.1	NM_008606 // Mmp11 // mat	Mmp11	NM_008606	chr10	8.82824	9.26963	9.02373	10.5249	9.10898	9.37416	8.57381	9.53358	0.128214	0.736427	-1.35791	4.11E-13	0.353263	-2.83075	0.358354	0.832095	-1.20179	0.0012937	0.51414	-1.945
34141	TC0700003413.mm.1	NM_026483 // Mphosph10 //	Mphosph10	NM_026483	chr7	8.6166	8.5474	11.041	8.67249	9.36841	8.86893	11.1003	9.26704	0.799606	1.04913	1.04913	1.42E-23	5.16412	5.16412	0.069934	1.4137	1.4137	2.87E-09	3.56344	3.56344
41498	TC0900002921.mm.1	NM_008624 // Mras // muscle	Mras	NM_008624	chr9	9.31309	9.06288	10.9875	9.48412	9.92539	9.34381	10.6339	9.75187	0.145144	1.18938	1.18938	6.38E-24	2.83503	2.83503	0.001014	1.49649	1.49649	1.77E-06	1.84294	1.84294
36463	TC0800001094.mm.1	NM_008630 // Mt2 // metallot	Mt2	NM_008630	chr8	17.2606	15.6147	15.9691	14.9389	16.5114	15.5464	16.1518	15.2458	0.000265	3.12947	3.12947	0.0001342	2.04237	2.04237	0.027675	1.95211	1.95211	0.0383393	1.87389	1.87389
54043	TC1200000675.mm.1	NM_138745 // Mthfd1 // meth	Mthfd1	NM_138745	chr12	9.10759	8.73616	10.1839	8.763	9.58813	9.01965	10.2726	9.27141	0.151391	1.29363	1.29363	4.17E-14	2.67755	2.67755	0.029574	1.48296	1.48296	0.000204598	2.0016	2.0016
63374	TC1500001819.mm.1	NM_022410 // Myh9 // myosir	Myh9	NM_022410	chr15	11.5223	11.488	12.1797	11.041	11.3093	11.483	12.1213	11.4723	0.847156	1.02409	1.02409	8.02E-17	2.20183	2.20183	0.330895	0.886525	-1.128	0.000477205	1.56808	1.56808
40185	TC0900001600.mm.1	NM_144557 // Myrip // myosi	Myrip	NM_144557	chr9	6.64495	6.38006	8.59362	6.33317	6.69379	6.46964	7.65313	6.63126	0.172672	1.20154	1.20154	3.21E-31	4.79143	4.79143	0.247662	1.16809	1.16809	1.10E-06	2.03055	2.03055
47455	TC1000001569.mm.1	ENSMUST00000133270 // Nab	Nab2	ENSMUST00000133270	chr10	7.56162	7.80231	10.0576	7.76447	8.46838	8.27256	9.04806	8.48351	0.343725	0.84634	-1.18156	1.50E-24	4.90133	4.90133	0.440648	1.14537	1.14537	0.0284252	1.47892	1.47892
48997	TC1000003120.mm.1	NM_001122895 // Nab2 // Ngf	Nab2	NM_001122895	chr10	8.67713	8.6675	10.7316	8.63327	9.23631	9.22534	9.62351	9.19475	0.966933	1.0067	1.0067	1.69E-24	4.28212	4.28212	0.962339	1.00764	1.00764	0.0681234	1.34608	1.34608
70300	TC1800001462.mm.1	NM_001142950 // Nars // aspa	Nars	NM_001142950	chr18	13.1208	12.8337	13.8318	12.7989	13.1577	12.8899	14.1983	13.3736	0.238699	1.22015	1.22015	4.50E-10	2.04611	2.04611	0.271274	1.20403	1.20403	0.00104708	1.77113	1.77113
26706	TC0500003268.mm.1	NM_001253904 // Ncor2 // nu	Ncor2	NM_001253904	chr5	8.66986	8.58252	10.1542	8.62848	8.77162	8.84746	9.55362	8.81651	0.681869	1.06241	1.06241	3.55E-19	2.87921	2.87921	0.721868	0.948792	-1.05397	0.000863285	1.66683	1.66683
69510	TC1800000665.mm.1	NM_001114386 // Nedd4l // n	Nedd4l	NM_001114386	chr18	9.70351	9.73997	12.0604	10.1242	10.0668	9.89743	11.5197	10.0114	0.901719	0.975048	-1.02559	2.45E-17	3.8269	3.8269	0.566644	1.12454	1.12454	2.28E-06	2.84469	2.84469
48421	TC1000002541.mm.1	NM_008688 // Nfic // nuclear	Nfic	NM_008688	chr10	9.68766	9.44638	8.81525	9.83983	10.0279	9.75536	9.32204	10.0549	0.265386	1.18204	1.18204	1.25E-11	0.491551	-2.03438	0.208943	1.20791	1.20791	0.00105926	0.601706	-1.66194
52670	TC1100003593.mm.1	NM_033217 // Ngfr // nerve g	Ngfr	NM_033217	chr11	7.5711	7.49792	9.13279	6.8365	7.81719	7.62438	8.5859	8.10937	0.850739	1.05204	1.05204	2.66E-15	4.91192	4.91192	0.620309	1.14299	1.14299	0.222741	1.39139	1.39139
49673	TC1100000573.mm.1	NM_026631 // Nhp2 // NHP2 r	Nhp2	NM_026631	chr11	7.70444	7.45457	9.0456	7.51875	8.05005	7.6202	9.46429	8.4945	0.393553	1.1891	1.1891	3.77E-13	2.88156	2.88156	0.14409	1.34709	1.34709	0.00135307	1.95855	1.95855
15475	TC0200004930.mm.1	NM_001001986 // Nol4l // nuc	Nol4l	NM_001001986	chr2	6.17811	6.09257	7.87971	5.98913	6.49907	6.36467	7.27517	6.42722	0.659652	1.06108	1.06108	2.19E-26	3.70783	3.70783	0.489364	1.09764	1.09764	3.80E-05	1.79994	1.79994
52765	TC1100003688.mm.1	NM_145434 // Nr1d1 // nuclea	Nr1d1	NM_145434	chr11	12.861	13.1863	10.524	12.974	12.2144	13.0887	10.1732	13.1947	0.367882	0.798103	-1.25297	4.50E-18	0.183006	-5.46429	0.017315	0.545506	-1.83316	2.13E-12	0.123148	-8.1203
62637	TC1500001067.mm.1	NM_010444 // Nr4a1 // nuclea	Nr4a1	NM_010444	chr15	7.31006	7.46802	11.6865	6.57007	7.8115	7.8289	10.4764	7.58819	0.788331	0.896288	-1.11571	1.36E-23	34.6895	34.6895	0.976402	0.988012	-1.01213	4.96E-06	7.40369	7.40369
37344	TC0800001984.mm.1	NM_178591 // Nrg1 // neureg	Nrg1	NM_178591	chr8	6.99459	7.22548	8.78962	7.38954	7.45539	7.52746	8.16214	7.42429	0.360727	0.85211	-1.17356	3.33E-14	2.63915	2.63915	0.77485	0.95127	-1.05123	0.00438904	1.66769	1.66769
70028	TC1800001186.mm.1	NM_001167891 // Nrg2 // neu	Nrg2	NM_001167891	chr18	7.81233	7.9471	9.43211	7.87755	8.0618	8.08186	8.70971	7.90002	0.591496	0.910819	-1.09791	3.25E-16	2.93744	2.93744	0.936278	0.986194	-1.014	0.0018003	1.75283	1.75283
65808	TC1600001922.mm.1	NM_173440 // Nrip1 // nuclea	Nrip1	NM_173440	chr16	9.6674	9.27527	13.0381	9.45124	9.89104	9.70745	11.8402	9.88298	0.080534	1.31233	1.31233	2.64E-40	12.0156	12.0156	0.409459	1.13571	1.13571	3.28E-13	3.88323	3.88323
36958	TC0800001594.mm.1	NM_008737 // Nrp1 // neurop	Nrp1	NM_008737	chr8	10.3947	9.77903	11.2385	9.69384	10.2619	10.1237	10.6805	10.1132	0.019721	1.53229	1.53229	1.80E-15	2.91735	2.91735	0.594467	1.10047	1.10047	0.0312294	1.48171	1.48171
50227	TC1100001131.mm.1	NM_001024205 // Nufip2 // nu	Nufip2	NM_001024205	chr11	11.1341	11.0691	12.1111	11.0997	11.3216	11.1267	11.9905	11.2209	0.620231	1.04605	1.04605	7.94E-21	2.01588	2.01588	0.139754	1.14459	1.14459	1.03E-07	1.70488	1.70488
29405	TC0600002250.mm.1	NM_001163645 // Osbpl3 // o	Osbpl3	NM_001163645	chr6	8.15602	8.10894	9.04897	7.977	7.76661	8.19703	8.5951	8.0969	0.807257	1.03317	1.03317	3.37E-14	2.10229	2.10229	0.028192	0.742044	-1.34763	0.0115207	1.41245	1.41245
18082	TC0300002051.mm.1	NM_001008497 // P2ry14 // p	P2ry14	NM_001008497	chr3	6.32292	6.3612	8.85855	6.85024	6.53331	6.71034	8.11323	7.03462	0.882097	0.973814	-1.02689	5.38E-21	4.02311	4.02311	0.493461	0.884522	-1.13055	7.54E-05	2.11201	2.11201
10231	TC0100003531.mm.1	NM_025557 // Pcp4l1 // Purki	Pcp4l1	NM_025557	chr1	11.1101	10.896	14.6619	11.3688	11.8796	11.8706	13.5697	12.5556	0.625024	1.16	1.16	3.07E-20	9.80172	9.80172	0.983719	1.00621	1.00621	0.0228602	2.01955	2.01955
52601	TC1100003523.mm.1	NM_008796 // Pctp // phosph	Pctp	NM_008796	chr11	7.94243	8.61651	7.40295	8.50656	8.29885	8.44414	7.64658	8.54404	0.001758	0.626731	-1.59558	2.25E-13	0.46535	-2.14892	0.486298	0.904195	-1.10596	4.75E-05	0.536832	-1.86278
66156	TC1700000092.mm.1	NM_011866 // Pde10a // phos	Pde10a	NM_011866	chr17	6.36794	6.38824	8.16144	6.46248	6.69954	6.72554	7.34147	6.59174	0.90932	0.98603	-1.01417	7.57E-26	3.24666	3.24666	0.884005	0.98214	-1.01819	6.81E-05	1.68148	1.68148
28968	TC0600001810.mm.1	NM_013743 // Pdk4 // pyruvat	Pdk4	NM_013743	chr6	11.2572	8.77437	12.7517	9.66679	9.3574	9.78752	10.5768	9.23447	6.47E-05	5.58977	5.58977	3.28E-13	8.4847	8.4847	0.465367	0.7422	-1.34735	0.0248575	2.53569	2.53569

Column #	Probeset ID	gene_assignment	Gene Symbol	RefSeq	seqname	Mean(Ex3aERKO-E2 2h)	Mean(Ex3aERKO-Saline)	Mean(WT-E2 2h)	Mean(WT-Saline)	Mean(ppKO E2 2h)	Mean(ppKO Saline)	Mean(ppWT E2 2h)	Mean(ppWT Saline)	p-value(Ex3aERKO-E2 2h vs. Ex3aERKO-Saline)	Ratio(Ex3aERKO-E2 2h vs. Ex3aERKO-Saline)	Fold-Change(Ex3aERKO-E2 2h vs. Ex3aERKO-Saline)	p-value(WT-E2 2h vs. WT-Saline)	Ratio(WT-E2 2h vs. WT-Saline)	Fold-Change(WT-E2 2h vs. WT-Saline)	p-value(ppKO E2 2h vs. ppKO Saline)	Ratio(ppKO E2 2h vs. ppKO Saline)	Fold-Change(ppKO E2 2h vs. ppKO Saline)	p-value(ppWT E2 2h vs. ppWT Saline)	Ratio(ppWT E2 2h vs. ppWT Saline)	Fold-Change(ppWT E2 2h vs. ppWT Saline)
9511	TC0100002801.mm.1	NM_011066 // Per2 // period (	Per2	NM_011066	chr1	8.55254	9.10339	10.529	8.80463	8.95651	9.41955	9.86856	9.15814	0.040222	0.682619	-1.46495	3.36E-17	3.30425	3.30425	0.083339	0.725453	-1.37845	0.00875212	1.63628	1.63628
46032	TC1000000133.mm.1	NM_022032 // Perp // PERP, T	Perp	NM_022032	chr10	10.012	9.15912	10.5403	8.77194	9.43351	9.34994	9.93926	9.28905	0.030607	1.80615	1.80615	5.21E-11	3.40667	3.40667	0.829578	1.05964	1.05964	0.097081	1.5694	1.5694
37757	TC0800002400.mm.1	NM_023217 // Pgpep1 // pyro	Pgpep1	NM_023217	chr8	8.04468	7.86899	9.48617	7.80709	8.25262	8.25807	8.65087	8.16213	0.336598	1.1295	1.1295	5.42E-25	3.20224	3.20224	0.97616	0.996232	-1.00378	0.00881278	1.40322	1.40322
63548	TC1500001993.mm.1	NM_001081166 // Phf21b // P	Phf21b	NM_001081166	chr15	5.92921	6.0698	9.09665	5.75902	6.20675	6.24233	7.63271	6.1947	0.672899	0.907146	-1.10236	3.96E-27	10.1094	10.1094	0.91486	0.975637	-1.02497	4.52E-05	2.70948	2.70948
6854	TC0100000112.mm.1	NM_053191 // Pi15 // peptida	Pi15	NM_053191	chr1	8.44728	8.67786	8.36054	9.88752	9.36298	8.56836	9.48794	9.64407	0.538525	0.852289	-1.17331	1.67E-09	0.347003	-2.88182	0.036546	1.73462	1.73462	0.676864	0.897427	-1.1143
66565	TC1700000505.mm.1	NM_008842 // Pim1 // provira	Pim1	NM_008842	chr17	8.55102	7.80189	9.93449	8.07316	7.85407	8.04793	8.64413	7.93093	0.011026	1.68078	1.68078	5.06E-17	3.63341	3.63341	0.501923	0.874263	-1.14382	0.0153169	1.63943	1.63943
62424	TC1500000854.mm.1	NM_145478 // Pim3 // provira	Pim3	NM_145478	chr15	6.83963	6.83467	7.73313	6.68295	6.70762	6.88927	7.17324	6.83811	0.983976	1.00345	1.00345	4.79E-10	2.07079	2.07079	0.463014	0.881698	-1.13417	0.177622	1.26149	1.26149
27822	TC0600000655.mm.1	NM_001001335 // Plekha8 // p	Plekha8	NM_001001335	chr6	7.69184	8.03851	9.80469	8.04663	8.24577	8.04289	9.79283	8.32454	0.066799	0.786396	-1.27162	1.68E-25	3.38243	3.38243	0.279803	1.15099	1.15099	2.19E-11	2.76694	2.76694
54050	TC1200000682.mm.1	NM_153804 // Plekhg3 // plec	Plekhg3	NM_153804	chr12	7.96476	8.06092	10.7078	7.76749	8.32001	8.21298	9.31388	8.10756	0.586254	0.93552	-1.06892	3.28E-41	7.67551	7.67551	0.544716	1.07701	1.07701	1.81E-09	2.30748	2.30748
57229	TC1300001242.mm.1	NM_152804 // Plk2 // polo-like	Plk2	NM_152804	chr13	9.37469	8.94316	14.4278	9.54636	9.91076	9.77463	13.1846	9.66574	0.291434	1.34867	1.34867	7.81E-32	29.475	29.475	0.738434	1.09895	1.09895	7.16E-13	11.4629	11.4629
23243	TC0400004004.mm.1	NM_011122 // Plod1 // procol	Plod1	NM_011122	chr4	8.38377	7.89882	10.6406	8.13931	8.70525	8.3776	9.72831	8.75985	0.075948	1.39953	1.39953	4.23E-25	5.66185	5.66185	0.227804	1.25497	1.25497	0.000582802	1.95676	1.95676
32796	TC0700002053.mm.1	NM_001163689 // Pnpla2 // pa	Pnpla2	NM_001163689	chr7	11.1919	9.75203	10.9088	9.64152	9.93326	9.97775	9.96245	10.5387	0.011163	2.71293	2.71293	0.0002491	2.40715	2.40715	0.936116	0.969633	-1.03132	0.300955	0.670714	-1.49095
32726	TC0700001983.mm.1	NM_026391 // Ppp2r2d // pro	Ppp2r2d	NM_026391	chr7	8.89096	8.76388	10.7473	8.90534	9.0934	8.96097	10.0816	8.99829	0.46907	1.09208	1.09208	2.39E-28	3.58498	3.58498	0.450655	1.09613	1.09613	2.88E-08	2.11896	2.11896
14702	TC0200004148.mm.1	NM_001177536 // Prdm11 // P	Prdm11	NM_001177536	chr2	6.91441	6.76592	7.59618	6.51989	6.9224	6.90499	7.12825	6.70485	0.299426	1.10841	1.10841	2.57E-20	2.10861	2.10861	0.902817	1.01214	1.01214	0.00390122	1.34109	1.34109
25548	TC0500002095.mm.1	NM_001170555 // Prkag2 // pr	Prkag2	NM_001170555	chr5	9.07007	8.81826	11.0531	8.84317	9.24458	9.07339	10.4905	9.13273	0.25853	1.1907	1.1907	5.95E-27	4.62665	4.62665	0.441348	1.12598	1.12598	3.76E-08	2.56282	2.56282
46713	TC1000000820.mm.1	NM_001077363 // Ptbp1 // po	Ptbp1	NM_001077363	chr10	12.0846	11.5267	13.5986	11.7929	12.2243	11.9862	13.2334	12.4734	0.049192	1.47216	1.47216	5.29E-17	3.49612	3.49612	0.396115	1.17947	1.17947	0.00804342	1.69345	1.69345
13167	TC0200002602.mm.1	NM_011201 // Ptpn1 // protei	Ptpn1	NM_011201	chr2	8.44958	7.78341	10.0666	7.95814	8.2847	8.11259	9.72706	8.26994	0.000373	1.58685	1.58685	2.42E-31	4.31229	4.31229	0.338404	1.12671	1.12671	6.52E-12	2.74561	2.74561
22893	TC0400003650.mm.1	NM_001083119 // Ptpru // pro	Ptpru	NM_001083119	chr4	8.13671	7.02839	8.49915	7.22003	7.40679	7.56209	7.96609	7.25514	3.56E-06	2.15594	2.15594	7.32E-15	2.42691	2.42691	0.484627	0.897942	-1.11366	0.00193177	1.63688	1.63688
49843	TC1100000745.mm.1	NM_001037764 // Rai1 // retir	Rai1	NM_001037764	chr11	8.04119	8.22963	9.49642	8.06214	8.40819	8.27083	9.00449	8.34293	0.22517	0.877552	-1.13953	3.61E-25	2.70248	2.70248	0.375537	1.09989	1.09989	5.25E-05	1.5818	1.5818
62773	TC1500001207.mm.1	NM_001166408 // Rai14 // ret	Rai14	NM_001166408	chr15	8.03703	7.63417	11.053	7.94471	8.10492	7.84185	10.1095	8.19836	0.112555	1.32213	1.32213	1.15E-32	8.62385	8.62385	0.297745	1.20003	1.20003	6.81E-11	3.76099	3.76099
12919	TC0200002352.mm.1	NM_001139511 // Raly // hnR	Raly	NM_001139511	chr2	8.02288	8.0196	9.54602	8.1017	8.31555	8.09434	9.35948	8.35562	0.977732	1.00227	1.00227	1.45E-32	2.72135	2.72135	0.06258	1.16571	1.16571	1.04E-12	2.00536	2.00536
50675	TC1100001583.mm.1	NM_001080925 // Rapgefl1 //	Rapgefl1	NM_001080925	chr11	6.27423	6.16138	7.47487	6.04838	6.23454	6.31219	6.75894	6.24322	0.515588	1.08136	1.08136	2.77E-22	2.68791	2.68791	0.654364	0.947598	-1.0553	0.00383651	1.42971	1.42971
50679	TC1100001587.mm.1	NM_001176528 // Rara // reti	Rara	NM_001176528	chr11	8.31989	8.22305	9.40005	8.2358	8.59928	8.46842	8.93167	8.58212	0.489425	1.06943	1.06943	1.51E-22	2.24116	2.24116	0.350934	1.09494	1.09494	0.0143515	1.27416	1.27416
51946	TC1100002865.mm.1	NM_009026 // Rasd1 // RAS, d	Rasd1	NM_009026	chr11	8.15254	6.34827	12.7097	7.11263	7.19766	7.30546	10.7584	7.65409	0.000856	3.49253	3.49253	6.39E-29	48.4043	48.4043	0.836065	0.928	-1.07759	7.30E-08	8.6001	8.6001
9763	TC0100003056.mm.1	NM_018750 // Rassf5 // Ras as	Rassf5	NM_018750	chr1	7.17074	7.19248	8.36651	7.17112	7.33842	7.14526	7.76872	7.17067	0.888909	0.985043	-1.01518	1.05E-20	2.29006	2.29006	0.216941	1.14327	1.14327	0.000244057	1.51367	1.51367
12860	TC0200002293.mm.1	NM_009047 // Rem1 // rad an	Rem1	NM_009047	chr2	7.29881	7.46487	6.696	7.72366	8.04436	7.67544	7.37405	8.02593	0.377385	0.891273	-1.12199	6.00E-14	0.490505	-2.03871	0.052241	1.29139	1.29139	0.000827809	0.636449	-1.57122
46551	TC1000000656.mm.1	NM_001081347 // Rhobtb1 //	Rhobtb1	NM_001081347	chr10	7.90932	7.8697	7.26126	8.54687	8.15618	8.18344	7.46749	8.29524	0.811201	1.02784	1.02784	6.52E-21	0.410195	-2.43787	0.869427	0.98128	-1.01908	3.62E-06	0.563407	-1.77491
17124	TC0300001081.mm.1	NM_007484 // Rhoc // ras hom	Rhoc	NM_007484	chr3	10.6605	10.0003	12.2833	10.1649	10.7684	10.5248	11.96	10.9578	0.035882	1.58033	1.58033	3.52E-18	4.34209	4.34209	0.432819	1.18397	1.18397	0.00176914	2.00301	2.00301
36896	TC0800001531.mm.1	NM_133955 // Rhou // ras hom	Rhou	NM_133955	chr8	8.90748	9.03097	11.4496	8.87219	8.98071	9.27082	10.2758	8.81028	0.65826	0.917962	-1.08937	4.63E-25	5.96877	5.96877	0.300197	0.817836	-1.22274	1.30E-06	2.76155	2.76155
25312	TC0500001859.mm.1	NM_001289564 // Rxfp2 // rel	Rxfp2	NM_001289564	chr5	5.57542	5.91212	7.53951	6.2716	6.34178	6.41094	6.61858	6.39305	0.146787	0.791853	-1.26286	4.96E-14	2.40813	2.40813	0.764116	0.953195	-1.0491	0.329208	1.1692	1.1692
38022	TC0800002665.mm.1	NM_021390 // Sall1 // sal-like	Sall1	NM_021390	chr8	10.2692	9.78057	8.93207	10.3055	10.0639	9.95541	9.56245	10.0912	0.002792	1.40311	1.40311	1.67E-23	0.385962	-2.59093	0.494187	1.07813	1.07813	0.0012853	0.693154	-1.44268
63535	TC1500001980.mm.1	NM_001271472 // Scube1 // si	Scube1	NM_001271472	chr15	7.65616	7.58892	11.3057	8.63956	8.2587	7.93684	11.1521	10.1205	0.900104	1.04772	1.04772	2.35E-12	6.34747	6.34747	0.548423	1.24994	1.24994	0.0571337	2.04437	2.04437
51780	TC1100002699.mm.1	NM_175255 // Sec24a // Sec24	Sec24a	NM_175255	chr11	9.71026	9.47326	10.7571	9.60305	9.99751	9.84262	10.7557	9.86874	0.110832	1.17854	1.17854	3.84E-21	2.22537	2.22537	0.295038	1.11333	1.11333	5.71E-08	1.84929	1.84929
16926	TC0300000880.mm.1	NM_009150 // Selenbp1 // sel	Selenbp1	NM_009150	chr3	10.5498	9.95913	9.12391	10.3009	9.76896	10.1017	8.71256	9.49342	0.017624	1.50599	1.50599	7.40E-12	0.442264	-2.2611	0.175637	0.794044	-1.25938	0.00196835	0.582017	-1.71816
41618	TC0900003042.mm.1	NM_011349 // Sema3f // sema	Sema3f	NM_011349	chr9	8.03837	7.58582	9.1774	7.62859	8.01955	7.94273	8.60329	8.10606	0.019997	1.36846	1.36846	6.06E-22	2.92577	2.92577	0.687645	1.05469	1.05469	0.0108775	1.4115	1.4115
38698	TC0900000100.mm.1	NM_030261 // Sesn3 // sestrin	Sesn3	NM_030261	chr9	11.0613	10.9056	9.84749	11.9415	10.6939	10.7728	10.399	11.3083	0.62302	1.11396	1.11396	1.63E-17	0.23423	-4.26931	0.80308	0.946757	-1.05624	0.00515432	0.532438	-1.87815
38701	TC0900000103.mm.1	uc009oek.1 // Sesn3 // sestrin	Sesn3	uc009oek.1	chr9	12.199	12.1944	11.1573	13.4625	11.482	12.2506	11.4308	12.881	0.990449	1.0032	1.0032	1.47E-15	0.20233	-4.94241	0.048857	0.587	-1.70358	0.000316233	0.365979	-2.7324
46070	TC1000000171.mm.1	NM_001161845 // Sgk1 // seru	Sgk1	NM_001161845	chr10	8.3213	7.29311	9.4037	7.46268	7.91024	7.63689	9.34857	7.85576	2.24E-06	2.03947	2.03947	3.67E-26	3.83976	3.83976	0.17664	1.20861	1.20861	1.41E-10	2.81438	2.81438
16724	TC0300000675.mm.1	NM_001082414 // Sh3d19 // S	Sh3d19	NM_001082414	chr3	10.0866	10.2528	9.62304	10.6785	10.0565	10.3947	9.44451	10.0669	0.422912	0.891175	-1.12211	9.55E-13	0.481138	-2.07841	0.105348	0.791039	-1.26416	0.00349643	0.649612	-1.53938
16264	TC0300000210.mm.1	NM_001039090 // Skil // SKI-li	Skil	NM_001039090	chr3	9.39641	8.85378	11.8037	9.07178	9.53726	9.34924	10.6311	9.5727	0.005485	1.45662	1.45662	6.81E-37	6.64333	6.64333	0.324722	1.1392	1.1392	3.74E-07	2.08263	2.08263
38197	TC0800002844.mm.1	NM_001253804 // Slc12a4 // s	Slc12a4	NM_001253804	chr8	8.35872	8.26191	11.0014	7.87212	8.65293	8.49724	10.0793	8.72889	0.723278	1.06941	1.06941	1.31E-30	8.74973	8.74973	0.569347	1.11395	1.11395	4.40E-06	2.54976	2.54976
17119	TC0300001076.mm.1	NM_009196 // Slc16a1 // solut	Slc16a1	NM_009196	chr3	7.79151	7.62521	10.6947	7.65768	7.94417	7.76491	9.66097	8.26792	0.597573	1.12218	1.12218	3.78E-26	8.20804	8.20804	0.569413	1.1323	1.1323	3.08E-05	2.62635	2.62635
50554	TC1100001460.mm.1	NM_016752 // Slc35b1 // solut	Slc35b1	NM_016752	chr11	10.0172	9.11849	11.3735	9.63943	10.495	9.95216	11.7716	10.7759	0.010375	1.86435	1.86435	1.30E-12	3.32673	3.32673	0.116356	1.45686	1.45686	0.00471317	1.99407	1.99407
36449	TC0800001080.mm.1	NM_009209 // Slc6a2 // solute	Slc6a2	NM_009209	chr8	8.11011	8.17234	10.61	8.45341	8.78962	8.86171	9.35388	9.0299	0.867455	0.957781	-1.04408	6.40E-15	4.45864	4.45864	0.846698	0.951257	-1.05124	0.386102	1.25178	1.25178
39887	TC0900001297.mm.1	NM_033314 // Slco2a1 // solut	Slco2a1	NM_033314	chr9	8.11886	7.35729	10.6775	8.0904	8.19561	8.0017	9.99144	8.45612	0.027059	1.69534	1.69534	1.43E-20	6.00876	6.00876	0.567504	1.14387	1.14387	2.08E-05	2.89853	2.89853
54118	TC1200000751.mm.1	NM_001146217 // Smoc1 // SP	Smoc1	NM_001146217	chr12	9.37505	9.45995	11.3556	9.53052	10.7361	9.86541	10.7225	9.33669	0.812497	0.94285	-1.06061	9.54E-13	3.54317	3.54317	0.017029	1.82849	1.82849	0.000220345	2.61319	2.61319
40220	TC0900001635.mm.1	NM_001164572 // Snrk // SNF	Snrk	NM_001164572	chr9	10.3426	10.2619	11.8137	10.2197	10.2853	10.2834	10.9311	10.4506	0.681747	1.05754	1.05754	6.36E-22	3.01879	3.01879	0.992293	1.00132	1.00132	0.0166042	1.39526	1.39526
15303	TC0200004756.mm.1	NM_001199188 // Snx5 // sort	Snx5	NM_001199188	chr2	12.1212	11.8758	13.4491	12.2128	12.1904	12.0624	12.8763	12.4456	0.065099	1.18539	1.18539	1.68E-25	2.35593	2.35593	0.331841	1.09278	1.09278	0.00155118	1.34789	1.34789
48605	TC1000002725.mm.1	NM_001168655 // Socs2 // sup	Socs2	NM_001168655	chr10	7.61841	7.70576	9.00537	7.9565	7.64528	7.8854	8.63791	8.10247	0.625617	0.941249	-1.06242	3.60E-15	2.06891	2.06891	0.182132	0.846671	-1.1811	0.00364196	1.44938	1.44938
28861	TC0600001703.mm.1	NR_040519 // Sox5os3 // SRY (	Sox5os3	NR_040519	chr6	5.92072	5.84599	7.94573	6.16336	5.98909	6.19812	7.21445	5.86	0.827663	1.05316	1.05316	4.82E-13	3.4399	3.4399	0.543029	0.865123	-1.15591	0.000170938	2.557	2.557
23294	TC0400004055.mm.1	NM_029035 // Spsb1 // splA/r	Spsb1	NM_029035	chr4	7.4298	7.0786	9.44179	7.01528	7.26573	7.4095	7.75949	7.27624	0.027875	1.27562	1.27562	5.29E-39	5.37593	5.37593	0.361442	0.905151	-1.10479	0.00284758	1.39789	1.39789
11167	TC0200000587.mm.1	NM_001025310 // St6galnac6	St6galnac6	NM_001025310	chr2	7.17953	7.0997	9.0094	6.89124	7.32039	7.31507	8.08949	7.37351	0.613361	1.05689	1.05689	5.59E-35	4.3414	4.3414	0.973113	1.00369	1.00369	2.05E-05	1.6426	1.6426
50724	TC1100001632.mm.1	NM_001164062 // Stat5a // sig	Stat5a	NM_001164062	chr11	8.05475	8.02036	9.84895	7.93516	8.19368	8.09824	9.26918	8.36378	0.832778	1.02413	1.02413	2.62E-31	3.76799	3.76799	0.558389	1.06839	1.06839	3.79E-07	1.87306	1.87306
52864	TC1100003787.mm.1	NM_001113563 // Stat5b // sig	Stat5b	NM_001113563	chr11	9.08689	8.85931	10.3604	9.05191	9.17994	9.14339	9.85137	9.23063	0.153995	1.17086	1.17086	2.37E-22	2.47689	2.47689	0.817716	1.02566	1.02566	0.000190173	1.53766	1.53766
70240	TC1800001402.mm.1	NM_001109975 // Synpo // sy	Synpo	NM_001109975	chr18	6.59564	6.68306	7.68147	6.58609	6.86232	6.76354	7.21565	6.79314	0.356822	0.941198	-1.06248	6.56E-31	2.13669	2.13669	0.298213	1.07087	1.07087	2.66E-05	1.34026	1.34026
42071	TC0X00000122.mm.1	NM_177704 // Sytl5 // synapto	Sytl5	NM_177704	chrX	6.09492	6.24505	8.72346	7.19577	6.41846	6.13449	9.28019	7.47924	0.649622	0.901167	-1.10967	3.10E-11	2.88324	2.88324	0.39105	1.21754	1.21754	5.80E-07	3.4845	3.4845
37266	TC0800001906.mm.1	NM_177089 // Tacc1 // transfo	Tacc1	NM_177089	chr8	11.0266	10.1384	12.088	10.5861	10.596	10.4103	11.8602	11.0785	1.67E-05	1.85092	1.85092	6.12E-21	2.83206	2.83206	0.338766	1.13734	1.13734	0.000123302	1.71916	1.71916
32649	TC0700001906.mm.1	NM_001004468 // Tacc2 // tra	Tacc2	NM_001004468	chr7	9.64173	9.72734	10.2092	8.91277	9.31708	9.50402	9.7747	9.2235	0.626971	0.942388	-1.06113	8.91E-20	2.45621	2.45621	0.290016	0.878467	-1.13835	0.00241119	1.4653	1.4653
53004	TC1100003928.mm.1	NM_198292 // Tex2 // testis e	Tex2	NM_198292	chr11	8.44525	8.44214	11.5944	8.58691	8.87581	8.84045	10.5792	9.25736	0.990755	1.00216	1.00216	5.53E-30	8.04182	8.04182	0.895365	1.02482	1.02482	4.84E-06	2.49992	2.49992
10450	TC0100003754.mm.1	NM_009367 // Tgfb2 // transfo	Tgfb2	NM_009367	chr1	8.37588	8.62777	10.4511	8.87044	9.25986	8.87689	10.0082	9.11426	0.399528	0.839798	-1.19076	2.21E-13	2.99107	2.99107	0.201651	1.30402	1.30402	0.00359919	1.85827	1.85827
22870	TC0400003627.mm.1	NM_001168333 // Tinagl1 // tu	Tinagl1	NM_001168333	chr4	8.16225	7.77022	9.62648	7.43707	8.01518	7.94821	9.39005	8.07435	0.044478	1.31224	1.31224	1.92E-30	4.56117	4.56117	0.727883	1.04752	1.04752	1.78E-09	2.48922	2.48922
16581	TC0300000528.mm.1	NM_178892 // Tiparp // TCDD	Tiparp	NM_178892	chr3	9.80538	9.68822	14.2375	9.72716	10.8373	10.2585	12.4073	9.92828	0.69202	1.0846	1.0846	1.21E-38	22.7902	22.7902	0.053202	1.49365	1.49365	2.13E-12	5.57528	5.57528
22103	TC0400002854.mm.1	NM_001285529 // Tle1 // tran	Tle1	NM_001285529	chr4	9.93977	9.95613	8.60389	10.2336	10.0197	10.2114	8.92733	9.66201	0.913667	0.988723	-1.01141	4.72E-29	0.323156	-3.09448	0.206453	0.875573	-1.14211	5.82E-06	0.600953	-1.66402
27264	TC0600000091.mm.1	NM_027992 // Tmem106b // t	Tmem106b	NM_027992	chr6	12.5637	12.5416	11.1371	12.2754	12.2706	12.2338	11.4218	12.0175	0.889609	1.01541	1.01541	3.62E-19	0.454305	-2.20117	0.81677	1.02586	1.02586	0.00033664	0.661738	-1.51117
40760	TC0900002179.mm.1	NM_027865 // Tmem25 // tra	Tmem25	NM_027865	chr9	6.07609	6.11775	7.28116	6.05593	6.21415	6.34717	6.55285	6.11722	0.802977	0.971532	-1.0293	1.08E-19	2.33792	2.33792	0.426635	0.91192	-1.09659	0.0107233	1.35251	1.35251
66035	TC1600002152.mm.1	NM_015775 // Tmprss2 // tra	Tmprss2	NM_015775	chr16	9.83871	9.17287	11.0724	8.69949	8.92083	9.11405	9.55661	8.88606	0.05003	1.58649	1.58649	6.55E-19	5.17966	5.17966	0.56492	0.87465	-1.14332	0.0484693	1.59169	1.59169
9291	TC0100002576.mm.1	NM_001289895 // Tns1 // tens	Tns1	NM_001289895	chr1	13.7929	13.0156	15.1409	13.6592	13.846	13.8837	14.2423	13.6835	0.009825	1.71389	1.71389	1.53E-12	2.79283	2.79283	0.898238	0.974252	-1.02643	0.0605865	1.47308	1.47308
20469	TC0400001209.mm.1	NM_001085549 // Trabd2b //	Trabd2b	NM_001085549	chr4	6.77247	6.86011	9.28529	7.08736	7.2013	7.25448	8.87464	7.60607	0.691718	0.941063	-1.06263	6.28E-27	4.58821	4.58821	0.809786	0.96381	-1.03755	1.79E-07	2.40921	2.40921
46227	TC1000000330.mm.1	NM_134000 // Traf3ip2 // TRA	Traf3ip2	NM_134000	chr10	10.143	10.2103	9.27266	10.5835	9.94147	10.1827	9.63343	10.3904	0.6905	0.954391	-1.04779	6.44E-21	0.40308	-2.4809	0.156387	0.846016	-1.18201	2.54E-05	0.591724	-1.68998
52365	TC1100003285.mm.1	NM_009423 // Traf4 // TNF re	Traf4	NM_009423	chr11	7.61779	7.73467	8.56126	7.45327	7.70618	7.75871	8.00677	7.82383	0.454537	0.922179	-1.08439	5.43E-19	2.15545	2.15545	0.73638	0.964242	-1.03708	0.243089	1.13519	1.13519
62233	TC1500000660.mm.1	NM_001024716 // Triobp // T	Triobp	NM_001024716	chr15	7.47686	7.50842	8.95626	7.22624	7.65574	7.55055	8.44137	7.69251	0.78879	0.978358	-1.02212	1.52E-37	3.31731	3.31731	0.373204	1.07563	1.07563	1.38E-08	1.68046	1.68046
12023	TC0200001448.mm.1	NM_001025246 // Trp53i11 //	Trp53i11	NM_001025246	chr2	8.76991	8.64008	11.0194	8.60484	8.86423	8.82465	9.8784	8.86164	0.602484	1.09417	1.09417	2.87E-26	5.33157	5.33157	0.873742	1.02781	1.02781	0.000106185	2.02338	2.02338
65415	TC1600001527.mm.1	NM_009471 // Umps // uridine	Umps	NM_009471	chr16	8.43342	8.53281	10.1501	8.53641	8.76109	8.48799	10.6408	8.90346	0.693548	0.933429	-1.07132	7.52E-17	3.06032	3.06032	0.28057	1.2084	1.2084	1.41E-09	3.33425	3.33425
16282	TC0300000228.mm.1	NM_001013024 // Usp13 // ub	Usp13	NM_001013024	chr3	6.96639	7.05002	8.52502	7.4045	7.35881	7.23149	8.33664	7.64331	0.639582	0.943676	-1.05969	1.81E-16	2.17425	2.17425	0.476357	1.09226	1.09226	0.000211243	1.61701	1.61701
53230	TC1100004156.mm.1	NM_001033528 // Usp36 // ub	Usp36	NM_001033528	chr11	8.38041	8.40472	10.0472	8.16804	8.5353	8.4551	9.77255	8.63063	0.897151	0.983289	-1.01699	4.93E-27	3.67852	3.67852	0.669966	1.05717	1.05717	4.59E-08	2.20675	2.20675
25296	TC0500001842.mm.1	NM_001013378 // Uspl1 // ubi	Uspl1	NM_001013378	chr5	9.92882	10.1488	11.5784	9.88904	10.1831	10.1435	11.2089	10.2197	0.120422	0.858581	-1.16471	6.13E-32	3.22518	3.22518	0.778241	1.02781	1.02781	7.44E-10	1.98501	1.98501
68440	TC1700002411.mm.1	NM_013933 // Vapa // vesicle-	Vapa	NM_013933	chr17	11.9928	11.4385	13.5184	11.8243	12.0535	11.8628	13.1164	12.3997	0.015014	1.46841	1.46841	2.00E-20	3.23585	3.23585	0.394334	1.14132	1.14132	0.00190513	1.64342	1.64342
68192	TC1700002162.mm.1	NM_001025250 // Vegfa // vas	Vegfa	NM_001025250	chr17	10.1104	9.88202	13.976	10.1137	10.7051	10.76	12.6991	11.4042	0.42452	1.17152	1.17152	3.19E-35	14.5432	14.5432	0.847342	0.962634	-1.03882	2.03E-05	2.45366	2.45366
25717	TC0500002268.mm.1	NM_011716 // Wfs1 // Wolfra	Wfs1	NM_011716	chr5	9.12013	8.90763	10.3467	8.62263	9.37369	9.0028	9.81896	9.10478	0.28995	1.15869	1.15869	2.25E-23	3.30371	3.30371	0.066812	1.29315	1.29315	0.000606809	1.64055	1.64055
20958	TC0400001701.mm.1	NM_009523 // Wnt4 // wingle	Wnt4	NM_009523	chr4	7.66241	7.63361	9.68932	7.4526	7.85253	7.86524	8.42131	7.92101	0.946555	1.02016	1.02016	4.34E-13	4.71325	4.71325	0.976389	0.991227	-1.00885	0.24629	1.41451	1.41451
37543	TC0800002184.mm.1	NM_133791 // Wwc2 // WW, (	Wwc2	NM_133791	chr8	8.65154	8.50169	11.2052	8.44693	9.0101	8.73406	10.3682	8.72282	0.529626	1.10946	1.10946	6.29E-31	6.76577	6.76577	0.248404	1.21087	1.21087	1.30E-09	3.12829	3.12829

Column #	Probeset ID	gene_assignment	Gene Symbol	RefSeq	seqname	Mean(Ex3aERKO-E2 2h)	Mean(Ex3aERKO-Saline)	Mean(WT-E2 2h)	Mean(WT-Saline)	Mean(ppKO E2 2h)	Mean(ppKO Saline)	Mean(ppWT E2 2h)	Mean(ppWT Saline)	p-value(Ex3aERKO-E2 2h vs. Ex3aERKO-Saline)	Ratio(Ex3aERKO-E2 2h vs. Ex3aERKO-Saline)	Fold-Change(Ex3aERKO-E2 2h vs. Ex3aERKO-Saline)	p-value(WT-E2 2h vs. WT-Saline)	Ratio(WT-E2 2h vs. WT-Saline)	Fold-Change(WT-E2 2h vs. WT-Saline)	p-value(ppKO E2 2h vs. ppKO Saline)	Ratio(ppKO E2 2h vs. ppKO Saline)	Fold-Change(ppKO E2 2h vs. ppKO Saline)	p-value(ppWT E2 2h vs. ppWT Saline)	Ratio(ppWT E2 2h vs. ppWT Saline)	Fold-Change(ppWT E2 2h vs. ppWT Saline)
54629	TC1200001265.mm.1	NM_001100460 // Zbtb42 // zi	Zbtb42	NM_001100460	chr12	5.55283	5.51303	7.16912	5.28408	5.66612	5.59861	5.87999	5.70932	0.87874	1.02797	1.02797	2.30E-19	3.69365	3.69365	0.795799	1.04791	1.04791	0.513513	1.12558	1.12558
15444	TC0200004899.mm.1	NM_175126 // Zcchc3 // zinc fi	Zcchc3	NM_175126	chr2	8.23322	8.24482	9.53964	8.20052	8.57642	8.54982	9.01045	8.46861	0.956972	0.991991	-1.00807	2.59E-16	2.52996	2.52996	0.901544	1.01861	1.01861	0.0135832	1.45582	1.45582
68675	TC1700002647.mm.1	NM_001001806 // Zfp36l2 // z	Zfp36l2	NM_001001806	chr17	12.2905	12.0442	13.461	12.4075	12.0587	12.1927	12.4005	12.6735	0.206668	1.18619	1.18619	8.46E-14	2.07566	2.07566	0.490587	0.911322	-1.09731	0.162234	0.827616	-1.20829
59665	TC1400000935.mm.1	NM_199029 // Zfp395 // zinc f	Zfp395	NM_199029	chr14	9.56552	9.47853	8.1387	9.31918	9.11852	9.45568	8.22172	8.96886	0.590711	1.06215	1.06215	1.35E-19	0.441204	-2.26653	0.039719	0.791596	-1.26327	1.48E-05	0.595786	-1.67845
36846	TC0800001481.mm.1	NM_009569 // Zfpm1 // zinc fi	Zfpm1	NM_009569	chr8	7.11089	7.19198	8.63114	6.96031	7.37119	7.22063	8.08402	7.36991	0.706833	0.945342	-1.05782	6.48E-21	3.18397	3.18397	0.485484	1.11	1.11	0.00137818	1.64047	1.64047
58989	TC1400000241.mm.1	NM_183208 // Zmiz1 // zinc fir	Zmiz1	NM_183208	chr14	10.8464	10.2927	13.3777	10.5248	10.7544	10.9946	12.1949	10.8324	0.070647	1.46789	1.46789	1.54E-25	7.22422	7.22422	0.428831	0.846638	-1.18114	2.36E-05	2.5713	2.5713

Table S5 Primer sequences for RT-PCR

Hoxd11_210F	TCGAATAAGCAAGGACAAGGACA
Hoxd11_306R	CGGATCTGGTACTTGGTGTAGG
Rara_1300F	CTTCACCACCCTCACCATCG
Rara_1403R	TGTCTTGCTCAGGCGTGTAC
Ncor2_2076F	GAGGCCAACCATGAGGAGAC
Ncor2_2167R	TCTTCCTCAGTCCAGCGAGA
PL7 F	AGCTGGCCTTTGTCATCAGAA
PL7 R	GACGAAGGAGCTGCAGAACCT
Zmiz1_3251F	CAGCTCCAACGACTACAGCA
Zmiz1_3344R	GTTCATGGATGTCCCTCCGG

Table S6 HiC QC

	V-1						V-2						V-3					
	MAPQ>0			MAPQ>30			MAPQ>0			MAPQ>30			MAPQ>0			MAPQ>30		
	#	% of all	% of uniq	#	% of all	% of uniq	#	% of all	% of uniq	#	% of all	% of uniq	#	% of all	% of uniq	#	% of all	% of uniq
Sequenced Reads	629,464,062			629,464,062			962,946,053			962,946,053			560,071,878			560,071,878		
Normal Pairs	585,375,643	93.0%		585,375,643	93.0%		905,019,501	94.0%		905,019,501	94.0%		183,027,758	32.7%		183,027,758	32.7%	
Chimeric Paired	3,166	0.0%		3,166	0.0%		2,846	0.0%		2,846	0.0%		302,360,827	54.0%		302,360,827	54.0%	
Chimeric Ambiguous	18,855	0.0%		18,855	0.0%		21,798	0.0%		21,798	0.0%		66,273,991	11.8%		66,273,991	11.8%	
Unmapped	44,066,398	7.0%		44,066,398	7.0%		57,901,908	6.0%		57,901,908	6.0%		8,409,302	1.5%		8,409,302	1.5%	
Alignable Reads	585,378,809	93.0%		585,378,809	93.0%		905,022,347	94.0%		905,022,347	94.0%		485,388,585	86.7%		485,388,585	86.7%	
Duplicates	297,034,719	47.2%		297,034,719	47.2%		103,738,011	10.8%		103,738,011	10.8%		21,472,911	3.8%		21,472,911	3.8%	
Unique Reads	288,344,090	45.8%	100.0%	288,344,090	45.8%	100.0%	801,284,336	83.2%	100.0%	801,284,336	83.2%	100.0%	463,915,674	82.8%	100.0%	463,915,674	82.8%	100.0%
Intra-fragment	1,577,562	0.3%	0.5%	1,577,562	0.3%	0.5%	7,628,914	0.8%	1.0%	7,628,914	0.8%	1.0%	679,265	0.1%	0.1%	679,265	0.1%	0.1%
Low Mapping Quality	87,545,112	13.9%	30.4%	102,124,373	16.2%	35.4%	201,629,580	20.9%	25.2%	256,179,472	26.6%	32.0%	52,105,001	9.3%	11.2%	77,986,333	13.9%	16.8%
HiC Contacts	199,221,416	31.6%	69.1%	184,642,155	29.3%	64.0%	592,025,842	61.5%	73.9%	537,475,950	55.8%	67.1%	411,131,408	73.4%	88.6%	385,250,076	68.8%	83.0%
Inter Chromosomal	28,901,981	4.6%	10.0%	26,136,968	4.2%	9.1%	89,857,971	9.3%	11.2%	80,051,498	8.3%	10.0%	85,455,890	15.3%	18.4%	78,895,436	14.1%	17.0%
Intra Chromosomal	170,319,435	27.1%	59.1%	158,505,187	25.2%	55.0%	502,167,871	52.1%	62.7%	457,424,452	47.5%	57.1%	325,675,518	58.1%	70.2%	306,354,640	54.7%	66.0%
Intra Short Range (<20 kb)	94,700,845	15.0%	32.8%	89,010,848	14.1%	30.9%	218,084,601	22.6%	27.2%	201,282,243	20.9%	25.1%	94,121,707	16.8%	20.3%	89,689,532	16.0%	19.3%
Intra Long Range (>20 kb)	75,616,534	12.0%	26.2%	69,492,413	11.0%	24.1%	284,081,489	29.5%	35.5%	256,140,548	26.6%	32.0%	231,553,482	41.3%	49.9%	216,664,804	38.7%	46.7%
Ligations	(Arima)	~	~	(Arima)	~	~	(Arima)	~	~	(Arima)	~	~	(Arima)	~	~	(Arima)	~	~
3' bias (long range)	65% - 35%			65% - 35%			63% - 37%			63% - 37%			63% - 37%			63% - 37%		
Read Pair Type (LIOR)	25% - 25% - 25% - 25%			25% - 25% - 25% - 25%			25% - 25% - 25% - 25%			25% - 25% - 25% - 25%			25% - 25% - 25% - 25%			25% - 25% - 25% - 25%		
	Table S5 QC metrics from Juicer output. Showing both all uniquely-mapped pairs (MAPQ>0) or results with a higher alignment score cutoff (MAPQ>30).																	

	P4-1h-1						P4-1h-2					
	MAPQ>0			MAPQ>30			MAPQ>0			MAPQ>30		
	#	% of all	% of uniq	#	% of all	% of uniq	#	% of all	% of uniq	#	% of all	% of uniq
Sequenced Reads	977,735,045			977,735,045			569,833,487			569,833,487		
Normal Pairs	908,549,195	92.9%		908,549,195	92.9%		197,380,068	34.6%		197,380,068	34.6%	
Chimeric Paired	3,776	0.0%		3,776	0.0%		301,564,475	52.9%		301,564,475	52.9%	
Chimeric Ambiguous	51,164	0.0%		51,164	0.0%		63,828,003	11.2%		63,828,003	11.2%	
Unmapped	69,130,910	7.1%		69,130,910	7.1%		7,060,941	1.2%		7,060,941	1.2%	
Alignable Reads	908,552,971	92.9%		908,552,971	92.9%		498,944,543	87.6%		498,944,543	87.6%	
Duplicates	390,802,598	40.0%		390,802,598	40.0%		20,698,739	3.6%		20,698,739	3.6%	
Unique Reads	517,750,373	53.0%	100.0%	517,750,373	53.0%	100.0%	478,245,804	83.9%	100.0%	478,245,804	83.9%	100.0%
Intra-fragment	2,295,765	0.2%	0.4%	2,295,765	0.2%	0.4%	1,031,829	0.2%	0.2%	1,031,829	0.2%	0.2%
Low Mapping Quality	148,079,981	15.1%	28.6%	176,209,001	18.0%	34.0%	53,160,053	9.3%	11.1%	79,260,210	13.9%	16.6%
HiC Contacts	367,374,627	37.6%	71.0%	339,245,607	34.7%	65.5%	424,053,922	74.4%	88.7%	397,953,765	69.8%	83.2%
Inter Chromosomal	50,488,377	5.2%	9.8%	45,431,238	4.6%	8.8%	78,509,166	13.8%	16.4%	72,368,604	12.7%	15.1%
Intra Chromosomal	316,886,250	32.4%	61.2%	293,814,369	30.1%	56.7%	345,544,756	60.6%	72.3%	325,585,161	57.1%	68.1%
Intra Short Range (<20 kb)	178,103,186	18.2%	34.4%	166,592,469	17.0%	32.2%	111,404,665	19.6%	23.3%	106,319,456	18.7%	22.2%
Intra Long Range (>20 kb)	138,778,498	14.2%	26.8%	127,217,621	13.0%	24.6%	234,139,667	41.1%	49.0%	219,265,304	38.5%	45.8%
Ligations	(Arima)	~	~	(Arima)	~	~	(Arima)	~	~	(Arima)	~	~
3' bias (long range)	64% - 36%			64% - 36%			63% - 37%			63% - 37%		
Read Pair Type (LIOR)	25% - 25% - 25% - 25%			25% - 25% - 25% - 25%			25% - 25% - 25% - 25%			25% - 25% - 25% - 25%		

	E2-1h						Ex3aERKO-V					
	MAPQ>0			MAPQ>30			MAPQ>0			MAPQ>30		
	#	% of all	% of uniq	#	% of all	% of uniq	#	% of all	% of uniq	#	% of all	% of uniq
Sequenced Reads	1,123,566,707			1,123,566,707			1,075,810,390			1,075,810,390		
Normal Pairs	1,052,887,996	93.7%		1,052,887,996	93.7%		1,016,539,785	94.5%		1,016,539,785	94.5%	
Chimeric Paired	4,258	0.0%		4,258	0.0%		2,882	0.0%		2,882	0.0%	
Chimeric Ambiguous	36,126	0.0%		36,126	0.0%		27,705	0.0%		27,705	0.0%	
Unmapped	70,638,327	6.3%		70,638,327	6.3%		59,240,018	5.5%		59,240,018	5.5%	
Alignable Reads	1,052,892,254	93.7%		1,052,892,254	93.7%		1,016,542,667	94.5%		1,016,542,667	94.5%	
Duplicates	465,203,148	41.4%		465,203,148	41.4%		359,549,214	33.4%		359,549,214	33.4%	
Unique Reads	587,689,106	52.3%	100.0%	587,689,106	52.3%	100.0%	656,993,453	61.1%	100.0%	656,993,453	61.1%	100.0%
Intra-fragment	2,636,953	0.2%	0.4%	2,636,953	0.2%	0.4%	7,804,849	0.7%	1.2%	7,804,849	0.7%	1.2%
Low Mapping Quality	170,685,442	15.2%	29.0%	202,388,116	18.0%	34.4%	190,877,208	17.7%	29.1%	230,709,543	21.4%	35.1%
HiC Contacts	414,366,711	36.9%	70.5%	382,664,037	34.1%	65.1%	458,311,396	42.6%	69.8%	418,479,061	38.9%	63.7%
Inter Chromosomal	55,444,898	4.9%	9.4%	49,910,330	4.4%	8.5%	69,619,556	6.5%	10.6%	62,064,452	5.8%	9.4%
Intra Chromosomal	358,921,813	31.9%	61.1%	332,753,707	29.6%	56.6%	388,691,840	36.1%	59.2%	356,414,609	33.1%	54.2%
Intra Short Range (<20 kb)	203,350,463	18.1%	34.6%	190,296,952	16.9%	32.4%	188,781,615	17.5%	28.7%	175,228,478	16.3%	26.7%
Intra Long Range (>20 kb)	155,565,974	13.8%	26.5%	142,451,710	12.7%	24.2%	199,907,371	18.6%	30.4%	181,183,479	16.8%	27.6%
Ligations	(Arima)	~	~	(Arima)	~	~	(Arima)	~	~	(Arima)	~	~
3' bias (long range)	64% - 36%			64% - 36%			61% - 39%			61% - 39%		
Read Pair Type (LIOR)	25% - 25% - 25% - 25%			25% - 25% - 25% - 25%			25% - 25% - 25% - 25%			25% - 25% - 25% - 25%		