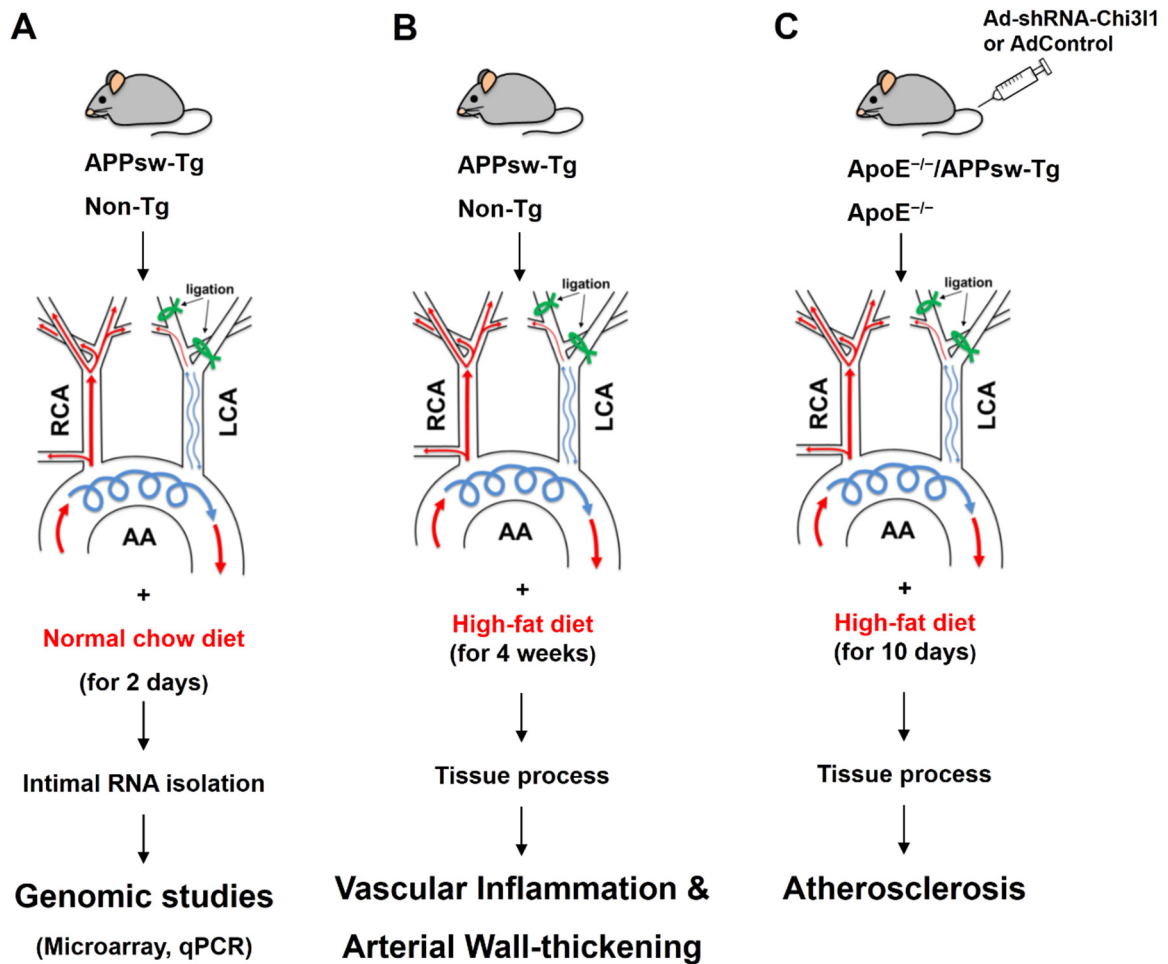
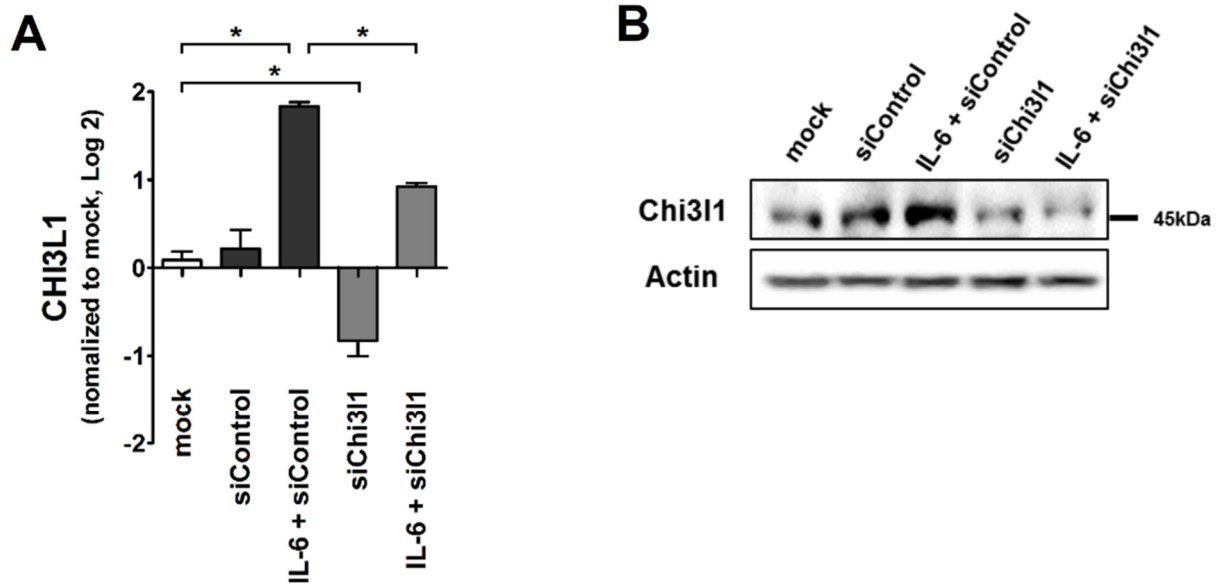


Supplemental Information

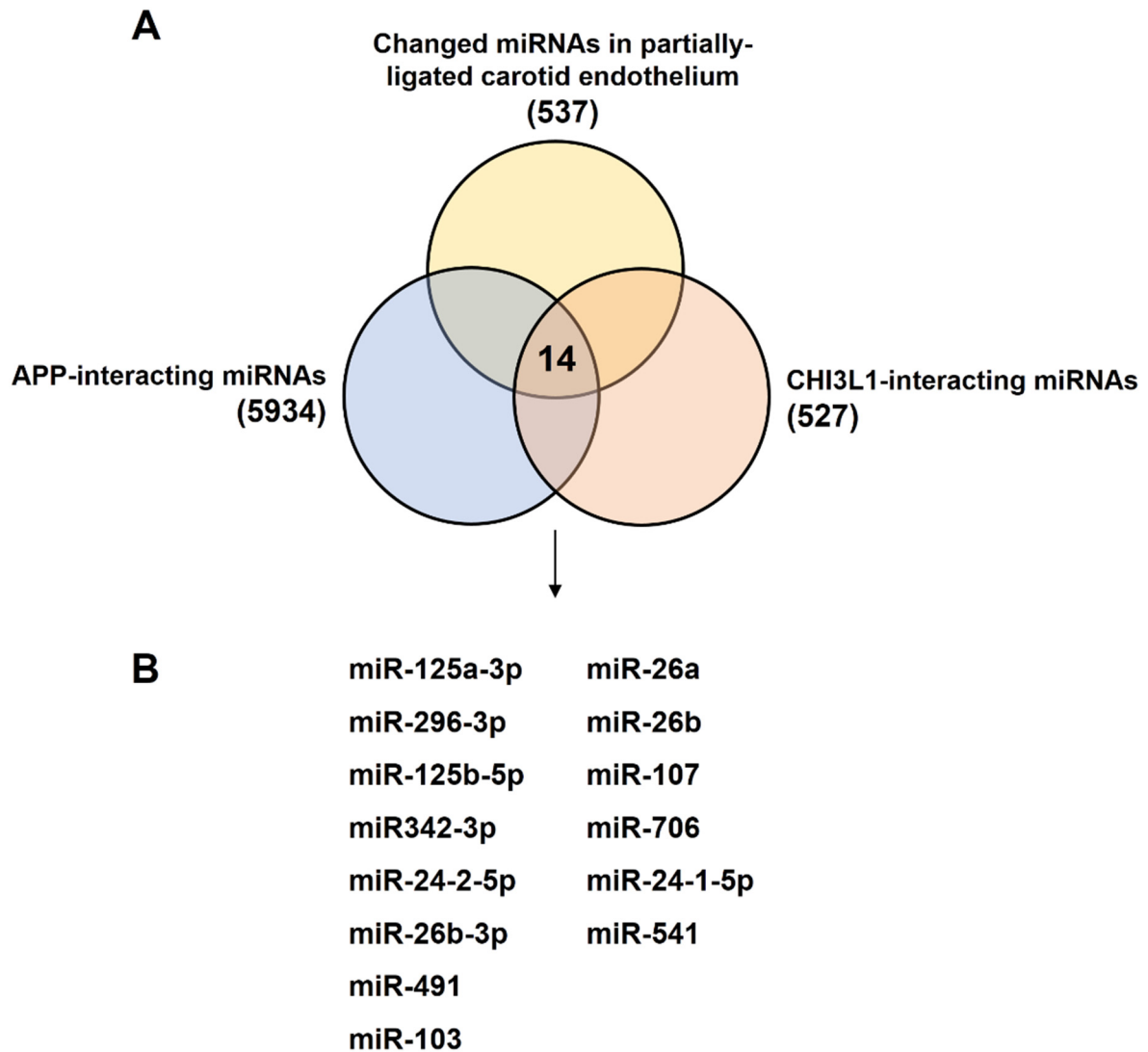
1. Supplementary Figures



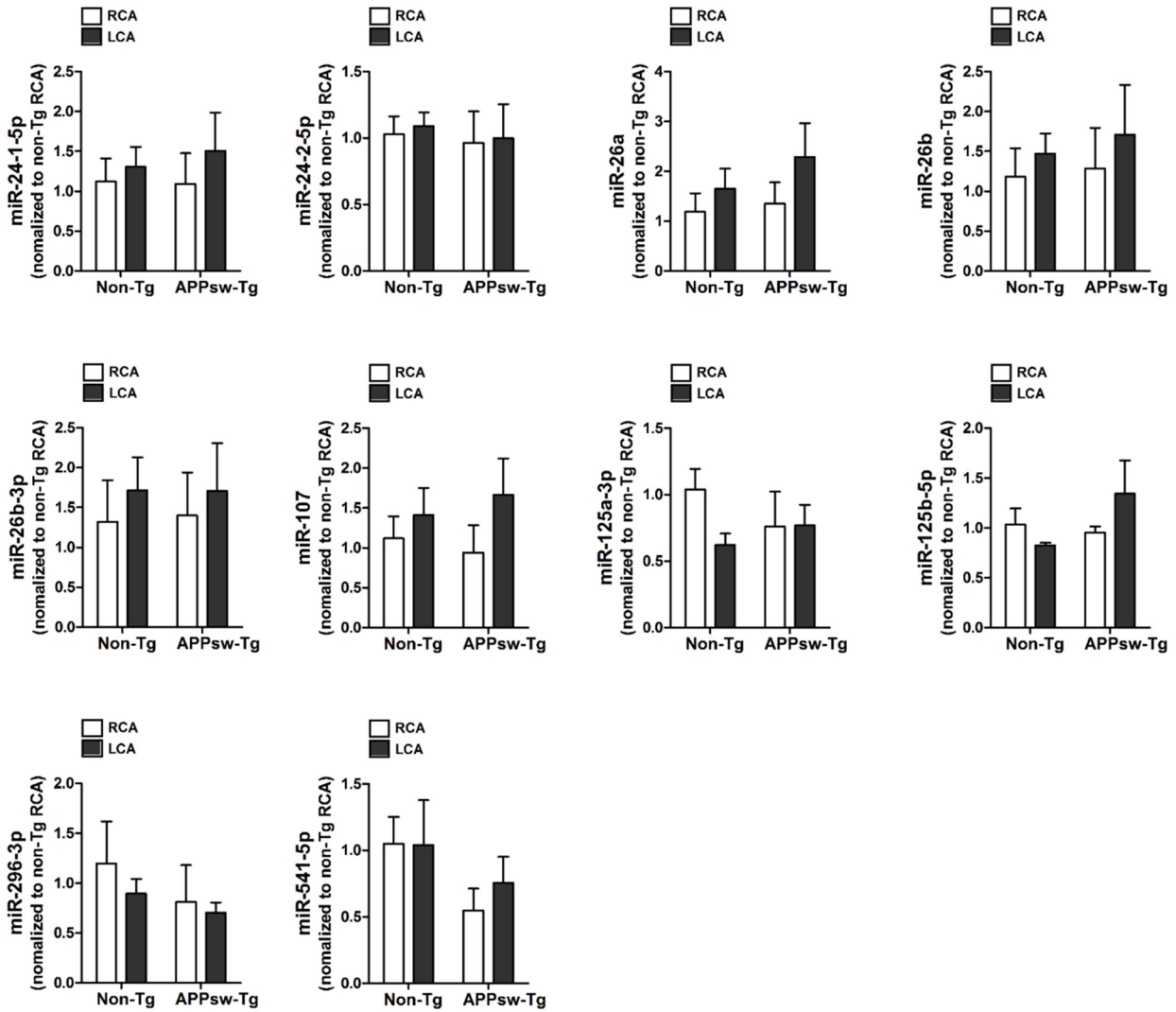
Supplementary Figure 1. Schematic diagram of the partial carotid ligation model, in which used in (A) genomic studies, (B) vascular inflammation and arterial wall-thickening, and (C) atherosclerosis functional studies.



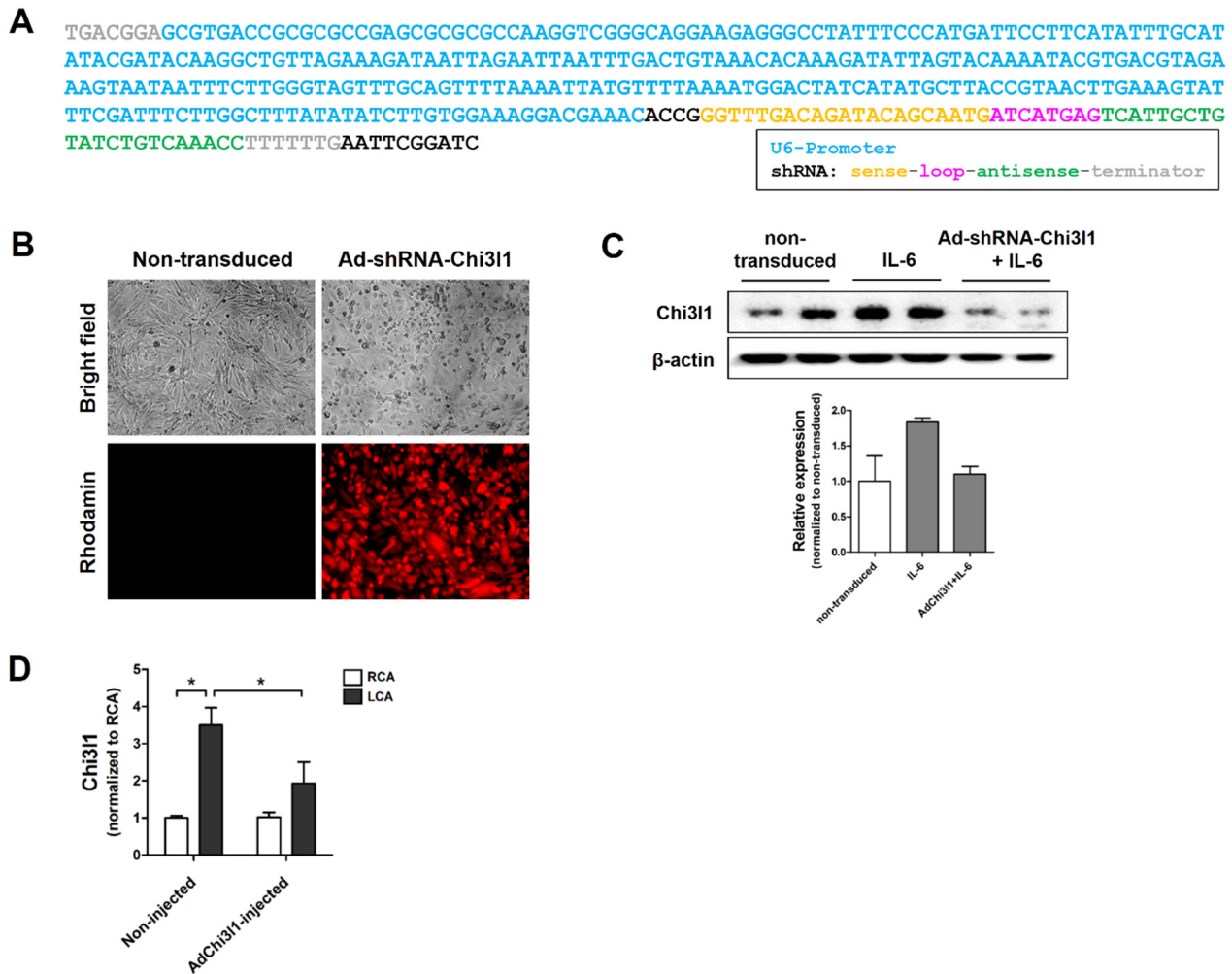
Supplementary Figure 2. Knockdown efficiency of Chi311 siRNA in iMAECs. (A) Knockdown of Chi311 mRNA by Chi311 siRNA (siChi311, 150 nM) in IL-6-stimulated iMAECs in comparison to control siRNA (siControl) was determined by qPCR ($n = 5$ each, data shown as mean \pm SEM, $*p < 0.05$ as determined by paired t -test). (B) Representative Western blots show a decreased expression of Chi311 protein stimulated by IL-6 upon treatment with siChi311 (150 nM) in iMAECs.



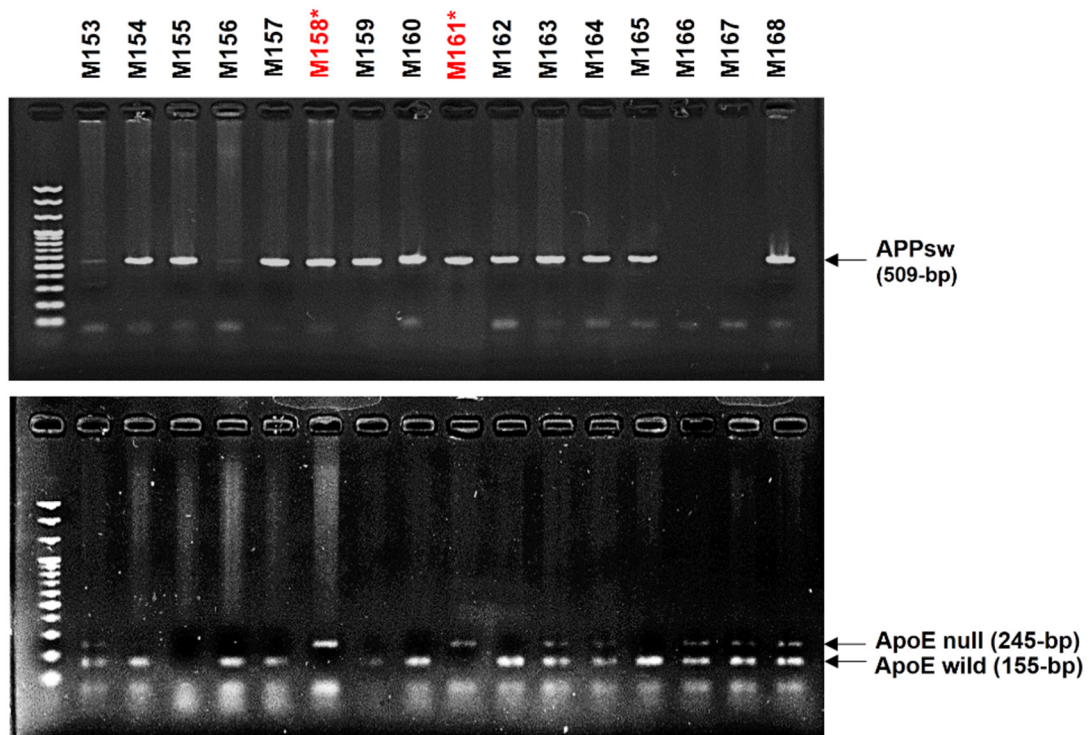
Supplementary Figure 3. The putative Chi3l1 targeting miRNAs. (A) The predicted miRNAs that target APP (5394 miRNAs) or Chi3l1 (527 miRNAs) from miRWalk were compared with a list of miRNAs (537 miRNAs) from a previous microarray data of mouse partial carotid ligation model. Venn diagram depicts the common miRNAs (14 miRNAs). (B) The list of 14 candidate miRNAs that regulates vascular inflammation and atherosclerosis development through targeting Chi3l1 in APPsw-Tg mice.



Supplementary Figure 4. Expression of the putative Chi311 targeting miRNAs in APPsw-Tg mice carotid endothelium. Expression of putative Chi311 targeting miRNAs was determined by qPCR using the Qiagen miScript miRNA-specific primer assay for each miRNAs in endothelial-enriched RNA obtained from the LCA and RCA following partial carotid ligation in APPsw-Tg or non-Tg mice at 2 days post-ligation ($n = 5$, data shown as mean \pm SEM).



Supplementary Figure 5. Adenoviral vector construction and Chi311 knockdown efficiency *in vitro* and *in vivo*. (A) The U6-shRNA-SV40-pA region of the shuttle plasmid was transferred via recombination in BAC vector containing the genome of a replication deficient Ad5-based vector deleted in E1/E3 genes. For the resulting vector cloning success was verified by restriction analysis and DNA sequencing. The successful shRNA sequence was obtained. (B-C) iMAECs were transduced at a confluency of about 70% with Ad-shRNA-Chi311 and were incubated for 24 h, then (B) transduction efficiency and (C) knockdown efficiency were determined. For Chi311 knockdown efficiency test in mouse carotid endothelium *in vivo*, C57BL/6 mice were injected with Ad-shRNA-Chi311 (10^8 p.f.u. per animal, *via* the tail vein) 2 days prior to partial carotid ligation, and Chi311 mRNA expression was determined by qPCR using endothelial-enriched RNAs obtained from the LCA and RCA following partial carotid ligation at 2 days post-ligation ($n = 4$, data shown as mean \pm SEM).



Supplementary Figure 6. Confirmation of transgenic status of ApoE^{-/-}/APPsw-Tg mice. DNA samples were extracted from tail tissues and the transgenic status of animal was confirmed by PCR using specific primers for human APP (509 bp) or ApoE (245 bp) as described in Methods.

2. Supplementary Tables

Supplementary Table 1. The list of endothelial genes in response to 48 h post partial carotid ligation and their fold-change expression in non-Tg mice LCA compared to non-Tg mice RCA.

Probe Set ID	Gene Accession	Gene Symbol	Non-Tg LCA-1	Non-Tg LCA-2	Non-Tg LCA-3	Non-Tg RCA-1	Non-Tg RCA-2	Non-Tg RCA-3	Non-Tg LCA/Non-Tg RCA (Fold-changes)	P-value
Upregulated genes (290)										
17491193	NM_011315	Saa3	2853.704032	2812.154221	660.6022165	20.7277699	23.10839251	23.80008795	93.53653456	0.39455023
17233226	NM_013532	Lilrb4	458.0902352	1080.901991	313.0262859	17.42043809	21.52196649	37.6320506	24.18585294	0.20550174
17400375	NM_001267695	Ctss	603.8004409	1040.232282	262.3769184	46.43555587	51.55005279	40.07709408	13.80828858	0.2510693
17439830	NM_001204201	Spp1	540.4772191	598.8554495	79.18246089	33.97585614	36.54970863	24.6576089	12.80179135	0.9551066
17212461	NM_009930	Col3a1	1240.735604	1287.654652	704.9035203	77.10523986	129.2047232	49.17898314	12.65531767	0.897469
17266952	NM_011338	Ccl9	658.9462593	842.0481957	285.0155851	45.90174198	57.23017051	46.19846461	11.96012543	0.62695915
17266960	NM_009139	Ccl6	470.5910263	568.1385549	173.9764233	31.99223769	45.98520925	26.81532809	11.57241999	0.0961448
17391565	NM_008361	Il1b	76.42962253	298.0062959	102.6130209	19.86712213	12.73583813	13.69976271	10.30282689	0.94831437
17502899	NM_009463	Ucp1	23.35659397	18.49326435	660.9237367	22.04697781	24.80546333	22.64619869	10.11204819	0.13397494
17233210	ENSMUST00000102894	Gp49a	48.66895861	247.736048	60.83830272	10.5132076	15.08943623	12.21075076	9.447533427	0.49868092
17383892	NM_008491	Lcn2	401.0135013	373.1564984	137.6338955	37.7635634	27.48594163	34.81987213	9.1117175	0.41461718
17286587	NM_010745	Ly86	212.4605244	472.3315188	96.22767724	28.7373475	20.17998224	37.03029147	9.087159242	0.90096104
17229658	NM_010185	Fcer1g	469.5278749	683.404056	266.3534209	40.25365836	67.23618673	60.25554057	8.460950185	0.6072606
17286830	NM_010104	Edn1	1411.242306	1840.803607	1768.830388	289.5143404	146.1034059	159.3158506	8.439389415	0.5409547
17230045	NM_008329	Ifi204	61.77464886	36.92671446	12.24755614	3.766391579	6.235472993	3.360199755	8.303276856	0.47208092
17227892	NM_021400	Prg4	534.7871536	579.0154362	261.7529525	89.79143929	45.59254379	41.32379941	7.784351787	0.10529035
17374488	NM_011580	Thbs1	716.1509997	1449.078464	802.454065	168.2152858	121.7805565	94.79906994	7.712377254	0.1207765
17264835	NM_009853	Cd68	522.9695002	758.6927809	234.1188034	65.79791666	63.65354685	73.13930436	7.48198499	0.7307995
17357671	NM_028595	Ms4a6c	93.22060688	159.4406846	42.59508311	12.3272236	14.71074086	14.58688574	7.093271764	0.50488627
17325324	NM_173869	Stfa2l1	9.024956636	84.16613712	18.81526886	5.884741324	5.16910318	4.785915749	7.071215778	0.681661
17512809	NM_017370	Hp	393.9798404	431.6242165	288.144166	37.85012081	47.75745327	76.14128433	6.885663577	0.97087485
17423577	ENSMUST00000029900	Atp6v0d2	114.0025275	86.11358826	97.36234425	12.63897883	14.70222907	16.47354338	6.78945906	0.15837772
17245223	ENSMUST00000092163	Lyz2	669.3950164	1383.378285	339.6956656	104.3529807	132.3941898	120.18558	6.702856387	0.4867249
17523650	ENSMUST00000168841	Ccr2	114.5238289	283.4406758	68.08957391	25.60032109	25.71274981	19.36742167	6.593814809	0.13224696
17483577	NM_001082960	Itgam	107.9614913	271.1239969	84.05915215	24.36301876	24.68026534	22.06827564	6.512930416	0.712665
17254047	NM_013654	Ccl7	356.9744479	291.0927303	155.3611527	51.46975464	39.1950076	37.65678688	6.261055422	0.5429484
17431607	NM_009777	C1qb	427.7585852	741.7144163	338.1939403	72.71433995	115.3768524	52.85276341	6.257334563	0.87215614
17408024	NM_010186	Fcgr1	212.5973789	183.5163764	51.66047488	16.08718506	29.21367598	26.97449415	6.195393008	0.76044804
17357640	XM_986941	Ms4a4a	121.0542567	239.7858972	49.11769656	16.74764108	28.60138292	20.90396921	6.187763458	0.82854617
17285546	NM_016687	Sfrp4	231.5845182	207.850153	94.81845629	14.51350434	57.06269579	15.76880032	6.116585092	0.589071
17476364	NM_011662	Tyropb	187.7247422	319.6118303	130.0655427	36.43542717	35.70719744	32.27906758	6.104115935	0.99270284
17362973	ENSMUST00000025582	Ms4a6d	44.14432261	81.54434917	16.06839582	5.62329604	10.22812647	7.517489772	6.066053305	0.3944778
17219662	NM_175026	Pyhin1	56.63150636	58.33779692	21.1232512	8.834876696	8.7479926	4.922994064	6.046982171	0.82337296

17408960	NM_007651	Cd53	167.087037	362.7472834	122.2165626	31.66846423	43.76015673	32.52806279	6.03993065	0.2833715
17350982	NM_001042605	Cd74	547.9407159	1525.345137	885.5297709	164.4904482	145.7827288	180.6877638	6.026580483	0.35997406
17404217	NM_001173459	LOC100038947	21.64833253	97.56379693	20.84493546	9.208301045	7.270260207	7.063068068	5.949336089	0.06375393
17227536	NM_001111316	Ptprc	121.7327887	258.84955	96.75799706	24.43997662	27.12407437	28.88164479	5.933696404	0.675267
17408897	NM_009892	Chi3l3	152.3496104	286.6481186	107.5492013	10.18007299	13.91837618	68.16763377	5.923595246	0.03566599
17254041	NM_011333	Ccl2	249.5131429	248.9090715	96.84737227	32.87140006	28.23005433	40.79495941	5.841909096	0.01433327
17255260	ENSMUST00000001547	Col1a1	799.9034145	961.9686047	594.572942	115.8858814	205.2332967	83.69322873	5.821078904	0.9358978
17533713	NM_001044384	Timp1	281.4545186	416.5012456	178.3012491	53.1050443	54.26920991	46.71878986	5.686544897	0.5384036
17514515	NM_010809	Mmp3	157.6561895	232.4500619	83.00895054	36.550494	30.69051607	16.25997349	5.665983582	0.5008412
17461205	NM_007697	Chl1	74.62370059	87.12682104	38.36689212	11.97203088	10.19554506	13.84239813	5.557277362	0.29208943
17230111	NM_172648	Ifi205	190.2847323	120.3260331	82.57956993	15.24799874	40.05301664	15.89740079	5.522459017	0.41417637
17239845	NM_007482	Arg1	103.4245593	361.99501	69.43147908	35.39093569	30.91088382	32.20170115	5.429765807	0.4091
17278328	NM_009252	Serpina3n	945.9748383	551.7940156	347.8653084	173.7043412	122.5088362	50.51647264	5.322977605	0.96364063
17470616	NM_009779	C3ar1	164.6669257	288.226465	74.93475003	30.28725659	30.30252273	39.95574363	5.249643398	0.4881593
17480018	NM_009982	Ctsc	283.171645	603.3159862	304.8709758	62.13218994	75.10978691	94.27621936	5.145853011	0.92264926
17232235	NM_010217	Ctgf	555.4914901	748.593131	387.2565955	145.0799155	117.6882925	71.87100725	5.054222994	0.8025477
17548315	XR_140674	LOC100862132	251.1542712	457.7871002	190.4498049	53.27755607	69.80386429	55.26913008	5.04282815	0.2180882
17336494	NM_207105	H2-Ab1	408.5599564	1134.200514	674.869152	144.0096821	169.3781539	145.1483136	4.836324518	0.45635393
17502573	NM_010442	Hmox1	130.290402	302.1185589	99.64572453	31.85860077	41.44941974	36.95621242	4.825269911	0.77882475
17472114	NM_025806	Plbd1	96.9214444	295.6335105	122.0092738	34.44892361	33.90337518	38.40145315	4.820104393	0.80835485
17434490	NM_054098	Steap4	194.0289345	157.3727564	95.34907251	29.62456367	34.933493	28.47121192	4.802260302	0.15853561
17495839	NM_030691	Igfbp6	80.42811485	216.5539984	108.367775	31.9522141	33.66025031	18.92113857	4.795133224	0.9775154
17279404	NM_178911	Pld4	114.5924354	255.4025289	85.78342421	30.76759986	30.7006437	33.8280474	4.782750555	0.5682341
17254176	NM_011410	Sifn4	140.4241247	74.40037563	38.91485294	15.63940802	15.80502048	21.66589606	4.777589957	0.15802813
17236811	NM_008524	Lum	247.5546091	369.3377711	221.316162	41.2280694	98.03615518	38.24737949	4.721992946	0.6667948
17321768	---	---	39.87329708	121.4627392	40.13452728	12.54852596	14.96498575	15.62220292	4.670620744	0.7718158
17229607	NM_001077189	Fcgr2b	136.9004141	406.3544829	105.9475929	40.78237813	54.84620903	45.71244244	4.593163724	0.2762405
17301968	NM_001247984	Lcp1	150.2923743	318.2366094	139.188094	37.01820408	49.8945039	48.48457726	4.488399281	0.00411807
17431174	NM_013706	Cd52	82.77263614	155.874919	50.6012809	19.11318099	25.26334908	20.16039499	4.481912265	0.33714092
17266967	NM_011337	Ccl3	84.04050931	189.172032	36.90084633	22.47446706	22.59566325	24.40633902	4.463574368	0.12985353
17357810	NM_010821	Mpeg1	90.12765818	172.6978127	52.77478899	23.52224737	23.1253132	25.2373408	4.390355329	0.33848202
17523659	NM_009917	Ccr5	33.29616236	50.44411277	17.85259636	7.892601998	7.922572737	7.882137955	4.287105159	0.5532042
17532569	NM_009912	Ccr1	33.67525581	96.66099899	38.38910445	10.3592525	15.65164079	13.51414187	4.268822497	0.511483
17254166	NM_011408	Sifn2	142.4787545	189.0036126	52.63997869	28.19804036	33.11155822	28.91665961	4.257323239	0.11566389
17343813	ENSMUST00000040655	H2-Aa	130.6345773	464.9394393	253.7901031	62.99013508	65.48215971	73.90786532	4.196874433	0.22923158
17287827	NM_009369	Tgfb1	433.7698593	941.4541335	378.5292565	114.6939117	231.2532771	77.45384744	4.142061779	0.652654
17287325	NM_010101	S1pr3	61.89328542	83.56361498	56.05118621	15.52011132	17.01340499	16.36453836	4.120983707	0.7291124
17508850	NM_001113326	Msr1	49.3414771	83.07312956	40.24113244	12.09538679	13.57295554	16.55856791	4.088760889	0.90187484
17462729	NM_199311	Clec4a1	73.06699651	161.8441041	41.81254635	21.67854462	22.59531869	23.80441055	4.064786478	0.9505217
17540154	NM_007807	Cybb	81.92852861	233.5369468	85.62908474	26.74047152	40.73965901	32.32931423	4.018603261	0.07247272
17378827	NM_008489	Lbp	245.7400171	215.7071219	79.15771157	46.53640952	58.2647332	29.82125359	4.015712582	0.01468381
17298473	ENSMUST00000022460	Galnt12	431.7023093	367.5014164	417.6975873	104.7938324	104.7641279	95.38351211	3.990606143	0.14786167
17537081	NM_205820	Tlr13	47.09170328	102.8687522	24.72474951	12.80598216	13.70157656	17.41471551	3.977143899	0.5356244
17450121	ENSMUST00000097437	Plac8	149.6993348	93.89516727	49.81913267	23.58399143	24.32117459	26.29728583	3.954230991	0.5802024

17222149	NM_153408	Neurl3	162.3656907	295.5302501	224.6627298	58.32344367	60.10653711	58.03571104	3.867939788	0.86631024
17462145	NM_145980	8430408G22Rik	148.6423082	147.6816739	157.6179465	32.34865895	46.37103427	38.98956084	3.856467634	0.79391867
17451437	NM_009151	Selplg	85.98529205	170.0063707	68.81399038	24.94462369	33.61809337	25.95594304	3.843005235	0.77474785
17399823	NM_013650	S100a8	32.70977658	84.76654028	36.5565242	11.63288476	12.35192506	16.19695826	3.833401276	0.12681131
17404091	NM_024406	Fabp4	237.6584685	287.9097827	906.9002078	115.0548508	98.13052	162.7016419	3.810901708	0.5369148
17470580	NM_031159	Apobec1	183.5512336	342.8008793	133.3262459	57.02750461	62.80349753	53.75462563	3.800305171	0.65316886
17357688	ENSMUST00000163078	Ms4a6b	59.26005253	60.24877487	27.16330274	11.33542832	14.46536679	13.11782838	3.768687508	0.9953316
17404209	NM_001173460	Sirpb1b	64.3980456	116.3573069	28.78080421	21.08064347	13.13548896	21.80596603	3.740241126	0.28655618
17283549	NM_029803	Ifi2712a	141.9681999	78.5611422	87.63686675	18.76416257	32.9538701	31.64612609	3.696627105	0.44543815
17510136	NM_023065	Ifi30	339.6561108	656.1600734	304.375199	87.87062193	139.2843157	126.1678045	3.679897239	0.42047763
17462796	NM_010819	Clec4d	27.12050242	84.54332804	22.8271683	11.21673587	13.84549761	11.75543483	3.652892889	0.05675953
17419287	ENSMUST00000151698	Laptm5	52.30427636	76.33882099	37.56470845	15.39295171	15.76281176	14.41688924	3.647095263	0.5007047
17464654	NM_013743	Pdk4	329.6485671	379.2588406	352.9047406	80.78205826	110.6272509	101.8408814	3.620840437	0.29785082
17362953	ENSMUST00000067532	Ms4a7	60.17402684	92.11058182	35.03864307	17.39232621	21.08615291	13.74687699	3.586825742	0.53652686
17344064	NM_008198	Cfb	284.7948011	259.8477938	88.55875285	55.81488447	75.54356694	47.65306154	3.53721019	0.24160087
17306477	NM_016972	Slc7a8	98.01461629	127.9203517	51.99957764	28.53006245	30.51688919	19.55195548	3.536112088	0.9519889
17234647	ENSMUST00000000299	Itgb2	104.8871405	202.0885818	86.77003464	34.99458999	43.26315579	34.70900252	3.485501379	0.9026452
17315570	NM_153505	Nckap11	78.51742745	171.9662929	70.13457814	25.92158445	32.44375725	33.65026591	3.484390386	0.02664633
17277794	NM_008152	Gpr65	38.7804597	59.66086542	26.13856437	12.16387508	11.95750923	11.94309626	3.454365279	0.7438377
17462149	NM_001012477	Cxcl12	769.7883354	745.7689905	461.3369382	217.1116001	201.456005	161.2765643	3.409354389	0.4166546
17267418	NR_002860 // NR_002860	A130040M12Rik // A130040M12Rik	54.82921829	103.7136519	50.69034226	25.36383515	14.9966151	21.11640008	3.403447174	0.9730902
17544061	ENSMUST00000113480	Cysltr1	17.02251147	34.06988092	16.88868389	5.518025027	7.155417763	7.336423897	3.397377771	0.29979712
17358598	NM_133775	Il33	200.2166301	170.9588147	99.26670499	33.5023177	67.681517	37.5023215	3.392134894	0.2699941
17430906	ENSMUST00000045154	BC013712	82.52532443	138.5871803	59.67898112	25.40599391	32.04896807	27.03958304	3.323190695	0.27160382
17309981	NM_011815	Fyb	42.92692719	92.12054237	37.80219232	16.8118898	17.88867963	17.40301061	3.317423903	0.16584834
17407363	ENSMUST00000117167	S100a9	29.66964994	75.74380542	26.04425023	14.42317622	12.67607328	12.55399818	3.31518131	0.914929
17289527	ENSMUST00000022124	Cd180	32.7810918	46.55044325	24.26234347	11.9701473	10.86093197	8.886978513	3.266085182	0.49911734
17396152	NM_007606	Car3	254.1247358	143.7450036	1408.261951	60.01761148	161.6652731	333.5901777	3.252690998	0.9627854
17462738	NM_153197	Clec4a3	52.83554789	95.89980656	26.94267144	14.58794742	25.69404276	13.86545448	3.244437978	0.06683109
17408856	NM_001033780	I830077J02Rik	43.36893167	62.43006228	47.59031175	17.42234603	15.62921052	14.50909873	3.225130201	0.89025736
17404200	ENSMUST00000099201	Sirpb1a	56.55540484	83.20405872	31.78129485	16.41311312	16.99274478	20.41721239	3.187123244	0.47456717
17218820	NM_011345	Sele	94.54780106	143.9804378	115.0144247	49.82890618	32.13723715	29.04618935	3.184715202	0.05784094
17248276	NM_001083955	Hba-a2	84.00253729	1819.252402	334.8081879	392.6810043	145.5110597	167.2301309	3.172657656	0.50735915
17438955	NM_009141	Cxcl5	54.29295115	79.48633755	53.26784458	22.33549	18.16986758	19.38126725	3.123354068	0.20650211
17387305	ENSMUST00000028389	Frzb	93.26908118	158.3913786	89.40744096	39.42724501	44.69495223	25.46267349	3.112363034	0.92830646
17336502	NM_010382	H2-Eb1	150.0964453	388.4580504	178.6648475	73.5523739	84.0634639	73.97921055	3.096868211	0.8487128
17439367	NM_018866	Cxcl13	128.3102843	114.4461404	80.23812564	32.71227067	30.00897214	42.68744768	3.064211773	0.45464566
17481232	NM_008220	Hbb-b1	15.51728229	103.1236913	26.60226165	17.36316446	17.15681678	13.01002654	3.055821826	0.29624176
17438975	NM_203320	Cxcl3	6.099102662	47.7028977	7.540410155	6.57911258	6.899835659	6.628079927	3.050794479	0.37673095
17260761	NM_019549	Plek	91.52278194	150.5189166	60.70582285	29.72627942	32.58569815	36.95482918	3.049836408	0.22664043
17230078	NM_001033450	Mnda	393.4667731	237.2872873	126.3245298	71.71107303	75.45423648	101.5397639	3.044081811	0.9830866
17261650	ENSMUST00000093193	Dock2	51.5663848	110.856688	43.6579051	18.92162384	24.78502828	24.04296639	3.041802779	0.00883616
17219418	NM_013489 // NM_013489	Cd84 // Cd84	45.285397	96.66836931	28.63802308	18.27861685	18.17756438	19.77718242	3.033640144	0.7164306

17266590	NM_001033711	Evi2a	77.63810501	132.3641849	57.18964321	30.52167007	29.89250717	28.2857006	3.012314555	0.6189651
17418485	NR_045561	Csf3r	64.07017385	157.8291636	58.89780648	29.47334705	30.9453557	32.93523639	3.007876759	0.14925183
17501633	ENSMUST00000015712	Lpl	59.95732028	74.23352643	288.4709037	36.75987613	50.83615462	53.60865372	2.993255868	0.5208018
17404191	NM_007606 // NR_007606	Car3 // Car3	51.01335215	25.59407568	228.8262894	13.69528136	27.09692056	62.25802905	2.963930448	0.5134701
17290083	NM_010330	Emb	166.5665619	336.3725109	259.9645331	70.5545882	79.15129229	109.7817171	2.940038803	0.5171216
17214142	NM_009909	Cxcr2	37.46566101	153.7041172	44.36373726	28.57376026	22.02808232	29.91723624	2.925188898	0.29696214
17453819	NM_008871	Serpine1	165.6920991	499.4671553	197.2168488	129.569469	93.50599765	72.6274489	2.916359825	0.25503665
17280590	NM_011158	Prkar2b	31.24618176	20.64560799	147.1120895	11.74613322	23.49443225	33.69314046	2.886887866	0.3800069
17294738	NM_001081249	Vcan	87.42863684	103.5792351	56.10638282	35.71100919	28.53447274	21.40560935	2.885126752	0.05359462
17227764	NM_009061	Rgs2	64.75209654	107.5120085	67.53914449	24.49862714	31.01131934	28.12111708	2.867394475	0.55405587
17309268	NM_007904	Ednrb	95.74305927	149.9214499	65.11432217	32.47559381	40.3198677	35.89106928	2.8594052	0.44735807
17452115	NM_011852	Oas1g	32.91976199	31.61784204	13.34235105	6.357537206	12.2008267	8.789596879	2.847742677	0.949643
17540521	ENSMUST00000001156	Cfp	99.43597537	177.8504729	66.53160812	37.69737077	42.18432173	41.7029345	2.82780862	0.8378093
17339013	NM_010130	Emr1	53.74058049	106.5484651	49.11885413	19.22730958	36.11236499	19.04448012	2.815221879	0.5208855
17219206	NR_004412 // NR_004412	Rnu1b1 // Rnu1b1	562.7650797	849.900417	318.3438316	181.3375641	231.6171065	203.8492728	2.806417415	0.62122804
17507799	ENSMUST00000033846	Angpt2	35.29177287	79.89520413	47.55835799	18.23757492	20.90146268	18.92172877	2.803017342	0.1528999
17219199	NM_144559	Fcgr4	46.38861925	66.77281697	18.05807245	13.66899245	17.25471812	16.16065761	2.786901763	0.84067875
17431612	ENSMUST00000046332	C1qc	96.29813816	143.9634729	69.22095785	36.27581193	41.36102404	34.43331082	2.761507661	0.3176268
17351053	NM_001037859	Csf1r	104.2256818	276.848904	96.52602072	43.41188011	75.53063443	54.17449895	2.758831133	0.59270066
17469754	ENSMUST00000113091	Cidec	59.04029398	57.96957486	208.6161445	30.99367663	41.00312608	46.24796562	2.753830194	0.8870407
17248380	ENSMUST00000169878	Lcp2	114.1712821	208.7880021	81.85411267	43.3981007	57.04671867	47.28071672	2.740307516	0.02546833
17507161	NM_133238	Cd209a	57.22465679	121.6715452	50.50169832	23.35873109	32.02045715	28.36773384	2.739180075	0.18691553
17367102	ENSMUST00000028045	Mrc1	160.6348376	273.4653055	111.0450289	55.31627103	98.49188794	45.46920895	2.735610058	0.05694432
17463501	NM_053109	Clec2d	1485.527915	1966.739274	2090.858913	638.150546	750.6106761	640.9819851	2.730949453	0.74250567
17291525	ENSMUST00000067230	Sox4	62.82435285	84.60716859	55.79032305	19.08221845	26.42057574	29.03159639	2.726551367	0.14472772
17391623	NM_019696	Cpxm1	205.3884153	122.7611282	76.61563878	48.30444341	54.59386758	45.91898985	2.71987988	0.93316936
17300279	NM_008608	Mmp14	231.6164643	294.0653521	190.7781318	87.93508546	96.43647416	79.2890096	2.717357208	0.6232212
17367536	ENSMUST00000014290	Apbb1ip	44.8404857	93.3020581	41.53388731	22.32555291	23.62705647	20.45636638	2.705604612	0.2374621
17547616	---	---	35.13848292	204.698114	60.37456566	44.84517919	35.96652821	30.63937578	2.693658546	0.45901906
17316197	NM_001242424	Fam105a	36.10212869	47.36107755	25.80772383	18.82043411	9.932659118	11.81637818	2.693427503	0.19017865
17254065	NM_021443	Ccl8	69.95207753	60.06930221	25.94286667	13.27615985	31.31456645	13.444172	2.687421723	0.571914
17485589	ENSMUST00000078451	Lilrb3	51.41085143	116.3739225	37.90283879	25.92014709	35.08255706	15.62700067	2.684175976	0.40877035
17462788	NM_020001	Clec4n	22.54242787	61.63179908	27.58452055	13.04155506	13.39871741	15.22339259	2.682403176	0.06869823
17435725	NM_031168	Il6	14.05131259	25.41000933	15.78596992	6.855210657	6.789616083	7.106301996	2.662375264	0.5552968
17445715	NM_007643	Cd36	52.19804975	82.52189237	157.6341167	34.83783343	45.09323163	30.12217417	2.656478454	0.63574547
17229020	NM_010231	Fmo1	1876.423814	1471.375746	1819.719035	678.0505392	710.448863	569.112872	2.63970484	0.11894051
17546101	ENSMUST00000112170	Tlr8	30.01273729	58.32283727	22.27707635	10.07087408	15.7398185	16.16374957	2.63523814	0.3348189
17391834	NM_011426	Siglec1	104.2232256	110.197295	53.01945738	35.03939597	32.44922237	34.31011366	2.627144491	0.46149105
17354282	NM_033037	Cdo1	244.6802763	205.3625066	297.5750996	100.360865	82.16197749	102.0910086	2.626779686	0.3346082
17520364	NM_001142916	Plod2	168.6672426	243.0051367	175.7544003	78.33173454	80.69917391	64.8158614	2.624236124	0.75185543
17285867	NM_175660	Hist1h2ab	16.69932634	20.82304287	16.21938262	5.919974658	7.717475512	6.883360167	2.618890334	0.09787317
17302141	NM_029495	Epsti1	50.50141828	54.6418718	35.20289079	12.85184873	9.643385625	14.81062892	2.594375085	0.09754205
17326075	NM_181596	Retnlg	13.64525074	41.96873285	13.77267606	7.451805402	26.897704702	9.651311493	2.569798086	0.91099536
17515238	NM_001198794	AB124611	63.45733373	130.6639185	60.81802238	29.14258606	39.20968102	30.92157714	2.568040722	0.14425975

17480740	NM_011671	Ucp2	123.1889464	261.9191982	114.5312117	55.71261003	73.24528565	65.83943271	2.564918936	0.02745808
17336114	NM_053214	Myo1f	47.45548693	86.97488734	37.21504306	18.7536174	30.74694144	17.48226249	2.562528928	0.45493674
17284349	---	---	72.29740702	133.9589349	55.37485075	30.46787549	44.7875238	27.43367514	2.547799696	0.03318829
17470796	NM_013545	Ptpn6	94.14750778	136.6966427	58.17070968	35.49881596	40.10899744	38.45600524	2.533799618	0.6752994
17291881	NM_028784	F13a1	162.8427861	325.9633607	104.2240925	69.66726394	111.9906129	52.45305877	2.533116353	0.08707952
17463509	NM_177686	Clec12a	27.80314153	49.94609565	15.88989845	12.6154783	13.35150066	11.14540394	2.523123775	0.82555014
17275704	---	---	24.85537561	44.19646264	23.54560683	9.570458216	14.86222283	12.33592505	2.518383341	0.97318524
17343628	ENSMUST00000002360	Angptl4	84.54309364	121.6653044	84.57556472	41.39326086	43.86501935	30.79012886	2.505712617	0.01922861
17395079	NM_021394	Zbp1	122.9470237	54.86875745	46.99537899	31.28460536	30.63871742	27.90365108	2.502713277	0.45451105
17319380	NM_011057	Pdgfb	252.4361998	269.9796769	237.537915	117.1165378	88.49413882	98.40290489	2.499736321	0.5774436
17438246	NM_001083316	Pdgfra	266.0458336	222.5011527	110.8019914	86.1680422	101.1154751	53.35409134	2.490670436	0.5509705
17331720	NM_011782	Adamts5	92.06194387	101.9085298	60.13316546	27.70433821	54.58811596	19.78889294	2.489226938	0.9065873
17283445	ENSMUST00000021607	Lgmn	875.8354289	1335.218376	899.9181624	351.5646003	455.0719963	445.608209	2.484316129	0.89727235
17454166	NM_153510	Pilra	23.68813972	36.32580842	28.46694954	9.507565678	15.7834644	10.33809171	2.483386995	0.2547529
17362874	NM_022430	Ms4a8a	44.39825285	74.3069372	24.70850813	16.71048846	19.32572992	21.913287	2.474804526	0.23217753
17433283	---	---	74.40455295	128.0291931	87.00334718	41.47514155	35.33651846	40.27693511	2.471949492	0.37382215
17498897	NM_033622	Tnfsf13b	103.8012495	114.2982892	61.82121057	35.97074164	46.62943358	31.20339282	2.459683419	0.22566287
17266851	NM_172796	Sifn9	29.21606551	24.6825749	43.71880312	6.929517973	10.7377216	22.03562635	2.458700178	0.20823741
17419437	ENSMUST00000070690	Ptafr	83.16951996	134.3266733	68.33733112	38.62007337	44.88781603	32.82841065	2.456959043	0.2767802
17438969	NM_019932	Pf4	84.8470738	95.36057303	49.59260142	30.59332483	31.33421619	31.64143225	2.455944959	0.70693254
17458520	NM_001164734	Mpp6	109.2893492	110.2264007	74.57462951	45.47450409	47.30615501	27.33154292	2.448463807	0.25665307
17286962	ENSMUST00000038275	Mylip	887.984079	728.6372796	855.4175523	394.2062938	315.363307	300.3829258	2.447678327	0.04837735
17218060	NM_011198	Ptgs2	252.1862837	695.5261755	435.974819	115.7985999	175.7500147	274.6546677	2.443799464	0.05593656
17428477	NM_007823	Cyp4b1	1301.437216	1063.084088	1160.797016	626.914114	511.2421586	317.5282188	2.421759894	0.6483734
17470627	NM_019948	Clec4e	23.70523845	44.12569205	19.6181351	12.45161526	11.18466391	12.62959088	2.411332349	0.89873207
17493632	NM_026384	Dgat2	55.76337593	61.39741456	237.5500994	47.94388788	46.71477454	52.54006208	2.4097416	0.31160292
17510685	NM_010332	Ednra	67.19504748	74.50291663	44.32147533	18.44590925	43.42283455	16.08482127	2.386285211	0.47359648
17332236	NM_001111021	Runx1	56.35321443	93.55034054	51.25639115	20.89178707	34.27576593	29.23685046	2.383287339	0.21714246
17448064	NM_144945	Lgi2	83.47764524	76.95253777	54.01780079	34.43099576	28.33513164	27.23003629	2.382856946	0.15347305
17346528	NM_009778	C3	1187.926615	784.5861184	506.7660267	303.0111349	596.249359	142.3907876	2.380142764	0.18328948
17289794	NM_152804	Plk2	267.541707	251.4308734	284.097042	117.8192938	121.1306374	98.67474632	2.378586862	0.9520394
17307837	NM_007940	Ephx2	1081.08182	1065.850959	1328.295116	560.146738	480.1794991	421.279528	2.377678015	0.39799595
17494677	AK156879	Gm1966	33.00917096	76.65850724	30.25335004	18.22328319	21.14491711	19.49533445	2.377040876	0.4042374
17229620	NM_010188	Fcgr3	77.15255345	135.4632778	66.48043883	45.64655255	43.43210585	29.10647047	2.361517669	0.25585058
17410845	ENSMUST00000059091	Clca1	35.00793356	46.81221094	51.15488108	19.6415925	18.87533049	17.92518371	2.355954328	0.40635195
17249787	NM_008161	Gpx3	92.47291744	78.51285596	119.4444492	34.23822487	46.48659978	42.72086638	2.352696316	0.01875637
17337796	ENSMUST00000024706	Pla2g7	45.28712345	116.3754551	49.01875713	28.61667205	33.40775195	27.72235666	2.347508559	0.09060112
17401335	NM_009196	Slc16a1	59.60696448	61.17647178	53.26393094	23.29602655	26.47999602	24.43054258	2.345444326	0.24957491
17338617	NM_139138	Emr4	15.22345591	45.44592396	16.62146914	10.45387566	9.705704927	12.84017535	2.342164262	0.8959883
17271724	ENSMUST00000045075	Cd300ld	37.07143355	71.03848947	39.77185645	16.24536215	19.39228632	27.50162574	2.342152033	0.52411306
17337152	---	---	54.28075942	114.1070405	55.52682498	25.94383773	32.34191052	37.4813497	2.338116428	0.13742158
17471828	NM_001170851	Klra2	12.02264983	24.8070968	14.21334287	7.003926772	7.141182558	7.704145767	2.336147812	0.93841386
17351457	NM_007702	Cidea	37.41842683	26.61388094	188.4863188	30.33360373	40.58168884	37.54362369	2.328242207	0.52904713
17362941	XM_357051	Ms4a14	19.9040209	40.95798965	13.56218759	11.46511563	11.64651972	8.885919059	2.325933951	0.31812146
17380222	NM_011044	Pck1	43.77165415	35.2618436	213.8727697	35.06140732	44.81730523	46.61279121	2.315620091	0.5502513
17357648	NM_029499	Ms4a4c	51.32827958	81.97726766	47.20850856	33.36001425	24.94638736	19.80014376	2.311125847	0.63944066

17372307	NM_010576	Itga4	59.38435528	123.5282326	54.87579384	32.72778365	34.0741792	36.47239414	2.302492009	0.5092989
17253707	ENSMUST00000018610	Nos2	67.95802404	106.0897158	45.09863928	31.58279617	33.83072055	29.92428767	2.298630439	0.18276256
17426022	// ENSMUST00000095049	Mup15 // Mup2	46.49932923	26.64025524	253.2190264	23.18244778	49.74301331	69.1082001	2.297755392	0.02486488
17212174	NM_010555	Il1r2	27.1602904	49.44449502	33.59088731	14.79279745	20.4601526	12.73911367	2.296122821	0.00840658
17216458	NM_011111	Serpinb2	7.006728524	24.323636	23.55494405	7.59174745	7.524830057	8.900621018	2.285250235	0.73379546
17526492	NM_008348	Il10ra	42.88469634	72.31705388	38.87786259	19.76616385	23.25412902	24.69633409	2.275358648	0.1468014
17238558	NM_021412	Mmp19	77.81028722	132.6000951	67.31905408	37.51261678	44.2009968	40.43797925	2.27364564	0.13840462
17470060	NM_178045	Rassf4	55.17034129	102.2587156	41.76701107	28.55598017	32.23169157	26.82495787	2.273599923	0.9714825
17545407	---	---	28.03004198	13.90236093	10.95674982	7.624892512	7.620100367	8.093327635	2.266193606	0.47163987
17301634	NM_033325 // NM_033325	Loxl2 // Loxl2	89.59870652	102.2563766	70.6234307	35.12253326	45.52026338	35.59616713	2.258094061	0.24750333
17363925	NR_002849	8430431K14Rik	78.02475408	71.22495994	81.07824748	41.55646409	28.16479372	32.39836268	2.255472165	0.7195809
17257100	NM_019679	Fmn1	63.05994471	126.5697646	67.79330968	39.63623434	42.63827005	32.8332578	2.23636542	0.46801305
17219397	ENSMUST00000068584	Cd48	39.77417221	72.63948152	23.25441916	16.59351938	24.5516997	19.71441506	2.229196327	0.7402461
17296558	AK172267	LOC100861753	104.089447	134.0861113	79.41254355	45.41673218	51.16165398	46.05270521	2.22664006	0.97136635
17347163	NM_011723	Xdh	100.85816	111.5480899	63.41753954	43.77632679	50.82854401	29.30961272	2.225920503	0.70862216
17230034	NM_001204910	Al607873	42.5411757	67.70568164	21.61543553	23.49054044	21.92203768	14.1822515	2.212647507	0.5586226
17265268	ENSMUST00000019064	Cxcl16	240.2240861	283.1184582	298.5076305	122.1234973	126.1205014	123.4508534	2.211088397	0.02590285
17240190	NM_172508	Dse	58.26255239	89.78801623	47.49922271	25.88641005	39.46790401	23.26346353	2.206665487	0.571629
17410974	NM_010516	Cyr61	821.9045219	1023.467092	1444.595634	509.6955686	436.0174305	546.0711015	2.205391012	0.17135113
17493949	NM_008035	Folr2	153.4911857	150.0469309	77.51802988	48.19464668	85.99143111	38.86334028	2.202007673	0.32379302
17425990	NM_001134675	Mup7	35.53271446	18.90019219	211.5264113	16.60907704	41.29362021	62.95901217	2.200525867	0.86243063
17245923	NM_008512	Lrp1	357.1471999	374.519493	201.1154353	154.1083262	181.598566	88.32990165	2.199766958	0.00735488
17302475	ENSMUST00000022722	Irg1	30.65127114	60.92004068	21.88327865	15.81895069	18.11639506	17.65322668	2.199219423	0.55489326
17413500	ENSMUST00000030202	Glipr2	50.75900908	59.49184435	45.05764481	23.04367643	24.62379123	23.16797427	2.192525296	0.4117871
17417858	NR_035483 // NR_035483	Mir1957 // Mir1957	34.83619142	40.51215712	26.18057721	18.05021354	11.42378637	16.86494841	2.191006258	0.9734596
17367652	NM_153511	Il1f9	11.0436028	37.83102604	10.33425154	8.839348253	9.171374725	9.123782153	2.182051233	0.6494271
17236288	ENSMUST00000062862	Igf1	95.79649722	91.8661205	60.7047709	31.70531928	44.76111285	37.38723825	2.181461413	0.19638617
17429454	NM_016748	Ctps	362.4813603	388.7605455	291.3238488	195.4070895	136.5899948	148.6162437	2.169240206	0.67788035
17411545	NR_028126	6330407A03Rik	34.22778433	41.93657108	28.20804938	17.75520361	13.66364981	16.90447141	2.159876315	0.57649547
17271733	NM_134158	AF251705	22.4691244	45.18039566	21.71186876	11.14939096	13.13989644	17.09329949	2.159395908	0.0044033
17235018	NM_013459	Cfd	139.38756	107.5750723	270.9682486	49.41684499	80.64308919	110.5829382	2.152280164	0.5648718
17346150	NM_029796	Lrg1	78.64373851	108.121978	71.05030808	38.3669453	39.99459119	41.69562186	2.147444002	0.62013614
17371374	ENSMUST00000028426	Lass6	52.3920134	112.8351695	53.41836817	29.74944812	40.45306191	31.66997888	2.146266901	0.44064078
17453288	NM_010876	Ncf1	67.56906563	109.2907886	54.06773443	32.99677221	42.39005696	32.50960225	2.140270865	0.10613766
17320907	NM_134086	Slc38a1	36.81697015	85.03153048	38.76221209	23.14598413	27.05542502	24.89444591	2.138742712	0.11905487
17373177	ENSMUST00000002180	Sfpi1	78.04098056	104.6440882	86.97838402	42.35469513	40.49811911	43.43785626	2.135260283	0.55035627
17432440	NM_010329	Pdpn	166.6730456	136.7992964	118.2598875	57.99220143	83.37875933	56.16829091	2.13492876	0.4614864
17357700	ENSMUST00000025581	Ms4a4d	70.27029256	36.99988804	37.49319849	17.7962825	31.88455851	18.39968293	2.126355244	0.7176452
17232731	NR_002842 // NR_002842	Rnu3a // Rnu3a	91.54384603	151.6757884	76.07064856	33.20031443	58.42775695	58.82807812	2.12214844	0.71132106
17480924	XR_105139 // XR_105139	Gm19765 // Gm19765	16.16809726	48.39942491	24.30880385	12.98610613	16.58289516	12.51935213	2.111660799	0.08227697

17375685	NM_008008	Fgf7	49.16552012	62.07695986	36.56990566	22.72050506	32.4757964	14.91694297	2.108194919	0.36181533
17391056	ENSMUST00000040128	Atp8b4	10.25540811	26.28544037	13.24031922	7.403194848	7.81237391	8.448820807	2.103632023	0.362386
17393868	NM_010658	Ma1b	78.53691371	124.8692123	71.74045549	41.92273689	54.95995813	33.92175719	2.103495537	0.14993486
17214197	NM_013612	Slc11a1	70.59910553	93.50074791	50.59829968	35.16335934	33.34803848	33.6859948	2.100818305	0.00181101
17224813	NM_175291	Dock10	50.8757411	92.11728592	50.96026943	33.93142231	31.3089235	27.20726439	2.09798064	0.1375782
17318950	NM_007781	Csf2rb2	33.74448896	73.55048756	36.02041755	23.69405143	21.58213972	23.32742243	2.089035644	0.35861135
17268103	---	---	1169.932841	1094.396647	1006.399224	495.7438277	596.6127504	478.1074248	2.082651182	0.09533147
17317637	ENSMUST00000164163	Sla	34.45267268	74.2817552	39.59962875	23.27297922	25.62869297	22.32347937	2.082607806	0.00980797
17471541	NM_020008	Clec7a	25.2464039	77.80786023	36.54441414	19.43513198	22.32576956	25.37797411	2.079252548	0.8248919
17280609	NM_020272	Pik3cg	28.45574409	56.16050487	41.9187851	20.98779939	25.19729571	14.68703224	2.078702349	0.74815744
17219139	ENSMUST00000027997	Rgs5	39.33773536	48.65354427	43.58832922	16.40217238	22.47178778	24.43259168	2.078451677	0.61230695
17219382	NM_018729	Cd244	24.16067741	36.87001249	27.49261057	15.34025968	13.29923172	14.06269309	2.073039156	0.5670965
17345775	NM_178796 // NM_178796	A530064D06Rik // A530064D06Rik	12.7725617	17.9189724	5.973535258	6.702168695	4.882344176	6.160271774	2.06624482	0.29936147
17404195	NM_001076679	Gm9733	20.69942805	49.25178135	19.13611421	14.84269333	11.93868473	16.36536643	2.064751922	0.5670566
17487361	ENSMUST00000142352	Apoc2	44.3840373	70.35577775	37.23408501	22.71984362	26.51077609	24.63528061	2.057429739	0.11956199
17213548	NM_001077406	Nrp2	37.15859376	58.77733326	42.54276804	19.74354299	22.42473451	25.24717389	2.054109143	0.7946842
17256264	NM_010517	Igfbp4	1316.306735	1370.237255	1172.790819	537.7761635	814.9902558	530.1199411	2.049690778	0.18896143
17312759	NM_028195	Cyth4	147.2313411	259.8694083	125.6757946	77.88194452	86.01396465	96.05787577	2.049504853	0.03306684
17471464	NM_030599	Klrb1b	12.72343228	30.59542427	11.44115661	8.841805509	8.366608915	9.545031773	2.046839602	0.41947138
17411527	NM_001111096	Lyn	115.9110261	146.6373694	89.59572552	49.81384956	61.49277466	60.74614703	2.046721587	0.06083049
17254289	NM_001081957	Gm11428	101.1355924	130.4215084	67.02637475	51.68164192	41.53201606	52.83415624	2.04442276	0.80859876
17501191	NM_153581	Gpm6a	121.2538714	134.030451	167.0509064	63.91306635	68.68956295	74.33707411	2.040861284	0.8661526
17241731	ENSMUST00000143791	Bicc1	117.6432716	108.688915	86.01980764	50.26948486	70.56221775	32.25252039	2.040393112	0.05856957
17301886	NM_175116	Lpar6	340.2959096	398.2658587	442.8495983	190.4185212	189.0752872	201.3781017	2.033858663	0.2917507
17425915	NM_001134676	Mup8	43.59621556	25.64932581	246.548899	31.14163962	48.65276863	75.48483871	2.033719551	0.8252996
17529575	NM_007536	Bcl2a1d	31.4009652	77.13180674	41.07028348	28.03627937	24.19803511	21.36289111	2.032727387	0.98086315
17485510	NM_177363	Tarm1	54.49942109	80.26927711	52.72422212	29.94883544	28.29389716	34.02548922	2.032042198	0.7371523
17434280	NM_011888	Ccl19	159.2873624	117.949705	82.03865873	61.55793793	60.77394336	54.60306386	2.030552675	0.5248179
17234436	NM_175329	Chchd10	45.46429259	58.1965611	99.91982188	31.69701327	36.50011236	32.36442573	2.024438494	0.14740741
17317486	NM_144846	Fam49b	108.5371409	211.7869669	96.33819576	65.2427641	66.13169618	74.68869573	2.022012627	0.07237852
17229059	NM_008030	Fmo3	82.88775022	102.4320229	102.8674687	61.70574885	58.74487138	22.191711	2.020348654	0.11966188
17452054	NM_145227	Oas2	100.9394276	81.46774103	53.92236992	39.1836259	38.78212633	39.09236603	2.018907719	0.15282266
17338982	NM_011691	Vav1	52.56344764	87.06687271	46.94348357	28.78305857	34.53219176	29.23194663	2.015985465	0.10799903
17353747	ENSMUST00000061829	Cd14	53.21326425	132.645599	55.34445981	36.44060484	47.76496823	35.58864254	2.01348055	0.5714285
17431619	NM_007572	C1qa	130.6286012	146.4521944	77.79583426	38.82782528	76.48728322	60.9605494	2.013191351	0.14322902
17448001	NM_008904	Ppargc1a	28.72529891	29.43569936	49.54223331	12.90656337	19.42644487	21.22109212	2.011110837	0.65778816
17448389	ENSMUST00000113726	Rbm47	19.98107087	35.68760055	21.94218057	10.5694837	12.57720983	15.46869945	2.009842346	0.6888541
17291190	ENSMUST00000105106 // ENSMUST00000105106 // ENSMUST00000105106 // ENSMUST00000105106 //	Hist1h2bn // Hist1h2bl // Hist1h2bj // Hist1h2bf	28.07587343	38.25779975	56.94451577	19.8941589	22.70668195	18.80171033	2.007704673	0.18463081

17455801	ENSMUST00000031668	Col1a2	382.5639179	429.965174	310.9045672	163.2066464	248.4082021	148.5457995	2.005556197	0.2525898
17512611	ENSMUST00000081998	Dpep2	73.90402325	134.7001829	75.94515372	39.0271444	55.37277811	47.75814844	2.001640554	0.11572506

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17283617	NM_009246	Serpina1d	6.490996598	4.366160001	6.370563545	321.3594306	61.20391352	84.26105066	0.03690407	0.3913305
17477220	NM_133712	Klk10	337.8537364	151.8757792	245.3468604	2505.772982	2545.794055	2959.771324	0.091754504	0.70749015
17502440	NM_008452	Klf2	110.3556741	107.3855452	102.1491933	455.8233438	649.2642666	695.3049258	0.177678149	0.13102439
17341179	ENSMUST00000014917	Dil1	47.08896148	37.08384678	44.67302364	163.8049336	216.3069185	239.0954723	0.208081892	0.44528058
17498032	NM_028308	Mob2	100.7670391	91.69956596	103.9012355	362.8061245	403.8559543	470.3611194	0.239581473	0.82175285
17425401	NM_010637	Klf4	199.4148448	137.893343	140.1006656	564.8010655	675.6077184	718.4789107	0.243714254	0.8737319
17321434	NM_007857	Dhh	114.5767094	101.5346261	109.4512788	427.1914611	409.9235317	443.3081267	0.254261743	0.866896
17477362	NM_010643	Klk1b24	22.60767929	28.73420044	11.91002057	115.1587321	50.99765483	68.88877411	0.269105307	0.85275406
17472903	ENSMUST00000052296	Pthlh	115.0080471	114.2231289	127.4688568	310.8858191	385.9582537	585.0649574	0.2782569	0.9827947
17436481	NM_008010	Fgfr3	43.88995847	36.07453767	36.75286979	132.6836689	134.4923217	140.5926145	0.286234311	0.66502166
17465365	NM_001101443	Prrt4	93.37238312	77.73589391	95.86092792	317.3581319	289.7693111	319.5367378	0.288097037	0.8018335
17341963	NM_023055	Slc9a3r2	503.3600818	329.2432379	481.6595632	1466.437633	1295.066083	1655.372293	0.297554851	0.9196361
17485039	NM_010844	Muc5ac	28.56447284	30.93463272	36.10137797	44.5579823	75.44314951	171.1093754	0.328399289	0.4369781
17377778	NM_010495	Id1	77.10892768	85.21414362	73.45363591	195.573759	271.6211481	232.1071251	0.337160049	0.56496835
17396024	NM_025285	Stmn2	299.4652932	307.8861158	256.7086323	766.6355025	790.7742045	924.0800354	0.348202141	0.82204074
17265164	NM_007528	Bcl6b	78.50409467	77.78731474	97.74588076	217.4320798	219.304864	290.2831459	0.349422655	0.16707698
17451390	NM_008153	Cmklr1	58.71173559	96.27858275	68.28784966	202.5544542	209.9377794	224.7688032	0.350371598	0.14887337
17376441	---	---	63.7396857	76.55464438	97.03888039	260.8898488	170.4242708	241.2988116	0.352852583	0.1385538
17282117	NM_013738	Plek2	186.9530244	165.7049627	203.2727478	479.0907006	494.0762851	554.7223334	0.363855371	0.51913863
17234786	NM_015790	Icosl	195.6481963	184.8962302	170.6144466	615.8290014	479.8797084	403.9564623	0.367521286	0.1824901
17453454	NM_007925	Eln	444.5558908	290.9303507	297.7785448	1166.321653	719.9315831	914.4446258	0.368931187	0.37613893
17318089	NM_001252057	Ly6c1	58.45445191	39.300452	36.62937044	140.9459292	105.4700815	116.0451164	0.370754998	0.91459626
17283641	ENSMUST00000122229	Serpina1e	36.06406211	24.1394684	28.15989403	99.90230085	55.23397301	82.26192914	0.372216063	0.47006792
17357486	NM_173068	Syt7	47.36002705	45.4180229	53.10272534	120.680352	142.5048292	128.6037588	0.372345312	0.7082105
17408885	AB081756	Chi3l7	31.46709299	24.45305819	21.47652988	65.97721611	66.28685958	71.89427564	0.379101225	0.03203686
17476752	ENSMUST00000032705	Rhpn2	102.1387855	84.93474822	91.40955042	269.7978423	217.2987402	241.6183139	0.382156431	0.51282054
17477339	NM_010642	Klk1b21	8.754950368	9.427687903	10.1909596	44.82274193	17.16926054	11.93629341	0.38379889	0.16075684
17376423	ENSMUST00000099349	Hspa12b	115.6795472	100.5860203	115.7589556	311.0552401	271.5712602	276.6770176	0.386387948	0.03020961
17340673	NM_001081416	Fndc1	138.389627	132.1021375	130.8411015	399.3550093	382.9032247	248.5447811	0.38934002	0.3318764
17474941	NM_001163510	Kcnn4	94.65816173	105.758294	107.9000707	255.0301492	242.7754954	293.9970767	0.389385535	0.40771094
17321823	NM_028770	Krt80	846.3132831	542.8508285	590.9625919	1811.287696	1492.370467	1717.70908	0.394340148	0.71133398
17477237	NM_008940	Klk8	95.42444596	101.872864	123.1182653	258.9816374	261.3437776	291.4331135	0.394717843	0.13909471
17271281	NM_153782	Fam20a	73.32417355	83.08982999	73.66395744	168.1589785	192.8549011	215.2468031	0.39926021	0.5570672
17224180	ENSMUST00000027377	Igfbp5	42.39431765	52.09821362	51.29331827	128.6198053	170.1919512	64.46365123	0.401309438	0.22310549
17487422	NM_020486	Bcam	593.2399727	592.6345803	642.1889362	1338.916244	1533.635583	1589.348735	0.409705116	0.42864937
17521422	NM_010489	Hyal2	122.4962692	103.7797388	117.9893636	304.5176416	260.5401675	274.9302801	0.409845539	0.00756623
17463747	NM_181444	Gprc5a	473.6064767	352.7858778	463.6421762	1039.482677	944.0640943	1159.55055	0.410434167	0.03402361
17233613	ENSMUST00000121820	Spock2	77.83779841	51.4453223	50.9292653	172.4271326	114.4417775	146.3483835	0.415986131	0.5929611
17315178	NM_010444	Nr4a1	114.2736528	116.6558624	185.731924	187.0952342	385.3159241	428.4093034	0.416319865	0.14271288
17328062	NM_007929	Emp2	569.0548865	395.2336576	460.1989878	1241.991858	1002.232839	1172.725788	0.41688855	0.07552438
17523309	NM_011703	Vipr1	50.42100607	38.74072371	45.14070358	120.8889861	109.2708669	91.60541648	0.417392572	0.80100155
17272019	ENSMUST00000041684	Caskin2	50.73438663	48.41912154	55.93839674	138.2149631	124.4615234	108.5968917	0.417729668	0.09463436

17488501	NM_027470	Pak4	69.09095747	73.59684418	68.60805204	158.9543844	181.6518187	164.0304675	0.418708877	0.27494833
17498041	NM_008748	Dusp8	64.19072721	39.94965115	44.43350367	91.87357098	116.7294679	145.8316446	0.419185506	0.18625024
17336175	NM_030697	Kank3	114.6375602	106.5186323	115.740743	292.2323333	264.4147779	235.4695993	0.425312244	0.28814065
17328368	NM_013607	Myh11	315.8903379	175.2692384	175.6574554	611.7167626	612.779405	340.9789811	0.425951847	0.05084864
17353957	NM_011898	Spry4	40.78319791	42.43133014	50.93851512	57.84109663	125.5643409	130.9477082	0.426759029	0.9854053
17236182	ENSMUST00000020234	Timp3	857.3324856	833.1301049	875.9465321	2139.577171	1803.782908	2004.810277	0.43146194	0.694561
17407017	ENSMUST00000171232	Adam15	313.8583976	266.1188695	279.355807	618.1546471	642.7954915	723.6042143	0.433010602	0.5111627
17280125	NM_001161111	Pqlc3	107.2476332	115.2949889	120.069091	264.8996266	236.1567562	289.8798012	0.433172385	0.5993008
17270877	ENSMUST00000001055	Icam2	229.9194969	216.6771185	220.9832177	513.5229701	512.8407173	506.4626259	0.435522164	0.03766792
17464248	NR_045598	Gm15706	32.45756801	31.60868255	28.02477723	72.59659611	62.23412634	76.02905742	0.436740605	0.97947615
17451549	NM_022017	Trpv4	124.7789704	120.0897327	122.1146094	317.7100683	256.2584913	266.0312657	0.436884987	0.5673464
17477391	NM_010639	Klk1	12.27959437	12.9706781	11.5066662	39.8417469	15.5962794	28.68731421	0.436930638	0.04572416
17470119	NM_001080780	Ret	37.98724026	35.0030565	32.57205865	73.32696894	76.67407756	91.03743469	0.437948144	0.24151844
17462663	ENSMUST00000148517	Mfap5	447.628474	328.4158623	280.2914642	974.8213241	844.7818332	590.8376697	0.43823345	0.30382344
17337852	NM_172621	Clic5	259.6857429	199.246283	260.611692	597.3654549	483.1334729	524.7054628	0.448256759	0.3159676
17256823	NM_025404	Arl4d	74.7119442	64.42233289	69.79147899	181.1723523	148.2543884	135.6073909	0.449269724	0.3601333
17409792	NM_023245	Palmd	503.052095	600.2164297	664.4666586	1139.227372	1296.152721	1488.609879	0.450494317	0.7380823
17217247	NM_001099276	Pik3c2b	114.7739163	107.8658968	122.0618034	259.4525671	258.2697739	246.4704708	0.45106629	0.27917966
17308242	NM_001253736	Pdlim2	97.41101413	71.04572813	68.38623221	182.8739791	174.471067	167.6078605	0.451169946	0.6929595
17218277	NM_175460	Nmnat2	47.3091718	45.2179913	38.76906401	102.1795729	85.52213712	99.69988946	0.456838888	0.40311894
17450387	NM_010097	Sparcl1	58.54544402	62.69941164	45.60910642	132.95415	151.4823608	79.17439319	0.458880524	0.878545
17467062	ENSMUST00000003569	Inmt	64.0327471	47.29887616	46.47496907	78.62880373	195.4891869	69.56496503	0.459163277	0.15269084
17454193	NM_007819	Cyp3a13	13.45921161	12.60074388	7.946777768	22.79646151	27.25562315	23.83272481	0.460266914	0.63485956
17377651	NM_027172	Slc52a3	126.067099	143.5858727	117.9212572	274.1939636	268.0737228	299.7930234	0.460268748	0.43719253
17388041	NM_001135657	Ptpnj	1169.349113	993.8001848	1026.501486	2399.203805	2192.893451	2332.158296	0.460648912	0.14389428
17287175	NM_008760	Ogn	236.6635968	148.145706	105.7099231	320.252717	590.3001917	153.3478363	0.46105732	0.31578755
17493875	NM_008773	P2ry2	55.27434044	44.38800612	62.46438738	113.0220929	117.9448815	119.8569702	0.462131324	0.29546258
17381717	NM_001001309	Itga8	153.8238077	81.51089487	78.56566205	274.18104	261.083776	140.3815959	0.464592661	0.5659048
17332228	NM_019466	Rcan1	97.8606527	111.9567731	114.8984878	173.3623735	226.1046732	297.4926057	0.46590346	0.037822
17435282	NM_008713	Nos3	334.749479	253.9588606	391.9535821	688.228583	680.6592829	727.8417509	0.467710244	0.8006139
17531001	NM_011349	Sema3f	417.4993091	362.0464514	397.9716908	813.076338	766.4075696	919.1700627	0.471260713	0.29768085
17400749	NM_008121	Gja5	256.7082765	274.9946993	268.2592299	561.3773321	565.7265229	566.9206461	0.472225877	0.27692196
17266038	NM_029658	Fam101b	56.61890724	51.00815453	68.1924919	145.499562	96.67701339	128.7560131	0.473993278	0.620657
17489384	NM_017405	Lsr	175.0736315	118.6016277	155.979649	370.4458856	267.4334286	307.2103476	0.475780158	0.24610208
17517132	NM_009964	Cryab	115.8225215	117.0531541	135.4104247	248.5082608	228.8661041	295.2988648	0.476638877	0.44098896
17395512	NM_001081171	Lama5	163.9041985	132.6623337	166.8500143	392.9091622	259.446093	319.0540418	0.47705591	0.71632123
17315167	NM_019518	Grasp	289.6960092	235.8999005	260.4217257	582.6246779	533.7668876	526.7154617	0.478372755	0.34277245
17399533	NM_172530	She	141.8375784	171.4154098	210.395057	324.672414	367.695319	397.5126606	0.480463772	0.37589645
17506356	NM_009569	Zfp1	81.34270148	73.62383524	102.6138032	200.0038554	146.2938184	189.4674226	0.480771035	0.35389966
17435957	NM_053085	Tcf23	55.93126286	33.75302735	45.04406112	108.1643299	84.84966155	86.9075735	0.48130751	0.40689385
17506137	NM_023395	Wfdc1	90.0737612	78.1434475	66.48684436	144.1770774	180.8404998	161.3815678	0.482533852	0.5956407
17349209	NM_144862	Lims2	363.7004751	325.9540973	367.4856233	706.9213972	751.8603962	717.489048	0.485757644	0.5574368
17326069	NM_020509	Retnla	22.30533638	15.36843122	37.46714128	60.13187335	65.46981513	28.97289616	0.486114254	0.38296118
17460891	ENSMUST00000041544	Fbln2	273.2199462	372.6077832	294.5588318	541.4716523	832.4553022	558.5102703	0.486632398	0.7628905
17315686	NM_001243837	C7	55.63978731	27.85273317	40.13408218	79.79846002	128.6135647	44.72839235	0.488371648	0.4296761
17394772	---	---	4.114610877	8.205578224	4.108312714	12.33698537	16.44936515	4.769308151	0.489589609	0.35089347

17309099	NM_010636	Klf12	115.8667654	88.33296298	109.3116988	234.0084799	173.0022511	231.4298266	0.491058131	0.08195947
17344453	NM_175242 // NM_175242	Ppp1r18 // Ppp1r18	17.68321879	16.23449947	16.92185708	30.50016199	29.57298568	43.25841799	0.492004307	0.06749874
17312127	NM_001166389	Ptp4a3	132.7970235	100.1125479	129.3420884	249.3267731	194.7890812	291.7140372	0.492303539	0.00366251
17324623	NM_008235	Hes1	54.34317679	63.6254478	53.46481995	108.8879124	117.8116174	121.2586621	0.492684031	0.7916324
17392151	ENSMUST00000028735	Jag1	182.4887857	190.3415877	198.507678	394.0833536	349.7077601	415.274651	0.492929796	0.40083256
17465620	NM_013723	Podxl	549.3093353	456.5446018	568.3540064	1056.824425	994.27974	1138.153951	0.493596908	0.48099574
17443486	NM_021719	Cldn15	56.28911263	64.44086703	84.96748752	146.5000148	139.7052087	130.0029004	0.494217809	0.3369351
17518238	NM_138304	Calml4	52.5373308	73.72443725	86.59062917	132.2791619	159.2723474	139.1082333	0.494247259	0.30100143
17458692	NM_001163640	Chn2	53.81740788	54.00821642	56.31276168	122.594717	96.21313775	113.0211528	0.494647491	0.9648149
17367852	NM_025980	Nrarp	82.52332238	88.61321742	85.63769144	161.6811861	183.4283724	171.3636139	0.497168575	0.64992243
17510338	NM_032398	Plvap	91.58668707	107.3690966	182.2596005	291.486246	235.7753363	237.4801304	0.498489069	0.8665022

Supplementary Table 2. The list of endothelial genes in response to 48 h post partial carotid ligation and their fold-change expression in APPsw-Tg mice LCA compared to APPsw-Tg mice RCA.

Probe Set ID	Gene Accession	Gene Symbol	Non-Tg LCA-1	Non-Tg LCA-2	Non-Tg LCA-3	Non-Tg RCA-1	Non-Tg RCA-2	Non-Tg RCA-3	APPsw-Tg LCA/APPsw-Tg RCA (Fold-changes)	P-value
Upregulated genes (433)										
17491193	NM_011315	Saa3	1028.830784	3950.364332	5382.721248	41.34113234	22.40632286	26.33902433	115.0218814	0.74820876
17408897	NM_009892	Chi3l3	101.7525401	142.0479302	1089.12966	11.91008662	20.40473402	6.473590016	34.3641337	0.3093723
17383892	NM_008491	Lcn2	170.1223643	392.4110889	1251.749358	31.78871953	31.44036367	23.58466167	20.89856639	0.99971837
17439367	NM_018866	Cxcl13	79.73620292	286.8814749	1388.777727	40.06556732	36.38409447	25.71882807	17.18137762	0.93447274
17254047	NM_013654	Ccl7	199.6804112	553.1542387	963.2984272	36.05186529	42.48651191	48.19491393	13.54129654	0.13365285
17461205	NM_007697	Chl1	31.9909959	161.6114943	320.895556	9.977366015	12.13822867	17.05996758	13.13313751	0.19763727
17400375	NM_001267695	Ctss	243.8885131	723.8570468	1564.135736	73.81565941	92.16876407	27.07210192	13.11471493	0.7715732
17435725	NM_031168	Il6	15.52021889	26.80412249	231.2258687	5.926638246	6.944106143	8.115781364	13.03456386	0.3941674
17233226	NM_013532	Lilrb4	209.5920231	428.6980367	1552.760922	73.1377328	83.81357348	15.57881938	12.69952696	0.7035315
17391565	NM_008361	Il1b	36.28514173	65.87065542	406.9808213	14.07398524	12.61748967	13.63472786	12.62545401	0.52904296
17230111	NM_172648	Ifi205	84.37659711	211.6817377	872.123115	45.26484158	39.99866655	14.33795138	11.72855755	0.43821195
17230045	NM_008329	Ifi204	12.31175054	61.27131884	235.208926	10.82266582	10.36563073	5.703814251	11.48262394	0.2197066
17286587	NM_010745	Ly86	95.64018397	348.77601	1063.305173	40.83985956	66.90517964	26.37046306	11.2419619	0.50117016
17266960	NM_009139	Ccl6	194.2552797	817.6524876	1266.893908	87.0389954	83.55753341	36.58833854	10.99888087	0.28876996
17362973	ENSMUST0000025582	Ms4a6d	18.80808423	54.05162176	215.7602069	8.982611884	10.30228892	8.07299501	10.54978478	0.07863718
17533713	NM_001044384	Timp1	353.7722312	409.9573454	1532.434823	72.73914183	111.2613727	44.01547708	10.07019018	0.7633805
17523650	ENSMUST00000168841	Ccr2	78.48788071	153.1326385	516.215625	23.57624414	27.45028076	25.22983734	9.806868861	0.25378832
17514515	NM_010809	Mmp3	125.4888176	544.8914337	1284.988738	72.03309561	102.2691355	30.29244243	9.557281992	0.30874145
17378827	NM_008489	Lbp	91.36660225	420.5099129	818.6721457	51.51065571	52.98286672	36.45730467	9.439807401	0.30401635
17229658	NM_010185	Fcer1g	212.5219433	445.436818	1448.174764	77.33625507	109.7537178	36.45093711	9.421691651	0.23048225
17408960	NM_007651	Cd53	104.1416962	230.6456063	738.4339126	38.2347623	49.75415135	26.59166118	9.366519733	0.03769186
17357671	NM_028595	Ms4a6c	43.82049876	117.0241925	468.3982904	21.20544716	21.85941671	27.78378025	8.881510572	0.29043984
17439830	NM_001204201	Spp1	85.4858658	132.2350669	448.2705775	25.3390231	31.27883772	19.91217625	8.70235447	0.67769694
17264835	NM_009853	Cd68	182.3237888	589.936965	1357.409218	84.39911699	93.42274949	72.00169677	8.524696166	0.29285756
17358598	NM_133775	Il33	128.3474658	608.0802827	1441.704723	94.31210185	131.0217942	34.13836359	8.394471435	0.23094133
17227892	NM_021400	Prg4	418.9661857	1378.353288	1946.774409	314.8993567	88.06464276	47.2816999	8.315668286	0.64411575
17278328	NM_009252	Serpina3n	526.5267433	2016.293579	3959.355792	492.5099292	229.7506288	68.60353441	8.221609979	0.7231973
17254041	NM_011333	Ccl2	146.6306613	275.8096262	539.8482066	29.51388634	44.77880119	44.453281	8.103757171	0.3356074
17219662	NM_175026	Pyhin1	30.42393802	42.27140032	187.5625515	15.1882632	8.840555348	8.55416479	7.987540219	0.8269274
17285546	NM_016687	Sfrp4	128.191074	594.4270671	714.7981053	50.75844615	110.0560008	19.27835436	7.981530833	0.61654073
17233210	ENSMUST00000102894	Gp49a	34.19129119	80.92098635	260.3024355	23.2128378	14.84421606	9.672628568	7.865434964	0.23968641
17467384	---	---	8.097485614	192.7255453	7.225297543	8.542521656	5.112082078	12.89662802	7.835731705	0.36989504
17266952	NM_011338	Ccl9	302.8131401	687.8823364	1260.499648	123.0245987	106.3971724	60.96562017	7.752385925	0.76028067
17434490	NM_054098	Steap4	93.27289556	504.4106757	982.8953438	89.76741837	95.92546844	21.78087489	7.618211103	0.03725633
17230078	NM_001033450	Mnda	167.9451124	386.4264402	1020.054839	94.0031372	79.91314899	34.77881808	7.544146268	0.5930525
17462729	NM_199311	Clec4a1	42.09800613	102.5970899	413.1580593	25.15949396	28.44789501	21.01853192	7.475326919	0.5503047
17495839	NM_030691	Igsf6	69.93491521	97.68824057	401.353314	25.34236042	37.9370081	14.2920801	7.334869722	0.66686034
17344064	NM_008198	Cfb	138.0858806	668.6910511	1187.877212	108.018679	121.5540372	48.18252184	7.181337632	0.87084943
17287325	NM_010101	S1pr3	40.37045663	121.8502161	195.0853997	19.99309613	16.55660537	13.49090289	7.140322881	0.8125109

17408024	NM_010186	Fcgr1	55.94712147	107.0764943	483.7004266	27.08910831	25.87778087	38.59788792	7.06302208	0.99757904
17254065	NM_021443	Ccl8	30.70911434	141.2959203	357.8335875	21.02654636	36.69966528	19.26428853	6.881870113	0.4849414
17357688	ENSMUST00000163078	Ms4a6b	32.24831778	60.42400893	244.088582	19.34944123	14.05935008	15.81941122	6.840812611	0.88165784
17227536	NM_001111316	Ptpnc	93.33491729	123.009165	419.7323936	29.30492013	39.55274726	25.11704783	6.768591684	0.09401629
17391623	NM_019696	Cpxm1	86.40836032	467.9524076	705.4729714	59.8479116	80.36191286	49.21229867	6.650932417	0.19127887
17476364	NM_011662	Tyropb	88.1921291	262.4840593	716.8224444	49.93425701	72.28297599	40.7662967	6.549733183	0.00557064
17357640	XM_986941	Ms4a4a	57.75300061	148.4806375	426.6942917	42.49876463	39.12530247	15.84629873	6.49354216	0.5117543
17404217	NM_001173459	LOC100038947	20.40285303	35.64925445	101.4639204	9.581416784	8.243305713	6.553102056	6.461447269	0.5695446
17374488	NM_011580	Thbs1	3093.469297	599.032306	391.0230924	230.934995	274.3200002	132.5875957	6.402088468	0.44465798
17450121	ENSMUST00000097437	Plac8	67.72605232	253.2320151	430.1845794	38.51669473	46.47748183	32.49554412	6.393262683	0.9945815
17212461	NM_009930	Col3a1	1106.087651	2353.839115	2313.770408	439.6543705	392.8857413	71.96791714	6.383245908	0.9691234
17254166	NM_011408	Slfn2	70.59034661	145.3405036	487.5995553	45.84148898	37.93748143	26.89667629	6.356686647	0.12054829
17357810	NM_010821	Mpeg1	47.10303124	92.84369274	292.1665087	18.96066948	25.82397174	23.24723131	6.351629267	0.5264798
17523659	NM_009917	Ccr5	18.50946127	37.31228996	102.2086155	8.512193815	8.865524586	7.971587179	6.234110287	0.7287362
17502573	NM_010442	Hmox1	71.39464683	207.099032	607.9833479	56.60525154	58.23077844	29.37825906	6.146943085	0.92582494
17532569	NM_009912	Ccr1	36.98947708	56.95185784	199.0319182	17.00139238	15.05165269	16.65389814	6.01502032	0.9774139
17431174	NM_013706	Cd52	57.15239296	89.50274347	316.3083871	24.60782085	25.18453171	28.47269207	5.915329452	0.18172322
17431607	NM_009777	C1qb	181.8833914	733.6483955	1537.840325	157.0140663	188.88400553	69.14964789	5.911686334	0.8375675
17498897	NM_033622	Tnfsf13b	48.36551983	276.5627416	637.9457791	59.69842646	71.49448236	35.70972206	5.769076469	0.1809824
17404209	NM_001173460	Sirpb1b	37.17101041	38.54051648	232.0649772	11.68117908	16.57138179	25.28270639	5.749042077	0.8773126
17508850	NM_001113326	Msr1	40.81866235	52.89351695	219.805397	20.76527395	17.4261867	16.35984302	5.747205937	0.50766003
17470616	NM_009779	C3ar1	77.85824931	142.3327652	416.1125527	36.24693242	46.28741211	28.97169124	5.706449546	0.33466858
17229607	NM_001077189	Fcgr2b	123.5522951	274.796344	671.6114425	68.71889819	84.24931201	35.47972691	5.677748974	0.94192785
17480018	NM_009982	Ctsc	185.7854874	394.0527611	1082.604069	109.1528508	118.8376359	68.42430639	5.608499833	0.74632305
17462738	NM_153197	Clec4a3	40.19781001	91.61176631	272.6786622	29.14153567	25.31644628	17.72646551	5.603537227	0.17440934
17321768	---	---	39.40221969	37.52444945	203.6662334	14.69259173	17.46048829	18.1153905	5.581886611	0.5476772
17434280	NM_011888	Ccl19	104.5833226	370.4458856	1112.184176	92.91038778	149.7335807	42.8086371	5.56033945	0.37844917
17437969	NM_001033415	Shisa3	91.22915189	412.1018129	659.9390603	70.5691144	86.72710216	54.09959917	5.502805347	0.87712145
17362953	ENSMUST00000067532	Ms4a7	27.91792864	96.56597231	289.1002407	24.86493923	34.13912082	16.64962755	5.466807433	0.87278193
17245223	ENSMUST00000092163	Lyz2	416.8761425	1302.926512	2097.027405	284.3287156	305.1090156	111.979901	5.441594116	0.05311649
17438955	NM_009141	Cxcl5	46.06608218	65.51843539	264.2705772	19.7153853	25.78637373	23.72955268	5.428975495	0.95732284
17343827	NM_010381	H2-Ea-ps	79.83375693	25.29902709	463.5701944	31.61589159	30.2689138	43.36932247	5.403141805	0.08414202
17483577	NM_001082960	Itgam	94.95815506	114.2869606	314.0596959	32.33715832	35.71172704	30.17389429	5.327733683	0.8126756
17254059	NM_011331	Ccl12	13.03868075	27.42823722	118.6920914	10.97019298	11.86588664	7.99288316	5.162645612	0.5464063
17404195	NM_001076679	Gm9733	27.17463966	36.15296334	138.084062	10.45328875	11.28637277	17.79074475	5.095107389	0.23059314
17329759	NM_007470	Apod	28.12246207	112.9376729	720.4432589	73.95988108	64.55692696	34.82066861	4.970093084	0.40305677
17507221	ENSMUST00000145007	Cd209f	18.86218627	63.36872135	264.8656601	21.42541138	33.04708235	15.51401289	4.959478399	0.04327312
17544061	ENSMUST00000113480	Cysltr1	11.56961539	24.85768433	92.03718796	8.155599895	8.632407679	9.29705635	4.924829322	0.21359865
17543365	NM_177789	Vsig4	7.389506404	48.73134038	98.57890153	16.01906458	7.903989334	7.574496545	4.911485054	0.19386496
17452115	NM_011852	Oas1g	13.23367638	23.90119755	94.72714511	9.155349747	11.42931472	6.860943567	4.804485252	0.4728625
17424373	NM_011888	Ccl19	122.1490641	357.1142765	1101.504749	118.3684676	161.9696843	53.060082	4.741381115	0.5055947
17309268	NM_007904	Ednrb	66.37485964	173.25678	419.1488904	46.31921827	60.2309872	32.63409214	4.733152672	0.36922953
17279404	NM_178911	Pld4	71.32445931	134.3777995	423.128778	49.39588651	56.53906029	28.16649221	4.689219156	0.86362135
17453819	NM_008871	Serpine1	1495.445895	128.958316	279.3062409	214.1099454	122.1513502	70.40143838	4.681300482	0.14305456
17286830	NM_010104	Edn1	2614.664275	1546.145098	471.9123117	322.6720934	443.0378047	225.435358	4.67410973	0.51423836
17540154	NM_007807	Cybb	58.76539726	140.0913434	363.0030853	45.2982057	43.23272894	33.84214247	4.591367964	0.26857287

17343813	ENSMUST0000040655	H2-Aa	122.6824438	204.2468474	604.3988059	49.30404131	81.41281509	72.48140419	4.583346799	0.13900207
17301968	NM_001247984	Lcp1	130.3428829	216.5559498	418.7945913	53.99927004	80.79986626	32.95647418	4.564338694	0.40176097
17216458	NM_011111	Serpinb2	18.79911707	11.13882384	71.18562341	7.445377505	7.58815422	7.159863086	4.556471202	0.86832184
17548315	XR_140674	LOC100862132	99.88415978	304.4038932	902.9285378	100.8143362	127.3711739	60.71141949	4.524854565	0.3254823
17404200	ENSMUST0000099201	Sirpb1a	39.92639749	43.02075683	204.3013603	20.55401029	17.60603334	25.47762691	4.51381253	0.29753324
17413033	NM_011888	Ccl19	102.3142299	354.1036734	1140.285998	106.6635175	174.6661218	75.34876706	4.476592563	0.03050149
17413131	NM_011888	Ccl19	102.3142299	354.1036734	1140.285998	106.6635175	174.6661218	75.34876706	4.476592563	0.3592736
17434224	NM_011888	Ccl19	102.3142299	354.1036734	1140.285998	106.6635175	174.6661218	75.34876706	4.476592563	0.87778217
17395079	NM_021394	Zbp1	49.56868221	132.0040149	391.2999186	39.73305999	39.74578591	48.9426733	4.460877113	0.99216485
17412973	NM_011888	Ccl19	99.80042125	364.6544021	1154.490031	109.0627781	180.2810566	75.25210326	4.440380942	0.13457052
17413084	NM_011888	Ccl19	99.80042125	364.6544021	1154.490031	109.0627781	180.2810566	75.25210326	4.440380942	0.9081607
17277794	NM_008152	Gpr65	30.67354487	36.38409447	119.6951595	17.92508432	15.63520251	8.832513199	4.405295208	0.28921202
17438969	NM_019932	Pf4	45.07332579	134.3226698	456.7797867	50.27509509	70.00417205	25.76813109	4.355954231	0.28914467
17537081	NM_205820	Tlr13	24.80382997	36.73331009	133.9056477	12.94600445	17.25602181	15.06982752	4.317092662	0.8943869
17219199	NM_144559	Fcgr4	24.72560642	43.53962268	147.3007535	14.61783754	15.60742902	20.70637353	4.232457117	0.8578261
17339013	NM_010130	Emr1	35.92108444	107.3145587	236.8006121	34.75850195	36.84977742	18.50370159	4.217377658	0.7661951
17350982	NM_001042605	Cd74	508.2473579	748.2854953	1326.096455	166.6821726	204.898555	242.3796893	4.206507842	0.7023027
17434141	NM_011888	Ccl19	118.4867561	374.9433953	1073.450537	116.7938906	191.5312514	67.86467917	4.165133132	0.8649583
17234647	ENSMUST0000000299	Itgb2	101.3354396	144.3256587	345.1926653	53.2185759	44.82914255	45.14136066	4.12638846	0.76287955
17463509	NM_177686	Clec12a	16.37055128	49.79790002	177.1316246	15.64487254	26.74200998	16.87349589	4.105611244	0.35730493
17375685	NM_008008	Fgf7	37.24996074	87.82854508	221.4825151	20.55899732	43.56745695	20.49664676	4.095347685	0.3193069
17434933	NM_010427	Hgf	20.09730295	54.22529156	127.5508763	18.01592723	18.59281101	12.9591483	4.072666495	0.5272868
17407363	ENSMUST00000117167	S100a9	19.3439699	23.40578099	86.11884109	10.43901729	11.26949529	10.41905841	4.011152665	0.01227749
17472114	NM_025806	Plbd1	102.0563401	150.3978361	395.9528954	60.2499442	33.78713227	68.64829577	3.985650724	0.22798088
17424421	NM_011888	Ccl19	119.8498256	379.5107653	1115.898428	117.208306	191.029151	97.35532592	3.982464893	0.28536984
17434190	NM_011888	Ccl19	119.8498256	379.5107653	1115.898428	117.208306	191.029151	97.35532592	3.982464893	0.12217332
17271724	ENSMUST0000045075	Cd300ld	29.88778341	66.86707013	169.7524987	28.86101234	20.62626933	18.02846923	3.947335972	0.21056493
17462796	NM_010819	Clec4d	20.251165	19.95513315	94.44771576	11.58920742	11.86137208	10.71237897	3.941520873	0.19805807
17367102	ENSMUST00000028045	Mrc1	122.5257358	446.3476438	1019.405976	135.4675032	220.6096364	47.7656304	3.932915167	0.5117977
17357648	NM_029499	Ms4a4c	47.73392288	54.46452713	128.0630975	12.21621116	25.04096057	21.57647078	3.913773441	0.9611458
17398115	NM_008987	Ptx3	43.64250479	51.7248625	196.0387442	21.84987316	25.84368696	26.8430928	3.909567979	0.8595437
17260761	NM_019549	Plek	52.61236509	101.920115	240.392654	28.70949403	43.58754369	28.99571884	3.898848718	0.58982146
17448064	NM_144945	Lgi2	55.30476953	186.9668906	328.9767918	58.13761567	72.90718025	16.41990642	3.873797884	0.667335
17510136	NM_023065	Ifi30	224.8439103	385.1490349	1050.259412	134.3530255	179.2714576	117.0840707	3.854700221	0.37546885
17462149	NM_001012477	Cxcl12	788.1208181	1456.792818	1997.804921	301.488675	642.7054964	160.5871896	3.840324165	0.02469031
17343628	ENSMUST00000002360	Angptl4	92.84015331	172.187428	378.5985302	65.87499308	64.53276786	37.32279178	3.837262211	0.6096694
17302141	NM_029495	Epsti1	29.86351337	57.83460203	183.6764686	21.33206908	31.77748405	17.62432379	3.836557473	0.67047143
17471828	NM_001170851	Klra2	16.98162954	8.160202761	44.10832285	5.511652762	6.880321595	5.66252298	3.83561801	0.24984773
17451437	NM_009151	Selplg	62.37634007	98.3650569	285.0300072	36.88747161	41.9106793	37.51261678	3.832589304	0.4323654
17540521	ENSMUST00000001156	Cfp	74.86725738	102.9165364	432.2367712	50.77195825	53.05798567	55.89440608	3.819208311	0.5632698
17262209	ENSMUST00000109212	Gm5431	12.30061889	24.20571828	62.25552617	6.180446209	7.65185216	12.13031408	3.804003297	0.24821112
17424346	NM_011888	Ccl19	115.0151422	363.5605876	1034.766831	123.1816032	182.7258583	94.4662445	3.779825044	0.04589163
17315570	NM_153505	Nckap1l	55.46696953	103.5221733	277.0917602	41.22555469	47.1826649	27.31343771	3.768360333	0.04923981
17266590	NM_001033711	Evi2a	49.84472745	78.86924899	277.5750335	34.24726801	43.46426973	31.23968497	3.72909087	0.01703664
17470580	NM_031159	Apobec1	101.4415581	197.7365834	479.6735238	71.80308872	77.48837582	59.92769585	3.722659358	0.9230717
17512809	NM_017370	Hp	187.236514	876.9738414	1155.674981	395.2320139	136.8442495	65.09460168	3.717336975	0.3025833

17229620	NM_010188	Fcgr3	64.02107514	139.9584711	368.8148665	52.76143872	58.30602235	43.79669197	3.698689474	0.5734408
17219418	NM_013489 // NM_013489	Cd84 // Cd84	30.18908237	61.34802524	147.1250403	25.24351666	19.58281147	19.79517615	3.693231078	0.67811674
17471541	NM_020008	Clec7a	32.41451316	39.64958883	142.2832477	15.31996398	18.39399566	24.98525436	3.651622145	0.9512431
17520364	NM_001142916	Plod2	184.7414773	345.8680647	638.2045129	127.325626	116.4906215	76.33876808	3.650775399	0.65315884
17419287	ENSMUST00000151698	Laptm5	47.79152835	58.92602321	113.6429203	19.20903314	26.56833659	14.779105	3.638925034	0.7807469
17434087	NM_011888	Ccl19	124.4418554	328.825871	937.1940599	122.1550757	164.9418861	95.51695895	3.634111858	0.5548362
17515238	NM_001198794	AB124611	58.30929603	84.81532153	238.0120821	33.67943427	40.03969279	31.17377578	3.633579483	0.66027397
17316197	NM_001242424	Fam105a	25.92025489	42.71518128	82.44830903	16.17227796	13.2440458	12.34879188	3.617462633	0.6080338
17271733	NM_134158	AF251705	14.78091832	28.22383252	89.9249159	13.00287734	12.9256417	10.97356205	3.602226834	0.75327206
17277387	NM_010234	Fos	99.15083383	530.1548501	88.5176963	50.32038308	104.4898502	44.56678546	3.600331597	0.5267341
17494677	AK156879	Gm1966	27.84479951	65.97963995	136.9887872	17.36197302	20.86993208	25.96573215	3.595353919	0.71610546
17336494	NM_207105	H2-Ab1	296.7857473	469.9159739	1194.937959	99.20266687	239.187635	209.2465462	3.582008199	0.01183721
17228234	NM_028749	Npl	31.39606834	99.01217284	233.7503962	34.49819561	37.92383612	30.2544405	3.546660977	0.25613967
17284607	BC018322 // BC018322	Igh-VJ558 // Igh-VJ558	22.47108686	213.6179397	26.88001429	26.17647631	26.47647218	21.52790463	3.544971914	0.17947656
17284631	BC018322 // BC018322	Igh-VJ558 // Igh-VJ558	22.47108686	213.6179397	26.88001429	26.17647631	26.47647218	21.52790463	3.544971914	0.9629905
17491199	NM_011316	Saa4	11.73373167	17.86935926	67.4911766	9.450096097	7.552461895	10.50020071	3.530346486	0.29931113
17370735	ENSMUST00000065927	Tnfaip6	38.38192061	39.32399527	105.0228907	15.24078175	18.31274302	18.54469969	3.507390289	0.77878255
17263174	ENSMUST00000108821	2210407C18Rik	54.87579384	100.5143728	205.0984815	53.17517607	25.57405454	24.57696732	3.488840733	0.37163547
17337796	ENSMUST00000024706	Pla2g7	46.46904208	83.81688497	315.8660344	50.22110963	45.01855984	32.92149622	3.481179022	0.753563
17448245	ENSMUST00000059349	Tlr1	29.3789107	41.05383241	142.2599745	19.46000263	19.36880444	22.74653674	3.45418644	0.7837602
17331720	NM_011782	Adamts5	71.70739485	219.0514569	309.1634585	73.59725229	79.24884478	20.87696371	3.453325699	0.16201837
17278321	NM_009253	Serpina3m	29.31751666	51.58837149	169.1429224	22.2972518	29.64592692	20.47446714	3.452871294	0.35539693
17546101	ENSMUST00000112170	Tlr8	23.4434339	48.21295664	154.833732	23.28443548	25.96323053	16.76248342	3.431140884	0.10944603
17481770	NM_009627	Adm	49.11980744	138.891163	318.6166832	57.04810265	59.68845476	30.92179147	3.431080311	0.33345047
17367536	ENSMUST00000014290	Apbb1ip	41.69700914	73.06679392	151.7739098	25.80326996	36.78164249	15.43602093	3.416233327	0.28084973
17407716	ENSMUST00000013851	Tnfaip8l2	43.65950898	86.60077316	172.6366542	32.95453252	40.28034123	15.49931982	3.413531179	0.3319142
17431612	ENSMUST00000046332	C1qc	39.44129456	126.0809937	336.1473579	56.70228621	66.70879148	23.96126218	3.404096363	0.44671923
17432440	NM_010329	Pdpr	149.7731289	227.1732256	560.7741357	95.7092196	120.620056	59.98791569	3.393637891	0.4870686
17493949	NM_008035	Folr2	70.8965245	312.4518344	673.3986413	115.734646	163.9311262	32.52837844	3.384903266	0.6687679
17431619	NM_007572	C1qa	82.91257381	229.1531012	574.1166159	93.34999241	114.0026856	54.50743021	3.3841821	0.48492324
17309981	NM_011815	Fyb	28.31363355	56.99656223	119.1056466	21.64714713	22.65712654	16.15482257	3.381060172	0.6050667
17408856	NM_001033780	I830077J02Rik	31.84500073	29.34736359	94.35401472	14.98965216	18.26141939	12.76426004	3.380316379	0.60069376
17301634	NM_033325 // NM_033325	Loxl2 // Loxl2	111.2376992	163.0229197	217.0676614	58.56411407	49.99278521	37.45104319	3.365079132	0.85508
17266851	NM_172796	Slnf9	29.80947372	34.37274108	107.9204905	20.51902109	15.01431759	15.91968627	3.344851065	0.9320539
17285867	NM_175660	Hist1h2ab	16.8356673	14.06614413	60.89424571	7.4783293	8.193466739	11.83068743	3.337737017	0.66814715
17411319	BC057661	Rabggtb	15.02561358	34.55946551	89.83769454	17.0940341	16.95749309	7.736076171	3.336462549	0.27758086
17470796	NM_013545	Ptpn6	63.08569505	97.93509252	237.4082073	43.88703804	43.07145037	32.81910521	3.326406741	0.69898665
17435249	NR_039541	Mir3096b	18.61826846	25.26485509	49.65475591	9.885240048	8.821811904	9.460280759	3.320792935	0.40100497
17514482	NM_008607	Mmp13	21.95188616	17.31997569	71.91476005	10.11296405	13.4864992	9.883513513	3.320691068	0.1569007
17219397	ENSMUST00000068584	Cd48	32.89804619	54.61248881	147.8175749	25.10335005	26.00166314	19.76599944	3.320512875	0.4871878
17254176	NM_011410	Slnf4	34.21737068	42.93040863	164.0866436	20.52960551	26.10240801	26.28057617	3.30854279	0.49740204
17238558	NM_021412	Mmp19	92.57861021	118.3644474	255.7587876	51.84147998	60.5194512	28.69988399	3.308515158	0.2211172

17230127	NM_011825	Grem2	64.27821674	219.0687668	383.6332617	65.26709852	98.24846757	38.22471924	3.306133151	0.3693443
17379871	ENSMUST00000136378	1500012F01Rik	64.02884142	105.301779	183.945682	39.69009196	46.14431458	21.13898205	3.302469026	0.6082311
17526492	NM_008348	Il10ra	31.02047774	66.98972851	174.0278028	31.32353215	27.99249158	23.19329679	3.297057924	0.7064081
17212185	NM_008362	Il1r1	192.9081118	380.9328778	824.288753	141.7595383	147.5115387	135.0372857	3.295079394	0.24703518
17291881	NM_028784	F13a1	130.0472426	413.2436956	916.9701751	174.3138026	215.743308	56.18725442	3.272335132	0.28732702
17285586	NM_012054	Aoah	15.00597339	39.04224208	76.76586318	13.59725947	11.36162274	15.11638224	3.264209992	0.80215305
17290083	NM_010330	Emb	141.5906314	183.1388426	409.7411561	73.25127673	70.02038067	82.56777938	3.252180578	0.78553504
17230023	NM_001177349	Pydc4	4.477104523	7.084475269	31.16372967	5.355461861	3.60973768	4.230364572	3.237853956	0.66750175
17261650	ENSMUST0000093193	Dock2	46.48775979	61.01267164	163.2773656	24.04404966	27.73413837	33.0268621	3.192944248	0.31440824
17498750	NM_027343	Cd209g	12.94406632	27.19964657	95.82545247	19.44854066	12.9477185	10.24194634	3.188904499	0.6455568
17248380	ENSMUST00000169878	Lcp2	89.71218221	164.9565209	334.2375472	61.95595281	68.43905812	54.87107746	3.178705047	0.33991006
17344303	NM_010734	Lst1	25.13345323	52.74937152	132.9813391	19.59376857	21.77319169	25.09075538	3.17290719	0.26028928
17493145	NM_016770	Folh1	19.24021479	47.54949125	297.5530303	40.31517278	55.74834224	18.99858412	3.166487827	0.72045785
17218820	NM_011345	Sele	217.7463914	48.2793049	47.41350034	33.2098891	33.07316022	33.07772252	3.154556782	0.7484334
17470060	NM_178045	Rassf4	58.3657049	74.15777225	195.0724188	39.5659365	36.27450444	28.14693643	3.1503429	0.92032146
17325324	NM_173869	Stfa2l1	5.789496959	9.220774915	47.83839228	8.03839237	6.205790526	5.738855305	3.145100536	0.6716079
17510685	NM_010332	Ednra	54.44848492	113.9789818	298.9884617	60.53262459	71.98113771	16.5330501	3.136034384	0.3333192
17357700	ENSMUST0000025581	Ms4a4d	28.36429302	137.0394067	379.8220892	49.58679239	99.44838242	24.9321605	3.134069898	2.07E-04
17458520	NM_001164734	Mpp6	75.10072864	186.6946791	375.5884791	95.73011916	83.47023919	25.45529712	3.114421077	0.33834672
17391834	NM_011426	Siglec1	42.75843071	131.8561452	359.8869553	62.65601021	66.0781779	43.80829009	3.097796767	0.36160424
17267418	NR_002860 // NR_002860	A130040M12Rik // A130040M12Rik	74.82201946	77.64671582	118.175487	42.0342667	22.90365597	22.98388859	3.078237566	0.39460787
17430906	ENSMUST0000045154	BC013712	46.33983493	82.53808151	187.6381017	38.8644717	38.85240499	25.14488413	3.077100913	0.15673347
17294738	NM_001081249	Vcan	81.46469175	82.88022417	270.1487132	73.2748904	40.99829476	27.70501033	3.060284205	0.26773313
17507161	NM_133238	Cd209a	47.59041071	58.06351475	200.5360777	26.90900237	38.54588641	34.62907629	3.059331262	0.81806034
17222149	NM_153408	Neurl3	171.3854708	130.0756404	251.9904065	52.44905957	72.50863954	56.20887363	3.054931764	0.54074967
17240190	NM_172508	Dse	47.15448202	110.1970658	265.0987395	55.89890045	62.30236397	20.18224838	3.052750134	0.86964124
17443803	NM_001013773	BC055004	21.07440508	39.32399527	92.07585604	13.52925038	16.74187261	19.70815748	3.05074933	0.60936517
17418485	NR_045561	Csf3r	48.03546339	59.73741895	170.0097881	27.21631804	33.65539771	30.32902049	3.045838026	0.16593175
17462843	NM_001170395	Cd163	44.42977715	122.3418341	413.8746284	81.45486708	75.33242154	34.01452412	3.043190373	0.5372658
17230034	NM_001204910	Al607873	43.41449809	59.17520936	173.4864288	24.16454626	35.49638006	31.07660504	3.042579318	0.48665586
17351053	NM_001037859	Csf1r	100.3322779	238.7778165	424.5206728	107.9605933	105.3835592	38.04911519	3.037594341	0.8411383
17349549	NR_035472	Mir1949	31.55115688	23.51339576	34.27574217	7.764591363	14.15271563	7.562063689	3.030603867	0.6732678
17480740	NM_011671	Ucp2	113.3029018	172.5945381	353.3223005	60.493742	79.77478997	70.6851867	3.030142083	0.5381389
17536383	NR_030718	F630028O10Rik	36.47992858	48.93951843	155.464029	25.85361293	32.03488708	22.03778008	3.013820682	0.30617362
17362874	NM_022430	Ms4a8a	33.11435838	41.559892	149.0314496	25.01552803	29.97730949	19.6823694	2.995715837	0.75574523
17452054	NM_145227	Oas2	71.93490127	87.67909487	290.9930729	55.70581385	55.2364999	39.69826359	2.99127285	0.14512703
17540188	NM_016911	Srpx	27.17612775	62.66586956	236.5240376	38.07892907	59.84749677	11.70770991	2.976865122	0.4768982
17387305	ENSMUST0000028389	Frzb	210.434436	67.167387	189.2694823	77.30677772	38.03735437	42.17268584	2.963945764	0.13571438
17487211	NM_008036	Fosb	345.5230149	131.310912	40.35283139	52.37364104	65.73140875	58.3795425	2.930492411	0.6855643
17285944	NM_001111110	Cmah	49.80905035	128.2787153	291.7619628	58.82946454	59.77279085	42.75982371	2.911772896	0.6025581
17513491	NM_028071	Cotl1	75.60925845	153.3414588	227.3129395	47.93411861	62.34279797	47.06191104	2.899879602	0.84529567
17442834	NM_001081342	Gpr133	84.6874333	186.3146102	387.3572683	90.65589935	122.467319	14.86159444	2.887733195	0.12057997
17419483	ENSMUST00000171223	Fgr	46.36765948	44.74231502	74.90623995	24.19236657	22.98586415	10.32389165	2.887131946	0.69187766
17255260	ENSMUST00000001547	Col1a1	976.1012536	1672.174856	1087.960151	610.6944823	580.4777666	104.792307	2.882977195	0.5580525

17317486	NM_144846	Fam49b	85.5946666	144.1834735	274.6030806	77.32119342	52.56701831	45.74369498	2.871808603	0.6951193
17306477	NM_016972	Slc7a8	51.30206525	96.02239399	233.6499632	54.66520769	54.39589963	23.65707824	2.87055177	0.5696487
17284839	ENSMUST00000026360	Itgb8	45.70851362	74.33001531	173.0382296	34.3266461	38.95023156	29.19711669	2.860011073	0.9966083
17438246	NM_001083316	Pdgfra	198.5151083	674.0940122	1322.507327	267.2773919	418.9505041	83.58313694	2.851500373	0.6204877
17507184	ENSMUST00000011445	Cd209d	14.86914719	26.25273819	94.41754068	14.10199139	16.24205192	17.2160826	2.849854231	0.48236188
17212174	NM_010555	Il1r2	27.08863889	22.86633112	85.15793139	13.54038636	20.75338841	13.22496501	2.843360367	0.38812175
17289527	ENSMUST00000022124	Cd180	15.82321659	20.98541371	81.1853776	11.5404614	16.67608817	13.38604626	2.836217442	0.3068328
17470627	NM_019948	Clec4e	21.26979171	20.85172741	72.82853907	13.67744643	13.73063079	13.15532513	2.833836698	0.15711981
17373177	ENSMUST00000002180	Sfpi1	64.01259988	106.084789	204.7934836	44.03528201	53.51776639	35.08494024	2.826421573	0.7891775
17423577	ENSMUST00000029900	Atp6v0d2	87.04744212	45.29277412	39.81499579	12.75225961	22.151385	26.15815713	2.819360175	0.1679228
17333731	NM_008039	Fpr2	11.97507677	11.97507677	50.96842968	6.836694692	8.271333852	11.5008533	2.815547969	0.3729958
17459423	---	---	53.49525404	179.154814	52.29891096	31.93007419	28.94094248	40.52723936	2.810196054	0.79355973
17386090	NM_009135	Scn7a	40.26278325	146.9575836	636.2760464	115.5860115	152.7519514	25.58382375	2.801753564	0.1574666
17401335	NM_009196	Slc16a1	50.94992085	89.88397362	224.3462097	65.286645	49.12729841	16.12923378	2.797389431	0.32679635
17453288	NM_010876	Ncf1	50.30960649	83.16110368	163.6706698	32.95325337	37.87906986	35.38916949	2.797375299	0.01943485
17211258	ENSMUST00000027053	Rdh10	99.22639261	140.2203567	196.7748459	46.03027	50.98093755	59.16450485	2.793146185	0.8042667
17462351	NM_008359	Il17ra	72.2174713	139.2830606	192.2652202	51.39887937	54.59118089	38.6765445	2.791008698	0.40020928
17514326	---	---	53.4196271	168.1280932	95.48981781	48.65816469	34.08157257	31.2423918	2.781467066	0.85774416
17544491	NM_013482	Btk	25.23851287	31.58846658	109.3820352	23.70691449	18.63390322	17.70053425	2.768242373	0.11987636
17214142	NM_009909	Cxcr2	35.96725119	30.90049406	174.6285943	29.41381479	31.6005519	26.23782088	2.767796856	0.2661024
17357815	BC038020	Fam111a	37.93261693	52.65136395	183.28679	36.90381346	33.70486636	28.69019761	2.758044984	0.7164151
17519112	NM_009022	Aldh1a2	38.78148117	153.2027092	328.0438809	51.4224342	69.12487206	68.1519485	2.755856519	0.94666684
17547624	XR_106231	Gm19984	7.605626013	22.78677737	29.81222194	7.688206039	6.271215082	8.086811594	2.730835064	0.5665117
17218060	NM_011198	Ptgs2	642.1497659	205.1162527	313.2077281	76.68263462	124.4934475	224.4877639	2.726268058	0.19203697
17236811	NM_008524	Lum	137.9447748	553.3076269	1737.358781	276.8253016	581.7760113	36.98283713	2.711762131	0.84810054
17347163	NM_011723	Xdh	56.60034729	180.2283306	371.3559799	102.9821154	98.70593988	22.73904879	2.709942992	0.52403355
17271751	NM_001101657	Gm11711	98.99089982	210.9101915	487.1694988	88.62064979	128.6711673	77.04241382	2.708045841	0.92355084
17498323	NM_024290	Tnfrsf23	380.1697681	146.8204379	203.8439036	84.74826923	97.3553934	88.36505215	2.702102201	0.36894068
17298364	NM_027289	Nt5dc2	52.22830577	65.44100503	170.2038664	37.308359	32.86622834	36.60523294	2.695951131	0.3995103
17346150	NM_029796	Lrg1	51.95569535	107.4864506	167.7319834	59.37509453	29.90751215	32.67841262	2.682612291	0.92708784
17411527	NM_001111096	Lyn	70.20875305	95.57298676	242.3724652	45.55460517	58.01383152	48.87788655	2.677363392	0.1878119
17336114	NM_053214	Myo1f	40.30254391	54.19207562	111.0017799	23.22642166	29.74377795	23.83439335	2.675574357	2.63E-04
17285523	---	---	21.55268942	16.49281781	35.23342941	9.251010746	9.359730564	8.971050917	2.656786624	0.9392199
17271757	NM_001101657	Gm11711	92.56372383	192.0992399	421.5760212	79.38794243	112.5236932	74.06253369	2.655291627	0.7282668
17494386	XM_485980	Trim30c	10.0680613	13.26894718	51.92009075	7.503876063	8.486972484	12.44900903	2.646184111	0.68742573
17482943	NM_001008700	Il4ra	196.7321593	239.6449951	497.7053207	120.8966116	135.8598165	96.9690201	2.640699107	0.04488748
17266967	NM_011337	Ccl3	34.28859774	39.83274504	88.29702961	19.75278264	20.41289645	21.54038305	2.63212992	0.29604807
17245231	NM_013590	Lyz1	22.59934415	26.12976057	112.4186823	18.79942981	17.10238946	25.37894161	2.629663613	0.6385735
17363470	NM_010266	Gda	276.5598661	403.6704023	768.7384397	193.1237788	194.5368969	164.1223606	2.625975452	0.01823456
17514337	---	---	154.0358127	447.3183091	293.6339557	145.8317457	95.96497191	99.39270067	2.623141368	0.30458552
17344289	NM_019467	Aif1	25.90119938	31.46397413	68.01254629	18.25724278	14.6474234	14.9672576	2.619024052	0.53847814
17282970	NM_010050	Dio2	38.92467261	53.91848294	227.0164451	55.28250176	40.22130538	26.62963963	2.618935346	0.46454442
17293348	NM_001145801	Ctla2b	46.22277596	37.44925205	55.83183236	28.53302894	18.6002744	6.188415222	2.616267145	0.08352897
17232235	NM_010217	Ctgf	1160.909665	411.8893462	460.5132959	509.4359636	196.5991127	72.59397951	2.611400502	0.3197709
17213021	NM_023617	Aox3	23.77888231	80.67467748	163.0837245	32.35554336	43.43707344	26.89121434	2.605447044	0.3633034
17319037	NM_009008	Rac2	88.8416942	161.3546115	330.5253237	63.67415483	75.75236367	83.93816388	2.599881159	0.20216224

17466228	NM_001038604	Clec5a	15.83495651	19.06286426	63.29510384	12.93438004	11.62762867	13.23416255	2.597959564	0.4964184
17486864	NM_001173550	C5ar1	38.40885363	46.33238361	117.9115309	30.57096102	35.12294713	13.03109127	2.574185705	0.8486164
17546109	ENSMUST00000112161	Tlr7	24.68289997	43.20636634	143.2844263	26.68309295	31.4331075	24.12717336	2.567668163	0.4383969
17525224	NM_001024139	Adamts15	44.55708663	106.0295071	134.0050909	46.71347935	38.54225294	25.64429491	2.566200314	0.4084782
17247389	NM_207655	Egfr	58.09890226	143.6282771	299.8645154	87.65247967	62.9366289	44.95105279	2.56515946	0.37407923
17437148	ENSMUST00000076939	C1qtnf7	30.60178707	76.13036025	176.8712806	37.30649712	51.92995248	21.43166455	2.562648059	0.01859688
17265526	NR_027858	Nlrp1c	10.36783674	25.89784233	48.92676531	9.730405983	15.97202135	7.579906224	2.559689639	0.3094952
17319380	NM_011057	Pdgfb	463.1449588	156.0773091	99.6992675	81.80731807	105.2039454	93.96281304	2.558675677	0.83722043
17300021	---	---	19.1475115	32.24331114	80.5623577	14.3370669	21.25079634	16.03223883	2.556236332	0.5459404
17362941	XM_357051	Ms4a14	12.63116672	19.99772529	73.36703107	12.94713516	19.51773858	9.035159064	2.554116609	0.28489518
17247336	NM_001025597	Ikzf1	40.7335317	34.0819978	67.26084507	17.39175962	19.90017207	18.42999788	2.549738957	0.52992785
17218261	NM_010877	Ncf2	50.16819058	64.75878441	165.0197626	38.23452378	35.89114391	36.06583699	2.540547371	0.17382663
17214197	NM_013612	Slc11a1	57.91025723	66.87416186	136.3098493	36.5619725	45.43023931	20.79210616	2.54021502	0.34047925
17254289	NM_001081957	Gm11428	71.18295899	123.9570916	275.3990934	55.76152066	63.79750063	65.72275263	2.539586782	0.6742002
17275704	---	---	14.34610311	78.80564111	62.73797244	26.45986875	16.02742775	18.90556421	2.539215715	0.00438871
17503937	NM_008630	Mt2	3977.703429	4096.198744	6394.917359	2640.398558	1818.937177	1240.847411	2.538307834	0.8811651
17326075	NM_181596	Retnlg	9.791188558	9.453339055	53.28970716	7.435599164	10.86394368	10.45918113	2.522164573	0.1586531
17253707	ENSMUST00000018610	Nos2	62.65001718	44.03317598	175.011753	36.4292402	40.33591282	34.93685892	2.521843083	0.7392066
17227797	ENSMUST00000027603	Rgs18	14.11141741	15.55918944	54.45512771	10.43913306	9.65503842	13.59919171	2.496804314	0.3917843
17290865	NM_134065	Epdr1	94.77876781	202.6263518	351.9534944	95.98559466	99.48933668	64.65159242	2.496318348	0.15262811
17487361	ENSMUST00000142352	Apoc2	32.70311148	48.72492298	107.848029	21.63190776	25.37913512	28.81134288	2.496308466	0.35758963
17371374	ENSMUST00000028426	Lass6	55.83160016	55.6334242	122.5050999	34.06225399	30.6134132	29.07116536	2.495765648	0.3493894
17336502	NM_010382	H2-Eb1	137.8619006	182.9789653	366.1974665	96.13514224	88.03925305	91.63945668	2.49094934	0.04142525
17368683	---	---	25.78204865	49.15441164	68.94222715	22.97450702	26.42112514	8.561722048	2.482492332	0.90591115
17485589	ENSMUST00000078451	Lilrb3	46.7183365	80.82042315	147.9438587	29.80709764	56.34032575	25.06393451	2.477108666	0.6529675
17419437	ENSMUST00000070690	Ptafr	69.71924301	102.2675051	241.0490611	61.93169387	70.72983546	34.62950835	2.468965552	0.764689
17287381	ENSMUST00000120135	Syk	33.16739958	62.05179331	104.1280541	29.27659771	30.57149078	20.94923998	2.467250474	0.7038356
17283445	ENSMUST00000021607	Lgmn	750.1961246	1157.486779	1532.26488	434.3764264	525.0561849	449.9235274	2.440793842	0.28460297
17241731	ENSMUST00000143791	Bicc1	91.89509799	255.1942478	491.0836567	114.4689098	185.7491759	44.95909219	2.428239919	0.6759354
17462788	NM_020001	Clec4n	21.22204825	31.91642152	71.89462447	16.45220445	16.04387805	19.28906088	2.414458783	0.28608236
17324322	NM_013465	Ahsg	89.00287289	83.36621903	184.1699661	54.39816194	60.36029702	32.98682456	2.413200946	0.59106207
17393868	NM_010658	Mafb	63.6458261	115.2302748	210.0906286	47.67156226	72.46397291	41.14633423	2.411720121	0.10053242
17388733	NM_009851	Cd44	75.39970637	57.61042517	148.4843427	37.25757833	43.14274299	36.62200821	2.40547659	0.992094
17353948	NM_011937	Gnpda1	43.2792022	82.21854865	209.0628629	43.6551514	51.42478671	44.23143061	2.40153131	0.24010082
17344086	NM_013484	C2	23.5017454	58.09028489	145.3788915	31.57163346	37.95565649	25.16631362	2.396898135	0.56811744
17296558	AK172267	LOC100861753	70.91962487	114.3280819	225.9415825	52.6089372	60.68823676	58.36538126	2.395334782	0.394624
17405482	NM_027571	P2ry12	32.66471167	73.17966976	167.2136718	41.81996647	42.62615438	29.58438501	2.394605296	0.5215132
17356002	NM_019449	Unc93b1	89.1763966	125.2402081	322.5461978	72.57662177	81.62606472	70.15431803	2.393340933	0.26720342
17300279	NM_008608	Mmp14	266.0808736	312.3797232	490.8991982	182.3914132	167.5403753	97.73653139	2.388732344	0.5737553
17408063	NR_004412 // NR_004412	Rnu1b1 // Rnu1b1	473.2550203	932.5226777	585.4462856	351.4040479	302.3521442	182.4661451	2.381213578	0.00603472
17219382	NM_018729	Cd244	24.45704166	25.26361175	59.22309571	15.04603034	14.65257178	16.05436836	2.38112953	0.5439234
17318950	NM_007781	Csf2rb2	25.9428307	43.07052488	88.42332009	23.8981991	22.28507637	19.94293719	2.380851244	0.23410937
17357872	NM_134152	Lpxn	39.39896976	52.77680096	106.4111856	29.82210109	28.75539997	24.88609565	2.37932421	0.27454382
17450319	NM_029415	Slc10a6	43.13691205	41.61313283	107.0193603	25.26329655	28.89099528	26.56108176	2.375872112	0.34948987
17406514	ENSMUST00000090986	Fcrls	45.00969864	68.90429462	227.6446904	48.96150501	52.93455876	41.94113504	2.374619963	0.07376967

17401066	NM_013609	Ngf	39.62736131	36.10342996	101.6852068	20.32562768	25.62274257	28.86081229	2.371580494	0.32797086
17343918	NM_009780	C4b	106.0353133	334.7343974	537.1465712	173.3475937	155.7125051	86.1004576	2.355513468	0.4805414
17454166	NM_153510	Pilra	32.4503245	26.91864713	46.74502745	12.31658165	14.13591142	18.67192803	2.351586934	0.34577173
17470031	NM_009662	Alox5	16.64445815	36.88358541	95.63024057	23.11507278	22.21778362	18.10339033	2.351310044	0.66553146
17373634	---	---	26.28986812	79.9675066	45.24746306	19.59872639	18.42562945	26.89667629	2.333678822	0.21610112
17364642	NM_031376	Pik3ap1	61.34577155	96.74136574	173.2751551	46.1107108	57.78803865	38.43591211	2.328050587	0.03759357
17548258	XR_140589	LOC100862291	4.938414731	16.22449872	27.17435712	7.011125211	6.982854926	6.772502401	2.327658066	0.75276583
17338416	NM_031254	Trem2	55.68450392	109.6343442	159.3837791	47.2102756	49.57280539	42.8540901	2.32533089	0.5196433
17539611	NM_001177956	Gpm6b	31.58840089	49.00656083	103.0593794	27.75631231	30.23800388	21.12231416	2.321311465	0.9487148
17433251	NM_173371	H6pd	120.5742478	163.9974986	327.7738614	103.165873	97.54912317	63.09076767	2.321198745	0.20504928
17399823	NM_013650	S100a8	18.2056204	19.69593499	59.01378144	15.06455341	9.840195646	16.90464717	2.318027658	0.6340863
17298473	ENSMUST0000022460	Galnt12	349.7560008	200.9241265	189.894854	101.7556435	124.6233851	93.15807996	2.317649379	0.2422336
17311846	ENSMUST00000160009	Myc	334.5643698	262.1313327	127.5172843	76.361895	114.8048675	121.5895979	2.315581963	0.7887558
17517105	NM_008360	Il18	20.79555091	31.10841532	97.64620026	16.60291897	28.80379502	19.28567853	2.31171179	0.6353618
17338617	NM_139138	Emr4	20.61520639	18.54955921	39.95809779	9.521685647	11.35820539	13.37768894	2.309645441	0.3551979
17518316	---	---	52.67483555	124.1654519	152.0338751	62.46360804	53.57666964	26.46617866	2.3077843	0.08691486
17217048	ENSMUST00000064679	5430435G22Rik	34.6486443	46.86461092	178.2874077	36.27701888	39.57194303	36.78610441	2.306569982	0.87192094
17312759	NM_028195	Cyth4	120.4653979	195.0506506	379.1113923	110.9747001	99.04409093	91.14951028	2.306442735	0.5878407
17512611	ENSMUST00000081998	Dpep2	53.33874592	75.5453473	145.3754654	37.87563051	44.91090845	36.30519257	2.302926955	0.35781115
17254660	NM_029478 // NM_029478	Vmp1 // Vmp1	12.60775937	20.76770658	44.03338963	7.752964183	12.42375173	13.48950964	2.299303064	0.1544187
17308299	NM_001135151	Slc39a14	167.9242762	174.4241509	291.7160593	103.0540933	83.34305044	89.49616763	2.29822348	0.88633466
17212199	NM_133193	Il1rl2	23.86077504	30.03517157	79.69117147	19.3528616	21.32011035	17.73445389	2.287159829	0.4069409
17353699	NM_010415	Hbegf	416.0773661	96.30094165	85.18745	77.2241403	89.75192643	94.37317922	2.286464442	0.72266257
17449488	NM_177872	Adamts3	32.39409616	44.43960228	66.21655273	20.47255133	20.77270227	21.53179963	2.278702867	0.9884776
17334846	NM_021793	Tmem8	37.33389174	48.12404479	101.820271	23.36524079	29.90347001	29.10806435	2.273434559	0.2906853
17283549	NM_029803	Ifi2712a	49.48989239	228.2534728	387.4955682	160.4520042	91.9873773	40.31601112	2.272337078	0.03213625
17484701	ENSMUST00000106042 //	Ifitm1 // Ifitm1	19.84257014	33.24494302	83.32745427	19.06659079	22.05286208	18.93230285	2.271623299	0.49637556
17439481	ENSMUST00000035635	Bmp2k	130.2735151	217.9768329	382.3632345	121.9558371	116.8559999	84.04412103	2.262970729	0.67094445
17372307	NM_010576	Itga4	53.01677467	74.88251578	155.5608271	50.18161511	44.70787283	30.38398093	2.262730649	0.7163813
17390879	ENSMUST00000103234	Fbn1	297.2279548	472.9726661	536.4433441	298.8283058	183.2063883	96.06766386	2.260229434	0.46264905
17514330	---	---	304.0175925	962.1766644	500.1274567	303.8591657	237.3854992	242.5546454	2.253538234	0.95249695
17284349	---	---	62.3266817	138.0384147	262.7571113	62.78230099	103.8414771	38.9621396	2.252694216	0.12343869
17300247	X01134	Trav9d-3	23.2051481	26.64668205	86.23382687	16.01416865	24.65931809	19.83381089	2.249078415	0.6358712
17249977	NM_001135115	Gm12250	35.47045668	30.87582969	108.7063947	24.26449619	28.60334566	25.01499051	2.247641435	0.6376863
17332236	NM_001111021	Runx1	54.89519614	64.43988436	122.6252273	35.37715188	41.36002063	31.39450151	2.237645075	0.0544547
17482766	NM_008855	Prkcb	32.77139088	52.66490539	108.9965756	29.31554555	36.46031195	21.24063512	2.234437013	0.8634297
17507637	ENSMUST00000117551	Rasa3	170.8539747	179.6498599	324.3401915	121.6706175	109.2979097	71.97659754	2.227611442	0.39572248
17219670	NM_001162938 // NM_001162938	Pydc3 // Pydc3	5.560620963	5.961651325	25.8379911	6.195535567	5.091493826	5.500691525	2.225451779	0.08308698
17516462	NM_009382	Thy1	65.46763691	131.9306538	330.4467508	82.04542593	107.2862962	48.25257404	2.221716882	0.33929056
17401269	NM_008979	Ptpn22	14.92065537	22.85351228	53.65858108	12.74956394	13.09588815	15.32323498	2.22092943	0.5465781
17523921	NM_027823	Arhgap42	47.89177494	77.18106253	148.4271293	47.81810324	51.60485872	23.84756402	2.218697167	0.26601103
17280609	NM_020272	Pik3cg	24.19038793	41.47226682	95.32125229	23.52785674	24.01555093	25.0530961	2.217515977	0.42230293

17370551	NM_153820	Arhgap15	27.40583146	42.78923556	123.4004632	31.86889297	27.94813289	27.510682	2.216885511	0.9507247
17346528	NM_009778	C3	646.0620846	2787.43027	3073.059532	1267.956908	1401.377575	270.6234413	2.21314456	0.55985314
17339772	NM_207246	Rasgrp3	19.4021416	26.66946539	75.46689436	16.93030431	21.22777121	16.90464717	2.20727373	0.18521874
17254194	NR_015519 //	Al662270 //	42.03024613	44.03317598	107.9674033	29.20122527	29.95151347	28.8184932	2.205616781	0.07213508
	NR_015519	Al662270								
17462145	NM_145980	8430408G22Rik	107.8753926	106.3182903	68.63264262	39.65764217	46.34561695	42.38691315	2.202865847	0.6870715
17497813	ENSMUST00000026571	lrf7	59.7795031	86.63745747	243.1598123	64.69216097	57.13140086	55.10521681	2.201884712	0.32582495
17258642	NR_028567	Snord1b	109.3366297	263.2513282	386.1396789	167.2778947	122.8348396	55.31573424	2.196482646	0.18488231
17462661	---	---	9.978645516	41.87496269	41.68114487	19.89349701	11.14903547	11.56102173	2.195468307	0.47261927
17501989	NM_153074	Lrrc25	32.72835078	48.0405841	97.5460805	29.93584316	28.20546859	23.12124213	2.194300833	0.46242887
17464950	NM_031198	Tfec	19.86069219	31.38421024	73.9940828	16.49429259	21.18097359	19.44374212	2.192597332	0.8624528
17467986	---	---	11.73488664	17.21962715	21.83822963	7.895797554	6.533531468	8.755951723	2.1907323	0.65151215
17240226	NM_008538	Marcks	124.5593059	192.8038433	356.7177018	93.85176683	125.0247578	89.31440668	2.18721832	0.5987632
17295136	NM_027711	lqgap2	49.87088846	85.42669126	163.8386588	47.32042087	50.39916756	39.04768193	2.187191699	0.39730293
17425631	ENSMUST00000042850	Svep1	56.18335996	187.0711145	291.1778897	102.1593896	106.0464121	37.78181228	2.172598675	0.18676226
17326318	NM_001014423	Abi3bp	239.9889217	532.5539966	963.2323264	269.7675484	349.2245084	180.9842069	2.169783434	0.28595465
17239845	NM_007482	Arg1	56.27904724	62.42564857	129.9494754	41.79600076	38.31243989	34.71910854	2.165457445	0.3428537
17225815	NM_009183	St8sia4	26.33132108	32.20382167	92.84330661	22.70518678	30.86645726	16.35919667	2.164687966	0.22062254
17467269	ENSMUST00000031982	Hpgds	24.0548517	34.08046228	96.74331039	20.11648031	32.34904014	19.17113703	2.162002386	0.91254735
17272619	NM_007707	Socs3	88.37258622	124.4452194	173.2456118	54.28467252	65.91971043	58.77431848	2.157035526	0.5272857
17447615	NM_010942	Nsg1	111.7237428	213.3259999	331.829422	90.87005204	128.3119742	86.61890323	2.148061374	0.6622127
17309905	NR_028091	Snord72	32.97244578	78.71463564	118.0370533	57.67895014	38.37056225	11.08060692	2.144346858	0.60006255
17514333	---	---	1041.08345	2097.594365	1464.659912	754.4162806	714.8332838	677.5703808	2.144258878	0.58117586
17256784	ENSMUST00000100403	Tmem106a	51.58676239	94.0618629	207.1966691	46.33032829	67.92854276	50.42359237	2.142579647	0.6004745
17394694	NM_019835	B4gal5	179.4324485	158.8828944	282.6907761	95.47644867	99.36101458	95.34147236	2.14007994	0.9511627
17216745	NM_027677	Gpr39	35.88751193	55.48954238	104.8182415	28.47105405	38.06810895	25.55307487	2.130421633	0.42534742
17224813	NM_175291	Dock10	49.87676534	63.39758589	172.4432682	59.24957909	48.53794083	26.67754493	2.124846478	0.4431527
17304514	NR_028523	Snord19	10.41180289	15.18094821	31.31541298	9.048000443	9.48937454	8.244940029	2.124841115	0.96902204
17472530	NM_008428	Kcnj8	48.58264055	137.5025916	353.2782205	90.90306287	134.1446772	28.99780914	2.12309743	0.6847752
17379873	---	---	75.08526964	148.3073204	165.6646524	79.67769461	70.93850395	32.75347334	2.121709869	0.52825695
17400365	NM_007802	Ctsk	46.57493982	94.78395791	262.8727889	70.69949476	99.47995846	20.44230538	2.120595727	0.2467744
17413500	ENSMUST00000030202	Glipr2	78.87356788	57.38405446	117.3964522	50.75900908	39.96192014	28.93795365	2.119809817	0.17247514
17221756	NM_001081079	Ogfr1	18.31830359	36.3354785	74.52145823	23.60183294	19.84356044	17.58943211	2.116418606	0.6173522
17504019	---	---	14.98184089	38.24456942	70.43023542	18.91168493	9.269625153	30.26117287	2.115869133	0.7127535
17429454	NM_016748	Ctps	451.6047969	305.8583813	256.8770158	171.533316	171.0960923	136.7924694	2.115757001	0.29591492
17287361	NM_011817	Gadd45g	105.3107571	137.5895414	139.6780972	72.76400261	64.16301366	44.14811699	2.112815762	0.98605794
17490149	NM_001111058 //	Cd33 // Cd33	36.7262579	60.60428931	156.055241	28.28852403	53.03151284	38.64580733	2.11214942	0.25820696
	NM_001111058									
17301670	NM_033325	Loxl2	65.4083538	92.55474183	88.19341285	36.85427314	50.70777265	29.36877122	2.105146571	0.3663119
17331380	ENSMUST00000064405	Epha3	73.97921055	134.2758459	373.946741	118.3223663	115.042889	43.29087333	2.104424002	0.46641946
17494370	NM_175648	Trim30b	15.22399407	12.87157775	44.79441618	11.81382302	10.24125064	12.65069728	2.100226735	0.8735316
17358832	NM_008331	lfit1	76.9899378	135.6109627	442.1138133	111.0675836	89.03403285	112.1790142	2.096558831	0.40572703
17341276	NM_013521	Fpr1	9.921099395	12.9826681	32.90445451	8.878758738	11.33147687	6.415510193	2.096024743	0.61034024
17438823	NM_007832	Dck	44.18675253	39.11529662	106.6465881	35.40138749	24.32098915	30.91615502	2.095672047	0.20787406
17539997	NM_009515	Was	31.00061648	52.23511218	121.6688464	36.78312124	34.03669379	27.22928132	2.089816048	0.14435604
17240342	NM_023323	Rpf2	64.99951283	69.12908859	136.7059286	48.81305021	42.17973131	38.7331519	2.087743929	0.8798567

17272785	ENSMUST00000043722	Lgals3bp	225.8632907	251.57731	578.5512686	210.5997626	160.7316243	136.9166416	2.077709721	0.21457164
17357597	NM_023044	Slc15a3	30.95569618	22.83300758	42.02206052	13.62114427	19.29594774	13.36500989	2.070147213	0.33098143
17286365	ENSMUST00000063191	Serpib9	550.3940257	291.7083757	440.8014013	225.8142938	185.6177671	208.8802096	2.068158029	0.4408335
17218707	NM_183391	Tnfsf18	6.658803652	7.558222555	30.42290471	7.150494419	6.81795936	7.632676256	2.066555354	0.12714136
17330203	NM_019388	Cd86	24.17382731	23.87127964	67.19099549	17.32280917	25.62393254	12.91990001	2.062699652	0.2261322
17532137	NM_010851	Myd88	129.3196771	192.4428153	343.8317591	114.6342229	112.1899007	96.28552347	2.059964033	0.42747444
17518314	---	---	14.88461499	9.598240748	25.54783265	5.444539384	11.54290142	7.303115261	2.059676536	0.97737706
17405478	NM_028808	P2ry13	18.5128743	27.93618281	73.80957101	21.28942382	22.55946579	14.58106305	2.058167475	0.25482136
17287827	NM_009369	Tgfb1	404.7437521	504.2537159	1290.469206	348.1791494	650.0153602	72.08449143	2.055040482	0.58554685
17304512	---	---	11.96876176	5.932320311	15.32320311	6.280441584	5.267615345	4.656329008	2.050327592	0.5169843
17547744	NM_025415	Cks2	9.362708879	16.23842721	38.42853306	10.1574686	11.88631818	9.238784141	2.046816079	0.78371465
17548303	NM_025415 // NM_025415	Cks2 // Cks2	9.362708879	16.23842721	38.42853306	10.1574686	11.88631818	9.238784141	2.046816079	0.9555617
17548955	NM_025415 // NM_025415	Cks2 // Cks2	9.362708879	16.23842721	38.42853306	10.1574686	11.88631818	9.238784141	2.046816079	0.6919266
17358815	NM_008332	Ifit2	46.7935572	74.58641603	92.20007378	35.65965895	42.94427768	25.74781316	2.046731822	0.55953825
17385564	NM_025422	Cd302	83.1836451	213.7346497	427.0756992	115.6304856	161.2250381	77.75723428	2.041646776	0.5810877
17290205	NM_001037925	BC147527	15.66547924	14.17670156	56.43365948	12.40185481	13.67505756	16.20205607	2.040632576	0.03408522
17392375	NM_001199188	Snx5	101.0874439	175.1738968	239.2665651	89.75671682	90.52692218	72.36067697	2.040528416	0.86401147
17325438	NM_008225	Hcls1	42.87958387	68.11128757	108.6678226	36.55520659	38.82064007	32.3832752	2.0384232	0.46524107
17304493	NM_153547	Gnl3	155.7647528	77.60480089	163.8967004	88.10164184	61.79276393	45.14004651	2.036902965	0.3590944
17497246	NM_007400	Adam12	58.30763896	72.03838833	82.40705791	49.13138487	35.6717478	19.7134312	2.035592037	0.41378254
17244949	NM_178610	Krr1	52.17410347	61.837239	193.1347559	77.14560161	45.72914373	28.32817979	2.031350241	0.67200106
17278779	---	---	53.83151041	34.59637559	42.15284207	29.37874779	24.00964222	10.92473212	2.030390125	0.5080736
17236288	ENSMUST00000062862	Igf1	49.55445988	130.2769465	287.3758464	90.88302815	103.1631557	36.17086013	2.029420779	0.22104305
17357425	NM_144538	Rab3il1	43.67966844	87.0013571	182.9567712	47.74484272	71.95240477	34.87267188	2.029099827	0.24605827
17487533	NM_001166737	Vmn1r103	14.83813637	30.11783163	21.36539375	12.92644806	11.59079004	8.201654668	2.027005077	0.20060553
17469634	---	---	9.437540955	14.48893852	14.53730566	6.579919802	5.154730491	7.255499806	2.025459774	0.67771584
17353747	ENSMUST00000061829	Cd14	38.30288086	64.64464676	196.4371519	40.03011902	51.24420641	56.61824007	2.024338941	0.17751603
17536191	NM_001163539	5430427O19Rik	6.440202268	11.65928974	17.41261529	6.86948526	5.54648202	5.142022774	2.022561078	0.5977257
17314693	NM_009448	Tuba1c	172.3724023	73.26056894	143.6725861	68.87535765	59.77676839	63.8425778	2.022422174	0.8066203
17328625	NM_022324	Sdf2l1	79.18679693	71.76353238	132.5056439	36.67985422	46.03642823	57.59381564	2.020210783	0.01817505
17391056	ENSMUST00000040128	Atp8b4	10.46767404	14.27812864	42.27708496	11.57297602	9.029768493	12.64094137	2.016108799	0.7325472
17239817	NM_134005	Enpp3	60.74277864	139.1724655	431.7334307	103.526694	161.852518	48.14836822	2.014651069	0.5436425
17503825	NM_008610	Mmp2	432.5295832	764.7853089	1058.774765	396.6082836	488.5860966	236.0296023	2.012166786	0.48404244
17514346	---	---	360.7200988	759.3072641	563.1322638	297.2757559	223.7334256	315.6451996	2.011774115	0.5421015
17351465	NM_026473	Tubb6	164.6218472	141.1763875	400.2379062	189.1543311	111.3636043	51.18502914	2.007478503	0.20754965
17514328	---	---	354.8513538	1116.053135	597.2528406	410.5129717	293.3731441	326.6285297	2.006916969	0.34314612
17514352	---	---	463.5669812	1024.163263	557.873418	394.9639039	314.8581061	310.285399	2.005282624	0.8204654
17251978	NM_001204252	Clec10a	19.85287443	38.88365685	113.0890159	40.37440238	31.69466249	13.67115284	2.004025086	0.33407873
17324402	---	---	113.7174624	332.6951443	278.7903858	192.4528199	112.8283653	56.9356355	2.002124007	0.13200979

Downregulated genes (89)

17477220	NM_133712	Klk10	215.8186903	337.4168007	72.05896375	1425.389019	1254.5463	2401.483199	0.123055098	0.9367153
17502899	NM_009463	Ucp1	21.51541854	22.86633112	22.55247712	287.7154731	27.81341523	71.80373573	0.172808131	0.694702
17351457	NM_007702	Cidea	40.2744505	30.97114897	34.72888049	468.3667986	55.78614674	64.86565956	0.179917033	0.5361774
17497704	NM_007751	Cox8b	26.11724833	37.8289283	34.45940772	358.1152139	50.84373112	48.20146199	0.215253952	0.06375395

17359918	NM_007703	Elov13	14.61410933	12.17576066	11.00416674	131.2157419	15.22032226	19.25542418	0.228098843	0.49477252
17283617	NM_009246	Serpina1d	6.006568387	29.88013995	4.718417244	66.18695525	49.64780395	59.93068672	0.231018818	0.6410726
17493432	ENSMUST00000043077	Thrsp	69.84965089	39.03439489	67.73811804	469.0519801	98.05606757	112.530089	0.25987677	0.8242627
17273348	NM_007988	Fasn	245.6579299	142.4574242	237.3970175	1249.564797	439.9241527	431.4540171	0.294921826	0.6419854
17341179	ENSMUST00000014917	Dll1	51.88835881	51.36180505	31.70441826	142.9210888	84.48662133	226.5231992	0.297302033	0.4228787
17502440	NM_008452	Klf2	85.08701051	202.062249	112.3514552	343.2295606	366.2172657	623.0883791	0.299804998	0.8284548
17484587	ENSMUST00000026552	Cyp2e1	84.04097533	137.0122427	188.3927975	879.9373501	225.1792374	137.9225937	0.329391078	0.5384908
17501633	ENSMUST00000015712	Lpl	48.58678274	77.50228818	162.2870419	628.3406034	145.3350636	91.32386416	0.33338297	0.78487563
17341963	NM_023055	Slc9a3r2	413.2485651	389.2429233	154.0553527	766.3586977	865.0183936	1207.317994	0.336967097	0.25694108
17224180	ENSMUST00000027377	Igfbp5	63.1550415	57.77802562	165.0553395	344.0549047	377.6704245	103.3847082	0.346606384	0.11814773
17396024	NM_025285	Stmn2	287.8718681	321.9261587	108.1169568	605.6552463	607.6951637	850.1378599	0.347913286	0.12405463
17472903	ENSMUST00000052296	Pthlh	81.81951045	114.491525	67.40431286	196.1599899	185.324653	370.8446125	0.350531827	0.25360343
17498032	NM_028308	Mob2	117.04066	107.7264719	119.0275725	323.3643894	212.5707082	425.5762999	0.357556557	0.5904746
17314888	ENSMUST00000023760	Gpd1	55.67327316	50.87926766	69.95590811	306.604487	71.54995726	112.0034996	0.36010525	0.27614564
17321434	NM_007857	Dhh	136.5419074	129.150373	47.20346957	265.5831855	230.3083647	369.9819298	0.361364284	0.75310516
17465365	NM_001101443	Prrt4	78.14101012	120.5633835	44.2730543	210.2724457	194.5584729	258.934071	0.366059451	0.07867662
17464614	NM_011134	Pon1	11.58117718	11.82103949	15.81014835	66.28203537	22.45016277	17.74463507	0.36827133	0.07196114
17425401	NM_010637	Klf4	145.7341324	232.5868949	136.392925	379.9276762	342.0819092	634.8940292	0.379329782	0.3563182
17436481	NM_008010	Fgfr3	45.97660393	30.69666459	19.49382104	78.10667818	61.82403882	112.7623782	0.380568727	0.11447971
17493632	NM_026384	Dgat2	58.91826328	56.38263509	81.00162806	360.9071713	84.90143304	64.80045329	0.384447795	0.2819839
17380222	NM_011044	Pck1	47.09748118	54.13272091	115.9156861	392.3300416	98.91250363	58.75615158	0.394811641	0.2602237
17234786	NM_015790	Icosl	143.0085903	159.8670714	148.6307692	348.0003628	345.3927524	447.3700917	0.395793297	0.48601165
17312070	---	---	3.745101969	4.154681836	3.448225204	4.279522996	3.940519936	20.34696909	0.397241721	0.20543559
17376441	---	---	67.61835434	78.73684503	40.96829649	154.0982855	120.2996804	187.9235419	0.405180146	0.3499409
17451390	NM_008153	Cmklr1	63.99024123	79.70879425	69.87691447	118.8780874	162.5503667	241.6069257	0.408339394	0.36328098
17487422	NM_020486	Bcam	707.6955316	571.0308978	354.1782969	1285.398519	1060.419948	1631.552844	0.410548726	0.41216728
17392817	---	---	2.633552098	2.558873804	2.560401395	3.455779098	2.839748177	12.41869782	0.414274556	0.5571782
17477339	NM_010642	Klk1b21	7.175602635	9.179171858	7.775265826	20.52128262	12.29903313	25.19865805	0.415899123	0.26507834
17270877	ENSMUST00000001055	Icam2	181.3996673	201.7675002	97.69474117	328.8363557	328.8682677	495.2066919	0.417084907	0.07716668
17476288	NM_009944	Cox7a1	27.24094789	30.51750262	31.40858404	143.1056676	42.38841157	27.98665191	0.417681887	0.46563485
17377778	NM_010495	Id1	65.8220019	89.42243957	71.05685841	133.7668665	122.042007	282.8052319	0.420154797	0.5946714
17366914	---	---	3.155360844	3.635419878	3.25416409	3.963104475	3.71720177	15.7470535	0.42876982	0.65274143
17477237	NM_008940	Klk8	105.9951909	78.65267893	53.10743698	171.4335897	163.8284383	214.3221279	0.432609464	0.16087219
17409792	NM_023245	Palmd	653.3815922	572.7675702	193.6915223	938.9346895	924.7739828	1410.293772	0.433671235	0.04136713
17282102	---	---	3.025196804	4.742533617	4.516399168	3.990490253	9.993492808	14.30163318	0.434288915	0.13910815
17302548	---	---	4.313583849	5.479487639	9.039794647	24.91438401	11.10752898	7.216978716	0.435553859	0.65070957
17425978	NM_001199995	Mup12	28.57376026	47.71926775	44.44246707	215.1358286	36.12172787	25.57068671	0.436138646	0.4222691
17388041	NM_001135657	Ptprj	883.166721	1106.547756	462.774641	1726.015853	1640.431913	2251.171104	0.436570934	0.3023053
17526663	NM_030069	Fam55b	29.65591541	62.30357315	24.15764641	79.45703202	70.77578792	113.3881449	0.440470033	0.23320618
17399485	NM_080466	Kcnn3	144.781454	169.2955216	67.05616168	229.0308295	303.7576642	331.4776984	0.44099045	0.45452872
17256607	ENSMUST00000129680	Ramp2	135.1758858	185.0997325	86.34729033	263.6240169	285.3271062	372.5594895	0.441256892	0.803838
17280590	NM_011158	Prkar2b	21.99215386	48.47002764	66.14664139	201.5747329	52.86675974	52.4260883	0.445171896	0.22075722
17377857	BC020535	BC020535	193.6101799	201.2601872	117.2925036	308.6602733	384.0592269	456.4325913	0.445687629	0.57315475
17282117	NM_013738	Plek2	208.49905	161.7308402	75.41334827	305.3825888	261.9108471	424.7876463	0.44920042	0.0470423
17356216	NM_001162946	Pcx	29.67820639	29.67820639	40.43430755	139.213663	52.54377685	29.61842458	0.450775068	0.19589686
17493310	---	---	4.562090291	3.48290229	3.429972477	3.828239262	3.555200685	17.87881236	0.454233649	0.52011335

17337852 NM_172621	Clic5	226.3695347	246.7097633	113.3754133	390.0182979	385.6937613	515.0672498	0.454341581	0.5802102
17516332 NM_153522	Scn3b	121.7624093	141.0981244	78.75387465	198.8702966	237.9256496	313.1143894	0.455540339	0.35837016
17248664 ---	---	16.96950998	34.21789248	12.01184618	39.19625734	38.129032	60.62828045	0.458119704	0.11233813
17300223 ---	---	8.363935869	3.864838153	6.861124284	13.21049847	6.50881541	21.84801039	0.459252517	0.930204
17526776 NM_001081445	Ncam1	172.3426545	190.9347651	190.7469264	418.9783829	429.2142011	354.0766754	0.46081553	0.5252919
17370787 ---	---	3.118905844	3.007921674	3.198263932	2.924798022	3.180877913	13.85640406	0.467140271	0.34308374
17435282 NM_008713	Nos3	303.4287547	284.1492308	121.0306807	440.4929136	473.2615811	582.9805737	0.473436269	0.12383359
17315167 NM_019518	Grasp	197.2488392	216.1416061	149.4308279	323.3717861	417.6133438	444.8493395	0.474620436	0.98908114
17323755 NM_013805	Cldn5	118.1116121	151.4626221	53.84106342	229.4202615	234.8982248	217.0616431	0.474647387	0.2569518
17465620 NM_013723	Podxl	453.8783931	424.2053483	166.4686847	615.1643123	634.9895326	950.3815376	0.474681041	0.9414855
17328580 ---	---	25.66741318	9.422801158	7.809098446	17.76777348	33.40062051	38.78438446	0.476909258	0.962277
17232195 NM_001010839	Taar7f	4.630249709	3.92736858	3.985790827	4.657384527	4.662232656	16.90464717	0.478313098	0.48183572
17523309 NM_011703	Vipr1	33.55111949	39.52487514	31.66032149	70.92316432	63.26935573	84.04132484	0.479927008	0.8891189
17218616 ---	---	3.238309776	3.18840744	3.334676937	4.062762415	4.627628335	11.64493757	0.480021468	0.03615699
17464706 NM_010056	Dlx5	221.2702987	301.8675774	104.4123822	349.1947358	474.3078712	476.4595736	0.482745012	0.4891495
17509962 ---	---	14.58006251	18.65006819	9.645546626	30.08004875	21.1946612	37.41215073	0.483450164	0.5800891
17370309 NM_008969	Ptgs1	251.8798669	362.8403272	195.5555946	462.5472703	539.8792656	667.9017111	0.485099734	0.24226828
17233074 ---	---	3.467993032	3.303556456	3.081972524	3.697325349	3.534651551	13.04663637	0.485907092	0.07893322
17252497 NM_001163336	Atp2a3	356.5533133	345.3302726	130.6880121	463.5971863	519.4539325	729.130378	0.486263635	0.6318494
17476752 ENSMUST00000032705	Rhpn2	92.30155193	83.13816497	48.67631335	174.8335197	126.8403541	159.0663654	0.486425997	0.23765492
17488501 NM_027470	Pak4	62.3507064	78.749999	60.91780271	131.2912537	135.8821368	147.3019787	0.487407752	0.5912582
17265164 NM_007528	Bcl6b	100.5473327	94.17381046	52.87496873	116.2197141	101.0662854	290.2648365	0.487825247	0.7965568
17370341 NM_146938	Olfir346	2.791916898	3.583302897	2.766448372	3.547161459	4.042682771	11.13680116	0.488163682	0.05441026
17477362 NM_010643	Klk1b24	18.78029735	20.73137643	27.52708619	51.31646902	30.8010793	55.1063245	0.488535694	0.9158513
17321823 NM_028770	Krt80	869.0708586	624.9521835	252.1911782	1105.091414	1160.933806	1308.066344	0.488575681	0.43206778
17473629 NM_146915	Olfir1336	24.22493686	14.25699474	10.37142339	19.43060612	27.55635187	52.93833811	0.488898776	0.36284247
17353378 NM_013512	Epb4.1l4a	68.88705512	80.88896521	41.71527931	114.5227969	123.2502703	153.7515346	0.489091359	0.08455111
ENSMUST00000093209									
17248263 //	Hba-a2 // Hba-a1	105.9243892	63.45658598	82.79421144	108.9612237	310.961034	95.57292052	0.489190195	0.3178532
ENSMUST00000093209									
17212719 NM_138741	Sdpr	918.9808575	847.5284573	306.6561342	1323.195025	1229.571572	1681.00698	0.489673198	0.58799034
17328062 NM_007929	Emp2	592.9205543	413.826436	337.2477482	931.0701118	794.3026465	1013.722456	0.490671055	0.43015927
17541232 ---	---	4.436321742	4.223453011	5.121058359	4.508701503	4.295696299	19.27180773	0.490836737	0.38802034
17474941 NM_001163510	Kcnn4	112.0155336	94.19685582	50.52067466	165.3968559	145.0243155	211.7915177	0.49162548	0.78032345
17438832 ENSMUST00000148750	Slc4a4	229.7155963	338.8443722	211.035954	453.9441502	500.6831175	626.896298	0.492939808	0.11168267
17320967 NM_178114	Amigo2	401.7168037	421.8730154	163.3129065	592.784946	627.7150548	772.510108	0.495181997	0.70460284
17489384 NM_017405	Lsr	152.1164115	127.3650823	64.68503161	246.541038	196.432931	250.7696599	0.496100448	0.18822052
17222775 ---	---	3.011877305	3.171756461	3.045487114	4.473214685	3.364989493	10.7430073	0.49669102	0.08659258
17521422 NM_010489	Hyal2	132.3148337	112.4240591	80.06456665	232.4864784	199.2364776	218.304491	0.499676531	0.01078988
17316272 ---	---	3.727928009	3.289497007	3.840126935	3.001319694	3.155529258	15.57025859	0.499723763	0.95157623
17285771 NM_134221	Vmn1r201	3.700991956	4.333726175	4.002534949	3.58325819	3.711460462	16.78512063	0.499889262	0.37550214

Supplementary Table 3. The list of endothelial genes in response to 48 h post partial carotid ligation and their fold-change expression in APPsw-Tg mice RCA compared to non-Tg mice RCA.

Probe Set ID	Gene Accession	Gene Symbol	APPsw-Tg RCA-1	APPsw-Tg RCA-2	APPsw-Tg RCA-3	Non-Tg RCA-1	Non-Tg RCA-2	Non-Tg RCA-3	APPsw-Tg RCA/Non-Tg RCA (Fold-changes)	P-value
Upregulated genes (210)										
17404091	NM_024406 ENSMUST00000095049	Fabp4	1988.327928	377.1056616	371.335903	115.0548508	98.13052	162.7016419	7.280830143	0.04814679
17426022	// ENSMUST00000095049	Mup15 // Mup2	784.9282644	110.3170521	73.64741587	23.18244778	49.74301331	69.1082001	6.821571198	0.15400992
17484587	ENSMUST0000026552	Cyp2e1	879.9373501	225.1792374	137.9225937	43.64416861	46.65555632	94.9586158	6.709760955	0.06077921
17396152	NM_007606	Car3	2287.982021	774.8321465	532.0422478	60.01761148	161.6652731	333.5901777	6.474033516	0.0446603
17404191	NM_007606 // NM_007606	Car3 // Car3	423.2070938	155.0848555	86.37746069	13.69528136	27.09692056	62.25802905	6.449955559	0.04743858
17425990	NM_001134675	Mup7	606.0205896	94.12584459	68.63701943	16.60907704	41.29362021	62.95901217	6.360852062	0.14046386
17426000	NM_001134674	Mup13	828.1159655	127.53514	86.41782405	26.72473987	46.12033222	94.19319952	6.238504024	0.15316525
17425915	NM_001134676	Mup8	773.7984346	107.8751683	82.37610457	31.14163962	48.65276863	75.48483871	6.208490358	0.16032386
17426011	NM_001134676	Mup8	606.1592257	84.75825613	64.0822101	23.47262035	38.20720982	60.93102057	6.157690673	0.16532469
17501633	ENSMUST00000015712	Lpl	628.3406034	145.3350636	91.32386416	36.75987613	50.83615462	53.60865372	6.125855771	0.08680784
17469754	ENSMUST00000113091	Cidec	506.7702419	124.3507156	89.32220743	30.99367663	41.00312608	46.24796562	6.092812181	0.06157083
17425978	NM_001199995 ENSMUST00000107483	Mup12	215.1358286	36.12172787	25.57068671	9.657059725	19.36205263	16.58291815	6.070524494	0.1594875
17426032	// ENSMUST00000107483	Mup19 // Mup16	470.6324542	65.83016917	50.17257228	25.70220092	33.11155822	43.92112186	5.710185186	0.18528318
17402181	NM_010171	F3	235.8515055	632.3883587	62.42608127	51.9647714	76.80940134	36.38409447	5.63499461	0.12579113
17502899	NM_009463	Ucp1	287.7154731	27.81341523	71.80373573	22.04697781	24.80546333	22.64619869	5.573240354	0.1574258
17425888	NM_001134675	Mup7	534.3217744	74.81553691	64.29550612	25.04175901	42.02031291	54.15084705	5.555784179	0.17625728
17497704	NM_007751	Cox8b	358.1152139	50.84373112	48.20146199	26.13434325	25.9645623	31.06973432	5.496788305	0.16399263
17351457	NM_007702	Cidea	468.3667986	55.78614674	64.86565956	30.33360373	40.58168884	37.54362369	5.430799285	0.18369147
17425941	NM_001163011	Mup1	722.1711615	102.2186052	85.36921452	46.22569162	51.26577146	74.51918547	5.288968961	0.17638367
17273348	NM_007988	Fasn	1249.564797	439.9241527	431.4540171	119.1467674	159.1981764	124.4939652	5.264990345	0.01447456
17236811	NM_008524	Lum	276.8253016	581.7760113	36.98283713	41.2280694	98.03615518	38.24737949	5.045214677	0.21495263
17235018	NM_013459	Cfd	691.5879874	299.5909015	123.878671	49.41684499	80.64308919	110.5829382	4.633661279	0.07229219
17445715	NM_007643 ENSMUST00000107484	Cd36	329.5594661	117.0555882	62.35036066	34.83783343	45.09323163	30.12217417	4.624719986	0.07106981
17426043	// ENSMUST00000107484	Gm2083 // Mup17	558.3326059	100.0885409	79.87765087	39.78997259	45.66870577	74.36851194	4.619356671	0.16609699
17493432	ENSMUST00000043077	Thrsp	469.0519801	98.05606757	112.530089	34.77108065	49.90152499	62.99035339	4.602631162	0.080943
17280590	NM_011158	Prkar2b	201.5747329	52.86675974	52.4260883	11.74613322	23.49443225	33.69314046	4.451633301	0.07917005
17380222	NM_011044	Pck1	392.3300416	98.91250363	58.75615158	35.06140732	44.81730523	46.61279121	4.348107822	0.13321319
17426062	NM_001134675	Mup7	607.3401771	116.3061036	83.43900217	51.85351919	52.88860434	90.50032073	4.133759367	0.1811521
17218927	NM_019759	Dpt	940.0912574	1940.146663	129.9117399	164.3381932	487.3417461	88.66556442	4.065871469	0.28098696
17234436	NM_175329	Chchd10	267.6576357	64.77359894	67.61198039	31.69701327	36.50011236	32.36442573	3.978093114	0.08891092
17359918	NM_007703	Elovl3	131.2157419	15.22032226	19.25542418	16.12824998	14.73591766	11.236626	3.935590616	0.29813898
17425900	NM_001134674	Mup13	318.2507271	63.74264589	53.19209668	29.5010214	33.11155822	51.78179243	3.804255943	0.18714418

17512809	NM_017370	Hp	395.2320139	136.8442495	65.09460168	37.85012081	47.75745327	76.14128433	3.691963398	0.13304096
17354282	NM_033037	Cdo1	679.934517	205.2616078	124.7663435	100.360865	82.16197749	102.0910086	3.5485359	0.12535374
17212461	NM_009930	Col3a1	439.6543705	392.8857413	71.96791714	77.10523986	129.2047232	49.17898314	3.540302006	0.1675648
17287160	NM_025711	Aspn	252.4914981	234.1265929	27.91206583	37.31448837	90.18646326	18.13182202	3.533065697	0.2522065
17314888	ENSMUST00000023760	Gpd1	306.604487	71.54995726	112.0034996	47.26865798	41.30655963	50.5891467	3.522151279	0.08099326
17397575	NM_015784	Postn	776.632354	420.3193313	104.1025069	153.0255772	155.8904781	61.35244782	3.513812763	0.18848649
17283549	NM_029803	Ifi27l2a	160.4520042	91.9873773	40.31601112	18.76416257	32.9538701	31.64612609	3.511765691	0.07033505
17493632	NM_026384	Dgat2	360.9071713	84.90143304	64.80045329	47.94388788	46.71477454	52.54006208	3.468841591	0.17072624
17411201	NM_199465	Nexn	241.6447767	78.5042035	34.87890879	43.24657575	35.85663007	28.59295855	3.296569484	0.20094718
17255260	ENSMUST00000001547	Col1a1	610.6944823	580.4777666	104.792307	115.8858814	205.2332967	83.69322873	3.201395348	0.19460817
17438246	NM_001083316	Pdgfra	267.2773919	418.9505041	83.58313694	86.1680422	101.1154751	53.35409134	3.199047053	0.1243947
17287175	NM_008760	Ogn	1406.301291	1717.423354	228.1642579	320.252717	590.3001917	153.3478363	3.150565425	0.2573205
17356216	NM_001162946	Pcx	139.213663	52.54377685	29.61842458	20.41641989	24.04940007	26.96591345	3.099124911	0.13278916
17274021	NM_011859	Osr1	741.8100483	940.712458	187.4935297	227.2756006	251.5807977	134.1727607	3.05045202	0.1528641
17324404	ENSMUST00000023593	Adipoq	182.9202518	81.08634057	57.53954868	31.76094647	38.59237698	35.91446203	3.025810123	0.06477433
17404337	NM_007753	Cpa3	197.6684761	123.7335564	39.39888783	49.53220703	33.47970707	41.07179229	2.907721979	0.14522181
17500996	ENSMUST00000110372	Acs1	317.7911196	108.7495786	61.03437065	60.76370777	58.18401709	48.77216128	2.907079655	0.16905664
17489420	NM_052992	Fxyd1	540.937086	445.645893	114.7140269	152.2196713	134.7052249	92.85785177	2.899807881	0.15204638
17271350	NM_153145	Abca8a	169.6975587	206.8703395	36.70190392	45.48156524	70.66921606	27.16430065	2.883644879	0.2021838
17515402	ENSMUST00000001384	Cnn1	1700.649358	707.8127797	186.8111816	410.1514731	325.8023049	168.1167894	2.870653479	0.3278084
17346528	NM_009778	C3	1267.956908	1401.377575	270.6234413	303.0111349	596.249359	142.3907876	2.822401293	0.21813375
17489871	---	---	9.617800493	8.015936056	23.30607251	3.965316439	5.338505796	5.279575736	2.80728875	0.11146534
17250585	ENSMUST00000064783	Mfap4	198.7893972	249.2560997	36.70551655	65.95293693	69.02547473	38.40145315	2.795889903	0.24321324
17249787	NM_008161	Gpx3	179.2905949	126.9815427	34.21428752	34.23822487	46.48659978	42.72086638	2.758188012	0.17759441
17275062	ENSMUST00000041183	Meox2	51.58754906	165.5914071	17.63634868	20.81382195	44.02695004	21.2577058	2.72728753	0.35958546
17528245	NR_002852 // NR_002852 // NR_002852 // NR_002852	Rnu5g // Rnu5g // Rnu5g // Rnu5g	14.77217138	4.650113726	8.838202584	3.220230593	4.22842972	2.99380032	2.706305408	0.09189247
17464614	NM_011134	Pon1	66.28203537	22.45016277	17.74463507	13.40926262	12.77118952	13.23972269	2.701074606	0.1601595
17312070	---	---	4.279522996	3.940519936	20.34696909	3.720307832	3.761301617	3.175386052	2.680587791	0.32483134
17461942	NM_001127330	Pparg	94.32458876	33.32714898	17.55423231	17.14003321	17.82671536	19.35243234	2.673198815	0.22317833
17498722	// ENSMUST00000012849	Retn // Retn	446.8853685	279.3226975	219.9131402	78.17113067	100.3309566	180.7844775	2.633333108	0.03538797
17211305	NM_053191	Pi15	168.074378	95.69276855	21.8882696	43.1152996	43.22562743	22.24259178	2.630743774	0.28935087
17474143	NM_009201	Slc1a5	267.3850512	166.0012161	53.31431329	64.34900787	67.51691123	53.20891204	2.629750234	0.18032295
17510772	NM_020259	Hhip	53.82665991	98.22517991	27.46217526	15.1237395	34.56971968	18.83212635	2.619664081	0.12826543
17398557	NM_009144	Sfrp2	233.6276147	313.5909251	51.62500102	85.59425129	102.8005377	41.85462075	2.600847236	0.26272464
17256697	NM_009675	Aoc3	313.9463001	119.2192176	57.53946891	74.65898552	74.43669006	39.77877656	2.598048498	0.2307598
17255058	NM_026433	Tmem100	76.08878921	90.69914212	19.17113703	22.64737601	32.03688558	16.93445908	2.596514802	0.18914852
17306960	NM_010779	Mcpt4	30.54658086	16.98703318	13.85194827	7.433676984	9.667762285	6.662783428	2.58310836	0.04499239
17313811	ENSMUST00000057410	Fbln1	291.6293274	478.4356222	79.11646163	90.93829184	163.520307	76.13906772	2.568624939	0.25485298
17466599	NM_177736 // NM_177736	Lrrc61 // Lrrc61	272.1354325	347.1605008	78.1068406	99.18410285	120.2951777	52.36442098	2.565454965	0.18702602

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17285846	ENSMUST00000102968	Hist1h4k //	9.243818928	8.338604715	16.01328066	3.760331887	5.176281223	4.198802705	2.557642999	0.03554998
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	ENSMUST00000102968	Hist1h4d //								
	//	Hist1h4c //								
	ENSMUST00000102968	Hist2h4 //								
	//	Hist1h4h								
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17357700	ENSMUST00000025581	Ms4a4d	49.58679239	99.44838242	24.9321605	17.7962825	31.88455851	18.39968293	2.555317222	0.14625208
17333465	NM_022315	Smoc2	173.0790144	271.6742463	44.14401662	73.92805232	75.62456324	42.02905169	2.551900108	0.25717863
17290850	---	---	12.65420528	5.016610748	24.21305143	6.711205808	4.707917372	5.001004836	2.550763759	0.19870871
17227892	NM_021400	Prg4	314.8993567	88.06464276	47.2816999	89.79143929	45.59254379	41.32379941	2.547967571	0.3294506
17509775	ENSMUST00000169749	Lpl	67.62252585	19.15234314	15.6866241	16.37206052	12.44604964	11.50904324	2.540756896	0.23935969
17527661	NM_001195431	Islr	284.9573115	415.491744	59.21016627	73.90161565	166.159158	60.18841833	2.530095808	0.31596804
17287827	NM_009369	Tgfb1	348.1791494	650.0153602	72.08449143	114.6939117	231.2532771	77.45384744	2.527813844	0.3810627
17545407	---	---	22.17149273	23.90075024	11.56094961	7.624892512	7.620100367	8.093327635	2.469466153	0.03241285
17315686	NM_001243837	C7	216.0535311	366.2809857	42.3195388	79.79846002	128.6135647	44.72839235	2.467618813	0.37439612
17339876	NM_027455	Qpct	113.5685845	146.1913357	34.55014835	37.19008139	59.35838767	23.1388298	2.458991651	0.18909818
17449084	NM_001159518	Igfbp7	2112.521047	1516.374095	586.1914032	665.8627388	675.0474011	377.9317725	2.452282851	0.13550913
17514515	NM_010809	Mmp3	72.03309561	102.2691355	30.29244243	36.550494	30.69051607	16.25997349	2.45020675	0.12678526
17387517	NM_009776	Serping1	1276.519623	2031.584983	485.4995001	451.219623	819.1171554	284.6619787	2.439618739	0.18601763
17236800	NM_007833	Dcn	2498.332879	4262.990131	701.7011906	934.0435453	1619.03673	512.2087186	2.43468861	0.2958717
17472536	NM_021041	Abcc9	506.4103217	557.8324305	120.6653798	188.5796251	203.5792908	95.63726713	2.429104968	0.24161632
17378663	ENSMUST00000088552	My19	2028.180026	1061.456843	443.7225307	625.3395699	514.601196	317.4703394	2.424408177	0.1983774
17227764	NM_009061	Rgs2	127.9569767	53.9997192	20.68756586	24.49862714	31.01131934	28.12111708	2.423074072	0.28543174
17476288	NM_009944	Cox7a1	143.1056676	42.38841157	27.98665191	29.75254139	32.10056978	26.27727922	2.422328213	0.26384553
17523566	NM_011606	Clec3b	166.4587617	273.6564404	50.05957022	64.1555424	98.43680996	39.83857116	2.421442158	0.25413817

17541232	---	---	4.508701503	4.295696299	19.27180773	4.033149824	4.023290748	3.557276213	2.417503892	0.3282232
17548532	NM_007743 // NM_007743	Col1a2 // Col1a2	93.60884825	105.4679614	37.0565072	28.34591628	39.46374595	29.95219858	2.415393027	0.08074302
17219185	NM_177068	Olfml2b	250.6836337	265.3671538	96.94254147	93.74390578	111.1663237	50.36826042	2.401272936	0.10523669
17272461	NM_030206	Cygb	430.3038684	857.5155364	89.39610071	154.9748181	333.3255277	88.39794951	2.388104	0.4285619
17296281	NM_027127	Gpx8	338.0823757	346.901195	107.5020231	113.2072073	132.3835451	87.00081436	2.382759134	0.13364723
17281479	---	---	9.216091242	9.679899037	17.65446259	6.270958621	4.012841018	5.125984087	2.371899146	0.04654132
17239919	NM_008481	Lama2	104.4847804	117.482495	40.53788738	37.94210985	49.00391133	23.86009695	2.369049356	0.10862441
17285771	NM_134221	Vmn1r201	3.58325819	3.711460462	16.78512063	3.110162585	3.954389553	3.137794781	2.360225492	0.34639043
17454082	ENSMUST00000031731	Pcolce	155.767452	285.1177408	116.628535	68.21461665	110.1186486	58.78735649	2.351181958	0.06122444
17434973	ENSMUST00000030568	Sema3c	148.7716684	133.3753272	32.64196493	47.20958841	60.55537011	26.14153587	2.350811751	0.24784227
17481550	NM_172907	Olfml1	93.59288798	157.5338445	50.69020172	39.92695099	49.73373926	38.9442654	2.346853064	0.09676875
17224771	ENSMUST00000027467	Serpine2	393.6686453	152.9083096	67.67358913	100.7920472	103.1466389	58.89752071	2.337008861	0.30554673
17232235	NM_010217	Ctgf	509.4359636	196.5991127	72.59397951	145.0799155	117.6882925	71.87100725	2.3267717	0.36720476
17298267	NM_018746	Itih4	354.9391738	128.4362823	81.55542828	86.12409424	99.68786562	57.92920657	2.317749163	0.22691151
17438189	NM_026878	Rasl11b	105.3454359	46.74953144	24.47225263	34.51462729	24.6410017	17.07342982	2.316271809	0.20667094
17464654	NM_013743	Pdk4	444.4354234	134.4898979	98.16548794	80.78205826	110.6272509	101.8408814	2.308918565	0.26207617
17232731	NR_002842 // NR_002842	Rnu3a // Rnu3a	166.8295452	146.3334724	32.67451689	33.20031443	58.42775695	58.82807812	2.298593548	0.27941257
17224971	NM_001003948	Pid1	162.0960359	195.1553225	39.05761634	55.83249026	79.42812269	37.17688529	2.298276064	0.26781526
17421074	NM_013868	Hspb7	634.3076801	329.3181006	113.9050579	216.5286323	173.9304841	79.30736802	2.29375844	0.29818225
17455801	ENSMUST00000031668	Col1a2	560.325368	542.9471636	176.8841539	163.2066464	248.4082021	148.5457995	2.285338483	0.14855486
17300243	---	---	11.38780666	7.914246496	13.73957049	4.239387966	4.970176206	5.259515841	2.283602249	0.01179038
17236100	---	---	6.584537004	3.924225646	16.01071687	2.894838773	4.25937278	4.459608301	2.283441611	0.22692865
17278328	NM_009252	Serpina3n	492.5099292	229.7506288	68.60353441	173.7043412	122.5088362	50.51647264	2.280924324	0.37517914
17224180	ENSMUST00000027377	Igfbp5	344.0549047	377.6704245	103.3847082	128.6198053	170.1919512	64.46365123	2.271307168	0.20790477
17468183	NM_009610	Actg2	314.0934396	112.1033826	47.42151996	93.00329983	73.12637795	42.52717154	2.269843256	0.3718519
17493310	---	---	3.828239262	3.555200685	17.87881236	3.731511158	3.225540653	4.17253167	2.269829086	0.38702753
17385838	---	---	138.9263067	86.34746988	48.35311739	44.58770381	35.79236578	40.23385302	2.268617819	0.0900125
17326069	NM_020509	Retnla	176.2592303	103.2904456	71.04282273	60.13187335	65.46981513	28.97289616	2.268112183	0.0922766
17366914	---	---	3.963104475	3.71720177	15.7470535	3.21019737	3.132878891	4.001272821	2.264749533	0.33463365
17241731	ENSMUST00000143791	Bicc1	114.4689098	185.7491759	44.95909219	50.26948486	70.56221775	32.25252039	2.25481876	0.20460765
17233226	NM_013532	Lilrb4	73.1377328	83.81357348	15.57881938	17.42043809	21.52196649	37.6320506	2.253102882	0.29136634
17245923	NM_008512	Lrp1	448.862263	413.5116026	92.65198628	154.1083262	181.598566	88.32990165	2.252224019	0.29886487
17548916	XR_140439	LOC100862127	13.09498952	9.501412477	5.754310219	4.016583865	4.342401126	4.279033578	2.243287748	0.05674013
17406221	NM_021896	Gucy1a3	302.6068845	111.3082718	55.36901685	83.91605782	73.62429453	51.69901899	2.24281009	0.3126279
17511693	ENSMUST00000034172	Ces1d	48.20396785	22.33374063	16.90464717	10.42137692	13.97922039	14.60175628	2.241976384	0.12310755
17257593	---	---	89.64020232	90.69807338	21.33390266	26.19922081	34.75288879	29.14020254	2.238505967	0.23279168
17306147	NM_013864	Ndrp2	450.1543654	269.6421082	114.3628763	153.5754712	119.7559893	100.3815279	2.23208552	0.18028061
17434490	NM_054098	Steap4	89.76741837	95.92546844	21.78087489	29.62456367	34.933493	28.47121192	2.230198784	0.2377587
17381717	NM_001001309	Itga8	901.1659544	448.4349771	156.5906216	274.18104	261.083776	140.3815959	2.229260048	0.32355547
17349552	NR_002905	Snora74a	734.1459029	596.1043124	156.6318723	216.0890264	302.7501784	148.4012054	2.228405331	0.27505246
17348248	---	---	51.54165651	20.86831195	16.25137633	15.32016574	12.12158121	12.35400573	2.227909734	0.17542547
17527694	NM_010729	Loxl1	372.6080415	305.7320525	85.3518193	113.1440572	159.5910571	70.56026138	2.224591321	0.2532236
17225169	NR_028478	Snora75	1026.90713	779.3858884	186.1482186	396.5511069	313.7833518	189.0606094	2.215312612	0.32936242
17526576	NM_011526	Tagln	1882.377153	1044.973035	385.9042173	683.8874005	543.8948669	273.6600444	2.206714424	0.27735245

17326781	---	---	18.00133503	11.30237455	32.86155854	9.919263464	8.793905321	9.478133621	2.205122248	0.11682147
17231423	NM_031185	Akap12	263.8971573	199.3103749	42.75816397	75.69273859	95.38278485	59.05723879	2.198581772	0.35733193
17370341	NM_146938	Olfr346	3.547161459	4.042682771	11.13680116	3.047624166	2.472259186	3.025865791	2.191340406	0.20998724
17545087	NM_001114385	Chrd1	53.6714887	113.1056352	18.97538168	21.39902263	43.85392296	19.65944924	2.187578221	0.32431224
17283380	NM_011812	Fbln5	818.8929175	920.9065791	706.8552502	324.3523317	475.2414956	319.1208365	2.187023042	0.00604048
17479974	ENSMUST00000032781	Nox4	268.8277017	221.5251978	62.71414628	84.72712438	102.7343622	65.52760964	2.186129971	0.243437
17400862	NM_008256	Hmgcs2	161.2837189	109.5942274	42.54975736	46.36547404	51.32813727	45.97720944	2.181568269	0.17482351
	ENSMUST00000122381									
	//									
	ENSMUST00000122381	LOC100861909								
17425926	//	// Mup19 //	20.4481724	6.518391481	4.414677346	3.564389509	5.514094529	5.324425986	2.178812558	0.3218263
	ENSMUST00000122381	Mup16 // Mup9								
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	ENSMUST00000122381									
17441808	---	---	965.2387338	1058.899533	228.1800736	288.1451647	478.1425543	268.6278363	2.176330551	0.30613047
17233074	---	---	3.697325349	3.534651551	13.04663637	3.013547907	3.216991223	3.090994313	2.175458941	0.28626043
17457785	---	---	8.239118544	12.3576713	12.29786526	4.959779558	3.965736989	6.20149049	2.174564673	0.01969024
17244862	---	---	30.92303463	19.67359904	15.45910616	10.29193253	12.06996845	8.093350075	2.16894419	0.04644912
17456084	NM_053242	Foxp2	63.4766902	62.65561934	31.75198762	25.83996122	25.27222883	21.7230986	2.167689592	0.03805726
17315305	NM_008344	Igfbp6	152.688331	315.6443244	48.90489602	56.73110265	122.2695204	60.23741688	2.16202052	0.3697987
17494801	NM_146310	Olfr493	4.449465376	4.104296622	15.90754172	4.353790536	2.507576996	4.462759311	2.160105062	0.3139961
17248424	---	---	8.235601367	10.11291499	18.80038108	4.902694955	5.728105245	6.578756887	2.158620192	0.08467008
17476728	NM_007678	Cebpa	112.7992762	53.24433017	35.29116131	25.1277049	32.88240692	35.48752364	2.15336748	0.1479085
17379887	---	---	93.40215944	125.5409308	186.6378781	52.80036509	54.00398636	82.43510871	2.143215627	0.04088873
17248426	ENSMUST00000069837	Slit3	362.3992099	358.2644291	78.079992	125.0478983	174.4986421	73.58781536	2.140632774	0.3277782
17300223	---	---	13.21049847	6.50881541	21.84801039	4.64297335	8.080407215	6.704677783	2.139551134	0.17439954
17476119	NM_026731	Ppp1r14a	682.4336615	306.2092385	169.7035577	261.7763584	145.4980492	134.1491404	2.139446025	0.23046516
17229454	NM_009062	Rgs4	109.1630652	35.68581954	14.75951081	31.21678376	17.36081775	26.28580477	2.131994836	0.43660912
17217596	NM_053106	Lmod1	459.3117881	196.3885488	104.3544997	139.5401036	115.9594029	101.1652498	2.131006283	0.25380844
17298731	ENSMUST00000022512	Gdf10	151.8299926	276.1991367	55.34963891	74.6550009	97.23622637	55.04409889	2.130028746	0.2920028
17540378	NM_172778	Maob	84.19484506	82.89889693	31.37294376	34.57753214	31.94207212	26.67290398	2.129642066	0.11689263
17364341	NM_001159487	Rbp4	262.4600443	124.2633463	106.5289695	77.12058018	77.54479274	77.02068238	2.1289687	0.07859132
17433815	NM_011985	Mmp23	131.0642128	149.9377658	40.32442342	47.60654416	62.32849619	41.210184	2.125944789	0.2113962
17412703	---	---	5.019149783	3.872287311	15.85679175	3.575668523	3.67749913	4.389279071	2.125689679	0.29796767
17249036	NM_013529	Gfpt2	277.0385632	165.5746502	50.43026845	77.95745024	105.3787382	48.84107332	2.123564892	0.33108833
17311551	NM_181277	Col14a1	269.338564	342.2057047	76.1152169	97.18629653	137.6440083	89.81876623	2.118162493	0.2797594
17547505	NM_009933 //	Col6a1 //								
	NM_009933	Col6a1	83.37864374	99.7036904	20.03117299	34.24389732	37.63627653	24.0790572	2.116664597	0.29539987
17239817	NM_134005	Enpp3	103.526694	161.852518	48.14836822	44.52877444	71.78144199	31.85950617	2.116003018	0.1770737
17343918	NM_009780	C4b	173.3475937	155.7125051	86.1004576	75.68618059	77.24882051	43.27500257	2.11589903	0.06063662
17386090	NM_009135	Scn7a	115.5860115	152.7519514	25.58382375	39.18354442	69.71363745	30.09909073	2.114601932	0.36211234
17540188	NM_016911	Srpx	38.07892907	59.84749677	11.70770991	19.14512268	17.33841362	15.36634346	2.114453038	0.27145928
17458439	NM_053110	Gpnmb	154.2508897	229.4945368	49.67393047	69.3118442	83.47382641	52.3352832	2.11299406	0.26914397
17472530	NM_008428	Kcnj8	90.90306287	134.1446772	28.99780914	45.60085596	38.24168003	36.52314258	2.110614523	0.26085567
17276139	NM_001190466	Dact1	61.72414319	111.6855709	41.87255364	30.69470714	42.9229105	28.59359277	2.106249078	0.10338751
17506532	NM_007876	Dpep1	261.0940915	254.4061965	46.93417842	99.72456361	106.2606771	61.28172489	2.104392008	0.39668643

17267766	---	---	6.305251863	7.795415925	24.90872032	5.704664334	7.377469238	5.471809485	2.102485061	0.29295772
17219139	ENSMUST00000027997	Rgs5	82.18891942	29.13345704	21.66505509	16.40217238	22.47178778	24.43259168	2.10068986	0.2654237
17541681	NM_016697	Gpc3	80.89905807	81.55118865	33.10391636	35.69049486	35.37119364	22.02939547	2.10067554	0.1106197
17248374	NM_031169	Kcnmb1	504.2886693	244.4739608	64.29613005	135.5636898	130.4215084	121.7933033	2.096709222	0.4784044
17435107	NM_028977	Lrrc17	155.5033661	148.2761756	67.56438226	62.29256181	64.45694916	50.7530986	2.092047688	0.07472383
17392817	---	---	3.455779098	2.839748177	12.41869782	2.690447211	2.766950817	3.50066498	2.089092818	0.34977034
17233147	---	---	55.97892977	32.41523215	35.17574319	17.98706635	23.38118265	17.79707198	2.088552941	0.026457
17410974	NM_010516	Cyr61	430.0006409	1613.278727	1065.68105	509.6955686	436.0174305	546.0711015	2.084055204	0.1999403
17299351	---	---	3.591941864	3.872289996	13.68951092	3.109020221	4.085441517	2.975516257	2.08001854	0.3506642
17331380	ENSMUST00000064405	Epha3	118.3223663	115.042889	43.29087333	33.70766997	62.44512318	37.25561569	2.073753304	0.14759685
17387717	NM_146843	Olfr1097	3.789782361	2.647919017	12.38928478	3.071901591	2.896324	3.115016921	2.072716449	0.31968734
17214823	---	---	19.09736913	14.61629751	11.33582118	7.479770474	5.317289441	8.969913047	2.069625754	0.02868816
17456381	NM_001081306	Ptprz1	71.06956678	20.67430605	11.03298299	16.40780106	19.79527219	13.49444745	2.06804795	0.41007695
17497058	NM_018867	Cpxm2	64.97523313	82.72457101	36.32945958	30.31916255	33.60923966	25.1847761	2.065118395	0.06522577
17487374	NM_007469	Apoc1	99.31784134	40.62058185	28.32425294	25.29606369	26.35394438	29.86904073	2.064090279	0.21184163
17285546	NM_016687	Sfrp4	50.75844615	110.0560008	19.27835436	14.51350434	57.06269579	15.76880032	2.061855863	0.36355895
17302360	---	---	6.512245104	7.401845385	21.45009304	7.683161077	3.610706114	5.895687269	2.057306582	0.28898236
17467062	ENSMUST00000003569	Inmt	128.9004062	507.7621337	68.94346963	78.62880373	195.4891869	69.56496503	2.053072455	0.50665975
17329759	NM_007470	Apod	73.95988108	64.55692696	34.82066861	30.85116363	34.68932829	18.99945328	2.050361829	0.07572376
17317046	NM_008764	Tnfrsf11b	58.29333353	65.22567211	38.57582216	21.20265463	32.80075232	25.14709772	2.047931703	0.02638047
17281684	---	---	136.7121827	52.09821362	51.8181642	46.75484604	27.56854075	43.52860861	2.041786053	0.1731768
17302136	---	---	18.30051065	17.2171805	14.52427252	5.562147487	12.29678273	6.805838891	2.028884335	0.02739624
	ENSMUST00000170094	LOC100044625								
17299158	//	//	5.487119517	5.553421887	14.95326892	3.713753346	4.981623534	4.119379382	2.028427993	0.21338929
	ENSMUST00000170094	LOC100044610								
17367102	ENSMUST00000028045	Mrc1	135.4675032	220.6096364	47.7656304	55.31627103	98.49188794	45.46920895	2.02653605	0.3040272
17328368	NM_013607	Myh11	1889.881419	888.0247032	389.7796606	611.7167626	612.779405	340.9789811	2.023466029	0.32980573
17236288	ENSMUST00000062862	Igf1	90.88302815	103.1631557	36.17086013	31.70531928	44.76111285	37.38723825	2.022043235	0.13583338
17227077	NM_054077	Prelp	1021.495406	866.8021971	269.7987773	391.7534039	449.8914066	226.2725867	2.020845794	0.26465586
17511731	NM_144930	Ces1f	63.41367138	18.40604812	16.54475474	12.48886964	15.37618826	20.87651512	2.018081653	0.34079075
17229891	NM_178405	Atp1a2	250.6012846	120.8120878	39.24067627	71.41345437	68.53295551	63.59502484	2.01754522	0.417979
17367031	NR_040353	E030013119Rik	199.7763509	93.53062999	51.67469273	60.58295316	60.430166	50.38512604	2.012749158	0.23911287
17230045	NM_008329	Ifi204	10.82266582	10.36563073	5.703814251	3.766391579	6.235472993	3.360199755	2.012571572	0.0750468
17492406	NM_175640	Plin1	121.8901723	55.70786034	42.27227934	30.04058495	37.94552894	41.39168285	2.010191452	0.15707196
17343827	NM_010381	H2-Ea-ps	31.61589159	30.2689138	43.36932247	19.50829786	18.97721	13.9039703	2.009069981	0.01179012
17269980	NM_024449	Sost	194.255145	91.75475376	55.33759347	64.68512128	51.39129138	53.85830792	2.008697758	0.20493808
17284349	---	---	62.78230099	103.8414771	38.9621396	30.46787549	44.7875238	27.43367514	2.002023281	0.1240946
17489510	---	---	3.691962758	3.165799746	12.68525838	3.42103058	3.162683088	3.184248657	2.00072648	0.35899478

Downregulated genes (9)

17514326	---	---	48.65816469	34.08157257	31.2423918	137.4229359	72.01152927	103.6509838	0.364060768	0.01367348
17283617	NM_009246	Serpina1d	66.18695525	49.64780395	59.93068672	321.3594306	61.20391352	84.26105066	0.376512984	0.25077966
17518314	---	---	5.444539384	11.54290142	7.303115261	23.94987133	16.73797392	23.80513656	0.37663875	0.00965253
17539534	---	---	12.68055513	9.656069098	5.5590255	17.19449691	23.52250824	28.25697258	0.404437306	0.02844779
17394772	---	---	4.664117067	4.434772201	5.436401467	12.33698537	16.44936515	4.769308151	0.433169585	0.13311483
17536026	---	---	34.57777182	20.2429129	21.43986624	58.65491097	49.99999342	56.04543645	0.463026066	0.00773408
17381587	---	---	19.37719716	17.30117361	15.74286269	43.85826998	33.22370358	33.18282938	0.475412208	0.00351832

17398266	NR_029735	Mir16-2	17.77844206	26.93189798	18.78312236	50.69002604	46.3964012	34.44362306	0.482729705	0.01167125
17485039	NM_010844	Muc5ac	28.17951741	61.57855037	53.05747079	44.5579823	75.44314951	171.1093754	0.490588746	0.25808087

Supplementary Table 4. The list of endothelial genes in response to 48 h post partial carotid ligation and their fold-change expression in APPsw-Tg mice LCA compared to non-Tg mice LCA.

Probe Set ID	Gene Accession	Gene Symbol	APPsw-Tg LCA-1	APPsw-Tg LCA-2	APPsw-Tg LCA-3	Non-Tg LCA-1	Non-Tg LCA-2	Non-Tg LCA-3	APPsw-Tg LCA/Non-Tg LCA (Fold-changes)	P-value
Upregulated genes (288)										
17467384	---	---	8.097485614	192.7255453	7.225297543	6.009637623	5.863162329	6.192401434	11.51652418	0.33466968
17343827	NM_010381	H2-Ea-ps	79.83375693	25.29902709	463.5701944	20.82419758	14.1856957	17.14196986	10.90474902	0.14219509
17329759	NM_007470	Apod	28.12246207	112.9376729	720.4432589	64.89812985	27.197799	23.00629881	7.484680457	0.24855044
17493145	NM_016770	Folh1	19.24021479	47.54949125	297.5530303	20.49506982	14.86530336	18.57396608	6.755301748	0.2183607
17386090	NM_009135	Scn7a	40.26278325	146.9575836	636.2760464	53.46893366	33.5544685	35.22217269	6.736410822	0.17185941
17315686	NM_001243837	C7	53.48075769	167.2806775	605.5121086	55.63978731	27.85273317	40.13408218	6.683622506	0.12189714
17507221	ENSMUST00000145007	Cd209f	18.86218627	63.36872135	264.8656601	21.72392677	16.56962446	13.64253651	6.683148131	0.1699686
17287175	NM_008760	Ogn	235.5713042	608.1633217	2376.413213	236.6635968	148.145706	105.7099231	6.564773957	0.10526308
17218927	NM_019759	Dpt	223.2562881	771.3741556	2280.935602	273.5995411	147.0024103	113.8996102	6.128262817	0.11052938
17439367	NM_018866	Cxcl13	79.73620292	286.8814749	1388.777727	128.3102843	114.4461404	80.23812564	5.43475239	0.25847757
17326069	NM_020509	Retnla	69.15084617	20.87417103	318.3462589	22.30533638	15.36843122	37.46714128	5.43473964	0.23134586
17435725	NM_031168	Il6	15.52021889	26.80412249	231.2258687	14.05131259	25.41000933	15.78596992	4.951377723	0.34069932
17358598	NM_133775	Il33	128.3474658	608.0802827	1441.704723	200.2166301	170.9588147	99.26670499	4.629968792	0.18724021
17402181	NM_010171	F3	42.67150236	146.2178872	435.1569416	46.87334995	50.98471878	38.04426275	4.591873622	0.17351323
17434280	NM_011888	Ccl19	104.5833226	370.4458856	1112.184176	159.2873624	117.949705	82.03865873	4.417814142	0.19392225
17545087	NM_001114385	Chrd1	24.43572493	64.5206917	212.090619	28.69029704	22.00307113	17.71146937	4.400961196	0.17283046
17413033	NM_011888	Ccl19	102.3142299	354.1036734	1140.285998	170.7816311	117.6936766	92.30199978	4.193274834	0.22717296
17413131	NM_011888	Ccl19	102.3142299	354.1036734	1140.285998	170.7816311	117.6936766	92.30199978	4.193274834	0.22193672
17434224	NM_011888	Ccl19	102.3142299	354.1036734	1140.285998	170.7816311	117.6936766	92.30199978	4.193274834	0.2300795
17543365	NM_177789	Vsig4	7.389506404	48.73134038	98.57890153	17.18220161	11.8406305	8.167406308	4.159686921	0.22129308
17507184	ENSMUST00000011445	Cd209d	14.86914719	26.25273819	94.41754068	10.55519993	8.203195435	13.96389975	4.142112452	0.15286674
17514515	NM_010809	Mmp3	125.4888176	544.8914337	1284.988738	157.6561895	232.4500619	83.00895054	4.132965885	0.20312823
17412973	NM_011888	Ccl19	99.80042125	364.6544021	1154.490031	173.1936229	121.0245567	99.92300785	4.107525185	0.23772117
17413084	NM_011888	Ccl19	99.80042125	364.6544021	1154.490031	173.1936229	121.0245567	99.92300785	4.107525185	0.23719487
17424373	NM_011888	Ccl19	122.1490641	357.1142765	1101.504749	154.6394927	140.71019	90.04847882	4.101649274	0.18020073
17271350	NM_153145	Abca8a	28.32413514	55.13933642	221.3525219	29.24443071	22.67609008	26.08753996	3.90749354	0.20355292
17434141	NM_011888	Ccl19	118.4867561	374.9433953	1073.450537	169.2385007	129.9615459	103.128409	3.894531113	0.19366674
17424421	NM_011888	Ccl19	119.8498256	379.5107653	1115.898428	178.7425127	131.9874548	105.2713467	3.882821914	0.20290111
17434190	NM_011888	Ccl19	119.8498256	379.5107653	1115.898428	178.7425127	131.9874548	105.2713467	3.882821914	0.20360921
17462843	NM_001170395	Cd163	44.42977715	122.3418341	413.8746284	56.60391754	53.12452015	42.72062948	3.808788407	0.22149867
17272461	NM_030206	Cygb	213.7036887	660.6205325	1698.740774	275.2179964	243.9427844	160.0729807	3.788187721	0.16900715
17424346	NM_011888	Ccl19	115.0151422	363.5605876	1034.766831	168.075077	124.4610058	107.6385462	3.781705415	0.20115711
17357700	ENSMUST00000025581	Ms4a4d	28.36429302	137.0394067	379.8220892	70.27029256	36.99988804	37.49319849	3.766323999	0.2894723
17333465	NM_022315	Smoc2	74.91480741	173.4646646	515.8890448	92.56449376	73.20092632	38.90244701	3.734189092	0.15868533
17467062	ENSMUST00000003569	Inmt	40.66340159	170.485	374.6277607	64.0327471	47.29887616	46.47496907	3.711987906	0.20878987
17275062	ENSMUST00000041183	Meox2	32.37818027	116.3656144	273.0412284	41.75479567	39.9553282	32.48255025	3.693625938	0.18789591
17438246	NM_001083316	Pdgfra	198.5151083	674.0940122	1322.507327	266.0458336	222.5011527	110.8019914	3.662501363	0.14941572
17466599	NM_177736 // NM_177736	Lrrc61 // Lrrc61	103.077597	280.2201713	727.217446	128.9469644	109.8091147	66.79411073	3.634477252	0.16037545

17381717	NM_001001309	Itga8	273.0603441	167.0914381	686.1327882	153.8238077	81.51089487	78.56566205	3.588032055	0.0714355
17434087	NM_011888	Ccl19	124.4418554	328.825871	937.1940599	169.9140097	126.7433286	95.34041499	3.547116723	0.1863748
17434490	NM_054098	Steap4	93.27289556	504.4106757	982.8953438	194.0289345	157.3727564	95.34907251	3.5379434	0.26654905
17278328	NM_009252	Serpina3n	526.5267433	2016.293579	3959.355792	945.9748383	551.7940156	347.8653084	3.523003771	0.1881977
17542220	NM_008067	Gabra3	52.39695252	93.73721326	372.5858307	63.82209227	47.39411423	38.04405179	3.475272001	0.20820403
17434973	ENSMUST00000030568	Sema3c	38.11769563	64.75375722	182.2137475	39.09149894	21.80696363	21.81493092	3.446663089	0.11406849
17287160	NM_025711	Aspn	49.75180629	114.7885554	210.3545188	45.78623398	43.0513329	19.94158254	3.446385474	0.08517027
17437969	NM_001033415	Shisa3	91.22915189	412.1018129	659.9390603	128.9845985	125.6808471	83.40245814	3.440936013	0.18451102
17498897	NM_033622	Tnfsf13b	48.36551983	276.5627416	637.9457791	103.8012495	114.2982892	61.82121057	3.439809456	0.3323621
17540188	NM_016911	Srpx	27.17612775	62.66586956	236.5240376	33.79076248	30.64203059	30.8196164	3.426328392	0.25621876
17284607	BC018322 // BC018322	Igh-VJ558 // Igh-VJ558	22.47108686	213.6179397	26.88001429	25.49964045	26.40883949	24.99152442	3.419623224	0.39531428
17284631	BC018322 // BC018322	Igh-VJ558 // Igh-VJ558	22.47108686	213.6179397	26.88001429	25.49964045	26.40883949	24.99152442	3.419623224	0.39272007
17254065	NM_021443	Ccl8	30.70911434	141.2959203	357.8335875	69.95207753	60.06930221	25.94286667	3.397180022	0.29211023
17254059	NM_011331	Ccl12	13.03868075	27.42823722	118.6920914	20.59870877	16.38837608	11.17647239	3.304552623	0.2943091
17481770	NM_009627	Adm	49.11980744	138.891163	318.6166832	63.60062334	48.20192974	42.02567248	3.293463549	0.1662805
17540378	NM_172778	Maob	34.95081034	53.92068802	206.1520504	34.90812589	22.22231174	33.31312985	3.261962757	0.19656117
17229481	NM_022563	Ddr2	146.2709031	290.8118002	625.0275621	131.8891432	108.6947915	85.7082396	3.255089607	0.08310845
17397575	NM_015784	Postn	253.2218347	212.6140314	633.0589331	125.169478	126.1839843	86.71117324	3.250546445	0.04293348
17400365	NM_007802	Ctsk	46.57493982	94.78395791	262.8727889	49.04927816	47.5515677	30.90957688	3.170185448	0.16054334
17311551	NM_181277	Col14a1	108.1044424	349.0243789	596.0543187	121.2546278	116.6276458	95.41029237	3.159935887	0.13782026
17527661	NM_001195431	Isir	75.93294195	132.6197656	331.0818239	80.38196831	53.63902097	37.27444587	3.150314724	0.11139687
17344064	NM_008198	Cfb	138.0858806	668.6910511	1187.877212	284.7948011	259.8477938	88.55875285	3.150110388	0.27277255
17450387	NM_010097	Sparcl1	102.4132095	108.1803005	309.7992841	58.54544402	62.69941164	45.60910642	3.118851885	0.06264339
17515402	ENSMUST00000001384	Cnn1	425.4645145	253.5152985	1036.166406	236.9621787	184.4881062	128.7608325	3.117251114	0.09063178
17391623	NM_019696	Cpxm1	86.40836032	467.9524076	705.4729714	205.3884153	122.7611282	76.61563878	3.112505211	0.26230663
17472530	NM_008428	Kcnj8	48.58264055	137.5025916	353.2782205	71.18113342	63.06121231	39.48237855	3.104701734	0.2222146
17458439	NM_053110	Gpymb	65.15536173	94.7524932	392.6086096	72.29209526	60.53896058	45.9436955	3.090573251	0.22589771
17506532	NM_007876	Dpep1	95.42986986	188.3662909	538.0904903	108.511941	87.30776105	70.20977502	3.089457078	0.16299973
17481550	NM_172907	Olfml1	33.39805079	88.57858218	256.4127161	41.33606063	38.95846689	42.26639026	3.087357339	0.24295294
17328368	NM_013607	Myh11	562.8610473	350.7197829	1139.377416	315.8903379	175.2692384	175.6574554	3.078742966	0.05702698
17211305	NM_053191	Pi15	65.12727686	78.9705044	293.6821966	53.47404844	53.05327842	37.1851323	3.046221465	0.15546656
17442834	NM_001081342	Gpr133	84.6874333	186.3146102	387.3572683	85.32602884	70.36445879	61.65346188	3.029112672	0.11086235
17423030	ENSMUST00000070375	Penk	28.75914738	65.41383988	153.261126	28.0767881	23.77509169	30.33080745	3.010781487	0.15682498
17498750	NM_027343	Cd209g	12.94406632	27.19964657	95.82545247	13.98393036	14.47076212	16.86006274	3.000549483	0.27310959
17305910	BC023359	3632451O06Rik	24.76715069	43.07386868	113.2977185	23.33765987	17.45522441	19.7153853	2.993619537	0.14805803
17331380	ENSMUST00000064405	Epha3	73.97921055	134.2758459	373.946741	75.16973434	73.52780438	46.05691902	2.989414487	0.15297534
17230111	NM_172648	Ifi205	84.37659711	211.6817377	872.123115	190.2847323	120.3260331	82.57956993	2.97103297	0.3781894
17425631	ENSMUST00000042850	Svep1	56.18335996	187.0711145	291.1778897	68.8253435	66.70943883	44.90876054	2.961770511	0.15088663
17497058	NM_018867	Cpxm2	29.60116395	35.52476006	171.0630076	30.78176389	25.41571654	23.67298949	2.957149642	0.267485
17249036	NM_013529	Gfpt2	122.0805029	197.3025785	567.2343145	135.8019137	79.88584561	84.60517468	2.952508353	0.14396095
17472536	NM_021041	Abcc9	219.5523247	614.8173211	1106.049318	288.8348472	219.3256904	149.0539709	2.952489542	0.14531764
17230127	NM_011825	Grem2	64.27821674	219.0687668	383.6332617	88.68898312	85.06141799	52.43124869	2.948869839	0.18857259
17278321	NM_009253	Serpina3m	29.31751666	51.58837149	169.1429224	31.70637417	28.14724859	24.95524219	2.948380581	0.20421576
17548258	XR_140589	LOC100862291	4.938414731	16.22449872	27.17435712	5.065079804	5.016429934	6.313653123	2.948264131	0.16040441

17367102	ENSMUST00000028045	Mrc1	122.5257358	446.3476438	1019.405976	160.6348376	273.4653055	111.0450289	2.913497976	0.28753144
17510772	NM_020259	Hhip	21.33832459	34.89769877	90.41962317	18.0293565	15.06571252	17.33026728	2.908372205	0.14323248
17277387	NM_010234	Fos	99.15083383	530.1548501	88.5176963	64.40407192	80.63582284	102.0201276	2.905461488	0.29600152
17236811	NM_008524	Lum	137.9447748	553.3076269	1737.358781	247.5546091	369.3377711	221.316162	2.897383003	0.44048524
17398557	NM_009144	Sfrp2	115.1445247	210.3064081	352.0327889	91.7842687	76.15141821	66.15461965	2.894112668	0.04639772
17254053	NM_011330	Ccl11	117.921012	380.4046312	860.7592683	239.2513077	128.4692258	104.7270272	2.876689446	0.25418818
17313811	ENSMUST00000057410	Fbln1	114.0459971	349.6309281	654.7484822	164.2757821	149.9934821	76.59323137	2.861429327	0.19418496
17335506	ENSMUST00000114701	Pi16	215.5398775	356.1178646	707.9737209	187.6025984	168.795192	95.16611028	2.833777149	0.07638954
17239817	NM_134005	Enpp3	60.74277864	139.1724655	431.7334307	74.71080491	87.84589706	60.53682053	2.831317861	0.26979426
17262209	ENSMUST00000109212	Gm5431	12.30061889	24.20571828	62.25552617	12.11462632	14.75043913	8.269373312	2.810970285	0.18833248
17255058	NM_026433	Tmem100	30.76365471	55.63338563	134.6077813	36.35245772	16.57132435	25.79459697	2.807537761	0.15136082
17462889	NM_144938 // NM_144938	C1s // C1s	11.79237988	22.11684971	78.6387781	16.00194093	14.36608449	9.873270134	2.796828635	0.28333127
17230045	NM_008329	Ifi204	12.31175054	61.27131884	235.208926	61.77464886	36.92671446	12.24755614	2.78319065	0.49954075
17434933	NM_010427	Hgf	20.09730295	54.22529156	127.5508763	24.80881636	28.45095156	19.43589987	2.776967004	0.22757855
17493949	NM_008035	Folr2	70.8965245	312.4518344	673.3986413	153.4911857	150.0469309	77.51802988	2.773205497	0.35715166
17541681	NM_016697	Gpc3	27.71878277	40.18867199	153.5315135	29.28849182	22.75188227	27.94024953	2.768657685	0.2559814
17438969	NM_019932	Pf4	45.07332579	134.3226698	456.7797867	84.8470738	95.36057303	49.59260142	2.768385966	0.4013413
17296281	NM_027127	Gpx8	155.1352797	224.6065204	857.9430054	153.4884195	163.3374727	132.2094967	2.75631907	0.23719938
17263174	ENSMUST00000108821	2210407C18Rik	54.87579384	100.5143728	205.0984815	33.00388605	73.12288061	24.77142572	2.753962003	0.12512305
17489420	NM_052992	Fxyd1	148.8210714	199.809449	522.5010043	107.2220639	114.3750053	96.96868403	2.734542292	0.09300153
17227892	NM_021400	Prg4	418.9661857	1378.353288	1946.774409	534.7871536	579.0154362	261.7529525	2.721877647	0.17713594
17504019	---	---	14.98184089	38.24456942	70.43023542	19.67561738	8.930426021	16.85240982	2.720212347	0.16891193
17224771	ENSMUST00000027467	Serpine2	130.8178864	102.474348	321.015022	77.7683918	78.44523983	48.14850172	2.712377519	0.08463719
17344086	NM_013484	C2	23.5017454	58.09028489	145.3788915	34.69699943	32.03151211	17.11974135	2.706924879	0.24776384
17285546	NM_016687	Sfrp4	128.191074	594.4270671	714.7981053	231.5845182	207.850153	94.81845629	2.690515361	0.24914435
17315305	NM_008344	Igfbp6	84.49458609	152.506191	333.5876342	77.74510835	83.28287688	51.22875764	2.688199223	0.11940084
17241731	ENSMUST00000143791	Bicc1	91.89509799	255.1942478	491.0836567	117.6432716	108.688915	86.01980764	2.683424527	0.19058181
17248374	NM_031169	Kcnmb1	127.7828135	122.7011534	392.3104623	86.03459576	80.09620592	73.60332317	2.681280479	0.10569649
17213021	NM_023617	Aox3	23.77888231	80.67467748	163.0837245	31.9299414	34.65359208	33.55684092	2.671622569	0.25693077
17282970	NM_010050	Dio2	38.92467261	53.91848294	227.0164451	33.9669553	44.30869711	41.57986013	2.668709965	0.28844655
17358098	NR_015502	E030003E18Rik	14.12193621	25.68524625	57.40311014	13.38616688	10.85893717	12.19151913	2.667928147	0.14395833
17448064	NM_144945	Lgi2	55.30476953	186.9668906	328.9767918	83.47764524	76.95253777	54.01780079	2.663808919	0.22779058
17285944	NM_001111110	Cmah	49.80905035	128.2787153	291.7619628	68.30579143	59.34390671	48.86159319	2.661867832	0.2135462
17378663	ENSMUST00000088552	MyI9	550.7489388	492.8445971	1424.361865	393.2816327	286.1877282	248.1309694	2.660580554	0.07377155
17300021	---	---	19.1475115	32.24331114	80.5623577	18.8064156	16.05982203	14.91777017	2.650513412	0.16477741
17479974	ENSMUST00000032781	Nox4	91.08199585	151.1597262	374.4366907	98.99933986	78.02345611	57.20887225	2.632771296	0.14566706
17346528	NM_009778	C3	646.0620846	2787.43027	3073.059532	1187.926615	784.5861184	506.7660267	2.624372859	0.2140818
17533713	NM_001044384	Timp1	353.7722312	409.9573454	1532.434823	281.4545186	416.5012456	178.3012491	2.62042342	0.20778197
17347983	---	---	10.10314813	66.06091284	40.4906248	7.934107803	20.28357435	16.32516875	2.618931734	0.2511582
17463509	NM_177686	Clec12a	16.37055128	49.79790002	177.1316246	27.80314153	49.94609565	15.88989845	2.598273406	0.42712584
17461205	NM_007697	Chl1	31.9909959	161.6114943	320.895556	74.62370059	87.12682104	38.36689212	2.570980888	0.39481318
17462661	---	---	9.978645516	41.87496269	41.68114487	8.713171864	14.84543024	12.85012956	2.569019815	0.16754499
17450121	ENSMUST00000097437	Plac8	67.72605232	253.2320151	430.1845794	149.6993348	93.89516727	49.81913267	2.560012753	0.278661
17545629	NM_011077	Phex	14.62248901	22.36301808	57.30610751	11.26822991	13.1300272	12.45985177	2.55823257	0.16129191
17395079	NM_021394	Zbp1	49.56868221	132.0040149	391.2999186	122.9470237	54.86875745	46.99537899	2.548239222	0.3490701

17248426	ENSMUST0000069837	Slit3	155.4635979	426.7386583	648.810789	212.348337	162.4507957	108.4570481	2.547330162	0.15516265
17524264	ENSMUST00000172171	Naalad2	29.79550924	44.0736966	116.4013516	30.19808166	25.80296591	18.7318437	2.546008246	0.16779211
17435107	NM_028977	Lrrc17	66.15764615	86.93781911	200.9653547	43.24915378	44.74591268	51.70228008	2.534484933	0.08649508
17290865	NM_134065	Epdr1	94.77876781	202.6263518	351.9534944	89.14364207	88.56421621	78.58396192	2.533668899	0.11006085
17411201	NM_199465	Nexn	65.83039732	60.73536884	167.3317034	39.27591552	42.89914532	33.9505255	2.530858864	0.08011559
17468183	NM_009610	Actg2	76.8544025	52.75584359	177.7485524	48.81102018	34.10825399	38.52937824	2.530771584	0.10897409
17523566	NM_011606	Clec3b	55.47692814	106.8773995	186.5571702	54.14510457	37.55182191	46.34288646	2.527614971	0.08902392
17247389	NM_207655	Egfr	58.09890226	143.6282771	299.8645154	79.07950854	69.83043235	50.09810055	2.52045943	0.20438802
17510685	NM_010332	Ednra	54.44848492	113.9789818	298.9884617	67.19504748	74.50291663	44.32147533	2.51272625	0.24541013
17343918	NM_009780	C4b	106.0353133	334.7343974	537.1465712	174.8194628	128.1410583	86.54616573	2.510653386	0.21202412
17431619	NM_007572	C1qa	82.91257381	229.1531012	574.1166159	130.6286012	146.4521944	77.79583426	2.497155959	0.31852028
17387517	NM_009776	Serping1	638.2009739	1794.778386	3760.894184	1007.067032	883.4838791	596.7695028	2.490179194	0.2612885
17219185	NM_177068	Olfml2b	149.6940429	235.2017526	575.2478994	158.8682479	135.8831728	90.99333684	2.489064792	0.14756458
17406221	NM_021896	Gucy1a3	80.68172363	54.1481071	193.8823951	47.70369127	41.6585581	43.09689422	2.481612194	0.12944917
17245231	NM_013590	Lyz1	22.59934415	26.12976057	112.4186823	22.11349265	21.19853999	21.66259243	2.48016494	0.3028558
17291881	NM_028784	F13a1	130.0472426	413.2436956	916.9701751	162.8427861	325.9633607	104.2240925	2.462372096	0.3240682
17378827	NM_008489	Lbp	91.36660225	420.5099129	818.6721457	245.7400171	215.7071219	79.15771157	2.461222202	0.4011417
17507194	NM_026972	Cd209b	20.780695	30.73681983	59.82920551	17.35512679	13.38228899	14.50582053	2.461068867	0.0851073
17434742	NM_028882	Sema3d	54.56749836	101.6962027	161.1531971	50.97796931	46.32021357	31.73808111	2.459904591	0.0780088
17421074	NM_013868	Hspb7	181.9082293	174.1976076	367.298196	126.332936	98.63248657	69.40318662	2.457476818	0.0445176
17229454	NM_009062	Rgs4	29.73771722	29.04999479	86.35004353	22.03645116	20.8114272	16.25109472	2.455842259	0.13209073
17370735	ENSMUST0000065927	Tnfaip6	38.38192061	39.32399527	105.0228907	22.59115301	35.47321045	16.55194671	2.448912391	0.1388195
17228792	---	---	38.55400953	105.551407	128.3626795	32.90493347	41.37452947	37.11660885	2.445939894	0.10728764
17411319	BC057661	Rabggtb	15.02561358	34.55946551	89.83769454	16.89231324	23.33303386	16.81849842	2.444133497	0.27202466
17250585	ENSMUST0000064783	Mfap4	84.43949234	66.56219018	160.016515	48.69443502	38.83094736	39.9109579	2.440576972	0.04542931
17408897	NM_009892	Chi3l3	101.7525401	142.0479302	1089.12966	152.3496104	286.6481186	107.5492013	2.438820998	0.61607575
17212199	NM_133193	Il1rl2	23.86077504	30.03517157	79.69117147	20.74809535	17.60227504	16.88754841	2.418395207	0.15079987
17427970	NM_172874	Podn	51.0185503	125.7245867	218.1489924	62.79109212	55.09318637	45.73028483	2.413551223	0.16930106
17406205	NM_017469	Gucy1b3	85.50056213	56.10937742	223.3733094	55.07936416	46.82012886	49.79486259	2.406043702	0.17957643
17437148	ENSMUST0000076939	C1qtnf7	30.60178707	76.13036025	176.8712806	36.78906231	46.72678915	34.59062078	2.401252214	0.27425697
17385564	NM_025422	Cd302	83.1836451	213.7346497	427.0756992	108.7718178	111.5265973	81.57555542	2.398331969	0.23426984
17516462	NM_009382	Thy1	65.46763691	131.9306538	330.4467508	79.53908165	82.15047432	59.01108175	2.391678823	0.24041459
17398115	NM_008987	Ptx3	43.64250479	51.7248625	196.0387442	43.16044995	42.32857454	37.64754801	2.366527715	0.2677306
17331720	NM_011782	Adamts5	71.70739485	219.0514569	309.1634585	92.06194387	101.9085298	60.13316546	2.360935532	0.19722429
17283617	NM_009246	Serpina1d	6.006568387	29.88013995	4.718417244	6.490996598	4.366160001	6.370563545	2.356964545	0.395108
17285586	NM_012054	Aoah	15.00597339	39.04224208	76.76586318	16.88097117	22.30556829	16.50632447	2.348848119	0.22946814
17375685	NM_008008	Fgf7	37.24996074	87.82854508	221.4825151	49.16552012	62.07695986	36.56990566	2.344600687	0.29870528
17212185	NM_008362	Il1r1	192.9081118	380.9328778	824.288753	206.2992834	218.8075941	175.0912284	2.329447109	0.18477385
17349549	NR_035472	Mir1949	31.55115688	23.51339576	34.27574217	11.83705266	19.29630887	7.227321137	2.328954768	0.02681502
17217596	NM_053106	Lmod1	104.84671259	115.9465433	237.374146	76.04413092	50.92234668	69.9322976	2.326918564	0.05457296
17274021	NM_011859	Osr1	255.1491455	647.1188984	1023.569253	348.4824037	249.5617464	230.9908669	2.322986674	0.17197353
17506206	ENSMUST00000108972	Crispld2	80.20070425	117.4134604	242.3943061	79.10818132	61.09362752	49.86086479	2.315070405	0.10092057
17462738	NM_153197	Clec4a3	40.19781001	91.61176631	272.6786622	52.83554789	95.89980656	26.94267144	2.302440709	0.37030602
17509315	NM_011857	Odz3	24.95285523	61.39124404	100.7914184	27.00369642	29.09289582	25.3022013	2.298996208	0.16903315
17519112	NM_009022	Aldh1a2	38.78148117	153.2027092	328.0438809	81.39904707	79.19151745	65.81210217	2.296916723	0.4223092
17357688	ENSMUST00000163078	Ms4a6b	32.24831778	60.42400893	244.088582	59.26005253	60.24877487	27.16330274	2.296011576	0.44442207

17456084	NM_053242	Foxp2	27.68153422	37.69671753	104.463635	25.03639608	25.55482842	23.52658473	2.291512505	0.19643848
17277788	NM_201518	Flrt2	40.00143914	60.13983481	152.3495048	42.26466179	33.44809173	34.83225574	2.284054073	0.18581225
17352981	---	---	38.60034936	191.2725456	172.7714469	24.17681006	82.74211901	70.09929355	2.274592615	0.29338408
17433815	NM_011985	Mmp23	61.16854269	111.3464691	188.3943646	62.82531088	52.29738845	43.7681955	2.271428937	0.1044419
17372552	ENSMUST00000051454	Fam171b	21.81352471	32.83084552	58.25459718	16.46177502	18.75842765	14.62623964	2.264935313	0.08750695
17404195	NM_001076679	Gm9733	27.17463966	36.15296334	138.084062	20.69942805	49.25178135	19.13611421	2.260834167	0.34782347
17239919	NM_008481	Lama2	36.44439384	68.91002616	155.1315161	43.36027496	37.93929591	34.01233152	2.258968335	0.20750256
17326318	NM_001014423	Abi3bp	239.9889217	532.5539966	963.2323264	314.2521925	231.9792572	222.6858379	2.257427779	0.17968284
17494386	XM_485980	Trim30c	10.0680613	13.26894718	51.92009075	12.32933429	11.90791563	9.129317439	2.255464232	0.35682783
17438189	NM_026878	Rasl11b	43.95416581	31.72547809	75.43677001	22.83618896	25.79465061	18.52090897	2.250371989	0.0625633
17271443	NM_147218	Abca6	19.33376894	33.9895416	94.35937777	24.19593861	20.12897773	21.36049241	2.248333247	0.27131203
17229988	NM_053199	Cadm3	30.37492623	63.94962526	89.09484159	28.95553002	27.57800136	25.07349148	2.247593242	0.09443491
17220526	NR_034044	Snora36b	28.88636972	107.6472012	65.81429184	21.46896892	46.52328295	22.05059989	2.247239607	0.18588749
17251959	NM_145137	Mgl2	19.6777996	13.74561927	86.25445093	16.86121975	17.3965823	19.09490715	2.243145129	0.41943714
17461240	ENSMUST00000089215	Cntn6	10.89900101	15.22953513	47.60426733	13.69989566	8.971660327	10.24762725	2.239812663	0.27777106
17487211	NM_008036	Fosb	345.5230149	131.310912	40.35283139	71.70888598	56.9472788	102.9437905	2.233103878	0.45828515
17432440	NM_010329	Pdpn	149.7731289	227.1732256	560.7741357	166.6730456	136.7992964	118.2598875	2.223497339	0.18646342
17454082	ENSMUST00000031731	Pcolce	124.7305453	276.4726579	502.9060155	148.0683004	153.1135339	106.1152358	2.219778351	0.19142452
17343628	ENSMUST00000002360	Angptl4	92.84015331	172.187428	378.5985302	84.54309364	121.6653044	84.57556472	2.213416811	0.20259513
17362953	ENSMUST00000067532	Ms4a7	27.91792864	96.56597231	289.1002407	60.17402684	92.11058182	35.03864307	2.207863348	0.5167644
17453819	NM_008871	Serpine1	1495.445895	128.958316	279.3062409	165.6920991	499.4671553	197.2168488	2.207517631	0.6371882
17347163	NM_011723	Xdh	56.60034729	180.2283306	371.3559799	100.85816	111.5480899	63.41753954	2.204975354	0.369443
17469406	BC147267	Gm765	13.06632025	21.85653806	63.66550484	16.15879823	14.70615306	14.06158191	2.19443514	0.29033723
17214711	NM_021342	Kcne4	35.25074883	49.74973721	129.0531012	34.77050222	27.25035274	35.75831871	2.189153162	0.20569594
17498722	ENSMUST00000012849 // ENSMUST00000012849	Retn // Retn	192.26562	185.8889239	668.7072738	92.52369647	64.65737356	321.5543954	2.186722926	0.2596687
17414057	---	---	22.6298168	74.14595068	63.31217267	27.10387085	31.60057709	14.59511831	2.184023022	0.1675963
17271757	NM_001101657	Gm11711	92.56372383	192.0992399	421.5760212	122.4651119	113.7137577	87.28936578	2.183333346	0.253348
17476877	---	---	54.81318265	191.2176653	151.6553938	43.54082987	89.16836136	49.65695872	2.180702076	0.18533997
17284593	---	---	6.319669011	10.40552607	18.04618531	5.186355142	6.374812901	4.386113058	2.180395527	0.12856424
17470031	NM_009662	Alox5	16.64445815	36.88358541	95.63024057	24.03718423	26.51559101	17.9191587	2.178385735	0.3273719
17430885	---	---	14.79102369	42.19446921	29.5757121	12.70676607	14.64380944	12.43284017	2.17581129	0.10313252
17526803	---	---	117.2227681	416.4308096	370.8392145	132.670334	167.7450053	115.5439572	2.174474281	0.18967783
17251514	NR_028566 // NR_028566	Snord118 // Snord118	55.17749285	88.09742829	135.9282017	48.6644721	52.12046319	27.73521492	2.172446285	0.08552461
17458520	NM_001164734	Mpp6	75.10072864	186.6946791	375.5884791	109.2893492	110.2264007	74.57462951	2.167306146	0.28610894
17527694	NM_010729	Loxl1	192.265087	343.2952297	448.8728414	167.785124	162.6293684	123.9249615	2.166734915	0.05498497
17526576	NM_011526	Tagln	999.3588472	572.6790433	1548.708598	544.0777423	504.5561431	392.9287715	2.164835829	0.08122461
17240190	NM_172508	Dse	47.15448202	110.1970658	265.0987395	58.26255239	89.78801623	47.49922271	2.160320829	0.33776662
17283549	NM_029803	Ifi2712a	49.48989239	228.2534728	387.4955682	141.9681999	78.5611422	87.63686675	2.158701747	0.447728
17488032	NM_009465	Axl	236.1012714	351.3867545	735.2886983	250.6911055	192.1823453	170.1447705	2.157809798	0.13056876
17367031	NR_040353	E030013l19Rik	52.67140359	67.25604321	155.9275454	46.91102114	48.17888164	32.80261671	2.156928281	0.13874577
17358832	NM_008331	Ifit1	76.9899378	135.6109627	442.1138133	124.8614228	76.43926494	102.410725	2.155713241	0.38148415
17219670	NM_001162938 // NM_001162938	Pydc3 // Pydc3	5.560620963	5.961651325	25.8379911	5.281720652	6.190847836	5.877908903	2.153270054	0.36566272

17230023	NM_001177349	Pydc4	4.477104523	7.084475269	31.16372967	8.773156474	7.052550054	4.038568472	2.150861759	0.4702011
17527735	NM_008684	Neo1	44.73065565	48.61120528	129.8931913	41.96937285	36.72633427	25.12234097	2.150252835	0.16502498
17239102	NM_177387	Ust	27.77553894	37.13863793	91.52278194	21.11754178	23.63154442	28.06056203	2.148574579	0.18307403
17479769	NM_001190374	Adamtsl3	39.24266189	60.96426793	163.7720101	41.47494032	36.37930307	45.10489172	2.146883513	0.25830105
17462149	NM_001012477	Cxcl12	788.1208181	1456.792818	1997.804921	769.7883354	745.7689905	461.3369382	2.146153507	0.08725809
17273304	ENSMUST00000026148	Cbr2	315.5640394	472.1933782	910.6589231	312.8263004	276.6797025	203.1858324	2.142593458	0.11094853
17298731	ENSMUST00000022512	Gdf10	90.75586666	231.7283908	370.5493798	118.9660407	122.776701	81.85859501	2.141627856	0.2197294
17254047	NM_013654	Ccl7	199.6804112	553.1542387	963.2984272	356.9744479	291.0927303	155.3611527	2.136012649	0.30009657
17228234	NM_028749	Npl	31.39606834	99.01217284	233.7503962	71.67022606	53.66765701	45.49862369	2.131620719	0.4360883
17501544	NM_010934	Npy1r	35.00689015	33.61573992	109.0586204	32.61647574	28.87872213	21.87117766	2.131329919	0.22704498
17357671	NM_028595	Ms4a6c	43.82049876	117.0241925	468.3982904	93.22060688	159.4406846	42.59508311	2.131174924	0.5729067
17476119	NM_026731	Ppp1r14a	178.547361	148.9156945	370.1442995	122.0215372	109.9180115	96.12334842	2.126443926	0.08200003
17424656	NM_009416	Tpm2	65.30741955	79.26005152	177.1606027	62.74084263	54.05739179	34.50647026	2.126358691	0.13361587
17280817	NM_001146196	Scin	24.01493502	30.01787614	95.44673882	23.98111777	23.14633709	23.26128675	2.123628673	0.2736839
17449084	NM_001159518	Igfbp7	879.2130562	1194.441101	2281.030465	804.3033953	708.1862389	539.700046	2.121969848	0.08749697
17547624	XR_106231	Gm19984	7.605626013	22.78677737	29.81222194	7.742776508	14.06649513	6.583980213	2.120385	0.2126343
17309268	NM_007904	Ednrb	66.37485964	173.25678	419.1488904	95.74305927	149.9214499	65.11432217	2.119772854	0.38408408
17337796	ENSMUST00000024706	Pla2g7	46.46904208	83.81688497	315.8660344	45.28712345	116.3754551	49.01875713	2.117662488	0.45909438
17357255	NM_001013019	Lrrn4cl	59.16585819	82.02700227	155.5922078	60.25762891	38.15070996	41.81301007	2.116546948	0.10284226
17390879	ENSMUST00000103234	Fbn1	297.2279548	472.9726661	536.4433441	232.0686769	219.9355489	165.7425255	2.115177397	0.02420089
17214025	---	---	1034.587535	4320.222798	2411.591777	1378.458387	1270.693175	1023.378419	2.114728035	0.23078097
17316348	NR_028575	Snord123	91.52988735	103.7191875	319.848964	75.95484031	78.2954736	89.33267142	2.114671672	0.22546747
17402321	NM_153422	Pde5a	87.35176809	147.7308173	309.9676833	98.79697744	78.30855383	81.30324333	2.10925604	0.17856139
17424352	BC059060	Gm3893	28.286328	59.63762913	120.4531239	41.24350393	27.52416705	30.20790023	2.105338504	0.2535041
17473155	NM_133189	Cacng7	43.22523793	49.31532034	140.9292241	44.59944957	31.54964791	34.81982386	2.103920445	0.20604327
17401335	NM_009196	Slc16a1	50.94992085	89.88397362	224.3462097	59.60696448	61.17647178	53.26393094	2.098165057	0.26666185
17290263	NM_134066	Akr1c18	26.21013719	41.93026375	65.71856165	23.09305282	16.58217103	24.20877209	2.095344235	0.08734611
17230034	NM_001204910	Al607873	43.41449809	59.17520936	173.4864288	42.5411757	67.70568164	21.61543553	2.093670072	0.29283616
17300122	BC111819	A630038E17Rik	7.682601913	7.048347235	21.35624352	5.614922072	5.260332523	6.423167862	2.086155125	0.21923195
17344694	---	---	45.24736897	63.05614207	65.64148627	26.63981207	30.13587397	26.69269374	2.083962786	0.00526438
17426011	NM_001134676	Mup8	74.00680351	237.0842476	196.1688281	31.27881604	19.25771998	193.2986833	2.080338848	0.24302089
17230078	NM_001033450	Mnda	167.9451124	386.4264402	1020.054839	393.4667731	237.2872873	126.3245298	2.079607603	0.39704028
17339876	NM_027455	Qpct	31.21379788	53.85905456	144.0404299	40.84144484	38.33560386	31.05728907	2.078420272	0.2917714
17544269	---	---	10.23199813	6.650076791	15.44402618	6.289590109	5.623479238	3.694888938	2.071129389	0.08361026
17520425	ENSMUST00000015498	Pcolce2	156.1168015	221.8105229	422.1307162	135.3739183	127.8292338	123.8449302	2.067076617	0.09917851
17298267	NM_018746	Itih4	210.5111734	298.5684681	444.9264327	172.2954747	187.7074369	101.6802026	2.066365533	0.06816139
17381519	---	---	16.90925274	15.04670825	24.41055176	14.15765088	5.586679278	7.543426515	2.065633809	0.06909794
17336681	NM_031176	Tnxb	126.9850634	221.3535959	296.3826119	133.0109307	93.75527768	85.62955957	2.063796431	0.07493668
17434890	NM_001110843	Cacna2d1	26.27272611	36.85532052	75.5575491	26.06440462	23.63136402	17.54620349	2.062485548	0.14670666
17216745	NM_027677	Gpr39	35.88751193	55.48954238	104.8182415	30.18500218	40.29899625	24.73189705	2.06053091	0.13875379
17278775	NR_028433	AF357355	90.87786268	90.89789626	175.9375967	55.62532673	78.29905552	40.05926372	2.056017125	0.07615703
17368683	---	---	25.78204865	49.15441164	68.94222715	23.69710639	21.56847098	24.8081973	2.053245856	0.10483299
17229620	NM_010188	Fcgr3	64.02107514	139.9584711	368.8148665	77.15255345	135.4632778	66.48043883	2.052318408	0.39051285
17525186	NM_023277	Jam3	30.31601037	35.36462357	86.87137695	23.67469607	26.65067189	24.05135051	2.051072083	0.15340556
17546109	ENSMUST00000112161	Tlr7	24.68289997	43.20636634	143.2844263	37.02936745	47.5641272	18.46581458	2.049050146	0.43405974
17546101	ENSMUST00000112170	Tlr8	23.4434339	48.21295664	154.833732	30.01273729	58.32283727	22.27707635	2.047596913	0.44520143

17317046	NM_008764	Tnfrsf11b	72.04857543	46.51635025	138.0755439	46.38694726	53.18955272	26.30888132	2.038683657	0.16832758
17362973	ENSMUST00000025582	Ms4a6d	18.80808423	54.05162176	215.7602069	44.14432261	81.54434917	16.06839582	2.0360178	0.60588676
17311519	ENSMUST00000050027	Nov	266.8153763	188.3703384	585.0596855	243.9072784	129.8938216	137.6988786	2.033715433	0.19071338
17490211	NM_009131	Clec11a	25.27760723	34.63176474	104.322895	29.6935566	29.63257308	21.47376119	2.032580307	0.30366138
17406514	ENSMUST00000090986	Fcrls	45.00969864	68.90429462	227.6446904	42.46834551	87.85411761	37.74524485	2.03226835	0.38484433
17308963	---	---	24.40975653	79.57271946	21.18502609	16.9117963	25.83725682	18.92113857	2.029627258	0.30508435
17291674	NM_001166030	Mylk4	54.36491547	39.7842363	100.3426407	43.09895547	28.33703683	24.47479719	2.027840595	0.11714476
17236800	NM_007833	Dcn	1127.232971	3201.628057	6756.310892	1935.096771	1887.354875	1647.154308	2.026685654	0.41569886
17364126	NM_001110517	Gm14446	5.81270221	13.49721641	9.996742081	5.449489172	3.907844335	5.105180605	2.0263877	0.07975499
17214039	---	---	980.0333269	4069.173276	1986.963974	1298.78778	1165.578132	1010.045802	2.025140127	0.25983122
17214041	---	---	980.0333269	4069.173276	1986.963974	1298.78778	1165.578132	1010.045802	2.025140127	0.25958714
17214043	---	---	980.0333269	4069.173276	1986.963974	1298.78778	1165.578132	1010.045802	2.025140127	0.25984704
17254200	---	---	980.0333269	4069.173276	1986.963974	1298.78778	1165.578132	1010.045802	2.025140127	0.26020133
17410435	NM_033525	Npnt	242.4828662	140.726479	275.9140284	135.8164106	108.1983734	81.63551394	2.024022019	0.05412094
17339729	NM_019919	Ltbp1	133.8430114	187.4740367	373.3963462	126.0035002	112.530323	104.9535387	2.022529709	0.11930332
17536436	ENSMUST00000052837	Ar	26.71462758	67.79730401	126.7645027	32.64081104	34.63774248	42.17774326	2.021596206	0.30656365
17306678	XM_993473	Gm8894	315.0041445	329.7589486	614.9562646	184.6464864	239.6697467	199.6885774	2.018765459	0.04315745
17227797	ENSMUST00000027603	Rgs18	14.11141741	15.55918944	54.45512771	13.04458372	16.24025072	12.3918871	2.018530524	0.33024436
17426000	NM_001134674	Mup13	102.7582204	334.7977449	220.3119591	46.35599427	25.37663725	254.235027	2.018199987	0.24789287
17462729	NM_199311	Clec4a1	42.09800613	102.5970899	413.1580593	73.06699651	161.8441041	41.81254635	2.015921521	0.60614
17411163	ENSMUST00000029670	Ptgr	42.41533349	58.71149141	121.6840276	35.19866971	39.74440845	35.81663757	2.011659663	0.13832721
17438955	NM_009141	Cxcl5	46.06608218	65.51843539	264.2705772	54.29295115	79.48633755	53.26784458	2.009413821	0.47789425
17447615	NM_010942	Nsg1	111.7237428	213.3259999	331.829422	118.1928538	121.4695589	87.25809062	2.009293262	0.13900277
17379871	ENSMUST00000136378	1500012F01Rik	64.02884142	105.301779	183.945682	53.52856232	67.53245034	54.87579384	2.007972689	0.1214835
17491199	NM_011316	Saa4	11.73373167	17.86935926	67.4911766	17.83083056	17.46242483	13.06600326	2.007769975	0.45453188
17507209	NM_130903 // NM_130903	Cd209c // Cd209c	22.71592266	24.26296572	59.33855953	16.20978443	18.88691284	17.91600415	2.005508964	0.1577364
17405482	NM_027571	P2ry12	32.66471167	73.17966976	167.2136718	47.50192255	48.4528291	40.40038118	2.002550601	0.37950727
Downregulated genes (14)										
17502899	NM_009463	Ucp1	21.51541854	22.86633112	22.55247712	23.35659397	18.49326435	660.9237367	0.095242945	0.3873962
17248276	NM_001083955	Hba-a2	78.27083876	86.46431916	276.806498	84.00253729	1819.252402	334.8081879	0.1972874	0.3204688
17494221	NM_008220	Hbb-b1	7.39830614	5.84845275	3.530589281	10.92877656	38.41268753	5.744809287	0.304564951	0.24167535
17481232	NM_008220	Hbb-b1	12.75613176	13.19567275	19.30992961	15.51728229	103.1236913	26.60226165	0.311627141	0.24944481
17547616	---	---	27.98645792	28.17768141	45.13832567	35.13848292	204.698114	60.37456566	0.337437369	0.21113619
17351457	NM_007702	Cidea	40.2744505	30.97114897	34.72888049	37.41842683	26.61388094	188.4863188	0.419669952	0.44566295
17487570	NM_001166726	Vmn1r127	78.42099273	65.30316453	46.61792871	151.5362351	105.5969972	159.379802	0.456989506	0.01587093
17239845	NM_007482	Arg1	56.27904724	62.42564857	129.9494754	103.4245593	361.99501	69.43147908	0.464903588	0.36830777
17229020	NM_010231	Fmo1	626.7642143	1098.409277	729.2906057	1876.423814	1471.375746	1819.719035	0.474979248	0.01388094
17471518	NM_001204223	Clec12b	47.22330142	47.88221544	26.88608895	93.22532394	63.27580274	99.85335522	0.475870774	0.03015218
17237490	---	---	11.34397222	18.09786992	6.975936946	16.11552184	27.96165793	31.97481263	0.478853715	0.07092478
17337122	NM_207648	H2-Q6	429.429949	448.5919745	275.3385873	675.6629796	823.5331989	889.5753491	0.482825795	0.01348044
17533280	---	---	7.857803006	6.992532238	10.9744216	11.04198009	23.93989634	17.57041059	0.491410713	0.06180606
17222527	NM_018775	Tbc1d8	128.4944289	126.8262878	96.59616446	204.6718668	231.1664148	271.2234295	0.49771735	0.00479277

Supplementary Table 5. Overrepresented Gene Ontology categories in mouse carotid endothelium *in vivo*.

Molecular and Cellular Functions	Number of Changed Genes (≥ 2 fold)			
	Non-Tg_LCA vs. Non-Tg RCA	APPsw-Tg LCA vs. APPsw-Tg RCA	APPsw-Tg RCA vs. Non-Tg RCA	APPsw-Tg LCA vs. Non-Tg LCA
Transport	74	103	43	59
Translation	0	1	0	1
Response to stress	108	145	29	69
Cell cycle	9	9	1	1
Cell adhesion	32	42	18	25
Signal transduction	117	136	53	58
Cell proliferation	26	29	9	14
Homeostasis	55	67	16	39
Cell differentiation	78	78	32	42
Immune response	59	76	7	28
Inflammatory response	42	55	6	21
Behavior	12	14	7	10
Apoptotic process	23	24	10	8
Total	635	779	231	375

Supplementary Table 6. Biological processes enriched in the endothelial genes in non-Tg mice LCA compared to non-Tg mice RCA.

GO Term	Count	%	P-value
Upregulated			
GO:0006955~immune response	57	20.87912	3.36E-35
GO:0006954~inflammatory response	42	15.38462	3.55E-33
GO:0009611~response to wounding	48	17.58242	5.68E-32
GO:0006952~defense response	51	18.68132	5.56E-30
GO:0042330~taxis	30	10.98901	1.16E-28
GO:0006935~chemotaxis	30	10.98901	1.16E-28
GO:0007626~locomotory behavior	31	11.35531	1.56E-19
GO:0002252~immune effector process	22	8.058608	1.65E-16
GO:0044421~extracellular region part	51	18.68132	1.69E-16
GO:0005576~extracellular region	77	28.20513	3.45E-16
GO:0048584~positive regulation of response to stimulus	24	8.791209	5.17E-15
GO:0007610~behavior	33	12.08791	8.48E-15
GO:0005615~extracellular space	39	14.28571	1.88E-14
GO:0002684~positive regulation of immune system process	24	8.791209	4.86E-14
GO:0050778~positive regulation of immune response	20	7.326007	1.44E-13
GO:0008009~chemokine activity	13	4.761905	1.46E-13
GO:0030246~carbohydrate binding	28	10.25641	1.52E-13
GO:0042379~chemokine receptor binding	13	4.761905	2.09E-13
GO:0001775~cell activation	24	8.791209	2.13E-12
GO:0060326~cell chemotaxis	11	4.029304	3.00E-12
GO:0030595~leukocyte chemotaxis	11	4.029304	3.00E-12
GO:0002443~leukocyte mediated immunity	16	5.860806	3.55E-12
GO:0002526~acute inflammatory response	15	5.494505	1.33E-11
GO:0050900~leukocyte migration	12	4.395604	2.39E-11
mmu04060:Cytokine-cytokine receptor interaction	26	9.52381	3.80E-11
GO:0002449~lymphocyte mediated immunity	14	5.128205	8.40E-11
GO:0045321~leukocyte activation	21	7.692308	9.65E-11
GO:0009986~cell surface	26	9.52381	1.06E-10
GO:0005125~cytokine activity	19	6.959707	1.58E-10
GO:0016477~cell migration	21	7.692308	4.98E-10
GO:0045087~innate immune response	15	5.494505	6.32E-10
GO:0002478~antigen processing and presentation of exogenous peptide antigen	9	3.296703	8.75E-10
mmu04062:Chemokine signaling pathway	21	7.692308	1.28E-09
GO:0005529~sugar binding	18	6.593407	1.38E-09
GO:0048002~antigen processing and presentation of peptide antigen	10	3.663004	1.57E-09
GO:0002274~myeloid leukocyte activation	10	3.663004	1.57E-09
GO:0019724~B cell mediated immunity	12	4.395604	2.79E-09
GO:0009897~external side of plasma membrane	20	7.326007	2.97E-09
GO:0002250~adaptive immune response	13	4.761905	3.93E-09
GO:0002460~adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	13	4.761905	3.93E-09
GO:0002253~activation of immune response	13	4.761905	5.19E-09
GO:0019884~antigen processing and presentation of exogenous antigen	9	3.296703	5.20E-09
GO:0051674~localization of cell	21	7.692308	9.24E-09
GO:0048870~cell motility	21	7.692308	9.24E-09
GO:0016064~immunoglobulin mediated immune response	11	4.029304	2.85E-08
GO:0050766~positive regulation of phagocytosis	8	2.930403	3.00E-08
GO:0006909~phagocytosis	10	3.663004	3.80E-08
GO:0050764~regulation of phagocytosis	8	2.930403	5.73E-08
GO:0019886~antigen processing and presentation of exogenous peptide antigen via MHC class II	7	2.564103	7.30E-08
GO:0002495~antigen processing and presentation of peptide antigen via MHC class II	7	2.564103	7.30E-08
GO:0030593~neutrophil chemotaxis	7	2.564103	1.11E-07
GO:0002822~regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	10	3.663004	1.28E-07
GO:0002819~regulation of adaptive immune response	10	3.663004	1.28E-07
GO:0006928~cell motion	22	8.058608	1.41E-07
GO:0002504~antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	7	2.564103	2.38E-07
GO:0030247~polysaccharide binding	13	4.761905	4.03E-07
GO:0001871~pattern binding	13	4.761905	4.03E-07
GO:0045807~positive regulation of endocytosis	8	2.930403	5.72E-07
GO:0002697~regulation of immune effector process	11	4.029304	7.27E-07
GO:0002703~regulation of leukocyte mediated immunity	10	3.663004	9.19E-07
GO:0042110~T cell activation	12	4.395604	1.26E-06
mmu04640:Hematopoietic cell lineage	12	4.395604	1.50E-06
GO:0032103~positive regulation of response to external stimulus	8	2.930403	1.54E-06

mmu05322:Systemic lupus erythematosus	13	4.761905	1.76E-06
GO:0009617~response to bacterium	13	4.761905	4.09E-06
GO:0002889~regulation of immunoglobulin mediated immune response	7	2.564103	4.55E-06
GO:0002712~regulation of B cell mediated immunity	7	2.564103	4.55E-06
GO:0002673~regulation of acute inflammatory response	6	2.197802	5.18E-06
GO:0002706~regulation of lymphocyte mediated immunity	9	3.296703	5.26E-06
GO:0019955~cytokine binding	10	3.663004	5.75E-06
GO:0019882~antigen processing and presentation	10	3.663004	5.82E-06
GO:0002698~negative regulation of immune effector process	6	2.197802	9.15E-06
GO:0002824~positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	7	2.564103	9.80E-06
GO:0002821~positive regulation of adaptive immune response	7	2.564103	9.80E-06
GO:0030100~regulation of endocytosis	8	2.930403	1.13E-05
GO:0002541~activation of plasma proteins involved in acute inflammatory response	7	2.564103	1.38E-05
GO:0006956~complement activation	7	2.564103	1.38E-05
GO:0006959~humoral immune response	8	2.930403	1.46E-05
GO:0002675~positive regulation of acute inflammatory response	5	1.831502	1.47E-05
GO:0019221~cytokine-mediated signaling pathway	8	2.930403	1.87E-05
GO:0008283~cell proliferation	15	5.494505	2.06E-05
GO:0031349~positive regulation of defense response	8	2.930403	2.10E-05
GO:0048534~hemopoietic or lymphoid organ development	16	5.860806	2.11E-05
GO:0032101~regulation of response to external stimulus	10	3.663004	2.32E-05
GO:0001944~vasculature development	15	5.494505	2.37E-05
GO:0050729~positive regulation of inflammatory response	6	2.197802	2.39E-05
GO:0030097~hemopoiesis	15	5.494505	2.47E-05
GO:0006897~endocytosis	13	4.761905	2.55E-05
GO:0010324~membrane invagination	13	4.761905	2.55E-05
GO:0008201~heparin binding	9	3.296703	2.97E-05
GO:0046649~lymphocyte activation	13	4.761905	2.98E-05
GO:0019864~IgG binding	4	1.465201	3.09E-05
GO:0002883~regulation of hypersensitivity	5	1.831502	3.11E-05
GO:0002864~regulation of acute inflammatory response to antigenic stimulus	5	1.831502	3.11E-05
GO:0060627~regulation of vesicle-mediated transport	9	3.296703	3.27E-05
GO:0007155~cell adhesion	23	8.424908	3.44E-05
GO:0022610~biological adhesion	23	8.424908	3.53E-05
GO:0002520~immune system development	16	5.860806	3.72E-05
GO:0002891~positive regulation of immunoglobulin mediated immune response	5	1.831502	4.31E-05
GO:0002707~negative regulation of lymphocyte mediated immunity	5	1.831502	4.31E-05
GO:0002714~positive regulation of B cell mediated immunity	5	1.831502	4.31E-05
GO:0002704~negative regulation of leukocyte mediated immunity	5	1.831502	4.31E-05
GO:0007159~leukocyte adhesion	5	1.831502	4.31E-05
GO:0001817~regulation of cytokine production	11	4.029304	4.44E-05
GO:0005539~glycosaminoglycan binding	10	3.663004	4.69E-05
GO:0051605~protein maturation by peptide bond cleavage	8	2.930403	5.01E-05
GO:0045765~regulation of angiogenesis	7	2.564103	5.18E-05
GO:0042098~T cell proliferation	6	2.197802	5.26E-05
GO:0002886~regulation of myeloid leukocyte mediated immunity	5	1.831502	5.80E-05
GO:0045576~mast cell activation	5	1.831502	5.80E-05
GO:0006911~phagocytosis, engulfment	5	1.831502	5.80E-05
GO:0001568~blood vessel development	14	5.128205	7.73E-05
GO:0019838~growth factor binding	8	2.930403	8.94E-05
GO:0002861~regulation of inflammatory response to antigenic stimulus	5	1.831502	1.26E-04
GO:0001525~angiogenesis	10	3.663004	1.71E-04
GO:0001798~positive regulation of type IIa hypersensitivity	4	1.465201	1.74E-04
GO:0001796~regulation of type IIa hypersensitivity	4	1.465201	1.74E-04
GO:0002888~positive regulation of myeloid leukocyte mediated immunity	4	1.465201	1.74E-04
GO:0002894~positive regulation of type II hypersensitivity	4	1.465201	1.74E-04
GO:0002892~regulation of type II hypersensitivity	4	1.465201	1.74E-04
mmu04610:Complement and coagulation cascades	9	3.296703	1.90E-04
GO:0048514~blood vessel morphogenesis	12	4.395604	1.92E-04
GO:0050727~regulation of inflammatory response	7	2.564103	1.99E-04
GO:0042742~defense response to bacterium	9	3.296703	2.12E-04
GO:0016044~membrane organization	14	5.128205	2.26E-04
GO:0032496~response to lipopolysaccharide	6	2.197802	2.38E-04
GO:0048407~platelet-derived growth factor binding	4	1.465201	2.49E-04
mmu04650:Natural killer cell mediated cytotoxicity	11	4.029304	2.75E-04
GO:0002429~immune response-activating cell surface receptor signaling pathway	6	2.197802	3.43E-04
GO:0002866~positive regulation of acute inflammatory response to antigenic stimulus	4	1.465201	3.65E-04
GO:0002885~positive regulation of hypersensitivity	4	1.465201	3.65E-04
GO:0006957~complement activation, alternative pathway	4	1.465201	3.65E-04

GO:0050829~defense response to Gram-negative bacterium	4	1.465201	3.65E-04
GO:0051094~positive regulation of developmental process	12	4.395604	3.75E-04
GO:0046651~lymphocyte proliferation	6	2.197802	3.85E-04
GO:0016485~protein processing	8	2.930403	3.92E-04
GO:0001816~cytokine production	6	2.197802	4.30E-04
GO:0070661~leukocyte proliferation	6	2.197802	4.30E-04
GO:0032943~mononuclear cell proliferation	6	2.197802	4.30E-04
GO:0019865~immunoglobulin binding	4	1.465201	4.78E-04
GO:0002768~immune response-regulating cell surface receptor signaling pathway	6	2.197802	4.79E-04
GO:0051130~positive regulation of cellular component organization	9	3.296703	4.86E-04
GO:0050865~regulation of cell activation	10	3.663004	5.59E-04
GO:0050777~negative regulation of immune response	5	1.831502	5.59E-04
GO:0051604~protein maturation	8	2.930403	5.81E-04
GO:0002699~positive regulation of immune effector process	6	2.197802	5.90E-04
GO:0045088~regulation of innate immune response	6	2.197802	5.90E-04
GO:0042277~peptide binding	10	3.663004	6.11E-04
GO:0032680~regulation of tumor necrosis factor production	5	1.831502	6.48E-04
GO:0001909~leukocyte mediated cytotoxicity	4	1.465201	6.54E-04
GO:0001803~regulation of type III hypersensitivity	3	1.098901	6.60E-04
GO:0001805~positive regulation of type III hypersensitivity	3	1.098901	6.60E-04
GO:0010744~positive regulation of foam cell differentiation	3	1.098901	6.60E-04
GO:0002757~immune response-activating signal transduction	6	2.197802	7.20E-04
GO:0002237~response to molecule of bacterial origin	6	2.197802	7.92E-04
GO:0002863~positive regulation of inflammatory response to antigenic stimulus	4	1.465201	8.41E-04
GO:0002683~negative regulation of immune system process	7	2.564103	9.47E-04
GO:0006958~complement activation, classical pathway	5	1.831502	9.77E-04
GO:0006953~acute-phase response	5	1.831502	9.77E-04
mmu04672:~Intestinal immune network for IgA production	7	2.564103	9.97E-04
GO:0002764~immune response-regulating signal transduction	6	2.197802	0.001041
GO:0042127~regulation of cell proliferation	19	6.959707	0.001191
GO:0045597~positive regulation of cell differentiation	10	3.663004	0.001264
GO:0019763~immunoglobulin receptor activity	3	1.098901	0.001274
GO:0010743~regulation of foam cell differentiation	3	1.098901	0.001307
GO:0010884~positive regulation of lipid storage	3	1.098901	0.001307
GO:0032760~positive regulation of tumor necrosis factor production	4	1.465201	0.001309
GO:0001906~cell killing	4	1.465201	0.001594
mmu04514:~Cell adhesion molecules (CAMs)	11	4.029304	0.001713
GO:0002455~humoral immune response mediated by circulating immunoglobulin	5	1.831502	0.001762
GO:0002444~myeloid leukocyte mediated immunity	4	1.465201	0.001914
GO:0033559~unsaturated fatty acid metabolic process	5	1.831502	0.001959
GO:0005578~proteinaceous extracellular matrix	14	5.128205	0.002057
GO:0042590~antigen processing and presentation of exogenous peptide antigen via MHC class I	3	1.098901	0.002156
GO:0030335~positive regulation of cell migration	5	1.831502	0.002171
GO:0002694~regulation of leukocyte activation	9	3.296703	0.002196
GO:0005886~plasma membrane	70	25.64103	0.002251
GO:0001819~positive regulation of cytokine production	6	2.197802	0.002299
GO:0030334~regulation of cell migration	7	2.564103	0.002537
GO:0001666~response to hypoxia	6	2.197802	0.002644
GO:0001763~morphogenesis of a branching structure	8	2.930403	0.002705
GO:0030155~regulation of cell adhesion	7	2.564103	0.002827
GO:0070482~response to oxygen levels	6	2.197802	0.002831
GO:0008217~regulation of blood pressure	6	2.197802	0.002831
GO:0048585~negative regulation of response to stimulus	6	2.197802	0.002831
GO:0031012~extracellular matrix	14	5.128205	0.002893
GO:0010810~regulation of cell-substrate adhesion	5	1.831502	0.002902
GO:0002705~positive regulation of leukocyte mediated immunity	5	1.831502	0.002902
GO:0002708~positive regulation of lymphocyte mediated immunity	5	1.831502	0.002902
GO:0016337~cell-cell adhesion	11	4.029304	0.002904
GO:0051272~positive regulation of cell motion	5	1.831502	0.003179
GO:0035272~exocrine system development	5	1.831502	0.003179
GO:0045123~cellular extravasation	3	1.098901	0.003202
GO:0051050~positive regulation of transport	8	2.930403	0.003664
GO:0044092~negative regulation of molecular function	8	2.930403	0.003664
GO:0042981~regulation of apoptosis	18	6.593407	0.0039
GO:0050660~FAD binding	6	2.197802	0.003931
GO:0004950~chemokine receptor activity	4	1.465201	0.003958
GO:0043086~negative regulation of catalytic activity	7	2.564103	0.004039
GO:0050867~positive regulation of cell activation	7	2.564103	0.004039
GO:0040017~positive regulation of locomotion	5	1.831502	0.004115
GO:0009968~negative regulation of signal transduction	9	3.296703	0.004175

GO:0042325~regulation of phosphorylation	12	4.395604	0.004267
GO:0043067~regulation of programmed cell death	18	6.593407	0.004421
GO:0010883~regulation of lipid storage	3	1.098901	0.004439
GO:0042953~lipoprotein transport	3	1.098901	0.004439
GO:0002437~inflammatory response to antigenic stimulus	3	1.098901	0.004439
GO:0019956~chemokine binding	4	1.465201	0.004503
GO:0010941~regulation of cell death	18	6.593407	0.004661
GO:0050830~defense response to Gram-positive bacterium	4	1.465201	0.004668
mmu04666:Fc gamma R-mediated phagocytosis	8	2.930403	0.005052
mmu04620:Toll-like receptor signaling pathway	8	2.930403	0.005341
GO:0051270~regulation of cell motion	7	2.564103	0.005352
GO:0002521~leukocyte differentiation	8	2.930403	0.005458
GO:0030217~T cell differentiation	6	2.197802	0.00555
GO:0007229~integrin-mediated signaling pathway	6	2.197802	0.00555
GO:0051174~regulation of phosphorus metabolic process	12	4.395604	0.005619
GO:0019220~regulation of phosphate metabolic process	12	4.395604	0.005619
GO:0001530~lipopolysaccharide binding	3	1.098901	0.005717
GO:0050840~extracellular matrix binding	4	1.465201	0.005723
GO:0008528~peptide receptor activity, G-protein coupled	7	2.564103	0.005748
GO:0001653~peptide receptor activity	7	2.564103	0.005748
GO:0031342~negative regulation of cell killing	3	1.098901	0.005861
GO:0045059~positive thymic T cell selection	3	1.098901	0.005861
GO:0001911~negative regulation of leukocyte mediated cytotoxicity	3	1.098901	0.005861
GO:0001810~regulation of type I hypersensitivity	3	1.098901	0.005861
GO:0032403~protein complex binding	6	2.197802	0.005869
GO:0005583~fibrillar collagen	3	1.098901	0.005944
GO:0040012~regulation of locomotion	7	2.564103	0.006115
mmu05020:Prion diseases	5	1.831502	0.006481
GO:0010648~negative regulation of cell communication	9	3.296703	0.006869
GO:0048872~homeostasis of number of cells	7	2.564103	0.006954
GO:0030098~lymphocyte differentiation	7	2.564103	0.007252
GO:0051048~negative regulation of secretion	4	1.465201	0.007379
GO:0045060~negative thymic T cell selection	3	1.098901	0.007462
GO:0050730~regulation of peptidyl-tyrosine phosphorylation	5	1.831502	0.008001
GO:0004896~cytokine receptor activity	5	1.831502	0.008712
mmu04512:ECM-receptor interaction	7	2.564103	0.008776
GO:0010033~response to organic substance	16	5.860806	0.008885
GO:0050873~brown fat cell differentiation	4	1.465201	0.009019
GO:0043383~negative T cell selection	3	1.098901	0.009236
GO:0043368~positive T cell selection	3	1.098901	0.009236
GO:0001932~regulation of protein amino acid phosphorylation	7	2.564103	0.009597
GO:0006979~response to oxidative stress	6	2.197802	0.009737
mmu04510:Focal adhesion	11	4.029304	0.010191
GO:0016192~vesicle-mediated transport	15	5.494505	0.010317
GO:0002366~leukocyte activation during immune response	4	1.465201	0.010856
GO:0002263~cell activation during immune response	4	1.465201	0.010856
GO:0045619~regulation of lymphocyte differentiation	5	1.831502	0.010944
GO:0032994~protein-lipid complex	4	1.465201	0.011093
GO:0034358~plasma lipoprotein particle	4	1.465201	0.011093
GO:0045582~positive regulation of T cell differentiation	4	1.465201	0.01185
GO:0042613~MHC class II protein complex	3	1.098901	0.012308
GO:0005764~lysosome	9	3.296703	0.012534
GO:0014033~neural crest cell differentiation	4	1.465201	0.012894
GO:0014032~neural crest cell development	4	1.465201	0.012894
GO:0005506~iron ion binding	12	4.395604	0.012908
GO:0000323~lytic vacuole	9	3.296703	0.012933
GO:0045444~fat cell differentiation	5	1.831502	0.013006
mmu04612:Antigen processing and presentation	7	2.564103	0.013485
GO:0045621~positive regulation of lymphocyte differentiation	4	1.465201	0.013989
GO:0006690~icosanoid metabolic process	4	1.465201	0.013989
mmu04670:Leukocyte transendothelial migration	8	2.930403	0.014116
GO:0042592~homeostatic process	17	6.227106	0.014339
GO:0030099~myeloid cell differentiation	6	2.197802	0.014475
GO:0043235~receptor complex	6	2.197802	0.014621
GO:0009967~positive regulation of signal transduction	8	2.930403	0.014785
GO:0030169~low-density lipoprotein binding	3	1.098901	0.015172
GO:0002820~negative regulation of adaptive immune response	3	1.098901	0.015545
GO:0006968~cellular defense response	3	1.098901	0.015545
GO:0002823~negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	3	1.098901	0.015545

GO:0006910~phagocytosis, recognition	3	1.098901	0.015545
GO:0030414~peptidase inhibitor activity	8	2.930403	0.015559
GO:0050851~antigen receptor-mediated signaling pathway	4	1.465201	0.016333
GO:0002696~positive regulation of leukocyte activation	6	2.197802	0.016347
GO:0050870~positive regulation of T cell activation	5	1.831502	0.016962
GO:0006692~prostanoid metabolic process	3	1.098901	0.01796
GO:0050853~B cell receptor signaling pathway	3	1.098901	0.01796
GO:0006693~prostaglandin metabolic process	3	1.098901	0.01796
GO:0008083~growth factor activity	7	2.564103	0.018136
GO:0005044~scavenger receptor activity	4	1.465201	0.019567
GO:0045061~thymic T cell selection	3	1.098901	0.020521
GO:0051249~regulation of lymphocyte activation	7	2.564103	0.021056
GO:0001503~ossification	6	2.197802	0.021323
GO:0004175~endopeptidase activity	13	4.761905	0.022333
GO:0050863~regulation of T cell activation	6	2.197802	0.022907
GO:0010647~positive regulation of cell communication	8	2.930403	0.02348
GO:0003013~circulatory system process	6	2.197802	0.025423
GO:0008015~blood circulation	6	2.197802	0.025423
GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	8	2.930403	0.025433
GO:0016493~C-C chemokine receptor activity	3	1.098901	0.025454
GO:0019957~C-C chemokine binding	3	1.098901	0.025454
GO:0045766~positive regulation of angiogenesis	3	1.098901	0.026066
GO:0030574~collagen catabolic process	3	1.098901	0.026066
GO:0002474~antigen processing and presentation of peptide antigen via MHC class I	3	1.098901	0.026066
GO:0060324~face development	3	1.098901	0.026066
GO:0046888~negative regulation of hormone secretion	3	1.098901	0.026066
GO:0005773~vacuole	9	3.296703	0.026088
GO:0045785~positive regulation of cell adhesion	4	1.465201	0.026172
GO:0008284~positive regulation of cell proliferation	10	3.663004	0.026993
GO:0043066~negative regulation of apoptosis	9	3.296703	0.027271
mmu03320:PPAR signaling pathway	6	2.197802	0.02749
GO:0004857~enzyme inhibitor activity	9	3.296703	0.027723
mmu04662:B cell receptor signaling pathway	6	2.197802	0.028831
GO:0060445~branching involved in salivary gland morphogenesis	3	1.098901	0.029041
GO:0044243~multicellular organismal catabolic process	3	1.098901	0.029041
GO:0019770~IgG receptor activity	2	0.732601	0.029284
GO:0004962~endothelin receptor activity	2	0.732601	0.029284
GO:0043069~negative regulation of programmed cell death	9	3.296703	0.030334
GO:0060548~negative regulation of cell death	9	3.296703	0.031047
GO:0060348~bone development	6	2.197802	0.031964
GO:0004866~endopeptidase inhibitor activity	7	2.564103	0.032118
GO:0006800~oxygen and reactive oxygen species metabolic process	4	1.465201	0.032938
GO:0014031~mesenchymal cell development	4	1.465201	0.032938
GO:0048771~tissue remodeling	4	1.465201	0.032938
GO:0008037~cell recognition	4	1.465201	0.032938
mmu05310:Asthma	4	1.465201	0.033547
GO:0005584~collagen type I	2	0.732601	0.034409
GO:0045580~regulation of T cell differentiation	4	1.465201	0.034759
GO:0030218~erythrocyte differentiation	4	1.465201	0.034759
GO:0042743~hydrogen peroxide metabolic process	3	1.098901	0.03537
GO:0051240~positive regulation of multicellular organismal process	7	2.564103	0.035877
mmu05332:Graft-versus-host disease	5	1.831502	0.035985
GO:0048762~mesenchymal cell differentiation	4	1.465201	0.03663
GO:0031399~regulation of protein modification process	7	2.564103	0.037521
GO:0008034~lipoprotein binding	3	1.098901	0.037824
GO:0050661~NADP or NADPH binding	3	1.098901	0.037824
GO:0060485~mesenchyme development	4	1.465201	0.038552
GO:0060322~head development	3	1.098901	0.038716
GO:0045058~T cell selection	3	1.098901	0.038716
GO:0034101~erythrocyte homeostasis	4	1.465201	0.040525
GO:0006469~negative regulation of protein kinase activity	4	1.465201	0.040525
GO:0033673~negative regulation of kinase activity	4	1.465201	0.040525
GO:0005770~late endosome	4	1.465201	0.040562
GO:0005520~insulin-like growth factor binding	3	1.098901	0.041211
GO:0016525~negative regulation of angiogenesis	3	1.098901	0.042177
GO:0009306~protein secretion	3	1.098901	0.042177
GO:0005581~collagen	3	1.098901	0.042235
GO:0010876~lipid localization	6	2.197802	0.042989
mmu04142:Lysosome	7	2.564103	0.043296
GO:0005887~integral to plasma membrane	16	5.860806	0.043674

GO:0010886~positive regulation of cholesterol storage	2	0.732601	0.044156
GO:0002713~negative regulation of B cell mediated immunity	2	0.732601	0.044156
GO:0010885~regulation of cholesterol storage	2	0.732601	0.044156
GO:0002890~negative regulation of immunoglobulin mediated immune response	2	0.732601	0.044156
GO:0032763~regulation of mast cell cytokine production	2	0.732601	0.044156
mmu04621:NOD-like receptor signaling pathway	5	1.831502	0.044334
mmu04810:Regulation of actin cytoskeleton	10	3.663004	0.044453
GO:0050866~negative regulation of cell activation	4	1.465201	0.044621
GO:0002695~negative regulation of leukocyte activation	4	1.465201	0.044621
GO:0051348~negative regulation of transferase activity	4	1.465201	0.044621
GO:0035295~tube development	9	3.296703	0.045192
GO:0032963~collagen metabolic process	3	1.098901	0.045749
GO:0050864~regulation of B cell activation	4	1.465201	0.048915
GO:0015837~amine transport	5	1.831502	0.048944
GO:0044259~multicellular organismal macromolecule metabolic process	3	1.098901	0.049429
GO:0001569~patterning of blood vessels	3	1.098901	0.049429
GO:0048754~branching morphogenesis of a tube	5	1.831502	0.050571
GO:0051251~positive regulation of lymphocyte activation	5	1.831502	0.052227
GO:0007585~respiratory gaseous exchange	3	1.098901	0.053211
GO:0007162~negative regulation of cell adhesion	3	1.098901	0.053211
GO:0007167~enzyme linked receptor protein signaling pathway	9	3.296703	0.053242
GO:0044236~multicellular organismal metabolic process	3	1.098901	0.057093
GO:0031226~intrinsic to plasma membrane	16	5.860806	0.057455
GO:0001846~opsonin binding	7	2.564103	0.057714
GO:0006631~fatty acid metabolic process	7	2.564103	0.058054
GO:0002445~type II hypersensitivity	2	0.732601	0.058439
GO:0030815~negative regulation of cAMP metabolic process	2	0.732601	0.058439
GO:0042832~defense response to protozoan	2	0.732601	0.058439
GO:0001794~type Ila hypersensitivity	2	0.732601	0.058439
GO:0030809~negative regulation of nucleotide biosynthetic process	2	0.732601	0.058439
GO:0030800~negative regulation of cyclic nucleotide metabolic process	2	0.732601	0.058439
GO:0030803~negative regulation of cyclic nucleotide biosynthetic process	2	0.732601	0.058439
GO:0030818~negative regulation of cAMP biosynthetic process	2	0.732601	0.058439
GO:0002523~leukocyte migration during inflammatory response	2	0.732601	0.058439
GO:0001788~antibody-dependent cellular cytotoxicity	2	0.732601	0.058439
GO:0048545~response to steroid hormone stimulus	4	1.465201	0.060492
GO:0045859~regulation of protein kinase activity	7	2.564103	0.06054
GO:0010811~positive regulation of cell-substrate adhesion	3	1.098901	0.06107
GO:0007435~salivary gland morphogenesis	3	1.098901	0.06107
GO:0020037~heme binding	6	2.197802	0.062088
GO:0070011~peptidase activity, acting on L-amino acid peptides	15	5.494505	0.062674
GO:0001501~skeletal system development	9	3.296703	0.064446
mmu05218:Melanoma	5	1.831502	0.066752
GO:0043549~regulation of kinase activity	7	2.564103	0.068706
GO:0031225~anchored to membrane	8	2.930403	0.068925
GO:0042035~regulation of cytokine biosynthetic process	4	1.465201	0.070589
GO:0008517~folic acid transporter activity	2	0.732601	0.071617
GO:0005201~extracellular matrix structural constituent	3	1.098901	0.071923
GO:0045953~negative regulation of natural killer cell mediated cytotoxicity	2	0.732601	0.07251
GO:0034381~lipoprotein particle clearance	2	0.732601	0.07251
GO:0002524~hypersensitivity	2	0.732601	0.07251
GO:0070391~response to lipoteichoic acid	2	0.732601	0.07251
GO:0050665~hydrogen peroxide biosynthetic process	2	0.732601	0.07251
GO:0043277~apoptotic cell clearance	2	0.732601	0.07251
GO:0046173~polyol biosynthetic process	2	0.732601	0.07251
GO:0002716~negative regulation of natural killer cell mediated immunity	2	0.732601	0.07251
GO:0002438~acute inflammatory response to antigenic stimulus	2	0.732601	0.07251
GO:0002687~positive regulation of leukocyte migration	2	0.732601	0.07251
GO:0046906~tetrapyrrole binding	6	2.197802	0.072899
GO:0002700~regulation of production of molecular mediator of immune response	3	1.098901	0.073538
GO:0031348~negative regulation of defense response	3	1.098901	0.073538
GO:0001910~regulation of leukocyte mediated cytotoxicity	3	1.098901	0.073538
GO:0031341~regulation of cell killing	3	1.098901	0.073538
GO:0006885~regulation of pH	3	1.098901	0.07786
GO:0007431~salivary gland development	3	1.098901	0.07786
GO:0051338~regulation of transferase activity	7	2.564103	0.078233
GO:0008233~peptidase activity	15	5.494505	0.082064
GO:0030888~regulation of B cell proliferation	3	1.098901	0.082261
GO:0033077~T cell differentiation in the thymus	3	1.098901	0.082261
GO:0008305~integrin complex	3	1.098901	0.084423

GO:0030324~lung development	5	1.831502	0.084783
GO:0048255~mRNA stabilization	2	0.732601	0.086371
GO:0045730~respiratory burst	2	0.732601	0.086371
GO:0043489~RNA stabilization	2	0.732601	0.086371
GO:0001878~response to yeast	2	0.732601	0.086371
GO:0006929~substrate-bound cell migration	2	0.732601	0.086371
GO:0045980~negative regulation of nucleotide metabolic process	2	0.732601	0.086371
GO:0050662~coenzyme binding	6	2.197802	0.088268
mmu05200:Pathways in cancer	12	4.395604	0.088639
GO:0030323~respiratory tube development	5	1.831502	0.089142
GO:0006865~amino acid transport	4	1.465201	0.08993
GO:0048871~multicellular organismal homeostasis	4	1.465201	0.08993
GO:0051051~negative regulation of transport	4	1.465201	0.092857
GO:0031667~response to nutrient levels	5	1.831502	0.093607
GO:0060341~regulation of cellular localization	6	2.197802	0.093807
GO:0005829~cytosol	15	5.494505	0.096822
GO:0004630~phospholipase D activity	2	0.732601	0.098814
GO:0008329~pattern recognition receptor activity	2	0.732601	0.098814

Downregulated

GO:0044421~extracellular region part	16	17.02128	9.03E-06
GO:0060113~inner ear receptor cell differentiation	5	5.319149	1.34E-05
GO:0005578~proteinaceous extracellular matrix	10	10.6383	2.41E-05
GO:0042490~mechanoreceptor differentiation	5	5.319149	2.82E-05
GO:0045596~negative regulation of cell differentiation	8	8.510638	3.04E-05
GO:0031012~extracellular matrix	10	10.6383	3.28E-05
GO:0048839~inner ear development	6	6.382979	7.15E-05
GO:0005576~extracellular region	22	23.40426	9.17E-05
GO:0043583~ear development	6	6.382979	1.58E-04
GO:0005886~plasma membrane	30	31.91489	1.58E-04
GO:0042491~auditory receptor cell differentiation	4	4.255319	1.65E-04
GO:0007423~sensory organ development	8	8.510638	2.64E-04
GO:0043062~extracellular structure organization	6	6.382979	8.29E-04
GO:0030198~extracellular matrix organization	5	5.319149	0.00154
GO:0007517~muscle organ development	6	6.382979	0.001739
GO:0005509~calcium ion binding	12	12.76596	0.0018
GO:0035295~tube development	7	7.446809	0.001882
GO:0030324~lung development	5	5.319149	0.002177
GO:0030323~respiratory tube development	5	5.319149	0.002323
GO:0060541~respiratory system development	5	5.319149	0.003251
GO:0045892~negative regulation of transcription, DNA-dependent	7	7.446809	0.004043
GO:0051253~negative regulation of RNA metabolic process	7	7.446809	0.004172
GO:0001755~neural crest cell migration	3	3.191489	0.005668
GO:0050840~extracellular matrix binding	3	3.191489	0.006187
GO:0048729~tissue morphogenesis	6	6.382979	0.006321
GO:0048598~embryonic morphogenesis	7	7.446809	0.008402
GO:0045608~negative regulation of auditory receptor cell differentiation	2	2.12766	0.009838
GO:0045632~negative regulation of mechanoreceptor differentiation	2	2.12766	0.009838
GO:0016481~negative regulation of transcription	7	7.446809	0.009913
GO:0002009~morphogenesis of an epithelium	5	5.319149	0.010439
GO:0060429~epithelium development	6	6.382979	0.010745
GO:0030155~regulation of cell adhesion	4	4.255319	0.011161
GO:0014032~neural crest cell development	3	3.191489	0.01146
GO:0014033~neural crest cell differentiation	3	3.191489	0.01146
GO:0004252~serine-type endopeptidase activity	5	5.319149	0.012299
GO:0044420~extracellular matrix part	4	4.255319	0.01263
GO:0045934~negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	7	7.446809	0.013348
GO:0030182~neuron differentiation	7	7.446809	0.013655
GO:0045664~regulation of neuron differentiation	4	4.255319	0.013904
GO:0051172~negative regulation of nitrogen compound metabolic process	7	7.446809	0.013967
GO:0045607~regulation of auditory receptor cell differentiation	2	2.12766	0.014721
GO:0045631~regulation of mechanoreceptor differentiation	2	2.12766	0.014721
GO:0010629~negative regulation of gene expression	7	7.446809	0.015432
GO:0005516~calmodulin binding	4	4.255319	0.016821
GO:0010558~negative regulation of macromolecule biosynthetic process	7	7.446809	0.016822
GO:0016564~transcription repressor activity	5	5.319149	0.017753
GO:0008236~serine-type peptidase activity	5	5.319149	0.018032
GO:0017171~serine hydrolase activity	5	5.319149	0.018313
GO:0031327~negative regulation of cellular biosynthetic process	7	7.446809	0.019066
GO:0009890~negative regulation of biosynthetic process	7	7.446809	0.019858
GO:0001667~ameboidal cell migration	3	3.191489	0.02069

GO:0014031~mesenchymal cell development	3	3.191489	0.02245
GO:0005112~Notch binding	2	2.12766	0.023485
GO:0007507~heart development	5	5.319149	0.024216
GO:0048762~mesenchymal cell differentiation	3	3.191489	0.02427
GO:0060120~inner ear receptor cell fate commitment	2	2.12766	0.024416
GO:0009912~auditory receptor cell fate commitment	2	2.12766	0.024416
GO:0060485~mesenchyme development	3	3.191489	0.025202
GO:0000122~negative regulation of transcription from RNA polymerase II promoter	5	5.319149	0.027112
GO:0044092~negative regulation of molecular function	4	4.255319	0.027346
GO:0050767~regulation of neurogenesis	4	4.255319	0.027346
mmu04330:Notch signaling pathway	3	3.191489	0.027715
GO:0032989~cellular component morphogenesis	6	6.382979	0.029294
GO:0043205~fibril	2	2.12766	0.031261
GO:0001656~metanephros development	3	3.191489	0.033164
GO:0051960~regulation of nervous system development	4	4.255319	0.036567
GO:0010605~negative regulation of macromolecule metabolic process	7	7.446809	0.038152
GO:0004866~endopeptidase inhibitor activity	4	4.255319	0.040871
GO:0042472~inner ear morphogenesis	3	3.191489	0.043128
GO:0044459~plasma membrane part	15	15.95745	0.04339
GO:0060284~regulation of cell development	4	4.255319	0.043723
mmu04514:Cell adhesion molecules (CAMs)	4	4.255319	0.045345
GO:0009725~response to hormone stimulus	4	4.255319	0.0479
GO:0042127~regulation of cell proliferation	7	7.446809	0.048931
GO:0004175~endopeptidase activity	6	6.382979	0.048976
GO:0030414~peptidase inhibitor activity	4	4.255319	0.050904
GO:0042471~ear morphogenesis	3	3.191489	0.054056
GO:0031328~positive regulation of cellular biosynthetic process	7	7.446809	0.054188
GO:0009891~positive regulation of biosynthetic process	7	7.446809	0.056146
GO:0007155~cell adhesion	7	7.446809	0.057744
mmu04610:Complement and coagulation cascades	3	3.191489	0.057953
GO:0022610~biological adhesion	7	7.446809	0.058148
GO:0005198~structural molecule activity	6	6.382979	0.061756
GO:0009719~response to endogenous stimulus	4	4.255319	0.062366
GO:0000902~cell morphogenesis	5	5.319149	0.065983
GO:0050771~negative regulation of axonogenesis	2	2.12766	0.076082
GO:0008233~peptidase activity	7	7.446809	0.076758
GO:0051129~negative regulation of cellular component organization	3	3.191489	0.076974
GO:0048471~perinuclear region of cytoplasm	4	4.255319	0.07796
GO:0007242~intracellular signaling cascade	9	9.574468	0.079835
GO:0006357~regulation of transcription from RNA polymerase II promoter	7	7.446809	0.082503
GO:0022604~regulation of cell morphogenesis	3	3.191489	0.082747
GO:0004725~protein tyrosine phosphatase activity	3	3.191489	0.082893
GO:0048483~autonomic nervous system development	2	2.12766	0.085182
GO:0043086~negative regulation of catalytic activity	3	3.191489	0.08865
GO:0010604~positive regulation of macromolecule metabolic process	7	7.446809	0.091205
GO:0031345~negative regulation of cell projection organization	2	2.12766	0.094194
GO:0005625~soluble fraction	3	3.191489	0.096128
GO:0001822~kidney development	3	3.191489	0.09773

Supplementary Table 7. Biological processes enriched in the endothelial genes in APPsw-Tg mice LCA compared to APPsw-Tg mice RCA.

GO Term	Count	%	P-value
Upregulated			
GO:0006955~immune response	72	19.40701	2.08E-43
GO:0006952~defense response	65	17.52022	1.70E-37
GO:0006954~inflammatory response	49	13.20755	2.31E-36
GO:0009611~response to wounding	57	15.36388	1.37E-35
GO:0042330~taxis	31	8.355795	1.81E-26
GO:0006935~chemotaxis	31	8.355795	1.81E-26
GO:0002252~immune effector process	29	7.816712	5.57E-22
GO:0005576~extracellular region	96	25.87601	4.91E-19
GO:0002684~positive regulation of immune system process	31	8.355795	5.63E-18
GO:0030246~carbohydrate binding	37	9.973046	1.60E-17
GO:0044421~extracellular region part	60	16.17251	2.71E-17
GO:0007626~locomotory behavior	32	8.625337	4.52E-17
GO:0002443~leukocyte mediated immunity	21	5.660377	4.01E-16
GO:0045087~innate immune response	22	5.929919	1.45E-15
GO:0050778~positive regulation of immune response	24	6.469003	1.85E-15
GO:0002460~adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	20	5.390836	2.07E-15
GO:0002250~adaptive immune response	20	5.390836	2.07E-15
GO:0048584~positive regulation of response to stimulus	27	7.277628	3.11E-15
GO:0002449~lymphocyte mediated immunity	19	5.121294	4.81E-15
GO:0001775~cell activation	29	7.816712	5.29E-14
mmu04060:Cytokine-cytokine receptor interaction	33	8.894879	6.92E-14
GO:0019724~B cell mediated immunity	17	4.58221	8.63E-14
GO:0002526~acute inflammatory response	18	4.851752	2.43E-13
GO:0005615~extracellular space	42	11.32075	8.54E-13
GO:0016064~immunoglobulin mediated immune response	16	4.312668	8.92E-13
GO:0007610~behavior	34	9.16442	3.70E-12
GO:0002253~activation of immune response	17	4.58221	8.91E-12
GO:0005529~sugar binding	23	6.199461	1.15E-11
GO:0030595~leukocyte chemotaxis	11	2.96496	4.56E-11
GO:0060326~cell chemotaxis	11	2.96496	4.56E-11
GO:0045321~leukocyte activation	24	6.469003	5.53E-11
GO:0008009~chemokine activity	12	3.234501	1.26E-10
GO:0042379~chemokine receptor binding	12	3.234501	1.72E-10
GO:0002478~antigen processing and presentation of exogenous peptide antigen	10	2.695418	2.45E-10
GO:0050766~positive regulation of phagocytosis	10	2.695418	2.45E-10
GO:0050900~leukocyte migration	12	3.234501	4.53E-10
GO:0050764~regulation of phagocytosis	10	2.695418	5.92E-10
mmu04062:Chemokine signaling pathway	24	6.469003	7.23E-10
GO:0002274~myeloid leukocyte activation	11	2.96496	8.64E-10
GO:0048002~antigen processing and presentation of peptide antigen	11	2.96496	8.64E-10
GO:0019884~antigen processing and presentation of exogenous antigen	10	2.695418	1.90E-09
GO:0030247~polysaccharide binding	17	4.58221	5.33E-09
GO:0001871~pattern binding	17	4.58221	5.33E-09
mmu04640:Hematopoietic cell lineage	16	4.312668	6.97E-09
GO:0019886~antigen processing and presentation of exogenous peptide antigen via MHC class II	8	2.156334	1.03E-08
GO:0002495~antigen processing and presentation of peptide antigen via MHC class II	8	2.156334	1.03E-08
GO:0009617~response to bacterium	18	4.851752	1.22E-08
GO:0045807~positive regulation of endocytosis	10	2.695418	1.30E-08
GO:0005125~cytokine activity	19	5.121294	2.10E-08
GO:0002504~antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	8	2.156334	4.31E-08
GO:0016477~cell migration	21	5.660377	5.56E-08
GO:0050865~regulation of cell activation	17	4.58221	7.15E-08
GO:0009986~cell surface	25	6.738544	9.08E-08
GO:0001817~regulation of cytokine production	16	4.312668	9.40E-08
GO:0002819~regulation of adaptive immune response	11	2.96496	1.17E-07
GO:0002822~regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	11	2.96496	1.17E-07
mmu05322:Systemic lupus erythematosus	16	4.312668	1.21E-07
GO:0019955~cytokine binding	13	3.504043	1.72E-07
GO:0009897~external side of plasma membrane	20	5.390836	1.82E-07
GO:0050830~defense response to Gram-positive bacterium	8	2.156334	1.96E-07
GO:0002694~regulation of leukocyte activation	16	4.312668	3.64E-07
GO:0042110~T cell activation	14	3.773585	4.42E-07
GO:0030593~neutrophil chemotaxis	7	1.886792	5.62E-07

GO:0030100~regulation of endocytosis	10	2.695418	6.71E-07
GO:0042127~regulation of cell proliferation	30	8.086253	8.29E-07
GO:0048870~cell motility	21	5.660377	8.44E-07
GO:0051674~localization of cell	21	5.660377	8.44E-07
GO:0006959~humoral immune response	10	2.695418	9.37E-07
GO:0019221~cytokine-mediated signaling pathway	10	2.695418	1.29E-06
GO:0042742~defense response to bacterium	13	3.504043	1.35E-06
GO:0006953~acute-phase response	8	2.156334	1.45E-06
GO:0001816~cytokine production	9	2.425876	1.60E-06
mmu04662:B cell receptor signaling pathway	13	3.504043	1.71E-06
GO:0007155~cell adhesion	30	8.086253	1.94E-06
GO:0022610~biological adhesion	30	8.086253	2.01E-06
GO:0001944~vasculature development	19	5.121294	2.22E-06
mmu04620:Toll-like receptor signaling pathway	14	3.773585	2.93E-06
GO:0002757~immune response-activating signal transduction	9	2.425876	3.82E-06
GO:0002455~humoral immune response mediated by circulating immunoglobulin	8	2.156334	4.39E-06
GO:0002237~response to molecule of bacterial origin	9	2.425876	4.49E-06
GO:0050867~positive regulation of cell activation	12	3.234501	4.57E-06
GO:0051605~protein maturation by peptide bond cleavage	10	2.695418	4.66E-06
GO:0051130~positive regulation of cellular component organization	13	3.504043	4.94E-06
GO:0060627~regulation of vesicle-mediated transport	11	2.96496	4.99E-06
GO:0051249~regulation of lymphocyte activation	14	3.773585	5.18E-06
GO:0002541~activation of plasma proteins involved in acute inflammatory response	8	2.156334	5.36E-06
GO:0006956~complement activation	8	2.156334	5.36E-06
GO:0031012~extracellular matrix	22	5.929919	6.14E-06
GO:0001568~blood vessel development	18	4.851752	6.62E-06
GO:0002764~immune response-regulating signal transduction	9	2.425876	7.12E-06
GO:0019882~antigen processing and presentation	11	2.96496	7.67E-06
GO:0016485~protein processing	11	2.96496	1.04E-05
GO:0051050~positive regulation of transport	13	3.504043	1.12E-05
GO:0032680~regulation of tumor necrosis factor production	7	1.886792	1.14E-05
GO:0005578~proteinaceous extracellular matrix	21	5.660377	1.19E-05
GO:0006928~cell motion	22	5.929919	1.20E-05
GO:0042098~T cell proliferation	7	1.886792	1.43E-05
GO:0031349~positive regulation of defense response	9	2.425876	1.44E-05
GO:0005539~glycosaminoglycan binding	12	3.234501	1.75E-05
GO:0051604~protein maturation	11	2.96496	1.85E-05
GO:0002673~regulation of acute inflammatory response	6	1.617251	1.96E-05
GO:0002889~regulation of immunoglobulin mediated immune response	7	1.886792	2.17E-05
GO:0006958~complement activation, classical pathway	7	1.886792	2.17E-05
GO:0002712~regulation of B cell mediated immunity	7	1.886792	2.17E-05
GO:0002696~positive regulation of leukocyte activation	11	2.96496	2.43E-05
GO:0046649~lymphocyte activation	15	4.043127	2.49E-05
GO:0001819~positive regulation of cytokine production	9	2.425876	2.70E-05
GO:0050829~defense response to Gram-negative bacterium	5	1.347709	2.79E-05
GO:0001666~response to hypoxia	9	2.425876	3.42E-05
GO:0032101~regulation of response to external stimulus	11	2.96496	3.43E-05
GO:0001763~morphogenesis of a branching structure	12	3.234501	3.52E-05
mmu04610:Complement and coagulation cascades	11	2.96496	3.73E-05
GO:0070482~response to oxygen levels	9	2.425876	3.83E-05
GO:0050870~positive regulation of T cell activation	9	2.425876	4.29E-05
GO:0002675~positive regulation of acute inflammatory response	5	1.347709	4.31E-05
GO:0006909~phagocytosis	8	2.156334	4.44E-05
GO:0002821~positive regulation of adaptive immune response	7	1.886792	4.61E-05
GO:0002824~positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	7	1.886792	4.61E-05
GO:0008284~positive regulation of cell proliferation	18	4.851752	4.69E-05
GO:0050863~regulation of T cell activation	11	2.96496	5.17E-05
GO:0019864~IgG binding	4	1.078167	7.70E-05
mmu04666:Fc gamma R-mediated phagocytosis	12	3.234501	7.75E-05
GO:0032496~response to lipopolysaccharide	7	1.886792	8.86E-05
GO:0042277~peptide binding	13	3.504043	9.01E-05
GO:0051240~positive regulation of multicellular organismal process	13	3.504043	9.05E-05
GO:0002883~regulation of hypersensitivity	5	1.347709	9.06E-05
GO:0002864~regulation of acute inflammatory response to antigenic stimulus	5	1.347709	9.06E-05
GO:0051251~positive regulation of lymphocyte activation	10	2.695418	9.45E-05
GO:0032103~positive regulation of response to external stimulus	7	1.886792	1.03E-04
GO:0004896~cytokine receptor activity	8	2.156334	1.06E-04
mmu04672:Intestinal immune network for IgA production	9	2.425876	1.07E-04
GO:0008283~cell proliferation	16	4.312668	1.12E-04

GO:0002683~negative regulation of immune system process	9	2.425876	1.19E-04
GO:0050727~regulation of inflammatory response	8	2.156334	1.19E-04
GO:0007159~leukocyte adhesion	5	1.347709	1.25E-04
GO:0002891~positive regulation of immunoglobulin mediated immune response	5	1.347709	1.25E-04
GO:0002714~positive regulation of B cell mediated immunity	5	1.347709	1.25E-04
mmu04650:Natural killer cell mediated cytotoxicity	13	3.504043	1.34E-04
GO:0002429~immune response-activating cell surface receptor signaling pathway	7	1.886792	1.37E-04
GO:0046651~lymphocyte proliferation	7	1.886792	1.58E-04
GO:0045576~mast cell activation	5	1.347709	1.68E-04
GO:0032760~positive regulation of tumor necrosis factor production	5	1.347709	1.68E-04
GO:0006911~phagocytosis, engulfment	5	1.347709	1.68E-04
GO:0002886~regulation of myeloid leukocyte mediated immunity	5	1.347709	1.68E-04
GO:0070661~leukocyte proliferation	7	1.886792	1.80E-04
GO:0032943~mononuclear cell proliferation	7	1.886792	1.80E-04
GO:0002768~immune response-regulating cell surface receptor signaling pathway	7	1.886792	2.05E-04
GO:0008201~heparin binding	9	2.425876	2.50E-04
GO:0009620~response to fungus	5	1.347709	2.84E-04
GO:0060324~face development	5	1.347709	2.84E-04
GO:0030574~collagen catabolic process	5	1.347709	2.84E-04
GO:0001525~angiogenesis	11	2.96496	2.93E-04
GO:0051094~positive regulation of developmental process	14	3.773585	3.18E-04
GO:0002697~regulation of immune effector process	9	2.425876	3.31E-04
GO:0002861~regulation of inflammatory response to antigenic stimulus	5	1.347709	3.59E-04
GO:0044243~multicellular organismal catabolic process	5	1.347709	3.59E-04
GO:0001653~peptide receptor activity	10	2.695418	3.59E-04
GO:0008528~peptide receptor activity, G-protein coupled	10	2.695418	3.59E-04
GO:0045582~positive regulation of T cell differentiation	6	1.617251	3.68E-04
GO:0001796~regulation of type II hypersensitivity	4	1.078167	3.91E-04
GO:0002892~regulation of type II hypersensitivity	4	1.078167	3.91E-04
GO:0002888~positive regulation of myeloid leukocyte mediated immunity	4	1.078167	3.91E-04
GO:0002894~positive regulation of type II hypersensitivity	4	1.078167	3.91E-04
GO:0001798~positive regulation of type II hypersensitivity	4	1.078167	3.91E-04
GO:0010033~response to organic substance	23	6.199461	4.15E-04
GO:0002703~regulation of leukocyte mediated immunity	8	2.156334	4.36E-04
mmu04670:Leukocyte transendothelial migration	12	3.234501	4.40E-04
GO:0030334~regulation of cell migration	9	2.425876	4.48E-04
GO:0006690~icosanoid metabolic process	6	1.617251	4.92E-04
GO:0045621~positive regulation of lymphocyte differentiation	6	1.617251	4.92E-04
GO:0048514~blood vessel morphogenesis	13	3.504043	5.49E-04
GO:0002695~negative regulation of leukocyte activation	7	1.886792	5.76E-04
GO:0050730~regulation of peptidyl-tyrosine phosphorylation	7	1.886792	5.76E-04
GO:0050866~negative regulation of cell activation	7	1.886792	5.76E-04
GO:0005886~plasma membrane	90	24.25876	5.82E-04
GO:0042325~regulation of phosphorylation	16	4.312668	6.26E-04
GO:0033559~unsaturated fatty acid metabolic process	6	1.617251	6.46E-04
GO:0005764~lysosome	13	3.504043	6.69E-04
GO:0060322~head development	5	1.347709	6.70E-04
GO:0045597~positive regulation of cell differentiation	12	3.234501	6.87E-04
GO:0000323~lytic vacuole	13	3.504043	7.03E-04
GO:0009615~response to virus	8	2.156334	7.20E-04
GO:0030335~positive regulation of cell migration	6	1.617251	7.35E-04
GO:0002866~positive regulation of acute inflammatory response to antigenic stimulus	4	1.078167	8.13E-04
GO:0002885~positive regulation of hypersensitivity	4	1.078167	8.13E-04
GO:0030414~peptidase inhibitor activity	12	3.234501	8.36E-04
GO:0004175~endopeptidase activity	20	5.390836	8.41E-04
GO:0051174~regulation of phosphorus metabolic process	16	4.312668	9.18E-04
GO:0019220~regulation of phosphate metabolic process	16	4.312668	9.18E-04
GO:0045619~regulation of lymphocyte differentiation	7	1.886792	9.36E-04
GO:0032963~collagen metabolic process	5	1.347709	9.61E-04
GO:0032944~regulation of mononuclear cell proliferation	8	2.156334	9.78E-04
GO:0050670~regulation of lymphocyte proliferation	8	2.156334	9.78E-04
GO:0005044~scavenger receptor activity	6	1.617251	0.001021
GO:0070663~regulation of leukocyte proliferation	8	2.156334	0.001133
GO:0044259~multicellular organismal macromolecule metabolic process	5	1.347709	0.001136
GO:0050729~positive regulation of inflammatory response	5	1.347709	0.001136
GO:0001803~regulation of type III hypersensitivity	3	0.808625	0.001139
GO:0001805~positive regulation of type III hypersensitivity	3	0.808625	0.001139
mmu04514:Cell adhesion molecules (CAMs)	13	3.504043	0.00114
GO:0001503~ossification	9	2.425876	0.001147
GO:0019865~immunoglobulin binding	4	1.078167	0.001162

GO:0051272~positive regulation of cell motion	6	1.617251	0.001186
GO:0051270~regulation of cell motion	9	2.425876	0.001219
GO:0006897~endocytosis	12	3.234501	0.001238
GO:0010324~membrane invagination	12	3.234501	0.001238
GO:0042108~positive regulation of cytokine biosynthetic process	6	1.617251	0.001325
GO:0048534~hemopoietic or lymphoid organ development	15	4.043127	0.001351
GO:0008237~metallopeptidase activity	12	3.234501	0.001371
GO:0030097~hemopoiesis	14	3.773585	0.001408
GO:0001909~leukocyte mediated cytotoxicity	4	1.078167	0.001447
GO:0040012~regulation of locomotion	9	2.425876	0.001457
GO:0004866~endopeptidase inhibitor activity	11	2.96496	0.001498
GO:0044236~multicellular organismal metabolic process	5	1.347709	0.00155
GO:0042035~regulation of cytokine biosynthetic process	7	1.886792	0.001571
GO:0040017~positive regulation of locomotion	6	1.617251	0.001638
GO:0048585~negative regulation of response to stimulus	7	1.886792	0.001703
GO:0002706~regulation of lymphocyte mediated immunity	7	1.886792	0.001703
GO:0045765~regulation of angiogenesis	6	1.617251	0.001814
GO:0002863~positive regulation of inflammatory response to antigenic stimulus	4	1.078167	0.001854
GO:0042089~cytokine biosynthetic process	4	1.078167	0.001854
GO:0045088~regulation of innate immune response	6	1.617251	0.002003
GO:0002699~positive regulation of immune effector process	6	1.617251	0.002003
GO:0004222~metalloendopeptidase activity	9	2.425876	0.002053
GO:0008083~growth factor activity	10	2.695418	0.00212
GO:0002520~immune system development	15	4.043127	0.002123
GO:0005773~vacuole	13	3.504043	0.002162
GO:0060348~bone development	9	2.425876	0.002275
GO:0042107~cytokine metabolic process	4	1.078167	0.002326
GO:0006692~prostanoid metabolic process	4	1.078167	0.002326
GO:0006693~prostaglandin metabolic process	4	1.078167	0.002326
GO:0070011~peptidase activity, acting on L-amino acid peptides	24	6.469003	0.002331
GO:0019763~immunoglobulin receptor activity	3	0.808625	0.002332
GO:0045580~regulation of T cell differentiation	6	1.617251	0.002424
GO:0051607~defense response to virus	4	1.078167	0.002865
GO:0002263~cell activation during immune response	5	1.347709	0.00302
GO:0002366~leukocyte activation during immune response	5	1.347709	0.00302
GO:0019838~growth factor binding	7	1.886792	0.003149
mmu04510:Focal adhesion	14	3.773585	0.003356
GO:0032675~regulation of interleukin-6 production	5	1.347709	0.003399
GO:0051250~negative regulation of lymphocyte activation	6	1.617251	0.003452
GO:0001906~cell killing	4	1.078167	0.003476
mmu05200:Pathways in cancer	19	5.121294	0.003607
GO:0004857~enzyme inhibitor activity	13	3.504043	0.003644
GO:0005537~mannose binding	4	1.078167	0.003662
GO:0042590~antigen processing and presentation of exogenous peptide antigen via MHC class I	3	0.808625	0.003699
GO:0007229~integrin-mediated signaling pathway	7	1.886792	0.00377
GO:0014032~neural crest cell development	5	1.347709	0.003809
GO:0014033~neural crest cell differentiation	5	1.347709	0.003809
GO:0008233~peptidase activity	24	6.469003	0.003959
GO:0002444~myeloid leukocyte mediated immunity	4	1.078167	0.00416
GO:0001501~skeletal system development	14	3.773585	0.004243
GO:0044092~negative regulation of molecular function	9	2.425876	0.004533
GO:0032403~protein complex binding	7	1.886792	0.004688
GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	11	2.96496	0.0047
GO:0032755~positive regulation of interleukin-6 production	4	1.078167	0.00492
GO:0050851~antigen receptor-mediated signaling pathway	5	1.347709	0.005237
GO:0045089~positive regulation of innate immune response	5	1.347709	0.005237
GO:0045123~cellular extravasation	3	0.808625	0.005477
GO:0001878~response to yeast	3	0.808625	0.005477
GO:0035295~tube development	13	3.504043	0.006029
GO:0042981~regulation of apoptosis	21	5.660377	0.006467
GO:0002698~negative regulation of immune effector process	4	1.078167	0.006677
GO:0009967~positive regulation of signal transduction	10	2.695418	0.006963
GO:0009612~response to mechanical stimulus	5	1.347709	0.006986
mmu04621:NOD-like receptor signaling pathway	7	1.886792	0.007249
GO:0007242~intracellular signaling cascade	30	8.086253	0.00735
GO:0043067~regulation of programmed cell death	21	5.660377	0.007374
GO:0045073~regulation of chemokine biosynthetic process	3	0.808625	0.007568
GO:0002437~inflammatory response to antigenic stimulus	3	0.808625	0.007568
GO:0046627~negative regulation of insulin receptor signaling pathway	3	0.808625	0.007568
mmu04664:Fc epsilon RI signaling pathway	8	2.156334	0.007573

GO:0016044~membrane organization	13	3.504043	0.007632
GO:0002708~positive regulation of lymphocyte mediated immunity	5	1.347709	0.007644
GO:0002705~positive regulation of leukocyte mediated immunity	5	1.347709	0.007644
GO:0010810~regulation of cell-substrate adhesion	5	1.347709	0.007644
GO:0010740~positive regulation of protein kinase cascade	7	1.886792	0.007695
GO:0043066~negative regulation of apoptosis	12	3.234501	0.007707
GO:0004908~interleukin-1 receptor activity	3	0.808625	0.007845
GO:0019966~interleukin-1 binding	3	0.808625	0.007845
GO:0010941~regulation of cell death	21	5.660377	0.007863
GO:0007167~enzyme linked receptor protein signaling pathway	13	3.504043	0.007936
GO:0035272~exocrine system development	5	1.347709	0.008342
GO:0043069~negative regulation of programmed cell death	12	3.234501	0.008955
GO:0060548~negative regulation of cell death	12	3.234501	0.009216
GO:0019239~deaminase activity	4	1.078167	0.009218
GO:0004950~chemokine receptor activity	4	1.078167	0.009218
GO:0001932~regulation of protein amino acid phosphorylation	8	2.156334	0.009889
GO:0001810~regulation of type I hypersensitivity	3	0.808625	0.009961
GO:0045059~positive thymic T cell selection	3	0.808625	0.009961
GO:0048754~branching morphogenesis of a tube	7	1.886792	0.009985
GO:0005509~calcium ion binding	28	7.54717	0.010115
GO:0001530~lipopolysaccharide binding	3	0.808625	0.010323
GO:0019956~chemokine binding	4	1.078167	0.010446
GO:0005164~tumor necrosis factor receptor binding	4	1.078167	0.010446
GO:0030155~regulation of cell adhesion	7	1.886792	0.010495
GO:0043235~receptor complex	7	1.886792	0.010697
GO:0045859~regulation of protein kinase activity	10	2.695418	0.011314
GO:0010647~positive regulation of cell communication	10	2.695418	0.012472
GO:0031226~intrinsic to plasma membrane	22	5.929919	0.012583
GO:0045060~negative thymic T cell selection	3	0.808625	0.012642
mmu05310:Asthma	5	1.347709	0.012692
GO:0048407~platelet-derived growth factor binding	3	0.808625	0.013098
GO:0014031~mesenchymal cell development	5	1.347709	0.013412
GO:0043549~regulation of kinase activity	10	2.695418	0.013707
mmu05218:Melanoma	7	1.886792	0.013767
GO:0046635~positive regulation of alpha-beta T cell activation	4	1.078167	0.013968
GO:0043086~negative regulation of catalytic activity	7	1.886792	0.014596
GO:0048029~monosaccharide binding	4	1.078167	0.014676
GO:0032813~tumor necrosis factor receptor superfamily binding	4	1.078167	0.014676
GO:0048762~mesenchymal cell differentiation	5	1.347709	0.015455
mmu04010:MAPK signaling pathway	15	4.043127	0.015456
GO:0046456~icosanoid biosynthetic process	4	1.078167	0.01549
GO:0007435~salivary gland morphogenesis	4	1.078167	0.01549
GO:0051048~negative regulation of secretion	4	1.078167	0.01549
mmu05020:Prion diseases	5	1.347709	0.015558
GO:0043383~negative T cell selection	3	0.808625	0.015599
GO:0042116~macrophage activation	3	0.808625	0.015599
GO:0046457~prostanoid biosynthetic process	3	0.808625	0.015599
GO:0002221~pattern recognition receptor signaling pathway	3	0.808625	0.015599
GO:0001516~prostaglandin biosynthetic process	3	0.808625	0.015599
GO:0006957~complement activation, alternative pathway	3	0.808625	0.015599
GO:0046626~regulation of insulin receptor signaling pathway	3	0.808625	0.015599
GO:0043368~positive T cell selection	3	0.808625	0.015599
GO:0005887~integral to plasma membrane	21	5.660377	0.016213
GO:0009725~response to hormone stimulus	9	2.425876	0.016319
GO:0007160~cell-matrix adhesion	5	1.347709	0.016547
GO:0060485~mesenchyme development	5	1.347709	0.016547
GO:0030217~T cell differentiation	6	1.617251	0.016807
GO:0051338~regulation of transferase activity	10	2.695418	0.016944
GO:0006636~unsaturated fatty acid biosynthetic process	4	1.078167	0.017102
mmu04810:Regulation of actin cytoskeleton	13	3.504043	0.017574
GO:0033673~negative regulation of kinase activity	5	1.347709	0.017685
GO:0006469~negative regulation of protein kinase activity	5	1.347709	0.017685
mmu04623:Cytosolic DNA-sensing pathway	6	1.617251	0.017935
GO:0031225~anchored to membrane	11	2.96496	0.018217
GO:0016337~cell-cell adhesion	11	2.96496	0.018397
GO:0007173~epidermal growth factor receptor signaling pathway	3	0.808625	0.018821
GO:0032642~regulation of chemokine production	3	0.808625	0.018821
GO:0009968~negative regulation of signal transduction	9	2.425876	0.019791
GO:0035239~tube morphogenesis	9	2.425876	0.019791
GO:0042613~MHC class II protein complex	3	0.808625	0.019969

GO:0051348~negative regulation of transferase activity	5	1.347709	0.020106
GO:0032994~protein-lipid complex	4	1.078167	0.021849
GO:0034358~plasma lipoprotein particle	4	1.078167	0.021849
GO:0002521~leukocyte differentiation	8	2.156334	0.022093
mmu05332:Graft-versus-host disease	6	1.617251	0.02211
GO:0030324~lung development	7	1.886792	0.022216
GO:0060325~face morphogenesis	3	0.808625	0.022296
GO:0002758~innate immune response-activating signal transduction	3	0.808625	0.022296
GO:0007431~salivary gland development	4	1.078167	0.022479
GO:0042060~wound healing	7	1.886792	0.023101
GO:0048872~homeostasis of number of cells	7	1.886792	0.02401
GO:0030323~respiratory tube development	7	1.886792	0.02401
GO:0008305~integrin complex	4	1.078167	0.024075
GO:0032649~regulation of interferon-gamma production	4	1.078167	0.024453
GO:0022612~gland morphogenesis	6	1.617251	0.024783
GO:0030098~lymphocyte differentiation	7	1.886792	0.024942
GO:0031589~cell-substrate adhesion	5	1.347709	0.025533
GO:0002823~negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	3	0.808625	0.026013
GO:0006910~phagocytosis, recognition	3	0.808625	0.026013
GO:0002820~negative regulation of adaptive immune response	3	0.808625	0.026013
GO:0050854~regulation of antigen receptor-mediated signaling pathway	3	0.808625	0.026013
mmu04512:ECM-receptor interaction	7	1.886792	0.027673
GO:0042129~regulation of T cell proliferation	5	1.347709	0.028546
GO:0046634~regulation of alpha-beta T cell activation	4	1.078167	0.028672
GO:0009719~response to endogenous stimulus	9	2.425876	0.029053
GO:0006916~anti-apoptosis	6	1.617251	0.029549
GO:0006739~NADP metabolic process	3	0.808625	0.029961
GO:0002707~negative regulation of lymphocyte mediated immunity	3	0.808625	0.029961
GO:0050853~B cell receptor signaling pathway	3	0.808625	0.029961
GO:0060323~head morphogenesis	3	0.808625	0.029961
GO:0002286~T cell activation during immune response	3	0.808625	0.029961
GO:0002218~activation of innate immune response	3	0.808625	0.029961
GO:0002704~negative regulation of leukocyte mediated immunity	3	0.808625	0.029961
GO:0010648~negative regulation of cell communication	9	2.425876	0.030701
GO:0032945~negative regulation of mononuclear cell proliferation	4	1.078167	0.030917
GO:0050672~negative regulation of lymphocyte proliferation	4	1.078167	0.030917
GO:0070664~negative regulation of leukocyte proliferation	4	1.078167	0.030917
mmu05214:Glioma	6	1.617251	0.03224
GO:0010627~regulation of protein kinase cascade	8	2.156334	0.033457
GO:0045061~thymic T cell selection	3	0.808625	0.034129
GO:0031224~intrinsic to membrane	149	40.16173	0.03415
GO:0060541~respiratory system development	7	1.886792	0.035613
GO:0045860~positive regulation of protein kinase activity	7	1.886792	0.035613
GO:0030168~platelet activation	3	0.808625	0.038508
GO:0008217~regulation of blood pressure	5	1.347709	0.038808
GO:0045630~positive regulation of T-helper 2 cell differentiation	2	0.539084	0.038915
GO:0060346~bone trabecula formation	2	0.539084	0.038915
GO:0030854~positive regulation of granulocyte differentiation	2	0.539084	0.038915
GO:0042095~interferon-gamma biosynthetic process	2	0.539084	0.038915
GO:0004962~endothelin receptor activity	2	0.539084	0.039637
GO:0019770~IgG receptor activity	2	0.539084	0.039637
GO:0004909~interleukin-1, Type I, activating receptor activity	2	0.539084	0.039637
GO:0030099~myeloid cell differentiation	6	1.617251	0.040719
GO:0048565~gut development	4	1.078167	0.040788
GO:0043603~cellular amide metabolic process	4	1.078167	0.040788
mmu04612:Antigen processing and presentation	7	1.886792	0.040838
GO:0016192~vesicle-mediated transport	16	4.312668	0.042206
GO:0045766~positive regulation of angiogenesis	3	0.808625	0.043088
GO:0046888~negative regulation of hormone secretion	3	0.808625	0.043088
GO:0060713~labyrinthine layer morphogenesis	3	0.808625	0.043088
GO:0002474~antigen processing and presentation of peptide antigen via MHC class I	3	0.808625	0.043088
GO:0033674~positive regulation of kinase activity	7	1.886792	0.043239
GO:0007243~protein kinase cascade	10	2.695418	0.04376
GO:0031399~regulation of protein modification process	8	2.156334	0.044469
GO:0019957~C-C chemokine binding	3	0.808625	0.044557
GO:0016493~C-C chemokine receptor activity	3	0.808625	0.044557
mmu05416:Viral myocarditis	7	1.886792	0.046647
GO:0019748~secondary metabolic process	5	1.347709	0.046677
GO:0012502~induction of programmed cell death	8	2.156334	0.04692

GO:0006917~induction of apoptosis	8	2.156334	0.04692
GO:0004713~protein tyrosine kinase activity	8	2.156334	0.046976
GO:0051241~negative regulation of multicellular organismal process	6	1.617251	0.047145
mmu04142:Lysosome	8	2.156334	0.047797
GO:0060445~branching involved in salivary gland morphogenesis	3	0.808625	0.047859
GO:0048568~embryonic organ development	10	2.695418	0.04884
GO:0030005~cellular di-, tri-valent inorganic cation homeostasis	7	1.886792	0.048851
GO:0050868~negative regulation of T cell activation	4	1.078167	0.049108
GO:0005100~Rho GTPase activator activity	3	0.808625	0.049479
GO:0051347~positive regulation of transferase activity	7	1.886792	0.050321
GO:0006508~proteolysis	29	7.816712	0.051911
GO:0002285~lymphocyte activation during immune response	3	0.808625	0.052812
GO:0046638~positive regulation of alpha-beta T cell differentiation	3	0.808625	0.052812
GO:0006801~superoxide metabolic process	3	0.808625	0.052812
GO:0051051~negative regulation of transport	5	1.347709	0.053118
GO:0050660~FAD binding	5	1.347709	0.053821
GO:0051537~2 iron, 2 sulfur cluster binding	3	0.808625	0.054587
GO:0042365~water-soluble vitamin catabolic process	2	0.539084	0.057802
GO:0002890~negative regulation of immunoglobulin mediated immune response	2	0.539084	0.057802
GO:0032763~regulation of mast cell cytokine production	2	0.539084	0.057802
GO:0002713~negative regulation of B cell mediated immunity	2	0.539084	0.057802
GO:0006742~NADP catabolic process	2	0.539084	0.057802
GO:0002238~response to molecule of fungal origin	2	0.539084	0.057802
GO:0019364~pyridine nucleotide catabolic process	2	0.539084	0.057802
GO:0008228~opsonization	2	0.539084	0.057802
GO:0010171~body morphogenesis	3	0.808625	0.057938
GO:0001872~zymosan binding	2	0.539084	0.058864
GO:0004942~anaphylatoxin receptor activity	2	0.539084	0.058864
GO:0005540~hyaluronic acid binding	3	0.808625	0.059871
mmu04630:Jak-STAT signaling pathway	9	2.425876	0.061296
GO:0001936~regulation of endothelial cell proliferation	3	0.808625	0.063228
GO:0045058~T cell selection	3	0.808625	0.063228
GO:0048771~tissue remodeling	4	1.078167	0.064648
GO:0006800~oxygen and reactive oxygen species metabolic process	4	1.078167	0.064648
GO:0008037~cell recognition	4	1.078167	0.064648
GO:0043410~positive regulation of MAPKKK cascade	4	1.078167	0.064648
GO:0001891~phagocytic cup	2	0.539084	0.065691
GO:0003013~circulatory system process	6	1.617251	0.067752
GO:0008015~blood circulation	6	1.617251	0.067752
GO:0030218~erythrocyte differentiation	4	1.078167	0.067998
GO:0055066~di-, tri-valent inorganic cation homeostasis	7	1.886792	0.068278
GO:0050852~T cell receptor signaling pathway	3	0.808625	0.068675
GO:0046637~regulation of alpha-beta T cell differentiation	3	0.808625	0.068675
GO:0009306~protein secretion	3	0.808625	0.068675
GO:0055080~cation homeostasis	8	2.156334	0.071235
GO:0000165~MAPKKK cascade	6	1.617251	0.074117
GO:0010604~positive regulation of macromolecule metabolic process	19	5.121294	0.074434
GO:0032946~positive regulation of mononuclear cell proliferation	4	1.078167	0.074927
GO:0050671~positive regulation of lymphocyte proliferation	4	1.078167	0.074927
GO:0005770~late endosome	4	1.078167	0.075186
GO:0030818~negative regulation of cAMP biosynthetic process	2	0.539084	0.07632
GO:0030809~negative regulation of nucleotide biosynthetic process	2	0.539084	0.07632
GO:0030803~negative regulation of cyclic nucleotide biosynthetic process	2	0.539084	0.07632
GO:0045416~positive regulation of interleukin-8 biosynthetic process	2	0.539084	0.07632
GO:0002523~leukocyte migration during inflammatory response	2	0.539084	0.07632
GO:0042535~positive regulation of tumor necrosis factor biosynthetic process	2	0.539084	0.07632
GO:0045354~regulation of interferon-alpha biosynthetic process	2	0.539084	0.07632
GO:0042832~defense response to protozoan	2	0.539084	0.07632
GO:0030800~negative regulation of cyclic nucleotide metabolic process	2	0.539084	0.07632
GO:0030815~negative regulation of cAMP metabolic process	2	0.539084	0.07632
GO:0032677~regulation of interleukin-8 production	2	0.539084	0.07632
GO:0045414~regulation of interleukin-8 biosynthetic process	2	0.539084	0.07632
GO:0002445~type II hypersensitivity	2	0.539084	0.07632
GO:0045356~positive regulation of interferon-alpha biosynthetic process	2	0.539084	0.07632
GO:0001788~antibody-dependent cellular cytotoxicity	2	0.539084	0.07632
GO:0046434~organophosphate catabolic process	2	0.539084	0.07632
GO:0030852~regulation of granulocyte differentiation	2	0.539084	0.07632
GO:0001794~type IIa hypersensitivity	2	0.539084	0.07632
mmu05330:Allograft rejection	5	1.347709	0.077471
GO:0008061~chitin binding	2	0.539084	0.077708

GO:0001846~opsonin binding	2	0.539084	0.077708
GO:0031328~positive regulation of cellular biosynthetic process	17	4.58221	0.078392
GO:0034101~erythrocyte homeostasis	4	1.078167	0.078505
GO:0032147~activation of protein kinase activity	4	1.078167	0.078505
GO:0030003~cellular cation homeostasis	7	1.886792	0.079456
GO:0005083~small GTPase regulator activity	9	2.425876	0.07965
GO:0046496~nicotinamide nucleotide metabolic process	3	0.808625	0.080004
GO:0001569~patterning of blood vessels	3	0.808625	0.080004
GO:0006769~nicotinamide metabolic process	3	0.808625	0.080004
GO:0001818~negative regulation of cytokine production	3	0.808625	0.080004
GO:0009820~alkaloid metabolic process	3	0.808625	0.080004
GO:0044093~positive regulation of molecular function	11	2.96496	0.08044
GO:0001701~in utero embryonic development	10	2.695418	0.081309
GO:0070665~positive regulation of leukocyte proliferation	4	1.078167	0.082156
GO:0019932~second-messenger-mediated signaling	6	1.617251	0.083092
GO:0043405~regulation of MAP kinase activity	5	1.347709	0.083395
GO:0009891~positive regulation of biosynthetic process	17	4.58221	0.083867
GO:0007162~negative regulation of cell adhesion	3	0.808625	0.085871
GO:0007585~respiratory gaseous exchange	3	0.808625	0.085871
GO:0030278~regulation of ossification	4	1.078167	0.085879
GO:0050840~extracellular matrix binding	3	0.808625	0.088633
mmu05210:Colorectal cancer	6	1.617251	0.091242
mmu04540:Gap junction	6	1.617251	0.091242
GO:0050777~negative regulation of immune response	3	0.808625	0.091862
GO:0006979~response to oxidative stress	5	1.347709	0.092048
GO:0050864~regulation of B cell activation	4	1.078167	0.093535
GO:0048732~gland development	8	2.156334	0.09426
GO:0009111~vitamin catabolic process	2	0.539084	0.094476
GO:0045351~type I interferon biosynthetic process	2	0.539084	0.094476
GO:0070391~response to lipoteichoic acid	2	0.539084	0.094476
GO:0032609~interferon-gamma production	2	0.539084	0.094476
GO:0002687~positive regulation of leukocyte migration	2	0.539084	0.094476
GO:0045080~positive regulation of chemokine biosynthetic process	2	0.539084	0.094476
GO:0045628~regulation of T-helper 2 cell differentiation	2	0.539084	0.094476
GO:0002524~hypersensitivity	2	0.539084	0.094476
GO:0002438~acute inflammatory response to antigenic stimulus	2	0.539084	0.094476
GO:0032606~type I interferon production	2	0.539084	0.094476
GO:0060665~regulation of branching involved in salivary gland morphogenesis by mesenchymal-epithelial signaling	2	0.539084	0.094476
GO:0001957~intramembranous ossification	2	0.539084	0.094476
GO:0050665~hydrogen peroxide biosynthetic process	2	0.539084	0.094476
GO:0045624~positive regulation of T-helper cell differentiation	2	0.539084	0.094476
mmu04210:Apoptosis	6	1.617251	0.094742
GO:0016814~hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines	3	0.808625	0.094797
GO:0016175~superoxide-generating NADPH oxidase activity	2	0.539084	0.096176
GO:0008517~folic acid transporter activity	2	0.539084	0.096176
GO:0050664~oxidoreductase activity, acting on NADH or NADPH, with oxygen as acceptor	2	0.539084	0.096176
GO:0010811~positive regulation of cell-substrate adhesion	3	0.808625	0.097972
mmu04940:Type I diabetes mellitus	5	1.347709	0.098
GO:0060341~regulation of cellular localization	7	1.886792	0.098032
GO:0050878~regulation of body fluid levels	5	1.347709	0.098046
Downregulated			
GO:0005886~plasma membrane	25	34.72222	0.001189
GO:0006094~gluconeogenesis	3	4.166667	0.003238
GO:0006071~glycerol metabolic process	3	4.166667	0.004277
GO:0006090~pyruvate metabolic process	3	4.166667	0.005044
GO:0019400~alditol metabolic process	3	4.166667	0.005044
GO:0019319~hexose biosynthetic process	3	4.166667	0.005044
GO:0000267~cell fraction	9	12.5	0.005334
GO:0048839~inner ear development	4	5.555556	0.006265
GO:0032994~protein-lipid complex	3	4.166667	0.006661
GO:0034358~plasma lipoprotein particle	3	4.166667	0.006661
GO:0060113~inner ear receptor cell differentiation	3	4.166667	0.007214
GO:0008610~lipid biosynthetic process	6	8.333333	0.007254
GO:0046364~monosaccharide biosynthetic process	3	4.166667	0.007691
GO:0005615~extracellular space	8	11.11111	0.008236
GO:0043583~ear development	4	5.555556	0.00991
GO:0006641~triglyceride metabolic process	3	4.166667	0.010278
GO:0042490~mechanoreceptor differentiation	3	4.166667	0.010278
GO:0005625~soluble fraction	4	5.555556	0.010342

GO:0046165~alcohol biosynthetic process	3	4.166667	0.010836
GO:0006639~acylglycerol metabolic process	3	4.166667	0.014454
GO:0019751~polyol metabolic process	3	4.166667	0.014454
GO:0030855~epithelial cell differentiation	4	5.555556	0.015558
GO:0006662~glycerol ether metabolic process	3	4.166667	0.015761
GO:0006638~neutral lipid metabolic process	3	4.166667	0.015761
GO:0018904~organic ether metabolic process	3	4.166667	0.017812
GO:0020037~heme binding	4	5.555556	0.018709
GO:0046906~tetrapyrrole binding	4	5.555556	0.021186
GO:0034637~cellular carbohydrate biosynthetic process	3	4.166667	0.023797
GO:0007423~sensory organ development	5	6.944444	0.023901
GO:0042127~regulation of cell proliferation	7	9.722222	0.026607
GO:0060429~epithelium development	5	6.944444	0.028325
GO:0044459~plasma membrane part	14	19.444444	0.029657
GO:0042472~inner ear morphogenesis	3	4.166667	0.033164
GO:0019432~triglyceride biosynthetic process	2	2.777778	0.03365
GO:0042627~chylomicron	2	2.777778	0.035902
GO:0004252~serine-type endopeptidase activity	4	5.555556	0.037636
GO:0042471~ear morphogenesis	3	4.166667	0.041724
GO:0045596~negative regulation of cell differentiation	4	5.555556	0.042644
GO:0006631~fatty acid metabolic process	4	5.555556	0.043814
GO:0034361~very-low-density lipoprotein particle	2	2.777778	0.044677
GO:0034385~triglyceride-rich lipoprotein particle	2	2.777778	0.044677
GO:0006633~fatty acid biosynthetic process	3	4.166667	0.046801
GO:0016051~carbohydrate biosynthetic process	3	4.166667	0.048892
mmu04514:Cell adhesion molecules (CAMs)	4	5.555556	0.049247
GO:0015269~calcium-activated potassium channel activity	2	2.777778	0.049717
GO:0008236~serine-type peptidase activity	4	5.555556	0.050013
GO:0046460~neutral lipid biosynthetic process	2	2.777778	0.050056
GO:0046463~acylglycerol biosynthetic process	2	2.777778	0.050056
GO:0017171~serine hydrolase activity	4	5.555556	0.050591
GO:0046504~glycerol ether biosynthetic process	2	2.777778	0.054114
GO:0005227~calcium activated cation channel activity	2	2.777778	0.060842
GO:0022839~ion gated channel activity	2	2.777778	0.060842
GO:0044421~extracellular region part	8	11.111111	0.060858
GO:0051094~positive regulation of developmental process	4	5.555556	0.063248
mmu03320:PPAR signaling pathway	3	4.166667	0.067319
GO:0005516~calmodulin binding	3	4.166667	0.073327
mmu05010:Alzheimer's disease	4	5.555556	0.073743
GO:0008034~lipoprotein binding	2	2.777778	0.079099
GO:0016337~cell-cell adhesion	4	5.555556	0.07964
GO:0008015~blood circulation	3	4.166667	0.081387
GO:0030324~lung development	3	4.166667	0.081387
GO:0003013~circulatory system process	3	4.166667	0.081387
GO:0030323~respiratory tube development	3	4.166667	0.083912
GO:0004129~cytochrome-c oxidase activity	2	2.777778	0.086304
GO:0016675~oxidoreductase activity, acting on heme group of donors	2	2.777778	0.086304
GO:0016676~oxidoreductase activity, acting on heme group of donors, oxygen as acceptor	2	2.777778	0.086304
GO:0015002~heme-copper terminal oxidase activity	2	2.777778	0.086304
GO:0022890~inorganic cation transmembrane transporter activity	3	4.166667	0.088252
GO:0042491~auditory receptor cell differentiation	2	2.777778	0.089881
GO:0030182~neuron differentiation	5	6.944444	0.090313
GO:0005887~integral to plasma membrane	6	8.333333	0.093607
GO:0022836~gated channel activity	4	5.555556	0.097192
GO:0060541~respiratory system development	3	4.166667	0.098214
GO:0031967~organelle envelope	6	8.333333	0.09881
GO:0031975~envelope	6	8.333333	0.099987

Supplementary Table 8. Biological processes enriched in the endothelial genes in APPsw-Tg mice RCA compared to non-Tg mice RCA.

GO Term	Count	%	P-value
Upregulated			
GO:0005576~extracellular region	64	40.25157	2.28E-23
GO:0044421~extracellular region part	44	27.67296	1.64E-21
GO:0031012~extracellular matrix	26	16.3522	3.24E-16
GO:0005578~proteinaceous extracellular matrix	25	15.72327	1.51E-15
GO:0030198~extracellular matrix organization	13	8.176101	1.06E-10
GO:0043062~extracellular structure organization	13	8.176101	9.80E-09
GO:0019838~growth factor binding	10	6.289308	1.56E-08
GO:0005615~extracellular space	22	13.83648	3.13E-08
mmu03320:PPAR signaling pathway	10	6.289308	1.45E-07
GO:0048407~platelet-derived growth factor binding	5	3.144654	7.70E-07
GO:0045444~fat cell differentiation	8	5.031447	1.22E-06
GO:0001871~pattern binding	10	6.289308	2.29E-06
GO:0030247~polysaccharide binding	10	6.289308	2.29E-06
GO:0050873~brown fat cell differentiation	6	3.773585	5.59E-06
GO:0005539~glycosaminoglycan binding	9	5.660377	8.67E-06
GO:0030246~carbohydrate binding	13	8.176101	2.91E-05
GO:0005520~insulin-like growth factor binding	5	3.144654	4.08E-05
GO:0006090~pyruvate metabolic process	5	3.144654	6.98E-05
GO:0008201~heparin binding	7	4.402516	1.02E-04
GO:0009968~negative regulation of signal transduction	9	5.660377	1.61E-04
GO:0007155~cell adhesion	16	10.06289	1.63E-04
GO:0022610~biological adhesion	16	10.06289	1.66E-04
mmu04512:ECM-receptor interaction	7	4.402516	2.69E-04
GO:0010648~negative regulation of cell communication	9	5.660377	2.86E-04
GO:0001503~ossification	7	4.402516	3.97E-04
GO:0060348~bone development	7	4.402516	7.02E-04
GO:0006094~gluconeogenesis	4	2.515723	7.37E-04
GO:0001501~skeletal system development	10	6.289308	0.001132
mmu04610:Complement and coagulation cascades	6	3.773585	0.001299
mmu04510:Focal adhesion	9	5.660377	0.001324
GO:0050840~extracellular matrix binding	4	2.515723	0.001429
GO:0019319~hexose biosynthetic process	4	2.515723	0.001439
GO:0005583~fibrillar collagen	3	1.886792	0.002015
GO:0044420~extracellular matrix part	6	3.773585	0.002265
GO:0046364~monosaccharide biosynthetic process	4	2.515723	0.002704
GO:0030324~lung development	6	3.773585	0.003345
GO:0030323~respiratory tube development	6	3.773585	0.003612
GO:0002541~activation of plasma proteins involved in acute inflammatory response	4	2.515723	0.004156
GO:0006956~complement activation	4	2.515723	0.004156
GO:0006641~triglyceride metabolic process	4	2.515723	0.004156
GO:0046165~alcohol biosynthetic process	4	2.515723	0.004494
GO:0030414~peptidase inhibitor activity	7	4.402516	0.00522
GO:0060541~respiratory system development	6	3.773585	0.005356
GO:0002252~immune effector process	6	3.773585	0.005728
GO:0002526~acute inflammatory response	5	3.144654	0.006222
GO:0004857~enzyme inhibitor activity	8	5.031447	0.006494
GO:0016051~carbohydrate biosynthetic process	5	3.144654	0.006778
GO:0006639~acylglycerol metabolic process	4	2.515723	0.006862
GO:0006638~neutral lipid metabolic process	4	2.515723	0.007788
GO:0006662~glycerol ether metabolic process	4	2.515723	0.007788
GO:0001649~osteoblast differentiation	4	2.515723	0.008783
GO:0006006~glucose metabolic process	6	3.773585	0.008853
GO:0018904~organic ether metabolic process	4	2.515723	0.009308
GO:0001558~regulation of cell growth	5	3.144654	0.009687
mmu04270:Vascular smooth muscle contraction	6	3.773585	0.009841
GO:0035295~tube development	8	5.031447	0.010159
GO:0001655~urogenital system development	6	3.773585	0.010496
GO:0043434~response to peptide hormone stimulus	5	3.144654	0.010812
GO:0016641~oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as acceptor	3	1.886792	0.011259
GO:0042383~sarcolemma	4	2.515723	0.011483
GO:0006959~humoral immune response	4	2.515723	0.012837
GO:0010171~body morphogenesis	3	1.886792	0.013882
GO:0034637~cellular carbohydrate biosynthetic process	4	2.515723	0.01416
GO:0005581~collagen	3	1.886792	0.01517
GO:0016638~oxidoreductase activity, acting on the CH-NH2 group of donors	3	1.886792	0.015183

GO:0004866~endopeptidase inhibitor activity	6	3.773585	0.015334
GO:0010033~response to organic substance	11	6.918239	0.016313
GO:0009725~response to hormone stimulus	6	3.773585	0.017053
GO:0006071~glycerol metabolic process	3	1.886792	0.018162
GO:0019318~hexose metabolic process	6	3.773585	0.018715
GO:0005584~collagen type I	2	1.257862	0.019894
GO:0051605~protein maturation by peptide bond cleavage	4	2.515723	0.021047
GO:0019400~alditol metabolic process	3	1.886792	0.021285
GO:0006631~fatty acid metabolic process	6	3.773585	0.025887
GO:0009719~response to endogenous stimulus	6	3.773585	0.025887
GO:0004601~peroxidase activity	3	1.886792	0.026234
GO:0016684~oxidoreductase activity, acting on peroxide as acceptor	3	1.886792	0.026234
GO:0010744~positive regulation of foam cell differentiation	2	1.257862	0.026913
GO:0040008~regulation of growth	7	4.402516	0.028875
GO:0010876~lipid localization	5	3.144654	0.028914
GO:0032994~protein-lipid complex	3	1.886792	0.029566
GO:0034358~plasma lipoprotein particle	3	1.886792	0.029566
GO:0005996~monosaccharide metabolic process	6	3.773585	0.029764
GO:0005201~extracellular matrix structural constituent	3	1.886792	0.02984
GO:0006958~complement activation, classical pathway	3	1.886792	0.029974
GO:0008235~metalloexopeptidase activity	3	1.886792	0.035593
GO:0010884~positive regulation of lipid storage	2	1.257862	0.035724
GO:0010743~regulation of foam cell differentiation	2	1.257862	0.035724
mmu04920:Adipocytokine signaling pathway	4	2.515723	0.036754
GO:0002455~humoral immune response mediated by circulating immunoglobulin	3	1.886792	0.039821
GO:0005887~integral to plasma membrane	11	6.918239	0.040009
GO:0005740~mitochondrial envelope	9	5.660377	0.042341
GO:0002253~activation of immune response	4	2.515723	0.043066
GO:0006979~response to oxidative stress	4	2.515723	0.044319
GO:0043277~apoptotic cell clearance	2	1.257862	0.044455
GO:0007611~learning or memory	4	2.515723	0.046879
GO:0016485~protein processing	4	2.515723	0.048186
GO:0031226~intrinsic to plasma membrane	11	6.918239	0.04975
GO:0016209~antioxidant activity	3	1.886792	0.05049
GO:0010810~regulation of cell-substrate adhesion	3	1.886792	0.050709
GO:0007507~heart development	6	3.773585	0.052021
GO:0008285~negative regulation of cell proliferation	6	3.773585	0.052839
GO:0008035~high-density lipoprotein binding	2	1.257862	0.052985
GO:0042470~melanosome	4	2.515723	0.053336
GO:0048770~pigment granule	4	2.515723	0.053336
GO:0030155~regulation of cell adhesion	4	2.515723	0.05359
GO:0006790~sulfur metabolic process	4	2.515723	0.05359
GO:0006954~inflammatory response	6	3.773585	0.053665
GO:0051604~protein maturation	4	2.515723	0.056397
GO:0019751~polyol metabolic process	3	1.886792	0.057695
GO:0045879~negative regulation of smoothed signaling pathway	2	1.257862	0.061683
GO:0010883~regulation of lipid storage	2	1.257862	0.061683
GO:0051241~negative regulation of multicellular organismal process	4	2.515723	0.062218
GO:0008131~amine oxidase activity	2	1.257862	0.070021
GO:0019432~triglyceride biosynthetic process	2	1.257862	0.070181
GO:0001568~blood vessel development	6	3.773585	0.070784
GO:0001822~kidney development	4	2.515723	0.073044
GO:0045087~innate immune response	4	2.515723	0.073044
GO:0007517~muscle organ development	5	3.144654	0.075735
GO:0031966~mitochondrial membrane	8	5.031447	0.075928
GO:0005743~mitochondrial inner membrane	7	4.402516	0.07644
GO:0005509~calcium ion binding	13	8.176101	0.076667
GO:0001944~vasculature development	6	3.773585	0.07675
GO:0009628~response to abiotic stimulus	6	3.773585	0.07777
GO:0045932~negative regulation of muscle contraction	2	1.257862	0.078603
GO:0008015~blood circulation	4	2.515723	0.079584
GO:0003013~circulatory system process	4	2.515723	0.079584
GO:0005179~hormone activity	4	2.515723	0.082476
GO:0055114~oxidation reduction	11	6.918239	0.083505
GO:0004867~serine-type endopeptidase inhibitor activity	4	2.515723	0.085883
GO:0004602~glutathione peroxidase activity	2	1.257862	0.086752
GO:0006957~complement activation, alternative pathway	2	1.257862	0.086949
GO:0050872~white fat cell differentiation	2	1.257862	0.086949
GO:0048584~positive regulation of response to stimulus	5	3.144654	0.08853
GO:0008237~metallopeptidase activity	5	3.144654	0.089241

GO:0031967~organelle envelope	10	6.289308	0.091492
GO:0019866~organelle inner membrane	7	4.402516	0.092762
GO:0031975~envelope	10	6.289308	0.093087
GO:0006869~lipid transport	4	2.515723	0.093393
GO:0050727~regulation of inflammatory response	3	1.886792	0.094082
GO:0007612~learning	3	1.886792	0.094082
GO:0009611~response to wounding	7	4.402516	0.095208
GO:0060343~trabecula formation	2	1.257862	0.09522
GO:0034385~triglyceride-rich lipoprotein particle	2	1.257862	0.095622
GO:0034361~very-low-density lipoprotein particle	2	1.257862	0.095622
GO:0001656~metanephros development	3	1.886792	0.096887
GO:0042803~protein homodimerization activity	5	3.144654	0.0974
GO:0005792~microsome	5	3.144654	0.099916
Downregulated			
GO:0005576~extracellular region	3	75	0.018043

Supplementary Table 9. Biological processes enriched in the endothelial genes in APPsw-Tg mice LCA compared to non-Tg mice LCA.

GO Term	Count	%	P-value
Upregulated			
GO:0005576~extracellular region	95	38.77551	1.12E-33
GO:0044421~extracellular region part	58	23.67347	7.85E-25
GO:0030246~carbohydrate binding	32	13.06122	6.39E-18
GO:0006954~inflammatory response	25	10.20408	7.70E-16
GO:0031012~extracellular matrix	30	12.2449	2.42E-15
GO:0009611~response to wounding	29	11.83673	3.36E-15
GO:0006952~defense response	31	12.65306	4.56E-14
GO:0005578~proteinaceous extracellular matrix	28	11.42857	5.23E-14
GO:0030247~polysaccharide binding	19	7.755102	1.68E-13
GO:0001871~pattern binding	19	7.755102	1.68E-13
GO:0005615~extracellular space	33	13.46939	5.93E-12
GO:0006955~immune response	29	11.83673	6.34E-12
GO:0002252~immune effector process	16	6.530612	5.20E-11
GO:0002526~acute inflammatory response	13	5.306122	3.57E-10
GO:0030198~extracellular matrix organization	13	5.306122	4.84E-09
GO:0005539~glycosaminoglycan binding	14	5.714286	6.15E-09
mmu04610:Complement and coagulation cascades	12	4.897959	1.84E-08
GO:0008009~chemokine activity	9	3.673469	4.15E-08
GO:0042379~chemokine receptor binding	9	3.673469	5.16E-08
GO:0045087~innate immune response	12	4.897959	9.91E-08
GO:0008201~heparin binding	11	4.489796	2.17E-07
GO:0002455~humoral immune response mediated by circulating immunoglobulin	8	3.265306	2.21E-07
GO:0005529~sugar binding	15	6.122449	2.30E-07
GO:0043062~extracellular structure organization	13	5.306122	3.83E-07
GO:0006935~chemotaxis	11	4.489796	1.12E-06
GO:0042330~taxis	11	4.489796	1.12E-06
GO:0050778~positive regulation of immune response	12	4.897959	1.14E-06
GO:0016064~immunoglobulin mediated immune response	9	3.673469	1.15E-06
GO:0005125~cytokine activity	14	5.714286	1.37E-06
GO:0019724~B cell mediated immunity	9	3.673469	1.46E-06
GO:0006958~complement activation, classical pathway	7	2.857143	1.68E-06
GO:0007155~cell adhesion	23	9.387755	2.15E-06
GO:0022610~biological adhesion	23	9.387755	2.21E-06
GO:0048584~positive regulation of response to stimulus	13	5.306122	4.02E-06
GO:0006959~humoral immune response	8	3.265306	4.76E-06
GO:0002449~lymphocyte mediated immunity	9	3.673469	4.86E-06
GO:0006956~complement activation	7	2.857143	5.18E-06
GO:0002541~activation of plasma proteins involved in acute inflammatory response	7	2.857143	5.18E-06
mmu04060:Cytokine-cytokine receptor interaction	16	6.530612	5.30E-06
GO:0002460~adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	9	3.673469	1.03E-05
GO:0002250~adaptive immune response	9	3.673469	1.03E-05
GO:0002684~positive regulation of immune system process	13	5.306122	1.14E-05
GO:0002443~leukocyte mediated immunity	9	3.673469	1.59E-05
GO:0001763~morphogenesis of a branching structure	10	4.081633	2.81E-05
GO:0035295~tube development	14	5.714286	2.95E-05
GO:0030414~peptidase inhibitor activity	12	4.897959	3.53E-05
GO:0004857~enzyme inhibitor activity	14	5.714286	3.58E-05
GO:0005509~calcium ion binding	28	11.42857	3.89E-05
GO:0007626~locomotory behavior	13	5.306122	4.97E-05
GO:0005537~mannose binding	5	2.040816	5.81E-05
GO:0002253~activation of immune response	8	3.265306	1.03E-04
GO:0051605~protein maturation by peptide bond cleavage	7	2.857143	1.63E-04
GO:0007610~behavior	16	6.530612	1.85E-04
GO:0004866~endopeptidase inhibitor activity	10	4.081633	4.20E-04
GO:0048029~monosaccharide binding	5	2.040816	4.28E-04
GO:0019838~growth factor binding	7	2.857143	4.90E-04
GO:0006953~acute-phase response	5	2.040816	5.14E-04
mmu04270:Vascular smooth muscle contraction	9	3.673469	5.78E-04
GO:0051607~defense response to virus	4	1.632653	7.97E-04
GO:0045807~positive regulation of endocytosis	5	2.040816	8.36E-04
GO:0016485~protein processing	7	2.857143	9.46E-04
mmu05322:Systemic lupus erythematosus	8	3.265306	0.001152
GO:0051604~protein maturation	7	2.857143	0.001325
GO:0002673~regulation of acute inflammatory response	4	1.632653	0.001391

GO:0044420~extracellular matrix part	7	2.857143	0.002679
GO:0030324~lung development	7	2.857143	0.002773
GO:0050766~positive regulation of phagocytosis	4	1.632653	0.002882
GO:0030323~respiratory tube development	7	2.857143	0.003031
GO:0008083~growth factor activity	8	3.265306	0.003575
GO:0050764~regulation of phagocytosis	4	1.632653	0.003675
GO:0030100~regulation of endocytosis	5	2.040816	0.004097
GO:0022612~gland morphogenesis	6	2.44898	0.004128
GO:0007435~salivary gland morphogenesis	4	1.632653	0.004588
GO:0008237~metallopeptidase activity	9	3.673469	0.004688
GO:0060541~respiratory system development	7	2.857143	0.004786
GO:0004867~serine-type endopeptidase inhibitor activity	7	2.857143	0.005401
GO:0050727~regulation of inflammatory response	5	2.040816	0.005695
GO:0035239~tube morphogenesis	8	3.265306	0.005914
GO:0002009~morphogenesis of an epithelium	8	3.265306	0.006283
GO:0048754~branching morphogenesis of a tube	6	2.44898	0.00635
GO:0051050~positive regulation of transport	7	2.857143	0.006466
GO:0007431~salivary gland development	4	1.632653	0.006796
GO:0050679~positive regulation of epithelial cell proliferation	4	1.632653	0.006796
GO:0008233~peptidase activity	18	7.346939	0.006809
GO:0004714~transmembrane receptor protein tyrosine kinase activity	5	2.040816	0.007603
mmu04062:Chemokine signaling pathway	9	3.673469	0.007904
GO:0002675~positive regulation of acute inflammatory response	3	1.22449	0.008037
GO:0016805~dipeptidase activity	3	1.22449	0.008061
GO:0042127~regulation of cell proliferation	15	6.122449	0.008066
GO:0014033~neural crest cell differentiation	4	1.632653	0.008099
GO:0014032~neural crest cell development	4	1.632653	0.008099
GO:0050678~regulation of epithelial cell proliferation	5	2.040816	0.008104
GO:0001817~regulation of cytokine production	7	2.857143	0.008256
GO:0042035~regulation of cytokine biosynthetic process	5	2.040816	0.008561
GO:0032101~regulation of response to external stimulus	6	2.44898	0.009679
mmu05410:Hypertrophic cardiomyopathy (HCM)	6	2.44898	0.010369
GO:0048729~tissue morphogenesis	9	3.673469	0.010532
GO:0050817~coagulation	5	2.040816	0.01166
GO:0007596~blood coagulation	5	2.040816	0.01166
GO:0007599~hemostasis	5	2.040816	0.012238
GO:0004180~carboxypeptidase activity	4	1.632653	0.012531
GO:0032103~positive regulation of response to external stimulus	4	1.632653	0.012843
GO:0008015~blood circulation	6	2.44898	0.013086
GO:0003013~circulatory system process	6	2.44898	0.013086
GO:0035272~exocrine system development	4	1.632653	0.01471
mmu05414:Dilated cardiomyopathy	6	2.44898	0.014968
GO:0009615~response to virus	5	2.040816	0.0154
GO:0042108~positive regulation of cytokine biosynthetic process	4	1.632653	0.015698
GO:0008238~exopeptidase activity	5	2.040816	0.016345
mmu04621:NOD-like receptor signaling pathway	5	2.040816	0.016405
GO:0045785~positive regulation of cell adhesion	4	1.632653	0.016722
GO:0046068~cGMP metabolic process	3	1.22449	0.016828
GO:0031668~cellular response to extracellular stimulus	4	1.632653	0.018881
GO:0031226~intrinsic to plasma membrane	16	6.530612	0.020319
GO:0060627~regulation of vesicle-mediated transport	5	2.040816	0.020625
GO:0060445~branching involved in salivary gland morphogenesis	3	1.22449	0.021107
GO:0014031~mesenchymal cell development	4	1.632653	0.021187
GO:0070011~peptidase activity, acting on L-amino acid peptides	16	6.530612	0.021352
GO:0035150~regulation of tube size	4	1.632653	0.022395
GO:0050880~regulation of blood vessel size	4	1.632653	0.022395
GO:0007507~heart development	8	3.265306	0.022692
GO:0006909~phagocytosis	4	1.632653	0.023641
GO:0048762~mesenchymal cell differentiation	4	1.632653	0.023641
GO:0005604~basement membrane	5	2.040816	0.024522
GO:0060485~mesenchyme development	4	1.632653	0.024923
GO:0007160~cell-matrix adhesion	4	1.632653	0.024923
GO:0003018~vascular process in circulatory system	4	1.632653	0.024923
GO:0050878~regulation of body fluid levels	5	2.040816	0.025876
GO:0008284~positive regulation of cell proliferation	9	3.673469	0.027344
GO:0006022~aminoglycan metabolic process	4	1.632653	0.027598
GO:0004962~endothelin receptor activity	2	0.816327	0.027652
GO:0004909~interleukin-1, Type I, activating receptor activity	2	0.816327	0.027652
GO:0051537~2 iron, 2 sulfur cluster binding	3	1.22449	0.028223
GO:0030334~regulation of cell migration	5	2.040816	0.028776

GO:0005976~polysaccharide metabolic process	5	2.040816	0.028776
GO:0005887~integral to plasma membrane	15	6.122449	0.030699
GO:0030155~regulation of cell adhesion	5	2.040816	0.030813
GO:0016477~cell migration	8	3.265306	0.032236
GO:0002819~regulation of adaptive immune response	4	1.632653	0.033387
GO:0002822~regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	4	1.632653	0.033387
GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	7	2.857143	0.034477
GO:0031349~positive regulation of defense response	4	1.632653	0.034926
GO:0031589~cell-substrate adhesion	4	1.632653	0.034926
GO:0006508~proteolysis	21	8.571429	0.03578
GO:0050729~positive regulation of inflammatory response	3	1.22449	0.036254
GO:0001656~metanephros development	4	1.632653	0.0365
GO:0005520~insulin-like growth factor binding	3	1.22449	0.037106
GO:0001655~urogenital system development	6	2.44898	0.037264
GO:0008228~opsonization	2	0.816327	0.037283
GO:0048732~gland development	7	2.857143	0.038431
GO:0060688~regulation of morphogenesis of a branching structure	3	1.22449	0.039087
GO:0001872~zymosan binding	2	0.816327	0.041191
GO:0006928~cell motion	10	4.081633	0.042619
GO:0042311~vasodilation	3	1.22449	0.044994
GO:0030595~leukocyte chemotaxis	3	1.22449	0.044994
GO:0060326~cell chemotaxis	3	1.22449	0.044994
GO:0010811~positive regulation of cell-substrate adhesion	3	1.22449	0.044994
GO:0032680~regulation of tumor necrosis factor production	3	1.22449	0.044994
GO:0051270~regulation of cell motion	5	2.040816	0.046086
GO:0001822~kidney development	5	2.040816	0.046086
GO:0005178~integrin binding	3	1.22449	0.046905
GO:0008217~regulation of blood pressure	4	1.632653	0.048519
GO:0045356~positive regulation of interferon-alpha biosynthetic process	2	0.816327	0.049402
GO:0045416~positive regulation of interleukin-8 biosynthetic process	2	0.816327	0.049402
GO:0042535~positive regulation of tumor necrosis factor biosynthetic process	2	0.816327	0.049402
GO:0048251~elastic fiber assembly	2	0.816327	0.049402
GO:0045414~regulation of interleukin-8 biosynthetic process	2	0.816327	0.049402
GO:0045354~regulation of interferon-alpha biosynthetic process	2	0.816327	0.049402
GO:0032677~regulation of interleukin-8 production	2	0.816327	0.049402
GO:0040012~regulation of locomotion	5	2.040816	0.050113
GO:0060562~epithelial tube morphogenesis	5	2.040816	0.051498
GO:0003012~muscle system process	4	1.632653	0.052267
GO:0042060~wound healing	5	2.040816	0.052903
mmu04672: Intestinal immune network for IgA production	4	1.632653	0.053597
GO:0008061~chitin binding	2	0.816327	0.054543
GO:0060429~epithelium development	8	3.265306	0.055569
GO:0007167~enzyme linked receptor protein signaling pathway	8	3.265306	0.057351
GO:0034097~response to cytokine stimulus	3	1.22449	0.061058
GO:0042447~hormone catabolic process	2	0.816327	0.061368
GO:0060665~regulation of branching involved in salivary gland morphogenesis by mesenchymal-epithelial signaling	2	0.816327	0.061368
GO:0008517~folic acid transporter activity	2	0.816327	0.06771
GO:0051674~localization of cell	8	3.265306	0.067828
GO:0048870~cell motility	8	3.265306	0.067828
GO:0002821~positive regulation of adaptive immune response	3	1.22449	0.067954
GO:0002824~positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	3	1.22449	0.067954
GO:0051130~positive regulation of cellular component organization	5	2.040816	0.068087
GO:0004175~endopeptidase activity	11	4.489796	0.070082
mmu04620: Toll-like receptor signaling pathway	5	2.040816	0.071525
GO:0001878~response to yeast	2	0.816327	0.073185
GO:0060638~mesenchymal-epithelial cell signaling	2	0.816327	0.073185
GO:0009187~cyclic nucleotide metabolic process	3	1.22449	0.075094
GO:0050660~FAD binding	4	1.632653	0.076403
GO:0008235~metalloexopeptidase activity	3	1.22449	0.07685
GO:0004713~protein tyrosine kinase activity	6	2.44898	0.079181
GO:0045359~positive regulation of interferon-beta biosynthetic process	2	0.816327	0.084854
GO:0045879~negative regulation of smoothed signaling pathway	2	0.816327	0.084854
GO:0045357~regulation of interferon-beta biosynthetic process	2	0.816327	0.084854
GO:0032647~regulation of interferon-alpha production	2	0.816327	0.084854
GO:0030511~positive regulation of transforming growth factor beta receptor signaling pathway	2	0.816327	0.084854
GO:0048565~gut development	3	1.22449	0.086223
GO:0009991~response to extracellular stimulus	5	2.040816	0.087106

GO:0006897~endocytosis	6	2.44898	0.089421
GO:0010324~membrane invagination	6	2.44898	0.089421
GO:0010810~regulation of cell-substrate adhesion	3	1.22449	0.090037
GO:0010647~positive regulation of cell communication	6	2.44898	0.090689
GO:0034702~ion channel complex	6	2.44898	0.091524
mmu04510:Focal adhesion	7	2.857143	0.093433
GO:0019966~interleukin-1 binding	2	0.816327	0.093499
GO:0004908~interleukin-1 receptor activity	2	0.816327	0.093499
GO:0032403~protein complex binding	4	1.632653	0.094943
GO:0001796~regulation of type IIa hypersensitivity	2	0.816327	0.096376
GO:0002892~regulation of type II hypersensitivity	2	0.816327	0.096376
GO:0001798~positive regulation of type IIa hypersensitivity	2	0.816327	0.096376
GO:0002894~positive regulation of type II hypersensitivity	2	0.816327	0.096376
GO:0002888~positive regulation of myeloid leukocyte mediated immunity	2	0.816327	0.096376
GO:0042534~regulation of tumor necrosis factor biosynthetic process	2	0.816327	0.096376
GO:0001944~vasculature development	7	2.857143	0.097428
GO:0002697~regulation of immune effector process	4	1.632653	0.099341

Downregulated

GO:0005833~hemoglobin complex	2	20	0.004471
GO:0015671~oxygen transport	2	20	0.005654
GO:0005344~oxygen transporter activity	2	20	0.006605
GO:0015669~gas transport	2	20	0.006679
GO:0019825~oxygen binding	2	20	0.0084
GO:0044445~cytosolic part	2	20	0.034748
GO:0020037~heme binding	2	20	0.083498
GO:0046906~tetrapyrrole binding	2	20	0.087397

Supplementary Table 10. Correlation coefficients and P-values between co-expression modules and Alzheimer's disease.

Module	R	P-value
AZ_M1	-0.0456	0.49092
AZ_M2	-0.4141	6.06E-11
AZ_M3	-0.0891	0.17824
AZ_M4	-0.0578	0.38294
AZ_M5	-0.1189	0.07182
AZ_M6	-0.1702	0.00973
AZ_M7	-0.0681	0.30368
AZ_M8	-0.4895	2.91E-15
AZ_M9	-0.0203	0.75929
AZ_M10	-0.0315	0.63421
AZ_M11	-0.2692	3.53E-05
AZ_M12	-0.3841	1.68E-09
AZ_M13	-0.3735	5.03E-09
AZ_M14	-0.5838	2.09E-22
AZ_M15	-0.6788	2.02E-32
AZ_M16	0.04722	0.47612
AZ_M17	-0.3678	8.92E-09
AZ_M18	-0.1376	0.03706
AZ_M19	0.10376	0.11658
AZ_M20	0.17108	0.00933
AZ_M21	0.09071	0.17038
AZ_M22	-0.1558	0.01804
AZ_M23	0.10057	0.12831
AZ_M24	-0.142	0.03132
AZ_M25	0.37708	3.48E-09
AZ_M26	0.01675	0.8005
AZ_M27	0.26948	3.45E-05
AZ_M28	0.2889	8.48E-06
AZ_M29	0.46722	7.14E-14
AZ_M30	0.1881	0.0042
AZ_M31	0.68214	7.76E-33
AZ_M32	0.4838	6.76E-15
AZ_M33	0.21509	0.00103
AZ_M34	0.65043	4.74E-29
AZ_M35	0.60471	2.52E-24
AZ_M36	-0.2347	0.00033
AZ_M37	0.06445	0.33046
AZ_M38	0.05517	0.40498
AZ_M39	0.27464	2.40E-05
AZ_M40	0.15886	0.01589
AZ_M41	0.29914	3.87E-06
AZ_M42	0.07616	0.24998
AZ_M43	0.23773	0.00027
AZ_M44	-0.1453	0.02758
AZ_M45	0.37835	3.06E-09

Supplementary Table 11. Biological processes enriched in the endothelial genes in the AZ_M32 module.

GO Term	Count	P-value
GO:0006954~inflammatory response	18	1.66E-10
GO:0032496~response to lipopolysaccharide	12	1.79E-08
GO:0006955~immune response	14	1.74E-06
GO:0007568~aging	9	3.67E-05
GO:0048711~positive regulation of astrocyte differentiation	4	4.74E-05
GO:0010332~response to gamma radiation	5	5.38E-05
GO:0071356~cellular response to tumor necrosis factor	7	6.20E-05
GO:0001938~positive regulation of endothelial cell proliferation	6	7.45E-05
GO:0042517~positive regulation of tyrosine phosphorylation of Stat3 protein	5	9.32E-05
GO:0071222~cellular response to lipopolysaccharide	7	1.37E-04
GO:0071347~cellular response to interleukin-1	6	1.48E-04
GO:0007165~signal transduction	19	2.33E-04
GO:0046697~decidualization	4	3.17E-04
GO:0009408~response to heat	5	4.40E-04
GO:0071407~cellular response to organic cyclic compound	5	6.40E-04
GO:0060326~cell chemotaxis	5	7.19E-04
GO:0070374~positive regulation of ERK1 and ERK2 cascade	7	8.96E-04
GO:0019221~cytokine-mediated signaling pathway	6	0.00123
GO:0008360~regulation of cell shape	6	0.00166
GO:0000122~negative regulation of transcription from RNA polymerase II promoter	13	0.00174
GO:0071260~cellular response to mechanical stimulus	5	0.00185
GO:0006468~protein phosphorylation	10	0.00199
GO:0002548~monocyte chemotaxis	4	0.00216
GO:0060707~trophoblast giant cell differentiation	3	0.00236
GO:0042060~wound healing	5	0.00237
GO:0007566~embryo implantation	4	0.00248
GO:0006953~acute-phase response	4	0.00248
GO:0045651~positive regulation of macrophage differentiation	3	0.00278
GO:0006879~cellular iron ion homeostasis	4	0.00281
GO:0006469~negative regulation of protein kinase activity	5	0.00334
GO:1900745~positive regulation of p38MAPK cascade	3	0.00423
GO:0050829~defense response to Gram-negative bacterium	4	0.00467
GO:0010628~positive regulation of gene expression	7	0.00504
GO:0021537~telencephalon development	3	0.00535
GO:0045766~positive regulation of angiogenesis	5	0.00566
GO:0045089~positive regulation of innate immune response	3	0.00596
GO:0042493~response to drug	8	0.00596
GO:0010951~negative regulation of endopeptidase activity	5	0.00656
GO:0001666~response to hypoxia	6	0.00702
GO:0070301~cellular response to hydrogen peroxide	4	0.00713
GO:0046330~positive regulation of JNK cascade	4	0.00744
GO:0031100~organ regeneration	4	0.00776
GO:0045471~response to ethanol	5	0.00776
GO:0009611~response to wounding	4	0.00842
GO:0035690~cellular response to drug	4	0.01061
GO:0038172~interleukin-33-mediated signaling pathway	2	0.01223
GO:0043065~positive regulation of apoptotic process	7	0.01266
GO:0060135~maternal process involved in female pregnancy	3	0.0127
GO:0008285~negative regulation of cell proliferation	8	0.01298
GO:0043410~positive regulation of MAPK cascade	4	0.014
GO:0045893~positive regulation of transcription, DNA-templated	9	0.01405
GO:0051384~response to glucocorticoid	4	0.0159
GO:0007259~JAK-STAT cascade	3	0.01739
GO:0045944~positive regulation of transcription from RNA polymerase II promoter	13	0.01779
GO:0070561~vitamin D receptor signaling pathway	2	0.0183
GO:0001837~epithelial to mesenchymal transition	3	0.01841
GO:0043491~protein kinase B signaling	3	0.01945
GO:0007267~cell-cell signaling	6	0.02013
GO:0070555~response to interleukin-1	3	0.02051

GO:0000165~MAPK cascade	6	0.02233
GO:0009409~response to cold	3	0.02271
GO:0006915~apoptotic process	9	0.02352
GO:0060708~spongiorophoblast differentiation	2	0.02432
GO:0010574~regulation of vascular endothelial growth factor production	2	0.02432
GO:0045637~regulation of myeloid cell differentiation	2	0.03031
GO:0071279~cellular response to cobalt ion	2	0.03031
GO:0045429~positive regulation of nitric oxide biosynthetic process	3	0.0311
GO:0030168~platelet activation	4	0.03454
GO:0032364~oxygen homeostasis	2	0.03626
GO:0032754~positive regulation of interleukin-5 production	2	0.03626
GO:0033132~negative regulation of glucokinase activity	2	0.03626
GO:0050900~leukocyte migration	4	0.04001
GO:0006935~chemotaxis	4	0.04001
GO:0032355~response to estradiol	4	0.04082
GO:0072678~T cell migration	2	0.04217
GO:0033591~response to L-ascorbic acid	2	0.04217
GO:0034351~negative regulation of glial cell apoptotic process	2	0.04217
GO:0043434~response to peptide hormone	3	0.04784
GO:0034097~response to cytokine	3	0.04784
GO:0001525~angiogenesis	5	0.0498

Supplementary Table 12. Correlation coefficients and P-values between co-expression modules and TNF α treatment in HUVECs.

Module	R	P-value
EC_M1	-0.22793	0.587196
EC_M2	-0.66553	0.071649
EC_M3	-0.70227	0.052126
EC_M4	0.097914	0.817581
EC_M5	-0.16648	0.693567
EC_M6	-0.11745	0.781806
EC_M7	-0.52345	0.183074
EC_M8	-0.7196	0.044173
EC_M9	-0.20496	0.626324
EC_M10	-0.74073	0.035538
EC_M11	0.095639	0.821768
EC_M12	-0.00611	0.98854
EC_M13	-0.09707	0.819141
EC_M14	-0.56991	0.140255
EC_M15	-0.39429	0.333757
EC_M16	-0.40764	0.316131
EC_M17	-0.44011	0.275156
EC_M18	-0.19365	0.645877
EC_M19	0.038087	0.928655
EC_M20	0.349737	0.395754
EC_M21	0.404819	0.319814
EC_M22	0.10209	0.809907
EC_M23	-0.06178	0.884453
EC_M24	0.359263	0.3821
EC_M25	-0.0193	0.963827
EC_M26	0.535346	0.171522
EC_M27	0.176652	0.675605
EC_M28	-0.11193	0.791881
EC_M29	0.034181	0.935961
EC_M30	0.489066	0.218731
EC_M31	0.215776	0.607803
EC_M32	0.374419	0.360817
EC_M33	0.327486	0.428453
EC_M34	0.066887	0.87496
EC_M35	0.328941	0.426282
EC_M36	-0.31697	0.444285
EC_M37	-0.38534	0.345828
EC_M38	-0.28592	0.492407
EC_M39	-0.73678	0.037066
EC_M40	-0.36459	0.374558
EC_M41	0.007166	0.986564
EC_M42	0.099867	0.813991
EC_M43	0.311326	0.452885
EC_M44	0.208869	0.619613
EC_M45	-0.11369	0.788659
EC_M46	-0.25521	0.541854
EC_M47	0.96468	0.000107

EC_M48	0.48917	0.218618
EC_M49	0.445442	0.2687
EC_M50	0.257759	0.537682
EC_M51	0.639863	0.087504
EC_M52	-0.40793	0.315754
EC_M53	-0.03845	0.927984
EC_M54	-0.16926	0.688654
EC_M55	-0.22307	0.59541
EC_M56	-0.15679	0.710807
EC_M57	0.154601	0.714709
EC_M58	-0.02501	0.953121
EC_M59	0.403063	0.32212
EC_M60	0.226827	0.589063
EC_M61	0.534125	0.172688

Supplementary Table 13. Biological processes enriched in the endothelial genes in the EC_M47 module.

GO Term	Count	P-value
GO:0007165--signal transduction	103	4.94E-08
GO:0060333--interferon-gamma-mediated signaling pathway	18	2.94E-07
GO:0006954--inflammatory response	46	3.27E-07
GO:0032496--response to lipopolysaccharide	28	5.43E-06
GO:0060326--cell chemotaxis	15	5.86E-06
GO:0006955--immune response	43	1.06E-05
GO:0045944--positive regulation of transcription from RNA polymerase II promoter	82	2.16E-05
GO:0006935--chemotaxis	20	2.58E-05
GO:0043065--positive regulation of apoptotic process	37	3.58E-05
GO:0042127--regulation of cell proliferation	25	5.16E-05
GO:0070098--chemokine-mediated signaling pathway	14	1.10E-04
GO:0000122--negative regulation of transcription from RNA polymerase II promoter	60	1.47E-04
GO:0070374--positive regulation of ERK1 and ERK2 cascade	23	1.97E-04
GO:0010628--positive regulation of gene expression	30	2.39E-04
GO:0016477--cell migration	22	3.28E-04
GO:0006915--apoptotic process	47	5.94E-04
GO:0030335--positive regulation of cell migration	23	6.80E-04
GO:0008285--negative regulation of cell proliferation	39	6.87E-04
GO:0043123--positive regulation of I-kappaB kinase/NF-kappaB signaling	20	7.53E-04
GO:0045599--negative regulation of fat cell differentiation	9	0.001389
GO:0007267--cell-cell signaling	27	0.001488
GO:0043066--negative regulation of apoptotic process	41	0.001734
GO:0001525--angiogenesis	25	0.002104
GO:0071222--cellular response to lipopolysaccharide	17	0.002188
GO:0045088--regulation of innate immune response	5	0.002318
GO:0032728--positive regulation of interferon-beta production	7	0.002927
GO:0050727--regulation of inflammatory response	10	0.00336
GO:0030728--ovulation	5	0.003465
GO:0033138--positive regulation of peptidyl-serine phosphorylation	11	0.003659
GO:0060337--type I interferon signaling pathway	11	0.004138
GO:0001657--ureteric bud development	8	0.004338
GO:0032727--positive regulation of interferon-alpha production	5	0.004943
GO:2000352--negative regulation of endothelial cell apoptotic process	7	0.005489
GO:0030593--neutrophil chemotaxis	10	0.006465
GO:0043433--negative regulation of sequence-specific DNA binding transcription factor activity	10	0.006465
GO:1902042--negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	7	0.006625
GO:0019885--antigen processing and presentation of endogenous peptide antigen via MHC class I	4	0.006976
GO:0051607--defense response to virus	17	0.007343
GO:0070373--negative regulation of ERK1 and ERK2 cascade	9	0.00789
GO:0034341--response to interferon-gamma	6	0.008165
GO:0019722--calcium-mediated signaling	8	0.008201
GO:0071347--cellular response to interleukin-1	11	0.00903
GO:0071498--cellular response to fluid shear stress	5	0.009048
GO:0030949--positive regulation of vascular endothelial growth factor receptor signaling pathway	5	0.009048
GO:0045766--positive regulation of angiogenesis	14	0.009756
GO:0007155--cell adhesion	37	0.009784
GO:0002480--antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent	4	0.010649
GO:0035234--ectopic germ cell programmed cell death	4	0.010649
GO:0070555--response to interleukin-1	7	0.011049
GO:0002474--antigen processing and presentation of peptide antigen via MHC class I	7	0.011049
GO:1901998--toxin transport	7	0.011049
GO:0060374--mast cell differentiation	3	0.01115
GO:0060544--regulation of necroptotic process	3	0.01115
GO:0016485--protein processing	10	0.011409
GO:0035556--intracellular signal transduction	32	0.011701
GO:0034142--toll-like receptor 4 signaling pathway	5	0.011739
GO:0030889--negative regulation of B cell proliferation	5	0.011739
GO:0090023--positive regulation of neutrophil chemotaxis	6	0.01218
GO:0045429--positive regulation of nitric oxide biosynthetic process	8	0.012435

GO:0001701~in utero embryonic development	19	0.012818
GO:0006816~calcium ion transport	10	0.014027
GO:0001666~response to hypoxia	20	0.01426
GO:0050860~negative regulation of T cell receptor signaling pathway	5	0.014895
GO:0034446~substrate adhesion-dependent cell spreading	7	0.014959
GO:0034405~response to fluid shear stress	4	0.015242
GO:0050729~positive regulation of inflammatory response	10	0.01549
GO:0001938~positive regulation of endothelial cell proliferation	10	0.01549
GO:0045444~fat cell differentiation	10	0.01549
GO:0051092~positive regulation of NF-kappaB transcription factor activity	15	0.015915
GO:0045786~negative regulation of cell cycle	7	0.017235
GO:0032480~negative regulation of type I interferon production	6	0.017357
GO:0007159~leukocyte cell-cell adhesion	6	0.017357
GO:0030168~platelet activation	14	0.017782
GO:0032481~positive regulation of type I interferon production	8	0.018051
GO:0006468~protein phosphorylation	35	0.018739
GO:0007596~blood coagulation	18	0.020437
GO:0007050~cell cycle arrest	15	0.020705
GO:0022409~positive regulation of cell-cell adhesion	4	0.02078
GO:0034121~regulation of toll-like receptor signaling pathway	3	0.021381
GO:0017145~stem cell division	3	0.021381
GO:1903800~positive regulation of production of miRNAs involved in gene silencing by miRNA	3	0.021381
GO:1903553~positive regulation of extracellular exosome assembly	3	0.021381
GO:0002690~positive regulation of leukocyte chemotaxis	5	0.022688
GO:0090090~negative regulation of canonical Wnt signaling pathway	16	0.02341
GO:0030217~T cell differentiation	6	0.02381
GO:0035666~TRIF-dependent toll-like receptor signaling pathway	6	0.02381
GO:0048010~vascular endothelial growth factor receptor signaling pathway	10	0.024531
GO:0010759~positive regulation of macrophage chemotaxis	4	0.027273
GO:0051894~positive regulation of focal adhesion assembly	5	0.027359
GO:0043171~peptide catabolic process	5	0.027359
GO:0007249~I-kappaB kinase/NF-kappaB signaling	8	0.028026
GO:0007507~heart development	18	0.028143
GO:0002250~adaptive immune response	14	0.028221
GO:0071260~cellular response to mechanical stimulus	11	0.028417
GO:0045087~innate immune response	29	0.029192
GO:0043124~negative regulation of I-kappaB kinase/NF-kappaB signaling	6	0.031634
GO:0050766~positive regulation of phagocytosis	6	0.031634
GO:0050900~leukocyte migration	14	0.031892
GO:0071356~cellular response to tumor necrosis factor	12	0.03374
GO:0035791~platelet-derived growth factor receptor-beta signaling pathway	3	0.034174
GO:0002551~mast cell chemotaxis	3	0.034174
GO:0034134~toll-like receptor 2 signaling pathway	3	0.034174
GO:0036499~PERK-mediated unfolded protein response	4	0.034717
GO:0043122~regulation of I-kappaB kinase/NF-kappaB signaling	4	0.034717
GO:0002523~leukocyte migration involved in inflammatory response	4	0.034717
GO:0031663~lipopolysaccharide-mediated signaling pathway	6	0.036082
GO:0030206~chondroitin sulfate biosynthetic process	5	0.038301
GO:0042346~positive regulation of NF-kappaB import into nucleus	5	0.038301
GO:0010595~positive regulation of endothelial cell migration	7	0.039986
GO:0006914~autophagy	12	0.041016
GO:0043303~mast cell degranulation	4	0.043094
GO:0001817~regulation of cytokine production	4	0.043094
GO:0061053~somite development	4	0.043094
GO:0043069~negative regulation of programmed cell death	4	0.043094
GO:0050927~positive regulation of positive chemotaxis	4	0.043094
GO:0032743~positive regulation of interleukin-2 production	4	0.043094
GO:0051926~negative regulation of calcium ion transport	4	0.043094
GO:0070498~interleukin-1-mediated signaling pathway	4	0.043094
GO:0070301~cellular response to hydrogen peroxide	9	0.044282
GO:0048844~artery morphogenesis	5	0.044582
GO:0045732~positive regulation of protein catabolic process	8	0.045025
GO:0007568~aging	19	0.045594

GO:0006974~cellular response to DNA damage stimulus	17	0.0474
GO:0030334~regulation of cell migration	9	0.047865
GO:0006260~DNA replication	15	0.048549
GO:2000391~positive regulation of neutrophil extravasation	3	0.049172
GO:0010818~T cell chemotaxis	3	0.049172
GO:0009615~response to virus	12	0.049313
