Supplemental Tables

Supplemental Table S1 Summary statistics for sequence quality in six samples

Sample	Raw Data		Valid Data		Valid Ratio(reads)	Q20%	Q30%	GC content%
	Read	Base	Read	Base				
Fb1_Fb	54546240	8.18G	53604580	8.04G	98.27	99.42	94.85	52
Fb2_Fb	56652684	8.50G	55640760	8.35G	98.21	99.42	94.51	52
Fb3_Fb	58430564	8.76G	57284110	8.59G	98.04	99.46	95.49	51.50
Pb1_Pb	55534776	8.33G	54405508	8.16G	97.97	99.49	95.32	51.50
Pb2_Pb	55682646	8.35G	54640098	8.20G	98.13	99.37	94.94	52
Pb3_Pb	55757216	8.36G	54623412	8.19G	97.97	99.51	94.78	51

Supplemental Table S2 Summary statistics for alignments in six samples

Sample	Fb1_Fb	Fb2_Fb	Fb3_Fb	Pb1_Pb	Pb2_Pb	Pb3_Pb
Valid reads	53604580	55640760	57284110	54405508	54640098	54623412
Mapped reads	48207741(89.93%)	49922983(89.72%)	51705584(90.26%)	49081433(90.21%)	49216958(90.07%)	49447796(90.52%)
Unique Mapped reads	47183247(88.02%)	48861303(87.82%)	50561574(88.26%)	47774287(87.81%)	48118304(88.06%)	48295470(88.42%)
Multi Mapped reads	1024494(1.91%)	1061680(1.91%)	1144010(2.00%)	1307146(2.40%)	1098654(2.01%)	1152326(2.11%)
PE Mapped reads	22362746(41.72%)	23074236(41.47%)	24217159(42.28%)	22897652(42.09%)	22875218(41.87%)	23192640(42.46%)
Mapped left reads	25243264(47.09%)	26251319(47.18%)	26909861(46.98%)	25569567(47.00%)	25728789(47.09%)	25641773(46.94%)
Mapped right reads	22964477(42.84%)	23671664(42.54%)	24795723(43.29%)	23511866(43.22%)	23488169(42.99%)	23806023(43.58%)
Reads map to sense strand	23332622(43.53%)	24154963(43.41%)	25023866(43.68%)	23639603(43.45%)	23787951(43.54%)	23930059(43.81%)
Reads map to antisense strand	23850625(44.49%)	24706340(44.40%)	25537708(44.58%)	24134684(44.36%)	24330353(44.53%)	24365411(44.61%)
Non-splice reads	26620773(49.66%)	27815911(49.99%)	29906641(52.21%)	27777251(51.06%)	27713011(50.72%)	28340065(51.88%)
Splice reads	20562474(38.36%)	21045392(37.82%)	20654933(36.06%)	19997036(36.76%)	20405293(37.34%)	19955405(36.53%)

Supplemental Table S3 Primers used for qRT-PCR and the fold changes detected from selected genes based on qRT-PCR and RNA-seq analysis

	Gene ID	*Forward primer (from 5' to 3')*	*Reverse primer (from 5' to 3')*	*size*	*Log2 FC by RNA-Seq*	*Log2 FC by qRT-PCR*
S100a8	ENSMUSG00000056054	AAATCACCATGCCCTCTACAAG	CCCACTTTTATCACCATCGCAA	165	5.69106	15.21177416
Tfap2b	ENSMUSG00000025927	GCGTCCCAAGCCATAGCTC	ACTCTGGTGGTAGGGTAGCG	152	4.94472	10.07475082
Sox10	ENSMUSG00000033006	CGGACGATGACAAGTTCCCC	GTGAGGGTACTGGTCGGCT	197	1.77112	0.655019084
Rgs6	ENSMUSG00000021219	CTCCCAACATGATTGTCTACTGC	GGGATTTTGGAGAGAAAGCTCTT	112	1.64007	2.027216987
Ostn	ENSMUST00000066852	CTGGAGATTGGCAAGTACACAC	CGCAGGAGCTTAGCCGAAA	174	1.71992	2.741750261

Col2a1	ENSMUSG00000022483	GGGTCACAGAGGTTACCCAG	ACCAGGGGAACCACTCTCAC	85	-2.63391	-2.069187794
Fgfr4	ENSMUSG00000005320	TCCATGACCGTCGTACACAAT	ATTTGACAGTATTCCCGGCAG	193	-2.00351	-1.899611303
Msx2	ENSMUSG00000021469	CTAAAGGCGGTGACTTGTTTTCG	CGGCTTCTTGTCGGACATGAG	161	-1.46778	0.03325983
Foxp2	ENSMUSG00000029563	AGTGTGCCCAATGTGGGAG	CATGATAGCCTGCCTTATGAGTG	153	-1.723	-1.940020226
Col9a1	ENSMUSG00000026147	CGACCGACCAGCACATCAA	AGGGGGACCCTTAATGCCT	209	-2.7724	0.002
TWIST2	ENSMUST00000186075	TACAGCAAGAAATCGAGCGAAG	GCTGAGCTTGTCAGAGGGG	204	-1.12285	0.072393962
NF2	ENSMUSG00000009073	CTAGTTCAAGAGATCACGCAACA	GGCAGTAGACCTTTTCATCCAAA	76	0.116892	0.126780692
GAPDH		CGTCCTCTCTGGCAAAGTCC	TTCCCGTTCTCAGCCTTGAC			

Supplemental Table S4 A total of DEGs between Fb and Pb tissues

Gene ID	Gne Name	log2(fold_change)	***p*_value**	***q*_value**
ENSMUST00000185352	Gm20257	7.19582	0.00005	0.00281617
ENSMUST00000069927	S100a8	5.69106	0.00155	0.0284139
ENSMUST00000035061	Ngp	5.13695	0.00005	0.00281617
ENSMUST00000112915	Gm11110	-4.9535	0.0001	0.00490324
ENSMUST00000027059	Tfap2b	4.94472	0.00005	0.00281617
ENSMUST00000102803	Myh7	-4.72223	0.00005	0.00281617
ENSMUST00000189288	F730311O21Rik	4.60865	0.00145	0.027817
ENSMUST00000147219	Lcn2	4.34394	0.00005	0.00281617
ENSMUST00000042097	Stfa1	4.27681	0.00085	0.0212865
ENSMUST00000088735	Olfm4	4.17201	0.00385	0.0422997
ENSMUST00000101368	Kcnip1	-3.92232	0.00465	0.0453122
ENSMUST00000069960	S100a9	3.87539	0.00005	0.00281617
ENSMUST00000023464	Mfi2	-3.7555	0.00005	0.00281617
ENSMUST00000065666	Retnlg	3.64626	0.00535	0.0461737
ENSMUST00000009018	Clec3a	-3.63989	0.00005	0.00281617
ENSMUST00000102576	Matn1	-3.56691	0.00005	0.00281617
ENSMUST00000106561	Cd300lf	3.48784	0.0001	0.00490324
ENSMUST00000057767	Upk1b	-3.41261	0.00075	0.0200233
ENSMUST00000187864	Ly6c2	3.34807	0.0004	0.0131891
ENSMUST00000078694	Ppp1r1b	-3.26073	0.00005	0.00281617
ENSMUST00000020899	Matn3	-3.18468	0.00005	0.00281617
ENSMUST00000022603	Lect1	-3.10197	0.00005	0.00281617
ENSMUST00000151197	Pih1d2	-3.08143	0.00165	0.029655
ENSMUST00000173664	Slc44a4	3.07924	0.0003	0.0107327
ENSMUST00000074898	Hp	3.05287	0.00005	0.00281617
ENSMUST00000097491	Sell	2.83803	0.0008	0.0202689
ENSMUST00000102939	Cacna1b	2.82496	0.0002	0.00835917
ENSMUST00000063063	Scml4	-2.81992	0.00005	0.00281617
ENSMUST00000094836	Stk32b	-2.81146	0.0017	0.0302225
ENSMUST00000078200	Brsk2	2.80087	0.001	0.0228178
ENSMUST00000156657	Bcas1	2.78685	0.00205	0.0321361

ENSMUST00000054588	Col9a1	-2.7724	0.00005	0.00281617
ENSMUST00000057428	Mylk4	-2.76917	0.0028	0.0395297
ENSMUST00000063820	F10	2.69603	0.00645	0.049732
ENSMUST00000140079	St18	2.69397	0.00005	0.00281617
ENSMUST00000068423	Cbln2	-2.69139	0.00005	0.00281617
ENSMUST00000054883	Pou3f3	-2.64734	0.00005	0.00281617
ENSMUST00000023123	Col2a1	-2.63391	0.00005	0.00281617
ENSMUST00000132527	Col9a3	-2.5661	0.00005	0.00281617
ENSMUST00000193252	Pcdh10	2.51983	0.00005	0.00281617
ENSMUST00000035077	Ltf	2.49387	0.00005	0.00281617
ENSMUST00000150014	Mbnl3	-2.44692	0.00295	0.0395297
ENSMUST00000030372	Col9a2	-2.41504	0.00005	0.00281617
ENSMUST00000171719	Ccr2	2.40207	0.00035	0.0119974
ENSMUST00000131443	Cytip	2.39882	0.00045	0.0145217
ENSMUST00000032159	Cntn3	-2.37759	0.0024	0.0347799
ENSMUST00000022108	Hapln1	-2.37187	0.00005	0.00281617
ENSMUST00000035935	Ccdc40	2.33904	0.00595	0.0496818
ENSMUST00000125174	B430306N03Rik	2.29151	0.00385	0.0422997
ENSMUST00000032200	Slc6a12	-2.27027	0.0008	0.0202689
ENSMUST00000040162	Gdf5	-2.26689	0.00185	0.0302225
ENSMUST00000110160	Tm6sf2	2.26366	0.00085	0.0212865
ENSMUST00000034023	Scrg1	-2.22602	0.00005	0.00281617
ENSMUST00000090469	Myoz1	-2.18772	0.00005	0.00281617
ENSMUST00000021506	Serpina3n	-2.18732	0.00035	0.0119974
ENSMUST00000112544	Gm15446	-2.16121	0.00025	0.00944576
ENSMUST00000048485	Sln	-2.13968	0.00055	0.016436
ENSMUST00000073554	Cytl1	-2.11114	0.00005	0.00281617
ENSMUST00000159329	Slc24a4	-2.07486	0.00715	0.049732
ENSMUST00000050567	1700019D03Rik	-2.06958	0.0017	0.0302225
ENSMUST00000000208	Slfn4	2.05452	0.0031	0.0395297
ENSMUST00000032203	A2m	-2.04203	0.00025	0.00944576
ENSMUST00000188495	Myb	2.03383	0.00635	0.0496818
ENSMUST00000005452	Fgfr4	-2.00351	0.00015	0.00678403
ENSMUST00000039178	Tnn	-2.00024	0.00005	0.00281617
ENSMUST00000033825	Adprhl1	-1.99823	0.0033	0.0406821
ENSMUST00000132836	Nfe2	1.99581	0.0004	0.0131891
ENSMUST00000071889	Car12	-1.95673	0.00005	0.00281617
ENSMUST00000027476	3110079O15Rik	-1.93667	0.00005	0.00281617
ENSMUST00000027861	Dpt	-1.92273	0.00005	0.00281617
ENSMUST00000114243	Gm973	-1.91982	0.00085	0.0212865
ENSMUST00000137663	Syt9	1.89128	0.00005	0.00281617
ENSMUST00000022519	Anxa8	-1.88846	0.00005	0.00281617
ENSMUST00000092163	Lyz2	1.87261	0.00005	0.00281617
ENSMUST00000170922	Vmn2r29	-1.86189	0.00345	0.0418871
ENSMUST00000093110	Medag	-1.86108	0.00005	0.00281617
ENSMUST00000032835	Acan	-1.85556	0.00005	0.00281617
ENSMUST00000167607	Ucma	-1.84834	0.00005	0.00281617
ENSMUST00000146270	Wfdc2	-1.84634	0.001	0.0228178

ENSMUST00000019625	Myh8	-1.84302	0.00005	0.00281617
ENSMUST00000080403	Magel2	-1.83194	0.00005	0.00281617
ENSMUST00000059805	Slc35d3	-1.81894	0.00695	0.049732
ENSMUST00000095580	Mypn	-1.81163	0.0026	0.0371979
ENSMUST00000157068	Shisa7	1.79303	0.0031	0.0395297
ENSMUST00000121629	Mybpc1	-1.78353	0.00005	0.00281617
ENSMUST00000016471	Atp1b4	-1.77274	0.00005	0.00281617
ENSMUST00000040019	Sox10	1.77112	0.00265	0.0377884
ENSMUST00000112712	Lypd6	-1.7707	0.00545	0.0469698
ENSMUST00000149964	Kcnq2	1.73586	0.00005	0.00281617
ENSMUST00000115477	Foxp2	-1.723	0.00005	0.00281617
ENSMUST00000066852	Ostn	1.71992	0.00005	0.00281617
ENSMUST00000121146	Tdrd5	1.70264	0.00385	0.0422997
ENSMUST00000019503	Gdpd2	1.6976	0.00005	0.00281617
ENSMUST00000017544	Stac2	-1.68819	0.00005	0.00281617
ENSMUST00000171324	Gcnt4	-1.67817	0.00005	0.00281617
ENSMUST00000032732	Apba2	-1.67289	0.00005	0.00281617
ENSMUST00000003643	Ckm	-1.66837	0.00005	0.00281617
ENSMUST00000125292	Gria1	-1.6669	0.00005	0.00281617
ENSMUST00000145763	Mmrn1	1.66082	0.00005	0.00281617
ENSMUST00000025349	Myot	-1.65755	0.00025	0.00944576
ENSMUST00000124451	Fgr	1.65027	0.0026	0.0371979
ENSMUST00000079491	Sez6l	1.64884	0.00055	0.016436
ENSMUST00000161801	Rgs6	1.64007	0.00055	0.016436
ENSMUST00000017561	Plxdc1	1.63698	0.0022	0.0330167
ENSMUST00000113861	Kcnj15	-1.6341	0.00005	0.00281617
ENSMUST00000160662	Cdk15	-1.63191	0.00005	0.00281617
ENSMUST00000167156	Alx1	1.62535	0.00005	0.00281617
ENSMUST00000181070	A530020G20Rik	1.6173	0.00005	0.00281617
ENSMUST00000143713	Spn	1.60563	0.00245	0.0352684
ENSMUST00000057612	Ssc5d	-1.60467	0.00005	0.00281617
ENSMUST00000181660	Pantr1	-1.58635	0.0062	0.0496818
ENSMUST00000049208	Hfe2	-1.58452	0.0045	0.0452415
ENSMUST00000014990	Tppp3	-1.582	0.00005	0.00281617
ENSMUST00000179893	Ryr1	-1.5655	0.00005	0.00281617
ENSMUST00000025724	Il33	-1.55118	0.00005	0.00281617
ENSMUST00000025500	Slc27a6	-1.5381	0.00005	0.00281617
ENSMUST00000153206	Gm12216	1.5367	0.00605	0.0496818
ENSMUST00000095655	Lmod3	-1.52723	0.00205	0.0321361
ENSMUST00000186103	Tmeff2	-1.52485	0.00005	0.00281617
ENSMUST00000168126	Nr5a2	-1.52474	0.00695	0.049732
ENSMUST00000099461	Duox1	-1.51529	0.00015	0.00678403
ENSMUST00000075422	Mab21l1	-1.51247	0.00125	0.0253701
ENSMUST00000104934	Adra2b	1.50098	0.00025	0.00944576
ENSMUST00000027885	Angptl1	-1.50011	0.00035	0.0119974
ENSMUST00000023154	Cldn1	-1.49592	0.0001	0.00490324
ENSMUST00000000305	Tpd52l1	-1.49407	0.00015	0.00678403
ENSMUST00000117762	Itgal	1.49147	0.00035	0.0119974

ENSMUST00000173342	Zic4	-1.48649	0.0023	0.033604
ENSMUST00000167156	Alx1	1.48557	0.00005	0.00281617
ENSMUST00000026886	Itih5	-1.4688	0.00005	0.00281617
ENSMUST00000021922	Msx2	-1.46778	0.00005	0.00281617
-;ENSMUST00000098789	Zc3h4	1.46721	0.00005	0.00281617
ENSMUST00000052296	Pthlh	-1.46668	0.0001	0.00490324
ENSMUST00000028955	Angpt4	1.46365	0.00005	0.00281617
ENSMUST00000054867	Gpr37	1.45797	0.00485	0.0453122
ENSMUST00000029964	Epha7	-1.45416	0.00005	0.00281617
ENSMUST00000027730	Myog	-1.45399	0.0063	0.0496818
ENSMUST00000181071	Zfp429	-1.45307	0.00675	0.049732
ENSMUST00000048770	Sh3bgr	-1.44968	0.00125	0.0253701
ENSMUST00000135338	Susd5	-1.44606	0.00005	0.00281617
ENSMUST00000062010	Zcchc5	-1.44358	0.00005	0.00281617
ENSMUST00000040398	Glb1l2	1.43961	0.00515	0.0453122
ENSMUST00000044705	Vstm2b	-1.43693	0.0001	0.00490324
ENSMUST00000049251	Cpa4	1.42812	0.00015	0.00678403
ENSMUST00000023053	Col14a1	-1.42142	0.00005	0.00281617
ENSMUST00000003659	Comp	-1.41904	0.00005	0.00281617
ENSMUST00000036934	Neb	-1.41706	0.0001	0.00490324
ENSMUST00000031868	Slc13a4	-1.41154	0.00005	0.00281617
ENSMUST00000122374	Serinc2	-1.41082	0.0011	0.0240991
ENSMUST00000021142	Atp2a3	1.40773	0.00205	0.0321361
ENSMUST00000026896	St8sia2	1.40454	0.00005	0.00281617
ENSMUST00000020759	Efemp1	-1.4043	0.00005	0.00281617
ENSMUST00000042221	Slc26a7	1.40366	0.0015	0.027817
ENSMUST00000032069	Add2	1.39633	0.0069	0.049732
ENSMUST00000085758	Radil	-1.39374	0.0056	0.0480984
ENSMUST00000044228	Cd79b	1.39225	0.0069	0.049732
ENSMUST00000031840	Gpnmb	-1.3881	0.00005	0.00281617
ENSMUST00000163313	Baalc	-1.38481	0.00005	0.00281617
ENSMUST00000194579	Pyurf	1.38397	0.0008	0.0202689
ENSMUST00000026428	Myl6b	-1.37959	0.00315	0.0395297
ENSMUST00000038815	Sox5	-1.37892	0.00005	0.00281617
ENSMUST00000014747	Alx3	1.37745	0.0008	0.0202689
ENSMUST00000033602	Tnmd	-1.37682	0.00005	0.00281617
ENSMUST00000038144	Esm1	1.37457	0.00005	0.00281617
ENSMUST00000114259	Ptgds	-1.3695	0.00005	0.00281617
ENSMUST00000069616	Tpsb2	-1.35967	0.00005	0.00281617
ENSMUST00000137427	Rbpjl	-1.35257	0.00665	0.049732
ENSMUST00000000808	Il12rb1	1.35226	0.0056	0.0480984
ENSMUST00000100050	Klhl41	-1.34857	0.00095	0.0226312
ENSMUST00000003554	Casq1	-1.34225	0.00065	0.01807
ENSMUST00000128349	Ptgfr	1.33835	0.0004	0.0131891
ENSMUST00000098441	Col6a6	-1.32766	0.0001	0.00490324
ENSMUST00000140217	Tppp	-1.326	0.00085	0.0212865
ENSMUST00000020057	Lin7a	-1.32445	0.00385	0.0422997
ENSMUST00000190367	Gpr55	1.31908	0.00055	0.016436

ENSMUST00000029946	Rragd	-1.31811	0.0005	0.0157168
ENSMUST00000160676	Fam19a3	1.3158	0.0034	0.0417789
ENSMUST00000141588	Myoz2	-1.31285	0.00015	0.00678403
ENSMUST00000066432	Scn3a	1.30693	0.00005	0.00281617
ENSMUST00000106248	Trim72	-1.30444	0.0008	0.0202689
ENSMUST00000085240	Gabrb3	1.30236	0.0003	0.0107327
ENSMUST00000026890	Clec3b	-1.29833	0.00005	0.00281617
ENSMUST00000142959	Aatk	1.29295	0.0051	0.0453122
ENSMUST00000045173	Tgfbi	-1.29007	0.00005	0.00281617
ENSMUST00000049124	C1rl	1.28957	0.00205	0.0321361
ENSMUST00000047812	Dpp4	-1.28797	0.0018	0.0302225
ENSMUST00000033049	Cox6a2	-1.28785	0.00105	0.0237264
ENSMUST00000164666	Mcc	-1.28303	0.00005	0.00281617
ENSMUST00000182750	Ntn5	1.28025	0.0019	0.0302225
ENSMUST00000064606	Lrrc15	-1.27958	0.00005	0.00281617
ENSMUST00000145461	AI662270,Gm11427	1.2795	0.00005	0.00281617
ENSMUST00000125664	Lppr4	-1.27807	0.0009	0.0219051
ENSMUST00000089883	Masp1	1.27571	0.00005	0.00281617
ENSMUST00000165122	Wnt11	-1.27367	0.00005	0.00281617
ENSMUST00000109859	Slc52a3	-1.26799	0.0001	0.00490324
ENSMUST00000002336	Zim1	-1.26107	0.00005	0.00281617
ENSMUST00000044683	Vmn1r90	-1.25811	0.0064	0.049732
ENSMUST00000076939	C1qtnf7	-1.25715	0.00315	0.0395297
ENSMUST00000030443	Ptch2	1.25186	0.00025	0.00944576
ENSMUST00000102766	Zfp354a	-1.25166	0.00025	0.00944576
ENSMUST00000041407	Sostdc1	1.2482	0.00005	0.00281617
ENSMUST00000075477	Cav3	-1.23739	0.0022	0.0330167
ENSMUST00000102600	Fndc5	-1.23689	0.0029	0.0395297
ENSMUST00000082209	Scn8a	-1.23586	0.00005	0.00281617
ENSMUST00000131723	Slc47a1	-1.23444	0.00005	0.00281617
ENSMUST00000018698	Ybx2	1.23406	0.0006	0.0172661
ENSMUST00000003640	Fosb	-1.22867	0.00005	0.00281617
ENSMUST00000145122	Cd52	1.22709	0.00005	0.00281617
ENSMUST00000138020	Cpm	-1.22145	0.00005	0.00281617
ENSMUST00000028648	Syt13	-1.22027	0.00315	0.0395297
ENSMUST00000050027	Nov	-1.21849	0.00005	0.00281617
ENSMUST00000174661	Pitx2	1.21618	0.00485	0.0453122
ENSMUST00000060847	Ssu2	-1.21541	0.00035	0.0119974
ENSMUST00000022853	C1qtnf3	-1.21298	0.00005	0.00281617
ENSMUST00000027151	Myl1	-1.21017	0.00005	0.00281617
ENSMUST00000036109	Fam101a	-1.20657	0.00045	0.0145217
ENSMUST00000033915	Gpm6a	1.20454	0.00125	0.0253701
ENSMUST00000189968	Me1	-1.2024	0.00005	0.00281617
ENSMUST00000109838	Ntrk2	-1.20139	0.00005	0.00281617
ENSMUST00000102961	Cntfr	-1.20132	0.00005	0.00281617
ENSMUST00000125867	Slc12a5	1.19991	0.00005	0.00281617
ENSMUST00000180749	Gm26903	1.19731	0.00045	0.0145217
ENSMUST00000135754	Pi16	-1.19728	0.00005	0.00281617

ENSMUST00000108587	Tnnt1	-1.19068	0.0008	0.0202689
ENSMUST00000169295	Lax1	1.1902	0.0045	0.0452415
ENSMUST00000111703	Bhlhe41	-1.1881	0.0035	0.0418871
ENSMUST00000102817	Gap43	-1.18663	0.00005	0.00281617
ENSMUST00000021685	Hhipl1	-1.18313	0.00025	0.00944576
ENSMUST00000130558	Arhgap36	-1.18198	0.00115	0.0240991
ENSMUST00000074541	Jazf1	-1.17008	0.0003	0.0107327
ENSMUST00000081872	Nell1	-1.16908	0.00135	0.0264432
ENSMUST00000105971	Tnni2	-1.1677	0.00005	0.00281617
ENSMUST00000139839	Dusp10	-1.16602	0.0001	0.00490324
ENSMUST00000023807	Igfbp6	-1.16521	0.00005	0.00281617
ENSMUST00000110347	Smoc1	-1.16197	0.00005	0.00281617
ENSMUST00000093245	Bean1	-1.16078	0.00185	0.0302225
ENSMUST00000025434	Slc14a2	1.16061	0.0049	0.0453122
ENSMUST00000032454	Slc6a1	-1.15396	0.00015	0.00678403
ENSMUST00000174539	Dlk1	-1.15348	0.00005	0.00281617
ENSMUST00000030568	Sema3c	-1.15006	0.00005	0.00281617
ENSMUST00000061498	Fut4	1.14941	0.0017	0.0302225
ENSMUST00000020024	Fabp7	1.14763	0.00015	0.00678403
ENSMUST00000058652	Hs3st3a1	-1.14614	0.00015	0.00678403
ENSMUST00000121292	Rpl39l	-1.14493	0.00005	0.00281617
ENSMUST00000098956	Bglap,Bglap2	1.1429	0.00005	0.00281617
ENSMUST00000015484	Cybb	1.13348	0.0029	0.0395297
ENSMUST00000033674	Itgb1bp2	-1.12711	0.00165	0.029655
ENSMUST00000173002	C1qtnf2	-1.12388	0.00005	0.00281617
ENSMUST00000007949	Twist2	-1.12285	0.0016	0.0292067
ENSMUST00000065927	Tnfaip6	-1.12223	0.00005	0.00281617
ENSMUST00000032336	Plbd1	1.12193	0.00005	0.00281617
ENSMUST00000160298	Gm8113	1.11711	0.00005	0.00281617
ENSMUST00000152790	2010001A14Rik	1.10407	0.00655	0.049732
ENSMUST00000094807	Pnmal2	-1.10337	0.00005	0.00281617
ENSMUST00000117373	Postn	-1.10102	0.00005	0.00281617
ENSMUST00000022536	Ska3	-1.09805	0.00345	0.0418871
ENSMUST00000090277	Efcab1	-1.09366	0.0027	0.038393
ENSMUST00000024736	Sgol1	-1.09324	0.0001	0.00490324
ENSMUST00000021284	Ntn1	-1.08967	0.00005	0.00281617
ENSMUST00000121834	Syt6	1.08944	0.00005	0.00281617
ENSMUST00000120397	Bdh2	1.08933	0.00005	0.00281617
ENSMUST00000091900	Prdm6	-1.08569	0.00005	0.00281617
ENSMUST00000036991	Hspb8	-1.07987	0.00005	0.00281617
ENSMUST00000064204	Actn2	-1.07717	0.00005	0.00281617
ENSMUST00000112963	Lhx6	1.0714	0.0047	0.0453122
ENSMUST00000082432	Dio2	-1.06878	0.00205	0.0321361
ENSMUST00000189545	Rasgrf1	-1.06835	0.00215	0.0330167
ENSMUST00000061287	Cep112	-1.06498	0.00555	0.0477502
ENSMUST00000081035	Mpeg1	1.05899	0.00005	0.00281617
ENSMUST00000008462	Relt	1.05715	0.0009	0.0219051
ENSMUST00000164415	A930018M24Rik,Klhl33	1.05682	0.00005	0.00281617

ENSMUST00000043249	Mcpt4	-1.05612	0.00035	0.0119974
ENSMUST00000062893	Cenpe	-1.05485	0.00565	0.0484455
ENSMUST00000015712	Lpl	1.05399	0.00005	0.00281617
ENSMUST00000008297	Clstn3	-1.05249	0.00055	0.016436
ENSMUST00000146033	Tnfrsf13b	1.04951	0.00575	0.0492194
ENSMUST00000132855	Wipf3	1.04862	0.00445	0.0450531
ENSMUST00000087241	Shisa3	-1.04494	0.00005	0.00281617
ENSMUST00000150156	Rtn1	1.0421	0.00385	0.0422997
ENSMUST00000064771	Swt1	-1.03421	0.0012	0.0248887
ENSMUST00000030400	Mycbp	-1.03288	0.00005	0.00281617
ENSMUST00000108325	Cp	1.03218	0.0007	0.0190922
ENSMUST00000171644	Pparg	1.03214	0.00025	0.00944576
ENSMUST00000058210	Eps8	-1.03086	0.00005	0.00281617
ENSMUST00000114766	Mtap7d3	-1.03075	0.00235	0.0341697
ENSMUST00000029548	Nup210l	-1.02782	0.0064	0.049732
ENSMUST00000156238	Slc4a4	-1.02419	0.00385	0.0422997
ENSMUST00000032997	Lat	1.02352	0.0021	0.0327505
ENSMUST00000048824	Gm5617	-1.02157	0.0014	0.0272465
ENSMUST00000125503	Sulf2	-1.02044	0.00005	0.00281617
ENSMUST00000042868	Camk4	-1.01909	0.0007	0.0190922
ENSMUST00000088132	Eya2	-1.0184	0.00435	0.0446065
ENSMUST00000000579	Sox9	-1.01638	0.00005	0.00281617
ENSMUST00000102820	Bnc2	-1.01579	0.00515	0.0453122
ENSMUST00000028858	Bub1	-1.01539	0.00015	0.00678403
ENSMUST00000000122	Ngfr	-1.01496	0.00005	0.00281617
ENSMUST00000164614	A4galt	-1.01457	0.00035	0.0119974
ENSMUST00000183144	Mir134,Mir3072	-1.01161	0.00005	0.00281617
ENSMUST00000146702	9330198N18Rik	1.00945	0.00025	0.00944576
ENSMUST00000160708	Stxbp2	1.00846	0.00005	0.00281617
ENSMUST00000050166	Adam22	-1.00464	0.00005	0.00281617
ENSMUST00000022213	Thbs4	-1.00356	0.00005	0.00281617
ENSMUST00000021802	Cap2	-1.00284	0.00565	0.0484455
ENSMUST00000049681	Itgbl1	-1.00265	0.00005	0.00281617
ENSMUST00000120593	Bcl7a	1.00227	0.0001	0.00490324
ENSMUST00000033591	Itm2a	-1.00217	0.00005	0.00281617

Supplemental Table S5 GO analysis of DEGs between Fb and Pb tissues

Category	Term	Count	*p* value	GenesID#
GOTERM_BP_DIRECT	GO:0007275~multicellular organism development	132	0.0000000	22771, 17313, 22772, 20438, 56198, 18012, 11877, 59004, 17684, 107449, 17385, 107250, 217558, 216795, 15213, 399558, 19876, 14370, 17286, 114715, 11727, 26456, 110075, 69539, 20377, 54725, 93840, 27279, 13542, 93842, 13842, 16765, 50932, 14726, 17305, 235472, 18187, 20361, 13838, 320398, 22253, 67784, 51791, 17268, 85030, 56177, 71093, 22160, 14369, 20563, 14367, 228357, 225207, 20356, 67916, 13798, 16917, 20354, 20460, 20353, 12778, 21892, 20661, 241226, 110648, 21385, 59036, 21389, 16450, 13175,

				93960, 15229, 14362, 65960, 13591, 13593, 212712, 21934, 77889, 12817, 433938, 21938, 219134, 15901, 15902, 29811, 13008, 12153, 20471, 20204, 17240, 20472, 71653, 23893, 16790, 56811, 26934, 83453, 13380, 229658, 22417, 15248, 12161, 18111, 65100, 233107, 74229, 22413, 14048, 12934, 13649, 14254, 94187, 14836, 22698, 20720, 67888, 16973, 15273, 24117, 74762, 20613, 22337, 18131, 228598, 320563, 11601, 12142, 223254, 24063, 230738, 50781
GOTERM_BP_DIRECT	GO:0007155~cell adhesion	76	0.0000000	84004, 12560, 94332, 15117, 12816, 11877, 12817, 12819, 22371, 64058, 20779, 21838, 20345, 16401, 29817, 23928, 399558, 19200, 16409, 12550, 100689, 12387, 380713, 54725, 18949, 14724, 27279, 21826, 21825, 13052, 12558, 13842, 12554, 12484, 117606, 14726, 22403, 68188, 70370, 233744, 12833, 11658, 26968, 240725, 19268, 12834, 15891, 77976, 18074, 13836, 18073, 13838, 12490, 16421, 12504, 20750, 23876, 14089, 57810, 68799, 56047, 16414, 114332, 67916, 240185, 12778, 16416, 30931, 234214, 76293, 241226, 11931, 19039, 74202, 76884, 78733
GOTERM_BP_DIRECT	GO:0016337~single organismal cell-cell adhesion	29	0.0000000	13649, 12560, 12741, 59308, 12817, 11877, 21838, 20779, 12490, 16401, 12508, 16409, 12550, 21687, 57810, 20563, 12387, 16414, 67896, 67916, 18949, 380928, 81877, 13052, 74202, 12558, 76884, 117606, 14726
GOTERM_BP_DIRECT	GO:0001503~ossification	26	0.0000000	19228, 17313, 65960, 12399, 13601, 19242, 12814, 21934, 74511, 15891, 12817, 107250, 12153, 14560, 242050, 20750, 12977, 22160, 83453, 110075, 17395, 20661, 12161, 18214, 16002, 215653
GOTERM_BP_DIRECT	GO:0007411~axon guidance	32	0.0000002	22323, 12934, 231876, 11658, 12399, 226251, 20266, 14251, 18187, 21808, 208968, 107449, 13838, 20779, 22253, 12978, 399558, 12569, 17263, 19876, 19277, 20563, 13637, 20356, 243743, 17181, 13542, 110648, 13842, 15229, 12484, 117606
GOTERM_BP_DIRECT	GO:0030198~extracellular matrix organization	27	0.0000003	241327, 74199, 64074, 373864, 21808, 15891, 18074, 17385, 107250, 18073, 320712, 23928, 13717, 57764, 23876, 53381, 234356, 320078, 69675, 67896, 17395, 81877, 241226, 229595, 53867, 12587, 11606
GOTERM_BP_DIRECT	GO:0016477~cell migration	36	0.0000008	22325, 14254, 19268, 17179, 21808, 13609, 18019, 13836, 13837, 68588, 20779, 13876, 18826, 319939, 16401, 20472, 226751, 66629, 19200, 219140, 11843, 230837, 20613, 11727, 14389, 16416, 234214, 21825, 72333, 12558, 17974, 23888, 70445, 12484, 19211, 16452
GOTERM_BP_DIRECT	GO:0007399~nervous system development	55	0.0000039	22771, 227541, 231876, 22772, 94190, 18012, 211401, 14586, 23859, 17135, 23921, 29811, 19876, 109241, 12751, 12387, 83453, 26456, 69539, 271564, 12166, 17755, 93842, 65100, 13842, 16765, 19211, 12934, 76829, 94187, 20720, 19268, 13605, 18187, 20361, 228662, 13838, 18760, 17965, 74762,

				56177, 72821, 71093, 20563, 20356, 20354, 243743, 20353, 233552, 241226, 320563, 59036, 13865, 230738, 13175
GOTERM_BP_DIRECT	GO:0001525~angiogenesis	40	0.0000039	84004, 22325, 14254, 59308, 13601, 18187, 67888, 13609, 19263, 21846, 107449, 18127, 20229, 13836, 21838, 18760, 18787, 15213, 67784, 17286, 105450, 14370, 17268, 12306, 16790, 14257, 14089, 21687, 14367, 11727, 67896, 51801, 12778, 27279, 11601, 57875, 230738, 16476, 15368, 19211
GOTERM_BP_DIRECT	GO:0048147~negative regulation of fibroblast proliferation	12	0.0000128	17395, 65972, 75613, 60599, 14870, 17869, 114774, 20656, 20481, 58801, 11609, 20377
GOTERM_BP_DIRECT	GO:0016311~dephosphorylation	23	0.0000181	19258, 19249, 15170, 19267, 19246, 19264, 19277, 75219, 19253, 19268, 56405, 320139, 18218, 19271, 19263, 17772, 70686, 19062, 59047, 11433, 319520, 13850, 19211
GOTERM_BP_DIRECT	GO:0043410~positive regulation of MAPK cascade	22	0.0000276	65086, 57810, 19264, 14254, 14184, 12387, 16590, 21858, 21934, 16416, 21938, 18753, 93834, 21939, 12558, 16002, 16706, 13842, 19156, 14257, 85030, 11606
GOTERM_BP_DIRECT	GO:0008285~negative regulation of cell proliferation	53	0.0000283	14955, 17988, 22368, 54353, 107503, 75079, 18127, 216795, 210530, 17984, 19876, 65973, 14184, 12387, 20481, 20377, 12062, 19054, 242608, 16476, 12554, 19211, 193740, 20680, 19228, 22403, 110532, 60599, 20720, 19268, 21808, 218820, 94040, 20556, 20656, 12978, 218772, 58208, 17263, 52679, 20563, 14367, 21858, 22337, 19271, 116701, 14609, 74754, 24063, 15368, 16452, 27206, 11606
GOTERM_BP_DIRECT	GO:0035335~peptidyl-tyrosine dephosphorylation	10	0.0000358	14048, 19249, 19246, 19277, 75219, 56405, 72828, 19268, 319520, 19271
GOTERM_BP_DIRECT	GO:0030032~lamellipodium assembly	11	0.0000804	22325, 19277, 319713, 226251, 219140, 17974, 50884, 16590, 12554, 13609, 66629
GOTERM_BP_DIRECT	GO:0001649~osteoblast differentiation	22	0.0000988	22160, 12833, 20613, 170574, 74511, 12033, 110075, 15891, 326618, 20361, 20377, 12359, 19656, 13836, 14609, 14560, 12161, 20750, 16002, 16842, 68728, 18619
GOTERM_BP_DIRECT	GO:0031032~actomyosin structure organization	10	0.0001043	218194, 11464, 77569, 226751, 12798, 13823, 54357, 58800, 269587, 13821
GOTERM_BP_DIRECT	GO:0015991~ATP hydrolysis coupled proton transport	11	0.0001076	11966, 27060, 108664, 114143, 242341, 76252, 232975, 11984, 11928, 11964, 11973
GOTERM_BP_DIRECT	GO:0006629~lipid metabolic process	58	0.0001377	67216, 68952, 60527, 18010, 20249, 54711, 18783, 18806, 28169, 15357, 234779, 12896, 18606, 20501, 13850, 382030, 26457, 71780, 27226, 57874, 14149, 19156, 67963, 19211, 96979, 11815, 11816, 14667, 52123, 15446, 18796, 14732, 216859, 20652, 19223, 16835, 54447, 171504, 110196, 433256,

				66569, 11364, 17772, 233552, 66659, 15450, 81877, 66469, 13360, 74754, 72999, 52538, 235293, 67469, 70999, 100340, 208715, 52430
GOTERM_BP_DIRECT	GO:0006979~response to oxidative stress	24	0.0001477	13649, 243864, 11816, 69675, 13010, 17751, 12359, 30931, 72774, 17395, 14778, 18753, 20856, 12350, 74754, 114886, 20656, 17250, 15368, 59047, 51791, 53901, 16452, 19122
GOTERM_BP_DIRECT	GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	20	0.0001540	13649, 21687, 14254, 76829, 17179, 16590, 15162, 14586, 13836, 13837, 13838, 26563, 11601, 18214, 12978, 13842, 16822, 12977, 17295, 14257
GOTERM_BP_DIRECT	GO:0007160~cell-matrix adhesion	17	0.0001996	21687, 12387, 16414, 56047, 12817, 16416, 18074, 81877, 18073, 241226, 53867, 12490, 16421, 16401, 105298, 12587, 11606
GOTERM_BP_DIRECT	GO:0030178~negative regulation of Wnt signaling pathway	14	0.0002150	56811, 14836, 228357, 13380, 14783, 20377, 24117, 219134, 15248, 59036, 17240, 50781, 93960, 666048
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia	20	0.0002302	22160, 17988, 19242, 68655, 56295, 16526, 17751, 12176, 58801, 20544, 20377, 20779, 20856, 52538, 12428, 20203, 19223, 15368, 63959, 19211
GOTERM_BP_DIRECT	GO:0009314~response to radiation	10	0.0002589	16177, 11601, 16478, 17869, 16476, 20656, 16590, 21934, 20315, 18619
GOTERM_BP_DIRECT	GO:0001666~response to hypoxia	30	0.0002591	14254, 16493, 21808, 18791, 12176, 17684, 12359, 12334, 18126, 18806, 94352, 20656, 19223, 21335, 21687, 11727, 13653, 26432, 13010, 18021, 17751, 17711, 11601, 11931, 57875, 114886, 15368, 12484, 20315, 18619
GOTERM_BP_DIRECT	GO:0045766~positive regulation of angiogenesis	22	0.0002676	21687, 14254, 13601, 16414, 17228, 20356, 16416, 76905, 18127, 17395, 21825, 11601, 18760, 18787, 12490, 230738, 14066, 19223, 15368, 15586, 20130, 15507
GOTERM_BP_DIRECT	GO:0030335~positive regulation of cell migration	31	0.0003011	84004, 13649, 50918, 14254, 15117, 21808, 11855, 12768, 13609, 20361, 329252, 218877, 18806, 12978, 12977, 66102, 277360, 20613, 16590, 26456, 20354, 20353, 16416, 21825, 17250, 12554, 16842, 17916, 20315, 16452, 14726
GOTERM_BP_DIRECT	GO:0060070~canonical Wnt signaling pathway	18	0.0003146	14369, 12560, 14367, 12387, 17869, 67916, 16973, 20377, 22417, 22289, 13542, 216795, 59036, 22413, 16842, 14370, 19211, 14362
GOTERM_BP_DIRECT	GO:0045453~bone resorption	9	0.0003489	19228, 19354, 20779, 12751, 12387, 13040, 13038, 11433, 19340
GOTERM_BP_DIRECT	GO:0001938~positive regulation of endothelial cell proliferation	15	0.0004020	14184, 13601, 11727, 20356, 228852, 16416, 76905, 18760, 12161, 16476, 14066, 22413, 12554, 14257, 20315
GOTERM_BP_DIRECT	GO:0043065~positive regulation of apoptotic process	44	0.0004381	227541, 22249, 60599, 56349, 19242, 16952, 19268, 13605, 21808, 18012, 56847, 12176, 58801, 58800, 242202, 18127, 18783, 109032, 57748, 20779, 22253, 20203, 218772, 13680, 27280, 20563, 105722, 12387, 12801, 114774, 12759, 20544, 20377, 17395, 27279,

				18753, 229595, 16476, 72565, 15368, 19211, 215653, 17279, 16452
GOTERM_BP_DIRECT	GO:0035556~intracellular signal transduction	50	0.0005379	18160, 22325, 56349, 11536, 17131, 170755, 23921, 142688, 20779, 319939, 234779, 226751, 238161, 13143, 97998, 277360, 26934, 69635, 14389, 13542, 54324, 26415, 16822, 17060, 50932, 13649, 22249, 210044, 13605, 18796, 77976, 18760, 11512, 51791, 74039, 15507, 15170, 21687, 219140, 18611, 16590, 18755, 18753, 54153, 104111, 16706, 15368, 13175, 11609, 16452
GOTERM_BP_DIRECT	GO:0003151~outflow tract morphogenesis	13	0.0005710	14048, 56198, 21808, 17684, 12166, 21385, 21825, 20471, 16476, 15213, 67784, 14362, 22762
GOTERM_BP_DIRECT	GO:0090090~negative regulation of canonical Wnt signaling pathway	19	0.0005811	12550, 56811, 19277, 228357, 13653, 13380, 21886, 20377, 74256, 24117, 22417, 106042, 68588, 216795, 59036, 12558, 50781, 93960, 16842
GOTERM_BP_DIRECT	GO:0030154~cell differentiation	85	0.0005840	22771, 65960, 17313, 22772, 17179, 18012, 12817, 17684, 56190, 29811, 13008, 107250, 12153, 13712, 15284, 23967, 17240, 19876, 26362, 16790, 26934, 14184, 12387, 11727, 26456, 83453, 110075, 20544, 20377, 100039795, 54725, 12166, 22417, 27279, 12161, 65100, 93842, 74229, 268564, 16765, 12934, 75766, 14254, 94187, 22698, 20720, 170676, 13605, 18187, 67888, 11790, 15162, 20361, 13836, 18760, 74762, 19725, 17263, 71093, 22160, 15170, 20563, 14367, 225207, 228357, 74614, 20356, 16590, 20354, 20353, 21892, 18755, 20661, 18131, 58521, 241226, 11601, 13360, 21804, 230738, 16450, 67469, 13175, 93960, 16452
GOTERM_BP_DIRECT	GO:0046777~protein autophosphorylation	28	0.0006043	13649, 14254, 231876, 15162, 58800, 21838, 12322, 13838, 20779, 18760, 108960, 56532, 12978, 14257, 21687, 14184, 69635, 16590, 102626, 73914, 18753, 18214, 13842, 70415, 17295, 50932, 17279, 16452
GOTERM_BP_DIRECT	GO:0030097~hemopoiesis	17	0.0006335	21687, 65960, 12399, 12387, 16590, 21808, 12798, 20377, 11601, 12490, 20656, 12978, 21335, 17268, 17279, 225049, 73046
GOTERM_BP_DIRECT	GO:0016055~Wnt signaling pathway	31	0.0006851	17869, 75723, 21886, 16973, 59004, 24117, 329252, 29811, 84035, 216795, 14370, 14369, 56811, 14367, 228357, 12387, 13380, 20377, 74256, 22417, 15248, 13542, 26563, 59036, 21804, 50781, 93960, 666048, 16842, 22413, 14362
GOTERM_BP_DIRECT	GO:0071526~semaphorin-plexin signaling pathway	10	0.0007212	218877, 20356, 26456, 235611, 67784, 20354, 243743, 17295, 20353, 54712
GOTERM_BP_DIRECT	GO:0009612~response to mechanical stimulus	14	0.0007266	27053, 16493, 16324, 16478, 16008, 16526, 17684, 21825, 20779, 171209, 11601, 667742, 16476, 20315

GOTERM_BP_DIRECT	GO:0006954~inflammatory response	44	0.0007579	227541, 13601, 230787, 16952, 70747, 15162, 12768, 20361, 107527, 21938, 54371, 18126, 13836, 93671, 18760, 108960, 20750, 12978, 12977, 15586, 26362, 85030, 106759, 13850, 19200, 13610, 12268, 18173, 16590, 243910, 53791, 13349, 27226, 12310, 21825, 12161, 21939, 230738, 19216, 100340, 109685, 11609, 20315, 16452
GOTERM_BP_DIRECT	GO:0014068~positive regulation of phosphatidylinositol 3-kinase signaling	14	0.0008498	216439, 21687, 15170, 14254, 22215, 21808, 20354, 12359, 107449, 18806, 83490, 235611, 16452, 11606
GOTERM_BP_DIRECT	GO:0030336~negative regulation of cell migration	19	0.0009294	110532, 20563, 60599, 240725, 19242, 12798, 19271, 17684, 20377, 21846, 22417, 21838, 109331, 242608, 66082, 18787, 20130, 19876, 19211
GOTERM_BP_DIRECT	GO:0048251~elastic fiber assembly	5	0.0009400	207596, 17880, 81877, 76293, 23876
GOTERM_BP_DIRECT	GO:0060763~mammary duct terminal end bud growth	5	0.0009400	20496, 20563, 75605, 12977, 19876
GOTERM_BP_DIRECT	GO:0007067~mitotic nuclear division	37	0.0009832	73804, 12236, 71819, 56150, 108911, 67849, 55947, 11799, 12442, 105988, 67166, 68743, 12428, 69736, 51791, 215387, 108907, 235072, 67052, 66977, 14793, 225182, 208628, 20878, 51944, 66131, 16551, 448987, 70099, 76464, 66442, 66156, 213582, 18817, 56742, 66616, 26886
GOTERM_BP_DIRECT	GO:0018108~peptidyl-tyrosine phosphorylation	14	0.0009901	15170, 13649, 21687, 14254, 14184, 16590, 15162, 20779, 13838, 18214, 12978, 14257, 16452, 17279
GOTERM_BP_DIRECT	GO:0030316~osteoclast differentiation	9	0.0010557	13836, 75766, 71982, 13637, 12387, 14389, 12978, 21934, 12977
GOTERM_BP_DIRECT	GO:0002040~sprouting angiogenesis	9	0.0010557	21687, 52679, 21825, 14254, 108961, 94352, 12554, 16842, 14257
GOTERM_BP_DIRECT	GO:0043392~negative regulation of DNA binding	9	0.0010557	17240, 16476, 22218, 278507, 15368, 16842, 16452, 15901, 15902
GOTERM_BP_DIRECT	GO:0046325~negative regulation of glucose import	7	0.0010955	23921, 18611, 98496, 17869, 13982, 18605, 14783
GOTERM_BP_DIRECT	GO:0043407~negative regulation of MAP kinase activity	11	0.0011145	15170, 19246, 18753, 24063, 14870, 15357, 11816, 19062, 51791, 73914, 19271
GOTERM_BP_DIRECT	GO:0048813~dendrite morphogenesis	11	0.0011145	13542, 12322, 223254, 228357, 18174, 59036, 13175, 17760, 50932, 75409, 228662
GOTERM_BP_DIRECT	GO:0002376~immune system process	47	0.0011897	19882, 73174, 75766, 12628, 11658, 12258, 12479, 15040, 230787, 16149, 16952, 217069, 15162, 246177, 107527, 13733, 109032, 20779, 18760, 12504, 12978, 12977, 26362, 21355, 106759, 19200, 18733, 65972, 14964, 100689, 69202, 53791, 54725, 381812, 11622, 16534, 12142, 21939, 18636, 230738, 54131, 26888, 100340, 268564, 22031, 16452, 13136

GOTERM_BP_DIRECT	GO:0032233~positive regulation of actin filament bundle assembly	6	0.0012290	68760, 20947, 18645, 211401, 118449, 15901
GOTERM_BP_DIRECT	GO:0043066~negative regulation of apoptotic process	64	0.0012454	227541, 16149, 56295, 56150, 107503, 54611, 17684, 15901, 407786, 20779, 12017, 15357, 11464, 20471, 23967, 26362, 53945, 14870, 69635, 17751, 12759, 231507, 20544, 15245, 20377, 83946, 68576, 17395, 21825, 57875, 16476, 19211, 216439, 13649, 66494, 18793, 21808, 105855, 15162, 12176, 12359, 11799, 14456, 20750, 20656, 12978, 218772, 58208, 14257, 66629, 19122, 27053, 22160, 21687, 11843, 53380, 20878, 20460, 15511, 74754, 18817, 16842, 22629, 16452
GOTERM_BP_DIRECT	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	102	0.0013086	22771, 22772, 15212, 56198, 14815, 12916, 98415, 18012, 16601, 17684, 54711, 20183, 18019, 12017, 13712, 108961, 15213, 17984, 17286, 14370, 53945, 433586, 22781, 16478, 66970, 18021, 13982, 110075, 18027, 75613, 18029, 30046, 98496, 16002, 16476, 17295, 216439, 170574, 17869, 13609, 24014, 218772, 58208, 17268, 22160, 57810, 14367, 11843, 18173, 16917, 13798, 110648, 21389, 320267, 15229, 18516, 16452, 13591, 226251, 13593, 212712, 107503, 75079, 19656, 407786, 20471, 23967, 20472, 21677, 22215, 12387, 20481, 231507, 20544, 83946, 12166, 12161, 52915, 22413, 12554, 13649, 14048, 238247, 12399, 16973, 69792, 15505, 18760, 319713, 52679, 13653, 66894, 22337, 18131, 228598, 21939, 13865, 230738, 17974, 16842, 18616, 22762
GOTERM_BP_DIRECT	GO:0000281~mitotic cytokinesis	9	0.0013455	26934, 108907, 12615, 235072, 18817, 68743, 66616, 71819, 16765
GOTERM_BP_DIRECT	GO:0046627~negative regulation of insulin receptor signaling pathway	10	0.0013932	19267, 387161, 18753, 50915, 19268, 98496, 19062, 53322, 18605, 14783
GOTERM_BP_DIRECT	GO:0031532~actin cytoskeleton reorganization	12	0.0014748	22350, 218194, 63873, 19246, 13052, 16952, 16590, 226751, 217692, 13609, 50932, 98366
GOTERM_BP_DIRECT	GO:0042474~middle ear morphogenesis	8	0.0015167	14048, 14836, 72999, 20204, 20471, 20472, 23967, 17869
GOTERM_BP_DIRECT	GO:0008152~metabolic process	54	0.0015744	217364, 227541, 15212, 15211, 18010, 18783, 28169, 12091, 59047, 216558, 18605, 18606, 224794, 13850, 110173, 14870, 26457, 14862, 107652, 69487, 56703, 236539, 329828, 20133, 66307, 109685, 23972, 17155, 240725, 52123, 665563, 56847, 72774, 110078, 242202, 17768, 14732, 12035, 83965, 15586, 80914, 140481, 433256, 234258, 11364, 110095, 56421, 52538, 11881, 100340, 545260, 208715, 52430, 270198

GOTERM_BP_DIRECT	GO:0010628~positive regulation of gene expression	48	0.0015843	227753, 12560, 60599, 18793, 21808, 54357, 17684, 15901, 15902, 18019, 63873, 20779, 18787, 14456, 12490, 11464, 75605, 23967, 18030, 16835, 12977, 109676, 56177, 13850, 22160, 18173, 404710, 12387, 13653, 114774, 16590, 66175, 12798, 17751, 22337, 16416, 230674, 22350, 22289, 14609, 12142, 98496, 230738, 320267, 15229, 17295, 16842, 11606
GOTERM_BP_DIRECT	GO:0030334~regulation of cell migration	15	0.0017014	21687, 219140, 108911, 243743, 54712, 16416, 13837, 21838, 22253, 235611, 67784, 54672, 18606, 50932, 20315
GOTERM_BP_DIRECT	GO:0071493~cellular response to UV-B	5	0.0017677	76293, 15586, 109685, 12925, 17380
GOTERM_BP_DIRECT	GO:0040037~negative regulation of fibroblast growth factor receptor signaling pathway	6	0.0018736	22417, 21825, 24063, 240725, 219134, 116701
GOTERM_BP_DIRECT	GO:0007035~vacuolar acidification	6	0.0018736	27060, 108664, 18173, 114143, 242341, 11984
GOTERM_BP_DIRECT	GO:0030514~negative regulation of BMP signaling pathway	11	0.0019270	65960, 73230, 17965, 78558, 83453, 13380, 20481, 17131, 23893, 20377, 14362
GOTERM_BP_DIRECT	GO:0048678~response to axon injury	9	0.0021125	17183, 16852, 17181, 11815, 11843, 14184, 20656, 13010, 16526
GOTERM_BP_DIRECT	GO:0006915~apoptotic process	63	0.0023572	13663, 20438, 22368, 66985, 107449, 29810, 64058, 109032, 16852, 217558, 69068, 29813, 12017, 20471, 13143, 14184, 333654, 69635, 13010, 73914, 54725, 27279, 229595, 19211, 22031, 22029, 227753, 21841, 60599, 240725, 66494, 170676, 12236, 14453, 12033, 58801, 12176, 11799, 13836, 22253, 18760, 67609, 66660, 106759, 27280, 14089, 223752, 54447, 18611, 56461, 53380, 114774, 99526, 66960, 14609, 18753, 230738, 15368, 70415, 76884, 18616, 13823, 17279
GOTERM_BP_DIRECT	GO:0001843~neural tube closure	17	0.0023768	22323, 12808, 22160, 22772, 18749, 50884, 21808, 20481, 20460, 20353, 17684, 20377, 93840, 22289, 106042, 65100, 21677
GOTERM_BP_DIRECT	GO:0001569~patterning of blood vessels	10	0.0024955	11622, 93840, 21687, 14254, 12387, 20356, 18021, 67784, 16842, 20315
GOTERM_BP_DIRECT	GO:0034446~substrate adhesion-dependent cell spreading	10	0.0024955	21687, 14369, 20779, 241226, 16401, 16421, 26362, 20377, 16416, 57373
GOTERM_BP_DIRECT	GO:0032147~activation of protein kinase activity	9	0.0026067	12310, 18753, 18173, 13605, 56532, 21808, 55984, 66197, 16416
GOTERM_BP_DIRECT	GO:0001501~skeletal system development	18	0.0026642	19228, 22771, 12387, 15212, 15211, 94111, 21808, 22337, 116701, 17395, 13836, 14118, 230484, 12577, 16450, 80752, 278507, 215653
GOTERM_BP_DIRECT	GO:0060444~branching involved in mammary gland duct morphogenesis	6	0.0027346	20496, 13836, 20779, 75605, 16973, 12977

GOTERM_BP_DIRECT	GO:0006883~cellular sodium ion homeostasis	7	0.0028200	170755, 11931, 232975, 11609, 20544, 11928, 11606
GOTERM_BP_DIRECT	GO:0045893~positive regulation of transcription, DNA-templated	63	0.0030565	22771, 13591, 22772, 13593, 18012, 107503, 77889, 73274, 17684, 15902, 18019, 20779, 13712, 20471, 12428, 12577, 12550, 12387, 18021, 13982, 17751, 18027, 66197, 21422, 20377, 83946, 12166, 22417, 11622, 13542, 109331, 56742, 65100, 75812, 16476, 20680, 96979, 14048, 12399, 94187, 60599, 17869, 16973, 19062, 17263, 68728, 67788, 71093, 14369, 68799, 20613, 13653, 80292, 21804, 58172, 320267, 16842, 11609, 22629, 14362, 67057, 22762, 11606
GOTERM_BP_DIRECT	GO:0048146~positive regulation of fibroblast proliferation	13	0.0031092	13649, 14456, 18787, 18214, 16149, 17869, 16476, 12428, 13982, 22413, 12306, 16416, 11606
GOTERM_BP_DIRECT	GO:0010811~positive regulation of cell-substrate adhesion	10	0.0035515	140709, 21825, 74199, 18073, 64074, 320712, 19242, 20750, 67896, 16452
GOTERM_BP_DIRECT	GO:0006470~protein dephosphorylation	21	0.0035971	19258, 19249, 14048, 15170, 19267, 19264, 19277, 19246, 75219, 19253, 66525, 19268, 56405, 320139, 18218, 19271, 19263, 17772, 19054, 319520, 19211
GOTERM_BP_DIRECT	GO:0001558~regulation of cell growth	12	0.0036690	170755, 22403, 107250, 12983, 110648, 16008, 29817, 78558, 13823, 67866, 23876, 13821
GOTERM_BP_DIRECT	GO:0015992~proton transport	12	0.0036690	11966, 108664, 114143, 18174, 242341, 76252, 11984, 246049, 17711, 97086, 11964, 11973
GOTERM_BP_DIRECT	GO:0030500~regulation of bone mineralization	7	0.0036990	22160, 17313, 14609, 13601, 18214, 13609, 11732
GOTERM_BP_DIRECT	GO:0048870~cell motility	7	0.0036990	218194, 13836, 18806, 12490, 67896, 17909, 14726
GOTERM_BP_DIRECT	GO:0051387~negative regulation of neurotrophin TRK receptor signaling pathway	4	0.0038226	24063, 19268, 11609, 11606
GOTERM_BP_DIRECT	GO:0007263~nitric oxide mediated signal transduction	6	0.0038493	17748, 18127, 18126, 11816, 17750, 18012
GOTERM_BP_DIRECT	GO:0048514~blood vessel morphogenesis	9	0.0038625	11622, 13836, 14609, 21825, 14254, 11601, 12558, 17268, 14257
GOTERM_BP_DIRECT	GO:0045765~regulation of angiogenesis	8	0.0039778	13836, 21687, 27279, 11601, 18787, 67784, 18606, 15901
GOTERM_BP_DIRECT	GO:0051259~protein oligomerization	13	0.0040282	21687, 16493, 20544, 20533, 67375, 15450, 17395, 14609, 67804, 230738, 20133, 56177, 20135
GOTERM_BP_DIRECT	GO:0001822~kidney development	20	0.0040707	68927, 228357, 12387, 240725, 15117, 12349, 21808, 17684, 12359, 20897, 22417, 241226, 14118, 12161, 20471, 20472, 12577, 15229, 11606, 17380
GOTERM_BP_DIRECT	GO:0097190~apoptotic signaling pathway	11	0.0042851	69635, 21939, 114774, 72565, 21934, 19223, 12507, 22337, 12484, 106759, 85030

GOTERM_BP_DIRECT	GO:0060021~palate development	15	0.0043841	22160, 65973, 20613, 212712, 21808, 20481, 22218, 12166, 21385, 72999, 231470, 23967, 278507, 17286, 16842
GOTERM_BP_DIRECT	GO:0001570~vasculogenesis	13	0.0045631	13836, 21687, 74376, 12387, 15117, 15213, 67888, 12778, 19271, 21677, 17684, 21846, 22762
GOTERM_BP_DIRECT	GO:0045669~positive regulation of osteoblast differentiation	13	0.0045631	12387, 16478, 56788, 12166, 22417, 14609, 68588, 18760, 12161, 14560, 18214, 80752, 15213
GOTERM_BP_DIRECT	GO:0006687~glycosphingolipid metabolic process	5	0.0046908	15212, 12916, 16590, 19156, 14421
GOTERM_BP_DIRECT	GO:0001889~liver development	16	0.0048970	27053, 12808, 68927, 19242, 17684, 54725, 11364, 22371, 22417, 11622, 15284, 16476, 20656, 208715, 17263, 17295
GOTERM_BP_DIRECT	GO:0030036~actin cytoskeleton organization	21	0.0049937	22323, 216439, 319713, 231003, 94190, 19240, 211401, 20377, 80837, 23921, 19354, 13007, 208846, 54324, 72333, 71409, 18645, 56419, 57778, 232227, 269587
GOTERM_BP_DIRECT	GO:0086004~regulation of cardiac muscle cell contraction	6	0.0052549	22218, 12373, 109676, 238161, 238871, 11928
GOTERM_BP_DIRECT	GO:0001764~neuron migration	19	0.0054683	22160, 215494, 73710, 12387, 212712, 18187, 16917, 20745, 17181, 14609, 14456, 13865, 74762, 13175, 12569, 17984, 26362, 17295, 20315
GOTERM_BP_DIRECT	GO:0042493~response to drug	40	0.0057127	12934, 12560, 11815, 13663, 19242, 16952, 21808, 18012, 105855, 54611, 67866, 12359, 18019, 16852, 20779, 11464, 20656, 11928, 12550, 66694, 14871, 12387, 16008, 16478, 103573, 13010, 17716, 21858, 17711, 20544, 20377, 17395, 21825, 232975, 16002, 16476, 17250, 208715, 19211, 14362
GOTERM_BP_DIRECT	GO:0045429~positive regulation of nitric oxide biosynthetic process	10	0.0057581	13649, 16414, 20656, 53791, 13982, 12759, 19288, 106759, 16452, 11606
GOTERM_BP_DIRECT	GO:0036120~cellular response to platelet-derived growth factor stimulus	7	0.0060426	20779, 19242, 15117, 17869, 12428, 15586, 16416
GOTERM_BP_DIRECT	GO:0000070~mitotic sister chromatid segregation	7	0.0060426	67052, 108907, 12615, 18817, 105988, 51944, 56150
GOTERM_BP_DIRECT	GO:0051301~cell division	43	0.0063581	100502766, 73804, 12236, 13605, 71819, 18951, 56150, 108911, 67849, 55947, 11799, 12442, 67166, 68743, 12428, 93737, 69736, 51791, 215387, 77891, 26934, 108907, 235072, 67052, 66977, 14793, 225182, 208628, 20878, 51944, 66131, 16551, 448987, 70099, 66197, 76464, 66442, 66156, 213582, 18817, 56742, 66616, 233406

GOTERM_BP_DIRECT	GO:0051091~positive regulation of sequence-specific DNA binding transcription factor activity	17	0.0064037	22772, 12387, 217069, 16590, 67916, 21934, 16973, 18012, 13982, 57748, 54324, 18214, 22413, 19211, 74039, 16452, 14362
GOTERM_BP_DIRECT	GO:0001656~metanephros development	9	0.0065630	22417, 14048, 241226, 20563, 24063, 14118, 20472, 23967, 15902
GOTERM_BP_DIRECT	GO:0007059~chromosome segregation	15	0.0066538	67052, 73804, 51944, 26900, 16551, 11740, 76464, 66442, 11799, 70012, 105988, 67166, 69736, 51791, 26886
GOTERM_BP_DIRECT	GO:0008203~cholesterol metabolic process	15	0.0066538	171504, 110196, 11816, 16973, 12359, 15450, 13360, 74754, 14149, 20652, 15357, 72999, 16835, 67963, 208715
GOTERM_BP_DIRECT	GO:0045577~regulation of B cell differentiation	5	0.0069346	15170, 19264, 12484, 74039, 74256
GOTERM_BP_DIRECT	GO:0003203~endocardial cushion morphogenesis	6	0.0069879	22160, 21385, 56198, 15213, 21808, 12166
GOTERM_BP_DIRECT	GO:0048812~neuron projection morphogenesis	12	0.0070293	13649, 14609, 20563, 23969, 67263, 17965, 235611, 12759, 243743, 71653, 13823, 16880
GOTERM_BP_DIRECT	GO:0006468~protein phosphorylation	61	0.0071612	18160, 227541, 231876, 17179, 18749, 170755, 20779, 108960, 56532, 12569, 226751, 26362, 13143, 14184, 69635, 73914, 12166, 26563, 18214, 26415, 55984, 13842, 17295, 50932, 19882, 13649, 18557, 12399, 14254, 12236, 11790, 21808, 15162, 77976, 21846, 58800, 11799, 13836, 13837, 13838, 12322, 18760, 14456, 24014, 12978, 320129, 14257, 21687, 20878, 16590, 102626, 18755, 18753, 18817, 80752, 16706, 13175, 70415, 16452, 17279, 27206
GOTERM_BP_DIRECT	GO:0035435~phosphate ion transmembrane transport	4	0.0072167	56857, 19775, 14385, 11732
GOTERM_BP_DIRECT	GO:2001028~positive regulation of endothelial cell chemotaxis	4	0.0072167	18760, 20356, 17295, 15507
GOTERM_BP_DIRECT	GO:0048704~embryonic skeletal system morphogenesis	11	0.0074615	22160, 14048, 21384, 14836, 216795, 20204, 20471, 17240, 20472, 212712, 12814
GOTERM_BP_DIRECT	GO:0030866~cortical actin cytoskeleton organization	7	0.0075512	109042, 71409, 105855, 57778, 13823, 269587, 13821
GOTERM_BP_DIRECT	GO:0007159~leukocyte cell-cell adhesion	7	0.0075512	22350, 19264, 23959, 16401, 16414, 12484, 16409
GOTERM_BP_DIRECT	GO:0016310~phosphorylation	64	0.0076125	227541, 231876, 17179, 18749, 170755, 20779, 16548, 56532, 59047, 226751, 26362, 13143, 14184, 69635, 73914, 12166, 18214, 26415, 74637, 55984, 13842, 17295, 50932, 269614, 23972, 19882, 13649, 18557, 14254, 12236, 11790, 15162, 77976, 21846, 58800, 13836, 13837, 13838, 12322, 12709, 18760, 110639, 235533, 12978, 320129,

				14257, 80914, 21687, 215015, 20878, 16590, 102626, 18755, 18655, 18753, 56421, 18817, 80752, 13175, 70415, 16452, 17279, 270198, 27206
GOTERM_BP_DIRECT	GO:0006641~triglyceride metabolic process	9	0.0077223	15450, 81877, 14732, 171504, 11816, 72999, 14385, 20249, 12359
GOTERM_BP_DIRECT	GO:0006874~cellular calcium ion homeostasis	16	0.0079078	19228, 11816, 15212, 53322, 12768, 22337, 16416, 63873, 12310, 20856, 11931, 224088, 21939, 20203, 14385, 109676
GOTERM_BP_DIRECT	GO:0042981~regulation of apoptotic process	26	0.0082841	22029, 17869, 21808, 21934, 16973, 58801, 21938, 12153, 14560, 108960, 19223, 109676, 85030, 12387, 18611, 13653, 13982, 73914, 110075, 12161, 21939, 70415, 11609, 215653, 22031, 11606
GOTERM_BP_DIRECT	GO:2001238~positive regulation of extrinsic apoptotic signaling pathway	8	0.0086819	19264, 27279, 12399, 14827, 11609, 20377, 74256, 11606
GOTERM_BP_DIRECT	GO:0001657~ureteric bud development	10	0.0088959	14048, 20563, 73230, 24063, 20471, 23967, 218772, 17131, 20377, 12359
GOTERM_BP_DIRECT	GO:0060048~cardiac muscle contraction	10	0.0088959	11931, 333654, 20266, 11464, 232975, 12373, 109676, 17295, 16511, 72821
GOTERM_BP_DIRECT	GO:0015012~heparan sulfate proteoglycan biosynthetic process	6	0.0090836	15450, 93840, 56219, 58193, 233781, 217119
GOTERM_BP_DIRECT	GO:0050860~negative regulation of T cell receptor signaling pathway	6	0.0090836	22350, 15170, 21838, 114774, 19271, 19122
GOTERM_BP_DIRECT	GO:0033137~negative regulation of peptidyl-serine phosphorylation	7	0.0093134	12062, 19062, 17974, 13380, 17131, 238871, 215653
GOTERM_BP_DIRECT	GO:0043542~endothelial cell migration	7	0.0093134	18127, 14089, 94352, 16414, 67784, 12554, 19211
GOTERM_BP_DIRECT	GO:0009408~response to heat	11	0.0096120	12310, 60599, 243864, 171209, 15511, 21804, 29817, 22368, 20315, 193740, 17711
GOTERM_BP_DIRECT	GO:0071276~cellular response to cadmium ion	5	0.0097874	227753, 17750, 15368, 17751, 105349
GOTERM_BP_DIRECT	GO:0010629~negative regulation of gene expression	32	0.0099652	14955, 50918, 60599, 56198, 17869, 21808, 218820, 12768, 17684, 15901, 15902, 18126, 20856, 18787, 12490, 15213, 16835, 56177, 20563, 14184, 404710, 12387, 114774, 66894, 13982, 20377, 230674, 22417, 14609, 12142, 230738, 17295
GOTERM_BP_DIRECT	GO:1900026~positive regulation of substrate adhesion-dependent cell spreading	8	0.0103175	277360, 50918, 70450, 56349, 15117, 18606, 68813, 16416

GOTERM_BP_DIRECT	GO:0050919~negative chemotaxis	7	0.0113504	218877, 20563, 26456, 18187, 20354, 20353, 16416
GOTERM_BP_DIRECT	GO:0048675~axon extension	7	0.0113504	13542, 17755, 20356, 13175, 235611, 17984, 20361
GOTERM_BP_DIRECT	GO:0034113~heterotypic cell-cell adhesion	6	0.0115752	19264, 64058, 16401, 16421, 16414, 16416
GOTERM_BP_DIRECT	GO:0042307~positive regulation of protein import into nucleus	6	0.0115752	22771, 21687, 18753, 13605, 230738, 72565
GOTERM_BP_DIRECT	GO:0045892~negative regulation of transcription, DNA-templated	60	0.0115871	22772, 70350, 56198, 12916, 94091, 107503, 208968, 17684, 59004, 15901, 15902, 20779, 75605, 15213, 100040972, 16950, 12569, 20893, 22781, 12387, 22218, 17751, 20377, 22417, 11622, 116871, 18029, 16476, 20680, 238247, 94187, 21886, 22200, 11799, 18037, 106042, 69009, 14456, 19062, 94352, 17263, 22160, 71093, 20613, 56461, 66894, 22337, 22666, 230674, 12310, 58521, 21385, 54670, 50781, 15229, 16842, 71041, 14362, 67057, 22762
GOTERM_BP_DIRECT	GO:0032956~regulation of actin cytoskeleton organization	10	0.0116124	93840, 18753, 13837, 54324, 73723, 620235, 21808, 12569, 17916, 16416
GOTERM_BP_DIRECT	GO:0001934~positive regulation of protein phosphorylation	24	0.0116457	21687, 13649, 57810, 404710, 14251, 68655, 18793, 17751, 20354, 20361, 17395, 13542, 93834, 16981, 14456, 21939, 16002, 12978, 320129, 238161, 14370, 12306, 14257, 14362
GOTERM_BP_DIRECT	GO:0006689~ganglioside catabolic process	4	0.0119242	15212, 15211, 18010, 14667
GOTERM_BP_DIRECT	GO:0072678~T cell migration	4	0.0119242	16401, 16421, 246177, 13609
GOTERM_BP_DIRECT	GO:0030155~regulation of cell adhesion	9	0.0121273	380928, 227753, 59308, 16450, 13842, 13609, 19271, 16452, 77976
GOTERM_BP_DIRECT	GO:0007049~cell cycle	63	0.0121346	71819, 56150, 75079, 56190, 55947, 20779, 29813, 67166, 68743, 108961, 12428, 12577, 69736, 17345, 77891, 26934, 235072, 108907, 66977, 225182, 51944, 231506, 66197, 69539, 66442, 76464, 11622, 66156, 213582, 56742, 26415, 77805, 215653, 233406, 19360, 73804, 12236, 13605, 14453, 18951, 108911, 67849, 22200, 11799, 12442, 56710, 93737, 51791, 215387, 52679, 67052, 14793, 208628, 20878, 66131, 16551, 448987, 70099, 58521, 18753, 18817, 66616, 17279
GOTERM_BP_DIRECT	GO:0010718~positive regulation of epithelial to mesenchymal transition	8	0.0121662	22160, 384009, 20613, 12387, 21804, 21808, 16842, 56177
GOTERM_BP_DIRECT	GO:0043408~regulation of MAPK cascade	11	0.0122055	12153, 16324, 14560, 83490, 12161, 21808, 21858, 19156, 12484, 110075, 15901
GOTERM_BP_DIRECT	GO:0035023~regulation of Rho protein signal transduction	13	0.0123533	277360, 22325, 219140, 56349, 14251, 13605, 213783, 223254, 54324, 235633, 12558, 213522, 263406

GOTERM_BP_DIRECT	GO:0060044~negative regulation of cardiac muscle cell proliferation	5	0.0133046	14609, 19662, 13052, 16526, 19211
GOTERM_BP_DIRECT	GO:0022407~regulation of cell-cell adhesion	5	0.0133046	22417, 20779, 12484, 16842, 50932
GOTERM_BP_DIRECT	GO:0003197~endocardial cushion development	5	0.0133046	13837, 21825, 13876, 67888, 17684
GOTERM_BP_DIRECT	GO:1902287~semaphorin-plexin signaling pathway involved in axon guidance	5	0.0133046	18187, 235611, 67784, 243743, 54712
GOTERM_BP_DIRECT	GO:0060317~cardiac epithelial to mesenchymal transition	5	0.0133046	56198, 15213, 21808, 22413, 56177
GOTERM_BP_DIRECT	GO:0009749~response to glucose	13	0.0136270	14609, 21825, 14732, 11601, 16548, 18111, 13653, 18012, 14385, 12834, 19211, 18640, 100039795
GOTERM_BP_DIRECT	GO:0071260~cellular response to mechanical stimulus	13	0.0136270	18127, 29810, 13649, 14609, 12161, 21939, 12387, 14489, 53791, 12798, 12176, 11928, 11606
GOTERM_BP_DIRECT	GO:0051260~protein homooligomerization	25	0.0136412	12550, 16493, 14251, 77782, 13605, 111368, 30931, 226153, 116701, 16504, 20389, 22371, 19656, 12495, 109168, 57875, 26434, 16538, 233107, 56532, 20656, 15368, 268564, 268935, 19122
GOTERM_BP_DIRECT	GO:0016126~sterol biosynthetic process	7	0.0136826	74754, 13360, 110196, 15357, 72999, 235293, 208715
GOTERM_BP_DIRECT	GO:0043525~positive regulation of neuron apoptotic process	12	0.0137930	14184, 12017, 12387, 19268, 114774, 16476, 13653, 14815, 21808, 14809, 12569, 58801
GOTERM_BP_DIRECT	GO:0043433~negative regulation of sequence-specific DNA binding transcription factor activity	12	0.0137930	22160, 20893, 14456, 108960, 66894, 22218, 13982, 15368, 17131, 15901, 19122, 15902
GOTERM_BP_DIRECT	GO:0090002~establishment of protein localization to plasma membrane	9	0.0139400	52588, 22417, 22350, 668212, 12550, 23969, 14251, 12558, 225049
GOTERM_BP_DIRECT	GO:0048013~ephrin receptor signaling pathway	9	0.0139400	13836, 13837, 20779, 13838, 13637, 17974, 13842, 12569, 217692
GOTERM_BP_DIRECT	GO:0007166~cell surface receptor signaling pathway	27	0.0144381	19228, 18160, 13649, 16952, 21912, 70747, 14131, 68498, 21938, 13733, 66109, 12504, 12508, 14370, 52588, 14369, 14367, 102626, 56496, 116701, 64540, 54672, 11609, 12484, 241556, 11606, 14362
GOTERM_BP_DIRECT	GO:0046597~negative regulation of viral entry into host cell	6	0.0144936	227753, 19360, 94091, 217069, 66949, 19288

GOTERM_BP_DIRECT	GO:0071560~cellular response to transforming growth factor beta stimulus	11	0.0152938	18127, 22417, 20779, 18787, 17131, 22413, 54611, 105349, 20377, 15901, 18619
GOTERM_BP_DIRECT	GO:1904037~positive regulation of epithelial cell apoptotic process	3	0.0162258	20661, 21841, 16452
GOTERM_BP_DIRECT	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	72	0.0162999	212712, 17131, 59004, 77128, 17684, 15901, 15902, 18019, 407786, 20471, 23967, 108961, 17240, 15213, 12577, 14370, 20893, 14184, 333654, 12387, 16478, 13380, 13982, 20481, 18027, 11568, 22350, 11622, 15248, 75613, 18029, 12161, 54131, 16476, 17295, 268564, 22294, 12399, 14836, 17869, 18767, 63873, 404634, 18030, 218772, 22160, 52679, 382639, 20613, 56461, 53380, 103573, 13653, 66894, 114774, 13798, 20354, 22337, 18131, 58521, 21385, 18817, 12142, 59036, 13865, 21389, 13864, 18616, 16842, 212276, 71041, 22762
GOTERM_BP_DIRECT	GO:0043113~receptor clustering	7	0.0163293	13542, 228357, 16401, 16421, 16414, 14809, 23859
GOTERM_BP_DIRECT	GO:0006024~glycosaminoglycan biosynthetic process	7	0.0163293	56219, 58193, 233781, 14735, 15211, 217119, 23888
GOTERM_BP_DIRECT	GO:0048661~positive regulation of smooth muscle cell proliferation	13	0.0164719	13649, 240725, 17869, 13653, 13609, 16416, 15902, 18131, 21825, 15357, 16476, 15368, 12554
GOTERM_BP_DIRECT	GO:0010634~positive regulation of epithelial cell migration	8	0.0165590	20779, 384009, 14389, 16476, 21808, 15586, 18606, 68813
GOTERM_BP_DIRECT	GO:0008360~regulation of cell shape	19	0.0170845	16952, 19242, 15212, 14453, 16590, 20354, 15162, 83946, 80837, 22350, 74202, 20203, 12978, 235611, 57778, 17909, 13823, 14726, 269587
GOTERM_BP_DIRECT	GO:0060307~regulation of ventricular cardiac muscle cell membrane repolarization	5	0.0175326	12293, 14609, 20266, 20648, 16511
GOTERM_BP_DIRECT	GO:0060993~kidney morphogenesis	5	0.0175326	22417, 11622, 14537, 93840, 11609
GOTERM_BP_DIRECT	GO:0090026~positive regulation of monocyte chemotaxis	5	0.0175326	27226, 105722, 18787, 12768, 20315
GOTERM_BP_DIRECT	GO:1901222~regulation of NIK/NF-kappaB signaling	4	0.0180181	21687, 72565, 215653, 57373
GOTERM_BP_DIRECT	GO:1903169~regulation of calcium ion transmembrane transport	4	0.0180181	15464, 11931, 66109, 22218

GOTERM_BP_DIRECT	GO:0051549~positive regulation of keratinocyte migration	4	0.0180181	17395, 18787, 15117, 54357
GOTERM_BP_DIRECT	GO:0016525~negative regulation of angiogenesis	12	0.0186203	13836, 21687, 21826, 21825, 11601, 19242, 240725, 17263, 12509, 15245, 21846, 11606
GOTERM_BP_DIRECT	GO:0008630~intrinsic apoptotic signaling pathway in response to DNA damage	10	0.0188372	15248, 13836, 13663, 17869, 20656, 72565, 15368, 58801, 12925, 21938
GOTERM_BP_DIRECT	GO:0030326~embryonic limb morphogenesis	11	0.0189284	22160, 228357, 20204, 231470, 66175, 21808, 13380, 20481, 16917, 13798, 16842
GOTERM_BP_DIRECT	GO:0071391~cellular response to estrogen stimulus	8	0.0191300	387161, 387163, 74614, 387166, 17869, 13982, 20377, 67788
GOTERM_BP_DIRECT	GO:0000910~cytokinesis	8	0.0191300	11799, 18817, 213582, 11853, 13605, 71819, 233406, 19200
GOTERM_BP_DIRECT	GO:0031214~biomineral tissue development	7	0.0193089	66695, 13601, 18214, 20750, 80752, 18605, 15891
GOTERM_BP_DIRECT	GO:0032355~response to estradiol	15	0.0193714	14870, 16952, 12387, 19242, 225182, 16008, 17869, 13010, 13982, 67866, 12359, 18127, 12504, 19211, 18619
GOTERM_BP_DIRECT	GO:0051216~cartilage development	13	0.0197428	17313, 14184, 234356, 240725, 212712, 12814, 110075, 12166, 12153, 12161, 20204, 109685, 15586
GOTERM_BP_DIRECT	GO:0007568~aging	22	0.0208194	19228, 227753, 11815, 12258, 11816, 16478, 16008, 12801, 16414, 21858, 238871, 12359, 21938, 20496, 12310, 15357, 16476, 12577, 20656, 19211, 11606, 18619
GOTERM_BP_DIRECT	GO:0042246~tissue regeneration	6	0.0217202	329252, 54381, 227753, 11815, 242050, 66175
GOTERM_BP_DIRECT	GO:0060412~ventricular septum morphogenesis	8	0.0219678	56198, 15213, 21808, 17131, 17684, 116701, 14362, 22762
GOTERM_BP_DIRECT	GO:0007229~integrin-mediated signaling pathway	14	0.0222360	14389, 11492, 16414, 108911, 20361, 16416, 110751, 20779, 241226, 22177, 16421, 16401, 330119, 16409
GOTERM_BP_DIRECT	GO:0050901~leukocyte tethering or rolling	5	0.0225084	14537, 20345, 16401, 16421, 66629
GOTERM_BP_DIRECT	GO:0051493~regulation of cytoskeleton organization	5	0.0225084	70292, 54324, 235611, 12338, 12334
GOTERM_BP_DIRECT	GO:0006693~prostaglandin metabolic process	5	0.0225084	66469, 19223, 15446, 14726, 96979
GOTERM_BP_DIRECT	GO:0071498~cellular response to fluid shear stress	5	0.0225084	20779, 15117, 20750, 12349, 211401
GOTERM_BP_DIRECT	GO:0033630~positive regulation of cell adhesion mediated by integrin	5	0.0225084	15170, 21808, 105855, 12484, 16416

GOTERM_BP_DIRECT	GO:0045785~positive regulation of cell adhesion	10	0.0234714	277360, 21687, 18806, 81877, 12310, 20779, 15586, 19271, 54357, 20315
GOTERM_BP_DIRECT	GO:0031100~organ regeneration	10	0.0234714	11601, 18826, 14870, 14456, 12428, 26362, 17345, 20315, 17711, 16880
GOTERM_BP_DIRECT	GO:0008202~steroid metabolic process	13	0.0234744	171504, 110196, 13360, 74754, 20652, 15357, 14149, 72999, 235293, 14385, 16835, 67963, 208715
GOTERM_BP_DIRECT	GO:0007596~blood coagulation	13	0.0234744	105722, 12258, 20720, 19271, 17135, 22371, 14724, 14456, 74145, 14066, 224794, 19124, 23972
GOTERM_BP_DIRECT	GO:0035690~cellular response to drug	12	0.0245991	13649, 18126, 67702, 14456, 18787, 17869, 18577, 17751, 14862, 16511, 11565, 19122
GOTERM_BP_DIRECT	GO:0034605~cellular response to heat	8	0.0250840	71145, 21426, 63873, 69068, 226101, 233781, 15368, 17345
GOTERM_BP_DIRECT	GO:0030199~collagen fibril organization	8	0.0250840	17385, 81877, 18214, 94352, 21808, 12814, 16917, 12306
GOTERM_BP_DIRECT	GO:0033077~T cell differentiation in thymus	8	0.0250840	22417, 14369, 14367, 12387, 56532, 58208, 14370, 268564
GOTERM_BP_DIRECT	GO:0032088~negative regulation of NF-kappaB transcription factor activity	11	0.0255132	108960, 53380, 230738, 100040972, 243910, 19223, 73914, 59004, 74256, 22031, 12359
GOTERM_BP_DIRECT	GO:0030948~negative regulation of vascular endothelial growth factor receptor signaling pathway	4	0.0255310	19246, 17263, 105450, 12509
GOTERM_BP_DIRECT	GO:0001960~negative regulation of cytokine-mediated signaling pathway	4	0.0255310	19264, 13601, 19268, 73914
GOTERM_BP_DIRECT	GO:0061045~negative regulation of wound healing	4	0.0255310	22417, 14609, 15357, 67866
GOTERM_BP_DIRECT	GO:0000578~embryonic axis specification	4	0.0255310	12808, 14367, 12387, 20460
GOTERM_BP_DIRECT	GO:0010873~positive regulation of cholesterol esterification	4	0.0255310	170459, 11816, 20249, 11606
GOTERM_BP_DIRECT	GO:0016043~cellular component organization	4	0.0255310	208846, 71409, 56419, 57778
GOTERM_BP_DIRECT	GO:0060947~cardiac vascular smooth muscle cell differentiation	4	0.0255310	93840, 387161, 387163, 12387
GOTERM_BP_DIRECT	GO:0006000~fructose metabolic process	4	0.0255310	170768, 16548, 18640, 270198
GOTERM_BP_DIRECT	GO:0007219~Notch signaling pathway	17	0.0260069	13610, 433586, 94187, 16493, 56198, 67888, 18131, 234214, 64058, 21385,

				243547, 207521, 16450, 15213, 76580, 53901, 14718
GOTERM_BP_DIRECT	GO:0045664~regulation of neuron differentiation	7	0.0263326	12934, 14048, 57810, 20471, 21858, 18012, 58208
GOTERM_BP_DIRECT	GO:0043029~T cell homeostasis	7	0.0263326	11622, 12442, 56532, 105855, 319817, 58801, 216892
GOTERM_BP_DIRECT	GO:0070374~positive regulation of ERK1 and ERK2 cascade	23	0.0266425	21687, 13649, 14184, 384009, 16149, 13982, 17751, 12768, 12778, 20361, 16416, 63873, 109042, 20779, 73230, 15357, 14456, 72514, 16476, 12978, 14257, 19211, 381126
GOTERM_BP_DIRECT	GO:0010666~positive regulation of cardiac muscle cell apoptotic process	5	0.0282595	12322, 15357, 68655, 12176, 11606
GOTERM_BP_DIRECT	GO:0002089~lens morphogenesis in camera-type eye	5	0.0282595	14184, 12387, 20481, 17268, 17684
GOTERM_BP_DIRECT	GO:2000353~positive regulation of endothelial cell apoptotic process	5	0.0282595	21825, 105722, 21939, 70445, 105349
GOTERM_BP_DIRECT	GO:0051898~negative regulation of protein kinase B signaling	8	0.0284895	109042, 13836, 387161, 19062, 19271, 19211, 27280, 17772
GOTERM_BP_DIRECT	GO:0048666~neuron development	10	0.0288656	56196, 23969, 13864, 20656, 21808, 20481, 18012, 13798, 17984, 18516
GOTERM_BP_DIRECT	GO:0051897~positive regulation of protein kinase B signaling	14	0.0303155	19882, 17537, 13649, 21687, 20356, 19271, 20779, 21825, 14456, 329828, 14066, 16002, 26362, 105349
GOTERM_BP_DIRECT	GO:0006695~cholesterol biosynthetic process	7	0.0304059	74754, 13360, 110196, 15357, 11816, 72999, 208715
GOTERM_BP_DIRECT	GO:0060349~bone morphogenesis	7	0.0304059	14184, 23850, 15117, 16973, 20481, 11433, 17684
GOTERM_BP_DIRECT	GO:1902732~positive regulation of chondrocyte proliferation	3	0.0308313	20472, 66175, 56788
GOTERM_BP_DIRECT	GO:1904395~positive regulation of skeletal muscle acetylcholine-gated channel clustering	3	0.0308313	228357, 19242, 16973
GOTERM_BP_DIRECT	GO:0043620~regulation of DNA-templated transcription in response to stress	3	0.0308313	57748, 69068, 51791
GOTERM_BP_DIRECT	GO:0071504~cellular response to heparin	3	0.0308313	20563, 13653, 20377
GOTERM_BP_DIRECT	GO:0002521~leukocyte differentiation	3	0.0308313	20130, 17684, 15902

GOTERM_BP_DIRECT	GO:0016050~vesicle organization	6	0.0309498	20661, 67804, 71982, 209131, 76561, 66616
GOTERM_BP_DIRECT	GO:0030511~positive regulation of transforming growth factor beta receptor signaling pathway	6	0.0309498	241226, 21825, 21804, 12577, 17684, 76905
GOTERM_BP_DIRECT	GO:0003148~outflow tract septum morphogenesis	6	0.0309498	93840, 21385, 21808, 218772, 12166, 22762
GOTERM_BP_DIRECT	GO:0046697~decidualization	6	0.0309498	18783, 12550, 20856, 19223, 22337, 17684
GOTERM_BP_DIRECT	GO:0050821~protein stabilization	17	0.0315973	65972, 50884, 67916, 22218, 17131, 17751, 12759, 29810, 407786, 13542, 72607, 11931, 18645, 109676, 215653, 19211, 71718
GOTERM_BP_DIRECT	GO:0030217~T cell differentiation	8	0.0321945	277360, 19264, 12387, 13653, 12504, 16450, 16590, 18021
GOTERM_BP_DIRECT	GO:0007017~microtubule-based process	8	0.0321945	71924, 22142, 22151, 227613, 73710, 17755, 22146, 22143
GOTERM_BP_DIRECT	GO:0010595~positive regulation of endothelial cell migration	8	0.0321945	71093, 21687, 21825, 18760, 230738, 14257, 16416, 11606
GOTERM_BP_DIRECT	GO:0030593~neutrophil chemotaxis	11	0.0335968	277360, 13052, 75458, 16414, 20750, 14131, 21808, 105855, 14385, 238871, 16409
GOTERM_BP_DIRECT	GO:0071305~cellular response to vitamin D	4	0.0344625	19242, 14827, 20377, 18619
GOTERM_BP_DIRECT	GO:0032963~collagen metabolic process	4	0.0344625	81877, 18753, 210530, 15901
GOTERM_BP_DIRECT	GO:0003149~membranous septum morphogenesis	4	0.0344625	93840, 21808, 14362, 15902
GOTERM_BP_DIRECT	GO:2000810~regulation of bicellular tight junction assembly	4	0.0344625	14609, 14367, 20613, 18755
GOTERM_BP_DIRECT	GO:0046850~regulation of bone remodeling	4	0.0344625	14609, 14184, 94111, 16973
GOTERM_BP_DIRECT	GO:0051092~positive regulation of NF-kappaB transcription factor activity	15	0.0348017	22029, 16414, 14489, 217069, 21934, 73914, 12759, 18755, 12359, 12322, 18760, 21939, 108960, 56532, 106759
GOTERM_BP_DIRECT	GO:0045670~regulation of osteoclast differentiation	5	0.0348047	14184, 12387, 72828, 70564, 215653
GOTERM_BP_DIRECT	GO:0035567~non-canonical Wnt signaling pathway	5	0.0348047	22417, 93840, 14369, 14367, 14370

GOTERM_BP_DIRECT	GO:0050732~negative regulation of peptidyl-tyrosine phosphorylation	5	0.0348047	15170, 19264, 18753, 20354, 20377
GOTERM_BP_DIRECT	GO:0071345~cellular response to cytokine stimulus	7	0.0348700	18126, 16401, 98496, 12978, 238161, 16842, 17380
GOTERM_BP_DIRECT	GO:0006898~receptor-mediated endocytosis	10	0.0350726	13649, 71145, 15505, 18806, 11816, 27008, 380713, 66616, 17533, 66102
GOTERM_BP_DIRECT	GO:0007611~learning or memory	9	0.0360662	13649, 29813, 18174, 12801, 13653, 14667, 20203, 19211, 19122
GOTERM_BP_DIRECT	GO:0021772~olfactory bulb development	6	0.0363588	12934, 20563, 13637, 12978, 20481, 15902
GOTERM_BP_DIRECT	GO:0008652~cellular amino acid biosynthetic process	6	0.0363588	27053, 236539, 12035, 209027, 665563, 14718
GOTERM_BP_DIRECT	GO:0048844~artery morphogenesis	6	0.0363588	18131, 12142, 11816, 20204, 17131, 20897
GOTERM_BP_DIRECT	GO:0045672~positive regulation of osteoclast differentiation	6	0.0363588	74614, 12349, 12978, 12977, 12768, 16416
GOTERM_BP_DIRECT	GO:0007420~brain development	25	0.0365674	22771, 12934, 11815, 70747, 13609, 15901, 29810, 22253, 404634, 12569, 231003, 11843, 13010, 17751, 54725, 170768, 241226, 110648, 18111, 13175, 208715, 17295, 16765, 20315, 211286
GOTERM_BP_DIRECT	GO:0007507~heart development	29	0.0378583	19242, 21808, 18187, 17684, 75691, 15901, 15902, 14118, 23967, 16401, 20656, 19876, 21687, 68927, 12387, 11492, 18021, 69821, 19271, 11364, 20897, 12166, 17395, 22289, 14609, 19662, 13052, 19211, 22762
GOTERM_BP_DIRECT	GO:0005975~carbohydrate metabolic process	24	0.0382029	140481, 110173, 15212, 15211, 18010, 319625, 15245, 110078, 18655, 54371, 16828, 110095, 14584, 16548, 12091, 329828, 16002, 74637, 235533, 21351, 15586, 109685, 52331, 53412
GOTERM_BP_DIRECT	GO:0050727~regulation of inflammatory response	10	0.0384959	16177, 83490, 11988, 16952, 74637, 13982, 20361, 107527, 16452, 11606
GOTERM_BP_DIRECT	GO:0032868~response to insulin	11	0.0398883	20661, 14537, 63873, 19662, 16548, 72999, 19062, 13653, 26457, 14783, 12359
GOTERM_BP_DIRECT	GO:0006909~phagocytosis	9	0.0399137	22141, 18173, 14456, 70450, 16952, 16414, 26362, 15162, 246177
GOTERM_BP_DIRECT	GO:0007157~heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	9	0.0399137	84004, 16852, 11658, 13052, 94332, 16401, 12558, 12484, 54725
GOTERM_BP_DIRECT	GO:0032720~negative regulation of tumor necrosis factor production	8	0.0405379	22160, 14870, 14456, 12490, 230738, 11433, 26362, 73914

GOTERM_BP_DIRECT	GO:0008217~regulation of blood pressure	10	0.0421394	18160, 11622, 12310, 12490, 20656, 74574, 16973, 15368, 11928, 11606
GOTERM_BP_DIRECT	GO:0072659~protein localization to plasma membrane	10	0.0421394	12550, 11931, 12297, 14251, 329877, 56461, 66053, 51801, 109676, 13823
GOTERM_BP_DIRECT	GO:0002076~osteoblast development	5	0.0421535	19228, 16478, 15213, 212712, 16973
GOTERM_BP_DIRECT	GO:0051145~smooth muscle cell differentiation	5	0.0421535	22417, 12387, 407831, 18021, 11606
GOTERM_BP_DIRECT	GO:0046849~bone remodeling	5	0.0421535	13836, 13637, 16973, 18605, 215653
GOTERM_BP_DIRECT	GO:0030111~regulation of Wnt signaling pathway	5	0.0421535	93840, 17240, 13380, 67916, 16842
GOTERM_BP_DIRECT	GO:0048856~anatomical structure development	5	0.0421535	22417, 14048, 216795, 228357, 20471
GOTERM_BP_DIRECT	GO:0048546~digestive tract morphogenesis	5	0.0421535	13649, 93840, 14184, 20377, 20897
GOTERM_BP_DIRECT	GO:0055093~response to hyperoxia	5	0.0421535	16493, 20656, 12176, 17711, 12359
GOTERM_BP_DIRECT	GO:0060707~trophoblast giant cell differentiation	5	0.0421535	52679, 12142, 20613, 17240, 108961
GOTERM_BP_DIRECT	GO:0050768~negative regulation of neurogenesis	6	0.0423132	94091, 56710, 107503, 17751, 12484, 12166
GOTERM_BP_DIRECT	GO:0001944~vasculature development	6	0.0423132	14367, 12387, 16973, 16842, 17684, 14257
GOTERM_BP_DIRECT	GO:0008283~cell proliferation	25	0.0438248	15170, 13649, 54447, 16149, 12387, 17869, 16917, 448987, 66197, 17684, 21938, 20779, 72607, 20471, 75458, 12490, 20472, 108961, 12978, 12977, 21335, 17345, 66629, 17279, 14726
GOTERM_BP_DIRECT	GO:0048103~somatic stem cell division	4	0.0447855	93840, 14369, 21808, 16590
GOTERM_BP_DIRECT	GO:0045332~phospholipid translocation	4	0.0447855	11304, 16534, 18670, 54670
GOTERM_BP_DIRECT	GO:0048643~positive regulation of skeletal muscle tissue development	4	0.0447855	57810, 15357, 14251, 12387
GOTERM_BP_DIRECT	GO:0097202~activation of cysteine-type endopeptidase activity	4	0.0447855	65973, 64058, 114774, 76884
GOTERM_BP_DIRECT	GO:0045603~positive regulation of endothelial cell differentiation	4	0.0447855	71093, 12161, 12387, 67888

GOTERM_BP_DIRECT	GO:0031953~negative regulation of protein autophosphorylation	4	0.0447855	19264, 16476, 18605, 14586
GOTERM_BP_DIRECT	GO:0061049~cell growth involved in cardiac muscle cell development	4	0.0447855	234214, 56376, 11609, 11606
GOTERM_BP_DIRECT	GO:0008347~glial cell migration	4	0.0447855	17181, 13838, 21808, 17984
GOTERM_BP_DIRECT	GO:0021785~branchiomotor neuron axon guidance	4	0.0447855	18187, 67784, 243743, 54712
GOTERM_BP_DIRECT	GO:0043206~extracellular fibril organization	4	0.0447855	81877, 76293, 50530, 13010
GOTERM_BP_DIRECT	GO:0003184~pulmonary valve morphogenesis	4	0.0447855	56198, 15213, 21808, 20897
GOTERM_BP_DIRECT	GO:0042177~negative regulation of protein catabolic process	7	0.0450095	216439, 13649, 18126, 20720, 56150, 73914, 280408
GOTERM_BP_DIRECT	GO:0043406~positive regulation of MAP kinase activity	9	0.0484057	19882, 13649, 18753, 20779, 14254, 21939, 16590, 12484, 242202
GOTERM_BP_DIRECT	GO:0071353~cellular response to interleukin-4	6	0.0488202	75766, 74637, 18030, 17533, 16842, 22143
GOTERM_BP_DIRECT	GO:0030325~adrenal gland development	6	0.0488202	22417, 12577, 14815, 50781, 17684, 20897
GOTERM_BP_DIRECT	GO:0046903~secretion	3	0.0488371	12349, 23876, 96979
GOTERM_BP_DIRECT	GO:0034435~cholesterol esterification	3	0.0488371	170459, 20652, 20249
GOTERM_BP_DIRECT	GO:0060033~anatomical structure regression	3	0.0488371	70445, 16973, 16842
GOTERM_BP_DIRECT	GO:0033591~response to L-ascorbic acid	3	0.0488371	14870, 20656, 12359
GOTERM_BP_DIRECT	GO:0050974~detection of mechanical stimulus involved in sensory perception	3	0.0488371	171209, 20720, 667742
GOTERM_BP_DIRECT	GO:0010757~negative regulation of plasminogen activation	3	0.0488371	21825, 18787, 20720
GOTERM_BP_DIRECT	GO:0015760~glucose-6-phosphate transport	3	0.0488371	56857, 68401, 14385
GOTERM_BP_DIRECT	GO:0006167~AMP biosynthetic process	3	0.0488371	110639, 11566, 11565
GOTERM_BP_DIRECT	GO:0045719~negative regulation of glycogen biosynthetic process	3	0.0488371	19062, 18605, 14783

GOTERM_BP_DIRECT	GO:0043535~regulation of blood vessel endothelial cell migration	3	0.0488371	13836, 72461, 73723
GOTERM_BP_DIRECT	GO:0001961~positive regulation of cytokine-mediated signaling pathway	3	0.0488371	14456, 16149, 26362
GOTERM_BP_DIRECT	GO:2001236~regulation of extrinsic apoptotic signaling pathway	3	0.0488371	97998, 22029, 19264

Supplemental Table S6 KEGG analysis DEGs between Fb and Pb

Category	Term	Count	*p* value	Genes ID#
KEGG_PATHWAY	mmu04142:Lysosome	30	0.00000004	27060, 15212, 242341, 15211, 18010, 14667, 17113, 12492, 114143, 12091, 108012, 13040, 11984, 229445, 16792, 110173, 18173, 12751, 18174, 64933, 13038, 20661, 12514, 108664, 11881, 56464, 19156, 11433, 67963, 211286
KEGG_PATHWAY	mmu04310:Wnt signaling pathway	31	0.00000029	20438, 18749, 17869, 16973, 18796, 24117, 18019, 106042, 12322, 208846, 216795, 14735, 14370, 14369, 56811, 14367, 12387, 13380, 18021, 20377, 229658, 22417, 93840, 19354, 13542, 243548, 16476, 93960, 16842, 22413, 14362
KEGG_PATHWAY	mmu04360:Axon guidance	28	0.00000162	12934, 226251, 20361, 54712, 107449, 18019, 218877, 13836, 13837, 13838, 22253, 235611, 19876, 57764, 319713, 20563, 13637, 26456, 20356, 18021, 20354, 243743, 20353, 19354, 17974, 13842, 17295, 20315
KEGG_PATHWAY	mmu04015:Rap1 signaling pathway	36	0.00001890	22323, 13649, 65086, 14254, 210044, 15901, 18796, 13836, 20779, 18760, 18645, 93737, 12978, 12977, 51791, 11512, 217692, 14257, 16409, 12550, 21687, 14184, 13637, 12387, 12801, 16414, 16590, 16416, 19354, 21825, 11601, 104111, 26415, 16822, 20130, 17295
KEGG_PATHWAY	mmu05323:Rheumatoid arthritis	19	0.00004540	21687, 27060, 14254, 76252, 242341, 16414, 13038, 21808, 21934, 11966, 108664, 114143, 16476, 11984, 12977, 11433, 20315, 11964, 11973
KEGG_PATHWAY	mmu04145:Phagosome	30	0.00006880	27060, 333715, 22151, 15040, 242341, 14131, 17113, 11966, 114143, 13040, 11984, 17533, 21355, 16409, 11964, 22142, 14964, 227613, 73710, 17972, 76252, 16414, 280408, 16416, 21826, 21825, 108664, 22146, 22143, 11973
KEGG_PATHWAY	mmu04640:Hematopoietic cell lineage	18	0.00021200	12479, 16590, 16416, 14724, 16177, 12982, 12490, 16401, 12504, 12978, 12977, 12507, 12484, 16790, 12509, 16409, 17380, 13136
KEGG_PATHWAY	mmu04510:Focal adhesion	32	0.00029600	22323, 13649, 22325, 14254, 12833, 11855, 373864, 12814, 15891, 12834, 12334, 22371, 329251, 20779, 13712, 16401, 16421, 20750, 23928, 17907, 14257, 12387, 16416, 19354, 21826,

				81877, 21825, 241226, 53867, 16476, 17295, 19211
KEGG_PATHWAY	mmu04974:Protein digestion and absorption	18	0.00037900	72461, 12833, 72472, 373864, 170745, 12814, 12816, 12834, 12817, 12819, 16534, 11931, 53867, 232975, 13717, 12873, 11928, 17380
KEGG_PATHWAY	mmu04512:ECM-receptor interaction	18	0.00037900	12833, 15366, 373864, 12814, 12834, 15891, 16416, 22371, 14724, 21826, 81877, 21825, 241226, 53867, 16421, 16401, 20750, 23928
KEGG_PATHWAY	mmu05205:Proteoglycans in cancer	31	0.00046500	13649, 18749, 17869, 18793, 21808, 329251, 12322, 20779, 234779, 216795, 13712, 109676, 14370, 22160, 14369, 15170, 14367, 12387, 13982, 20544, 16416, 22350, 22417, 17395, 21825, 26415, 16002, 20130, 17295, 22413, 14362
KEGG_PATHWAY	mmu04390:Hippo signaling pathway	25	0.00058800	17869, 21808, 23859, 15901, 15902, 11799, 216795, 18787, 12695, 93737, 14370, 21677, 12550, 14369, 14367, 12387, 16414, 12166, 22417, 13542, 12161, 16842, 22413, 22629, 14362
KEGG_PATHWAY	mmu04380:Osteoclast differentiation	22	0.00067500	18733, 17972, 16478, 14389, 13038, 21808, 14131, 21934, 16416, 74256, 18019, 16177, 22177, 234779, 26415, 16476, 12978, 16822, 17060, 12977, 11433, 232790
KEGG_PATHWAY	mmu04966:Collecting duct acid secretion	9	0.00076400	11966, 27060, 242341, 76252, 12349, 11984, 11964, 11973, 20533
KEGG_PATHWAY	mmu04978:Mineral absorption	11	0.00094200	17748, 53945, 11931, 18173, 18174, 232975, 17750, 15368, 22337, 11928, 58800
KEGG_PATHWAY	mmu04919:Thyroid hormone signaling pathway	20	0.00107447	68975, 72472, 12387, 18749, 17869, 13982, 20544, 18640, 16416, 18796, 20183, 22417, 18131, 20779, 11931, 234779, 232975, 53901, 20502, 11928
KEGG_PATHWAY	mmu04520:Adherens junction	15	0.00114026	15170, 13649, 12550, 19246, 20613, 20411, 19268, 12387, 19271, 19263, 19354, 380928, 20779, 16842, 17295
KEGG_PATHWAY	mmu04916:Melanogenesis	17	0.00390698	14369, 14367, 210044, 12387, 18749, 16590, 18796, 22417, 13542, 12322, 216795, 104111, 11512, 22413, 14370, 16842, 14362
KEGG_PATHWAY	mmu00330:Arginine and proline metabolism	11	0.00392103	18127, 20229, 18126, 320452, 18452, 107239, 12709, 228608, 209027, 20810, 14718
KEGG_PATHWAY	mmu05414:Dilated cardiomyopathy	15	0.00455975	12293, 12297, 210044, 18749, 13346, 21808, 326618, 16416, 22004, 241226, 11464, 16421, 104111, 16401, 11512
KEGG_PATHWAY	mmu05166:HTLV-I infection	35	0.00549203	60599, 333715, 15040, 210044, 18749, 12916, 12236, 17869, 21808, 56150, 18019, 216795, 13712, 11512, 14370, 14369, 14964, 14367, 110196, 12387, 103573, 13653, 16414, 18021, 11740, 22417, 16177, 66156, 13542, 21939, 104111, 16476, 20130, 22413, 14362
KEGG_PATHWAY	mmu00534:Glycosaminoglycan biosynthesis - heparan sulfate / heparin	7	0.00875421	54710, 15476, 56219, 58193, 233781, 50786, 217119
KEGG_PATHWAY	mmu05217:Basal cell carcinoma	11	0.00915476	22417, 14369, 13542, 14367, 216795, 12387, 22413, 14370, 16842, 15245, 14362
KEGG_PATHWAY	mmu04971:Gastric acid secretion	13	0.00916411	22350, 12322, 11931, 210044, 18749, 104111, 232975, 12349, 11512, 16526, 20544, 11928, 18796

KEGG_PATHWAY	mmu05140:Leishmaniasis	12	0.00982990	18126, 15170, 13712, 17972, 26415, 16401, 16476, 16414, 14131, 21808, 16452, 16409
KEGG_PATHWAY	mmu00511:Other glycan degradation	6	0.01033598	217364, 110173, 12091, 15212, 15211, 18010
KEGG_PATHWAY	mmu05200:Pathways in cancer	45	0.01041266	22029, 13649, 65086, 210044, 18749, 17869, 21808, 18796, 20183, 18126, 11799, 234779, 216795, 23928, 12978, 218772, 11512, 14370, 13143, 12550, 14369, 14367, 14184, 69635, 14696, 12387, 16590, 66197, 15245, 22417, 19354, 17395, 12062, 13542, 12982, 104111, 19216, 16476, 17295, 16842, 22413, 20315, 19211, 22031, 14362
KEGG_PATHWAY	mmu04550:Signaling pathways regulating pluripotency of stem cells	20	0.01043214	14369, 14367, 14184, 16324, 12387, 17869, 15901, 16880, 15902, 12166, 22417, 13542, 216795, 26415, 22413, 14370, 17268, 71041, 16452, 14362
KEGG_PATHWAY	mmu05219:Bladder cancer	9	0.01249112	17395, 13649, 12550, 20779, 21825, 14184, 69635, 17869, 13143
KEGG_PATHWAY	mmu04540:Gap junction	14	0.01522451	22142, 13649, 14609, 20779, 22151, 227613, 210044, 73710, 18749, 104111, 11512, 22146, 22143, 18796
KEGG_PATHWAY	mmu04961:Endocrine and other factor-regulated calcium reabsorption	10	0.01788418	19228, 12062, 11931, 18749, 232975, 13982, 11512, 22337, 11928, 18796
KEGG_PATHWAY	mmu04912:GnRH signaling pathway	14	0.01821842	13649, 210044, 18749, 18796, 18783, 18753, 18806, 20779, 12322, 13712, 104111, 26415, 16476, 11512
KEGG_PATHWAY	mmu05202:Transcriptional misregulation in cancer	22	0.01826882	22029, 14048, 14254, 21912, 53623, 17869, 18791, 15446, 15902, 20183, 17395, 22289, 13876, 20471, 21939, 16421, 12978, 17295, 17268, 66629, 18516, 16409
KEGG_PATHWAY	mmu00531:Glycosaminoglycan degradation	6	0.02021816	12091, 15212, 15211, 11881, 15586, 109685
KEGG_PATHWAY	mmu04976:Bile secretion	12	0.02068904	18670, 11931, 15357, 210044, 18749, 104111, 232975, 12349, 16835, 11512, 20544, 11928
KEGG_PATHWAY	mmu04151:PI3K-Akt signaling pathway	39	0.02319681	13649, 65086, 14254, 12833, 17869, 373864, 12814, 15891, 12834, 22371, 170755, 18127, 13836, 68401, 16401, 16421, 20750, 23928, 12978, 12977, 14257, 21687, 14184, 13637, 14696, 16590, 16416, 21826, 81877, 19054, 21825, 241226, 11601, 83490, 53867, 17295, 19211, 22629, 16452
KEGG_PATHWAY	mmu04261:Adrenergic signaling in cardiomyocytes	20	0.02371151	12293, 12297, 20266, 210044, 18749, 12916, 326618, 20544, 18796, 22004, 19054, 12322, 11931, 11464, 26415, 104111, 232975, 11512, 11609, 11928
KEGG_PATHWAY	mmu04670:Leukocyte transendothelial migration	17	0.02526138	22323, 22325, 12741, 12387, 17972, 16414, 11855, 22350, 17395, 19354, 21838, 234779, 16401, 26415, 17907, 20315, 16409
KEGG_PATHWAY	mmu04611:Platelet activation	18	0.02539804	22323, 210044, 18749, 373864, 12814, 16416, 18796, 22371, 18127, 14724, 18783, 20779, 234779, 53867, 104111, 26415, 16822, 11512
KEGG_PATHWAY	mmu04514:Cell adhesion molecules (CAMs)	21	0.02650021	12550, 12560, 14964, 19264, 12741, 11658, 333715, 15040, 94332, 19268, 16414, 54725, 241226, 20345, 12490, 21939, 16401, 16421, 12558, 12504, 16409
KEGG_PATHWAY	mmu01130:Biosynthesis of antibiotics	26	0.02655897	71776, 319625, 12359, 14584, 12035, 15357, 209027, 110639, 21351, 216558, 14718, 110196, 434437, 107652, 71780,

				11364, 18655, 16828, 27226, 236539, 56421, 52538, 235293, 239017, 208715, 23972
KEGG_PATHWAY	mmu04666:Fc gamma R-mediated phagocytosis	13	0.02886036	22323, 227753, 19354, 22325, 18806, 19264, 18753, 230837, 234779, 14389, 67916, 17909, 15162
KEGG_PATHWAY	mmu04610:Complement and coagulation cascades	12	0.03262003	12268, 22371, 12062, 12628, 18787, 12258, 74145, 14066, 18793, 18791, 12509, 13136
KEGG_PATHWAY	mmu04750:Inflammatory mediator regulation of TRP channels	17	0.03523154	210044, 18749, 22368, 18755, 18796, 16177, 18783, 63873, 18753, 12062, 20779, 12322, 171209, 234779, 104111, 26415, 11512
KEGG_PATHWAY	mmu04970:Salivary secretion	12	0.03549351	20496, 16534, 11931, 210044, 18749, 104111, 232975, 13010, 11512, 20544, 11928, 18796
KEGG_PATHWAY	mmu04921:Oxytocin signaling pathway	20	0.03799827	18160, 12293, 227541, 13649, 12297, 210044, 18749, 18021, 18796, 18127, 18019, 18783, 329251, 20779, 12322, 13712, 104111, 16476, 55984, 11512
KEGG_PATHWAY	mmu00230:Purine metabolism	22	0.03820587	18160, 210044, 14544, 54611, 11566, 238871, 11565, 242202, 29863, 12495, 23959, 215446, 19075, 110639, 104111, 20133, 18577, 18605, 224794, 11512, 20135, 23972
KEGG_PATHWAY	mmu04915:Estrogen signaling pathway	14	0.04018900	18127, 17395, 13649, 18753, 20779, 15511, 210044, 18749, 104111, 16476, 13982, 11512, 193740, 18796
KEGG_PATHWAY	mmu05412:Arrhythmogenic right ventricular cardiomyopathy (ARVC)	11	0.04754148	12293, 14609, 241226, 12297, 12387, 16401, 16421, 12558, 13346, 16842, 16416
KEGG_PATHWAY	mmu04721:Synaptic vesicle cycle	10	0.04965302	11966, 22249, 27060, 108664, 114143, 242341, 76252, 11984, 11964, 11973