

Table S1	meta_sig_genes_metap	UG 290 DEG	
EntrezID	Name	Combine	CombinedPval
10769	PLK2	-75.763	000E-11
1591	CYP24A1	-59.072	000E-08
7128	TNFAIP3	-54.414	000E-07
3569	IL6	-53.09	000E-07
1906	EDN1	-52.685	000E-07
5743	PTGS2	-52.335	000E-07
154	ADRB2	-51.163	000E-07
3399	ID3	-50.168	000E-07
1490	CTGF	-49.837	000E-07
10468	FST	-49.696	000E-07
1847	DUSP5	-49.125	000E-07
1647	GADD45	-48.243	000E-07
688	KLF5	-47.733	000E-06
11010	GLIPR1	-47.307	000E-06
3491	CYR61	-46.897	000E-06
11221	DUSP10	-46.685	000E-06
389136	VGLL3	-46.265	000E-06
3553	IL1B	-44.656	000E-06
10116	FEM1B	-44.385	000E-06
390	RND3	-43.556	000E-06
3664	IRF6	-43.364	000E-06
3280	HES1	-41.743	000E-05
6446	SGK1	-40.336	000E-05
3872	KRT17	-40.316	000E-05
1316	KLF6	-39.373	000E-05
56300	IL36G	-39.371	000E-05
2625	GATA3	-38.924	000E-05
5327	PLAT	-38.318	000E-05
5017	OVOL1	-37.741	000E-05
2633	GBP1	-36.633	000E-05
65983	GRAMD3	-36.627	000E-05
116039	OSR2	-36.28	000E-05
5734	PTGER4	-36.242	000E-05
597	BCL2A1	-36.23	000E-05
29094	LGALS1	-35.556	0012256
5055	SERPINB	-35.305	0013192
2919	CXCL1	-35.29	0013192
9957	HX3ST1	-35.205	0013389
2729	GCLC	-35.145	0013417
3576	IL8	-35.097	0013417
2152	F3	-34.954	0014021
9982	FGFBP1	-34.651	0015813
8507	ENC1	-33.998	0020666
1843	DUSP1	-33.959	0020666
6662	SOX9	-33.93	0020666
7357	UGCG	-33.879	0020666
54407	SLC38A2	-33.857	0020666
7020	TFAP2A	-33.778	0021021
6659	SOX4	-33.298	0025847
27071	DAPP1	-33.014	0028984
8660	IRS2	-32.945	0029382
9076	CLDN1	-32.679	0003269
5328	PLAU	-32.608	0033175
79669	C3orf52	-32.484	0034544
4929	NR4A2	-32.23	0038251
7538	ZFP36	-31.979	000423
5450	POU2AF1	-31.773	0045822
23766	GABARA6	-31.605	0048759
22914	KLRK1	-31.062	0061923
51421	AMOTL2	-30.902	0065675
1825	DSC3	-30.713	0070623
7159	TP53BP2	-30.659	0071309
9152	SLC6A5	-30.485	0076173
23529	CLCF1	-30.404	0077933
6722	SRF	-30.366	0078135
8843	HCAR3	-30.271	000805
3854	KRT6B	-29.903	0094285
7764	ZNF217	-29.774	0098715
4616	GADD45	-29.66	0010269
694	BTG1	-29.403	0011423
4430	MYO1B	-29.052	0013272
9021	SOC3	-28.989	0013487
0506658	OCLN	-28.864	0014105
25956	SEC31B	-28.333	0017614
51085	MLXIPL	-28.21	0018416
2150	F2RL1	-27.97	0020049
10979	FERMT2	-27.945	0020049
221823	PRPS1L1	-27.934	0020049
1948	EFNB2	-27.921	0020049
1942	EFNA1	-27.715	000218
3861	KRT14	-27.667	0022031
7168	TPM1	-27.604	0022417
5329	PLAUR	-27.513	0023119
7403	KDM6A	-27.485	0023156
23353	SUN1	-27.458	0023176
1022	CDK7	-27.426	0023258
5292	PIM1	-27.147	0026196
80352	RNF39	-27.053	0027066
7056	THBD	-26.906	0028677
4081	MAB21L1	-26.487	0033395
3868	KRT16	-26.367	0034624
696	BTN1A1	-26.365	0034624
57817	HAMP	-26.256	0035687
79098	C1orf116	-26.162	0036909
29930	PCDH11	-26.019	0003867
0169750	PRINS	-25.685	0004474
2250	FGF5	-25.616	0045348
148022	TICAM1	-25.614	0045348
1472	CST4	-25.481	0047778
9590	AKAP12	-25.386	0049478
3777	KCNK3	-25.294	0051168
1075	CTSC	-25.113	0054652
4609	MYC	-25.112	0054652
313	AOAH	-25.053	0055677
55679	LIMS2	-24.803	000615
1793	DOCK1	-24.767	0006189
10627	MYL12A	-24.606	0066106
760	CA2	-24.548	0066869
9052	GPRC5A	-24.537	0066869
3037	HAS2	-24.508	0066869
9314	KLF4	-24.412	0069301
639	PRDM1	-24.36	0070418
2627	GATA6	-24.246	0072339
10447	FAM3C	-24.237	0072339
54101	RIPK4	-24.143	0073756
23078	KIAA056	-24.137	0073756
2294	FOXF1	-24.122	0073756
10398	MYL9	-24.074	0074832
10741	RBBP9	-24.051	0075029
2155	F7	-24.007	0075458
3909	LAMA3	-23.835	0081103
1543	CYP1A1	-23.567	0090804
4211	MEIS1	-23.558	0090804
7286	TUFT1	-23.374	0096044
55859	BEX1	-23.335	0096626
5099	PCDH7	-23.176	0010106
29881	NPC1L1	-23.173	0010106
23237	ARC	-23.012	0010807
9388	LIPG	-22.979	0010897
3400	ID4	-22.906	001115
4335	MNT	-22.9	001115
2550	GABBR1	-22.882	0011172
301	ANXA1	-22.733	0011853
53635	PTOV1	-22.681	0012014
57053	CHRNA10	-22.635	0012195
7050	TGIF1	-22.589	0012332
580	BARD1	-22.583	0012332
9048	ARTN	-22.544	0012444
7465	WEE1	-22.536	0012444
54626	HES2	-22.52	0012453
238	ALK	-22.502	0012479
64063	PRSS22	-22.473	0012494
57132	CHMP1B	-22.434	0012524
10261	IGSF6	-22.427	0012524
1809	DPYSL3	-22.426	0012524
4633	MYL2	-22.415	0012524
10626	TRIM16	-22.369	0012719
80342	TRAF3IP3	-22.356	0012719
115207	KCTD12	-22.325	0012825
54438	GFOD1	-22.294	0012935
2355	FOSL2	-22.266	0013023
9450	LY86	-22.213	0013242
5912	RAP2B	-22.205	0013242
9414	TJP2	-22.18	0013318
23339	VPS39	-22.107	0013696
8200	GDF5	-21.993	0014314
2172	FABP6	-21.965	0014332
6585	SLIT1	-21.959	0014332
5676	PSG7	-21.897	0014623
3552	IL1A	-21.891	0014623
3459	IFNGR1	-21.871	0014679
6575	SLC20A2	-21.757	0015216
800	CALD1	-21.686	0015162
79170	PRR15L	-21.663	0015163
3493	IGHA1	-21.646	0015674
8416	ANXA9	-21.6	0015692
79586	CHXF1	-21.587	0015692
5076	PAX2	-21.56	0015728
201134	CEP112	-21.502	0016067
81931	ZNF93	-21.484	001612
30844	EHD4	-21.459	0016228
9465	AKAP7	-21.408	0016521
7057	THBS1	-21.381	0016646
2158	F9	-21.324	0017008
5366	PMAIP1	-21.29	0017186
440915	POTEKP	-21.277	0017206
83937	RASSF4	-21.185	0017857
752014	CEMP1	-21.12	0018219
1822	ATN1	-21.059	0018643
168544	ZNF467	-20.964	0019285
4884	NPTX1	-20.95	0019314
79740	ZBNX	-20.94	0019314
5783	PTPN13	-20.907	0019522
6698	SPRR1A	-20.721	0021151
107	ADCY1	-20.696	0021295
483	ATP1B3	-20.682	0021334
27134	TJP3	-20.661	0021433
8609	KLF7	-20.645	0021455
4214	MAP3K1	-20.614	0021606
7380	ADPK3A	-20.54	0022416
108	ADCY2	-20.51	0022416
80271	ITPKC	-20.504	0022416
8837	CFLAR	-20.446	0022808
3484	IGFBP1	-20.43	0022808
27115	PDE7B	-20.43	0022808
55203	LGI2	-20.425	0022808
2312	FLG	-20.417	0022808
11259	SLIPL1L	-20.318	0023508
6590	FILIP1	-20.317	0023508
268	AMH	-20.313	0023508
357	SHROOM	-20.248	0024112
6247	RS1	-20.221	0024309
51286	CEND1	-20.207	0024344
2248	FGF3	-20.165	0024616
1545	CYP1B1	-20.136	0024848
11250	GPR45	-20.117	0024954
27010	TPK1	-20.065	0025341
4993	OR2C1	-20.051	0025403
1465	CSRP1	-20.04	0025421
84159	ARID5B	-20.031	0025426
4353	MPO	-20.021	0025436
27042	DIEXF	-19.895	002683
1053	CEBPE	-19.881	0026891
81628	TSC2D4	-19.822	0027397
1068	CETN1	-19.81	0027435
79885	HDAC11	-19.765	0027899
58483	LINC004	-19.735	0028143
50835	TAS2R9	-19.728	0028143
1485	NKX2-5	-19.692	0028499
1609	DGKQ	-19.641	0028935
2972	BRF1	-19.633	0028935
23022	PALLD	-19.594	0029267
4070	TACSTD2	-19.576	0029351
84909	C9orf3	-19.523	0029949
1960	EGR3	-19.505	002998
79037	PVRIG	-19.504	002998
7091	TLE4	-19.491	0030004
1439	CSF2RB	-19.435	0030571
441151	TMEM15	-19.426	0030571
22898	DENND3	-19.414	0030571
63967	CLSPN	-19.411	0030571
55317	AP5S1	-19.403	0030571
83700	JAM3	-19.321	0031465
8698	S1PR4	-19.316	0031465
4745	NELL1	-19.258	0032052
4071	TM4SF1	-19.214	0032477
28234	SLCO1B3	-19.198	0032591
3081	HGD	-19.189	003261
2354	FOSB	-19.177	003261
29974	A1CF	-19.173	003261
26959	HBP1	-19.138	0033014
26040	SETBP1	-19.12	0033163
1039	CDR2	-19.113	0033163
962	CD48	-19.018	0034391
375449	MAST4	-18.952	0035176
3725	JUN	-18.912	0035579
55478	PRO2012	-18.895	0035727
1832	DSP	-18.876	0035801
9182	RASSF9	-18.875	0035801
58473	PLEKHB1	-18.772	0036896
596	BCL2	-18.65	003846
3448	IFNA14	-18.556	0039491
3249	HPN	-18.548	0039502
57165	GJC2	-18.541	0039502
79097	TRIM48	-18.525	0039658
26509	MYOF	-18.462	004041
57213	SPRYD7	-18.432	0040698
10957	PNRC1	-18.392	0041315
5268	SERPINB	-18.372	0041556
79962	DNAJC22	-18.352	0041715
80223	RAB11F1	-18.35	0041715
54769	DIRAS2	-18.307	0041999
79825	CCDC48	-18.304	0041999
1846	DUSP4	-18.302	0041999
8412	BCAR3	-18.301	0041999
6876	TAGLN	-18.292	0041999
0289255	LOC1002	-18.285	0041999
7293	TNFRSF4	-18.283	0041999
23053	KIAA091	-18.241	0042526
80258	EFHC2	-18.205	0042793
140	ADORA3	-18.173	0043277
2597			

Table S2 meta_sig_genes_metap DG 72 DEG

EntrezID	Name	Combine	CombinedPval
54541	DDIT4	39.654	0.000E-05
6591	SNAI2	35.697	0.0011782
7071	KLF10	28.802	0.0014331
26276	VPS33B	26.858	0.0029001
11067	C10orf10	26.815	0.0029282
6574	SLC20A1	26.779	0.0029459
55844	PPP2R2D	26.31	0.0035159
117247	SLC16A1	26.115	0.0037347
10224	ZNF443	24.8	0.00615
4016	LOXL1	24.512	0.0066869
79759	ZNF668	24.307	0.0071582
10561	IFI44	24.232	0.0072339
27034	ACAD8	24.179	0.0073529
54014	BRWD1	24.036	0.0075029
9778	KIAA023	23.467	0.0093984
5154	PDGFA	23.45	0.0094071
8772	FADD	23.374	0.0096044
1390	CREM	23.33	0.0096626
211	ALAS1	23.256	0.0099284
283871	PGP	23.211	0.010065
668	FOXL2	22.725	0.011853
80055	PGAP1	22.475	0.012494
9997	SCO2	21.986	0.014314
4857	NOVA1	21.82	0.014944
5834	PYGB	21.778	0.015151
10628	TXNIP	21.676	0.01562
80304	C2orf44	21.622	0.015692
27346	TMEM97	21.616	0.015692
200424	TET3	21.596	0.015692
55654	TMEM127	21.574	0.015704
8793	TNFRSF1	21.123	0.018219
8894	EIF2S2	20.985	0.01919
56937	PMEPA1	20.639	0.021455
643376	BTBD18	20.369	0.023212
3421	IDH3G	20.199	0.024344
23221	RHOBTB2	20.101	0.025035
57396	CLK4	19.823	0.027397
79778	MICALL2	19.635	0.028935
1594	CYP27B1	19.591	0.029267
10948	STARD3	19.408	0.030571
55143	CDCA8	19.386	0.030706
9524	TECR	19.265	0.032052
114625	ERMAP	19.251	0.032052
10363	HMG20A	19.017	0.034391
79908	BTNL8	18.981	0.034846
79888	LPCAT1	18.924	0.035499
115353	LRRC42	18.847	0.036146
63917	GALNT11	18.837	0.036189
23250	ATP11A	18.805	0.036589
9015	TAF1A	18.785	0.03679
9416	DDX23	18.745	0.03722
79819	WDR78	18.664	0.03846
54948	MRPL16	18.652	0.03846
7086	TKT	18.637	0.038566
8464	SUPT3H	18.588	0.039281
11320	MGAT4A	18.582	0.039281
58529	MYOZ1	18.563	0.039478
8225	GTPBP6	18.499	0.039991
10253	SPRY2	18.488	0.040069
53916	RAB4B	18.433	0.040698
30012	TLX3	18.28	0.041999
10885	WDR3	18.239	0.042526
65987	KCTD14	18.232	0.042526
51167	CYB5R4	18.209	0.042793
1581	CYP7A1	18.109	0.044191
10123	ARL4C	18.107	0.044191
10467	ZNHIT1	17.873	0.047406
5900	RALGDS	17.844	0.04747
648	BMI1	17.833	0.04747
55039	TRMT12	17.744	0.048861
55695	NSUN5	17.725	0.04914
79762	C1orf115	17.705	0.049451

Table S3 GO Biological Process terms of up-regulated genes												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferro	Benjamir	FDR
GOTERM	GO:0043066--negative regulation of apoptotic process	26	41.37931	3.86322	597, 596	259	455	16792	3.704798	7.996557	9.96554	6.66879
GOTERM	GO:0008284--positive regulation of cell proliferation	24	8.275862	9.14216	3037, 99	259	466	16792	3.339088	0.001899	0.45767	0.001576
GOTERM	GO:0007568--aging	14	4.827586	1.64399	3725, 59	259	165	16792	5.501066	0.003399	0.00113	0.00283
GOTERM	GO:0007596--blood coagulation	14	4.827586	5.51298	2158, 26	259	184	16792	4.933019	0.01134	0.00284	0.00951
GOTERM	GO:000122--negative regulation of transcription from RNA polymerase II promoter	29	10	6.33587	10320, 7	259	720	16792	1.611366	0.01302	0.00261	0.01303
GOTERM	GO:0042493--response to drug	17	5.86206	2.00345	3725, 59	259	304	16792	3.625584	0.006688	0.00347	0.00347
GOTERM	GO:0045944--positive regulation of transcription from RNA polymerase II promoter	33	11.37931	4.65135	3725, 10	259	981	16792	2.180959	0.091790	0.01366	0.08026
GOTERM	GO:0045429--positive regulation of nitric oxide biosynthetic process	7	2.41379	4.69768	22914, 1	259	43	16792	10.55430	0.09266	0.01208	0.08106
GOTERM	GO:0032496--response to lipopolysaccharide	12	4.13793	4.71470	3725, 11	259	164	16792	4.743949	0.09298	0.01078	0.08135
GOTERM	GO:0008544--epidermis development	9	3.10344	4.83106	7357, 50	259	85	16792	8.664774	0.09516	0.00995	0.03478
GOTERM	GO:0045766--positive regulation of angiogenesis	10	3.44827	7.07348	694, 801	259	115	16792	5.63773	0.13621	0.01322	0.12203
GOTERM	GO:0007165--signal transduction	36	12.4137	9.86222	9982, 14	259	1161	16792	2.010355	0.18470	0.01687	0.17014
GOTERM	GO:0071260--cellular response to mechanical stimulus	8	2.57862	1.07203	1647, 42	259	71	16792	7.305236	0.19902	0.01692	0.14849
GOTERM	GO:0030335--positive regulation of cell migration	12	4.13793	1.32676	80310, 3	259	184	16792	4.22830	0.24016	0.01942	0.22878
GOTERM	GO:0006366--transcription from RNA polymerase II promoter	21	7.24137	1.36109	3725, 67	259	513	16792	6.54022	0.24554	0.01860	0.23469
GOTERM	GO:0008285--negative regulation of cell proliferation	18	6.20689	1.40831	3725, 67	259	396	16792	2.94699	0.25288	0.01805	0.24282
GOTERM	GO:0004594--positive regulation of transcription, DNA-templated	21	7.24137	1.43419	3725, 68	259	515	16792	2.64371	0.25688	0.01731	0.24728
GOTERM	GO:0007267--cell-cell signaling	14	4.82758	1.59249	9982, 19	259	254	16792	2821877	0.28084	0.01814	0.27454
GOTERM	GO:0050728--negative regulation of inflammatory response	8	2.57862	2.10567	7538, 26	259	79	16792	6.56546	0.35330	0.02268	0.36286
GOTERM	GO:0070301--cellular response to hydrogen peroxide	7	2.41379	2.33689	80310, 5	259	57	16792	7.96206	0.38355	0.02389	0.40263
GOTERM	GO:0006954--inflammatory response	17	5.86206	2.64465	148022,	259	379	16792	2.90812	0.42161	0.02573	0.45544
GOTERM	GO:0045892--negative regulation of transcription, DNA-templated	20	6.8955	2.69442	3725, 10	259	499	16792	2.598556	0.42754	0.02503	0.46411
GOTERM	GO:0009612--response to mechanical stimulus	7	2.41379	2.82832	3725, 57	259	59	16792	7.99216	0.44319	0.02513	0.48710
GOTERM	GO:0071356--cellular response to tumor necrosis factor	9	3.10344	2.95913	3037, 75	259	110	16792	5.30459	0.45807	0.02520	0.50958
GOTERM	GO:0048661--positive regulation of smooth muscle cell proliferation	7	2.41379	3.10266	80310, 3	259	60	16792	7.56396	0.47394	0.02536	0.53442
GOTERM	GO:0071222--cellular response to lipopolysaccharide	9	3.10344	3.55308	7538, 22	259	113	16792	5.16376	0.52079	0.02789	0.61275
GOTERM	GO:0001822--kidney development	8	2.57862	0.0000	4037, 50	259	86	16792	6.03106	0.52185	0.02695	0.61341
GOTERM	GO:0050927--positive regulation of positive chemotaxis	4	1.37931	5.39937	3791, 21	259	11	16792	23.5759	0.67305	0.03914	0.92797
GOTERM	GO:0008283--cell proliferation	16	5.51274	5.58986	596, 291	259	366	16792	2.83427	0.68570	0.03912	0.90606
GOTERM	GO:0010628--positive regulation of gene expression	13	4.82758	7.65519	639, 355	259	262	16792	3.21695	0.79509	0.05146	1.31266
GOTERM	GO:0071347--cellular response to interleukin-1	7	2.41379	7.71306	3037, 80	259	71	16792	6.39208	0.79754	0.05021	1.32313
GOTERM	GO:0009791--post-embryonic development	7	2.41379	8.93706	4633, 63	259	73	16792	6.21695	0.84288	0.05619	1.53158
GOTERM	GO:0061029--eyelid development in camera-type eye	4	1.37931	9.14822	3725, 67	259	13	16792	19.9489	0.84961	0.05579	1.56749
GOTERM	GO:0019221--cytokine-mediated signaling pathway	9	3.10344	9.48497	3448, 90	259	131	16792	4.5424	0.85974	0.05613	1.62455
GOTERM	GO:0043444--cellular response to fibroblast growth factor stimulus	5	1.72413	0.00108	7538, 27	259	30	16792	10.8056	0.89527	0.06243	1.75298
GOTERM	GO:0002009--morphogenesis of an epithelium	4	1.37931	0.00115	54101, 7	259	14	16792	18.5239	0.90784	0.06408	1.96856
GOTERM	GO:0002042--cell migration involved in sprouting angiogenesis	4	1.37931	0.00142	6722, 19	259	15	16792	17.2890	0.94750	0.07656	2.42766
GOTERM	GO:0006959--humoral immune response	6	2.06896	0.00179	596, 262	259	57	16792	6.24625	0.97589	0.09383	3.05897
GOTERM	GO:0072593--reactive oxygen species metabolic process	5	1.72413	0.00196	5076, 59	259	35	16792	9056812	0.98277	0.09890	3.33076
GOTERM	GO:0071407--cellular response to organic cyclic compound	6	2.06896	0.00209	688, 229	259	59	16792	6.59328	0.98703	0.10295	3.55920
GOTERM	GO:0007598--blood coagulation, extrinsic pathway	3	1.03448	0.00228	2158, 21	259	5	16792	1003861	0.99114	0.10888	3.86493
GOTERM	GO:0045597--positive regulation of cell differentiation	5	1.72413	0.00241	3725, 67	259	37	16792	2080768	0.99328	0.11229	4.08623
GOTERM	GO:0001525--angiogenesis	11	7.9310	0.00241	3725, 83	259	223	16792	3.19808	0.99333	0.10999	4.09233
GOTERM	GO:0030890--positive regulation of B cell proliferation	5	1.72413	0.00293	596, 148	259	39	16792	8.31204	0.99772	0.12915	4.94754
GOTERM	GO:0046330--positive regulation of JNK cascade	6	2.06896	0.00321	4616, 16	259	65	16792	5.98467	0.99871	0.13756	5.40247
GOTERM	GO:0008584--male gonad development	7	2.41379	0.00347	221823,	259	94	16792	0465785	0.99887	0.13719	5.50344
GOTERM	GO:0030336--negative regulation of cell migration	7	2.41379	0.00345	6722, 71	259	95	16792	4.77724	0.99921	0.14121	5.72288
GOTERM	GO:0070527--platelet aggregation	5	1.72413	0.00352	10627, 1	259	41	16792	7.90658	0.99933	0.14138	5.91908
GOTERM	GO:0071456--cellular response to hypoxia	7	2.41379	0.00363	3777, 59	259	96	16792	4.72747	0.99946	0.14256	7052286
GOTERM	GO:0042730--fibrinolysis	4	1.37931	0.00388	5327, 53	259	21	16792	12.3493	0.99968	0.14884	9866019
GOTERM	GO:0001836--release of cytochrome c from mitochondria	4	1.37931	0.00505	3725, 59	259	23	16792	11.2754	0.99997	0.18601	8.38101
GOTERM	GO:0016477--cell migration	9	3.10344	0.00517	23237, 6	259	172	16792	3.39247	0.99997	0.18651	8.56277
GOTERM	GO:0010595--positive regulation of endothelial cell migration	5	1.72413	0.00535	2625, 80	259	46	16792	7.04717	0.99998	0.18921	8.85367
GOTERM	GO:0090102--cochlear development	4	1.37931	0.00571	3777, 50	259	24	16792	10.8056	0.99999	0.19259	9.42066
GOTERM	GO:0051781--positive regulation of cell division	5	1.72413	0.00578	80310, 2	259	47	16792	6.89723	0.99999	0.19615	9.52965
GOTERM	GO:0007623--circadian rhythm	6	2.06896	0.00593	3725, 10	259	75	16792	5.18671	0.99999	0.19741	9.76055
GOTERM	GO:0007050--cell cycle arrest	8	2.57862	0.00617	1022, 58	259	141	16792	3.67852	0.99999	0.20110	10.1291
GOTERM	GO:0030216--keratinocyte differentiation	6	2.06896	0.00627	1832, 30	259	76	16792	5.11847	0.99999	0.20112	10.2917
GOTERM	GO:0000188--inactivation of MAPK activity	4	1.37931	0.00642	1843, 11	259	25	16792	10.3734	0.99999	0.20231	11.6250
GOTERM	GO:0002053--positive regulation of mesenchymal cell proliferation	4	1.37931	0.00717	2294, 86	259	26	16792	9.97445	0.99999	0.22068	11.5945
GOTERM	GO:0031018--endocrine pancreas development	4	1.37931	0.00717	301, 665	259	26	16792	9.97445	0.99999	0.22068	11.6940
GOTERM	GO:0007189--adenylate cyclase-activating G-protein coupled receptor signaling pathway	5	1.72413	0.00720	8698, 57	259	50	16792	6.48339	0.99999	0.21644	11.7387
GOTERM	GO:000165--MAPK cascade	11	3.79310	0.00746	2248, 75	259	262	16792	2.22203	0.99999	0.22125	12.858
GOTERM	GO:0043583--ear development	3	1.03448	0.00788	596, 262	259	9	16792	21.6113	0.99999	0.22899	12.7707
GOTERM	GO:0010575--positive regulation of vascular endothelial growth factor production	4	1.37931	0.00798	5743, 35	259	27	16792	9.60503	0.99999	0.22841	12.9247
GOTERM	GO:0071333--cellular response to glucose stimulus	5	1.72413	0.00827	6722, 50	259	52	16792	6.23403	0.99999	0.23245	13.3593
GOTERM	GO:0001701--in utero embryonic development	9	3.10344	0.00842	6722, 71	259	187	16792	3.12035	0.99999	0.23304	13.5871
GOTERM	GO:0003281--ventricular septum development	4	1.37931	0.00884	639, 349	259	28	16792	9056812	0.99999	0.24001	14.2159
GOTERM	GO:0060070--canonical Wnt signaling pathway	6	2.06896	0.00904	6659, 49	259	83	16792	4.68679	0.99999	0.24159	14.5135
GOTERM	GO:0035556--intracellular signal transduction	14	4.82758	0.00969	7538, 29	259	403	16792	2.25229	0.99999	0.25336	15.4749
GOTERM	GO:0048008--platelet-derived growth factor receptor signaling pathway	4	1.37931	0.00975	80310, 8	259	29	16792	8.94261	0.99999	0.25161	15.6596
GOTERM	GO:0006928--movement of cell or subcellular component	6	2.06896	0.01045	7168, 80	259	86	16792	4.52330	0.99999	0.26391	16.5913
GOTERM	GO:0001570--vasculogenesis	5	1.72413	0.01070	3037, 22	259	56	16792	5.78874	0.99999	0.26608	16.9520
GOTERM	GO:0030513--positive regulation of BMP signaling pathway	4	1.37931	0.01173	3491, 32	259	31	16792	6.36567	0.99999	0.28440	18.4308
GOTERM	GO:004871											

Table S4 KEGG pathway of up-regulated genes												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferro	Benjamin	FDR
KEGG_PA	hsa04064:NF-kappa B signaling pathway	9	3.103448	3.526536	597, 596	141	87	6910	5.069699	0.063829	0.063829	0.436269
KEGG_PA	hsa04668:TNF signaling pathway	9	3.103448	0.001318	3725, 88	141	106	6910	4.160979	0.218661	0.116066	1.622340
KEGG_PA	hsa04350:TGF-beta signaling pathway	8	2.758620	0.001488	7050, 33	141	84	6910	4.667342	0.243174	0.088691	1.829992
KEGG_PA	hsa04010:MAPK signaling pathway	14	4.827586	0.001903	3725, 67	141	255	6910	2.690585	0.299686	0.085206	2.333712
KEGG_PA	hsa04060:Cytokine-cytokine receptor interaction	13	4.482758	0.002343	3459, 34	141	230	6910	2.769966	1477103	0.084023	2.866997
KEGG_PA	hsa04610:Complement and coagulation cascades	7	2.413793	0.002612	2158, 53	141	69	6910	4.971733	0.386876	0.078296	3.190736
KEGG_PA	hsa05142:Chagas disease (American trypanosomiasis)	8	2.758620	0.004997	3725, 34	141	104	6910	3.769776	0.608186	0.125281	6.022061
KEGG_PA	hsa04530:Tight junction	9	3.103448	0.006474	4633, 83	141	137	6910	3.219444	0.703173	0.140862	7.735840
KEGG_PA	hsa05132:Salmonella infection	7	2.413793	0.006533	3725, 34	141	83	6910	4.133128	0.706471	0.127329	7.804136
KEGG_PA	hsa05202:Transcriptional misregulation in cancer	10	3.448275	0.006899	597, 435	141	168	6910	2.917088	0.726038	0.121444	8.224788
KEGG_PA	hsa05161:Hepatitis B	9	3.103448	0.009015	3725, 59	141	145	6910	3.041819	0.816138	0.142694	10.61920
KEGG_PA	hsa04913:Ovarian steroidogenesis	5	1.724137	0.016903	108, 574	141	49	6910	5.000723	0.958744	0.233304	19.04899
KEGG_PA	hsa05144:Malaria	5	1.724137	0.016903	22914, 3	141	49	6910	5.000723	0.958744	0.233304	19.04899
KEGG_PA	hsa05133:Pertussis	6	2.068965	0.017660	3725, 14	141	75	6910	3.920567	0.964277	0.226095	19.81806
KEGG_PA	hsa04024:cAMP signaling pathway	10	3.448275	0.018842	3725, 25	141	198	6910	2.475105	0.971478	0.224369	21.00573
KEGG_PA	hsa04510:Focal adhesion	10	3.448275	0.023687	80310, 3	141	206	6910	2.378985	0.988699	0.258336	25.70774
KEGG_PA	hsa05164:Influenza A	9	3.103448	0.024654	3725, 34	141	174	6910	2.534849	0.990611	0.253057	26.61510
KEGG_PA	hsa04923:Regulation of lipolysis in adipocytes	5	1.724137	0.026306	108, 574	141	56	6910	4.375633	0.993161	0.254158	28.14036
KEGG_PA	hsa04630:Jak-STAT signaling pathway	8	2.758620	0.027514	5292, 34	141	145	6910	2.703839	0.994578	0.251626	29.23809
KEGG_PA	hsa04932:Non-alcoholic fatty liver disease (NAFLD)	8	2.758620	0.033303	3725, 51	141	151	6910	3568644	0.998224	0.283490	34.28643
KEGG_PA	hsa05321:Inflammatory bowel disease (IBD)	5	1.724137	0.040255	3725, 34	141	64	6910	3.828679	0.999539	0.318989	39.91021
KEGG_PA	hsa04115:p53 signaling pathway	5	1.724137	0.046388	4616, 16	141	67	6910	3.657245	0.999861	0.344900	44.50039
KEGG_PA	hsa04380:Osteoclast differentiation	7	2.413793	0.049555	3725, 34	141	131	6910	2.618699	0.999925	0.350802	46.74249
KEGG_PA	hsa05219:Bladder cancer	4	1.379310	0.049603	7380, 70	141	41	6910	4.781179	0.999926	0.338763	46.77562
KEGG_PA	hsa04976:Bile secretion	5	1.724137	0.050750	28234, 4	141	69	6910	3.551238	0.999941	0.333569	47.56667
KEGG_PA	hsa04022:cGMP-PKG signaling pathway	8	2.758620	0.051185	6722, 48	141	166	6910	2.361787	0.999945	0.324979	47.86343
KEGG_PA	hsa04068:FoxO signaling pathway	7	2.413793	0.054234	4616, 10	141	134	6910	2.560071	0.999970	0.330379	49.90250
KEGG_PA	hsa05140:Leishmaniasis	5	1.724137	0.055330	3725, 34	141	71	6910	3.451203	0.999976	0.325798	50.61789
KEGG_PA	hsa05206:MicroRNAs in cancer	11	3.793103	0.063146	5292, 15	141	285	6910	1.891501	0.999994	0.353143	55.45027
KEGG_PA	hsa04620:Toll-like receptor signaling pathway	6	2.068965	0.063510	3725, 14	141	106	6910	2.773986	0.999995	0.344997	55.66439
KEGG_PA	hsa05146:Amoebiasis	6	2.068965	0.063510	107, 355	141	106	6910	2.773986	0.999995	0.344997	55.66439
KEGG_PA	hsa04261:Adrenergic signaling in cardiomyocytes	7	2.413793	0.075558	4633, 71	141	146	6910	2.349655	0.999999	0.387206	62.23914
KEGG_PA	hsa04925:Aldosterone synthesis and secretion	5	1.724137	0.081431	3777, 57	141	81	6910	3.025129	0.999999	0.400928	65.10752
KEGG_PA	hsa04151:PI3K-Akt signaling pathway	12	4.137931	0.090176	80310, 2	141	345	6910	1.704594	0.999999	0.424355	69.00918
KEGG_PA	hsa04670:Leukocyte transendothelial migration	6	2.068965	0.090908	4633, 83	141	118	6910	2.491886	0.999999	0.417304	69.31682
KEGG_PA	hsa05134:Legionellosis	4	1.379310	0.095789	2919, 35	141	54	6910	3.630154	0.999999	0.425246	71.29759
KEGG_PA	hsa04970:Salivary secretion	5	1.724137	0.096403	483, 108	141	86	6910	2.849249	0.999999	0.418193	1790749
KEGG_PA	hsa04621:NOD-like receptor signaling pathway	4	1.379310	0.099885	7128, 35	141	55	6910	3.564152	0.999999	0.421100	72.86806