

GO ID	GO Name	Gene Counts	Gene Amount in	Enrichment Score	p-value	FDR
GO:0007155	cell adhesion	127	500	8.2896234	1.33E-77	5.12E-74
GO:0001525	angiogenesis	70	189	12.087523	1.32E-55	2.54E-52
GO:0007275	multicellular	142	954	4.8578159	4.78E-55	6.14E-52
GO:0030154	cell differentiation	101	636	5.1828106	8.78E-42	8.45E-39
GO:0008285	negative regulation	69	315	7.1489066	6.16E-38	4.74E-35
GO:0045944	positive regulation	104	745	4.5559416	7.48E-38	4.80E-35
GO:0043065	positive regulation	62	258	7.8428348	1.07E-36	5.91E-34
GO:0008284	positive regulation	73	382	6.2367822	7.15E-36	3.44E-33
GO:0043066	negative regulation	81	480	5.5073777	1.32E-35	5.64E-33
GO:0030335	positive regulation	45	129	11.38476	9.21E-35	3.55E-32
GO:0008152	metabolic process	109	991	3.5896651	2.82E-30	9.86E-28
GO:0007395	nervous system	60	307	6.3784324	3.18E-30	1.02E-27
GO:0016310	phosphorylation	87	684	4.1511099	8.55E-29	2.53E-26
GO:0000122	negative regulation	77	561	4.4794939	9.49E-28	2.61E-25
GO:0016477	cell migration	38	125	9.921439	5.30E-27	1.36E-24
GO:0006468	protein phosphorylation	79	611	4.2197524	1.06E-26	2.54E-24
GO:0007507	heart development	41	167	8.0125079	4.98E-25	1.13E-22
GO:0006355	regulation of	145	1852	2.5552189	2.09E-24	4.48E-22
GO:0006915	apoptotic process	70	540	4.2306331	7.71E-24	1.56E-21
GO:0001938	positive regulation	24	49	15.985133	2.441E-23	4.70E-21

Gene Symbols	Rank
Cdh23 Srp2 Negr1 Cdh19 Pdpn Prkca Cdh11 Parvb Thbs1 Svep1 Ret Scarb2 Postn Cx	1
Tmem100 Mmp2 Meis1 Nos3 Nrp1 Robo4 Srp2 Tnfrsf2 Arhgap24 Prkd1 Ptk2 Prkd2 Ct	2
Sema3c Lrp1 Sema6b Wnt9a Smo Eya2 Dli1 Adcyap1r1 Spred2 Dact1 Ift81 Heyl Efna5 F	3
Dock7 Adcyap1r1 Pgf Gata2 Slfn5 Sdc2 Slit3 Robo4 Hip1 Gli2 Musk Cbfa2t3 Itgav Sema	4
Gli3 Hmox1 Timp2 Sox7 Cav1 Notch2 Tgfb2 Slfn3 Prkca Smad3 Rgcc Skap2 Wt1 Ptgs2	5
Plscr1 Nfix Nr1h4 Mkl2 Pparg Epas1 Lmo4 Hexb Gli1 Tbx20 Lif Cebpa Pygo1 Foxs1 Mef	6
Maged1 Casp1 Slit2 Alox12 G0s2 Sept4 Sfrp2 Anxa1 Map3k1 Wnt11 Bmp2 Bmp4 Uaca	7
Ptgs2 Kdr Ddr2 Acer2 Adrb2 Il6ra Bcl2l1 Vegfa Ctgf Igf1 Smo Avpr1a Rogdi Ednrb Hlx Zf	8
Sox9 Dpep1 Notch1 Bmp4 Pdgfrb Cryab Ctsh Gimap5 Vimp Timp1 ApoE Foxc2 Smad3 C	9
Ctsh Pdgfra Pld1 Egfr Itgav Ptp4a1 Snai1 Trip6 Ret Irs1 Aqp1 Irs2 Zfp703 Has2 Smad3 C	10
Ust Isoc1 Pde5a Bdh2 Gfod1 Enpp2 Acsf2 Arb Cd38 Alpl Kifc3 Dusp3 Dusp6 Zdhc18 C	11
Epha7 Atoh8 Igf1 Ndr2 Efnb2 Ephb1 Mtss1 Ret Nrp1 Srgap2 Hdac9 Mef2c Camk1d Efn	12
Map3k11 Nik Ptpn3 Jak3 Prkd2 Rps6kl1 Flt1 Mst1r Itpkb Snrk Ddr2 Pik3cb Gk5 Pak1 Prk	13
Nr1h4 Dach1 Tgif1 Dact1 Ripply3 Tbx20 Glis2 Bhlhe40 Cebpa Efna1 Gli3 Cdkn1c Eng B	14
Thbs1 Snai1 Fmn1 Cd248 Nck2 Podxl Kdr Lrrc16a Eng Ctgf Vegfa Pdgfra Lamb1 Nck1 C	15
Ephb1 Epha7 Jak3 Mapk11 Mertk Prkd1 Tgfb3 Pdgfra Ddr2 Snrk Sgk1 Ror1 Lyn Prkab2	16
Hdac9 Pkd1 Fbn1 Gli3 Tnnt2 Mkl2 Adap2 Pdlim3 Bmp4 Tgfb1 Bmpr1a Ptprij Sema3c Co	17
Cdk8 Gata2 Nr4a1 Zfp354c Mapk11 Nfkbiz Heyl Apbb2 Atf5 Ralgapa1 Eya4 Bhlhe40 Elk	18
Tnfrsf21 Dram2 Xaf1 Tnfrsf12a Dapk1 Tmem173 Epha7 Nr4a1 Tgfb1 Gadd45b Mef2c G	19
Egr3 Bmp4 Nrarp Ccl11 Prkd1 Cav1 Fgf2 Pdgfb Cav2 Ecm1 Kdr Prkd2 Pgf Cdh13 Cxcl12	20