

Table S1a. GO term enrichment of DEGs

ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	Count
BP	GO:0030198	extracellular matrix organization	72/807	368/18670	9.75385E-28	2.90356E-24	2.29121E-24	72
BP	GO:0043062	extracellular structure organization	72/807	369/18670	1.16398E-27	2.90356E-24	2.29121E-24	72
BP	GO:0006936	muscle contraction	58/807	363/18670	4.28837E-18	7.13157E-15	5.62755E-15	58
BP	GO:0031589	cell-substrate adhesion	56/807	354/18670	2.62641E-17	3.27579E-14	2.58494E-14	56
BP	GO:0003012	muscle system process	63/807	472/18670	1.26651E-15	1.26372E-12	9.97207E-13	63
BP	GO:0060485	mesenchyme development	46/807	279/18670	4.03209E-15	3.35268E-12	2.64562E-12	46
BP	GO:0001655	urogenital system development	48/807	330/18670	1.38776E-13	9.00136E-11	7.10302E-11	48
BP	GO:0001763	morphogenesis of a branching structure	36/807	196/18670	1.44339E-13	9.00136E-11	7.10302E-11	36
BP	GO:0048762	mesenchymal cell differentiation	38/807	220/18670	2.28385E-13	1.26601E-10	9.99017E-11	38
BP	GO:0060537	muscle tissue development	53/807	408/18670	7.47736E-13	3.73045E-10	2.94372E-10	53
BP	GO:0060047	heart contraction	42/807	282/18670	2.1638E-12	9.09522E-10	7.17708E-10	42
BP	GO:0061138	morphogenesis of a branching epithelium	33/807	182/18670	2.18766E-12	9.09522E-10	7.17708E-10	33
BP	GO:0034329	cell junction assembly	52/807	409/18670	2.86386E-12	1.075E-09	8.48291E-10	52
BP	GO:0061448	connective tissue development	41/807	273/18670	3.01665E-12	1.075E-09	8.48291E-10	41
BP	GO:0030323	respiratory tube development	32/807	176/18670	4.37461E-12	1.455E-09	1.14814E-09	32
BP	GO:0003015	heart process	42/807	292/18670	6.95579E-12	2.1689E-09	1.71149E-09	42
BP	GO:0001503	ossification	50/807	398/18670	1.18537E-11	3.32486E-09	2.62366E-09	50
BP	GO:0030324	lung development	31/807	172/18670	1.19959E-11	3.32486E-09	2.62366E-09	31
BP	GO:0072001	renal system development	41/807	293/18670	3.01507E-11	7.91694E-09	6.24729E-09	41
BP	GO:0008016	regulation of heart contraction	37/807	251/18670	6.1062E-11	1.52319E-08	1.20196E-08	37
BP	GO:0060348	bone development	34/807	217/18670	6.81311E-11	1.6186E-08	1.27725E-08	34
BP	GO:0060541	respiratory system development	32/807	198/18670	1.09115E-10	2.47442E-08	1.95258E-08	32
BP	GO:1903522	regulation of blood circulation	40/807	297/18670	1.71992E-10	3.73072E-08	2.94393E-08	40
BP	GO:0014706	striated muscle tissue development	47/807	390/18670	2.0765E-10	4.31652E-08	3.40618E-08	47
BP	GO:0010810	regulation of cell-substrate adhesion	33/807	215/18670	2.26696E-10	4.52394E-08	3.56986E-08	33

BP	GO:0085029	extracellular matrix assembly	14/807	41/18670	8.43977E-10	1.61946E-07	1.27792E-07	14
BP	GO:0007517	muscle organ development	47/807	410/18670	1.1072E-09	2.04586E-07	1.6144E-07	47
BP	GO:0010721	negative regulation of cell development	42/807	344/18670	1.29998E-09	2.21079E-07	1.74454E-07	42
BP	GO:0048754	branching morphogenesis of an epithelial tube	26/807	150/18670	1.31147E-09	2.21079E-07	1.74454E-07	26
BP	GO:0090287	regulation of cellular response to growth factor stimulus	38/807	292/18670	1.3294E-09	2.21079E-07	1.74454E-07	38
BP	GO:0070252	actin-mediated cell contraction	23/807	121/18670	1.83559E-09	2.92992E-07	2.31202E-07	23
BP	GO:0051216	cartilage development	31/807	209/18670	1.87928E-09	2.92992E-07	2.31202E-07	31
BP	GO:0030048	actin filament-based movement	25/807	143/18670	2.26274E-09	3.42086E-07	2.69941E-07	25
BP	GO:0003416	endochondral bone growth	14/807	44/18670	2.43951E-09	3.57963E-07	2.8247E-07	14
BP	GO:0048565	digestive tract development	24/807	134/18670	2.86247E-09	4.08024E-07	3.21974E-07	24
BP	GO:0030282	bone mineralization	22/807	114/18670	3.0665E-09	4.24966E-07	3.35343E-07	22
BP	GO:0061337	cardiac conduction	25/807	146/18670	3.52965E-09	4.7593E-07	3.75559E-07	25
BP	GO:0051271	negative regulation of cellular component movement	44/807	384/18670	3.84801E-09	4.88563E-07	3.85527E-07	44
BP	GO:0045666	positive regulation of neuron differentiation	43/807	371/18670	4.09976E-09	4.88563E-07	3.85527E-07	43
BP	GO:0010975	regulation of neuron projection development	52/807	499/18670	4.13451E-09	4.88563E-07	3.85527E-07	52
BP	GO:0001822	kidney development	36/807	278/18670	4.13512E-09	4.88563E-07	3.85527E-07	36
BP	GO:0035265	organ growth	30/807	204/18670	4.21091E-09	4.88563E-07	3.85527E-07	30
BP	GO:0035637	multicellular organismal signaling	30/807	204/18670	4.21091E-09	4.88563E-07	3.85527E-07	30
BP	GO:0098868	bone growth	14/807	47/18670	6.42467E-09	7.2847E-07	5.74839E-07	14
BP	GO:0060048	cardiac muscle contraction	24/807	140/18670	7.07658E-09	7.77768E-07	6.1374E-07	24
BP	GO:0048738	cardiac muscle tissue development	32/807	233/18670	7.17124E-09	7.77768E-07	6.1374E-07	32
BP	GO:0001837	epithelial to mesenchymal transition	24/807	141/18670	8.18561E-09	8.65198E-07	6.82731E-07	24
BP	GO:0022612	gland morphogenesis	22/807	120/18670	8.32421E-09	8.65198E-07	6.82731E-07	22

BP	GO:0040013	negative regulation of locomotion	43/807	381/18670	9.13144E-09	9.29729E-07	7.33654E-07	43
BP	GO:0060350	endochondral bone morphogenesis	17/807	73/18670	9.86105E-09	9.83936E-07	7.76428E-07	17
BP	GO:0006941	striated muscle contraction	27/807	177/18670	1.12709E-08	1.10256E-06	8.70033E-07	27
BP	GO:0001101	response to acid chemical	40/807	343/18670	1.2045E-08	1.15563E-06	9.1191E-07	40
BP	GO:0086003	cardiac muscle cell contraction	17/807	74/18670	1.22927E-08	1.15714E-06	9.13103E-07	17
BP	GO:0002062	chondrocyte differentiation	22/807	123/18670	1.33699E-08	1.23523E-06	9.74724E-07	22
BP	GO:0050769	positive regulation of neurogenesis	49/807	474/18670	1.51618E-08	1.37531E-06	1.08527E-06	49
BP	GO:0055123	digestive system development	24/807	146/18670	1.65954E-08	1.45308E-06	1.14663E-06	24
BP	GO:0060349	bone morphogenesis	21/807	114/18670	1.66016E-08	1.45308E-06	1.14663E-06	21
BP	GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	40/807	349/18670	1.96371E-08	1.6605E-06	1.31031E-06	40
BP	GO:2000146	negative regulation of cell motility	40/807	349/18670	1.96371E-08	1.6605E-06	1.31031E-06	40
BP	GO:0072132	mesenchyme morphogenesis	14/807	52/18670	2.71998E-08	2.26166E-06	1.78469E-06	14
BP	GO:0007044	cell-substrate junction assembly	19/807	97/18670	2.81837E-08	2.26788E-06	1.78959E-06	19
BP	GO:0150115	cell-substrate junction organization	19/807	97/18670	2.81837E-08	2.26788E-06	1.78959E-06	19
BP	GO:0071229	cellular response to acid chemical	29/807	209/18670	2.87918E-08	2.28003E-06	1.79918E-06	29
BP	GO:0071560	cellular response to transforming growth factor beta stimulus	32/807	249/18670	3.61193E-08	2.81561E-06	2.22181E-06	32
BP	GO:0050678	regulation of epithelial cell proliferation	41/807	378/18670	6.19294E-08	4.75332E-06	3.75087E-06	41
BP	GO:0071559	response to transforming growth factor beta	32/807	255/18670	6.36277E-08	4.80968E-06	3.79534E-06	32
BP	GO:0010959	regulation of metal ion transport	42/807	394/18670	6.97991E-08	5.19743E-06	4.10132E-06	42
BP	GO:0086002	cardiac muscle cell action potential involved in contraction	14/807	56/18670	7.59867E-08	5.57496E-06	4.39923E-06	14
BP	GO:0086001	cardiac muscle cell action potential	16/807	74/18670	8.21313E-08	5.93845E-06	4.68606E-06	16
BP	GO:0042692	muscle cell differentiation	41/807	385/18670	1.02753E-07	7.32335E-06	5.77889E-06	41
BP	GO:0048880	sensory system development	40/807	371/18670	1.05552E-07	7.41686E-06	5.85267E-06	40

BP	GO:0032970	regulation of actin filament-based process	41/807	388/18670	1.2706E-07	8.80422E-06	6.94745E-06	41
BP	GO:0031214	biomineral tissue development	24/807	163/18670	1.44884E-07	9.76793E-06	7.70792E-06	24
BP	GO:0110148	biomineralization	24/807	163/18670	1.44884E-07	9.76793E-06	7.70792E-06	24
BP	GO:0051146	striated muscle cell differentiation	34/807	293/18670	1.69133E-07	1.12507E-05	8.87799E-06	34
BP	GO:0006813	potassium ion transport	30/807	240/18670	1.78454E-07	1.17145E-05	9.244E-06	30
BP	GO:0090092	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	30/807	241/18670	1.95618E-07	1.26745E-05	1.00015E-05	30
BP	GO:0060441	epithelial tube branching involved in lung morphogenesis	10/807	29/18670	2.04089E-07	1.30538E-05	1.03008E-05	10
BP	GO:0006939	smooth muscle contraction	19/807	110/18670	2.29603E-07	1.44999E-05	1.14419E-05	19
BP	GO:0006937	regulation of muscle contraction	24/807	171/18670	3.59918E-07	2.24454E-05	1.77118E-05	24
BP	GO:0003418	growth plate cartilage chondrocyte differentiation	9/807	24/18670	3.66776E-07	2.25907E-05	1.78264E-05	9
BP	GO:0060560	developmental growth involved in morphogenesis	29/807	235/18670	3.7516E-07	2.28253E-05	1.80115E-05	29
BP	GO:0050673	epithelial cell proliferation	43/807	434/18670	3.79749E-07	2.28261E-05	1.80122E-05	43
BP	GO:0048638	regulation of developmental growth	37/807	347/18670	4.17549E-07	2.47994E-05	1.95694E-05	37
BP	GO:0001654	eye development	38/807	362/18670	4.33387E-07	2.54372E-05	2.00726E-05	38
BP	GO:0030336	negative regulation of cell migration	36/807	334/18670	4.60455E-07	2.66511E-05	2.10305E-05	36
BP	GO:0034765	regulation of ion transmembrane transport	46/807	483/18670	4.64751E-07	2.66511E-05	2.10305E-05	46
BP	GO:0016049	cell growth	46/807	484/18670	4.92824E-07	2.74833E-05	2.16872E-05	46
BP	GO:0045665	negative regulation of neuron differentiation	28/807	225/18670	5.00076E-07	2.74833E-05	2.16872E-05	28
BP	GO:0070167	regulation of biomineral tissue development	17/807	94/18670	5.01299E-07	2.74833E-05	2.16872E-05	17

BP	GO:0110149	regulation of biomineralization	17/807	94/18670	5.01299E-07	2.74833E-05	2.16872E-05	17
BP	GO:0055074	calcium ion homeostasis	45/807	471/18670	5.67325E-07	3.06275E-05	2.41683E-05	45
BP	GO:0150063	visual system development	38/807	366/18670	5.70928E-07	3.06275E-05	2.41683E-05	38
BP	GO:0050768	negative regulation of neurogenesis	33/807	295/18670	5.9709E-07	3.16902E-05	2.50069E-05	33
BP	GO:0006874	cellular calcium ion homeostasis	44/807	458/18670	6.5202E-07	3.42414E-05	2.702E-05	44
BP	GO:0071805	potassium ion transmembrane transport	27/807	217/18670	7.99539E-07	4.15511E-05	3.27881E-05	27
BP	GO:0001558	regulation of cell growth	41/807	416/18670	8.12692E-07	4.17992E-05	3.29839E-05	41
BP	GO:0090257	regulation of muscle system process	30/807	259/18670	9.28651E-07	4.72759E-05	3.73056E-05	30
BP	GO:0048732	gland development	42/807	434/18670	9.67163E-07	4.87392E-05	3.84603E-05	42
BP	GO:0051961	negative regulation of nervous system development	34/807	316/18670	9.96285E-07	4.97047E-05	3.92222E-05	34
BP	GO:0060425	lung morphogenesis	12/807	50/18670	1.0453E-06	5.09606E-05	4.02133E-05	12
BP	GO:0001704	formation of primary germ layer	19/807	121/18670	1.0521E-06	5.09606E-05	4.02133E-05	19
BP	GO:0010811	positive regulation of cell-substrate adhesion	19/807	121/18670	1.0521E-06	5.09606E-05	4.02133E-05	19
BP	GO:0001508	action potential	20/807	133/18670	1.11543E-06	5.35083E-05	4.22236E-05	20
BP	GO:0071772	response to BMP	23/807	170/18670	1.20929E-06	5.69166E-05	4.49131E-05	23
BP	GO:0071773	cellular response to BMP stimulus	23/807	170/18670	1.20929E-06	5.69166E-05	4.49131E-05	23
BP	GO:0007160	cell-matrix adhesion	27/807	225/18670	1.62957E-06	7.59805E-05	5.99565E-05	27
BP	GO:0060512	prostate gland morphogenesis	9/807	28/18670	1.65765E-06	7.65743E-05	6.04251E-05	9
BP	GO:0033002	muscle cell proliferation	28/807	239/18670	1.69836E-06	7.74568E-05	6.11215E-05	28
BP	GO:0034109	homotypic cell-cell adhesion	15/807	81/18670	1.71079E-06	7.74568E-05	6.11215E-05	15
BP	GO:2000027	regulation of animal organ morphogenesis	29/807	253/18670	1.74066E-06	7.74568E-05	6.11215E-05	29
BP	GO:0031346	positive regulation of cell projection organization	38/807	383/18670	1.74377E-06	7.74568E-05	6.11215E-05	38

BP	GO:0010976	positive regulation of neuron projection development	31/807	281/18670	1.75438E-06	7.74568E-05	6.11215E-05	31
BP	GO:0003417	growth plate cartilage development	10/807	36/18670	1.96667E-06	8.56943E-05	6.76218E-05	10
BP	GO:0072503	cellular divalent inorganic cation homeostasis	45/807	493/18670	1.97532E-06	8.56943E-05	6.76218E-05	45
BP	GO:0048608	reproductive structure development	41/807	431/18670	2.01419E-06	8.66275E-05	6.83582E-05	41
BP	GO:0060536	cartilage morphogenesis	9/807	29/18670	2.31175E-06	9.85756E-05	7.77864E-05	9
BP	GO:0006816	calcium ion transport	41/807	434/18670	2.39899E-06	0.000100576	7.93651E-05	41
BP	GO:0061458	reproductive system development	41/807	434/18670	2.39899E-06	0.000100576	7.93651E-05	41
BP	GO:0030278	regulation of ossification	25/807	203/18670	2.45152E-06	0.000101922	8.04272E-05	25
BP	GO:0006029	proteoglycan metabolic process	16/807	94/18670	2.49809E-06	0.000103	8.12777E-05	16
BP	GO:0022604	regulation of cell morphogenesis	44/807	484/18670	2.85356E-06	0.000116692	9.2082E-05	44
BP	GO:0090288	negative regulation of cellular response to growth factor stimulus	22/807	166/18670	2.90575E-06	0.00011786	9.3004E-05	22
BP	GO:1901342	regulation of vasculature development	40/807	422/18670	2.9294E-06	0.000117861	9.30047E-05	40
BP	GO:0044272	sulfur compound biosynthetic process	24/807	192/18670	2.98215E-06	0.000119023	9.39219E-05	24
BP	GO:0003413	chondrocyte differentiation involved in endochondral bone morphogenesis	9/807	30/18670	3.17637E-06	0.000125769	9.9245E-05	9
BP	GO:0060688	regulation of morphogenesis of a branching structure	12/807	56/18670	3.78751E-06	0.000148787	0.000117408	12
BP	GO:0030500	regulation of bone mineralization	14/807	76/18670	4.03092E-06	0.000157111	0.000123977	14
BP	GO:0060562	epithelial tube morphogenesis	33/807	322/18670	4.16023E-06	0.000160768	0.000126862	33
BP	GO:0030509	BMP signaling pathway	21/807	157/18670	4.18918E-06	0.000160768	0.000126862	21
BP	GO:0042659	regulation of cell fate specification	6/807	12/18670	4.72967E-06	0.000180125	0.000142137	6
BP	GO:0002063	chondrocyte development	11/807	48/18670	4.79282E-06	0.000181147	0.000142944	11
BP	GO:0001649	osteoblast differentiation	26/807	225/18670	5.09579E-06	0.00019115	0.000150837	26
BP	GO:0048705	skeletal system morphogenesis	27/807	239/18670	5.17284E-06	0.000192592	0.000151975	27

BP	GO:0007179	transforming growth factor beta receptor signaling pathway	24/807	199/18670	5.59046E-06	0.000206599	0.000163028	24
BP	GO:0003414	chondrocyte morphogenesis involved in endochondral bone morphogenesis	7/807	18/18670	5.75349E-06	0.000208001	0.000164135	7
BP	GO:0003429	growth plate cartilage chondrocyte morphogenesis	7/807	18/18670	5.75349E-06	0.000208001	0.000164135	7
BP	GO:0090171	chondrocyte morphogenesis	7/807	18/18670	5.75349E-06	0.000208001	0.000164135	7
BP	GO:0070527	platelet aggregation	12/807	59/18670	6.74065E-06	0.000241936	0.000190913	12
BP	GO:0086009	membrane repolarization	11/807	50/18670	7.32173E-06	0.000260915	0.000205889	11
BP	GO:0090101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	18/807	126/18670	7.95984E-06	0.000281643	0.000222246	18
BP	GO:0003007	heart morphogenesis	28/807	259/18670	8.09962E-06	0.000283454	0.000223675	28
BP	GO:0050920	regulation of chemotaxis	25/807	217/18670	8.12467E-06	0.000283454	0.000223675	25
BP	GO:0042178	xenobiotic catabolic process	6/807	13/18670	8.46204E-06	0.000293174	0.000231345	6
BP	GO:0003422	growth plate cartilage morphogenesis	7/807	19/18670	8.77024E-06	0.000301757	0.000238118	7
BP	GO:0060740	prostate gland epithelium morphogenesis	8/807	26/18670	9.18405E-06	0.00031383	0.000247645	8
BP	GO:0007411	axon guidance	29/807	276/18670	9.7596E-06	0.000331229	0.000261374	29
BP	GO:0002576	platelet degranulation	18/807	128/18670	9.9529E-06	0.000335507	0.00026475	18
BP	GO:0050679	positive regulation of epithelial cell proliferation	24/807	206/18670	1.01352E-05	0.000337314	0.000266176	24
BP	GO:0055117	regulation of cardiac muscle contraction	14/807	82/18670	1.01417E-05	0.000337314	0.000266176	14
BP	GO:0097485	neuron projection guidance	29/807	277/18670	1.04629E-05	0.000345693	0.000272788	29
BP	GO:0043405	regulation of MAP kinase activity	33/807	337/18670	1.09116E-05	0.000358146	0.000282614	33
BP	GO:0070838	divalent metal ion transport	42/807	479/18670	1.16423E-05	0.00037963	0.000299568	42
BP	GO:0010977	negative regulation of neuron projection development	20/807	155/18670	1.21788E-05	0.000394547	0.000311338	20

BP	GO:1903779	regulation of cardiac conduction	13/807	73/18670	1.30353E-05	0.000419568	0.000331083	13
BP	GO:0003197	endocardial cushion development	10/807	44/18670	1.40272E-05	0.000442924	0.000349513	10
BP	GO:0010463	mesenchymal cell proliferation	10/807	44/18670	1.40272E-05	0.000442924	0.000349513	10
BP	GO:0050654	chondroitin sulfate proteoglycan metabolic process	10/807	44/18670	1.40272E-05	0.000442924	0.000349513	10
BP	GO:0001666	response to hypoxia	34/807	359/18670	1.63419E-05	0.000512765	0.000404625	34
BP	GO:0072511	divalent inorganic cation transport	42/807	486/18670	1.64961E-05	0.00051437	0.000405892	42
BP	GO:0006942	regulation of striated muscle contraction	15/807	97/18670	1.70917E-05	0.000529629	0.000417933	15
BP	GO:0035987	endodermal cell differentiation	10/807	45/18670	1.73424E-05	0.000534083	0.000421447	10
BP	GO:0019932	second-messenger-mediated signaling	39/807	439/18670	1.76792E-05	0.000541114	0.000426995	39
BP	GO:0045165	cell fate commitment	28/807	271/18670	1.88752E-05	0.000574197	0.000453102	28
BP	GO:1903844	regulation of cellular response to transforming growth factor beta stimulus	17/807	122/18670	1.97107E-05	0.000595981	0.000470291	17
BP	GO:0070482	response to oxygen levels	36/807	394/18670	2.02986E-05	0.000610059	0.0004814	36
BP	GO:0050921	positive regulation of chemotaxis	18/807	135/18670	2.09318E-05	0.000625322	0.000493445	18
BP	GO:0031345	negative regulation of cell projection organization	22/807	188/18670	2.18857E-05	0.000649926	0.00051286	22
BP	GO:0048568	embryonic organ development	38/807	428/18670	2.28933E-05	0.000673855	0.000531742	38
BP	GO:0086065	cell communication involved in cardiac conduction	11/807	56/18670	2.30369E-05	0.000673855	0.000531742	11
BP	GO:0007204	positive regulation of cytosolic calcium ion concentration	31/807	319/18670	2.32317E-05	0.000673855	0.000531742	31
BP	GO:0043010	camera-type eye development	31/807	319/18670	2.32317E-05	0.000673855	0.000531742	31
BP	GO:0055024	regulation of cardiac muscle tissue development	15/807	100/18670	2.48093E-05	0.000715455	0.000564569	15

BP	GO:0060351	cartilage development involved in endochondral bone morphogenesis	10/807	47/18670	2.60296E-05	0.000742066	0.000585567	10
BP	GO:1903115	regulation of actin filament-based movement	10/807	47/18670	2.60296E-05	0.000742066	0.000585567	10
BP	GO:0045765	regulation of angiogenesis	35/807	383/18670	2.6283E-05	0.000745034	0.00058791	35
BP	GO:0086005	ventricular cardiac muscle cell action potential	9/807	38/18670	2.6519E-05	0.000747477	0.000589837	9
BP	GO:0002027	regulation of heart rate	15/807	101/18670	2.79915E-05	0.000784549	0.000619091	15
BP	GO:0043583	ear development	24/807	219/18670	2.82233E-05	0.000786625	0.00062073	24
BP	GO:0010717	regulation of epithelial to mesenchymal transition	14/807	90/18670	3.02799E-05	0.00083583	0.000659557	14
BP	GO:0048839	inner ear development	22/807	192/18670	3.03854E-05	0.00083583	0.000659557	22
BP	GO:0036293	response to decreased oxygen levels	34/807	370/18670	3.04913E-05	0.00083583	0.000659557	34
BP	GO:0001823	mesonephros development	15/807	102/18670	3.15283E-05	0.000857299	0.000676499	15
BP	GO:0030850	prostate gland development	10/807	48/18670	3.16182E-05	0.000857299	0.000676499	10
BP	GO:0048736	appendage development	21/807	179/18670	3.21682E-05	0.000862834	0.000680867	21
BP	GO:0060173	limb development	21/807	179/18670	3.21682E-05	0.000862834	0.000680867	21
BP	GO:0051480	regulation of cytosolic calcium ion concentration	33/807	357/18670	3.53265E-05	0.000940819	0.000742405	33
BP	GO:0007229	integrin-mediated signaling pathway	15/807	103/18670	3.54528E-05	0.000940819	0.000742405	15
BP	GO:0030166	proteoglycan biosynthetic process	12/807	69/18670	3.57069E-05	0.00094255	0.00074377	12
BP	GO:0048546	digestive tract morphogenesis	10/807	49/18670	3.82021E-05	0.001003106	0.000791556	10
BP	GO:0032956	regulation of actin cytoskeleton organization	32/807	343/18670	3.86198E-05	0.001008765	0.000796021	32
BP	GO:0014032	neural crest cell development	13/807	81/18670	4.12524E-05	0.001071918	0.000845855	13
BP	GO:0002685	regulation of leukocyte migration	22/807	196/18670	4.17387E-05	0.001078935	0.000851392	22
BP	GO:0043266	regulation of potassium ion transport	15/807	105/18670	4.46111E-05	0.001147241	0.000905293	15
BP	GO:0001706	endoderm formation	10/807	50/18670	4.59222E-05	0.001168907	0.00092239	10

BP	GO:0002931	response to ischemia	10/807	50/18670	4.59222E-05	0.001168907	0.00092239	10
BP	GO:0003433	chondrocyte development involved in endochondral bone morphogenesis	7/807	24/18670	4.98412E-05	0.001262223	0.000996026	7
BP	GO:0048286	lung alveolus development	9/807	41/18670	5.07359E-05	0.001278392	0.001008785	9
BP	GO:0070371	ERK1 and ERK2 cascade	30/807	317/18670	5.13561E-05	0.001287515	0.001015984	30
BP	GO:0007369	gastrulation	21/807	185/18670	5.25042E-05	0.001305705	0.001030338	21
BP	GO:0031032	actomyosin structure organization	22/807	199/18670	5.26051E-05	0.001305705	0.001030338	22
BP	GO:0001667	ameboidal-type cell migration	39/807	462/18670	5.49625E-05	0.001354394	0.001068759	39
BP	GO:0016264	gap junction assembly	5/807	11/18670	5.53811E-05	0.001354394	0.001068759	5
BP	GO:0060525	prostate glandular acinus development	5/807	11/18670	5.53811E-05	0.001354394	0.001068759	5
BP	GO:0043406	positive regulation of MAP kinase activity	26/807	258/18670	5.66274E-05	0.00137628	0.001086029	26
BP	GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	27/807	273/18670	5.68278E-05	0.00137628	0.001086029	27
BP	GO:0070588	calcium ion transmembrane transport	30/807	319/18670	5.76679E-05	0.00138988	0.00109676	30
BP	GO:0060326	cell chemotaxis	29/807	304/18670	5.90485E-05	0.001416312	0.001117618	29
BP	GO:0017015	regulation of transforming growth factor beta receptor signaling pathway	16/807	120/18670	5.93441E-05	0.001416593	0.00111784	16
BP	GO:0007162	negative regulation of cell adhesion	28/807	289/18670	6.00257E-05	0.001426039	0.001125294	28
BP	GO:0055002	striated muscle cell development	20/807	173/18670	6.06815E-05	0.001434786	0.001132196	20
BP	GO:0060420	regulation of heart growth	13/807	84/18670	6.10424E-05	0.001436512	0.001133558	13
BP	GO:0010464	regulation of mesenchymal cell proliferation	8/807	33/18670	6.23814E-05	0.00146113	0.001152984	8
BP	GO:0050900	leukocyte migration	41/807	499/18670	6.548E-05	0.00152654	0.0012046	41
BP	GO:0060571	morphogenesis of an epithelial fold	7/807	25/18670	6.66543E-05	0.001546689	0.0012205	7
BP	GO:0002028	regulation of sodium ion transport	13/807	85/18670	6.92574E-05	0.001584977	0.001250713	13
BP	GO:0014031	mesenchymal cell development	13/807	85/18670	6.92574E-05	0.001584977	0.001250713	13
BP	GO:0048864	stem cell development	13/807	85/18670	6.92574E-05	0.001584977	0.001250713	13

BP	GO:0001657	ureteric bud development	14/807	97/18670	7.08514E-05	0.001609596	0.001270139	14
BP	GO:0003018	vascular process in circulatory system	20/807	175/18670	7.13847E-05	0.001609596	0.001270139	20
BP	GO:0071695	anatomical structure maturation	24/807	232/18670	7.15332E-05	0.001609596	0.001270139	24
BP	GO:0035107	appendage morphogenesis	18/807	148/18670	7.22255E-05	0.001609596	0.001270139	18
BP	GO:0035108	limb morphogenesis	18/807	148/18670	7.22255E-05	0.001609596	0.001270139	18
BP	GO:0034394	protein localization to cell surface	11/807	63/18670	7.23315E-05	0.001609596	0.001270139	11
BP	GO:0007409	axonogenesis	39/807	468/18670	7.25915E-05	0.001609596	0.001270139	39
BP	GO:0045785	positive regulation of cell adhesion	35/807	403/18670	7.44941E-05	0.001644473	0.001297661	35
BP	GO:0086004	regulation of cardiac muscle cell contraction	9/807	43/18670	7.55789E-05	0.001661072	0.001310759	9
BP	GO:0048566	embryonic digestive tract development	8/807	34/18670	7.8509E-05	0.0017179	0.001355603	8
BP	GO:0072163	mesonephric epithelium development	14/807	98/18670	7.94288E-05	0.001722914	0.001359559	14
BP	GO:0072164	mesonephric tubule development	14/807	98/18670	7.94288E-05	0.001722914	0.001359559	14
BP	GO:0048588	developmental cell growth	24/807	234/18670	8.19092E-05	0.001769025	0.001395946	24
BP	GO:0045600	positive regulation of fat cell differentiation	11/807	64/18670	8.39779E-05	0.001805886	0.001425033	11
BP	GO:1904062	regulation of cation transmembrane transport	31/807	342/18670	8.69405E-05	0.001861572	0.001468975	31
BP	GO:0045992	negative regulation of embryonic development	7/807	26/18670	8.78275E-05	0.00186456	0.001471332	7
BP	GO:0071711	basement membrane organization	7/807	26/18670	8.78275E-05	0.00186456	0.001471332	7
BP	GO:1901888	regulation of cell junction assembly	21/807	192/18670	9.01488E-05	0.001905731	0.001503821	21
BP	GO:0030199	collagen fibril organization	10/807	54/18670	9.15122E-05	0.001919313	0.001514539	10
BP	GO:0031581	hemidesmosome assembly	5/807	12/18670	9.15607E-05	0.001919313	0.001514539	5
BP	GO:1901617	organic hydroxy compound biosynthetic process	26/807	266/18670	9.41035E-05	0.001964361	0.001550086	26
BP	GO:0060419	heart growth	15/807	112/18670	9.50674E-05	0.001976213	0.001559438	15

BP	GO:0060389	pathway-restricted SMAD protein phosphorylation	11/807	65/18670	9.71905E-05	0.002011963	0.001587649	11
BP	GO:0048333	mesodermal cell differentiation	8/807	35/18670	9.7947E-05	0.002019247	0.001593397	8
BP	GO:0034446	substrate adhesion-dependent cell spreading	14/807	100/18670	9.93285E-05	0.002039299	0.00160922	14
BP	GO:0048640	negative regulation of developmental growth	15/807	113/18670	0.000105321	0.002153474	0.001699316	15
BP	GO:0060973	cell migration involved in heart development	6/807	19/18670	0.000107031	0.002179498	0.001719852	6
BP	GO:1900274	regulation of phospholipase C activity	9/807	45/18670	0.000109923	0.002229283	0.001759137	9
BP	GO:0018108	peptidyl-tyrosine phosphorylation	32/807	363/18670	0.000113502	0.002292557	0.001809067	32
BP	GO:0002026	regulation of the force of heart contraction	7/807	27/18670	0.000114172	0.002296784	0.001812402	7
BP	GO:0072073	kidney epithelium development	17/807	140/18670	0.000115874	0.002321671	0.001832041	17
BP	GO:0030900	forebrain development	33/807	381/18670	0.000124708	0.00248867	0.001963821	33
BP	GO:0014033	neural crest cell differentiation	13/807	90/18670	0.000126324	0.002491037	0.001965688	13
BP	GO:0045778	positive regulation of ossification	13/807	90/18670	0.000126324	0.002491037	0.001965688	13
BP	GO:1901379	regulation of potassium ion transmembrane transport	13/807	90/18670	0.000126324	0.002491037	0.001965688	13
BP	GO:0032963	collagen metabolic process	15/807	115/18670	0.000128753	0.002528941	0.001995599	15
BP	GO:0018212	peptidyl-tyrosine modification	32/807	366/18670	0.000132175	0.002575967	0.002032707	32
BP	GO:0071902	positive regulation of protein serine/threonine kinase activity	30/807	334/18670	0.00013218	0.002575967	0.002032707	30
BP	GO:0048660	regulation of smooth muscle cell proliferation	19/807	169/18670	0.000133558	0.002592697	0.002045909	19
BP	GO:0050803	regulation of synapse structure or activity	23/807	227/18670	0.000137359	0.002656147	0.002095978	23
BP	GO:0038065	collagen-activated signaling pathway	5/807	13/18670	0.000143497	0.002753495	0.002172795	5

BP	GO:0070208	protein heterotrimerization	5/807	13/18670	0.000143497	0.002753495	0.002172795	5
BP	GO:0001755	neural crest cell migration	10/807	57/18670	0.000146904	0.002773771	0.002188795	10
BP	GO:0071398	cellular response to fatty acid	10/807	57/18670	0.000146904	0.002773771	0.002188795	10
BP	GO:0086014	atrial cardiac muscle cell action potential	6/807	20/18670	0.000147334	0.002773771	0.002188795	6
BP	GO:0086026	atrial cardiac muscle cell to AV node cell signaling	6/807	20/18670	0.000147334	0.002773771	0.002188795	6
BP	GO:0086066	atrial cardiac muscle cell to AV node cell communication	6/807	20/18670	0.000147334	0.002773771	0.002188795	6
BP	GO:0010812	negative regulation of cell-substrate adhesion	11/807	68/18670	0.000147972	0.002775304	0.002190005	11
BP	GO:0035296	regulation of tube diameter	17/807	143/18670	0.000150574	0.002803045	0.002211895	17
BP	GO:0097746	regulation of blood vessel diameter	17/807	143/18670	0.000150574	0.002803045	0.002211895	17
BP	GO:0007568	aging	29/807	321/18670	0.000153875	0.002853839	0.002251977	29
BP	GO:0048659	smooth muscle cell proliferation	19/807	171/18670	0.000156036	0.00288281	0.002274839	19
BP	GO:0051153	regulation of striated muscle cell differentiation	15/807	117/18670	0.000156593	0.00288281	0.002274839	15
BP	GO:0070509	calcium ion import	12/807	80/18670	0.000158002	0.002898065	0.002286876	12
BP	GO:0035150	regulation of tube size	17/807	144/18670	0.000164005	0.00299715	0.002365064	17
BP	GO:0055001	muscle cell development	20/807	186/18670	0.000165891	0.003020543	0.002383524	20
BP	GO:1904018	positive regulation of vasculature development	23/807	230/18670	0.000167038	0.003030367	0.002391276	23
BP	GO:0007009	plasma membrane organization	14/807	105/18670	0.000169004	0.003054932	0.00241066	14
BP	GO:0048041	focal adhesion assembly	12/807	81/18670	0.000178307	0.003211451	0.00253417	12
BP	GO:0006575	cellular modified amino acid metabolic process	20/807	188/18670	0.000191722	0.003440648	0.002715031	20
BP	GO:0030203	glycosaminoglycan metabolic process	18/807	160/18670	0.000197043	0.003510332	0.002770019	18
BP	GO:0060993	kidney morphogenesis	13/807	94/18670	0.000197588	0.003510332	0.002770019	13

BP	GO:0045843	negative regulation of striated muscle tissue development	10/807	59/18670	0.000197716	0.003510332	0.002770019	10
BP	GO:0050807	regulation of synapse organization	22/807	218/18670	0.000201578	0.003566213	0.002814115	22
BP	GO:0045926	negative regulation of growth	24/807	249/18670	0.000213213	0.003758735	0.002966035	24
BP	GO:0002523	leukocyte migration involved in inflammatory response	5/807	14/18670	0.000215292	0.003782018	0.002984407	5
BP	GO:0030204	chondroitin sulfate metabolic process	8/807	39/18670	0.00021972	0.003832801	0.003024481	8
BP	GO:0030501	positive regulation of bone mineralization	8/807	39/18670	0.00021972	0.003832801	0.003024481	8
BP	GO:1903845	negative regulation of cellular response to transforming growth factor beta stimulus	12/807	83/18670	0.000225661	0.003922719	0.003095435	12
BP	GO:0048635	negative regulation of muscle organ development	10/807	60/18670	0.0002282	0.003943569	0.003111888	10
BP	GO:0032526	response to retinoic acid	14/807	108/18670	0.000228441	0.003943569	0.003111888	14
BP	GO:0007389	pattern specification process	36/807	446/18670	0.000253337	0.004358274	0.003439133	36
BP	GO:0060976	coronary vasculature development	9/807	50/18670	0.000256197	0.004392319	0.003465998	9
BP	GO:0001759	organ induction	6/807	22/18670	0.000263366	0.004454003	0.003514674	6
BP	GO:0033622	integrin activation	6/807	22/18670	0.000263366	0.004454003	0.003514674	6
BP	GO:1901685	glutathione derivative metabolic process	6/807	22/18670	0.000263366	0.004454003	0.003514674	6
BP	GO:1901687	glutathione derivative biosynthetic process	6/807	22/18670	0.000263366	0.004454003	0.003514674	6
BP	GO:0045444	fat cell differentiation	22/807	223/18670	0.000278032	0.004686147	0.003697859	22
BP	GO:0010769	regulation of cell morphogenesis involved in differentiation	27/807	301/18670	0.000287307	0.004818932	0.003802641	27
BP	GO:0050680	negative regulation of epithelial cell proliferation	18/807	165/18670	0.000289258	0.004818932	0.003802641	18

BP	GO:0003401	axis elongation	7/807	31/18670	0.000290739	0.004818932	0.003802641	7
BP	GO:0050650	chondroitin sulfate proteoglycan biosynthetic process	7/807	31/18670	0.000290739	0.004818932	0.003802641	7
BP	GO:0090075	relaxation of muscle	7/807	31/18670	0.000290739	0.004818932	0.003802641	7
BP	GO:0010830	regulation of myotube differentiation	10/807	62/18670	0.000301072	0.004940955	0.003898929	10
BP	GO:0060393	regulation of pathway-restricted SMAD protein phosphorylation	10/807	62/18670	0.000301072	0.004940955	0.003898929	10
BP	GO:1901862	negative regulation of muscle tissue development	10/807	62/18670	0.000301072	0.004940955	0.003898929	10
BP	GO:1905330	regulation of morphogenesis of an epithelium	19/807	180/18670	0.000303504	0.004964529	0.003917532	19
BP	GO:0150146	cell junction disassembly	5/807	15/18670	0.000311484	0.005078412	0.004007398	5
BP	GO:0060070	canonical Wnt signaling pathway	29/807	335/18670	0.000316735	0.005147203	0.004061681	29
BP	GO:0090596	sensory organ morphogenesis	24/807	256/18670	0.000322282	0.005220348	0.0041194	24
BP	GO:0030326	embryonic limb morphogenesis	15/807	125/18670	0.000326656	0.005257049	0.00414836	15
BP	GO:0035113	embryonic appendage morphogenesis	15/807	125/18670	0.000326656	0.005257049	0.00414836	15
BP	GO:0001708	cell fate specification	13/807	99/18670	0.000332907	0.005340435	0.004214161	13
BP	GO:1903510	mucopolysaccharide metabolic process	14/807	112/18670	0.000335031	0.005348025	0.00422015	14
BP	GO:0035051	cardiocyte differentiation	18/807	167/18670	0.000335525	0.005348025	0.00422015	18
BP	GO:0030168	platelet activation	17/807	153/18670	0.000340097	0.005403641	0.004264037	17
BP	GO:0048863	stem cell differentiation	24/807	257/18670	0.000341323	0.005405901	0.004265821	24
BP	GO:0009226	nucleotide-sugar biosynthetic process	6/807	23/18670	0.000343377	0.005416876	0.004274481	6
BP	GO:1902903	regulation of supramolecular fiber organization	30/807	353/18670	0.000344187	0.005416876	0.004274481	30
BP	GO:0008217	regulation of blood pressure	19/807	182/18670	0.000349302	0.005480085	0.004324359	19
BP	GO:0045667	regulation of osteoblast differentiation	15/807	126/18670	0.000356304	0.005572413	0.004397216	15
BP	GO:0071295	cellular response to vitamin	7/807	32/18670	0.000358397	0.00558763	0.004409223	7

BP	GO:0099622	cardiac muscle cell membrane repolarization	8/807	42/18670	0.000375917	0.005842521	0.00461036	8
BP	GO:0031099	regeneration	20/807	198/18670	0.000381183	0.00590597	0.004660427	20
BP	GO:0006790	sulfur compound metabolic process	31/807	372/18670	0.000387585	0.005986566	0.004724026	31
BP	GO:1901861	regulation of muscle tissue development	17/807	155/18670	0.000396296	0.006083442	0.004800471	17
BP	GO:2001236	regulation of extrinsic apoptotic signaling pathway	17/807	155/18670	0.000396296	0.006083442	0.004800471	17
BP	GO:0048639	positive regulation of developmental growth	19/807	184/18670	0.000400998	0.00613675	0.004842537	19
BP	GO:0007492	endoderm development	11/807	76/18670	0.000404051	0.00614576	0.004849647	11
BP	GO:0042310	vasoconstriction	11/807	76/18670	0.000404051	0.00614576	0.004849647	11
BP	GO:0006022	aminoglycan metabolic process	18/807	170/18670	0.000416941	0.006322554	0.004989156	18
BP	GO:0072006	nephron development	16/807	142/18670	0.000429955	0.006500134	0.005129284	16
BP	GO:0055119	relaxation of cardiac muscle	5/807	16/18670	0.000437016	0.006567081	0.005182113	5
BP	GO:0060572	morphogenesis of an epithelial bud	5/807	16/18670	0.000437016	0.006567081	0.005182113	5
BP	GO:0010863	positive regulation of phospholipase C activity	8/807	43/18670	0.000444566	0.006660473	0.005255809	8
BP	GO:0060675	ureteric bud morphogenesis	10/807	65/18670	0.000446105	0.006663531	0.005258222	10
BP	GO:0003205	cardiac chamber development	18/807	171/18670	0.000447636	0.006666437	0.005260515	18
BP	GO:0030308	negative regulation of cell growth	19/807	186/18670	0.000459213	0.0068185	0.005380509	19
BP	GO:0070206	protein trimerization	9/807	54/18670	0.000466095	0.006900137	0.005444929	9
BP	GO:0072171	mesonephric tubule morphogenesis	10/807	66/18670	0.000505742	0.007446789	0.005876294	10
BP	GO:0055021	regulation of cardiac muscle tissue growth	11/807	78/18670	0.000507498	0.007446789	0.005876294	11
BP	GO:0061333	renal tubule morphogenesis	11/807	78/18670	0.000507498	0.007446789	0.005876294	11
BP	GO:0001659	temperature homeostasis	18/807	173/18670	0.000514929	0.007533672	0.005944854	18
BP	GO:0010092	specification of animal organ identity	7/807	34/18670	0.000531319	0.007728132	0.006098303	7

BP	GO:0098901	regulation of cardiac muscle cell action potential	7/807	34/18670	0.000531319	0.007728132	0.006098303	7
BP	GO:0061098	positive regulation of protein tyrosine kinase activity	9/807	55/18670	0.000536241	0.007736098	0.006104589	9
BP	GO:0098900	regulation of action potential	9/807	55/18670	0.000536241	0.007736098	0.006104589	9
BP	GO:0051899	membrane depolarization	12/807	91/18670	0.000536518	0.007736098	0.006104589	12
BP	GO:0014829	vascular smooth muscle contraction	6/807	25/18670	0.000559507	0.007986109	0.006301874	6
BP	GO:0034110	regulation of homotypic cell-cell adhesion	6/807	25/18670	0.000559507	0.007986109	0.006301874	6
BP	GO:0045766	positive regulation of angiogenesis	20/807	204/18670	0.00056026	0.007986109	0.006301874	20
BP	GO:1902905	positive regulation of supramolecular fiber organization	20/807	204/18670	0.00056026	0.007986109	0.006301874	20
BP	GO:0042476	odontogenesis	15/807	132/18670	0.00058729	0.008296731	0.006546988	15
BP	GO:0055007	cardiac muscle cell differentiation	15/807	132/18670	0.00058729	0.008296731	0.006546988	15
BP	GO:0038063	collagen-activated tyrosine kinase receptor signaling pathway	4/807	10/18670	0.000590367	0.008296731	0.006546988	4
BP	GO:0060281	regulation of oocyte development	4/807	10/18670	0.000590367	0.008296731	0.006546988	4
BP	GO:1905879	regulation of oogenesis	4/807	10/18670	0.000590367	0.008296731	0.006546988	4
BP	GO:0055017	cardiac muscle tissue growth	13/807	105/18670	0.000592698	0.00830609	0.006554372	13
BP	GO:0032409	regulation of transporter activity	25/807	283/18670	0.000595003	0.00831504	0.006561435	25
BP	GO:0006749	glutathione metabolic process	9/807	56/18670	0.000614808	0.008567814	0.0067609	9
BP	GO:0070372	regulation of ERK1 and ERK2 cascade	26/807	300/18670	0.000622519	0.008651103	0.006826624	26
BP	GO:0022898	regulation of transmembrane transporter activity	24/807	268/18670	0.000625702	0.008657545	0.006831707	24
BP	GO:0021700	developmental maturation	25/807	284/18670	0.000626453	0.008657545	0.006831707	25
BP	GO:0002088	lens development in camera-type eye	11/807	80/18670	0.000632195	0.008712768	0.006875284	11
BP	GO:0042391	regulation of membrane potential	34/807	434/18670	0.000634935	0.008726426	0.006886062	34
BP	GO:0003203	endocardial cushion morphogenesis	7/807	35/18670	0.000639662	0.008767231	0.006918261	7

BP	GO:0050918	positive chemotaxis	10/807	68/18670	0.000644918	0.008815058	0.006956002	10
BP	GO:0033273	response to vitamin	12/807	93/18670	0.000654854	0.008926416	0.007043875	12
BP	GO:0002064	epithelial cell development	20/807	207/18670	0.000674394	0.009166381	0.007233232	20
BP	GO:0051260	protein homooligomerization	29/807	351/18670	0.000676133	0.009166381	0.007233232	29
BP	GO:0072089	stem cell proliferation	14/807	120/18670	0.00067952	0.009187332	0.007249765	14
BP	GO:0051924	regulation of calcium ion transport	23/807	254/18670	0.000690962	0.009316777	0.00735191	23
BP	GO:0045927	positive regulation of growth	24/807	270/18670	0.00069524	0.009349201	0.007377496	24
BP	GO:0060043	regulation of cardiac muscle cell proliferation	9/807	57/18670	0.00070254	0.009384663	0.00740548	9
BP	GO:0014855	striated muscle cell proliferation	11/807	81/18670	0.000703521	0.009384663	0.00740548	11
BP	GO:0030512	negative regulation of transforming growth factor beta receptor signaling pathway	11/807	81/18670	0.000703521	0.009384663	0.00740548	11
BP	GO:1901654	response to ketone	19/807	193/18670	0.000724421	0.00962688	0.007596614	19
BP	GO:0071300	cellular response to retinoic acid	10/807	69/18670	0.000725538	0.00962688	0.007596614	10
BP	GO:0030595	leukocyte chemotaxis	21/807	224/18670	0.000743169	0.009834673	0.007760585	21
CC	GO:0062023	collagen-containing extracellular matrix	92/835	406/19717	1.94437E-41	9.39131E-39	7.63422E-39	92
CC	GO:0005604	basement membrane	27/835	95/19717	1.3761E-15	3.32328E-13	2.7015E-13	27
CC	GO:0005581	collagen trimer	24/835	87/19717	1.08752E-13	1.75091E-11	1.42331E-11	24
CC	GO:0042383	sarcolemma	29/835	136/19717	4.22477E-13	5.10141E-11	4.14695E-11	29
CC	GO:0043292	contractile fiber	35/835	234/19717	7.86051E-11	7.19499E-09	5.84882E-09	35
CC	GO:0005788	endoplasmic reticulum lumen	41/835	309/19717	8.93788E-11	7.19499E-09	5.84882E-09	41
CC	GO:0045121	membrane raft	40/835	315/19717	5.75506E-10	3.709E-08	3.01506E-08	40
CC	GO:0098857	membrane microdomain	40/835	316/19717	6.32825E-10	3.709E-08	3.01506E-08	40
CC	GO:0030055	cell-substrate junction	47/835	412/19717	6.91119E-10	3.709E-08	3.01506E-08	47
CC	GO:0005925	focal adhesion	46/835	405/19717	1.21289E-09	5.85825E-08	4.76218E-08	46
CC	GO:0031674	I band	25/835	143/19717	1.511E-09	6.63466E-08	5.39332E-08	25
CC	GO:0030016	myofibril	32/835	224/19717	1.65749E-09	6.6714E-08	5.42319E-08	32

CC	GO:0098589	membrane region	40/835	328/19717	1.90973E-09	7.09538E-08	5.76785E-08	40
CC	GO:0030018	Z disc	23/835	132/19717	7.2732E-09	2.50925E-07	2.03978E-07	23
CC	GO:0005911	cell-cell junction	45/835	416/19717	8.44542E-09	2.71943E-07	2.21063E-07	45
CC	GO:0030017	sarcomere	29/835	204/19717	1.07531E-08	3.24608E-07	2.63874E-07	29
CC	GO:0005901	caveola	15/835	80/19717	1.13011E-06	3.21084E-05	2.61009E-05	15
CC	GO:0043025	neuronal cell body	45/835	497/19717	1.45352E-06	3.90027E-05	3.17053E-05	45
CC	GO:0044853	plasma membrane raft	17/835	109/19717	3.23996E-06	8.23633E-05	6.69533E-05	17
CC	GO:0014704	intercalated disc	11/835	50/19717	6.04456E-06	0.000145976	0.000118664	11
CC	GO:0098644	complex of collagen trimers	7/835	19/19717	7.67736E-06	0.000176579	0.000143542	7
CC	GO:0008305	integrin complex	8/835	31/19717	3.31173E-05	0.000727076	0.000591042	8
CC	GO:0044291	cell-cell contact zone	12/835	71/19717	3.93983E-05	0.000827364	0.000672566	12
CC	GO:0030315	T-tubule	10/835	52/19717	5.5209E-05	0.001111081	0.0009032	10
CC	GO:0098636	protein complex involved in cell adhesion	8/835	34/19717	6.80967E-05	0.001315628	0.001069476	8
CC	GO:0016010	dystrophin-associated glycoprotein complex	6/835	19/19717	9.56612E-05	0.001650156	0.001341415	6
CC	GO:0043034	costamere	6/835	19/19717	9.56612E-05	0.001650156	0.001341415	6
CC	GO:0090665	glycoprotein complex	6/835	19/19717	9.56612E-05	0.001650156	0.001341415	6
CC	GO:0031093	platelet alpha granule lumen	11/835	67/19717	0.00010793	0.001797593	0.001461267	11
CC	GO:0042827	platelet dense granule	6/835	21/19717	0.000177915	0.002864436	0.002328505	6
CC	GO:0031091	platelet alpha granule	12/835	91/19717	0.00044813	0.006936931	0.005639044	12
CC	GO:0042641	actomyosin	11/835	79/19717	0.000478834	0.006936931	0.005639044	11
CC	GO:0001725	stress fiber	10/835	67/19717	0.000488314	0.006936931	0.005639044	10
CC	GO:0097517	contractile actin filament bundle	10/835	67/19717	0.000488314	0.006936931	0.005639044	10
CC	GO:0001527	microfibril	4/835	10/19717	0.000546438	0.007540841	0.006129964	4
MF	GO:0005201	extracellular matrix structural constituent	50/792	163/17696	1.93333E-28	1.5834E-25	1.35943E-25	50
MF	GO:0005539	glycosaminoglycan binding	44/792	229/17696	1.62404E-16	6.65046E-14	5.70979E-14	44

MF	GO:0005518	collagen binding	22/792	67/17696	6.28997E-14	1.71716E-11	1.47428E-11	22
MF	GO:0005178	integrin binding	29/792	132/17696	7.20773E-13	1.47578E-10	1.26704E-10	29
MF	GO:1901681	sulfur compound binding	38/792	250/17696	3.56562E-11	5.84048E-09	5.01438E-09	38
MF	GO:0030020	extracellular matrix structural constituent conferring tensile strength	15/792	41/17696	1.0849E-10	1.48089E-08	1.27143E-08	15
MF	GO:0008201	heparin binding	29/792	169/17696	4.18117E-10	4.89197E-08	4.20003E-08	29
MF	GO:0050840	extracellular matrix binding	15/792	57/17696	1.93017E-08	1.97602E-06	1.69652E-06	15
MF	GO:0019199	transmembrane receptor protein kinase activity	15/792	79/17696	1.88263E-06	0.00017132	0.000147088	15
MF	GO:0030021	extracellular matrix structural constituent conferring compression resistance	8/792	22/17696	2.83986E-06	0.000232585	0.000199687	8
MF	GO:1900750	oligopeptide binding	6/792	12/17696	5.7799E-06	0.00043034	0.000369471	6
MF	GO:0015267	channel activity	43/792	474/17696	9.11904E-06	0.000562061	0.000482561	43
MF	GO:0098631	cell adhesion mediator activity	12/792	59/17696	9.55985E-06	0.000562061	0.000482561	12
MF	GO:0022803	passive transmembrane transporter activity	43/792	475/17696	9.60788E-06	0.000562061	0.000482561	43
MF	GO:0003779	actin binding	40/792	431/17696	1.09584E-05	0.00059833	0.0005137	40
MF	GO:0048018	receptor ligand activity	42/792	482/17696	3.01604E-05	0.001543835	0.00132547	42
MF	GO:0030546	signaling receptor activator activity	42/792	487/17696	3.83282E-05	0.001830224	0.001571351	42
MF	GO:0019838	growth factor binding	18/792	137/17696	4.02247E-05	0.001830224	0.001571351	18
MF	GO:0043295	glutathione binding	5/792	11/17696	6.53845E-05	0.002520932	0.002164363	5
MF	GO:0048407	platelet-derived growth factor binding	5/792	11/17696	6.53845E-05	0.002520932	0.002164363	5
MF	GO:0097493	structural molecule activity conferring elasticity	5/792	11/17696	6.53845E-05	0.002520932	0.002164363	5
MF	GO:0005216	ion channel activity	38/792	435/17696	6.77173E-05	0.002520932	0.002164363	38
MF	GO:0016247	channel regulator activity	18/792	144/17696	7.81052E-05	0.002781224	0.002387838	18
MF	GO:0061134	peptidase regulator activity	23/792	219/17696	0.000132876	0.004534402	0.003893041	23

MF	GO:0046873	metal ion transmembrane transporter activity	37/792	439/17696	0.000173945	0.005698452	0.004892444	37
MF	GO:0046332	SMAD binding	12/792	80/17696	0.000217603	0.006854479	0.005884959	12
MF	GO:0099106	ion channel regulator activity	15/792	118/17696	0.000250165	0.007514417	0.006451553	15
MF	GO:0005516	calmodulin binding	21/792	200/17696	0.000256903	0.007514417	0.006451553	21
MF	GO:0015079	potassium ion transmembrane transporter activity	18/792	159/17696	0.000277101	0.007590036	0.006516476	18
MF	GO:0005109	frizzled binding	8/792	39/17696	0.000278023	0.007590036	0.006516476	8
MF	GO:0098632	cell-cell adhesion mediator activity	9/792	50/17696	0.000330849	0.008740815	0.007504485	9
MF	GO:0001664	G protein-coupled receptor binding	26/792	280/17696	0.000365335	0.009013288	0.007738418	26
MF	GO:0005024	transforming growth factor beta-activated receptor activity	5/792	15/17696	0.000365853	0.009013288	0.007738418	5
MF	GO:0008083	growth factor activity	18/792	163/17696	0.000376315	0.009013288	0.007738418	18
MF	GO:0005267	potassium channel activity	15/792	123/17696	0.000394409	0.009013288	0.007738418	15
MF	GO:0004714	transmembrane receptor protein tyrosine kinase activity	10/792	62/17696	0.000396188	0.009013288	0.007738418	10

GO: Gene Ontology; DEGs: differentially expressed genes.

Table S2b. KEGG pathway enrichment of DEGs

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	Count
hsa04510	Focal adhesion	36/413	201/8049	2.71567E-11	7.63103E-09	6.48902E-09	36
hsa04512	ECM-receptor interaction	21/413	88/8049	2.0415E-09	2.8683E-07	2.43905E-07	21
hsa05412	Arrhythmogenic right ventricular cardiomyopathy	18/413	77/8049	4.1768E-08	3.91227E-06	3.32678E-06	18
hsa05414	Dilated cardiomyopathy	20/413	96/8049	5.90121E-08	4.1456E-06	3.5252E-06	20
hsa05410	Hypertrophic cardiomyopathy	19/413	90/8049	1.01608E-07	5.71036E-06	4.85579E-06	19
hsa04022	cGMP-PKG signaling pathway	25/413	167/8049	1.15445E-06	5.40668E-05	4.59755E-05	25
hsa04974	Protein digestion and absorption	17/413	95/8049	5.41068E-06	0.0002172	0.000184695	17
hsa04270	Vascular smooth muscle contraction	20/413	135/8049	1.61004E-05	0.000565526	0.000480893	20
hsa04350	TGF-beta signaling pathway	16/413	94/8049	1.9736E-05	0.000616201	0.000523985	16
hsa04151	PI3K-Akt signaling pathway	37/413	354/8049	2.51642E-05	0.000707115	0.000601293	37
hsa04310	Wnt signaling pathway	21/413	160/8049	6.35865E-05	0.001624347	0.001381257	21
hsa00480	Glutathione metabolism	11/413	57/8049	0.000123309	0.002677615	0.002276901	11
hsa05205	Proteoglycans in cancer	24/413	205/8049	0.000123875	0.002677615	0.002276901	24
hsa04020	Calcium signaling pathway	23/413	201/8049	0.000240454	0.004826265	0.004103997	23

KEGG: Kyoto Encyclopedia of Genes and Genomes; DEGs: differentially expressed genes.