

Table S3a. GO term enrichment of MCODE 1

ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	Count
BP	GO:0030198	extracellular matrix organization	24/25	368/18670	1.36963E-40	4.2187E-38	2.69066E-38	24
BP	GO:0043062	extracellular structure organization	24/25	369/18670	1.46483E-40	4.2187E-38	2.69066E-38	24
BP	GO:0001704	formation of primary germ layer	9/25	121/18670	2.79182E-14	5.3603E-12	3.41876E-12	9
BP	GO:0035987	endodermal cell differentiation	7/25	45/18670	1.34804E-13	1.94117E-11	1.23807E-11	7
BP	GO:0001706	endoderm formation	7/25	50/18670	2.95463E-13	3.40373E-11	2.17087E-11	7
BP	GO:0007229	integrin-mediated signaling pathway	8/25	103/18670	6.51232E-13	6.25182E-11	3.98737E-11	8
BP	GO:0007369	gastrulation	9/25	185/18670	1.34988E-12	1.11076E-10	7.08431E-11	9
BP	GO:0007492	endoderm development	7/25	76/18670	6.32618E-12	4.55485E-10	2.90505E-10	7
BP	GO:0031589	cell-substrate adhesion	10/25	354/18670	1.34364E-11	8.59931E-10	5.48457E-10	10
BP	GO:0007160	cell-matrix adhesion	8/25	225/18670	3.56206E-10	2.05175E-08	1.30859E-08	8
BP	GO:0038065	collagen-activated signaling pathway	4/25	13/18670	1.77276E-09	9.28283E-08	5.92052E-08	4
BP	GO:0071230	cellular response to amino acid stimulus	5/25	68/18670	2.77086E-08	1.33001E-06	8.48272E-07	5
BP	GO:0001101	response to acid chemical	7/25	343/18670	2.40298E-07	1.04065E-05	6.63717E-06	7
BP	GO:0038063	collagen-activated tyrosine kinase receptor signaling pathway	3/25	10/18670	2.52935E-07	1.04065E-05	6.63717E-06	3
BP	GO:0043200	response to amino acid	5/25	113/18670	3.5838E-07	1.37618E-05	8.77716E-06	5
BP	GO:0070208	protein heterotrimerization	3/25	13/18670	6.01232E-07	2.16443E-05	1.38046E-05	3
BP	GO:0030199	collagen fibril organization	4/25	54/18670	7.55683E-07	2.56043E-05	1.63302E-05	4
BP	GO:0003414	chondrocyte morphogenesis involved in endochondral bone morphogenesis	3/25	18/18670	1.70784E-06	4.91857E-05	3.13702E-05	3
BP	GO:0003429	growth plate cartilage chondrocyte morphogenesis	3/25	18/18670	1.70784E-06	4.91857E-05	3.13702E-05	3
BP	GO:0090171	chondrocyte morphogenesis	3/25	18/18670	1.70784E-06	4.91857E-05	3.13702E-05	3
BP	GO:0003422	growth plate cartilage morphogenesis	3/25	19/18670	2.02626E-06	5.55775E-05	3.54469E-05	3
BP	GO:0060350	endochondral bone morphogenesis	4/25	73/18670	2.55667E-06	6.69384E-05	4.26928E-05	4

BP	GO:0003418	growth plate cartilage chondrocyte differentiation	3/25	24/18670	4.21369E-06	0.000101129	6.4499E-05	3
BP	GO:0003433	chondrocyte development involved in endochondral bone morphogenesis	3/25	24/18670	4.21369E-06	0.000101129	6.4499E-05	3
BP	GO:0071711	basement membrane organization	3/25	26/18670	5.40328E-06	0.000124492	7.93998E-05	3
BP	GO:0071229	cellular response to acid chemical	5/25	209/18670	7.419E-06	0.00016157	0.000103048	5
BP	GO:0060536	cartilage morphogenesis	3/25	29/18670	7.57358E-06	0.00016157	0.000103048	3
BP	GO:0003413	chondrocyte differentiation involved in endochondral bone morphogenesis	3/25	30/18670	8.40765E-06	0.000172957	0.000110311	3
BP	GO:0060348	bone development	5/25	217/18670	8.90376E-06	0.000176847	0.000112792	5
BP	GO:0003417	growth plate cartilage development	3/25	36/18670	1.47077E-05	0.000280677	0.000179013	3
BP	GO:0060349	bone morphogenesis	4/25	114/18670	1.51059E-05	0.000280677	0.000179013	4
BP	GO:0032963	collagen metabolic process	4/25	115/18670	1.56361E-05	0.00028145	0.000179507	4
BP	GO:0061448	connective tissue development	5/25	273/18670	2.69412E-05	0.000458921	0.000292696	5
BP	GO:0003416	endochondral bone growth	3/25	44/18670	2.70891E-05	0.000458921	0.000292696	3
BP	GO:0060351	cartilage development involved in endochondral bone morphogenesis	3/25	47/18670	3.30781E-05	0.00052925	0.000337551	3
BP	GO:0098868	bone growth	3/25	47/18670	3.30781E-05	0.00052925	0.000337551	3
BP	GO:0002063	chondrocyte development	3/25	48/18670	3.52522E-05	0.00054879	0.000350014	3
BP	GO:0050900	leukocyte migration	6/25	499/18670	4.06445E-05	0.000616085	0.000392934	6
BP	GO:0070206	protein trimerization	3/25	54/18670	5.02874E-05	0.000742706	0.000473692	3
BP	GO:0033627	cell adhesion mediated by integrin	3/25	68/18670	0.000100356	0.001445123	0.000921689	3
BP	GO:0045765	regulation of angiogenesis	5/25	383/18670	0.00013405	0.001883242	0.001201118	5
BP	GO:0001503	ossification	5/25	398/18670	0.00016042	0.002139995	0.001364872	5
BP	GO:0051216	cartilage development	4/25	209/18670	0.000160503	0.002139995	0.001364872	4
BP	GO:0009612	response to mechanical stimulus	4/25	210/18670	0.000163472	0.002139995	0.001364872	4
BP	GO:0010810	regulation of cell-substrate adhesion	4/25	215/18670	0.000178918	0.002290148	0.001460639	4
BP	GO:0043588	skin development	5/25	419/18670	0.000203823	0.002552219	0.001627786	5

BP	GO:1901342	regulation of vasculature development	5/25	422/18670	0.000210691	0.002582089	0.001646837	5
BP	GO:0035313	wound healing, spreading of epidermal cells	2/25	17/18670	0.000231246	0.002774952	0.001769843	2
BP	GO:0048705	skeletal system morphogenesis	4/25	239/18670	0.000268117	0.003151739	0.002010155	4
BP	GO:0007044	cell-substrate junction assembly	3/25	97/18670	0.000287779	0.003250208	0.002072958	3
BP	GO:0150115	cell-substrate junction organization	3/25	97/18670	0.000287779	0.003250208	0.002072958	3
BP	GO:0071560	cellular response to transforming growth factor beta stimulus	4/25	249/18670	0.000313369	0.003471163	0.002213881	4
BP	GO:0048745	smooth muscle tissue development	2/25	20/18670	0.00032227	0.003502402	0.002233805	2
BP	GO:0071559	response to transforming growth factor beta	4/25	255/18670	0.000343019	0.003658869	0.002333599	4
BP	GO:0045992	negative regulation of embryonic development	2/25	26/18670	0.000548543	0.005660306	0.0036101	2
BP	GO:0010811	positive regulation of cell-substrate adhesion	3/25	121/18670	0.000550308	0.005660306	0.0036101	3
BP	GO:0002062	chondrocyte differentiation	3/25	123/18670	0.000577266	0.005755422	0.003670764	3
BP	GO:0072001	renal system development	4/25	293/18670	0.000579539	0.005755422	0.003670764	4
BP	GO:0051291	protein heterooligomerization	3/25	128/18670	0.000648326	0.00632942	0.004036856	3
BP	GO:0044319	wound healing, spreading of cells	2/25	31/18670	0.000781626	0.007380598	0.004707289	2
BP	GO:0090505	epiboly involved in wound healing	2/25	31/18670	0.000781626	0.007380598	0.004707289	2
BP	GO:0090504	epiboly	2/25	32/18670	0.000833051	0.00773931	0.004936073	2
BP	GO:0001655	urogenital system development	4/25	330/18670	0.000904025	0.008265371	0.005271591	4
BP	GO:0010922	positive regulation of phosphatase activity	2/25	34/18670	0.000940676	0.008466088	0.005399607	2
BP	GO:0048333	mesodermal cell differentiation	2/25	35/18670	0.000996869	0.008833796	0.005634128	2
BP	GO:0010470	regulation of gastrulation	2/25	42/18670	0.001434274	0.012517298	0.007983438	2
BP	GO:0016525	negative regulation of angiogenesis	3/25	173/18670	0.001547899	0.013307309	0.008487301	3

BP	GO:2000181	negative regulation of blood vessel morphogenesis	3/25	175/18670	0.001599704	0.013550432	0.008642362	3
BP	GO:0045785	positive regulation of cell adhesion	4/25	403/18670	0.001888805	0.01576742	0.01005634	4
BP	GO:1901343	negative regulation of vasculature development	3/25	187/18670	0.001933475	0.015909737	0.01014711	3
BP	GO:0007517	muscle organ development	4/25	410/18670	0.002011273	0.016316808	0.010406736	4
BP	GO:0032964	collagen biosynthetic process	2/25	53/18670	0.002274908	0.018199263	0.011607352	2
BP	GO:0007179	transforming growth factor beta receptor signaling pathway	3/25	199/18670	0.002307831	0.018209735	0.011614031	3
BP	GO:0002011	morphogenesis of an epithelial sheet	2/25	55/18670	0.002447539	0.019017131	0.012128981	2
BP	GO:0035265	organ growth	3/25	204/18670	0.002476189	0.019017131	0.012128981	3
BP	GO:0034284	response to monosaccharide	3/25	207/18670	0.002580773	0.019559539	0.012474925	3
BP	GO:0097529	myeloid leukocyte migration	3/25	210/18670	0.002688063	0.020069522	0.012800188	3
BP	GO:0035306	positive regulation of dephosphorylation	2/25	58/18670	0.002717748	0.020069522	0.012800188	2
BP	GO:0018149	peptide cross-linking	2/25	60/18670	0.00290535	0.021183308	0.013510553	2
BP	GO:0034113	heterotypic cell-cell adhesion	2/25	61/18670	0.003001378	0.02160992	0.013782643	2
BP	GO:0014823	response to activity	2/25	65/18670	0.003400251	0.024179562	0.015421541	2
BP	GO:0009743	response to carbohydrate	3/25	230/18670	0.003474227	0.02440433	0.015564896	3
BP	GO:0001707	mesoderm formation	2/25	75/18670	0.004499428	0.031224948	0.019915034	2
BP	GO:0090596	sensory organ morphogenesis	3/25	256/18670	0.004688493	0.032096808	0.0204711	3
BP	GO:0048332	mesoderm morphogenesis	2/25	77/18670	0.004736508	0.032096808	0.0204711	2
BP	GO:0048041	focal adhesion assembly	2/25	81/18670	0.005227674	0.035013259	0.02233119	2
BP	GO:0001822	kidney development	3/25	278/18670	0.005894488	0.039025573	0.024890214	3
BP	GO:0010632	regulation of epithelial cell migration	3/25	291/18670	0.006687063	0.043688884	0.027864438	3
BP	GO:0090287	regulation of cellular response to growth factor stimulus	3/25	292/18670	0.006750539	0.043688884	0.027864438	3
BP	GO:0033273	response to vitamin	2/25	93/18670	0.006835103	0.043744661	0.027900012	2

CC	GO:0062023	collagen-containing extracellular matrix	17/25	406/19717	1.43486E-23	9.32657E-22	6.0415E-22	17
CC	GO:0005581	collagen trimer	12/25	87/19717	1.22667E-22	3.98667E-21	2.58246E-21	12
CC	GO:0098644	complex of collagen trimers	7/25	19/19717	1.04482E-16	2.26378E-15	1.46641E-15	7
CC	GO:0005604	basement membrane	9/25	95/19717	1.81946E-15	2.95662E-14	1.91522E-14	9
CC	GO:0008305	integrin complex	7/25	31/19717	5.40047E-15	7.02061E-14	4.54776E-14	7
CC	GO:0098636	protein complex involved in cell adhesion	7/25	34/19717	1.10219E-14	1.19403E-13	7.73464E-14	7
CC	GO:0005788	endoplasmic reticulum lumen	11/25	309/19717	4.30082E-14	3.99362E-13	2.58696E-13	11
CC	GO:0005583	fibrillar collagen trimer	4/25	11/19717	6.59163E-10	4.76062E-09	3.0838E-09	4
CC	GO:0098643	banded collagen fibril	4/25	11/19717	6.59163E-10	4.76062E-09	3.0838E-09	4
CC	GO:0098802	plasma membrane signaling receptor complex	7/25	295/19717	5.96497E-08	3.87723E-07	2.51157E-07	7
CC	GO:0005925	focal adhesion	6/25	405/19717	9.20624E-06	5.44005E-05	3.52392E-05	6
CC	GO:0030055	cell-substrate junction	6/25	412/19717	1.01501E-05	5.49798E-05	3.56145E-05	6
CC	GO:0045178	basal part of cell	3/25	51/19717	3.60213E-05	0.000180106	0.000116668	3
CC	GO:0042383	sarcolemma	3/25	136/19717	0.000660596	0.003067051	0.001986754	3
CC	GO:0005796	Golgi lumen	2/25	102/19717	0.007356878	0.031879806	0.020650887	2
CC	GO:0043204	perikaryon	2/25	134/19717	0.012416287	0.04991822	0.032335689	2
CC	GO:0009897	external side of plasma membrane	3/25	393/19717	0.013055534	0.04991822	0.032335689	3
MF	GO:0005201	extracellular matrix structural constituent	16/25	163/17696	2.40507E-27	1.15443E-25	4.81014E-26	16
MF	GO:0030020	extracellular matrix structural constituent conferring tensile strength	11/25	41/17696	1.0354E-23	2.48497E-22	1.0354E-22	11
MF	GO:0048407	platelet-derived growth factor binding	5/25	11/17696	1.68879E-12	2.70207E-11	1.12586E-11	5
MF	GO:0005518	collagen binding	7/25	67/17696	3.67961E-12	4.41553E-11	1.8398E-11	7
MF	GO:0050840	extracellular matrix binding	6/25	57/17696	1.43886E-10	1.38131E-09	5.75545E-10	6
MF	GO:0005178	integrin binding	6/25	132/17696	2.42233E-08	1.93786E-07	8.07442E-08	6

MF	GO:0019838	growth factor binding	5/25	137/17696	1.21242E-06	8.3137E-06	3.46404E-06	5
MF	GO:0043236	laminin binding	3/25	29/17696	8.88307E-06	5.32984E-05	2.22077E-05	3
MF	GO:0043394	proteoglycan binding	3/25	36/17696	1.72448E-05	9.19722E-05	3.83217E-05	3
MF	GO:0050839	cell adhesion molecule binding	6/25	499/17696	5.47262E-05	0.000262686	0.000109452	6
MF	GO:0046332	SMAD binding	3/25	80/17696	0.000190462	0.000831107	0.000346295	3
MF	GO:0002020	protease binding	3/25	128/17696	0.000756775	0.0030271	0.001261292	3
MF	GO:0098631	cell adhesion mediator activity	2/25	59/17696	0.003120716	0.011522645	0.004801102	2
MF	GO:0001618	virus receptor activity	2/25	74/17696	0.004863013	0.015561642	0.006484018	2
MF	GO:0140272	exogenous protein binding	2/25	74/17696	0.004863013	0.015561642	0.006484018	2
MF	GO:0097493	structural molecule activity conferring elasticity	1/25	11/17696	0.015435258	0.046305773	0.019294072	1

GO: Gene Ontology.

Table S3b. KEGG pathway enrichment of MCODE 1

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	Count
hsa04512	ECM-receptor interaction	15/21	88/8049	5.62004E-26	1.57361E-24	6.50741E-25	15
hsa04510	Focal adhesion	15/21	201/8049	2.58391E-20	3.61747E-19	1.49595E-19	15
hsa05165	Human papillomavirus infection	15/21	331/8049	5.17313E-17	4.82825E-16	1.99665E-16	15
hsa04974	Protein digestion and absorption	11/21	95/8049	1.0943E-16	7.66009E-16	3.16771E-16	11
hsa04151	PI3K-Akt signaling pathway	15/21	354/8049	1.4234E-16	7.97104E-16	3.29629E-16	15
hsa05412	Arrhythmogenic right ventricular cardiomyopathy	7/21	77/8049	5.80062E-10	2.70696E-09	1.11942E-09	7
hsa05410	Hypertrophic cardiomyopathy	7/21	90/8049	1.76657E-09	7.06629E-09	2.92215E-09	7
hsa05414	Dilated cardiomyopathy	7/21	96/8049	2.79239E-09	9.77337E-09	4.04162E-09	7
hsa04810	Regulation of actin cytoskeleton	7/21	214/8049	7.2114E-07	2.24355E-06	9.27783E-07	7
hsa04933	AGE-RAGE signaling pathway in diabetic complications	5/21	100/8049	4.65206E-06	1.30258E-05	5.38659E-06	5
hsa05146	Amoebiasis	5/21	102/8049	5.1295E-06	1.30569E-05	5.39947E-06	5
hsa04926	Relaxin signaling pathway	5/21	129/8049	1.62031E-05	3.78073E-05	1.56346E-05	5
hsa05222	Small cell lung cancer	4/21	92/8049	8.24386E-05	0.00017756	7.34271E-05	4
hsa05205	Proteoglycans in cancer	5/21	205/8049	0.000148895	0.00029779	0.000123146	5
hsa04640	Hematopoietic cell lineage	3/21	99/8049	0.002043896	0.003815273	0.001577744	3
hsa04611	Platelet activation	3/21	124/8049	0.003875372	0.006781901	0.002804546	3
hsa04514	Cell adhesion molecules	3/21	149/8049	0.006474456	0.010663809	0.004409846	3

KEGG: Kyoto Encyclopedia of Genes and Genomes.

Table S3c. GO term enrichment of MCODE 2

ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	Count
BP	GO:0043687	post-translational protein modification	17/21	361/18670	2.8295E-26	2.7616E-23	1.70366E-23	17
BP	GO:0030198	extracellular matrix organization	10/21	368/18670	2.27994E-12	7.61987E-10	4.70078E-10	10
BP	GO:0043062	extracellular structure organization	10/21	369/18670	2.34217E-12	7.61987E-10	4.70078E-10	10
BP	GO:0031589	cell-substrate adhesion	6/21	354/18670	1.90012E-06	0.00046363	0.000286019	6
BP	GO:0001503	ossification	6/21	398/18670	3.7393E-06	0.000729911	0.00045029	6
BP	GO:0071295	cellular response to vitamin	3/21	32/18670	5.95676E-06	0.000968967	0.000597767	3
BP	GO:0085029	extracellular matrix assembly	3/21	41/18670	1.27192E-05	0.001773415	0.00109404	3
BP	GO:1900115	extracellular regulation of signal transduction	2/21	11/18670	6.5871E-05	0.00670084	0.004133823	2
BP	GO:1900116	extracellular negative regulation of signal transduction	2/21	11/18670	6.5871E-05	0.00670084	0.004133823	2
BP	GO:0060350	endochondral bone morphogenesis	3/21	73/18670	7.25125E-05	0.00670084	0.004133823	3
BP	GO:0031670	cellular response to nutrient	3/21	74/18670	7.55218E-05	0.00670084	0.004133823	3
BP	GO:0060348	bone development	4/21	217/18670	9.09643E-05	0.007398428	0.004564173	4
BP	GO:0001649	osteoblast differentiation	4/21	225/18670	0.000104629	0.007855256	0.004845995	4
BP	GO:0090092	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	4/21	241/18670	0.00013636	0.009096203	0.005611549	4
BP	GO:0030510	regulation of BMP signaling pathway	3/21	91/18670	0.000139804	0.009096203	0.005611549	3
BP	GO:0033273	response to vitamin	3/21	93/18670	0.000149118	0.009096203	0.005611549	3
BP	GO:0060602	branch elongation of an epithelium	2/21	20/18670	0.000226169	0.012984775	0.008010452	2
BP	GO:0060349	bone morphogenesis	3/21	114/18670	0.000272161	0.013876416	0.008560516	3
BP	GO:0007162	negative regulation of cell adhesion	4/21	289/18670	0.000273387	0.013876416	0.008560516	4
BP	GO:0090287	regulation of cellular response to growth factor stimulus	4/21	292/18670	0.000284353	0.013876416	0.008560516	4

BP	GO:0071305	cellular response to vitamin D negative regulation of transmembrane	2/21	23/18670	0.00030055	0.013968423	0.008617276	2
BP	GO:0090101	receptor protein serine/threonine kinase signaling pathway	3/21	126/18670	0.000365224	0.015599388	0.009623436	3
BP	GO:0002576	platelet degranulation	3/21	128/18670	0.000382484	0.015599388	0.009623436	3
BP	GO:0060740	prostate gland epithelium morphogenesis	2/21	26/18670	0.000385298	0.015599388	0.009623436	2
BP	GO:0042476	odontogenesis	3/21	132/18670	0.000418564	0.015599388	0.009623436	3
BP	GO:0001958	endochondral ossification	2/21	28/18670	0.000447523	0.015599388	0.009623436	2
BP	GO:0036075	replacement ossification	2/21	28/18670	0.000447523	0.015599388	0.009623436	2
BP	GO:0060512	prostate gland morphogenesis	2/21	28/18670	0.000447523	0.015599388	0.009623436	2
BP	GO:0060441	epithelial tube branching involved in lung morphogenesis	2/21	29/18670	0.000480348	0.016166179	0.009973096	2
BP	GO:0003401	axis elongation	2/21	31/18670	0.000549406	0.017581957	0.010846505	2
BP	GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	4/21	349/18670	0.000558443	0.017581957	0.010846505	4
BP	GO:0030509	BMP signaling pathway	3/21	157/18670	0.000694194	0.021172921	0.013061811	3
BP	GO:0033280	response to vitamin D	2/21	37/18670	0.000783698	0.023178464	0.014299053	2
BP	GO:0090288	negative regulation of cellular response to growth factor stimulus	3/21	166/18670	0.000816086	0.023426475	0.014452053	3
BP	GO:0071772	response to BMP	3/21	170/18670	0.000874359	0.023704836	0.014623777	3
BP	GO:0071773	cellular response to BMP stimulus	3/21	170/18670	0.000874359	0.023704836	0.014623777	3
BP	GO:2000107	negative regulation of leukocyte apoptotic process	2/21	47/18670	0.001263449	0.03298854	0.020350997	2
BP	GO:0030850	prostate gland development	2/21	48/18670	0.001317489	0.03298854	0.020350997	2
BP	GO:0001763	morphogenesis of a branching structure	3/21	196/18670	0.00131819	0.03298854	0.020350997	3

BP	GO:0060425	lung morphogenesis	2/21	50/18670	0.001428847	0.03401352	0.020983319	2
BP	GO:0060976	coronary vasculature development	2/21	50/18670	0.001428847	0.03401352	0.020983319	2
BP	GO:0030514	negative regulation of BMP signaling pathway	2/21	52/18670	0.00154456	0.035892633	0.022142565	2
BP	GO:0006888	endoplasmic reticulum to Golgi vesicle-mediated transport	3/21	212/18670	0.001650832	0.037470045	0.023115688	3
BP	GO:0007584	response to nutrient	3/21	219/18670	0.001811463	0.040181541	0.02478844	3
BP	GO:0007160	cell-matrix adhesion	3/21	225/18670	0.001956691	0.04243845	0.026180752	3
BP	GO:0031669	cellular response to nutrient levels	3/21	237/18670	0.002268562	0.048132976	0.029693768	3
BP	GO:0048705	skeletal system morphogenesis	3/21	239/18670	0.00232337	0.048247002	0.029764113	3
CC	GO:0005788	endoplasmic reticulum lumen	21/21	309/19717	6.31239E-39	3.02995E-37	2.12628E-37	21
CC	GO:0062023	collagen-containing extracellular matrix	11/21	406/19717	7.23299E-14	1.73592E-12	1.21819E-12	11
CC	GO:0005581	collagen trimer	4/21	87/19717	1.99829E-06	3.19726E-05	2.24369E-05	4
CC	GO:0005604	basement membrane	4/21	95/19717	2.84226E-06	3.41071E-05	2.39348E-05	4
CC	GO:0031093	platelet alpha granule lumen	3/21	67/19717	4.77409E-05	0.000386954	0.000271547	3
CC	GO:0001527	microfibril	2/21	10/19717	4.83693E-05	0.000386954	0.000271547	2
CC	GO:0031091	platelet alpha granule	3/21	91/19717	0.000119095	0.000816654	0.000573091	3
CC	GO:0034774	secretory granule lumen	4/21	321/19717	0.000331514	0.001707099	0.001197964	4
CC	GO:0060205	cytoplasmic vesicle lumen	4/21	325/19717	0.000347466	0.001707099	0.001197964	4
CC	GO:0031983	vesicle lumen	4/21	327/19717	0.000355646	0.001707099	0.001197964	4
CC	GO:0005796	Golgi lumen	2/21	102/19717	0.005219499	0.022775994	0.015983154	2
CC	GO:0043256	laminin complex	1/21	10/19717	0.010602214	0.042408855	0.0297606	1
CC	GO:0032280	symmetric synapse	1/21	11/19717	0.011656527	0.043039485	0.030203147	1
CC	GO:0005614	interstitial matrix	1/21	12/19717	0.01270977	0.043576356	0.030579899	1
MF	GO:0005201	extracellular matrix structural constituent	9/20	163/17696	5.88429E-14	5.06049E-12	3.03506E-12	9

MF	GO:0030020	extracellular matrix structural constituent conferring tensile strength	4/20	41/17696	1.1695E-07	5.02884E-06	3.01607E-06	4
MF	GO:0005539	glycosaminoglycan binding	4/20	229/17696	0.000112459	0.002928172	0.001756186	4
MF	GO:0048018	receptor ligand activity	5/20	482/17696	0.000162226	0.002928172	0.001756186	5
MF	GO:0030546	signaling receptor activator activity	5/20	487/17696	0.000170243	0.002928172	0.001756186	5
MF	GO:0005179	hormone activity	3/20	122/17696	0.000334527	0.004794886	0.002875758	3
MF	GO:0005178	integrin binding	3/20	132/17696	0.000421467	0.005178028	0.003105549	3
MF	GO:0008201	heparin binding	3/20	169/17696	0.000865587	0.00930506	0.005580758	3
MF	GO:0050840	extracellular matrix binding	2/20	57/17696	0.00186597	0.017830376	0.010693861	2
MF	GO:0005518	collagen binding	2/20	67/17696	0.002567566	0.020785423	0.012466166	2
MF	GO:1901681	sulfur compound binding	3/20	250/17696	0.002658601	0.020785423	0.012466166	3

GO: Gene Ontology.

Table S3d. KEGG pathway enrichment of MCODE 2

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	Count
hsa04350	TGF-beta signaling pathway	3/13	94/8049	0.000405307	0.004599453	0.003961252	3
hsa04974	Protein digestion and absorption	3/13	95/8049	0.000418132	0.004599453	0.003961252	3

KEGG: Kyoto Encyclopedia of Genes and Genomes.

Table S3e. GO term enrichment of MCODE 3

ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	Count
BP	GO:0006939	smooth muscle contraction	10/33	110/18670	2.74258E-15	3.48307E-12	2.03528E-12	10
BP	GO:0007204	positive regulation of cytosolic calcium ion concentration	12/33	319/18670	1.29664E-13	8.23369E-11	4.81123E-11	12
BP	GO:0006874	cellular calcium ion homeostasis	13/33	458/18670	3.60924E-13	1.26724E-10	7.4049E-11	13
BP	GO:0051480	regulation of cytosolic calcium ion concentration	12/33	357/18670	4.91743E-13	1.26724E-10	7.4049E-11	12
BP	GO:0055074	calcium ion homeostasis	13/33	471/18670	5.14964E-13	1.26724E-10	7.4049E-11	13
BP	GO:0006936	muscle contraction	12/33	363/18670	5.98694E-13	1.26724E-10	7.4049E-11	12
BP	GO:0072503	cellular divalent inorganic cation homeostasis	13/33	493/18670	9.18465E-13	1.66636E-10	9.73711E-11	13
BP	GO:0003012	muscle system process	12/33	472/18670	1.30055E-11	2.06462E-09	1.20643E-09	12
BP	GO:0007187	G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	9/33	256/18670	4.30877E-10	6.08015E-08	3.55284E-08	9
BP	GO:0014829	vascular smooth muscle contraction	5/33	25/18670	6.50923E-10	8.26672E-08	4.83053E-08	5
BP	GO:0007188	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	8/33	221/18670	3.65504E-09	3.99714E-07	2.33567E-07	8
BP	GO:0042310	vasoconstriction	6/33	76/18670	3.77683E-09	3.99714E-07	2.33567E-07	6
BP	GO:0097756	negative regulation of blood vessel diameter	6/33	84/18670	6.95285E-09	6.7924E-07	3.96904E-07	6
BP	GO:0003018	vascular process in circulatory system	7/33	175/18670	1.96068E-08	1.69236E-06	9.88906E-07	7
BP	GO:0007200	phospholipase C-activating G protein-coupled receptor signaling pathway	6/33	100/18670	1.99885E-08	1.69236E-06	9.88906E-07	6
BP	GO:0060326	cell chemotaxis	8/33	304/18670	4.39295E-08	3.4869E-06	2.03752E-06	8
BP	GO:0019932	second-messenger-mediated signaling	9/33	439/18670	4.73252E-08	3.53547E-06	2.0659E-06	9

BP	GO:0019935	cyclic-nucleotide-mediated signaling	7/33	212/18670	7.32987E-08	5.17163E-06	3.02196E-06	7
BP	GO:0035296	regulation of tube diameter	6/33	143/18670	1.69743E-07	1.06984E-05	6.25147E-06	6
BP	GO:0097746	regulation of blood vessel diameter	6/33	143/18670	1.69743E-07	1.06984E-05	6.25147E-06	6
BP	GO:0035150	regulation of tube size	6/33	144/18670	1.76903E-07	1.06984E-05	6.25147E-06	6
BP	GO:0007202	activation of phospholipase C activity	4/33	31/18670	2.46011E-07	1.42016E-05	8.29847E-06	4
BP	GO:0019933	cAMP-mediated signaling	6/33	184/18670	7.49736E-07	4.13985E-05	2.41906E-05	6
BP	GO:0014820	tonic smooth muscle contraction	3/33	11/18670	8.22161E-07	4.3506E-05	2.54221E-05	3
BP	GO:0010863	positive regulation of phospholipase C activity	4/33	43/18670	9.506E-07	4.82905E-05	2.82178E-05	4
BP	GO:1900274	regulation of phospholipase C activity	4/33	45/18670	1.14483E-06	5.57401E-05	3.25709E-05	4
BP	GO:0031032	actomyosin structure organization	6/33	199/18670	1.18503E-06	5.57401E-05	3.25709E-05	6
BP	GO:0150146	cell junction disassembly	3/33	15/18670	2.25626E-06	0.000102338	5.97995E-05	3
BP	GO:0030595	leukocyte chemotaxis	6/33	224/18670	2.35662E-06	0.000103204	6.03055E-05	6
BP	GO:0002576	platelet degranulation	5/33	128/18670	2.84925E-06	0.000120618	7.04815E-05	5
BP	GO:0010518	positive regulation of phospholipase activity	4/33	59/18670	3.43669E-06	0.000140793	8.22705E-05	4
BP	GO:0014821	phasic smooth muscle contraction	3/33	21/18670	6.5477E-06	0.000255102	0.000149065	3
BP	GO:0051017	actin filament bundle assembly	5/33	153/18670	6.82663E-06	0.000255102	0.000149065	5
BP	GO:0010517	regulation of phospholipase activity	4/33	70/18670	6.82951E-06	0.000255102	0.000149065	4
BP	GO:0060193	positive regulation of lipase activity	4/33	72/18670	7.64394E-06	0.000273093	0.000159578	4
BP	GO:0061572	actin filament bundle organization	5/33	157/18670	7.74121E-06	0.000273093	0.000159578	5
BP	GO:0051047	positive regulation of secretion	7/33	428/18670	8.0816E-06	0.000277396	0.000162092	7
BP	GO:0050886	endocrine process	4/33	84/18670	1.4124E-05	0.000472039	0.000275829	4
BP	GO:0008217	regulation of blood pressure	5/33	182/18670	1.58465E-05	0.000516029	0.000301533	5
BP	GO:0007193	adenylate cyclase-inhibiting G protein-coupled receptor signaling pathway	4/33	89/18670	1.77621E-05	0.000563945	0.000329533	4
BP	GO:0007568	aging	6/33	321/18670	1.84586E-05	0.000571766	0.000334103	6
BP	GO:0050900	leukocyte migration	7/33	499/18670	2.18313E-05	0.000660138	0.000385741	7

BP	GO:0032231	regulation of actin filament bundle assembly	4/33	97/18670	2.49563E-05	0.000715382	0.000418022	4
BP	GO:0030038	contractile actin filament bundle assembly	4/33	98/18670	2.59859E-05	0.000715382	0.000418022	4
BP	GO:0043149	stress fiber assembly	4/33	98/18670	2.59859E-05	0.000715382	0.000418022	4
BP	GO:0060191	regulation of lipase activity	4/33	98/18670	2.59859E-05	0.000715382	0.000418022	4
BP	GO:2001025	positive regulation of response to drug	3/33	33/18670	2.64747E-05	0.000715382	0.000418022	3
BP	GO:0010721	negative regulation of cell development	6/33	344/18670	2.72532E-05	0.000721076	0.00042135	6
BP	GO:0097529	myeloid leukocyte migration	5/33	210/18670	3.1526E-05	0.000817102	0.000477461	5
BP	GO:2001023	regulation of response to drug	4/33	106/18670	3.53829E-05	0.000898726	0.000525157	4
BP	GO:0071695	anatomical structure maturation	5/33	232/18670	5.07022E-05	0.001262583	0.000737771	5
BP	GO:0044060	regulation of endocrine process	3/33	44/18670	6.34195E-05	0.001548899	0.000905076	3
BP	GO:1903532	positive regulation of secretion by cell	6/33	403/18670	6.58687E-05	0.001578363	0.000922293	6
BP	GO:0060986	endocrine hormone secretion	3/33	47/18670	7.73663E-05	0.00181954	0.001063221	3
BP	GO:0046883	regulation of hormone secretion	5/33	262/18670	9.0143E-05	0.002061861	0.001204818	5
BP	GO:0050921	positive regulation of chemotaxis	4/33	135/18670	9.09167E-05	0.002061861	0.001204818	4
BP	GO:0007189	adenylate cyclase-activating G protein-coupled receptor signaling pathway	4/33	139/18670	0.000101806	0.002268318	0.001325457	4
BP	GO:1905517	macrophage migration	3/33	53/18670	0.000110967	0.002429805	0.00141982	3
BP	GO:0043270	positive regulation of ion transport	5/33	275/18670	0.000113189	0.002436437	0.001423695	5
BP	GO:0060485	mesenchyme development	5/33	279/18670	0.000121119	0.002563684	0.00149805	5
BP	GO:0021700	developmental maturation	5/33	284/18670	0.000131625	0.002681561	0.00156693	5
BP	GO:0003376	sphingosine-1-phosphate receptor signaling pathway	2/33	10/18670	0.000135134	0.002681561	0.00156693	2
BP	GO:2000833	positive regulation of steroid hormone secretion	2/33	10/18670	0.000135134	0.002681561	0.00156693	2

BP	GO:2000849	regulation of glucocorticoid secretion	2/33	10/18670	0.000135134	0.002681561	0.00156693	2
BP	GO:0019229	regulation of vasoconstriction	3/33	58/18670	0.000145286	0.002838664	0.00165873	3
BP	GO:0032060	bleb assembly	2/33	11/18670	0.000164981	0.003081259	0.001800487	2
BP	GO:0035933	glucocorticoid secretion	2/33	11/18670	0.000164981	0.003081259	0.001800487	2
BP	GO:0098883	synapse pruning	2/33	11/18670	0.000164981	0.003081259	0.001800487	2
BP	GO:0032233	positive regulation of actin filament bundle assembly	3/33	61/18670	0.000168849	0.003107796	0.001815993	3
BP	GO:0007588	excretion	3/33	63/18670	0.000185858	0.003371998	0.001970376	3
BP	GO:0046879	hormone secretion	5/33	308/18670	0.000192147	0.003436999	0.002008358	5
BP	GO:0048484	enteric nervous system development	2/33	12/18670	0.000197758	0.003440447	0.002010373	2
BP	GO:0090520	sphingolipid mediated signaling pathway	2/33	12/18670	0.000197758	0.003440447	0.002010373	2
BP	GO:0006940	regulation of smooth muscle contraction	3/33	65/18670	0.000203943	0.003500099	0.00204523	3
BP	GO:0048660	regulation of smooth muscle cell proliferation	4/33	169/18670	0.000216003	0.003657653	0.002137294	4
BP	GO:0009914	hormone transport	5/33	317/18670	0.000219624	0.003670031	0.002144527	5
BP	GO:0006937	regulation of muscle contraction	4/33	171/18670	0.000225945	0.003678841	0.002149675	4
BP	GO:0048659	smooth muscle cell proliferation	4/33	171/18670	0.000225945	0.003678841	0.002149675	4
BP	GO:0072091	regulation of stem cell proliferation	3/33	70/18670	0.000254049	0.004084084	0.002386473	3
BP	GO:0032496	response to lipopolysaccharide	5/33	330/18670	0.000264495	0.00419886	0.00245354	5
BP	GO:0002523	leukocyte migration involved in inflammatory response	2/33	14/18670	0.000272064	0.004265688	0.00249259	2
BP	GO:1903524	positive regulation of blood circulation	3/33	73/18670	0.000287613	0.004454494	0.002602916	3
BP	GO:0002237	response to molecule of bacterial origin	5/33	343/18670	0.000316039	0.004835783	0.002825716	5
BP	GO:2000846	regulation of corticosteroid hormone secretion	2/33	16/18670	0.000357972	0.0053882	0.003148513	2

BP	GO:1902903	regulation of supramolecular fiber organization	5/33	353/18670	0.000360628	0.0053882	0.003148513	5
BP	GO:0001505	regulation of neurotransmitter levels	5/33	355/18670	0.00037009	0.005465286	0.003193557	5
BP	GO:0014032	neural crest cell development	3/33	81/18670	0.000390768	0.005704309	0.003333226	3
BP	GO:0035930	corticosteroid hormone secretion	2/33	17/18670	0.000405253	0.005848542	0.003417507	2
BP	GO:0051492	regulation of stress fiber assembly	3/33	84/18670	0.000434832	0.005962532	0.003484115	3
BP	GO:0034764	positive regulation of transmembrane transport	4/33	204/18670	0.000441815	0.005962532	0.003484115	4
BP	GO:1902905	positive regulation of supramolecular fiber organization	4/33	204/18670	0.000441815	0.005962532	0.003484115	4
BP	GO:0015893	drug transport	4/33	205/18670	0.000450049	0.005962532	0.003484115	4
BP	GO:0071222	cellular response to lipopolysaccharide	4/33	205/18670	0.000450049	0.005962532	0.003484115	4
BP	GO:0014031	mesenchymal cell development	3/33	85/18670	0.000450199	0.005962532	0.003484115	3
BP	GO:0048864	stem cell development	3/33	85/18670	0.000450199	0.005962532	0.003484115	3
BP	GO:0007194	negative regulation of adenylate cyclase activity	2/33	18/18670	0.000455406	0.005962532	0.003484115	2
BP	GO:0007252	I-kappaB phosphorylation	2/33	18/18670	0.000455406	0.005962532	0.003484115	2
BP	GO:0070098	chemokine-mediated signaling pathway	3/33	88/18670	0.000498382	0.006458618	0.003773995	3
BP	GO:2000831	regulation of steroid hormone secretion	2/33	19/18670	0.000508421	0.006486973	0.003790564	2
BP	GO:0071219	cellular response to molecule of bacterial origin	4/33	212/18670	0.000510785	0.006486973	0.003790564	4
BP	GO:0014033	neural crest cell differentiation	3/33	90/18670	0.000532271	0.006627294	0.003872559	3
BP	GO:0032651	regulation of interleukin-1 beta production	3/33	90/18670	0.000532271	0.006627294	0.003872559	3
BP	GO:0050920	regulation of chemotaxis	4/33	217/18670	0.000557603	0.006875297	0.004017476	4

BP	GO:0031280	negative regulation of cyclase activity	2/33	20/18670	0.000564287	0.006890818	0.004026545	2
BP	GO:0048762	mesenchymal cell differentiation	4/33	220/18670	0.000587118	0.00710133	0.004149554	4
BP	GO:0010959	regulation of metal ion transport	5/33	394/18670	0.000595144	0.007130494	0.004166596	5
BP	GO:0110020	regulation of actomyosin structure organization	3/33	95/18670	0.000623365	0.007398813	0.004323384	3
BP	GO:0007015	actin filament organization	5/33	400/18670	0.000637292	0.007494078	0.004379051	5
BP	GO:1990868	response to chemokine	3/33	97/18670	0.000662416	0.007647888	0.004468928	3
BP	GO:1990869	cellular response to chemokine	3/33	97/18670	0.000662416	0.007647888	0.004468928	3
BP	GO:0002052	positive regulation of neuroblast proliferation	2/33	22/18670	0.000684539	0.007693495	0.004495577	2
BP	GO:0033622	integrin activation	2/33	22/18670	0.000684539	0.007693495	0.004495577	2
BP	GO:0035929	steroid hormone secretion	2/33	22/18670	0.000684539	0.007693495	0.004495577	2
BP	GO:0032611	interleukin-1 beta production	3/33	101/18670	0.000745132	0.00819922	0.00479109	3
BP	GO:0051350	negative regulation of lyase activity	2/33	23/18670	0.000748905	0.00819922	0.00479109	2
BP	GO:1903429	regulation of cell maturation	2/33	23/18670	0.000748905	0.00819922	0.00479109	2
BP	GO:0071216	cellular response to biotic stimulus	4/33	236/18670	0.000763608	0.008288741	0.0048434	4
BP	GO:0032652	regulation of interleukin-1 production	3/33	103/18670	0.000788845	0.008490116	0.004961071	3
BP	GO:0033002	muscle cell proliferation	4/33	239/18670	0.000800456	0.00851531	0.004975793	4
BP	GO:0030593	neutrophil chemotaxis	3/33	104/18670	0.000811301	0.00851531	0.004975793	3
BP	GO:0046928	regulation of neurotransmitter secretion	3/33	104/18670	0.000811301	0.00851531	0.004975793	3
BP	GO:0043266	regulation of potassium ion transport	3/33	105/18670	0.00083416	0.008683473	0.005074056	3
BP	GO:0050804	modulation of chemical synaptic transmission	5/33	436/18670	0.0009392	0.009588477	0.005602881	5
BP	GO:0030072	peptide hormone secretion	4/33	250/18670	0.000946375	0.009588477	0.005602881	4
BP	GO:0099177	regulation of trans-synaptic signaling	5/33	437/18670	0.00094888	0.009588477	0.005602881	5
BP	GO:0010460	positive regulation of heart rate	2/33	26/18670	0.000958848	0.009588477	0.005602881	2
BP	GO:0030318	melanocyte differentiation	2/33	26/18670	0.000958848	0.009588477	0.005602881	2

BP	GO:0072676	lymphocyte migration	3/33	111/18670	0.000979946	0.009722901	0.00568143	3
BP	GO:0072376	protein activation cascade	2/33	27/18670	0.001034412	0.010105408	0.005904942	2
BP	GO:0072378	blood coagulation, fibrin clot formation	2/33	27/18670	0.001034412	0.010105408	0.005904942	2
BP	GO:0043406	positive regulation of MAP kinase activity	4/33	258/18670	0.001063648	0.010311704	0.006025488	4
BP	GO:0090257	regulation of muscle system process	4/33	259/18670	0.001078994	0.010365902	0.006057158	4
BP	GO:0032612	interleukin-1 production	3/33	115/18670	0.001085563	0.010365902	0.006057158	3
BP	GO:0110053	regulation of actin filament organization	4/33	261/18670	0.001110151	0.010468109	0.006116881	4
BP	GO:0045761	regulation of adenylate cyclase activity	2/33	28/18670	0.001112752	0.010468109	0.006116881	2
BP	GO:0015850	organic hydroxy compound transport	4/33	262/18670	0.001125965	0.010514529	0.006144006	4
BP	GO:1990266	neutrophil migration	3/33	118/18670	0.001169325	0.010839732	0.006334033	3
BP	GO:0072089	stem cell proliferation	3/33	120/18670	0.001227374	0.0112954	0.006600296	3
BP	GO:0071621	granulocyte chemotaxis	3/33	123/18670	0.001317811	0.01204043	0.007035643	3
BP	GO:0051482	positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G protein-coupled signaling pathway	2/33	31/18670	0.001364332	0.012288666	0.007180696	2
BP	GO:0071880	adenylate cyclase-activating adrenergic receptor signaling pathway	2/33	31/18670	0.001364332	0.012288666	0.007180696	2
BP	GO:0046887	positive regulation of hormone secretion	3/33	127/18670	0.001444781	0.012820661	0.007491559	3
BP	GO:0045907	positive regulation of vasoconstriction	2/33	32/18670	0.001453681	0.012820661	0.007491559	2
BP	GO:0045987	positive regulation of smooth muscle contraction	2/33	32/18670	0.001453681	0.012820661	0.007491559	2
BP	GO:0032691	negative regulation of interleukin-1 beta production	2/33	33/18670	0.001545759	0.013445986	0.007856959	2

BP	GO:1902692	regulation of neuroblast proliferation	2/33	33/18670	0.001545759	0.013445986	0.007856959	2
BP	GO:0042063	gliogenesis	4/33	290/18670	0.00163606	0.014077747	0.008226118	4
BP	GO:0071875	adrenergic receptor signaling pathway	2/33	34/18670	0.001640556	0.014077747	0.008226118	2
BP	GO:0002920	regulation of humoral immune response	3/33	134/18670	0.001685001	0.01436209	0.00839227	3
BP	GO:0050931	pigment cell differentiation	2/33	36/18670	0.001838272	0.015564039	0.00909461	2
BP	GO:0070372	regulation of ERK1 and ERK2 cascade	4/33	300/18670	0.001851865	0.015575289	0.009101184	4
BP	GO:0051588	regulation of neurotransmitter transport	3/33	139/18670	0.001871024	0.015632894	0.009134845	3
BP	GO:0035023	regulation of Rho protein signal transduction	3/33	140/18670	0.001909703	0.015851782	0.009262749	3
BP	GO:0097530	granulocyte migration	3/33	141/18670	0.001948879	0.016071925	0.009391386	3
BP	GO:0048246	macrophage chemotaxis	2/33	38/18670	0.002046755	0.016662683	0.009736586	2
BP	GO:1904706	negative regulation of vascular smooth muscle cell proliferation	2/33	38/18670	0.002046755	0.016662683	0.009736586	2
BP	GO:1904064	positive regulation of cation transmembrane transport	3/33	144/18670	0.002069413	0.01673984	0.009781672	3
BP	GO:0032692	negative regulation of interleukin-1 production	2/33	39/18670	0.00215501	0.017153388	0.010023322	2
BP	GO:2000648	positive regulation of stem cell proliferation	2/33	39/18670	0.00215501	0.017153388	0.010023322	2
BP	GO:1901214	regulation of neuron death	4/33	313/18670	0.002161057	0.017153388	0.010023322	4
BP	GO:0043524	negative regulation of neuron apoptotic process	3/33	147/18670	0.002194503	0.017310675	0.01011523	3
BP	GO:0070371	ERK1 and ERK2 cascade	4/33	317/18670	0.002262968	0.01765479	0.010316309	4
BP	GO:0045823	positive regulation of heart contraction	2/33	40/18670	0.00226593	0.01765479	0.010316309	2

BP	GO:0051092	positive regulation of NF-kappaB transcription factor activity	3/33	149/18670	0.002280456	0.017659632	0.010319139	3
BP	GO:0140353	lipid export from cell	2/33	41/18670	0.002379504	0.01820464	0.010637606	2
BP	GO:1901381	positive regulation of potassium ion transmembrane transport	2/33	41/18670	0.002379504	0.01820464	0.010637606	2
BP	GO:0034767	positive regulation of ion transmembrane transport	3/33	156/18670	0.0025977	0.019754963	0.011543514	3
BP	GO:0031279	regulation of cyclase activity	2/33	43/18670	0.002614581	0.019764984	0.011549369	2
BP	GO:0060402	calcium ion transport into cytosol	3/33	158/18670	0.002693098	0.020238076	0.011825813	3
BP	GO:0071902	positive regulation of protein serine/threonine kinase activity	4/33	334/18670	0.002733371	0.020320478	0.011873964	4
BP	GO:0014003	oligodendrocyte development	2/33	44/18670	0.002736064	0.020320478	0.011873964	2
BP	GO:0032680	regulation of tumor necrosis factor production	3/33	160/18670	0.002790642	0.020605319	0.012040406	3
BP	GO:0043405	regulation of MAP kinase activity	4/33	337/18670	0.002822285	0.020722655	0.01210897	4
BP	GO:0048483	autonomic nervous system development	2/33	45/18670	0.002860167	0.020875928	0.012198533	2
BP	GO:0032640	tumor necrosis factor production	3/33	163/18670	0.002941014	0.021222088	0.012400805	3
BP	GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	3/33	163/18670	0.002941014	0.021222088	0.012400805	3
BP	GO:0002673	regulation of acute inflammatory response	2/33	46/18670	0.002986878	0.021310871	0.012452685	2
BP	GO:0051339	regulation of lyase activity	2/33	46/18670	0.002986878	0.021310871	0.012452685	2
BP	GO:0032956	regulation of actin cytoskeleton organization	4/33	343/18670	0.003007822	0.021340413	0.012469947	4
BP	GO:0042551	neuron maturation	2/33	47/18670	0.00311619	0.021825806	0.012753579	2
BP	GO:0048066	developmental pigmentation	2/33	47/18670	0.00311619	0.021825806	0.012753579	2
BP	GO:0070997	neuron death	4/33	348/18670	0.003168197	0.021825806	0.012753579	4

BP	GO:2000146	negative regulation of cell motility	4/33	349/18670	0.003200961	0.021825806	0.012753579	4
BP	GO:0050806	positive regulation of synaptic transmission	3/33	168/18670	0.003202585	0.021825806	0.012753579	3
BP	GO:0071706	tumor necrosis factor superfamily cytokine production	3/33	168/18670	0.003202585	0.021825806	0.012753579	3
BP	GO:0001774	microglial cell activation	2/33	48/18670	0.003248092	0.021825806	0.012753579	2
BP	GO:0002269	leukocyte activation involved in inflammatory response	2/33	48/18670	0.003248092	0.021825806	0.012753579	2
BP	GO:0043268	positive regulation of potassium ion transport	2/33	48/18670	0.003248092	0.021825806	0.012753579	2
BP	GO:0045933	positive regulation of muscle contraction	2/33	48/18670	0.003248092	0.021825806	0.012753579	2
BP	GO:0007269	neurotransmitter secretion	3/33	170/18670	0.003311091	0.022016158	0.012864808	3
BP	GO:0099643	signal release from synapse	3/33	170/18670	0.003311091	0.022016158	0.012864808	3
BP	GO:0003044	regulation of systemic arterial blood pressure mediated by a chemical signal	2/33	49/18670	0.003382577	0.02237434	0.013074107	2
BP	GO:0006959	humoral immune response	4/33	356/18670	0.003436848	0.022615529	0.013215042	4
BP	GO:0055002	striated muscle cell development	3/33	173/18670	0.003478054	0.022768702	0.013304546	3
BP	GO:0002931	response to ischemia	2/33	50/18670	0.003519636	0.022805803	0.013326225	2
BP	GO:0014009	glial cell proliferation	2/33	50/18670	0.003519636	0.022805803	0.013326225	2
BP	GO:0006956	complement activation	3/33	175/18670	0.003592185	0.023157742	0.013531876	3
BP	GO:0060401	cytosolic calcium ion transport	3/33	176/18670	0.003650103	0.023353055	0.013646004	3
BP	GO:0051496	positive regulation of stress fiber assembly	2/33	51/18670	0.003659258	0.023353055	0.013646004	2
BP	GO:0048469	cell maturation	3/33	177/18670	0.003708592	0.02354956	0.013760829	3
BP	GO:2000179	positive regulation of neural precursor cell proliferation	2/33	52/18670	0.003801436	0.024019024	0.014035153	2

BP	GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	3/33	183/18670	0.004071609	0.025598728	0.014958229	3
BP	GO:0055001	muscle cell development	3/33	186/18670	0.004260963	0.026657255	0.015576763	3
BP	GO:0040013	negative regulation of locomotion	4/33	381/18670	0.004376193	0.027243947	0.015919588	4
BP	GO:0051271	negative regulation of cellular component movement	4/33	384/18670	0.004499476	0.027783351	0.01623478	4
BP	GO:0042692	muscle cell differentiation	4/33	385/18670	0.004541088	0.027783351	0.01623478	4
BP	GO:0001755	neural crest cell migration	2/33	57/18670	0.004550344	0.027783351	0.01623478	2
BP	GO:0071398	cellular response to fatty acid	2/33	57/18670	0.004550344	0.027783351	0.01623478	2
BP	GO:0032970	regulation of actin filament-based process	4/33	388/18670	0.00466749	0.028362259	0.016573057	4
BP	GO:0061900	glial cell activation	2/33	58/18670	0.004707668	0.02847018	0.016636119	2
BP	GO:0002685	regulation of leukocyte migration	3/33	196/18670	0.004930603	0.029677088	0.017341357	3
BP	GO:0007405	neuroblast proliferation	2/33	61/18670	0.005194564	0.030827551	0.018013612	2
BP	GO:0032370	positive regulation of lipid transport	2/33	61/18670	0.005194564	0.030827551	0.018013612	2
BP	GO:0045123	cellular extravasation	2/33	61/18670	0.005194564	0.030827551	0.018013612	2
BP	GO:0007266	Rho protein signal transduction	3/33	203/18670	0.005435182	0.032105496	0.01876036	3
BP	GO:0060537	muscle tissue development	4/33	408/18670	0.005571546	0.032758628	0.019142008	4
BP	GO:0048247	lymphocyte chemotaxis	2/33	64/18670	0.005703665	0.033380896	0.019505621	2
BP	GO:1901215	negative regulation of neuron death	3/33	208/18670	0.005813992	0.033870504	0.019791716	3
BP	GO:0072678	T cell migration	2/33	65/18670	0.005878259	0.034088535	0.019919119	2
BP	GO:0010876	lipid localization	4/33	415/18670	0.00591389	0.034139275	0.019948768	4
BP	GO:0043523	regulation of neuron apoptotic process	3/33	210/18670	0.005969855	0.034306405	0.020046428	3
BP	GO:0045428	regulation of nitric oxide biosynthetic process	2/33	66/18670	0.006055286	0.034640601	0.020241711	2
BP	GO:0048662	negative regulation of smooth muscle cell proliferation	2/33	67/18670	0.006234737	0.035348733	0.020655496	2

BP	GO:0048747	muscle fiber development	2/33	67/18670	0.006234737	0.035348733	0.020655496	2
BP	GO:0070374	positive regulation of ERK1 and ERK2 cascade	3/33	215/18670	0.006370454	0.035899059	0.020977071	3
BP	GO:0010812	negative regulation of cell-substrate adhesion	2/33	68/18670	0.006416603	0.035899059	0.020977071	2
BP	GO:0050918	positive chemotaxis	2/33	68/18670	0.006416603	0.035899059	0.020977071	2
BP	GO:0019722	calcium-mediated signaling	3/33	218/18670	0.00661837	0.036865482	0.021541786	3
BP	GO:0006816	calcium ion transport	4/33	434/18670	0.006913625	0.038315304	0.022388967	4
BP	GO:0044706	multi-multicellular organism process	3/33	222/18670	0.006957812	0.038315304	0.022388967	3
BP	GO:0002683	negative regulation of immune system process	4/33	435/18670	0.006969162	0.038315304	0.022388967	4
BP	GO:0051495	positive regulation of cytoskeleton organization	3/33	226/18670	0.007307482	0.040002165	0.023374659	3
BP	GO:0043627	response to estrogen	2/33	73/18670	0.007361867	0.040126912	0.023447553	2
BP	GO:2001234	negative regulation of apoptotic signaling pathway	3/33	230/18670	0.007667458	0.04161398	0.024316499	3
BP	GO:0150076	neuroinflammatory response	2/33	75/18670	0.007756581	0.041918546	0.024494468	2
BP	GO:0048738	cardiac muscle tissue development	3/33	233/18670	0.007944246	0.042641264	0.024916777	3
BP	GO:0030500	regulation of bone mineralization	2/33	76/18670	0.007957464	0.042641264	0.024916777	2
BP	GO:0006809	nitric oxide biosynthetic process	2/33	77/18670	0.008160686	0.043546518	0.025445748	2
BP	GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	3/33	237/18670	0.008322243	0.043905467	0.025655495	3
BP	GO:0010827	regulation of glucose transmembrane transport	2/33	78/18670	0.008366239	0.043905467	0.025655495	2
BP	GO:2000243	positive regulation of reproductive process	2/33	78/18670	0.008366239	0.043905467	0.025655495	2
BP	GO:2000300	regulation of synaptic vesicle exocytosis	2/33	78/18670	0.008366239	0.043905467	0.025655495	2

BP	GO:0046578	regulation of Ras protein signal transduction	3/33	238/18670	0.008418613	0.043998515	0.025709866	3
BP	GO:0051402	neuron apoptotic process	3/33	239/18670	0.008515454	0.044285227	0.025877402	3
BP	GO:0045913	positive regulation of carbohydrate metabolic process	2/33	79/18670	0.008574114	0.044285227	0.025877402	2
BP	GO:0002697	regulation of immune effector process	4/33	462/18670	0.008583018	0.044285227	0.025877402	4
BP	GO:0006813	potassium ion transport	3/33	240/18670	0.008612954	0.044285227	0.025877402	3
BP	GO:0046209	nitric oxide metabolic process	2/33	82/18670	0.009211589	0.046794872	0.027343874	2
BP	GO:0060415	muscle tissue morphogenesis	2/33	82/18670	0.009211589	0.046794872	0.027343874	2
BP	GO:1905954	positive regulation of lipid localization	2/33	82/18670	0.009211589	0.046794872	0.027343874	2
BP	GO:0002718	regulation of cytokine production involved in immune response	2/33	84/18670	0.009648032	0.048623018	0.028412124	2
BP	GO:0046889	positive regulation of lipid biosynthetic process	2/33	84/18670	0.009648032	0.048623018	0.028412124	2
BP	GO:0070838	divalent metal ion transport	4/33	479/18670	0.009715994	0.048771987	0.028499172	4
BP	GO:1904705	regulation of vascular smooth muscle cell proliferation	2/33	85/18670	0.009869666	0.048962798	0.028610669	2
BP	GO:1990874	vascular smooth muscle cell proliferation	2/33	85/18670	0.009869666	0.048962798	0.028610669	2
BP	GO:2001057	reactive nitrogen species metabolic process	2/33	85/18670	0.009869666	0.048962798	0.028610669	2
BP	GO:0070542	response to fatty acid	2/33	86/18670	0.010093565	0.049878708	0.029145868	2
CC	GO:0031093	platelet alpha granule lumen	5/33	67/19717	8.58087E-08	7.63698E-06	3.52267E-06	5
CC	GO:0031091	platelet alpha granule	5/33	91/19717	4.01607E-07	1.78715E-05	8.24351E-06	5
CC	GO:0043292	contractile fiber	6/33	234/19717	2.21977E-06	6.58532E-05	3.03758E-05	6
CC	GO:0043025	neuronal cell body	6/33	497/19717	0.000154519	0.001483502	0.000684288	6
CC	GO:0045121	membrane raft	5/33	315/19717	0.000165735	0.001483502	0.000684288	5
CC	GO:0098857	membrane microdomain	5/33	316/19717	0.0001682	0.001483502	0.000684288	5

CC	GO:0034774	secretory granule lumen	5/33	321/19717	0.000180948	0.001483502	0.000684288	5
CC	GO:0001725	stress fiber	3/33	67/19717	0.000190215	0.001483502	0.000684288	3
CC	GO:0097517	contractile actin filament bundle	3/33	67/19717	0.000190215	0.001483502	0.000684288	3
CC	GO:0060205	cytoplasmic vesicle lumen	5/33	325/19717	0.000191668	0.001483502	0.000684288	5
CC	GO:0031983	vesicle lumen	5/33	327/19717	0.000197208	0.001483502	0.000684288	5
CC	GO:0098589	membrane region	5/33	328/19717	0.000200023	0.001483502	0.000684288	5
CC	GO:0032432	actin filament bundle	3/33	75/19717	0.000265688	0.0017887	0.000825065	3
CC	GO:0005859	muscle myosin complex	2/33	15/19717	0.000281368	0.0017887	0.000825065	2
CC	GO:0042641	actomyosin	3/33	79/19717	0.000309734	0.001837757	0.000847694	3
CC	GO:0030017	sarcomere	4/33	204/19717	0.000359896	0.002001924	0.000923418	4
CC	GO:0016460	myosin II complex	2/33	19/19717	0.000456313	0.002388932	0.001101932	2
CC	GO:0030016	myofibril	4/33	224/19717	0.000512381	0.002496396	0.001151501	4
CC	GO:0062023	collagen-containing extracellular matrix	5/33	406/19717	0.000532938	0.002496396	0.001151501	5
CC	GO:0030018	Z disc	3/33	132/19717	0.001381593	0.006148087	0.002835901	3
CC	GO:0042383	sarcolemma	3/33	136/19717	0.001505202	0.006379191	0.002942501	3
CC	GO:0043198	dendritic shaft	2/33	36/19717	0.001651512	0.006681119	0.00308177	2
CC	GO:0031674	I band	3/33	143/19717	0.001737829	0.006724643	0.003101846	3
CC	GO:0030315	T-tubule	2/33	52/19717	0.00341842	0.012676639	0.005847297	2
CC	GO:0016459	myosin complex	2/33	55/19717	0.003816352	0.013586212	0.006266851	2
CC	GO:0099056	integral component of presynaptic membrane	2/33	73/19717	0.006628207	0.022688863	0.01046559	2
CC	GO:0005901	caveola	2/33	80/19717	0.007912099	0.026080624	0.012030093	2
CC	GO:0098889	intrinsic component of presynaptic membrane	2/33	82/19717	0.008297922	0.026375537	0.012166126	2
CC	GO:0005623	cell	2/33	90/19717	0.009924028	0.030456498	0.014048533	2
CC	GO:0044853	plasma membrane raft	2/33	109/19717	0.014299849	0.042422884	0.019568214	2

CC	GO:0099055	integral component of postsynaptic membrane	2/33	117/19717	0.016350071	0.046940528	0.021652047	2
CC	GO:0098936	intrinsic component of postsynaptic membrane	2/33	122/19717	0.017691681	0.049204988	0.022696564	2
CC	GO:0061827	sperm head	1/33	11/19717	0.018261806	0.049251537	0.022718036	1
MF	GO:0008528	G protein-coupled peptide receptor activity	6/32	146/17696	2.16022E-07	1.45288E-05	7.21388E-06	6
MF	GO:0001653	peptide receptor activity	6/32	152/17696	2.74128E-07	1.45288E-05	7.21388E-06	6
MF	GO:0045125	bioactive lipid receptor activity	3/32	14/17696	1.92889E-06	6.81541E-05	3.38402E-05	3
MF	GO:0001664	G protein-coupled receptor binding	6/32	280/17696	9.53678E-06	0.000252725	0.000125484	6
MF	GO:0008188	neuropeptide receptor activity	3/32	50/17696	9.93691E-05	0.001885473	0.000936183	3
MF	GO:0003779	actin binding	6/32	431/17696	0.000106725	0.001885473	0.000936183	6
MF	GO:0004966	galanin receptor activity	2/32	10/17696	0.000141277	0.00203139	0.001008634	2
MF	GO:0008227	G protein-coupled amine receptor activity	3/32	59/17696	0.000163005	0.00203139	0.001008634	3
MF	GO:0045236	CXCR chemokine receptor binding	2/32	11/17696	0.000172476	0.00203139	0.001008634	2
MF	GO:0004935	adrenergic receptor activity	2/32	17/17696	0.000423606	0.004490227	0.002229507	2
MF	GO:0001965	G-protein alpha-subunit binding	2/32	24/17696	0.000852905	0.008218901	0.004080884	2
MF	GO:0071855	neuropeptide receptor binding	2/32	32/17696	0.001518986	0.01275647	0.006333898	2
MF	GO:0048018	receptor ligand activity	5/32	482/17696	0.001609996	0.01275647	0.006333898	5
MF	GO:0030546	signaling receptor activator activity	5/32	487/17696	0.001684817	0.01275647	0.006333898	5
MF	GO:0048020	CCR chemokine receptor binding	2/32	43/17696	0.002731341	0.019301476	0.009583652	2
MF	GO:0008307	structural constituent of muscle	2/32	46/17696	0.003120047	0.020670314	0.010263314	2
MF	GO:0008009	chemokine activity	2/32	49/17696	0.003533144	0.020806291	0.01033083	2
MF	GO:0017046	peptide hormone binding	2/32	49/17696	0.003533144	0.020806291	0.01033083	2
MF	GO:0005516	calmodulin binding	3/32	200/17696	0.005541724	0.030916989	0.015351037	3
MF	GO:0042379	chemokine receptor binding	2/32	66/17696	0.006322336	0.033508383	0.016637727	2
MF	GO:0005125	cytokine activity	3/32	220/17696	0.007208181	0.036362216	0.018054725	3

MF	GO:0001618	virus receptor activity	2/32	74/17696	0.007889915	0.036362216	0.018054725	2
MF	GO:0140272	exogenous protein binding	2/32	74/17696	0.007889915	0.036362216	0.018054725	2

GO: Gene Ontology.

Table S3f. KEGG pathway enrichment of MCODE 3

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	Count
hsa04080	Neuroactive ligand-receptor interaction	13/28	341/8049	2.38022E-11	1.64235E-09	1.37802E-09	13
hsa04270	Vascular smooth muscle contraction	8/28	135/8049	1.19186E-08	4.11191E-07	3.45012E-07	8
hsa04020	Calcium signaling pathway	8/28	201/8049	2.66291E-07	6.12469E-06	5.13894E-06	8
hsa04022	cGMP-PKG signaling pathway	6/28	167/8049	1.88088E-05	0.000324452	0.000272233	6
hsa04610	Complement and coagulation cascades	3/28	85/8049	0.003077323	0.042467056	0.03563216	3

KEGG: Kyoto Encyclopedia of Genes and Genomes.