

Table S4a. GO term enrichment of MCODE 4

ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	Count
BP	GO:0006936	muscle contraction	7/10	363/18670	1.13189E-10	3.59942E-08	1.91826E-08	7
BP	GO:0003012	muscle system process	7/10	472/18670	7.09794E-10	1.12857E-07	6.01457E-08	7
BP	GO:0031032	actomyosin structure organization	4/10	199/18670	2.50132E-06	2.65140E-04	1.41303E-04	4
BP	GO:0070527	platelet aggregation	3/10	59/18670	3.54101E-06	2.81510E-04	1.50027E-04	3
BP	GO:0034109	homotypic cell-cell adhesion	3/10	81/18670	9.23598E-06	5.87408E-04	3.13051E-04	3
BP	GO:0030168	platelet activation	3/10	153/18670	6.20831E-05	3.29040E-03	1.75357E-03	3
BP	GO:0006937	regulation of muscle contraction	3/10	171/18670	8.64143E-05	3.92568E-03	2.09214E-03	3
BP	GO:0090257	regulation of muscle system process	3/10	259/18670	2.94647E-04	1.17122E-02	6.24186E-03	3
BP	GO:0007596	blood coagulation	3/10	336/18670	6.31114E-04	1.76212E-02	9.39099E-03	3
BP	GO:0007599	hemostasis	3/10	341/18670	6.58862E-04	1.76212E-02	9.39099E-03	3
BP	GO:0050817	coagulation	3/10	342/18670	6.64504E-04	1.76212E-02	9.39099E-03	3
BP	GO:0030239	myofibril assembly	2/10	73/18670	6.64952E-04	1.76212E-02	9.39099E-03	2
BP	GO:0007015	actin filament organization	3/10	400/18670	1.04714E-03	2.56148E-02	1.36510E-02	3
BP	GO:0006939	smooth muscle contraction	2/10	110/18670	1.50093E-03	3.40926E-02	1.81692E-02	2
BP	GO:0010927	cellular component assembly involved in morphogenesis	2/10	115/18670	1.63879E-03	3.47424E-02	1.85155E-02	2
BP	GO:0070252	actin-mediated cell contraction	2/10	121/18670	1.81194E-03	3.60122E-02	1.91922E-02	2
BP	GO:0030048	actin filament-based movement	2/10	143/18670	2.51808E-03	4.71029E-02	2.51028E-02	2
CC	GO:0043292	contractile fiber	6/10	234/19717	5.28974E-10	2.22169E-08	1.00227E-08	6
CC	GO:0030016	myofibril	5/10	224/19717	4.35460E-08	9.14467E-07	4.12541E-07	5
CC	GO:0030017	sarcomere	4/10	204/19717	2.22557E-06	3.11580E-05	1.40562E-05	4
CC	GO:0005859	muscle myosin complex	2/10	15/19717	2.42239E-05	2.01537E-04	9.09191E-05	2
CC	GO:0005925	focal adhesion	4/10	405/19717	3.33943E-05	2.01537E-04	9.09191E-05	4
CC	GO:0030018	Z disc	3/10	132/19717	3.40071E-05	2.01537E-04	9.09191E-05	3
CC	GO:0030055	cell-substrate junction	4/10	412/19717	3.57109E-05	2.01537E-04	9.09191E-05	4

CC	GO:0016460	myosin II complex	2/10	19/19717	3.94077E-05	2.01537E-04	9.09191E-05	2
CC	GO:0031674	I band	3/10	143/19717	4.31866E-05	2.01537E-04	9.09191E-05	3
CC	GO:0016459	myosin complex	2/10	55/19717	3.38907E-04	1.42341E-03	6.42140E-04	2
CC	GO:0001725	stress fiber	2/10	67/19717	5.02959E-04	1.76036E-03	7.94147E-04	2
CC	GO:0097517	contractile actin filament bundle	2/10	67/19717	5.02959E-04	1.76036E-03	7.94147E-04	2
CC	GO:0032432	actin filament bundle	2/10	75/19717	6.29893E-04	1.94023E-03	8.75290E-04	2
CC	GO:0005912	adherens junction	2/10	76/19717	6.46742E-04	1.94023E-03	8.75290E-04	2
CC	GO:0042641	actomyosin	2/10	79/19717	6.98595E-04	1.95607E-03	8.82436E-04	2
CC	GO:0005911	cell-cell junction	3/10	416/19717	1.00201E-03	2.63027E-03	1.18659E-03	3
CC	GO:0005884	actin filament	2/10	111/19717	1.37233E-03	3.39046E-03	1.52953E-03	2
CC	GO:0097440	apical dendrite	1/10	17/19717	8.59058E-03	2.00447E-02	9.04271E-03	1
CC	GO:0043034	costamere	1/10	19/19717	9.59686E-03	2.12141E-02	9.57027E-03	1
CC	GO:0032982	myosin filament	1/10	22/19717	1.11045E-02	2.22091E-02	1.00191E-02	1
CC	GO:0101031	chaperone complex	1/10	22/19717	1.11045E-02	2.22091E-02	1.00191E-02	1
CC	GO:0005865	striated muscle thin filament	1/10	31/19717	1.56152E-02	2.94279E-02	1.32757E-02	1
CC	GO:0036379	myofilament	1/10	32/19717	1.61153E-02	2.94279E-02	1.32757E-02	1
CC	GO:0043198	dendritic shaft	1/10	36/19717	1.81132E-02	3.16980E-02	1.42999E-02	1
MF	GO:0008307	structural constituent of muscle	5/10	46/17696	2.36708E-11	6.15442E-10	2.74083E-10	5
MF	GO:0003779	actin binding	6/10	431/17696	3.89848E-08	5.06803E-07	2.25702E-07	6
MF	GO:0051015	actin filament binding	4/10	198/17696	3.02934E-06	2.62542E-05	1.16922E-05	4
MF	GO:0005516	calmodulin binding	2/10	200/17696	5.38810E-03	2.74507E-02	1.22250E-02	2
MF	GO:0017166	vinculin binding	1/10	11/17696	6.20031E-03	2.74507E-02	1.22250E-02	1
MF	GO:0032036	myosin heavy chain binding	1/10	12/17696	6.76225E-03	2.74507E-02	1.22250E-02	1
MF	GO:0017160	Ral GTPase binding	1/10	15/17696	8.44637E-03	2.74507E-02	1.22250E-02	1
MF	GO:0019215	intermediate filament binding	1/10	15/17696	8.44637E-03	2.74507E-02	1.22250E-02	1
MF	GO:0005158	insulin receptor binding	1/10	22/17696	1.23660E-02	3.57240E-02	1.59095E-02	1

GO: Gene Ontology.

Table S4b. KEGG pathway enrichment of MCODE 4

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	Count
hsa04270	Vascular smooth muscle contraction	2/5	135/8049	2.70142E-03	2.80270E-02	1.96681E-02	2
hsa04530	Tight junction	2/5	162/8049	3.86859E-03	2.80270E-02	1.96681E-02	2
hsa04510	Focal adhesion	2/5	201/8049	5.90447E-03	2.80270E-02	1.96681E-02	2
hsa05132	Salmonella infection	2/5	213/8049	6.61239E-03	2.80270E-02	1.96681E-02	2
hsa04810	Regulation of actin cytoskeleton	2/5	214/8049	6.67309E-03	2.80270E-02	1.96681E-02	2

KEGG: Kyoto Encyclopedia of Genes and Genomes.