

**Supplemental\_Table\_S1: Complete list of significant GO terms in each cluster for m6A-mRNAs (FDR < 0,05)**

Cluster	GOID	GO Term	Ontology Source	FDR	% Associated Genes	Nr. Genes
None Specific Cluster	GO:0007548	sex differentiation	BP	0,02	11,78	41,00
None Specific Cluster	GO:0008092	cytoskeletal protein binding	MF	0,00	14,29	35,00
None Specific Cluster	GO:0016358	dendrite development	BP	0,04	14,42	15,00
None Specific Cluster	GO:0060627	regulation of vesicle-mediated transport	BP	0,02	18,33	11,00
None Specific Cluster	GO:0097193	intrinsic apoptotic signaling pathway	BP	0,05	18,60	8,00
None Specific Cluster	GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	BP	0,03	26,09	6,00
None Specific Cluster	GO:0098858	actin-based cell projection	CC	0,01	22,92	11,00
None Specific Cluster	GO:0007391	dorsal closure	BP	0,01	37,50	6,00
None Specific Cluster	GO:0120031	plasma membrane bounded cell projection assembly	BP	0,01	16,98	18,00
None Specific Cluster	GO:0051489	regulation of filopodium assembly	BP	0,01	30,43	7,00
None Specific Cluster	GO:0071363	cellular response to growth factor stimulus	BP	0,03	11,38	43,00
None Specific Cluster	GO:0071560	cellular response to transforming growth factor beta stimulus	BP	0,01	12,89	33,00
None Specific Cluster	GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	0,04	11,66	33,00
None Specific Cluster	GO:0007179	transforming growth factor beta receptor signaling pathway	BP	0,02	12,40	31,00
None Specific Cluster	GO:0045944	positive regulation of transcription by RNA polymerase II	BP	0,02	11,29	49,00
None Specific Cluster	GO:0000775	chromosome, centromeric region	CC	0,00	15,23	37,00
None Specific Cluster	GO:0000792	heterochromatin	CC	0,01	13,92	27,00
None Specific Cluster	GO:0000793	condensed chromosome	CC	0,03	12,24	30,00
None Specific Cluster	GO:0005819	spindle	CC	0,03	14,18	19,00
None Specific Cluster	GO:0045815	positive regulation of gene expression, epigenetic	BP	0,05	12,72	22,00
None Specific Cluster	GO:0005721	pericentric heterochromatin	CC	0,01	14,12	25,00
None Specific Cluster	GO:0034401	chromatin organization involved in regulation of transcription	BP	0,05	12,50	23,00
None Specific Cluster	GO:0001501	skeletal system development	BP	0,01	14,29	26,00
None Specific Cluster	GO:0051216	cartilage development	BP	0,01	16,96	19,00
None Specific Cluster	GO:0072657	protein localization to membrane	BP	0,03	15,46	15,00

None Specific Cluster	GO:0002062	chondrocyte differentiation	BP	0,01	18,48	17,00
None Specific Cluster	GO:0032330	regulation of chondrocyte differentiation	BP	0,00	20,73	17,00
None Specific Cluster	GO:0006605	protein targeting	BP	0,00	16,20	23,00
None Specific Cluster	GO:0006612	protein targeting to membrane	BP	0,00	23,53	12,00
None Specific Cluster	GO:0006607	NLS-bearing protein import into nucleus	BP	0,01	19,74	15,00
None Specific Cluster	GO:0007389	pattern specification process	BP	0,02	13,07	26,00
None Specific Cluster	GO:0048736	appendage development	BP	0,03	15,56	14,00
None Specific Cluster	GO:0007498	mesoderm development	BP	0,00	28,89	13,00
None Specific Cluster	GO:0048332	mesoderm morphogenesis	BP	0,00	33,33	8,00
None Specific Cluster	GO:0045669	positive regulation of osteoblast differentiation	BP	0,00	46,15	6,00
None Specific Cluster	GO:0090100	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	0,03	23,33	7,00
None Specific Cluster	GO:0032507	maintenance of protein location in cell	BP	0,00	20,90	14,00
None Specific Cluster	GO:0000775	chromosome, centromeric region	CC	0,00	15,23	37,00
None Specific Cluster	GO:0005819	spindle	CC	0,03	14,18	19,00
None Specific Cluster	GO:0015630	microtubule cytoskeleton	CC	0,01	12,28	48,00
None Specific Cluster	GO:0099513	polymeric cytoskeletal fiber	CC	0,02	13,21	28,00
None Specific Cluster	GO:0005874	microtubule	CC	0,01	14,20	25,00
None Specific Cluster	GO:0051258	protein polymerization	BP	0,00	18,02	20,00
None Specific Cluster	GO:0045202	synapse	CC	0,00	14,59	34,00
None Specific Cluster	GO:0005911	cell-cell junction	CC	0,00	14,94	39,00
None Specific Cluster	GO:0032507	maintenance of protein location in cell	BP	0,00	20,90	14,00
None Specific Cluster	GO:0044304	main axon	CC	0,00	21,21	14,00
None Specific Cluster	GO:0045211	postsynaptic membrane	CC	0,01	17,65	18,00
None Specific Cluster	GO:0072657	protein localization to membrane	BP	0,03	15,46	15,00
None Specific Cluster	GO:0006605	protein targeting	BP	0,00	16,20	23,00
None Specific Cluster	GO:0006612	protein targeting to membrane	BP	0,00	23,53	12,00
None Specific Cluster	GO:0007389	pattern specification process	BP	0,02	13,07	26,00

None Specific Cluster	GO:0009791	post-embryonic development	BP	0,00	21,92	16,00
None Specific Cluster	GO:0007552	metamorphosis	BP	0,00	26,83	11,00
None Specific Cluster	GO:0048729	tissue morphogenesis	BP	0,00	14,89	42,00
None Specific Cluster	GO:0048736	appendage development	BP	0,03	15,56	14,00
None Specific Cluster	GO:0002165	instar larval or pupal development	BP	0,00	28,57	12,00
None Specific Cluster	GO:0007498	mesoderm development	BP	0,00	28,89	13,00
None Specific Cluster	GO:0001655	urogenital system development	BP	0,03	13,73	21,00
None Specific Cluster	GO:0002009	morphogenesis of an epithelium	BP	0,00	15,56	40,00
None Specific Cluster	GO:0060541	respiratory system development	BP	0,00	18,10	19,00
None Specific Cluster	GO:0007444	imaginal disc development	BP	0,01	22,73	10,00
None Specific Cluster	GO:0016331	morphogenesis of embryonic epithelium	BP	0,02	18,64	11,00
None Specific Cluster	GO:0043296	apical junction complex	CC	0,01	24,32	9,00
None Specific Cluster	GO:0048732	gland development	BP	0,01	13,76	26,00
None Specific Cluster	GO:0060562	epithelial tube morphogenesis	BP	0,00	17,39	24,00
None Specific Cluster	GO:0007424	open tracheal system development	BP	0,02	21,62	8,00
None Specific Cluster	GO:0022612	gland morphogenesis	BP	0,01	17,12	19,00
None Specific Cluster	GO:0030324	lung development	BP	0,03	17,86	10,00
None Specific Cluster	GO:0007043	cell-cell junction assembly	BP	0,03	15,91	14,00
None Specific Cluster	GO:0007391	dorsal closure	BP	0,01	37,50	6,00
None Specific Cluster	GO:0007560	imaginal disc morphogenesis	BP	0,01	24,24	8,00
None Specific Cluster	GO:0120031	plasma membrane bounded cell projection assembly	BP	0,01	16,98	18,00
None Specific Cluster	GO:0007435	salivary gland morphogenesis	BP	0,00	34,62	9,00
None Specific Cluster	GO:0061333	renal tubule morphogenesis	BP	0,00	34,48	10,00
None Specific Cluster	GO:0072073	kidney epithelium development	BP	0,03	19,15	9,00
None Specific Cluster	GO:0051258	protein polymerization	BP	0,00	18,02	20,00
None Specific Cluster	GO:0051489	regulation of filopodium assembly	BP	0,01	30,43	7,00
None Specific Cluster	GO:0007476	imaginal disc-derived wing morphogenesis	BP	0,02	25,00	7,00
Specific for Cluster #1	GO:0005758	mitochondrial intermembrane space	CC	0,00	50,00	5,00

Specific for Cluster #1	GO:0007367	segment polarity determination	BP	0,03	50,00	3,00
Specific for Cluster #1	GO:0032011	ARF protein signal transduction	BP	0,00	47,06	8,00
Specific for Cluster #1	GO:0032012	regulation of ARF protein signal transduction	BP	0,00	47,06	8,00
Specific for Cluster #1	GO:0072331	signal transduction by p53 class mediator	BP	0,01	25,81	8,00
Specific for Cluster #1	GO:0031571	mitotic G1 DNA damage checkpoint	BP	0,05	30,77	4,00
Specific for Cluster #1	GO:0046847	filopodium assembly	BP	0,00	34,21	13,00
Specific for Cluster #1	GO:0030507	spectrin binding	MF	0,00	58,33	7,00
Specific for Cluster #1	GO:0072659	protein localization to plasma membrane	BP	0,00	27,78	10,00
Specific for Cluster #1	GO:0008154	actin polymerization or depolymerization	BP	0,02	17,91	12,00
Specific for Cluster #1	GO:0000910	cytokinesis	BP	0,01	19,67	12,00
Specific for Cluster #1	GO:0030315	T-tubule	CC	0,00	43,75	7,00
Specific for Cluster #1	GO:0030507	spectrin binding	MF	0,00	58,33	7,00
Specific for Cluster #1	GO:0001508	action potential	BP	0,05	15,94	11,00
Specific for Cluster #1	GO:0033268	node of Ranvier	CC	0,03	17,86	10,00
Specific for Cluster #1	GO:0042383	sarcolemma	CC	0,01	21,74	10,00
Specific for Cluster #1	GO:0045838	positive regulation of membrane potential	BP	0,00	42,86	6,00
Specific for Cluster #1	GO:0000281	mitotic cytokinesis	BP	0,00	61,54	8,00
Specific for Cluster #1	GO:0006892	post-Golgi vesicle-mediated transport	BP	0,03	19,57	9,00
Specific for Cluster #1	GO:0071709	membrane assembly	BP	0,01	30,00	6,00
Specific for Cluster #1	GO:0086001	cardiac muscle cell action potential	BP	0,00	43,75	7,00
Specific for Cluster #1	GO:0014704	intercalated disc	CC	0,01	30,00	6,00
Specific for Cluster #1	GO:0032414	positive regulation of ion transmembrane transporter activity	BP	0,02	25,93	7,00
Specific for Cluster #1	GO:0072659	protein localization to plasma membrane	BP	0,00	27,78	10,00
Specific for Cluster #1	GO:0072660	maintenance of protein location in plasma membrane	BP	0,00	66,67	6,00
Specific for Cluster #1	GO:1900827	positive regulation of membrane depolarization during cardiac muscle cell action potential	BP	0,00	85,71	6,00
Specific for Cluster #1	GO:0043001	Golgi to plasma membrane protein transport	BP	0,00	54,55	6,00
Specific for Cluster #1	GO:0006813	potassium ion transport	BP	0,03	17,86	10,00

Specific for Cluster #1	GO:0071498	cellular response to fluid shear stress	BP	0,00	83,33	5,00
Specific for Cluster #1	GO:0003785	actin monomer binding	MF	0,00	71,43	5,00
Specific for Cluster #1	GO:0048286	lung alveolus development	BP	0,00	42,86	6,00
Specific for Cluster #1	GO:0061005	cell differentiation involved in kidney development	BP	0,01	31,82	7,00
Specific for Cluster #1	GO:0008154	actin polymerization or depolymerization	BP	0,02	17,91	12,00
Specific for Cluster #1	GO:2001013	epithelial cell proliferation involved in renal tubule morphogenesis	BP	0,00	66,67	6,00
Specific for Cluster #1	GO:0046847	filopodium assembly	BP	0,00	34,21	13,00
Specific for Cluster #1	GO:0072080	nephron tubule development	BP	0,02	22,22	8,00
Specific for Cluster #2	GO:0045740	positive regulation of DNA replication	BP	0,03	33,33	4,00
Specific for Cluster #2	GO:0010369	chromocenter	CC	0,00	80,00	4,00
Specific for Cluster #2	GO:0001939	female pronucleus	CC	0,00	66,67	4,00
Specific for Cluster #2	GO:0001940	male pronucleus	CC	0,00	80,00	4,00
Specific for Cluster #2	GO:0060389	pathway-restricted SMAD protein phosphorylation	BP	0,01	38,46	5,00
Specific for Cluster #2	GO:0010862	positive regulation of pathway-restricted SMAD protein phosphorylation	BP	0,00	62,50	5,00
Specific for Cluster #2	GO:0018210	peptidyl-threonine modification	BP	0,01	33,33	6,00
Specific for Cluster #2	GO:0007527	adult somatic muscle development	BP	0,00	100,00	3,00
Specific for Cluster #2	GO:0009954	proximal/distal pattern formation	BP	0,01	38,46	5,00
Specific for Cluster #2	GO:0070160	tight junction	CC	0,01	24,24	8,00
Specific for Cluster #2	GO:0008362	chitin-based embryonic cuticle biosynthetic process	BP	0,03	50,00	3,00
Specific for Cluster #2	GO:0005918	septate junction	CC	0,00	62,50	5,00
Specific for Cluster #2	GO:0035151	regulation of tube size, open tracheal system	BP	0,01	35,71	5,00
Specific for Cluster #2	GO:0005920	smooth septate junction	CC	0,01	75,00	3,00
Specific for Cluster #2	GO:0043297	apical junction assembly	BP	0,00	42,86	6,00
Specific for Cluster #2	GO:0120192	tight junction assembly	BP	0,00	42,86	6,00
Specific for Cluster #2	GO:0060857	establishment of glial blood-brain barrier	BP	0,00	80,00	4,00
Specific for Cluster #2	GO:0035317	imaginal disc-derived wing hair organization	BP	0,05	30,77	4,00
Specific for Cluster #3	GO:0038032	termination of G protein-coupled receptor signaling pathway	BP	0,04	42,86	3,00
Specific for Cluster #3	GO:0010921	regulation of phosphatase activity	BP	0,02	22,22	8,00

Specific for Cluster #3	GO:0010923	negative regulation of phosphatase activity	BP	0,02	27,27	6,00
Specific for Cluster #3	GO:0016776	phosphotransferase activity, phosphate group as acceptor	MF	0,02	33,33	5,00
Specific for Cluster #3	GO:0004550	nucleoside diphosphate kinase activity	BP	0,03	50,00	3,00
Specific for Cluster #3	GO:0006183	GTP biosynthetic process	BP	0,03	50,00	3,00
Specific for Cluster #3	GO:0006228	UTP biosynthetic process	BP	0,03	50,00	3,00
Specific for Cluster #3	GO:0031109	microtubule polymerization or depolymerization	BP	0,01	27,59	8,00
Specific for Cluster #3	GO:0034453	microtubule anchoring	BP	0,00	61,54	8,00
Specific for Cluster #3	GO:0007020	microtubule nucleation	BP	0,00	60,00	6,00
Specific for Cluster #3	GO:0034453	microtubule anchoring	BP	0,00	61,54	8,00
Specific for Cluster #4	GO:0004360	glutamine-fructose-6-phosphate transaminase (isomerizing) activity	MF	0,00	100,00	3,00
Specific for Cluster #4	GO:0009226	nucleotide-sugar biosynthetic process	BP	0,01	44,44	4,00
Specific for Cluster #4	GO:0060395	SMAD protein signal transduction	BP	0,01	57,14	4,00