

**Table S1.** Go enrichment analysis of upregulated DEGs (adjusted P-value < 0.05)

Term type	NO.	GO accession	Description	Corrected P Value	Protein number
Biological process	1	GO:0007264	small GTPase mediated signal transduction	1.10E-07	186
	2	GO:006509	regulation of molecular function	3.17E-05	152
	3	GO:0051056	regulation of small GTPase mediated signal transduction	3.95E-05	35
	4	GO:0050790	regulation of catalytic activity	4.71E-05	141
	5	GO:0051641	cellular localization	0.000131	626
	6	GO:0033036	macromolecule localization	0.000469	624
	7	GO:0043087	regulation of GTPase activity	0.000469	59
	8	GO:0007266	Rho protein signal transduction	0.000469	18
	9	GO:0035023	regulation of Rho protein signal transduction	0.000469	18
	10	GO:0051649	establishment of localization in cell	0.001253	584
	11	GO:0051336	regulation of hydrolase activity	0.001483	77
	12	GO:0007265	Ras protein signal transduction	0.001895	25
	13	GO:0046578	regulation of Ras protein signal transduction	0.001895	25
	14	GO:0008104	protein localization	0.003145	548
	15	GO:0045184	establishment of protein localization	0.003437	523
	16	GO:1902531	regulation of intracellular signal transduction	0.004585	45
	17	GO:0006470	protein dephosphorylation	0.009589	50
	18	GO:0015031	protein transport	0.009749	505
	19	GO:0035556	intracellular signal transduction	0.009756	298

20	GO:004690 7	intracellular transport	0.010529	509
21	GO:000704 9	cell cycle	0.012566	301
22	GO:000996 6	regulation of signal transduction	0.025295	67
23	GO:003336 5	protein localization to organelle	0.025295	148
24	GO:005125 8	protein polymerization	0.026491	91
25	GO:002305 1	regulation of signaling	0.030259	69
26	GO:003461 3	cellular protein localization	0.030259	449
27	GO:007072 7	cellular macromolecule localization	0.030259	449
28	GO:000177 5	cell activation	0.030259	70
29	GO:003250 5	reproduction of a single-celled organism	0.030939	61
30	GO:003016 8	platelet activation	0.030939	64
31	GO:000639 7	mRNA processing	0.032502	123
32	GO:001607 1	mRNA metabolic process	0.032502	141
33	GO:000091 7	barrier septum assembly	0.032502	63
34	GO:003250 6	cytokinetic process	0.032502	63
35	GO:009052 9	cell septum assembly	0.032502	63
36	GO:190241 0	mitotic cytokinetic process	0.032502	63
37	GO:000027 8	mitotic cell cycle	0.032502	125
38	GO:190304 7	mitotic cell cycle process	0.032502	125
39	GO:001064 6	regulation of cell communication	0.033484	68
40	GO:190258 2	single-organism intracellular transport	0.035609	274
41	GO:000691 3	nucleocytoplasmic transport	0.042165	71

	42	GO:0000281	mitotic cytokinesis	0.042165	64
	43	GO:0061640	cytoskeleton-dependent cytokinesis	0.042165	64
	44	GO:0007596	blood coagulation	0.044018	65
	45	GO:1902580	single-organism cellular localization	0.044754	153
	46	GO:0048870	cell motility	0.046942	83
	47	GO:0051674	localization of cell	0.046942	83
Cellular component	1	GO:0044422	organelle part	0.000469	1307
	2	GO:0044446	intracellular organelle part	0.000472	1298
	3	GO:0031974	membrane-enclosed lumen	0.000518	405
	4	GO:0005654	nucleoplasm	0.000664	187
	5	GO:0044451	nucleoplasm part	0.000664	187
	6	GO:0043233	organelle lumen	0.001659	399
	7	GO:0070013	intracellular organelle lumen	0.001659	399
	8	GO:0031981	nuclear lumen	0.003079	379
	9	GO:0044428	nuclear part	0.005163	550
	10	GO:0000428	DNA-directed RNA polymerase complex	0.011971	81
	11	GO:0055029	nuclear DNA-directed RNA polymerase complex	0.011971	81
	12	GO:0016591	DNA-directed RNA polymerase II, holoenzyme	0.015103	76
	13	GO:0044430	cytoskeletal part	0.020102	280
	14	GO:0005856	cytoskeleton	0.020102	290
	15	GO:0090575	RNA polymerase II transcription factor complex	0.030259	63
	16	GO:0043231	intracellular membrane-bounded organelle	0.030259	1618

	17	GO:000557 7	fibrinogen complex	0.030939	64
	18	GO:004322 7	membrane-bounded organelle	0.031324	1619
	19	GO:000931 8	exodeoxyribonuclease VII complex	0.036221	49
	20	GO:003151 4	motile cilium	0.044386	53
Molecular function	1	GO:001642 3	tRNA (guanine) methyltransferase activity	2.91E-05	66
	2	GO:000817 6	tRNA (guanine-N7-)-methyltransferase activity	4.09E-05	56
	3	GO:000817 5	tRNA methyltransferase activity	5.15E-05	73
	4	GO:000509 6	GTPase activator activity	0.001633	50
	5	GO:003509 1	phosphatidylinositol binding	0.00209	34
	6	GO:000804 7	enzyme activator activity	0.004002	69
	7	GO:000508 5	guanyl-nucleotide exchange factor activity	0.004075	45
	8	GO:003069 5	GTPase regulator activity	0.005717	55
	9	GO:000828 9	lipid binding	0.011733	111
	10	GO:006058 9	nucleoside-triphosphatase regulator activity	0.019029	96
	11	GO:000813 8	protein tyrosine/serine/threonine phosphatase activity	0.019029	30
	12	GO:000472 1	phosphoprotein phosphatase activity	0.028217	39
	13	GO:000551 5	protein binding	0.030939	2455
	14	GO:001679 6	exonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	0.032502	62
	15	GO:000885 5	exodeoxyribonuclease VII activity	0.036221	49
	16	GO:000452 7	exonuclease activity	0.036221	83
	17	GO:004573 5	nutrient reservoir activity	0.036637	26
	18	GO:000554	phospholipid binding	0.040345	52

	3				
19	GO:000875	S-adenosylmethionine-dependent	0.04293	116	
	7	methyltransferase activity			
20	GO:000452	exodeoxyribonuclease activity	0.044018	51	
	9				
21	GO:001689	exodeoxyribonuclease activity, producing	0.044018	51	
	5	5'-phosphomonoesters			
22	GO:000817	RNA methyltransferase activity	0.048527	79	
	3				

---