

**Table S9: GO analysis of upregulated unknown transcript in developmental stage.**

Level	GO ID	GO Name	Nodescore	#Seqs
1	GO:0008150	biological_process	2.8	11
2	GO:0009987	cellular process	4.04	10
2	GO:0008152	metabolic process	1.43	7
2	GO:0051179	localization	0.86	4
2	GO:0050789	regulation of biological process	0.49	3
2	GO:0065007	biological regulation	0.29	3
2	GO:0050896	response to stimulus	0.35	2
2	GO:0048519	negative regulation of biological process	0.04	1
2	GO:0048518	positive regulation of biological process	0.21	1
3	GO:0044237	cellular metabolic process	1.31	6
3	GO:0071704	organic substance metabolic process	1.33	5
3	GO:0044238	primary metabolic process	1.59	5
3	GO:0006807	nitrogen compound metabolic process	0.7	4
3	GO:0055085	transmembrane transport	4	4
3	GO:0051234	establishment of localization	1.44	4

3	GO:0009058	biosynthetic process	0.52	3
3	GO:0050794	regulation of cellular process	0.72	3
3	GO:0051716	cellular response to stimulus	0.58	2
3	GO:0019222	regulation of metabolic process	0.31	2
3	GO:0007154	cell communication	0.49	2
3	GO:0009056	catabolic process	0.36	1
3	GO:0007165	signal transduction	0.6	1
3	GO:0060148	positive regulation of post-transcriptional gene silencing	0.13	1
3	GO:0048523	negative regulation of cellular process	0.04	1
3	GO:0007049	cell cycle	0.22	1
3	GO:0023052	signaling	0.36	1
3	GO:0009605	response to external stimulus	0.08	1
3	GO:0061919	process utilizing autophagic mechanism	0.6	1
3	GO:0071840	cellular component organization or biogenesis	0.09	1
3	GO:0006950	response to stress	0.22	1
3	GO:0009892	negative regulation of metabolic process	0.06	1
3	GO:0022402	cell cycle process	0.36	1

3	GO:0009893	positive regulation of metabolic process	0.35	1
3	GO:0048522	positive regulation of cellular process	0.21	1
4	GO:0006810	transport	2.4	4
4	GO:0034641	cellular nitrogen compound metabolic process	0.53	4
4	GO:0043170	macromolecule metabolic process	1.22	4
4	GO:0044249	cellular biosynthetic process	0.87	3
4	GO:1901576	organic substance biosynthetic process	0.87	3
4	GO:0043603	amide metabolic process	0.43	2
4	GO:1901564	organonitrogen compound metabolic process	0.72	2
4	GO:0031323	regulation of cellular metabolic process	0.31	2
4	GO:0080090	regulation of primary metabolic process	0.29	2
4	GO:0006725	cellular aromatic compound metabolic process	0.27	2
4	GO:0019538	protein metabolic process	1.2	2
4	GO:0060255	regulation of macromolecule metabolic process	0.52	2
4	GO:0051171	regulation of nitrogen compound metabolic process	0.29	2
4	GO:0006139	nucleobase-containing compound metabolic process	0.45	2
4	GO:1901360	organic cyclic compound metabolic process	0.27	2

4	GO:0046483	heterocycle metabolic process	0.27	2
4	GO:0016043	cellular component organization	0.09	1
4	GO:0009991	response to extracellular stimulus	0.13	1
4	GO:0071496	cellular response to external stimulus	0.13	1
4	GO:0006914	autophagy	1	1
4	GO:0051726	regulation of cell cycle	0.36	1
4	GO:0006793	phosphorus metabolic process	0.36	1
4	GO:0009889	regulation of biosynthetic process	0.07	1
4	GO:0005975	carbohydrate metabolic process	1	1
4	GO:0035556	intracellular signal transduction	1	1
4	GO:0051173	positive regulation of nitrogen compound metabolic process	0.35	1
4	GO:0009890	negative regulation of biosynthetic process	0.06	1
4	GO:0009891	positive regulation of biosynthetic process	0.08	1
4	GO:0042594	response to starvation	0.36	1
4	GO:0031324	negative regulation of cellular metabolic process	0.06	1
4	GO:0044248	cellular catabolic process	0.6	1
4	GO:0031325	positive regulation of cellular metabolic process	0.35	1

4	GO:0031668	cellular response to extracellular stimulus	0.22	1
4	GO:0044085	cellular component biogenesis	0.13	1
4	GO:0010605	negative regulation of macromolecule metabolic process	0.11	1
4	GO:0044786	cell cycle DNA replication	0.36	1
4	GO:0010564	regulation of cell cycle process	0.6	1
4	GO:1900370	positive regulation of post-transcriptional gene silencing by RNA	0.22	1
4	GO:0010604	positive regulation of macromolecule metabolic process	0.58	1
4	GO:0033554	cellular response to stress	0.36	1
5	GO:0009059	macromolecule biosynthetic process	1.45	3
5	GO:0006518	peptide metabolic process	0.72	2
5	GO:0019219	regulation of nucleobase-containing compound metabolic process	0.48	2
5	GO:0006412	translation	2	2
5	GO:0044271	cellular nitrogen compound biosynthetic process	0.43	2
5	GO:0043604	amide biosynthetic process	0.72	2
5	GO:1901566	organonitrogen compound biosynthetic process	0.72	2
5	GO:0090304	nucleic acid metabolic process	0.47	2
5	GO:0031327	negative regulation of cellular biosynthetic process	0.11	1

5	GO:0045935	positive regulation of nucleobase-containing compound metabolic process	0.58	1
5	GO:0022607	cellular component assembly	0.13	1
5	GO:0009267	cellular response to starvation	0.6	1
5	GO:0006796	phosphate-containing compound metabolic process	0.6	1
5	GO:0031669	cellular response to nutrient levels	0.36	1
5	GO:0022613	ribonucleoprotein complex biogenesis	0.22	1
5	GO:0010557	positive regulation of macromolecule biosynthetic process	0.22	1
5	GO:0042023	DNA endoreduplication	0.6	1
5	GO:0031326	regulation of cellular biosynthetic process	0.12	1
5	GO:2000637	positive regulation of miRNA-mediated gene silencing	0.36	1
5	GO:0032875	regulation of DNA endoreduplication	1	1
5	GO:0010556	regulation of macromolecule biosynthetic process	0.21	1
5	GO:0031667	response to nutrient levels	0.22	1
5	GO:0043933	protein-containing complex organization	0.16	1
5	GO:0010558	negative regulation of macromolecule biosynthetic process	0.18	1
5	GO:0031328	positive regulation of cellular biosynthetic process	0.13	1
5	GO:0051052	regulation of DNA metabolic process	0.22	1

5	GO:0051252	regulation of RNA metabolic process	0.58	1
5	GO:0051254	positive regulation of RNA metabolic process	0.96	1
6	GO:0010467	gene expression	1.62	3
6	GO:0043043	peptide biosynthetic process	1.2	2
6	GO:0010468	regulation of gene expression	0.35	1
6	GO:2000630	positive regulation of miRNA metabolic process	1	1
6	GO:0070920	regulation of regulatory ncRNA processing	0.22	1
6	GO:1903800	positive regulation of miRNA processing	0.6	1
6	GO:0071824	protein-DNA complex organization	0.05	1
6	GO:0006275	regulation of DNA replication	0.36	1
6	GO:0043562	cellular response to nitrogen levels	0.6	1
6	GO:0071826	protein-RNA complex organization	0.22	1
6	GO:0016070	RNA metabolic process	0.65	1
6	GO:0006995	cellular response to nitrogen starvation	1	1
6	GO:0022618	protein-RNA complex assembly	0.36	1
6	GO:2000628	regulation of miRNA metabolic process	0.6	1
6	GO:0016310	phosphorylation	1	1

6	GO:0010629	negative regulation of gene expression	0.29	1
6	GO:0006259	DNA metabolic process	0.13	1
6	GO:0065003	protein-containing complex assembly	0.22	1
6	GO:0010628	positive regulation of gene expression	0.36	1
7	GO:0060147	regulation of post-transcriptional gene silencing	0.08	1
7	GO:1903798	regulation of miRNA processing	0.36	1
7	GO:0040029	epigenetic regulation of gene expression	0.13	1
7	GO:0016441	post-transcriptional gene silencing	0.08	1
7	GO:0031047	regulatory ncRNA-mediated gene silencing	0.49	1
7	GO:0090329	regulation of DNA-templated DNA replication	0.6	1
7	GO:0000387	spliceosomal snRNP assembly	0.6	1
7	GO:0016071	mRNA metabolic process	0.13	1
7	GO:0010608	post-transcriptional regulation of gene expression	0.05	1
7	GO:0006396	RNA processing	0.21	1
7	GO:2000636	positive regulation of primary miRNA processing	1	1
7	GO:0006325	chromatin organization	0.08	1
7	GO:0060966	regulation of gene silencing by regulatory ncRNA	0.13	1



7	GO:0045814	negative regulation of gene expression, epigenetic	0.22	1
7	GO:0006260	DNA replication	0.22	1
7	GO:0034660	ncRNA metabolic process	0.44	1
8	GO:0006261	DNA-templated DNA replication	0.36	1
8	GO:0000244	spliceosomal tri-snRNP complex assembly	1	1
8	GO:0034470	ncRNA processing	0.13	1
8	GO:0070918	regulatory ncRNA processing	0.22	1
8	GO:0010586	miRNA metabolic process	0.6	1
8	GO:0006338	chromatin remodeling	0.13	1
8	GO:0035194	regulatory ncRNA-mediated post-transcriptional gene silencing	0.13	1
8	GO:0031507	heterochromatin formation	0.36	1
8	GO:0006397	mRNA processing	0.22	1
8	GO:0031048	regulatory ncRNA-mediated heterochromatin formation	0.6	1
8	GO:2000634	regulation of primary miRNA processing	0.6	1
8	GO:0008380	RNA splicing	0.08	1
8	GO:1900368	regulation of post-transcriptional gene silencing by regulatory ncRNA	0.13	1
9	GO:0035195	miRNA-mediated post-transcriptional gene silencing	0.22	1

9	GO:0080188	gene silencing by RNA-directed DNA methylation	1	1
9	GO:0060964	regulation of miRNA-mediated gene silencing	0.22	1
9	GO:0000398	mRNA splicing, via spliceosome	0.36	1
9	GO:0035196	miRNA processing	0.36	1
9	GO:0070828	heterochromatin organization	0.22	1
9	GO:0000375	RNA splicing, via transesterification reactions	0.13	1
9	GO:0140718	facultative heterochromatin formation	0.36	1
10	GO:0031053	primary miRNA processing	0.6	1
10	GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	0.22	1
10	GO:0006346	DNA methylation-dependent heterochromatin formation	0.6	1

Level	GO ID	GO Name	Nodescore	#Seqs
1	GO:0003674	molecular_function	3.96	8
2	GO:0005215	transporter activity	0.31	4
2	GO:0003824	catalytic activity	0.4	5
2	GO:0005198	structural molecule activity	1.2	2
2	GO:0005488	binding	1.21	7

2	GO:0098772	molecular function regulator activity	0.13	1
2	GO:0140657	ATP-dependent activity	3.84	4
3	GO:0003735	structural constituent of ribosome	2	2
3	GO:0036094	small molecule binding	1.08	5
3	GO:0016740	transferase activity	0.13	1
3	GO:0016787	hydrolase activity	0.31	4
3	GO:0140096	catalytic activity, acting on a protein	0.36	1
3	GO:0097367	carbohydrate derivative binding	0.65	5
3	GO:0022857	transmembrane transporter activity	0.52	4
3	GO:0042626	ATPase-coupled transmembrane transporter activity	2.4	4
3	GO:0097159	organic cyclic compound binding	2.02	7
3	GO:0016887	ATP hydrolysis activity	4	4
3	GO:0030234	enzyme regulator activity	0.22	1
3	GO:0140678	molecular function inhibitor activity	0.22	1
4	GO:0140359	ABC-type transporter activity	4	4
4	GO:0016772	transferase activity, transferring phosphorus-containing groups	0.22	1
4	GO:0019207	kinase regulator activity	0.36	1

4	GO:1901363	heterocyclic compound binding	1.8	5
4	GO:0032553	ribonucleotide binding	1.08	5
4	GO:0043167	ion binding	1.08	5
4	GO:0003676	nucleic acid binding	1.56	2
4	GO:0022804	active transmembrane transporter activity	0.86	4
4	GO:0016817	hydrolase activity, acting on acid anhydrides	0.52	4
4	GO:0004857	enzyme inhibitor activity	0.36	1
4	GO:0004672	protein kinase activity	0.6	1
4	GO:1901265	nucleoside phosphate binding	1.8	5
5	GO:0000166	nucleotide binding	0.65	5
5	GO:0032555	purine ribonucleotide binding	1.8	5
5	GO:0016818	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	0.86	4
5	GO:0015399	primary active transmembrane transporter activity	1.44	4
5	GO:0019887	protein kinase regulator activity	0.6	1
5	GO:0043168	anion binding	1.8	5
5	GO:0016773	phosphotransferase activity, alcohol group as acceptor	0.36	1
5	GO:0019210	kinase inhibitor activity	0.6	1

5	GO:0004674	protein serine/threonine kinase activity	1	1
5	GO:0003723	RNA binding	2.6	2
5	GO:0035639	purine ribonucleoside triphosphate binding	3	5
5	GO:0016301	kinase activity	0.36	1
6	GO:0032559	adenyl ribonucleotide binding	3	5
6	GO:0005524	ATP binding	5	5
6	GO:0003729	mRNA binding	1	1
6	GO:0017076	purine nucleotide binding	1.08	5
6	GO:0004860	protein kinase inhibitor activity	1	1
6	GO:0016462	pyrophosphatase activity	1.44	4
7	GO:0030554	adenyl nucleotide binding	1.8	5
7	GO:0017111	ribonucleoside triphosphate phosphatase activity	2.4	4

Level	GO ID	GO Name	Nodescore	#Seqs
1	GO:0005575	cellular_component	5.71	11
2	GO:0110165	cellular anatomical entity	8.61	11
2	GO:0032991	protein-containing complex	1.09	3

3	GO:0012505	endomembrane system	0.6	1
3	GO:0099080	supramolecular complex	0.13	1
3	GO:0043226	organelle	1.07	5
3	GO:0005622	intracellular anatomical structure	3.93	6
3	GO:0120114	Sm-like protein family complex	0.13	1
3	GO:0016020	membrane	8	8
3	GO:1902494	catalytic complex	0.6	1
3	GO:0140513	nuclear protein-containing complex	0.49	1
3	GO:0005737	cytoplasm	5.92	4
3	GO:1990904	ribonucleoprotein complex	1.57	3
4	GO:0005681	spliceosomal complex	0.6	1
4	GO:0005739	mitochondrion	1	1
4	GO:0005773	vacuole	0.6	1
4	GO:0009536	plastid	0.6	1
4	GO:0043229	intracellular organelle	1.78	5
4	GO:0030532	small nuclear ribonucleoprotein complex	0.22	1
4	GO:0071013	catalytic step 2 spliceosome	1	1

4	GO:0099081	supramolecular polymer	0.22	1
4	GO:0043227	membrane-bounded organelle	1.26	4
4	GO:0005783	endoplasmic reticulum	1	1
4	GO:0043228	non-membrane-bounded organelle	0.52	3
4	GO:0044391	ribosomal subunit	1.8	2
5	GO:0043232	intracellular non-membrane-bounded organelle	0.86	3
5	GO:0043231	intracellular membrane-bounded organelle	2.1	4
5	GO:0009507	chloroplast	1	1
5	GO:0005776	autophagosome	1	1
5	GO:0015935	small ribosomal subunit	2	2
5	GO:0015934	large ribosomal subunit	1	1
5	GO:0099512	supramolecular fiber	0.36	1
5	GO:0097525	spliceosomal snRNP complex	0.36	1
6	GO:0005840	ribosome	1.08	2
6	GO:0005634	nucleus	0.29	1
6	GO:0097526	spliceosomal tri-snRNP complex	0.6	1
6	GO:0005856	cytoskeleton	0.36	1

6	GO:0099513	polymeric cytoskeletal fiber	0.6	1
7	GO:0015630	microtubule cytoskeleton	0.6	1
7	GO:0005874	microtubule	1	1
7	GO:0046540	U4/U6 x U5 tri-snRNP complex	1	1