S3 Table. Top 10 significant GOs in the three samples

GO ID	Total Gene num	DEGs num	FDR	Level	Terms
Wat6					
GO:0016491	1856	571	1.81E-14	3	oxidoreductase activity
GO:1901700	1372	428	2.33E-11	4	response to oxygen-containing compound
GO:0005576	1222	387	2.98E-11	2	extracellular region
GO:0001071	1345	417	6.13E-11	2	nucleic acid binding transcription factor activity
GO:0003700	1345	417	6.13E-11	3	sequence-specific DNA binding transcription factor activity
GO:0015979	192	86	5.45E-09	4	photosynthesis
GO:0042221	2287	643	1.21E-08	3	response to chemical stimulus
GO:0009637	73	43	1.60E-08	6	response to blue light
GO:0006979	368	138	2.59E-08	4	response to oxidative stress
GO:0046906	485	171	4.00E-08	4	tetrapyrrole binding
Wat24					
GO:0003735	471	283	1.37E-75	3	structural constituent of ribosome
GO:0005840	538	307	6.59E-75	4	ribosome
GO:0005198	606	304	5.99E-57	2	structural molecule activity
GO:0044391	216	147	3.23E-48	4	ribosomal subunit
GO:0022626	198	135	2.37E-44	5	cytosolic ribosome
GO:0006412	671	301	1.24E-43	6	translation
GO:0030529	801	328	1.31E-37	3	ribonucleoprotein complex
GO:0044445	243	139	3.99E-33	5	cytosolic part
GO:0022625	96	74	1.64E-29	6	cytosolic large ribosomal subunit
GO:0015934	125	85	2.00E-27	5	large ribosomal subunit
GO:0005576	1222	415	2.65E-26	2	extracellular region
Wat24:Wat6					
GO:0005840	538	175	1.03E-26	4	ribosome
GO:0003735	471	156	8.92E-25	3	structural constituent of ribosome
GO:0005198	606	175	1.68E-20	2	structural molecule activity
GO:0006412	671	176	6.93E-16	6	translation
GO:0005576	1222	272	7.80E-15	2	extracellular region
GO:0044391	216	77	1.19E-13	4	ribosomal subunit
GO:0046906	485	133	1.75E-13	4	tetrapyrrole binding
GO:0016491	1856	372	1.75E-13	3	oxidoreductase activity
GO:0020037	452	125	6.13E-13	5	heme binding
GO:0022626	198	71	7.60E-13	5	cytosolic ribosome