

Supplementary Table 12: GO profiling of essential orthologous pairs in fission yeast and budding yeast

GO ID	GO term	Corrected P-value	Non-essential pair gene annotation	Total gene annotation
1. Macromolecule metabolism and cellular biosynthesis				
GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	4.41e-46	343	1,236
GO:0043283	biopolymer metabolic process	3.28e-42	461	2,017
GO:0034960	cellular biopolymer metabolic process	8.20e-37	365	1,472
GO:0006506	GPI anchor biosynthetic process	1.29e-10	21	27
GO:0034645	cellular macromolecule biosynthetic process	1.66e-10	228	1,058
GO:0046489	phosphoinositide biosynthetic process	7.99e-10	22	31
GO:0042158	lipoprotein biosynthetic process	9.01e-10	26	42
GO:0008610	lipid biosynthetic process	2.20e-06	45	130
GO:0008654	phospholipid biosynthetic process	3.87e-06	25	52
GO:0046467	membrane lipid biosynthetic process	3.33e-05	28	68
GO:0034961	cellular biopolymer biosynthetic process	3.68e-05	191	957
2. Macromolecular complex assembly				
GO:0022613	ribonucleoprotein complex biogenesis and assembly	9.23e-54	151	289
GO:0042254	ribosome biogenesis	1.99e-48	125	222
GO:0016043	cellular component organization	1.37e-35	336	1,314
GO:0043933	macromolecular complex subunit organization	2.42e-17	117	359
GO:0034621	cellular macromolecular complex subunit organization	7.14e-16	107	326
GO:0065003	macromolecular complex assembly	4.98e-15	106	329
GO:0034622	cellular macromolecular complex assembly	1.38e-13	96	296
GO:0022607	cellular component assembly	6.651e-12	116	410
GO:0022618	ribonucleoprotein complex assembly	1.35e-07	35	81
GO:0065004	protein-DNA complex assembly	0.0005	41	134
GO:0000245	spliceosome assembly	0.0007	9	11
3. Gene expression				
GO:0016070	RNA metabolic process	9.54e-50	284	885
GO:0006396	RNA processing	1.91e-48	173	393
GO:0006364	rRNA processing	4.25e-40	91	144
GO:0016072	rRNA metabolic process	9.96e-40	91	145
GO:0034660	ncRNA metabolic process	2.60e-36	122	259

GO:0010467	gene expression	1.21e-33	303	1,147
GO:0034470	ncRNA processing	3.19e-30	103	218
GO:0006397	mRNA processing	1.57e-21	74	154
GO:0016071	mRNA metabolic process	2.70e-17	82	207
GO:0008380	RNA splicing	5.03e-17	60	125
GO:0000398	nuclear mRNA splicing, via spliceosome	8.36e-15	54	114
GO:0006352	transcription initiation	5.49e-14	34	53
GO:0006383	transcription from RNA polymerase III promoter	2.68e-12	24	31
GO:0006367	transcription initiation from RNA polymerase II promoter	5.58e-12	25	34
GO:0030490	maturation of SSU-rRNA	1.29e-10	21	27
GO:0006360	transcription from RNA polymerase I promoter	2.05e-08	20	29
GO:0006378	mRNA polyadenylation	8.10e-05	13	19
GO:0006384	transcription initiation from RNA polymerase III promoter	0.0007	9	11
GO:0006366	transcription from RNA polymerase II promoter	0.0012	54	202
GO:0032774	RNA biosynthetic process	0.0012	95	424
GO:0031124	mRNA 3'-end processing	0.0019	13	23
GO:0006418	tRNA aminoacylation for protein translation	0.0025	17	37
GO:0000394	RNA splicing, via endonucleolytic cleavage and ligation	0.0060	6	6
GO:0006388	tRNA splicing	0.0061	6	6
GO:0043631	RNA polyadenylation	0.0067	13	25
GO:0006399	tRNA metabolic process	0.0079	36	123
4. Cell cycle related processes				
GO:0000278	mitotic cell cycle	9.39e-13	90	276
GO:0006270	DNA replication initiation	1.18e-11	34	60

Fission yeast annotations are used. The number of essential orthologous pairs is 715 and the total gene number is 4,836.