

Supplementary Table 5: GO profiling of all essential genes in fission yeast (A) and budding yeast (B)

GO ID	GO term	Corrected <i>P</i> -value	Essential gene annotation	Total gene annotation
A. Fission yeast				
1. Macromolecule metabolism and cellular biosynthesis				
GO:0034960	cellular biopolymer metabolic process	3.97e-43	581	1,148
GO:0044260	cellular macromolecule metabolic process	9.59e-43	771	2,133
GO:0043283	biopolymer metabolic process	1.64e-41	730	1,991
GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	6.56e-32	482	1,208
GO:0034645	cellular macromolecule biosynthetic process	1.83e-22	406	1,042
GO:0004429	Cellular biosynthetic process	2.28e-25	504	1,375
GO:0034961	cellular biopolymer biosynthetic process	3.90e-16	356	941
GO:0006506	GPI anchor biosynthetic process	4.52e-10	25	27
GO:0046489	phosphoinositide biosynthetic process	1.51e-09	27	31
GO:004215	lipoprotein biosynthetic process	1.40e-08	32	42
GO:000865	phospholipid biosynthetic process	1.44e-05	33	52
GO:0008610	lipid biosynthetic process	6.90e-05	62	130
GO:0046467	membrane lipid biosynthetic process	0.00015	38	68
GO:0044267	cellular protein metabolic process	0.00019	368	1,153
2. Macromolecular complex assembly				
GO:0022613	ribonucleoprotein complex biogenesis and assembly	4.62e-43	186	287
GO:0042254	ribosome biogenesis	2.08e-34	146	221
GO:0016043	cellular component organization	4.35e-33	511	1,295
GO:0006996	organelle organization	1.59e-22	379	953
GO:0043933	macromolecular complex subunit organization	4.26e-12	157	352
GO:0065003	macromolecular complex assembly	8.29e-12	146	322
GO:0034621	cellular macromolecular complex subunit organization	2.047e-11	144	319
GO:0034622	cellular macromolecular complex assembly	3.67e-11	133	289
GO:0007005	mitochondrion organization and biogenesis	3.18e-13	127	259
GO:0022618	ribonucleoprotein complex assembly	5.56e-09	50	80
GO:0022607	cellular component assembly	1.55e-08	164	403
GO:006500	protein-DNA complex assembly	0.009	57	131
3. Gene expression				
GO:0010467	gene expression	1.31e-44	488	1,130
GO:0006396	RNA processing	2.43e-41	225	387
GO:0016070	RNA metabolic process	2.36e-38	392	872
GO:0034660	ncRNA metabolic process	6.27e-33	160	258
GO:0006364	rRNA processing	2.67e-29	104	143
GO:0016072	rRNA metabolic process	7.27e-29	104	144
GO:0006397	mRNA processing	2.18e-22	99	150
GO:0034470	ncRNA processing	1.90e-21	126	217

GO:0008380	RNA splicing	6.07e-21	84	121
GO:0000398	nuclear mRNA splicing, via spliceosome	5.47e-19	77	111
GO:0016071	mRNA metabolic process	8.56e-16	111	203
GO:0006418	tRNA aminoacylation for protein translation	1.73e-11	32	37
GO:0006412	translation	2.62e-10	152	351
GO:0006367	transcription initiation from RNA polymerase II promoter	2.19e-09	28	33
GO:0032543	mitochondrial translation	1.45e-22	84	117
GO:0006352	transcription initiation	4.26e-09	37	51
GO:0006383	transcription from RNA polymerase III promoter	7.8e-08	25	30
GO:0030490	maturation of SSU-rRNA	1.95e-07	23	27
GO:0006399	tRNA metabolic process	1.51e-06	63	123
GO:0006360	transcription from RNA polymerase I promoter	2.89e-05	22	29
GO:0006379	mRNA cleavage	0.0020	14	17
4. Cell cycle related processes				
GO:0000278	mitotic cell cycle	9.61e-13	131	273
GO:0000087	M phase of mitotic cell cycle	6.84e-10	68	120
GO:0007067	mitosis	1.167e-09	66	116
GO:0006270	DNA replication initiation	1.22e-06	38	60
GO:0007091	mitotic metaphase/anaphase transition	2.63e-06	22	27
GO:0006260	DNA replication	3.43e-06	70	144
GO:0007049	cell cycle	5.97e-06	196	534
GO:0051726	regulation of cell cycle	6.15e-06	98	226
GO:0000910	cytokinesis	0.0072	59	136
GO:0031145	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	0.006	13	16
5. Intracellular protein transport				
GO:0033036	macromolecule localization	1.93e-06	185	492
GO:0008104	protein localization	4.27e-05	166	447
GO:0017038	protein import	0.00020	35	61
GO:0015031	protein transport	0.000228	119	305
GO:0043681	protein import into mitochondrion	0.00066	25	39
GO:0006626	protein targeting to mitochondrion	0.00667	28	50
GO:0030150	protein import into mitochondrial matrix	0.0069	14	18
6. Miscellaneous				
GO:0015991	ATP hydrolysis coupled proton transport	6.84e-06	14	14
GO:0007035	vacuolar acidification	0.0022	17	23
B. Budding yeast				
1. Macromolecule metabolism and cellular biosynthesis				
GO:0043283	biopolymer metabolic process	8.57e-67	671	2,335
GO:0044260	cellular macromolecule metabolic process	1.63e-65	702	2,519
GO:0034960	cellular biopolymer metabolic process	3.03e-57	549	1,800
GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	5.30e-60	513	1,600

GO:0034645	cellular macromolecule biosynthetic process	4.56e-16	358	1,369
GO:0034961	cellular biopolymer biosynthetic process	8.36e-11	314	1,246
GO:0046489	phosphoinositide biosynthetic process	1.80e-10	24	30
GO:0006506	GPI anchor biosynthetic process	9.63e-10	22	27
GO:0008610	lipid biosynthetic process	9.26e-07	58	150
GO:0042158	lipoprotein biosynthetic process	7.67e-06	27	50
GO:0046467	membrane lipid biosynthetic process	0.0030	34	88
GO:0006696	ergosterol biosynthetic process	0.0061	15	26 *
2. Macromolecular complex assembly				
GO:0022613	ribonucleoprotein complex biogenesis and assembly	2.14e-85	233	375
GO:0016043	cellular component organization	7.63e-71	566	1,758
GO:0042254	ribosome biogenesis	3.86e-70	187	292
GO:0006996	organelle organization	6.54e-64	435	1,214
GO:0034621	cellular macromolecular complex subunit organization	1.95e-48	199	404
GO:0034622	cellular macromolecular complex assembly	1.30e-39	168	343
GO:0022618	ribonucleoprotein complex assembly	2.98e-23	83	148
GO:0065004	protein-DNA complex assembly	1.84e-19	65	110
GO:0042273	ribosomal large subunit biogenesis	6.23e-14	42	65*
GO:0006267	pre-replicative complex assembly	5.74e-09	15	15 *
GO:0042255	ribosome assembly	4.73e-08	34	62 *
GO:0000027	ribosomal large subunit assembly and maintenance	6.23e-14	26	41*
GO:0051123	transcriptional preinitiation complex assembly	5.89e-06	11	11 *
GO:0034623	cellular macromolecular complex disassembly	2.36e-06	32	63 *
GO:0042257	ribosomal subunit assembly	2.51e-06	30	57 *
GO:0043624	cellular protein complex disassembly	0.00015	28	59 *
3. Gene expression				
GO:0006396	RNA processing	1.75e-81	260	466
GO:0016070	RNA metabolic process	9.58e-72	438	1,170
GO:0034660	ncRNA metabolic process	7.13e-65	199	341
GO:0006364	rRNA processing	2.44e-63	150	214
GO:0010467	gene expression	1.90e-62	488	1,462
GO:0016072	rRNA metabolic process	9.58e-72	151	219
GO:0034470	ncRNA processing	1.98e-57	176	299
GO:0006397	mRNA processing	7.83e-33	168	343
GO:0016071	mRNA metabolic process	3.79e-29	124	249
GO:0000398	nuclear mRNA splicing, via	8.43e-25	65	95

	spliceosome			
GO:0008380	RNA splicing	9.73e-22	78	139
GO:0030490	maturation of SSU-rRNA	7.47e-17	47	70
GO:0006352	transcription initiation	3.35e-16	41	57
GO:0006379	mRNA cleavage	9.16e-16	24	24
GO:0000966	RNA 5'-end processing	3.02e-13	25	28 *
GO:0006383	transcription from RNA polymerase III promoter	4.62e-12	29	38
GO:0006399	tRNA metabolic process	5.27e-10	61	139
GO:0006367	transcription initiation from RNA polymerase II promoter	5.63e-10	30	45
GO:0006360	transcription from RNA polymerase I promoter	8.33e-09	26	38
GO:0006378	mRNA polyadenylation	1.07e-07	16	18 *
GO:0006366	transcription from RNA polymerase II promoter	2.27e-07	111	357 *
GO:0032774	RNA biosynthetic process	4.37e-07	181	675 *
GO:0043144	snoRNA processing	5.69e-07	16	19 *
GO:0006384	transcription initiation from RNA polymerase III promoter	1.04e-06	12	12 *
GO:0031123	RNA 3'-end processing	2.50e-06	29	54 *
GO:0006413	translational initiation	0.00012	25	49
GO:0006418	tRNA aminoacylation for protein translation	2.07e-07	21	38
GO:0006353	transcription termination	0.00021	14	20 *
GO:0008033	tRNA processing	0.00088	37	95*
4. Cell cycle related processes				
GO:0000278	mitotic cell cycle	3.94e-25	141	327
GO:0007049	cell cycle	1.68e-21	206	605
GO:0000087	M phase of mitotic cell cycle	4.32e-18	90	192
GO:0007067	mitosis	3.85e-16	83	179
GO:0006270	DNA replication initiation	6.77e-19	31	36
GO:0007059	chromosome segregation	3.57e-13	68	145 *
GO:0022402	cell cycle process	4.66e-13	156	482
GO:0006260	DNA replication	8.58e-13	71	157
GO:0000226	microtubule cytoskeleton organization and biogenesis	1.69e-13	51	91*
GO:0007010	cytoskeleton organization and biogenesis	1.92e-11	88	226*
GO:0006271	DNA strand elongation during DNA replication	5.10e-10	25	33 *
GO:0007017	microtubule-based process	2.96e-10	53	111*
GO:0000070	mitotic sister chromatid segregation	7.65e-07	34	67 *
GO:0007020	microtubule nucleation	1.107e-10	18	22*
GO:0051300	spindle pole body organization and biogenesis	2.72e-06	14	16*
GO:0030474	spindle pole body duplication	2.15e-06	13	14*
GO:0007052	mitotic spindle organization and biogenesis	7.32e-05	24	45*
GO:0051276	chromosome organization and biogenesis	3.96e-05	117	414 *
GO:0007051	spindle organization and biogenesis	1.34e-05	26	48*

GO:0051329	interphase of mitotic cell cycle	0.00012	45	118 *
GO:0007062	sister chromatid cohesion	0.0036	19	37 *
GO:0006272	leading strand elongation	0.0012	11	14 *
5. Intracellular Protein Transport				
GO:0000054	ribosome export from nucleus	9.10e-12	25	30 *
GO:0051168	nuclear export	3.98e-09	50	107 *
GO:0033036	macromolecule localization	2.72e-08	167	591
GO:0008104	protein localization	6.45e-08	152	529
GO:0006913	nucleocytoplasmic transport	2.54e-07	55	135*
GO:0015031	protein transport	4.05e-07	140	487
GO:0051640	organelle localization	2.48e-05	40	95 *
GO:0006906	vesicle fusion	4.05e-05	20	33 *
GO:0043681	protein import into mitochondrion	0.00012	22	40
GO:0006886	intracellular protein transport	0.00014	91	307 *
GO:0006888	ER to Golgi vesicle-mediated transport	0.00021	36	87 *
GO:0006626	protein targeting to mitochondrion	0.00053	25	52
GO:0017038	protein import	0.00054	42	112
GO:0048193	Golgi vesicle transport	0.00069	58	176 *
GO:0045047	protein targeting to ER	0.0035	16	28 *
GO:0006890	retrograde vesicle-mediated transport, Golgi to ER	0.0065	16	29 *
GO:0030150	protein import into mitochondrial matrix	0.0089	13	21
6. Miscellaneous				
GO:0006511	ubiquitin-dependent protein catabolic process	5.10e-06	57	182
GO:0006405	RNA export from nucleus	0.0046	32	82 *
GO:0050657	nucleic acid transport	2.71e-06	37	99 *

For our analyses we have used the 4,836 dataset modified by the previously published data for the 19 previously characterized genes where we had different dispensability. This increased the number of essential genes from 1,249 to 1,260 and from this analysis dataset we conclude that 26.1% of fission yeast genes are essential for viability under the conditions used. Terms marked with an asterisk* are those enriched in the set of budding yeast essential genes but not in the fission yeast essential gene set, but where the differences are a result of annotation differences (i.e., the fission yeast genes are annotated to higher level terms), and not to biological differences. Most of these terms are enriched in fission yeast but the enrichment is below the 95% significance threshold. They are not significant biological differences. The number of essential genes is 1,260 from fission yeast and 1,033 from budding yeast. The total number of genes is 4,836 from fission yeast and 5,776 from budding yeast. The GO analysis is described in Methods in the main text. GO terms used to generate the data in **Fig. 2d** in the main text are cellular biosynthetic (process) (GO:0044249); cellular comp(onent) org(anization) (GO:0016043); (nucleobase) nucleotide (nucleoside) & nucleic (acid metabolic process) (GO:0006139); RNA processing (GO:0006396); ribosome biogenesis (GO:0042254); protein localization (GO:0008104); translation (GO:0006412); mitotic cell cycle (GO:0000278); DNA replication (GO:0006260); general transcription (union of GO:0006360, GO:0006383 and GO:0006352). Except where mentioned for transmembrane transport, all figures were taken from the enrichment data in **Supplementary Tables 5 and 6**. The terms used were selected to provide broad genome coverage of highly significant but also biologically informative terms.