

**Table S11.1.** GO molecular function enrichments (p-value < 0.1) for undetected proteins in *S. pombe* with high (Top 25% quantile), medium (middle 50% quantile) and low (bottom 25% quantile) mRNA concentration. Background set of genes in a given class (high, medium, low) are all genes in the respective class that have a GO annotation.

mRNA Concentration	GO.ID	Term	Annotated	Significant	Expected	pvalue
High (n=222)	GO:0015171	amino acid transmembrane transporter activity	8	7	0.96	2.10E-06
	GO:0003735	structural constituent of ribosome	156	33	18.7	0.00014
	GO:0019843	rRNA binding	18	8	2.16	0.0005
	GO:0008270	zinc ion binding	59	16	7.07	0.00072
	GO:0003677	DNA binding	74	20	8.87	0.00125
	GO:0000978	RNA polymerase II core promoter proximal region sequence-specific DNA binding	27	7	3.24	0.03327
	GO:0004842	ubiquitin-protein ligase activity	15	4	1.8	0.09351
Medium (n=468)	GO:0022857	transmembrane transporter activity	61	23	8.71	0.00013
	GO:0015171	amino acid transmembrane transporter activity	11	7	1.57	0.00022
	GO:0008270	zinc ion binding	160	36	22.84	0.00176
	GO:0004674	protein serine/threonine kinase activity	62	16	8.85	0.01005
	GO:0030674	protein binding, bridging	11	5	1.57	0.01253
	GO:0004842	ubiquitin-protein ligase activity	47	12	6.71	0.02694
	GO:0046982	protein heterodimerization activity	19	6	2.71	0.0423
	GO:0000978	RNA polymerase II core promoter proximal region sequence-specific DNA binding	53	12	7.57	0.06317
	GO:0003684	damaged DNA binding	12	4	1.71	0.07855
	GO:0005515	protein binding	325	56	46.39	0.08339
Low (n=240)	GO:0003677	DNA binding	161	34	22.98	0.09341
	GO:0003677	DNA binding	54	22	11.51	0.0043
	GO:0003684	damaged DNA binding	6	4	1.28	0.0204

**Table S11.2.** GO biological process enrichments (p-value < 0.1) for non-detected proteins in *S. pombe* with high (Top 25% quantile), medium (middle 50% quantile) and low (bottom 25% quantile) mRNA concentration. Background set of genes in a given class (high, medium, low) are all genes in the respective class that have a GO annotation.

mRNA Concentration	GO.ID	Term	Annotated	Significant	Expected	pvalue
High (n=222)	GO:0003333	amino acid transmembrane transport	9	8	1.24	8.60E-07
	GO:0006974	response to DNA damage stimulus	21	8	2.89	0.0035
	GO:0034220	ion transmembrane transport	9	5	1.24	0.0037
	GO:0000122	negative regulation of transcription from RNA polymerase II promoter	9	5	1.24	0.0037
	GO:0010389	regulation of G2/M transition of mitotic cell cycle	7	4	0.96	0.0086
	GO:0030071	regulation of mitotic metaphase/anaphase transition	10	6	1.38	0.0088
	GO:0007093	mitotic cell cycle checkpoint	8	5	1.1	0.0183
	GO:0010948	negative regulation of cell cycle process	19	6	2.61	0.0184
	GO:0031570	DNA integrity checkpoint	7	4	0.96	0.0185
	GO:0006334	nucleosome assembly	13	5	1.79	0.0235
	GO:0055085	transmembrane transport	37	19	5.09	0.0254
	GO:0006355	regulation of transcription, DNA-dependent	68	17	9.36	0.0334
	GO:0042254	ribosome biogenesis	71	13	9.77	0.0341
	GO:0007094	mitotic cell cycle spindle assembly checkpoint	6	3	0.83	0.0372
	GO:0002181	cytoplasmic translation	181	30	24.91	0.055
	GO:0033365	protein localization to organelle	7	3	0.96	0.0587
Medium (n=468)	GO:0055085	transmembrane transport	79	37	12.59	1.50E-08
	GO:0007131	reciprocal meiotic recombination	24	12	3.83	9.70E-05
	GO:0003333	amino acid transmembrane transport	14	8	2.23	0.00048
	GO:0006914	autophagy	18	9	2.87	0.00076
	GO:0006995	cellular response to nitrogen starvation	27	11	4.3	0.00167
	GO:0007165	signal transduction	100	24	15.94	0.00346
	GO:0006506	GPI anchor biosynthetic process	18	8	2.87	0.00385
	GO:0033314	mitotic cell cycle DNA replication checkpoint	22	9	3.51	0.0043
	GO:0000724	double-strand break repair via homologous recombination	15	7	2.39	0.00495
	GO:0030071	regulation of mitotic metaphase/anaphase transition	25	8	3.98	0.01248
	GO:0006470	protein dephosphorylation	26	9	4.14	0.01497
	GO:0016567	protein ubiquitination	58	16	9.24	0.01558
	GO:0030437	ascospore formation	45	13	7.17	0.01922
	GO:0006468	protein phosphorylation	84	20	13.39	0.03606
	GO:0046379	extracellular polysaccharide metabolic process	18	6	2.87	0.05341
	GO:0006281	DNA repair	49	16	7.81	0.07292
GO:0006974	response to DNA damage stimulus	70	22	11.16	0.07621	
GO:0000070	mitotic sister chromatid segregation	51	12	8.13	0.09949	
Low (n=240)	GO:0007131	reciprocal meiotic recombination	23	11	4.1	0.00077
	GO:0045892	negative regulation of transcription, DNA-dependent	25	5	4.46	0.00583
	GO:0000002	mitochondrial genome maintenance	9	5	1.61	0.01154
	GO:0071852	fungal-type cell wall organization or biogenesis	7	3	1.25	0.03159
	GO:0006200	ATP catabolic process	44	13	7.85	0.03496
	GO:0055085	transmembrane transport	15	6	2.68	0.03568
	GO:0034613	cellular protein localization	85	16	15.17	0.04889
	GO:0033554	cellular response to stress	78	22	13.92	0.05616
	GO:0006506	GPI anchor biosynthetic process	6	3	1.07	0.0734
	GO:0030437	ascospore formation	18	6	3.21	0.08339
GO:0031570	DNA integrity checkpoint	8	3	1.43	0.08364	
GO:0007093	mitotic cell cycle checkpoint	9	3	1.61	0.08385	

**Table S11.3.** GO cellular compartment enrichments (p-value < 0.1) for non-detected proteins in *S. pombe* with high (Top 25% quantile), medium (middle 50% quantile) and low (bottom 25% quantile) mRNA concentration. Background set of genes in a given class (high, medium, low) are all genes in the respective class that have a GO annotation.

mRNA Concentration	GO.ID	Term	Annotated	Significant	Expected	pvalue
High (n=222)	GO:0005886	plasma membrane	53	21	7.86	1.20E-07
	GO:0016021	integral to membrane	204	41	30.24	0.014
	GO:0022625	cytosolic large ribosomal subunit	76	17	11.27	0.043
	GO:0022627	cytosolic small ribosomal subunit	57	13	8.45	0.064
	GO:0005819	spindle	28	6	4.15	0.088
Medium (n=468)	GO:0016021	integral to membrane	520	129	88.4	8.00E-08
	GO:0005886	plasma membrane	86	36	14.62	1.20E-05
	GO:0000329	fungal-type vacuole membrane	53	22	9.01	1.60E-05
	GO:0005783	endoplasmic reticulum	318	74	54.06	0.00034
	GO:0005794	Golgi apparatus	165	44	28.05	0.0004
	GO:0005938	cell cortex	63	11	10.71	0.01004
	GO:0009277	fungal-type cell wall	11	5	1.87	0.02613
	GO:0032153	cell division site	154	31	26.18	0.07393
Low (n=240)	GO:0005783	endoplasmic reticulum	98	39	20.4	4.60E-05
	GO:0016021	integral to membrane	174	56	36.22	0.00013
	GO:0000139	Golgi membrane	11	7	2.29	0.00229
	GO:0005887	integral to plasma membrane	5	4	1.04	0.00758
	GO:0005789	endoplasmic reticulum membrane	30	12	6.24	0.02514
	GO:0005886	plasma membrane	19	10	3.95	0.03375

**Table S11.4.** GO molecular function enrichments (p-value < 0.1) for non-detected proteins in *S. cerevisiae* with high (Top 25% quantile), medium (middle 50% quantile) and low (bottom 25% quantile) mRNA concentration. Background set of genes in a given class (high, medium, low) are all genes in the respective class that have a GO annotation.

mRNA Concentration	GO.ID	Term	Annotated	Significant	Expected	pvalue
High (n=69)	GO:0015171	amino acid transmembrane transporter activity	11	2	0.19	0.014
	GO:0003735	structural constituent of ribosome	161	6	2.79	0.049
Medium (n=468)	GO:0016787	hydrolase activity	437	72	55.61	5.70E-06
	GO:0000030	mannosyltransferase activity	16	8	2.04	0.00032
	GO:0005215	transporter activity	102	20	12.98	0.00104
	GO:0016757	transferase activity, transferring glycosyl groups	51	17	6.49	0.02316
	GO:0015171	amino acid transmembrane transporter activity	7	3	0.89	0.04819
	GO:0008757	S-adenosylmethionine-dependent methyltransferase activity	12	4	1.53	0.05529
	GO:0016740	transferase activity	370	61	47.08	0.07795
	GO:0004721	phosphoprotein phosphatase activity	39	7	4.96	0.08369
Low (n=315)	GO:0003887	DNA-directed DNA polymerase activity	14	4	1.78	0.0913
	GO:0043169	cation binding	157	51	49	0.00032
	GO:0016798	hydrolase activity, acting on glycosyl bonds	12	9	3.75	0.00211
	GO:0003690	double-stranded DNA binding	9	7	2.81	0.0052
	GO:0005506	iron ion binding	13	6	4.06	0.03403
	GO:0016787	hydrolase activity	123	48	38.39	0.03908
	GO:0009055	electron carrier activity	10	6	3.12	0.05543
	GO:0016740	transferase activity	112	39	34.96	0.07356
	GO:0043130	ubiquitin binding	6	4	1.87	0.07953
	GO:0050660	flavin adenine dinucleotide binding	11	6	3.43	0.09088

**Table S11.5.** GO biological process enrichments (p-value < 0.1) for non-detected proteins in *S.cerevisiae* with high (Top 25% quantile), medium (middle 50% quantile) and low (bottom 25% quantile) mRNA concentration. Background set of genes in a given class (high, medium, low) are all genes in the respective class that have a GO annotation.

mRNA Concentration	GO.ID	Term	Annotated	Significant	Expected	pvalue
High (n=69)	GO:0032543	mitochondrial translation	23	4	0.47	0.00097
	GO:0003333	amino acid transmembrane transport	11	2	0.23	0.02007
	GO:0000087	M phase of mitotic cell cycle	22	2	0.45	0.07819
	GO:0016236	macroautophagy	5	1	0.1	0.09904
Medium (n=468)	GO:0055085	transmembrane transport	165	41	23.77	0.00035
	GO:0006506	GPI anchor biosynthetic process	23	10	3.31	0.00067
	GO:0008380	RNA splicing	77	24	11.09	0.00122
	GO:0006811	ion transport	42	14	6.05	0.0029
	GO:0006865	amino acid transport	23	10	3.31	0.00415
	GO:0008643	carbohydrate transport	9	5	1.3	0.00462
	GO:0006629	lipid metabolic process	101	28	14.55	0.00517
	GO:0000070	mitotic sister chromatid segregation	35	8	5.04	0.00945
	GO:0006487	protein N-linked glycosylation	19	7	2.74	0.01285
	GO:0000398	nuclear mRNA splicing, via spliceosome	48	13	6.92	0.01499
	GO:0006397	mRNA processing	132	32	19.02	0.03451
	GO:0006281	DNA repair	140	27	20.17	0.03508
	GO:0006470	protein dephosphorylation	28	8	4.03	0.03855
	GO:0016236	macroautophagy	14	5	2.02	0.03964
	GO:0055072	iron ion homeostasis	21	6	3.03	0.04208
	GO:0016042	lipid catabolic process	19	6	2.74	0.04463
	GO:0006623	protein targeting to vacuole	44	10	6.34	0.05682
GO:0003333	amino acid transmembrane transport	7	3	1.01	0.06637	
GO:0006260	DNA replication	58	11	8.36	0.0916	
Low (n=315)	GO:0006811	ion transport	18	11	5.25	0.0029
	GO:0006260	DNA replication	12	6	3.5	0.0251
	GO:0016567	protein ubiquitination	12	7	3.5	0.0321
	GO:0022900	electron transport chain	10	6	2.92	0.0404
	GO:0005975	carbohydrate metabolic process	43	18	12.54	0.0506
	GO:0007047	cellular cell wall organization	69	20	20.12	0.0536
	GO:0034727	piecemeal microautophagy of nucleus	16	8	4.67	0.0619
	GO:0001302	replicative cell aging	6	4	1.75	0.0632
	GO:0030472	mitotic spindle organization in nucleus	6	4	1.75	0.0632
	GO:0006281	DNA repair	59	21	17.21	0.0727
	GO:0033036	macromolecule localization	55	16	16.04	0.0789
	GO:0071702	organic substance transport	25	8	7.29	0.0853
	GO:0000282	cellular bud site selection	8	3	2.33	0.0853
	GO:0006139	nucleobase-containing compound metabolic process	234	58	68.24	0.0982

**Table S11.6.** GO cellular compartment enrichments (p-value < 0.1) for non-detected proteins in *S. cerevisiae* with high (Top 25% quantile), medium (middle 50% quantile) and low (bottom 25% quantile) mRNA concentration. Background set of genes in a given class (high, medium, low) are all genes in the respective class that have a GO annotation.

mRNA Concentration	GO.ID	Term	Annotated	Significant	Expected	pvalue
High (n=69)	GO:0005762	mitochondrial large ribosomal subunit	14	5	0.34	1.10E-05
	GO:0005886	plasma membrane	108	8	2.65	0.0031
	GO:0010008	endosome membrane	14	2	0.34	0.0441
Medium (n=468)	GO:0005681	spliceosomal complex	52	19	8.37	0.00031
	GO:0005789	endoplasmic reticulum membrane	154	35	24.79	0.0171
	GO:0005743	mitochondrial inner membrane	114	27	18.35	0.0195
	GO:0005758	mitochondrial intermembrane space	21	7	3.38	0.03975
	GO:0005774	vacuolar membrane	107	26	17.23	0.0472
	GO:0005886	plasma membrane	173	36	27.85	0.06562
	GO:0000790	nuclear chromatin	28	8	4.51	0.06762
	GO:0000329	fungus-type vacuole membrane	71	16	11.43	0.09384
Low (n=315)	GO:0005743	mitochondrial inner membrane	31	14	8.42	0.021
	GO:0005874	microtubule	16	8	4.35	0.042
	GO:0000790	nuclear chromatin	14	7	3.8	0.056
	GO:0000324	fungus-type vacuole	25	10	6.79	0.066
	GO:0031974	membrane-enclosed lumen	90	24	24.45	0.075
	GO:0005886	plasma membrane	79	27	21.46	0.09

**Table S11.7.** GO term enrichments (p-value < 0.1) for non-detected *S. pombe* proteins with known orthologs in *S. cerevisiae* that are also not detected in *S. cerevisiae* (n=392 genes matching this criteria). Background set is all genes with a known ortholog.

GO Ontology Type	GO.ID	Term	Annotated	Significant	Expected	pvalue
Molecular Function	GO:0015171	amino acid transmembrane transporter activity	21	17	1.7	5.70E-16
	GO:0022857	transmembrane transporter activity	84	40	6.81	1.30E-15
	GO:0008270	zinc ion binding	203	37	16.45	5.80E-07
	GO:0000978	RNA polymerase II core promoter proximal region sequence-specific DNA binding	43	11	3.48	0.00041
	GO:0000981	sequence-specific DNA binding RNA polymerase II transcription factor activity	17	5	1.38	0.00912
	GO:0003677	DNA binding	219	35	17.75	0.01236
	GO:0003684	damaged DNA binding	19	4	1.54	0.06163
Biological Process	GO:0003333	amino acid transmembrane transport	26	20	2.47	2.60E-16
	GO:0055085	transmembrane transport	110	54	10.46	6.10E-14
	GO:0007131	reciprocal meiotic recombination	34	15	3.23	1.10E-07
	GO:0006506	GPI anchor biosynthetic process	23	8	2.19	0.00083
	GO:0006914	autophagy	26	8	2.47	0.00206
	GO:0000724	double-strand break repair via homologous recombination	27	8	2.57	0.00269
	GO:0006974	response to DNA damage stimulus	109	23	10.37	0.00355
	GO:0006995	cellular response to nitrogen starvation	37	9	3.52	0.00636
	GO:0034220	ion transmembrane transport	19	6	1.81	0.00655
	GO:0033314	mitotic cell cycle DNA replication checkpoint	25	7	2.38	0.00698
	GO:0030071	regulation of mitotic metaphase/anaphase transition	45	10	4.28	0.0108
	GO:0030437	ascospore formation	52	9	4.95	0.05343
GO:0006879	cellular iron ion homeostasis	17	4	1.62	0.07069	
Cellular Compartment	GO:0016021	integral to membrane	700	143	77.56	1.40E-18
	GO:0005886	plasma membrane	132	42	14.63	1.90E-08
	GO:0005783	endoplasmic reticulum	451	73	49.97	0.00012
	GO:0005794	Golgi apparatus	232	40	25.71	0.00116
	GO:0000329	fungus-type vacuole membrane	78	18	8.64	0.00158
	GO:0009277	fungus-type cell wall	22	8	2.44	0.00163
	GO:0009897	external side of plasma membrane	14	6	1.55	0.00244
	GO:0005576	extracellular region	15	6	1.66	0.00369
	GO:0030176	integral to endoplasmic reticulum membrane	48	11	5.32	0.01341
	GO:0005887	integral to plasma membrane	42	10	4.65	0.01384
	GO:0009986	cell surface	33	11	3.66	0.0479
	GO:0032153	cell division site	220	30	24.38	0.04924
	GO:0005938	cell cortex	104	7	11.52	0.06514