

**Table S1**

ORFs designated by the consortium to be essential but had high integration densities.

Gene	Gene function	integration/kb/million insertions
SPBC21C3.10c	5-amino-6-(5-phosphoribosylamino) uracil reductase	161.5
tim10 SPAC222.03c	Tim9-Tim10 complex subunit Tim10 (predicted)	130.2
mrpl16 SPBC1105.03c	mitochondrial ribosomal protein subunit L16	128.4
SPBP8B7.05c	carbonic anhydrase (predicted)	124.5
SPBC2D10.08c	mitochondrial ribosomal protein subunit Yml6	123.5
mrpl31 SPCC16A11.11	mitochondrial ribosomal protein subunit L31	111.6
ste11 aff1 stex SPBC32C12.0	transcription factor Ste11	108.4
SPAC1486.07c mrpl19	mitochondrial ribosomal protein subunit L19	102.0
SPCC1672.01	histidinol-phosphatase (predicted)	100.8
SPCC2H8.04	sequence orphan	99.4
met9 met5 SPAC56F8.10	methylenetetrahydrofolate reductase Met9	94.9
SPAC17H9.07	signal recognition particle subunit Srp21 (predicted)	94.6
tpx1 SPCC576.03c	thioredoxin peroxidase Tpx1	86.2
vph2 SPCC757.10	endoplasmic reticulum membrane involved in assembly of the V-ATPase	84.5
ups1 ups SPAC31G5.08	uroporphyrinogen-III synthase Ups1	80.7
mmf1 pmf1 SPBC2G2.04c	YjgF family protein Mmf1	79.4
grx4 SPBC26H8.06	glutaredoxin Grx4	79.3
SPAC30C2.03	sequence orphan	78.9
SPBC2A9.10	Bin3 family	78.4
SPAC12B10.02c	sequence orphan	78.4
mrp10 SPAC24C9.13c	mitochondrial ribosomal protein subunit Mrp10	78.0
SPBC3B9.14c mrpl3	mitochondrial ribosomal protein subunit L3	77.3
SPCC1682.09c	guanine nucleotide transporter	74.1
SPAC1002.16c	nicotinic acid plasma membrane transporter (predicted)	74.0
SPAC688.09	mitochondrial pyrimidine nucleotide transporter (predicted)	70.9
SPBC577.09	ERCC-8 DNA repair homolog (predicted)	70.3
SPAC17G8.02	uridine ribohydrolase (predicted)	69.8
SPAC31G5.06	mitochondrial protein	69.8
dea2 SPBC1198.02	adenine deaminase Dea2	67.8
SPCC63.10c	dolichol kinase (predicted)	67.4
SPAC24C9.06c	aconitate hydratase	66.5
SPBC354.06 mrps16	mitochondrial ribosomal protein subunit S16	65.5
SPBP4H10.15	aconitate hydratase/mitochondrial ribosomal protein subunit L49, fusion protein	64.9
bet5 SPAC688.15 SPAC3G9.1	TRAPP complex subunit Bet5 (predicted)	64.6
usp103 yhc1 SPBP35G2.09	U1 snRNP-associated protein Usp103 (predicted)	63.6
crk1 mop1 mcs6 SPBC19F8.(	cyclin-dependent kinase activating kinase Crk1	63.3
SPAPB17E12.09	sequence orphan	63.2
mrp20 SPAC31A2.08	mitochondrial ribosomal protein subunit L23 (predicted)	62.8
fta3 SPBP8B7.12c sma3	Sim4 and Mal2 associated (4 and 2 associated) protein 3	62.8
SPBC887.07 mrpl38	mitochondrial ribosomal protein subunit L38	62.7
SPBC2F12.10	mitochondrial ribosomal protein subunit L35	62.3
SPCC4B3.09c	mitochondrial ribosomal protein subunit L12	62.1
SPAPB24D3.06c	DUF1749 family protein	61.3
SPBC119.18	mitochondrial distribution and morphology protein Mdm35 (predicted)	61.2
SPBC17G9.13c	sequence orphan	61.1
SPAC2F7.15 rsm24	mitochondrial ribosomal protein subunit S24 (predicted)	60.9
SPBC16H5.15	conserved fungal protein	60.9
SPCC1393.11	mitochondrial ribosomal protein subunit L20	60.7
sum2 SPBC800.09	G2/M transition checkpoint protein Sum2	60.6
alr2 SPBC359.02	alanine racemase Alr2	59.8
SPAC3A12.19	mitochondrial ribosomal protein subunit L27	59.4