APPENDIX

Sen1 is required for effective termination of RNA polymerase III transcription.

Julieta Rivosecchi, Marc Larochelle, Camille Teste, Frédéric Grenier, Amélie Malapert, Emiliano P. Ricci, Pascal Bernard, François Bachand and Vincent Vanoosthuyse.

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Appendix Table S1: List of the proteins identified as protein partners of Flag-tagged Sen1 and Flag-tagged Dbl8 using mass-spectrometry analysis. The flag-tagged strains were expressed from the endogenous loci. The no-tag strain was used as negative control.

	no tag								
Accession	Description	Score	Coverage	# Proteins	# Unique Peptides	# Peptides	MW [kDa]	calc. pI
P40847	Switch-activating protein 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=sap1 PE=1 SV=2 - [SAP1_SCHPO]	151,91	29,92	1	7	7	29,1	7,88
B5BP45	Uncharacterized amino-acid permease C460.01c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPBC460.01c PE=3 SV=1 - [YP51_SCHPO]	137,37	6,64	1	3	3	62,7	6,68
P78958	Glyceraldehyde-3-phosphate dehydrogenase 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=tdh1 PE=1 SV=1 - [G3P1_SCHPO]	135,39	7,74	1	2	2	35,8	6,70
Q92372	Replication factor A protein 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=ssb1 PE=1 SV=1 - [RFA1_SCHPO]	129,17	9,36	1	5	5	68,2	6,74
O94514	Nucleolar protein 56 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=nop56 PE=3 SV=1 - [NOP56_SCHPO]	96,67	11,07	1	5	5	55,4	8,90
O13370	ATP-dependent RNA helicase ded1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=ded1 PE=1 SV=1 - [DED1_SCHPO]	90,86	6,13	1	3	3	69,7	8,50
O14007	H/ACA ribonucleoprotein complex subunit 4 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=cbf5 PE=3 SV=1 - [CBF5_SCHPO]	82,53	9,49	1	4	4	53,1	8,97
Q09781	40S ribosomal protein S1-A OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps101 PE=3 SV=2 - [RS3A1_SCHPO]	64,06	9,52	1	1	2	28,5	9,99
O94438	40S ribosomal protein S1-B OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps102 PE=1 SV=3 - [RS3A2_SCHPO]	60,46	14,29	1	2	3	28,5	10,14
O94754	40S ribosomal protein S18 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps18a PE=1 SV=1 - [RS18_SCHPO]	58,56	15,13	1	2	2	17,4	10,49
P00332	Alcohol dehydrogenase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=adh1 PE=1 SV=2 - [ADH_SCHPO]	53,80	6,00	1	2	2	37,4	6,93
O14460	Elongation factor 2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=eft201 PE=1 SV=2 - [EF2_SCHPO]	53,60	2,85	1	2	2	93,2	6,43
Q09188	ADP,ATP carrier protein OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=anc1 PE=2 SV=1 - [ADT_SCHPO]	50,60	6,52	1	2	2	35,0	9,96

	Sen1-3flag							
Accession	Description	Score	Coverage	# Proteins	# Unique Peptides	# Peptides	MW [kDa]	calc. pI
Q92355	Helicase sen1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=sen1 PE=1 SV=1 - [SEN1_SCHPO]	2066,75	39,18	1	63	63	192,4	7,05
O94666	DNA-directed RNA polymerase III subunit rpc1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpc1 PE=2 SV=1 - [RPC1_SCHPO]	1159,97	39,43	1	43	43	157,5	7,71
Q10233	DNA-directed RNA polymerase III subunit RPC2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpc2 PE=2 SV=1 - [RPC2_SCHPO]	873,66	42,66	1	39	39	130,2	8,41
O74883	DNA-directed RNA polymerase III subunit rpc5 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpc37 PE=3 SV=1 - [RPC5_SCHPO]	627,02	57,85	1	14	14	27,4	6,57
Q9US25	Chromodomain helicase hrp1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=hrp1 PE=1 SV=1 - [HRP1_SCHPO]	608,38	27,68	1	31	31	158,5	5,83
Q9C106	DNA-directed RNA polymerase III subunit rpc3 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpc82 PE=1 SV=1 - [RPC3_SCHPO]	552,12	36,55	1	22	22	68,3	7,61
O94616	DNA-directed RNA polymerases I and III subunit RPAC1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpc40 PE=3 SV=1 - [RPAC1_SCHPO]	294,39	40,23	1	11	11	39,1	5,63
P50522	Elongation factor 1-alpha-A OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=tef1a PE=1 SV=2 - [EF1A1_SCHPO]	247,65	20,65	2	9	9	49,6	9,00
Q8WZJ8	DNA-directed RNA polymerase III subunit rpc31 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpc31 PE=1 SV=1 - [RPC7_SCHPO]	228,89	42,38	1	9	9	24,3	4,60
O74857	DNA-directed RNA polymerase III subunit rpc4 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpc53 PE=2 SV=1 - [RPC4_SCHPO]	218,55	44,85	1	10	10	36,8	5,11
Q10264	DNA cross-link repair protein pso2/snm1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=pso2 PE=3 SV=3 - [PSO2_SCHPO]	198,92	19,82	1	10	10	63,0	8,16
O94438	40S ribosomal protein S1-B OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps102 PE=1 SV=3 - [RS3A2_SCHPO]	194,81	25,40	1	6	6	28,5	10,14
O13896	DNA-directed RNA polymerase III subunit RPC10 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpc11 PE=3 SV=1 - [RPC10_SCHPO]	181,26	66,06	1	4	4	12,8	5,06
Q9C0Z9	DNA-directed RNA polymerase III subunit rpc9 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpc17 PE=1 SV=1 - [RPC9_SCHPO]	159,16	51,16	1	6	6	14,9	4,77
O94553	Probable DNA-directed RNA polymerase III subunit rpc6 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpc6 PE=2 SV=1 - [RPC6_SCHPO]	156,24	39,53	1	7	7	33,9	7,97
Q10284	Heat shock protein sks2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=sks2 PE=1 SV=2 - [HSP75_SCHPO]	155,21	15,50	1	6	6	67,2	6,09
P78958	Glyceraldehyde-3-phosphate dehydrogenase 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=tdh1 PE=1 SV=1 - [G3P1_SCHPO]	151,22	16,67	1	5	5	35,8	6,70
P09322	Histone H4 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=hhf1 PE=1 SV=2 - [H4_SCHPO]	149,88	30,10	1	4	4	11,4	11,36
P35551	rRNA 2'-O-methyltransferase fibrillarin OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=fib1 PE=1 SV=1 - [FBRL_SCHPO]	147,53	15,74	1	4	4	32,0	10,17
O94514	Nucleolar protein 56 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=nop56 PE=3 SV=1 - [NOP56_SCHPO]	145,16	8,05	1	4	4	55,4	8,90
P09627	Plasma membrane ATPase 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=pma1 PE=1 SV=1 - [PMA1_SCHPO]	140,32	6,64	1	5	5	99,8	5,19
Q9P7S7	Nucleolar protein 58 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=nop58 PE=1 SV=1 - [NOP58_SCHPO]	138,63	12,40	1	5	5	55,7	9,06
O13370	ATP-dependent RNA helicase ded1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=ded1 PE=1 SV=1 - [DED1_SCHPO]	132,83	14,78	1	7	7	69,7	8,50
O60176	Uncharacterized RNA-binding protein C23E6.01c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPBC23E6.01c PE=1 SV=2 - [YG41_SCHPO]	119,15	26,85	1	7	7	51,7	5,15

P36595	DNA-directed RNA polymerases I, II, and III subunit RPABC2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpb6 PE=1 SV=1 - [RPAB2_SCHPO]	114,25	26,76	1	3	3	15,7	4,37
O14049	40S ribosomal protein S8-A OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps8a PE=3 SV=1 - [RS8A_SCHPO]	106,35	15,50	2	3	3	22,6	10,93
Q09177	DNA-directed RNA polymerases I and III subunit RPAC2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpc19 PE=2 SV=1 - [RPAC2_SCHPO]	102,28	29,60	1	3	3	13,7	4,68
O42867	60S ribosomal protein L23 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl23a PE=3 SV=1 - [RL23_SCHPO]	99,43	22,30	1	3	3	14,9	10,21
O74895	60S ribosomal protein L15-A OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl15a PE=3 SV=1 - [RL15A_SCHPO]	97,20	24,88	2	5	5	23,8	11,25
P09988	Histone H3.1/H3.2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=hht1 PE=1 SV=2 - [H31_SCHPO]	93,18	43,38	1	4	4	15,3	11,27
Q9C0Z7	40S ribosomal protein S6-B OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps6b PE=1 SV=1 - [RS6B_SCHPO]	93,05	12,97	1	2	2	27,5	10,77
P31209	Polyadenylate-binding protein, cytoplasmic and nuclear OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=pab1 PE=1 SV=2 - [PABP_SCHPO]	91,89	4,59	1	3	3	71,5	5,38
O74391	60S ribosomal protein L25-B OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl25b PE=3 SV=1 - [RL25B_SCHPO]	90,78	18,44	2	2	2	15,8	10,48
O94285	DNA-directed RNA polymerase III subunit rpc8 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpc25 PE=1 SV=1 - [RPC8_SCHPO]	90,55	23,15	1	4	4	23,2	5,03
O94754	40S ribosomal protein S18 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps18a PE=1 SV=1 - [RS18_SCHPO]	89,76	28,95	1	4	4	17,4	10,49
O59855	Probable heat shock protein ssa2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=ssa2 PE=1 SV=3 - [HSP72_SCHPO]	88,15	9,58	1	4	4	70,2	5,25
O60128	40S ribosomal protein S3 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps3 PE=1 SV=1 - [RS3_SCHPO]	87,92	16,87	1	3	3	27,5	9,20
Q09191	DNA-directed RNA polymerases I, II, and III subunit RPABC1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpb5 PE=1 SV=1 - [RPAB1_SCHPO]	87,31	11,43	1	2	2	23,9	9,23
Q10157	60S ribosomal protein L11 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl11a PE=1 SV=1 - [RL11_SCHPO]	85,71	13,79	1	2	2	19,9	10,07
O74976	Putative peroxisomal-coenzyme A synthetase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPCC1827.03c PE=1 SV=1 - [FAT2_SCHPO]	84,00	9,38	1	4	4	56,2	9,29
B5BP45	Uncharacterized amino-acid permease C460.01c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPBC460.01c PE=3 SV=1 - [YP51_SCHPO]	82,88	4,02	1	3	3	62,7	6,68
P04909	Histone H2A-alpha OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=hta1 PE=1 SV=3 - [H2A1_SCHPO]	81,24	34,09	1	5	5	13,9	10,64
Q10208	Pyruvate kinase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=pyk1 PE=1 SV=1 - [KPYK_SCHPO]	79,36	7,27	1	3	3	55,5	7,96
P36584	60S ribosomal protein L3-B OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl3b PE=3 SV=2 - [RL3B_SCHPO]	73,70	4,90	2	2	2	43,8	10,27
O14388	60S ribosomal protein L27-A OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl27a PE=2 SV=2 - [RL27A_SCHPO]	73,47	15,44	1	2	2	15,4	10,84
P28189	40S ribosomal protein S13 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps13 PE=1 SV=2 - [RS13_SCHPO]	69,32	23,84	1	4	4	16,9	10,37
Q9P785	LisH domain-containing protein C1711.05 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPBC1711.05 PE=4 SV=1 - [YNY5_SCHPO]	69,22	6,87	1	2	2	47,4	4,37
P40370	Enolase 1-1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=eno101 PE=1 SV=2 - [ENO11_SCHPO]	65,82	11,16	1	3	3	47,4	6,67
O42699	60S ribosomal protein L19-B OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl19b PE=2 SV=2 - [RL19B_SCHPO]	63,18	19,69	2	3	3	22,7	11,40
P40847	Switch-activating protein 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=sap1 PE=1 SV=2 - [SAP1_SCHPO]	58,97	6,30	1	2	2	29,1	7,88
Q9USZ4	DNA-directed RNA polymerase I subunit rpa34 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpa34 PE=1 SV=1 - [RPA34_SCHPO]	58,50	15,14	1	2	2	28,0	5,52
Q92372	Replication factor A protein 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=ssb1 PE=1 SV=1 - [RFA1_SCHPO]	57,10	10,02	1	5	5	68,2	6,74
P04913	Histone H2B-alpha OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=htb1 PE=1 SV=3 - [H2B1_SCHPO]	55,99	15,08	1	2	2	13,8	10,07
P10989	Actin OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=act1 PE=1 SV=1 - [ACT_SCHPO]	55,80	7,20	1	2	2	41,7	5,48
O14469	40S ribosomal protein S22 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps22a PE=2 SV=1 - [RS22_SCHPO]	52,29	14,62	1	2	2	14,8	10,27
Q09188	ADP,ATP carrier protein OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=anc1 PE=2 SV=1 - [ADT_SCHPO]	49,72	9,94	1	3	3	35,0	9,96
O13672	60S ribosomal protein L8 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl8 PE=1 SV=3 - [RL8_SCHPO]	49,60	12,36	1	3	3	28,6	10,35
O14086	DNA-directed RNA polymerase I subunit rpa49 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpa49 PE=2 SV=1 - [RPA49_SCHPO]	48,75	5,88	1	2	2	48,0	9,58
P36604	78 kDa glucose-regulated protein homolog OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=bip1 PE=3 SV=2 - [GRP78_SCHPO]	48,37	3,47	1	2	2	73,2	4,96
O94529	FACT complex subunit pob3 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=pob3 PE=3 SV=1 - [POB3_SCHPO]	42,47	3,91	1	2	2	57,4	4,53
Q10475	Eukaryotic translation initiation factor 4 gamma OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=tif471 PE=1 SV=1 - [IF4G_SCHPO]	41,46	4,56	1	3	3	153,9	9,23
P78946	60S ribosomal protein L26 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl26 PE=3 SV=1 - [RL26_SCHPO]	40,17	11,90	1	2	2	14,3	11,17
Q9UT19	Probable 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=met26 PE=1 SV=1 - [METE_SCHPO]	33,30	2,62	1	2	2	85,3	6,38
P41891	Protein gar2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=gar2 PE=1 SV=2 - [GAR2_SCHPO]	32,39	6,60	1	2	2	53,0	4,97
P00332	Alcohol dehydrogenase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=adh1 PE=1 SV=2 - [ADH_SCHPO]	30,42	9,43	1	2	2	37,4	6,93

	Dbl8-3flag							
Accession	Description	Score	Coverage	# Proteins	# Unique Peptides	# Peptides	MW [kDa]	calc. pI
Q9US25	Chromodomain helicase hrp1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=hrp1 PE=1 SV=1 - [HRP1_SCHPO]	640,16	36,64	1	32	32	158,5	5,83

O94387	Uncharacterized ATP-dependent helicase C29A10.10c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPBC29A10.10c PE=3 SV=1 - [YGSA_SCHPO]	551,74	16,00	1	25	25	222,1	8,41
P40370	Enolase 1-1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=eno101 PE=1 SV=2 - [ENO11_SCHPO]	329,57	39,41	1	11	11	47,4	6,67
P09322	Histone H4 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=hhf1 PE=1 SV=2 - [H4_SCHPO]	325,47	41,75	1	5	5	11,4	11,36
P78958	Glyceraldehyde-3-phosphate dehydrogenase 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=tdh1 PE=1 SV=1 - [G3P1_SCHPO]	278,53	27,38	1	10	10	35,8	6,70
P09627	Plasma membrane ATPase 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=pma1 PE=1 SV=1 - [PMA1_SCHPO]	267,36	10,23	1	7	7	99,8	5,19
O59855	Probable heat shock protein ssa2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=ssa2 PE=1 SV=3 - [HSP72_SCHPO]	239,93	20,09	1	10	10	70,2	5,25
O60101	Phosphoglycerate kinase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=pgk1 PE=1 SV=1 - [PGK_SCHPO]	234,20	35,02	1	10	10	43,9	8,15
Q92345	Probable pyruvate decarboxylase C1F8.07c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPAC1F8.07c PE=1 SV=3 - [PDC2_SCHPO]	231,42	19,16	1	9	9	61,7	5,64
P50522	Elongation factor 1-alpha-A OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=tef1a PE=1 SV=2 - [EF1A1_SCHPO]	214,21	15,43	2	8	8	49,6	9,00
P36580	Fructose-bisphosphate aldolase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=fba1 PE=1 SV=2 - [ALF_SCHPO]	202,03	36,03	1	7	7	39,5	6,35
Q9P7L5	Ornithine aminotransferase car2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=car2 PE=2 SV=1 - [OAT_SCHPO]	193,51	9,59	1	3	3	48,2	6,34
Q10208	Pyruvate kinase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=pyk1 PE=1 SV=1 - [KPYK_SCHPO]	180,45	27,90	1	9	9	55,5	7,96
Q9UT19	Probable 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=met26 PE=1 SV=1 - [METE_SCHPO]	173,80	12,83	1	9	9	85,3	6,38
O74391	60S ribosomal protein L25-B OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl25b PE=3 SV=1 - [RL25B_SCHPO]	172,17	18,44	2	2	2	15,8	10,48
O14460	Elongation factor 2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=eft201 PE=1 SV=2 - [EF2_SCHPO]	158,38	10,45	1	6	6	93,2	6,43
O60128	40S ribosomal protein S3 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps3 PE=1 SV=1 - [RS3_SCHPO]	140,92	17,67	1	4	4	27,5	9,20
O59838	Heat shock protein homolog pss1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=pss1 PE=1 SV=2 - [HSP7F_SCHPO]	140,91	7,50	1	4	4	80,3	5,07
P40847	Switch-activating protein 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=sap1 PE=1 SV=2 - [SAP1_SCHPO]	130,47	20,47	1	4	4	29,1	7,88
P22774-2	Isoform Short of Heat shock 70 kDa protein, mitochondrial OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=ssp1 - [HSP7M_SCHPO]	126,55	11,39	2	5	5	69,4	5,97
Q10284	Heat shock protein sks2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=sks2 PE=1 SV=2 - [HSP75_SCHPO]	122,21	8,81	1	4	4	67,2	6,09
Q9USZ4	DNA-directed RNA polymerase I subunit rpa34 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpa34 PE=1 SV=1 - [RPA34_SCHPO]	121,87	35,86	1	6	6	28,0	5,52
P00332	Alcohol dehydrogenase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=adh1 PE=1 SV=2 - [ADH_SCHPO]	121,82	21,71	1	6	6	37,4	6,93
P15398	DNA-directed RNA polymerase I subunit rpa1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpa1 PE=1 SV=2 - [RPA1_SCHPO]	119,91	5,51	1	8	8	189,1	6,64
O60176	Uncharacterized RNA-binding protein C23E6.01c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPBC23E6.01c PE=1 SV=2 - [YG41_SCHPO]	117,05	18,82	1	5	5	51,7	5,15
O14027	Probable pyridoxine biosynthesis PDX1-like protein OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=snz1 PE=1 SV=1 - [PDX1_SCHPO]	115,48	8,11	1	2	2	31,4	6,27
O14049	40S ribosomal protein S8-A OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps8a PE=3 SV=1 - [RS8A_SCHPO]	113,05	15,50	2	2	2	22,6	10,93
Q9US22	60S ribosomal protein L15-B OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl15b PE=1 SV=1 - [RL15B_SCHPO]	109,54	17,91	1	3	3	23,8	11,18
O74766	Probable delta-1-pyrroline-5-carboxylate dehydrogenase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPBC24C6.04 PE=1 SV=1 - [PUT2_SCHPO]	107,87	7,85	1	3	3	60,2	7,33
O42700	Transaldolase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=tal1 PE=1 SV=2 - [TAL1_SCHPO]	107,23	9,94	1	3	3	35,2	5,86
P31209	Polyadenylate-binding protein, cytoplasmic and nuclear OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=pab1 PE=1 SV=2 - [PABP_SCHPO]	105,83	7,04	1	4	4	71,5	5,38
P41887	Heat shock protein 90 homolog OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=swo1 PE=1 SV=2 - [HSP90_SCHPO]	102,78	7,39	1	4	4	80,5	4,96
P78827	Probable ketol-acid reductoisomerase, mitochondrial OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=ilv5 PE=1 SV=2 - [ILV5_SCHPO]	102,71	9,16	1	3	3	45,2	9,45
P78854	Lysophospholipase 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=plb1 PE=2 SV=2 - [PLB1_SCHPO]	102,40	4,57	1	2	2	67,1	4,92
O13639	Adenosylhomocysteinase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=pi047 PE=3 SV=1 - [SAHH_SCHPO]	102,38	11,78	1	4	4	47,4	5,94
O13370	ATP-dependent RNA helicase ded1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=ded1 PE=1 SV=1 - [DED1_SCHPO]	100,01	7,23	1	4	4	69,7	8,50
O74779	Microtubule-associated protein mug164 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=mug164 PE=1 SV=4 - [MU164_SCHPO]	98,92	10,06	1	3	3	55,4	11,81
O94514	Nucleolar protein 56 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=nop56 PE=3 SV=1 - [NOP56_SCHPO]	96,05	4,43	1	3	3	55,4	8,90
P05752	40S ribosomal protein S6-A OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps6a PE=1 SV=2 - [RS6A_SCHPO]	95,15	17,15	1	3	3	27,5	10,83
O42938	6-phosphofructokinase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=pfk1 PE=1 SV=1 - [K6PF_SCHPO]	94,45	6,58	1	5	5	102,5	6,19
P87167	Uba3-binding protein but2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=but2 PE=1 SV=1 - [BUT2_SCHPO]	94,13	7,69	1	2	2	43,6	9,00
O74836	60S ribosomal protein L1-B OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl1b PE=1 SV=1 - [RL1B_SCHPO]	93,87	19,91	1	3	3	23,9	9,82
Q9UT09	Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=aro4 PE=3 SV=1 - [AROG_SCHPO]	93,02	9,95	1	2	3	40,6	7,23
P36623	Phosphoglycerate mutase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=gpm1 PE=1 SV=1 - [PMGY_SCHPO]	91,55	25,59	1	5	5	23,8	7,47
O42699	60S ribosomal protein L19-B OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl19b PE=2 SV=2 - [RL19B_SCHPO]	90,03	19,69	2	3	3	22,7	11,40
Q10192	60S ribosomal protein L18-A OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl18a PE=1 SV=1 - [RL18A_SCHPO]	89,39	14,44	1	2	2	21,2	11,66
O74835	rRNA biogenesis protein rrp5 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rrp5 PE=1 SV=1 - [RRP5_SCHPO]	88,22	2,78	1	4	4	187,4	5,49
O74173	Elongation factor 1-beta OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=tef5 PE=2 SV=1 - [EF1B_SCHPO]	87,09	12,62	1	2	2	23,5	4,50
P08096	DNA topoisomerase 2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=top2 PE=1 SV=2 - [TOP2_SCHPO]	87,05	3,23	1	4	4	167,8	7,28

P36584	60S ribosomal protein L3-B OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl3b PE=3 SV=2 - [RL3B_SCHPO]	85,87	6,44	2	2	2	43,8	10,27
Q9P7S7	Nucleolar protein 58 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=nop58 PE=1 SV=1 - [NOP58_SCHPO]	84,97	6,89	1	3	3	55,7	9,06
O13972	Probable serine hydroxymethyltransferase, cytosolic OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPAC24C9.12c PE=3 SV=1 - [GLYD_SCHPO]	84,19	7,71	1	3	3	51,8	7,81
P07669	Triosephosphate isomerase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=tpi1 PE=1 SV=4 - [TPIS_SCHPO]	84,09	17,67	1	4	4	27,2	7,03
O94754	40S ribosomal protein S18 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps18a PE=1 SV=1 - [RS18_SCHPO]	83,96	25,66	1	4	4	17,4	10,49
Q09781	40S ribosomal protein S1-A OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps101 PE=3 SV=2 - [RS3A1_SCHPO]	82,15	22,22	1	2	5	28,5	9,99
O94438	40S ribosomal protein S1-B OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps102 PE=1 SV=3 - [RS3A2_SCHPO]	79,88	25,00	1	3	6	28,5	10,14
Q09755	Putative phospho-2-dehydro-3-deoxyheptonate aldolase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPAC24H6.10c PE=3 SV=1 - [AROF_SCHPO]	78,31	10,33	1	2	3	39,7	6,80
P42656	DNA damage checkpoint protein rad24 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rad24 PE=1 SV=2 - [RAD24_SCHPO]	78,02	8,89	1	2	2	30,1	4,72
Q10289	Fatty acid synthase subunit alpha OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=fas2 PE=1 SV=2 - [FAS2_SCHPO]	77,95	1,19	1	2	2	202,0	6,18
Q9P3T6	40S ribosomal protein S5-B OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps5b PE=3 SV=1 - [RS5B_SCHPO]	77,71	22,66	1	3	3	22,3	9,85
O94703	DNA-directed RNA polymerase I subunit RPA12 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpa12 PE=3 SV=1 - [RPA12_SCHPO]	77,00	27,73	1	2	2	13,1	5,15
P35551	rRNA 2'-O-methyltransferase fibrillarin OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=fib1 PE=1 SV=1 - [FBRL_SCHPO]	75,96	10,16	1	3	3	32,0	10,17
P22068	ATP synthase subunit beta, mitochondrial OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=atp2 PE=1 SV=1 - [ATPB_SCHPO]	75,47	14,10	1	5	5	56,8	5,99
Q10157	60S ribosomal protein L11 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl11a PE=1 SV=1 - [RL11_SCHPO]	74,56	13,79	1	2	2	19,9	10,07
O94658	60S ribosomal protein L36-B OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl36b PE=3 SV=1 - [RL36B_SCHPO]	70,08	20,20	2	2	2	11,3	11,84
O94238	60S ribosomal protein L14 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl14 PE=2 SV=1 - [RL14_SCHPO]	67,82	19,40	1	3	3	15,2	10,35
O74175	60S ribosomal protein L13 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl13 PE=1 SV=1 - [RL13_SCHPO]	67,70	27,88	1	3	3	23,5	10,70
O42867	60S ribosomal protein L23 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl23a PE=3 SV=1 - [RL23_SCHPO]	67,08	39,57	1	4	4	14,9	10,21
Q09668	60S ribosomal protein L22 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl22 PE=1 SV=3 - [RL22_SCHPO]	66,40	17,95	1	2	2	13,3	9,64
O13672	60S ribosomal protein L8 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl8 PE=1 SV=3 - [RL8_SCHPO]	65,38	9,65	1	2	2	28,6	10,35
Q42598	Threonine synthase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=thrc PE=1 SV=1 - [THRC_SCHPO]	63,87	5,64	1	2	2	57,6	5,59
P41891	Protein gar2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=gar2 PE=1 SV=2 - [GAR2_SCHPO]	63,74	10,20	1	3	3	53,0	4,97
O94489	Elongation factor 3 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=tef3 PE=1 SV=1 - [EF3_SCHPO]	63,33	6,69	1	5	5	115,7	6,49
O94700	Multiprotein-bridging factor 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=mbf1 PE=3 SV=1 - [MBF1_SCHPO]	63,20	23,65	1	3	3	16,0	10,49
Q9P784	60S ribosomal protein L4-B OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl4b PE=3 SV=1 - [RL4B_SCHPO]	62,92	10,74	1	3	3	39,9	10,71
O14351	Uncharacterized oxidoreductase C30D10.05c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPBC30D10.05c PE=3 SV=1 - [YB45_SCHPO]	62,86	9,72	1	2	2	26,6	8,35
P05733	60S ribosomal protein L37-B OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl37b PE=1 SV=4 - [RL37B_SCHPO]	62,48	26,37	1	2	2	10,1	11,46
O42914	Uncharacterized protein C16A3.08c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPBC16A3.08c PE=1 SV=1 - [YBI8_SCHPO]	60,56	16,20	1	3	3	30,9	10,14
Q09757	40S ribosomal protein S9-A OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps9a PE=1 SV=2 - [RS9A_SCHPO]	59,63	13,61	2	3	3	22,1	10,37
Q09864	Heat shock protein 60, mitochondrial OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=hsp60 PE=1 SV=1 - [HSP60_SCHPO]	59,20	4,12	1	2	2	62,1	5,99
O42945	Probable pre-mRNA-splicing factor ATP-dependent RNA helicase prp43 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=prp43 PE=3 SV=1 - [DHX15_SCHPO]	57,56	2,86	1	2	2	83,8	6,32
P04910	Histone H2A-beta OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=hta2 PE=1 SV=2 - [H2A2_SCHPO]	54,52	29,77	2	3	3	13,8	10,52
O60198	S-adenosylmethionine synthase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=sam1 PE=3 SV=1 - [METK_SCHPO]	52,88	4,97	1	2	2	41,8	6,04
P79071	60S ribosomal protein L6 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl6 PE=1 SV=2 - [RL6_SCHPO]	50,32	23,08	1	4	4	21,2	10,26
Q92372	Replication factor A protein 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=ssb1 PE=1 SV=1 - [RFA1_SCHPO]	48,98	6,08	1	3	3	68,2	6,74
O13907	Probable ATP-citrate synthase subunit 2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPAC22A12.16 PE=1 SV=1 - [ACL2_SCHPO]	48,75	4,27	1	2	2	53,9	6,09
O74892	40S ribosomal protein S2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps2 PE=1 SV=1 - [RS2_SCHPO]	48,09	9,49	1	2	2	27,6	10,08
O94267	FACT complex subunit spt16 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=spt16 PE=1 SV=1 - [SPT16_SCHPO]	48,01	2,16	1	2	2	116,4	5,26
O94692	RuvB-like helicase 2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rvb2 PE=1 SV=1 - [RUVB2_SCHPO]	47,33	4,73	1	2	2	51,5	5,39
O42848	60S ribosomal protein L16-A OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl16a PE=1 SV=1 - [RL16A_SCHPO]	47,04	7,61	1	2	2	22,0	10,55
P40375	NAD-dependent malic enzyme OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=mae2 PE=1 SV=1 - [MAOX_SCHPO]	44,80	2,83	1	2	2	62,5	6,01
O14370	Branched-chain-amino-acid aminotransferase, mitochondrial OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=eca39 PE=1 SV=3 - [BCA1_SCHPO]	44,30	4,92	1	2	2	47,8	8,70
P58234	40S ribosomal protein S19-A OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps19a PE=2 SV=1 - [RS19A_SCHPO]	43,91	14,58	1	2	2	16,1	9,70
P05732	60S ribosomal protein L20 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl20a PE=1 SV=3 - [RL20_SCHPO]	43,36	25,00	1	3	3	20,6	10,42
P47943	ATP-dependent RNA helicase eIF4A OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=tif1 PE=1 SV=2 - [IF4A_SCHPO]	42,93	5,36	1	2	2	44,4	5,02
O14007	H/ACA ribonucleoprotein complex subunit 4 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=cbf5 PE=3 SV=1 - [CBF5_SCHPO]	41,76	4,22	1	2	2	53,1	8,97
O60144	40S ribosomal protein S16 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps16a PE=2 SV=1 - [RS16_SCHPO]	41,11	22,86	1	3	3	15,4	10,13

O59804	10 kDa heat shock protein, mitochondrial OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=hsp10 PE=1 SV=1 - [CH10_SCHPO]	40,32	22,12	1	2	2	11,3	9,36
P87142	Heat shock protein 70 homolog C57A7.12 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPAC57A7.12 PE=1 SV=3 - [YDMC_SCHPO]	40,06	3,71	1	2	2	61,2	4,89
Q9URM2	Probable transketolase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPBC2G5.05 PE=2 SV=1 - [TKT_SCHPO]	37,91	4,09	1	2	2	75,1	6,80
P36592	DNA repair and recombination protein rad22 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rad22 PE=1 SV=2 - [RAD22_SCHPO]	36,72	9,17	1	2	2	51,9	8,40
O42952	40S ribosomal protein S30 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps30a PE=3 SV=2 - [RS30_SCHPO]	34,77	19,67	1	2	2	6,9	11,68
O75000	60S ribosomal protein L12 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl1201 PE=1 SV=1 - [RL12_SCHPO]	34,18	20,61	1	2	2	17,7	9,31
P56289	Eukaryotic translation initiation factor 5A-1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=tif51a PE=1 SV=1 - [IF5A1_SCHPO]	33,96	19,11	2	2	2	17,1	4,89
O14086	DNA-directed RNA polymerase I subunit rpa49 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpa49 PE=2 SV=1 - [RPA49_SCHPO]	33,05	5,18	1	2	2	48,0	9,58
O14344	Inosine-5'-monophosphate dehydrogenase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=gua1 PE=2 SV=1 - [IMDH_SCHPO]	32,60	4,20	1	2	2	57,0	6,87
Q9USU7	HMG box-containing protein C28F2.11 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPBC28F2.11 PE=1 SV=1 - [YHHB_SCHPO]	32,52	14,19	1	3	3	33,9	9,32
P09988	Histone H3.1/H3.2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=hht1 PE=1 SV=2 - [H31_SCHPO]	31,92	30,15	1	2	2	15,3	11,27
P78812	6-phosphogluconate dehydrogenase, decarboxylating OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPBC660.16 PE=1 SV=2 - [6PGD_SCHPO]	31,25	11,18	1	4	4	53,6	7,14
P78811	Probable UTP--glucose-1-phosphate uridylyltransferase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=fuy1 PE=1 SV=2 - [UGPA1_SCHPO]	30,66	4,55	1	2	2	56,4	7,52
O14069	Probable 60S ribosomal protein L28e OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl28e PE=1 SV=1 - [RL28E_SCHPO]	30,58	35,82	1	4	4	14,7	11,22
P78946	60S ribosomal protein L26 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpl26 PE=3 SV=1 - [RL26_SCHPO]	30,34	16,67	1	2	2	14,3	11,17
P10989	Actin OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=act1 PE=1 SV=1 - [ACT_SCHPO]	29,00	13,33	1	3	3	41,7	5,48
P36604	78 kDa glucose-regulated protein homolog OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=bip1 PE=3 SV=2 - [GRP78_SCHPO]	28,55	4,07	1	2	2	73,2	4,96
P24487	ATP synthase subunit alpha, mitochondrial OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=atp1 PE=3 SV=1 - [ATPA_SCHPO]	28,00	5,60	1	2	2	58,6	9,09
O59865	40S ribosomal protein S24-B OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps24b PE=2 SV=3 - [RS24B_SCHPO]	26,76	17,16	1	2	2	15,5	10,92
Q02061	DNA-directed RNA polymerase II subunit RPB2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rpb2 PE=1 SV=2 - [RPB2_SCHPO]	23,71	1,82	1	2	2	137,8	6,83

Appendix Table S2: Fission yeast strains used in this study

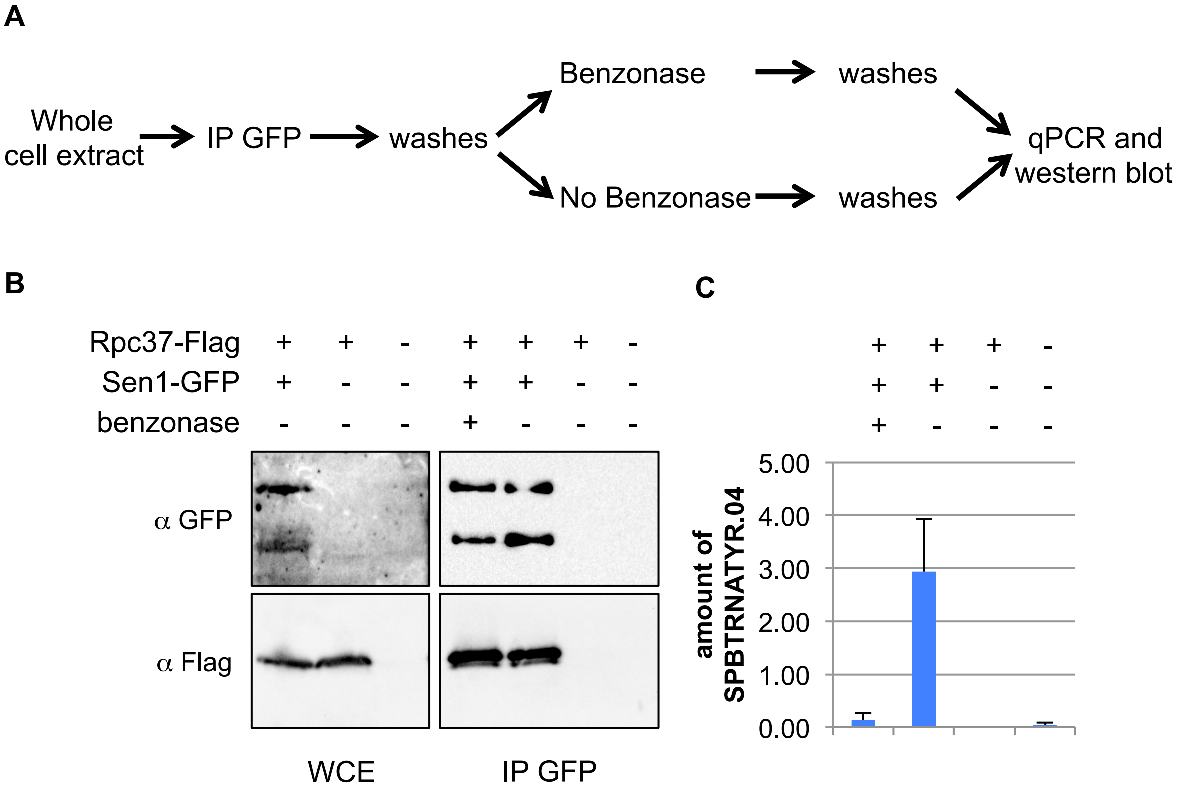
Strain number	Mating type	Leu Ura Ade His	Genotype	Origin
LY5	*h+*	*leu1-32*		lab stock
LY6	*h-*	*leu1-32*		lab stock
LY11	*h+*	*leu1-32 ura4D18*		lab stock
LY12	*h-*	*leu1-32 ura4D18*		lab stock
LY112	*h+*	*leu1-32 ura4D18 ade6-210*		lab stock
LY113	*h-*	*leu1-32 ura4D18 ade6-210*		lab stock
LY1052	*h-*	*leu1-32*	*rrp6Δ::KanR*	lab stock
LY1053	*h+*	*leu1-32*	*rrp6Δ::KanR*	lab stock
LY1334	*h-*	*leu1-32*	*sen1Δ::KanR*	lab stock
LY2528	*h-*	*leu1-32 ura? ade?*	*rnh1D129N-GFP-KanR*	lab stock
LY2529	*h-*	*leu1-32 ura? ade?*	*rnh1D129N-GFP-KanR*	lab stock
LY2544	*h+*	*leu1-32 ura4- ade6-210*	*rnh1D129N-GFP-KanR ARS::nmt1-RnhA::LEU2+*	lab stock
LY2545	*h-*	*leu1-32 ura4- ade6-216*	*rnh1D129N-GFP-KanR ARS::nmt1-RnhA::LEU2+*	lab stock
LY2638	*h+*	*leu1-32 ura4D18*	*sen1Δ::NatR*	lab stock
LY2639	*h-*	*leu1-32 ura4D18 ade6-210*	*sen1Δ::NatR*	lab stock
LY3159	*h+*	*leu1-32 ura4D-*	*rpc25-13myc-KanR sen1Δ::NatR*	lab stock
LY3160	*h+*	*leu1-32 ura4D- ade6-210*	*rpc25-13myc-KanR sen1Δ::NatR*	lab stock
LY3161	*h+*	*leu1-32 ura4D- ade6-210*	*rpc25-13myc-KanR sen1Δ::NatR*	lab stock
LY3681	*h90?*	*leu1-32 ura4D- ade6-216*	*rpc25-13myc-KanR rnh1Δ::HygroR rnh201Δ::KanR*	lab stock
LY3747	*h-?*	*leu1-32 ura- ade6-216*	*rrp6Δ::KanR*	lab stock
LY3790	*h+*	*leu1-32 ura4-*	*sen1Δ::NatR rrp6Δ::KanR*	lab stock
LY3791	*h-*	*leu1-32 ura4- ade6-216*	*sen1Δ::NatR rrp6Δ::KanR*	lab stock
LY3843	*h-*	*leu1-32 ura4-*	*sen1Δ::KanR*	lab stock
LY3844	*h+*	*leu1-32 ura4-*	*sen1Δ::KanR*	lab stock
LY3929	*h-*	*leu1-32 ura4- ade6-210*	*sen1-3flag-NatR*	lab stock
LY3930	*h+*	*leu1-32 ura4- ade6-210*	*sen1-3flag-NatR*	lab stock
LY3966	*h-*	*leu1-32 ura4D18 ade6? his3D1*	*P81nmt1-dis3::KanR*	François Bachand
LY4127	*h-*	*leu1-32 ura4D18 ade6-704*		Richard J. Maraia
LY4130	*h-*	*ura4D18 ade6-704*	*leu1-32::[DRT5T::leu1+]*	Richard J. Maraia
LY4156	*h-*	*leu1-32 ade6-704*	*sen1Δ::KanR*	this study
LY4157	*h+*	*leu1-32 ade6-704*	*sen1Δ::KanR*	this study
LY4164	*h+*	*ade6-704*	*sen1Δ::KanR leu1-32::[DRT5T::leu1+]*	this study
LY4165	*h-*	*ade6-704*	*sen1Δ::KanR leu1-32::[DRT5T::leu1+]*	this study
LY4174	*h-*	*leu1-32 ura4- ade6-704*	*dbl8Δ::NatR*	this study
LY4175	*h+*	*leu1-32 ura4- ade6-704*	*dbl8Δ::NatR*	this study
LY4183	*h+*	*leu1-32 ura4- ade6-704*	*dbl8Δ::NatR leu1-32::[DRT5T::leu1+]*	this study
LY4184	*h-*	*leu1-32 ura4- ade6-704*	*dbl8Δ::NatR leu1-32::[DRT5T::leu1+]*	this study
LY4285	*h-*	*leu1-32 ura4D18 ade6-704*	*rpc37-3flag-NatR*	this study
LY4290	*h-*	*leu1-32 ura4D18 ade6-704*	*rpc37-V189D-3flag-NatR*	this study
LY4294	*h+*	*leu1-32 ura4D18 ade6-704*		this study
LY4316	*h+*	*leu1-32 ura4D18 ade6-704*	*rpc37-V189D-3flag-NatR*	this study
LY4331	*h+*	*ura4D18 ade6-704*	*rpc37-3flag-NatR leu1-32::[DRT5T::leu1+]*	this study
LY4332	*h+*	*ura4D18 ade6-704*	*rpc37-3flag-NatR leu1-32::[DRT5T::leu1+]*	this study
LY4333	*h+*	*ura4D18 ade6-704*	*rpc37-3flag-NatR sen1Δ::KanR leu1-32::[DRT5T::leu1+]*	this study
LY4334	*h+*	*ura4D18 ade6-704*	*rpc37-3flag-NatR sen1Δ::KanR leu1-32::[DRT5T::leu1+]*	this study
LY4349	*h+*	*leu1-32 ade6-704*	*rpc37-3flag-NatR*	this study
LY4350	*h-*	*leu1-32 ade6-704*	*rpc37-3flag-NatR*	this study
LY4355	*h-*	*ade6-704*	*rpc37-V189D-3flag-NatR leu1-32::[DRT5T::leu1+]*	this study
LY4356	*h-*	*ade6-704*	*rpc37-V189D-3flag-NatR leu1-32::[DRT5T::leu1+]*	this study
LY4523	*h-*	*leu1-32 ura4D*	*sen1Δ::NatR*	lab stock
LY4524	*h+*	*leu1-32 ura4D ade6-210*	*sen1Δ::NatR*	lab stock
LY4681	*h+*	*leu1-32 ura4D18*	*cdc2asM17*	Iain Hagan
LY4682	*h-*	*leu1-32 ura4D18*	*cdc2asM17*	Iain Hagan
LY4757	*h-*	*ura4D- ade6-704*	*cdc2asM17 rpc37-3flag-NatR*	lab stock
LY4781	*h-*		*cdc2asM17 sen1Δ::KanR*	lab stock
LY4793	*h+*	*leu1-32 ura4D18 ade6-210*	*arg10-2T*	this study
LY4795	*h+*	*leu1-32 ura4D18 ade6-210*	*arg10-2T*	this study
LY4880	*h+*	*leu1-32 ura4D18 ade6-210*	*sen1Δ::NatR arg10-2T*	this study
LY4881	*h+*	*leu1-32 ura4D18 ade6-210*	*sen1Δ::NatR arg10-2T*	this study
LY4882	*h-*	*leu1-32 ura4D18 ade6-210*	*sen1Δ::NatR arg10-2T*	this study
LY4938	*h-*	*leu1-32 ura4D18 ade6-704/210?*	*rpc37-3flag-NatR arg10-2T*	this study
LY4975	*h+*	*leu1-32 ade6-704*	*cdc2asM17 rpc37-3flag-NatR*	this study
LY4976	*h-*	*leu1-32 ade6-704*	*cdc2asM17 rpc37-3flag-NatR*	this study
LY4977	*h-*	*leu1-32 ade6-704*	*cdc2asM17 rpc37-3flag-NatR sen1Δ::KanR*	this study
LY4978	*h-*	*leu1-32 ade6-704*	*cdc2asM17 rpc37-3flag-NatR sen1Δ::KanR*	this study
LY5218	*h+*	*leu1-32 ura4D-*	*rpc25-13myc-KanR sen1Δ::NatR ARS::nmt1-RnhA::LEU2+*	this study
LY5219	*h+*	*leu1-32 ura4D-*	*rpc25-13myc-KanR sen1Δ::NatR ARS::nmt1-RnhA::LEU2+*	this study
LY5220	*h-*	*leu1-32 ura4D- ade6-210*	*rpc25-13myc-KanR sen1Δ::NatR ARS::nmt1-RnhA::LEU2+*	this study
LY5221	*h+*	*leu1-32 ura4D- ade6-210*	*rpc25-13myc-KanR sen1Δ::NatR ARS::nmt1-RnhA::LEU2+*	this study
LY5242	*h-*	*leu1-32 ura4D- ade6-210 his2-Mat1M*	*rpc25-13myc-KanR*	Ken Noma
LY5277	*h+*	*leu1-32 ura4D-*	*rpc25-13myc-KanR ARS::nmt1-RnhA::LEU2+*	this study
LY5278	*h-*	*leu1-32 ura4D- his2-Mat1M*	*rpc25-13myc-KanR ARS::nmt1-RnhA::LEU2+*	this study
LY5357	*h-*	*leu1-32 ura4D- ade6-210/216?*	*rnh1-D129N-GFP-KanR sen1Δ::NatR*	this study
LY5358	*h-*	*leu1-32 ura4D- ade6-210/216?*	*rnh1-D129N-GFP-KanR sen1Δ::NatR*	this study
LY5359	*h+*	*leu1-32 ura4D- ade6-210/216?*	*rnh1-D129N-GFP-KanR sen1Δ::NatR*	this study
LY5360	*h+*	*leu1-32 ura4D- ade6-210/216?*	*rnh1-D129N-GFP-KanR sen1Δ::NatR ARS::nmt1-RnhA::LEU2+*	this study
LY5361	*h-*	*leu1-32 ura4D- ade6-210/216?*	*rnh1-D129N-GFP-KanR sen1Δ::NatR ARS::nmt1-RnhA::LEU2+*	this study
LY5362	*h+*	*leu1-32 ura4D- ade6-210/216?*	*rnh1-D129N-GFP-KanR sen1Δ::NatR ARS::nmt1-RnhA::LEU2+*	this study
LY5465	*h-*	*leu1-32 ura4D- ade6-210/704?*	*rpc37-3flag-NatR sen1Δ::KanR arg10-2T*	this study
LY5466	*h+*	*leu1-32 ura4D- ade6-210/704?*	*rpc37-3flag-NatR sen1Δ::KanR arg10-2T*	this study
LY5467	*h-*	*leu1-32 ura4D- ade6-210/704?*	*rpc37-3flag-NatR sen1Δ::KanR arg10-2T*	this study
LY5521	*h-*	*leu1-32 ura4D- ade6-? his3D1*	*sen1Δ::NatR P81nmt1-dis3::KanR*	this study
LY5522	*h+*	*leu1-32 ura4D- ade6-?*	*sen1Δ::NatR P81nmt1-dis3::KanR*	this study
LY5524	*h-*	*leu1-32 ura4D- ade6-? his3D1*	*sen1Δ::NatR P81nmt1-dis3::KanR*	this study
LY5724	*h+*	*leu1-32 ura4D18 ade6-210*	*arg10-23T*	this study
LY5762	*h-*	*leu1-32 ura4D- ade6-210/704?*	*cdc2asM17 rpc37-3flag-NatR sen1Δ::KanR arg10-23T*	this study
LY5763	*h+*	*leu1-32 ura4D- ade6-210/704?*	*cdc2asM17 rpc37-3flag-NatR sen1Δ::KanR arg10-23T*	this study
LY5766	*h-*	*leu1-32 ura4D- ade6-210/704?*	*cdc2asM17 rpc37-3flag-NatR arg10-23T*	this study
LY5767	*h+*	*leu1-32 ura4D- ade6-210/704?*	*cdc2asM17 rpc37-3flag-NatR arg10-23T*	this study
LY5955	*h+*	*leu1-32 ura4D- ade6-210*	*sen1-3flag-NatR arg10-TATAless*	this study
LY5956	*h-*	*leu1-32 ura4D- ade6-210*	*sen1-3flag-NatR arg10-TATAless*	this study
LY5961	*h-*	*leu1-32 ura4D- ade6-210*	*sen1Δ::NatR arg10-23T*	this study
LY5962	*h-*	*leu1-32 ura4D- ade6-210*	*sen1Δ::NatR arg10-23T*	this study
LY5965	*h-*	*leu1-32 ura4D- ade6-*	*rpc37-3flag-NatR arg10-TATAless*	this study
LY5966	*h-*	*leu1-32 ura4D- ade6-*	*rpc37-3flag-NatR arg10-TATAless*	this study
FBY2103	*h+*	*leu1-32 ura4-D18 his3-D1 ade6-M216*	*Sen1-HTP::kanMX6*	this study
FBY2209	*h+*	*leu1-32 ura4-D18 his3-D1 ade6-M216*	*Rpc1-TAP::natMX6*	this study
FBY2210	*h+*	*leu1-32 ura4-D18 his3-D1 ade6-M216*	*Rpc2-TAP::natMX6*	this study
FBY2212	*h?*	*leu1-32 ura4-D18 his3-D1 ade6?*	*sen1Δ::kanMX6 Rpc1-TAP::natMX6*	this study
FBY2213	*h?*	*leu1-32 ura4-D18 his3-D1 ade6?*	*sen1Δ::kanMX6 Rpc2-TAP::natMX6*	this study
LY3811	*h-*	*leu1-32 ura4-*	*dbl8Δ::NatR*	this study
LY3812	*h+*	*leu1-32 ura4-*	*dbl8Δ::NatR*	this study
LY3815	*h-*	*leu1-32 ura4D18 ade6-210*	*dbl8-3flag-NatR*	this study
LY3859	*h-*	*leu1-32 ura4- ade6-210*	*sen1-GFP-KanR dbl8Δ::NatR*	this study
LY3860	*h-*	*leu1-32 ura4- ade6-210*	*sen1-GFP-KanR dbl8Δ::NatR*	this study
LY3861	*h+*	*leu1-32 ura4- ade6-210*	*sen1-GFP-KanR dbl8Δ::NatR*	this study
LY3921	*h+*	*leu1-32 ura4- ade6-210*	*rpa43-GFP-KanR*	this study
LY3923	*h-*	*leu1-32 ura4- ade6-210*	*rpa43-GFP-KanR dbl8-3flag-NatR*	this study
LY6180	*h+*	*leu1-32 ura4D ade6-210/704?*	*rpc37-3flag-NatR sen1Δ::KanR thr10-20T*	this study
LY6211	*h+*	*leu1-32 ura4D ade6-210/704?*	*sen1Δ::KanR thr10-20T*	this study

Appendix Table S3: Primers used in this study

Figure	Chromosome site	Name on figure	Use	Primer name	Primer sequence
1F/2A/3C	18S ribosomal RNA	18S	ChIP	18SqL1 18SqR1	tttctaggaccgccgtaatg tgctttcgcagtagttcgtc
1F	28S ribosomal RNA	28S	ChIP	28SqL1 28SqR1	cccttgtcgcttaattggac tacattccggcaccttaacc
1F/2A	SPCC13B11.01	adh1	ChIP	adh1ORFqL1 adh1ORFqR1	tcaccatggtcactgtttc cgggaaacgtattcaagagc
1F	SPAC27E2.11c	27E2.11c	ChIP	27E2.11cqL1 27E2.11cqR1	tcccctgtttagcatggaag caagggctgttttgtcactg
1F	SPBC19C2.07	fba1	ChIP	fba1qL1 fba1qR1	tcaagaccaccaacgacaag aggcgaattgggtatcagtg
1F	SPCC417.08	tef3	ChIP	Tef3 qL1 Tef3 qR1	ATGTTGCCTGGTTGGAGAAC AACGTGGTCCAAGAAACCAG
1F	SPBC18H10.14	rps1601	ChIP	rps1601qL1 rps1601qR1	cgtgctcgtcaacaaaagtc aacggttggctcgtacacag
1F/1G/2A/2C/3B/3C/4E/5B/6B/6C/6D/6E	SPCTRNAARG.10	arg10.1	ChIP/RTqPCR	arg10qL1 arg10qR1	GGTGTGTAGCCTAATGGTTAAGG GAGTGTGACAGGACTCGAACC
1G/4E/6B/6D	SPCTRNAARG.10	arg10.2	ChIP	arg10qL2 arg10qR2	GGAAGGATACAATATCCACAACG GCTGTTATCCATCCACTTACGG
1G/4E/6B/6D	SPCTRNAARG.10	arg10.3	ChIP	arg10 -300 FW arg10qR3	TGCGACTCAGCATAAAGGTG GGCATTCGTCGATTTTGC
1G/4E/6B/6D	SPCTRNAARG.10	arg10.4	ChIP	arg10qL4 arg10qR4	AAGCCGCCTTTCGTTAACAC CTGCTTGACCAGCTTTTGTG
1G/4E/6B/6D	SPCTRNAARG.10	arg10.5	ChIP	arg10qL5 arg10qR5	ACCAAACTGCCCGATACAAC GCAAACAGAGTCCAATTGAGG
2C/	SPCTRNAARG.10	arg10	RTqPCR	arg10RTT1	CAATATTTCTATTGCATGTTGACAG
1F/1G/2A/3B/3C/4E/	SPCTRNATHR.10	thr10.1	ChIP	thr10qL1 thr10qR1	CAATCAACGTTGCCCCTATG ATACAAATTGCCCCCACTCG
4E	SPCTRNATHR.10	thr10.2	ChIP	thr10qL2 thr10qR2	ATTAGGAGGAGCATCGTACAGC CACATAAAAGTGATATGCAAAAACG
4E	SPCTRNATHR.10	thr10.4	ChIP	thr10qL4 thr10qR4	AGTCACGGACTTGGTCTTTACC TTCTTTGCACCCCATAGCAC
4E	SPCTRNATHR.10	thr10.5	ChIP	thr10qL5 thr10qR5	AATGAGATTCATCCAGCGTTC GCAGGTACCGTAATTAGCCTTC
4E	SPCTRNATHR.10	thr10.6	ChIP	thr10qL6 thr10qR6	GTGGGATGTACTAAACCACGTC ACGGATGACAGTAAAAGGAATG
1F/2A/2C/3B/3C/4E/5B	SPBTRNATYR.04	tyr04	ChIP/RTqPCR	tyr04FW tyr04RV	TGGTGTAGTTGGTTATCACATCC AATCTCCTGAGCCAGAATCG
4E	SPBTRNATYR.04	lys09	ChIP	lys09qL1 lys09qR1	GCTTTATGAGCGGCGTAAAC GAGCATTAGGTTTTTGGCGTAG
4E	SPBTRNATYR.04	tyr04.2	ChIP	tyr04qL2 tyr04qR2	ttgcccttgcatcctatctc tgaatttagcacgtttctctcaa
4E	SPBTRNATYR.04	tyr04.3	ChIP	tyr04qL3 tyr04qR3	TCCTTTCACGCCCCTTTC ACAAATCCTGTTCAAAATTAGCC
5B	SPBTRNATYR.04	tyr04	RTqPCR	tyr04RTT2	TACCACAAGTAGCCAGGGTG
1F/2A/3B/3C/5B	SPATRNAPRO.02	pro02	ChIP/RTqPCR	pro02qL1 pro02qR1	ACATACCTCTTTCGGGTAATCC GGGCCTAACCAGGATTCG
5B	SPATRNAPRO.02	pro02	RTqPCR	pro02RTT1	GGTAATCAAGCAAGGTGTAAGG
5C	SPATRNAPRO.02	pro02	Northern	pro02qR3	TCTAAACTCAGCATACAAGTGGGG
1F/2A/3B/3C	SPCTRNAMET.07	met07	ChIP	c417qL1 c417qR1	AGGTTCAAATCCTGCTGGTG TGGGACCTACGGGTTATGAG
1F/2A/3B/3C	5S ribosomal RNA	5S	ChIP	5SqL1 5SqR1	TAGGCGAAAACACCAGTTCC TTCCCATGTTGTCTCCAACC
1F/2A/3B/3C	SPRRNA.20	5S20	ChIP	5S20qL2 5S20qR2	CATGGCTAAATTGTTCAAATCC GTGGTAATTCGCCCATTGTC
1F/2A/3B/3C	snu6	snu6	ChIP	snu6qL1 snu6qR1	GATCTTCGGATCACTTTGGTC ATGTCGCAGTGTCATCCTTG
1F/2A	Chromosome-Organizing Clamp 3*	COC3	ChIP	COC3qL COC3qR	CGAATCGCCCTTATGGATTC ATGCTACATCCCGATGATCC
1F/2A	Chromosome-Organizing Clamp 4*	COC4	ChIP	COC4qL COC4qR	TGTCGATATTAGACCGAGCAAC TTCGAACCCACAGACTTTGC
1F/2A	Chromosome-Organizing Clamp 5*	COC5	ChIP	COC5qL COC5qR	CCGAATTGACGCTAGTCTCC TTGTTGCTACCAGCGTATCC
1F/2C/5B/6C/6E	act1	act1	ChIP/RTqPCR	act1qL0 act1qR0	aacgctcgtttccgatagtg acgtcgctttggactttgag
2C	SPBTRNAARG.05	arg05	RTqPCR	arg05qL2 arg05qR2	ATGGTAGCGCATCTCATTCC ACAATCTTACACGACGGGACTC
2C	SPBTRNAARG.05	arg05	RTqPCR	arg05RTT2	CATGAGCAAAACAAAATACCACA
6C	SPCTRNASER.09	ser.09	RTqPCR	ser.09 qL1 ser.09 qR1	AGAAATCTGTTGCGGTCTCC CCGTAAGTGGATGGATAACAGC

* see Noma et al., 2006

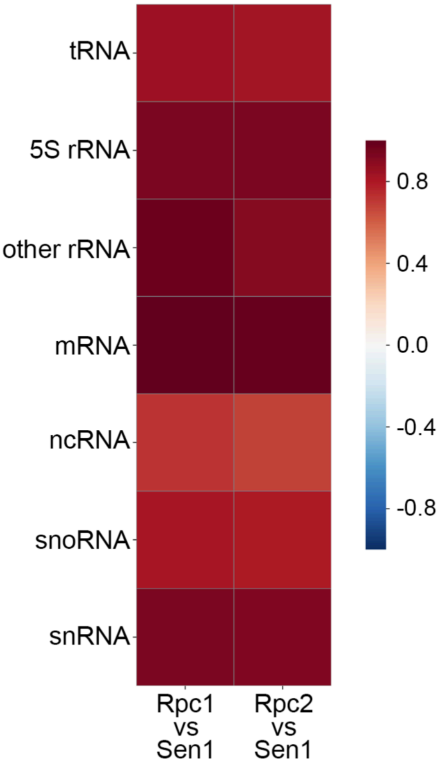
Appendix Figure S1



Appendix Figure S1: The Sen1/RNAP3 physical association is not mediated by RNA or DNA.

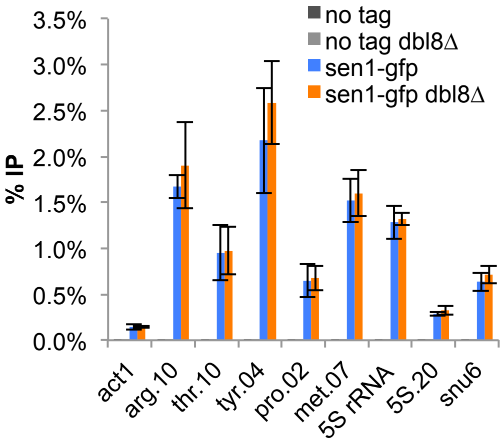
A. Principle of the experiment.
B. Result of the Sen1-GFP immuno-precipitation. Sen1 was difficult to detect in the whole cell extract (WCE) and as a result the blot was exposed for longer than in the IP.
C. The DNA co-immunoprecipitated with Sen1 was quantified by qPCR, using the RNAP3-transcribed SPBTRNATYR.04 locus as reference. This confirmed that the benzonase treatment was efficient.

Appendix Figure S2



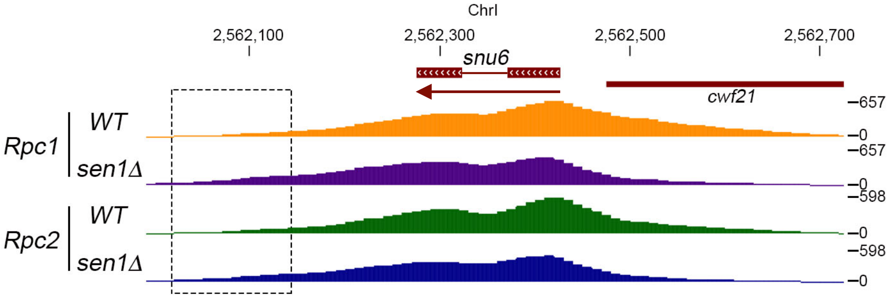
Appendix Figure S2: Correlation analysis of ChIP-seq data from Sen1 and RNAP3 for different classes of genes. Pairwise Pearson correlation analysis of read coverage between Sen1 and Rpc1/Rpc2 for the indicated gene types.

Appendix Figure S3



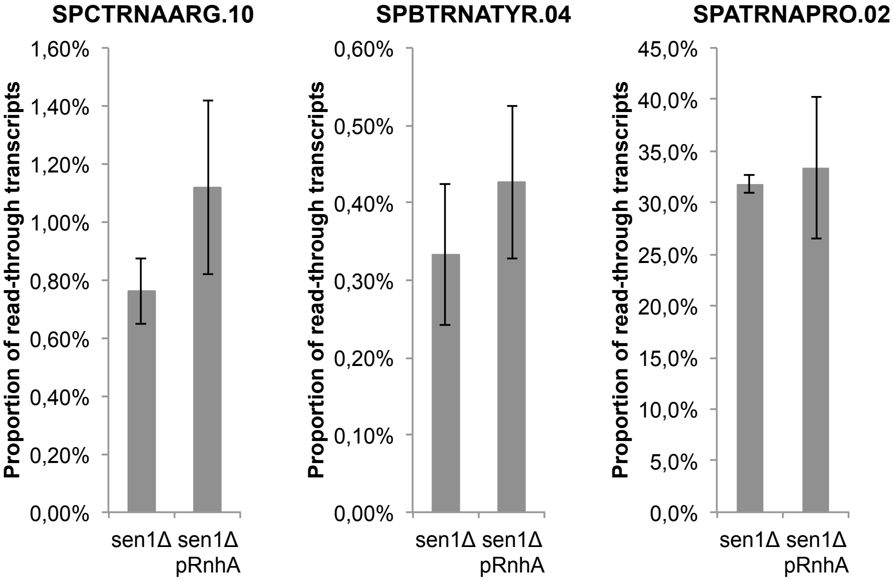
Appendix Figure S3: Lack of Dbl8 does not impact the recruitment of Sen1 at RNAP3-transcribed genes. ChIP-qPCR analysis of GFP-tagged Sen1 in the indicated genotypes and at the indicated loci in a population of cycling cells (mean ± standard deviation from 3 biological replicates).

Appendix Figure S4



Appendix Figure S4: Lack of Sen1 results in modest transcription termination defects at *snu6*. Snapshots of ChIP-seq signals of the RNAP3 subunits Rpc1 and Rpc2 in the presence or absence of Sen1 across the *snu6* locus. Boxed region highlights the increased density of reads downstream of *snu6* in the absence of Sen1.

Appendix Figure S5



Appendix Figure S5: RnhA expression does not change the proportion of read-through transcripts in the absence of Sen1. Strand-specific RT-qPCR was used to quantify the levels of read-through transcripts (see Methods). The mean ± standard deviation from 3 biological replicates is represented here.