

Appendices

Gene Name	Gene Description	Adjusted <i>p</i> -value (Benjamini-Hochberg)	Log 2 fold change (<i>no19^{sa1022}</i> /wild-type)
<i>no19</i>	<i>nucleolar protein 9</i>	0.0127	-1.16
<i>senp3b</i>	<i>SUMO1/sentrin/SMT3 specific peptidase 3b</i>	1.13x10 ⁻⁵	1.14
<i>las11</i>	<i>LAS1-like (S. cerevisiae)</i>	1	-0.166935452
<i>senp3a</i>	<i>SUMO1/sentrin/SMT3 specific peptidase 3a</i>	1	0.098424375
<i>tex10</i>	<i>testis expressed 10</i>	1	0.451582269
<i>wdr18</i>	<i>WD repeat domain 18</i>	1	0.357977686

Table A - 1 The list of genes encoding proteins that interact with *No19* in *no19^{sa1022}* mutants. The gene name and description, the adjusted *p*-value and the fold change of mutant versus wild-type sibling are shown.

GO Term ID	Term	K-S value
GO:0048565	digestive tract development	0.0043
GO:0001889	liver development	0.02733
GO:0055123	digestive system development	0.04959
GO:0031017	exocrine pancreas development	0.11301
GO:0031016	pancreas development	0.14306
GO:0048546	digestive tract morphogenesis	0.29657
GO:0031018	endocrine pancreas development	0.47669

Table A - 2 The list of GO terms associated with the digestive organs in *no19^{sa1022}* mutants. The GO Term ID and name and the K-S value using topGO are shown.

Gene Name	Gene Description	Adjusted <i>p</i> -value (Benjamini-Hochberg)	Log 2 fold change (<i>no19^{sa1022}</i> /wild-type)
<i>yars</i>	<i>tyrosyl-tRNA synthetase</i>	1.38x10 ⁻⁷	1.42
<i>tars</i>	<i>threonyl-tRNA synthetase</i>	5.78x10 ⁻⁶	1.22
<i>qars</i>	<i>glutamyl-tRNA synthetase</i>	5.87x10 ⁻⁵	1.27
<i>eprs</i>	<i>glutamyl-prolyl-tRNA synthetase</i>	8.17x10 ⁻⁵	1.17
<i>iars</i>	<i>isoleucyl-tRNA synthetase</i>	8.35x10 ⁻⁵	1.28
<i>kars</i>	<i>lysyl-tRNA synthetase</i>	0.000389147	0.97
<i>iars</i>	<i>isoleucyl-tRNA synthetase</i>	0.000619223	1.48
<i>hars</i>	<i>histidyl-tRNA synthetase</i>	0.0007359	0.99
<i>farsa</i>	<i>phenylalanyl-tRNA synthetase, alpha subunit</i>	0.001796306	0.94
<i>rars</i>	<i>arginyl-tRNA synthetase</i>	0.005236793	0.89
<i>farsb</i>	<i>phenylalanyl-tRNA synthetase, beta subunit</i>	0.013378278	0.86
<i>nars</i>	<i>asparaginyl-tRNA synthetase</i>	0.028617189	0.81
<i>larsb</i>	<i>leucyl-tRNA synthetase b</i>	0.030845695	0.84

Table A - 3 The differentially expressed genes belonging to the KEGG term 'Aminoacyl-tRNA biosynthesis' in *no19^{sa1022}* mutants. The gene name and description, the adjusted *p*-value and the fold change of mutant versus wild-type sibling are shown.

Gene Name	Gene Description	Adjusted <i>p</i> -value (Benjamini-Hochberg)	Log 2 fold change (<i>noI9</i> ^{sa1022} /wild-type)
<i>ctps1a</i>	<i>CTP synthase 1a</i>	2.03x10 ⁻⁸	1.57
<i>POLR1D</i>	<i>polymerase (RNA) I polypeptide D, 16kDa</i>	7.10x10 ⁻⁷	1.56
<i>cad</i>	<i>carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase</i>	2.77x10 ⁻⁵	1.22
<i>polr1c</i>	<i>polymerase (RNA) I polypeptide C</i>	0.000232932	1.31
<i>polr1e</i>	<i>polymerase (RNA) I polypeptide E</i>	0.000331795	1.22
<i>upp2</i>	<i>uridine phosphorylase 2</i>	0.000487591	-1.37
<i>POLR3D</i>	<i>polymerase (RNA) III (DNA directed) polypeptide D, 44kDa</i>	0.00213729	1.09
<i>znr1</i>	<i>zinc ribbon domain containing 1</i>	0.00557888	1.52
<i>txnr1</i>	<i>thioredoxin reductase 1</i>	0.005973931	0.85
<i>zgc:110540</i>	<i>zgc:110540</i>	0.014289753	-0.87
<i>polr1a</i>	<i>polymerase (RNA) I polypeptide A</i>	0.036743601	0.90
<i>umps</i>	<i>uridine monophosphate synthetase</i>	0.044072318	1.05
<i>znr1</i>	<i>zinc ribbon domain containing 1</i>	0.04613515	1.65

Table A - 4 The differentially expressed genes belonging to the KEGG term 'Pyrimidine metabolism in *noI9*^{sa1022} mutants.. The gene name and description, the adjusted *p*-value and the fold change of mutant versus wild-type sibling are shown.

Gene Name	Gene Description	Adjusted <i>p</i> -value (Benjamini-Hochberg)	Log 2 fold change (<i>noI9</i> ^{sa1022} /wild-type)
<i>POLR1D</i>	<i>polymerase (RNA) I polypeptide D, 16kDa</i>	7.10x10 ⁻⁷	1.56
<i>polr1c</i>	<i>polymerase (RNA) I polypeptide C</i>	0.000232932	1.31
<i>polr1e</i>	<i>polymerase (RNA) I polypeptide E</i>	0.000331795	1.22
<i>POLR3D</i>	<i>polymerase (RNA) III (DNA directed) polypeptide D, 44kDa</i>	0.00213729	1.09
<i>znr1</i>	<i>zinc ribbon domain containing 1</i>	0.00557888	1.52
<i>polr1a</i>	<i>polymerase (RNA) I polypeptide A</i>	0.036743601	0.90
<i>znr1</i>	<i>zinc ribbon domain containing 1</i>	0.04613515	1.65

Table A - 5 The differentially expressed genes belonging to the KEGG term 'RNA polymerase' in *noI9*^{sa1022} mutants. The gene name and description, the adjusted *p*-value and the fold change of mutant versus wild-type sibling are shown.

Gene Name	Gene Description	Adjusted <i>p</i> -value (Benjamini-Hochberg)	Log 2 fold change (<i>noI9</i> ^{sa1022} /wild-type)
<i>las11</i>	<i>LAS1-like (S. cerevisiae)</i>	1	-0.448606006
<i>noI9</i>	<i>nucleolar protein 9</i>	1	0.229556284
<i>senp3a</i>	<i>SUMO1/sentrin/SMT3 specific peptidase 3a</i>	1	0.236577597
<i>senp3b</i>	<i>SUMO1/sentrin/SMT3 specific peptidase 3b</i>	1	0.273886684
<i>tex10</i>	<i>testis expressed 10</i>	1	0.070232461
<i>wdr18</i>	<i>WD repeat domain 18</i>	1	0.618400968

Table A - 6 The list of genes encoding proteins that interact with Las11 in *las11*^{sa674} mutants. The gene name and description, the adjusted *p*-value and the fold change of mutant versus wild-type sibling are shown.

GO Term ID	Term	K-S value
GO:0031016	pancreas development	0.00447
GO:0048565	digestive tract development	0.00941
GO:0031017	exocrine pancreas development	0.0102
GO:0001889	liver development	0.0472
GO:0048546	digestive tract morphogenesis	0.13953
GO:0055123	digestive system development	0.25312
GO:0031018	endocrine pancreas development	0.28337

Table A - 7 The list of GO terms associated with the digestive organs in *las1l^{sa674}* mutants. The GO Term ID and name and the K-S value using topGO are shown.

KEGG Term	Genes		Fold Enrichment	<i>p</i> -value	Adjusted <i>p</i> -value (Benjamini-Hochberg)
	#	%			
Aminoacyl-tRNA biosynthesis	16	2.46	7.14	2.64x10 ⁻¹⁰	2.77 x10 ⁻⁸
PPAR signaling pathway	11	1.69	3.72	4.08x10 ⁻⁴	0.021191437
Steroid biosynthesis	6	0.92	6.82	9.34x10 ⁻⁴	0.032179842
Pyrimidine metabolism	12	1.84	2.42	0.008207939	0.194544645
Glutathione metabolism	7	1.08	3.50	0.01145079	0.21482917
Purine metabolism	14	2.15	1.99	0.019360768	0.289748562
Steroid hormone biosynthesis	5	0.77	4.46	0.020533482	0.267438789
Drug metabolism	6	0.92	3.57	0.021400618	0.247182337
Spliceosome	15	2.30	1.86	0.025918624	0.263887035
RNA polymerase	5	0.77	3.92	0.032950845	0.296587998

Table A - 8 The enriched KEGG terms of differentially expressed genes of *tti^{s450}* mutants at a statistical significance of *p*-value less than 0.05 using a modified Fisher's exact test. The KEGG term, the number of genes involved in the terms and the percentage of involved genes over total number of genes, the fold enrichment, the *p*-value and the adjusted *p*-value using Benjamini-Hochberg procedure are shown.

KEGG Term	Genes		Fold Enrichment	<i>p</i> -value	Adjusted <i>p</i> -value (Benjamini-Hochberg)
	#	%			
Aminoacyl-tRNA biosynthesis	15	2.81	7.87	3.45x10 ⁻¹⁰	3.38x10 ⁻⁸
PPAR signaling pathway	11	2.06	4.58	6.45x10 ⁻⁵	0.003154475
Steroid biosynthesis	7	1.31	8.26	6.99x10 ⁻⁵	0.002281903
Glutathione metabolism	7	1.31	3.96	0.006238015	0.142136284
Retinol metabolism	6	1.13	4.05	0.012889366	0.22452057
Steroid hormone biosynthesis	5	0.94	5.06	0.013361798	0.197251552
Purine metabolism	13	2.44	2.09	0.017599578	0.220098841
RNA polymerase	5	0.94	4.16	0.026950046	0.284424572
p53 signaling pathway	8	1.50	2.52	0.034401259	0.316949433
Metabolism of xenobiotics by cytochrome P450	4	0.75	4.72	0.046546298	0.373189632

Table A - 9 The enriched KEGG terms of differentially expressed genes of *set^{s453}* mutants at a statistical significance of *p*-value less than 0.05 using a modified Fisher's exact test. The KEGG term, the number of genes involved in the terms and the percentage of involved genes over total number of genes, the fold enrichment, the *p*-value and the adjusted *p*-value using Benjamini-Hochberg procedure are shown.

GO Term ID	Term	K-S value
Digestive organs		
GO:0031017	exocrine pancreas development	0.04942
GO:0048546	digestive tract morphogenesis	0.05708
GO:0001889	liver development	0.10248
GO:0031018	endocrine pancreas development	0.22476
GO:0055123	digestive system development	0.30988
GO:0048565	digestive tract development	0.31777
GO:0031016	pancreas development	0.36157
Eye		
GO:0031076	embryonic camera-type eye development	0.19883
GO:0048596	embryonic camera-type eye morphogenesis	0.34133
GO:0048048	embryonic eye morphogenesis	0.64118
GO:0001754	eye photoreceptor cell differentiation	0.70683
GO:0048593	camera-type eye morphogenesis	0.72337
GO:0048592	eye morphogenesis	0.78997
GO:0042462	eye photoreceptor cell development	0.92979
GO:0043010	camera-type eye development	0.95017
GO:0001654	eye development	0.95104
GO:0060041	retina development in camera-type eye	0.96029
GO:0060042	retina morphogenesis in camera-type eye	0.98179
Brain		
GO:0030902	hindbrain development	0.3064
GO:0007420	brain development	0.6693
GO:0030900	forebrain development	0.87958
GO:0030901	midbrain development	0.893
Cartilage		
GO:0051216	cartilage development	0.12518
Skeletal		
GO:0001501	skeletal system development	0.0204
GO:0048706	embryonic skeletal system development	0.26733
GO:0060538	skeletal muscle organ development	0.29114
GO:0048704	embryonic skeletal system morphogenesis	0.29273
GO:0048705	skeletal system morphogenesis	0.41744
GO:0007519	skeletal muscle tissue development	0.48451
GO:0048741	skeletal muscle fiber development	0.75617

Table A - 10 The list of GO terms associated with the digestive organs, eye, brain, cartilage and skeletal muscle in *titi*^{s450} mutants. The GO Term ID and name and the K-S value using topGO are shown.

GO Term ID	Term	K-S value
Digestive organs		
GO:0048565	digestive tract development	0.02479
GO:0055123	digestive system development	0.02639
GO:0001889	liver development	0.17341
GO:0031016	pancreas development	0.19378
GO:0031017	exocrine pancreas development	0.27094
GO:0048546	digestive tract morphogenesis	0.28365
GO:0031018	endocrine pancreas development	0.31304
Eye		
GO:0001654	eye development	0.08402
GO:0042462	eye photoreceptor cell development	0.17352
GO:0048048	embryonic eye morphogenesis	0.18294
GO:0043010	camera-type eye development	0.22899
GO:0048592	eye morphogenesis	0.24795
GO:0001754	eye photoreceptor cell differentiation	0.26204
GO:0031076	embryonic camera-type eye development	0.46281
GO:0048596	embryonic camera-type eye morphogenesis	0.55498
GO:0048593	camera-type eye morphogenesis	0.64427
GO:0060041	retina development in camera-type eye	0.75822
GO:0060042	retina morphogenesis in camera-type eye	0.89389
Cartilage		
GO:0051216	cartilage development	0.27115
Skeletal		
GO:0007519	skeletal muscle tissue development	0.00688
GO:0001501	skeletal system development	0.03697
GO:0048741	skeletal muscle fiber development	0.04216
GO:0060538	skeletal muscle organ development	0.0603
GO:0048705	skeletal system morphogenesis	0.12181
GO:0048704	embryonic skeletal system morphogenesis	0.14073
GO:0048706	embryonic skeletal system development	0.17811

Table A - 11 The list of GO terms associated with the digestive organs, eye, brain, cartilage and skeletal muscle in *set*^{s453} mutants. The GO Term ID and name and the K-S value using topGO are shown.

Gene Name	Gene Description	Adjusted <i>p</i> -value (Benjamini-Hochberg)	Log 2 fold change (<i>nol9</i> ^{sa1022} /wild-type)
<i>tti</i> ^{sa450} mutant			
<i>atg16l1</i>	ATG16 autophagy related 16-like 1 (<i>S. cerevisiae</i>)	0.388405483	0.746690463
<i>atg4b</i>	ATG4 autophagy related 4 homolog B (<i>S. cerevisiae</i>)	0.488785713	0.817575752
<i>atg9a</i>	ATG9 autophagy related 9 homolog A (<i>S. cerevisiae</i>)	0.611158802	-0.772274754
<i>atg5</i>	ATG5 autophagy related 5 homolog (<i>S. cerevisiae</i>)	0.788039883	0.513492925
<i>atg9a</i>	ATG9 autophagy related 9 homolog A (<i>S. cerevisiae</i>)	0.818836971	-0.470201462
<i>atg4c</i>	autophagy-related 4C (yeast)	0.876251962	-0.476068028
<i>atg10</i>	ATG10 autophagy related 10 homolog (<i>S. cerevisiae</i>)	0.982750495	0.153372409
<i>atg13</i>	ATG13 autophagy related 13 homolog (<i>S. cerevisiae</i>)	0.983675464	-0.049780343
<i>set</i> ^{sa453} mutant			
<i>atg16l1</i>	ATG16 autophagy related 16-like 1 (<i>S. cerevisiae</i>)	0.609960781	0.648996789
<i>atg10</i>	ATG10 autophagy related 10 homolog (<i>S. cerevisiae</i>)	0.81602828	0.940493174
<i>atg5</i>	ATG5 autophagy related 5 homolog (<i>S. cerevisiae</i>)	0.833919644	0.638757882
<i>atg12</i>	ATG12 autophagy related 12 homolog (<i>S. cerevisiae</i>)	0.994165769	0.652995621
<i>atg4b</i>	ATG4 autophagy related 4 homolog B (<i>S. cerevisiae</i>)	0.99897654	0.516784842
<i>atg13</i>	ATG13 autophagy related 13 homolog (<i>S. cerevisiae</i>)	0.999674861	0.226912478
<i>atg4c</i>	autophagy-related 4C (yeast)	0.999674861	-0.204736068
<i>atg9a</i>	ATG9 autophagy related 9 homolog A (<i>S. cerevisiae</i>)	0.999674861	0.217419046
<i>atg9a</i>	ATG9 autophagy related 9 homolog A (<i>S. cerevisiae</i>)	0.999674861	-0.630197512
<i>nol9</i> ^{sa1022} mutant			
<i>atg4b</i>	ATG4 autophagy related 4 homolog B (<i>S. cerevisiae</i>)	1	-0.18992073
<i>atg13</i>	ATG13 autophagy related 13 homolog (<i>S. cerevisiae</i>)	1	0.190786591
<i>atg16l1</i>	ATG16 autophagy related 16-like 1 (<i>S. cerevisiae</i>)	1	0.249922058
<i>atg10</i>	ATG10 autophagy related 10 homolog (<i>S. cerevisiae</i>)	1	0.486924121
<i>atg4c</i>	autophagy-related 4C (yeast)	1	0.241821933
<i>atg5</i>	ATG5 autophagy related 5 homolog (<i>S. cerevisiae</i>)	1	0.174871634
<i>atg9a</i>	ATG9 autophagy related 9 homolog A (<i>S. cerevisiae</i>)	1	-0.212406566
<i>atg9a</i>	ATG9 autophagy related 9 homolog A (<i>S. cerevisiae</i>)	1	-0.095397584
<i>las1</i> ^{sa674} mutant			
<i>atg4b</i>	ATG4 autophagy related 4 homolog B (<i>S. cerevisiae</i>)	1	0.014990544
<i>atg13</i>	ATG13 autophagy related 13 homolog (<i>S. cerevisiae</i>)	1	0.137029624
<i>atg16l1</i>	ATG16 autophagy related 16-like 1 (<i>S. cerevisiae</i>)	1	0.112731025
<i>atg4c</i>	autophagy-related 4C (yeast)	1	0.599221648
<i>atg9a</i>	ATG9 autophagy related 9 homolog A (<i>S. cerevisiae</i>)	1	-0.081416492
<i>atg10</i>	ATG10 autophagy related 10 homolog (<i>S. cerevisiae</i>)	1	0.162001033
<i>atg5</i>	ATG5 autophagy related 5 homolog (<i>S. cerevisiae</i>)	1	0.152707837
<i>atg9a</i>	ATG9 autophagy related 9 homolog A (<i>S. cerevisiae</i>)	1	-0.755265462

Table A - 12 The list of autophagy-related genes (*atg*) in *nol9*^{sa1022}, *las1*^{sa674}, *tti*^{sa450} and *set*^{sa453} mutants. The gene name and description, the adjusted *p*-value and the fold change of mutant over wild-type sibling are shown.

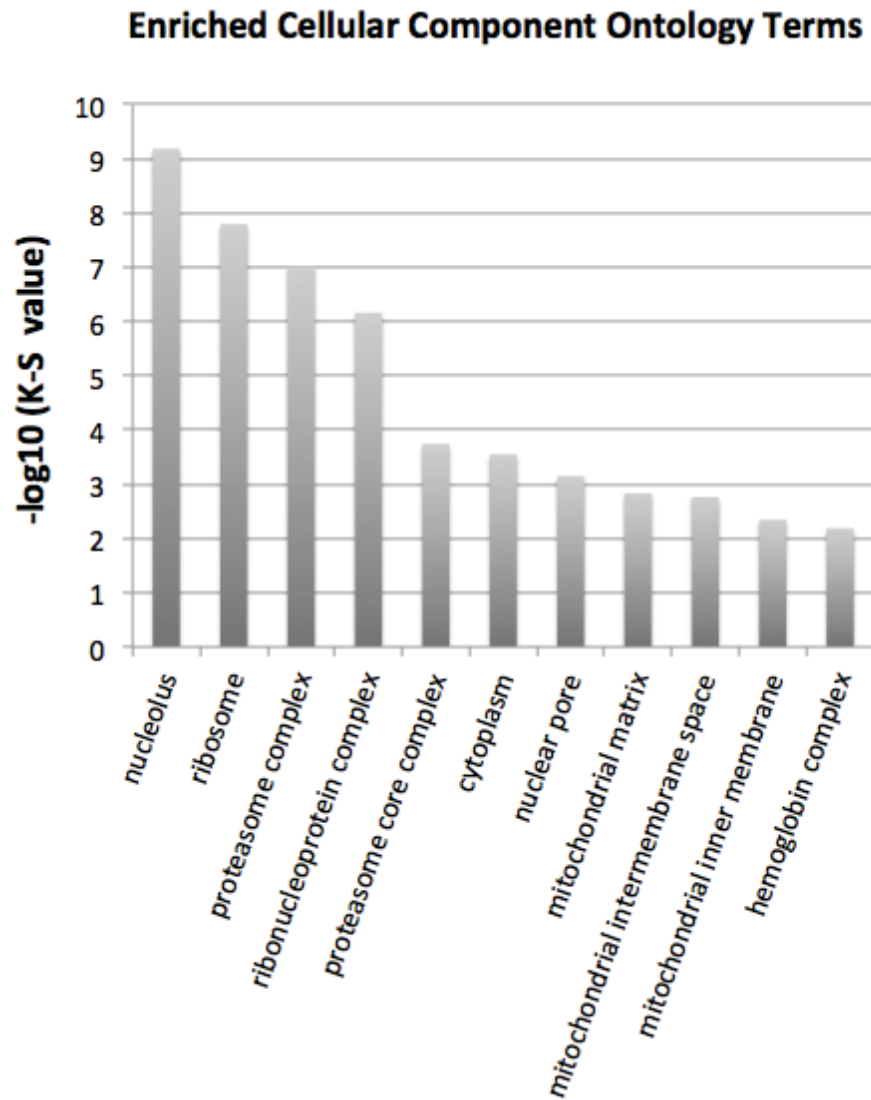


Figure A - 1 The enriched cellular component ontology terms in *tit^{s450}* mutants at statistical significance of K-S value less than 0.01 ($-\log_{10}(\text{K-S value})$ more than 2.0).

Enriched Molecular Function Ontology Terms

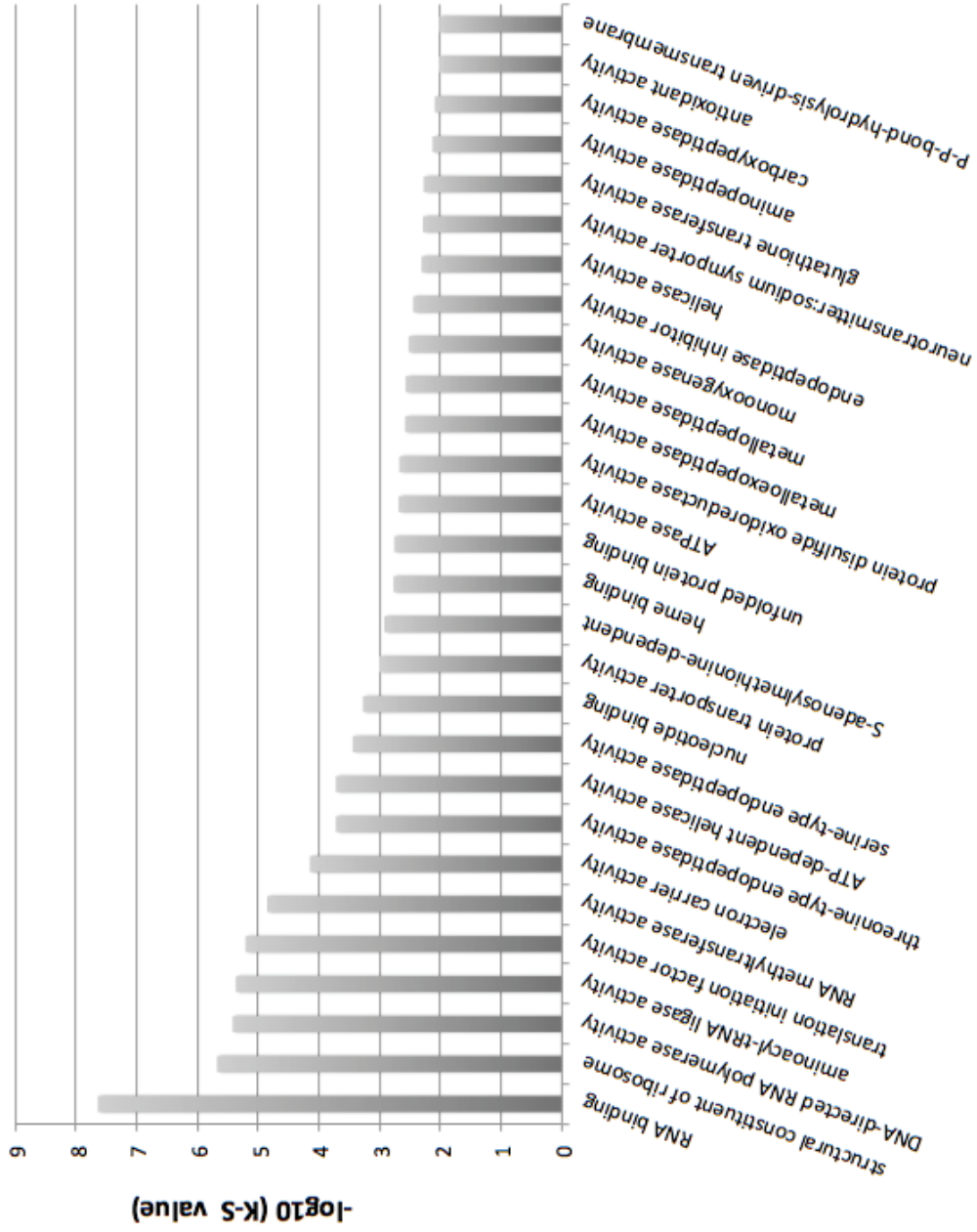


Figure A - 2 The enriched molecular function ontology terms in *ttf1⁸⁴⁵⁰* mutants at statistical significance of K-S value less than 0.01 ($-\log_{10}(\text{K-S value})$ more than 2.0).

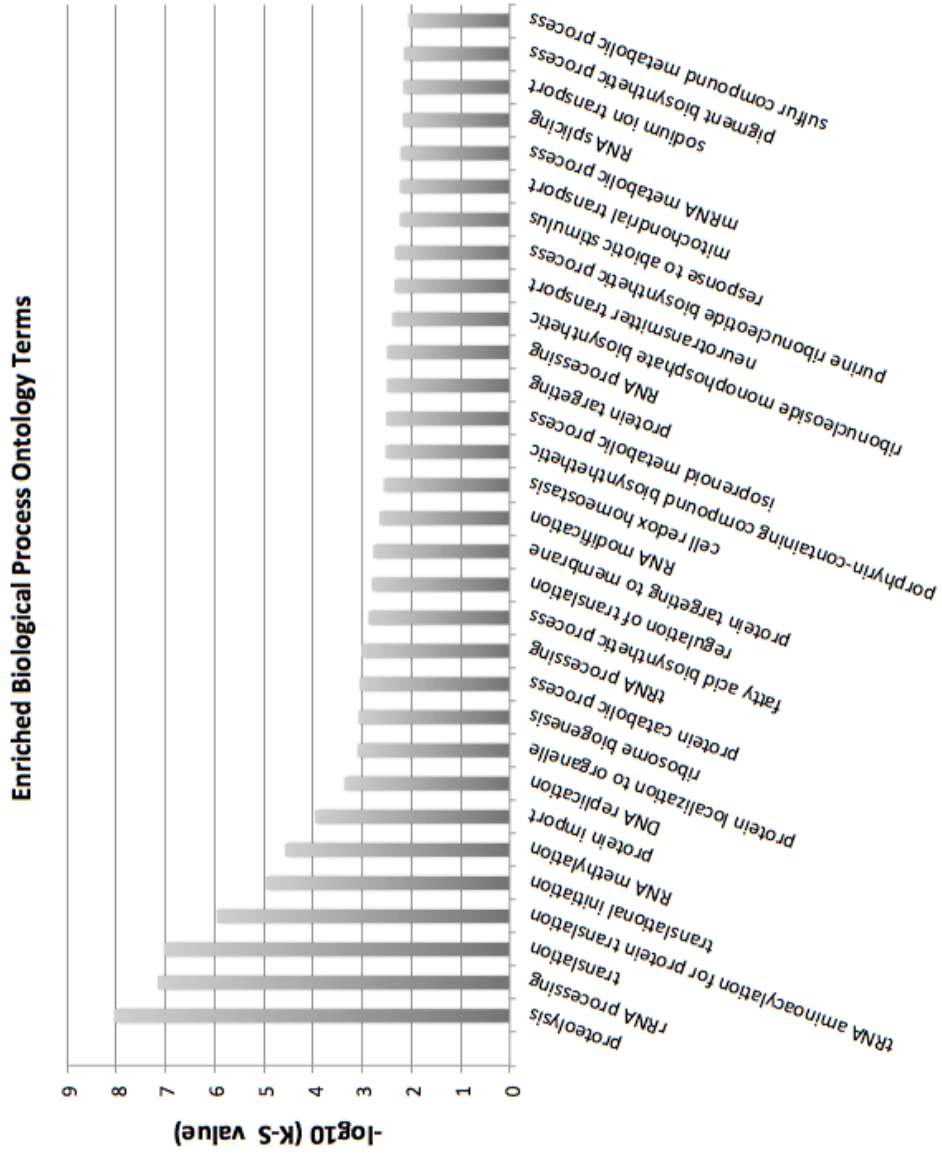


Figure A - 3 The enriched biological process ontology terms in *tit*⁴⁵⁰ mutants at statistical significance of K-S value less than 0.01 ($-\log_{10}(\text{K-S value})$ more than 2.0).

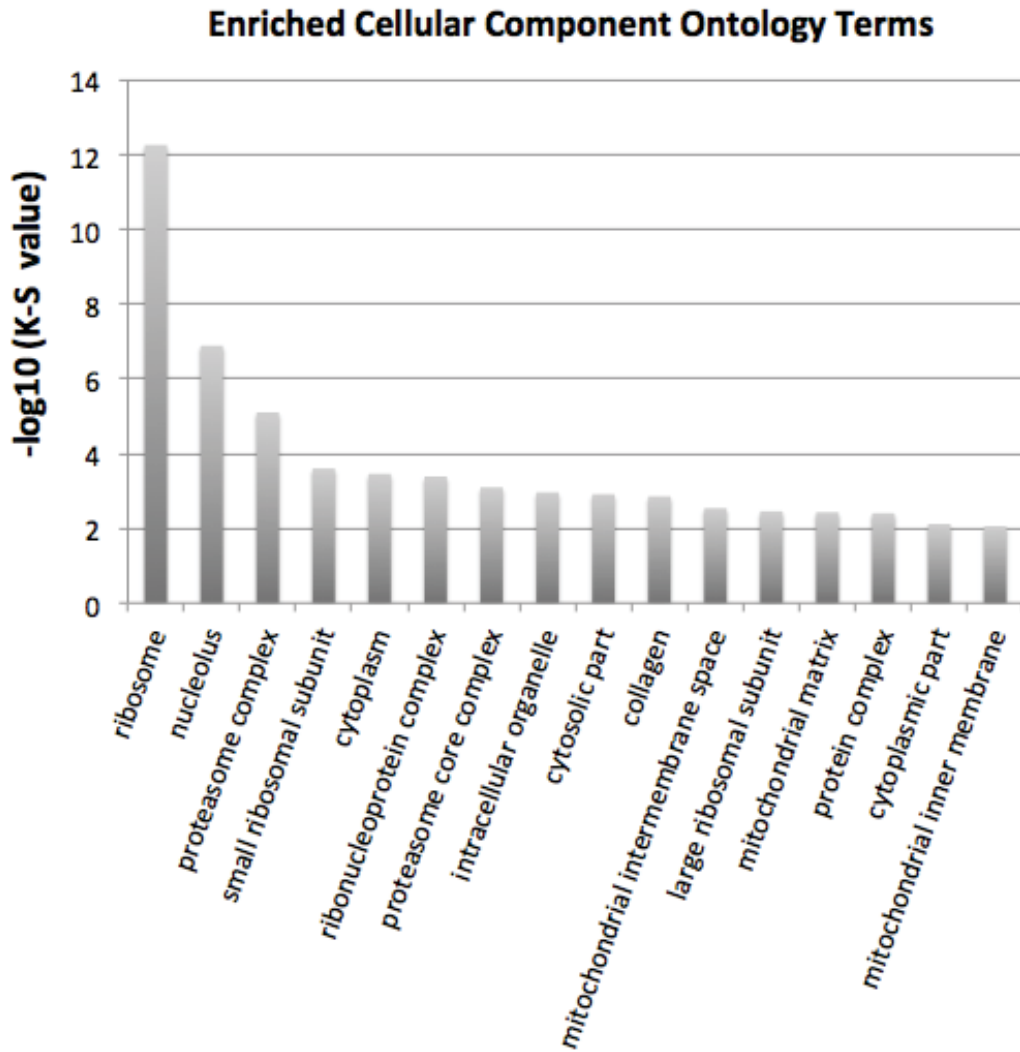


Figure A - 4 The enriched cellular component ontology terms in *set*⁴⁵³ mutants at statistical significance of K-S value less than 0.01 ($-\log_{10}(\text{K-S value})$ more than 2.0).

Enriched Molecular Function Ontology Terms

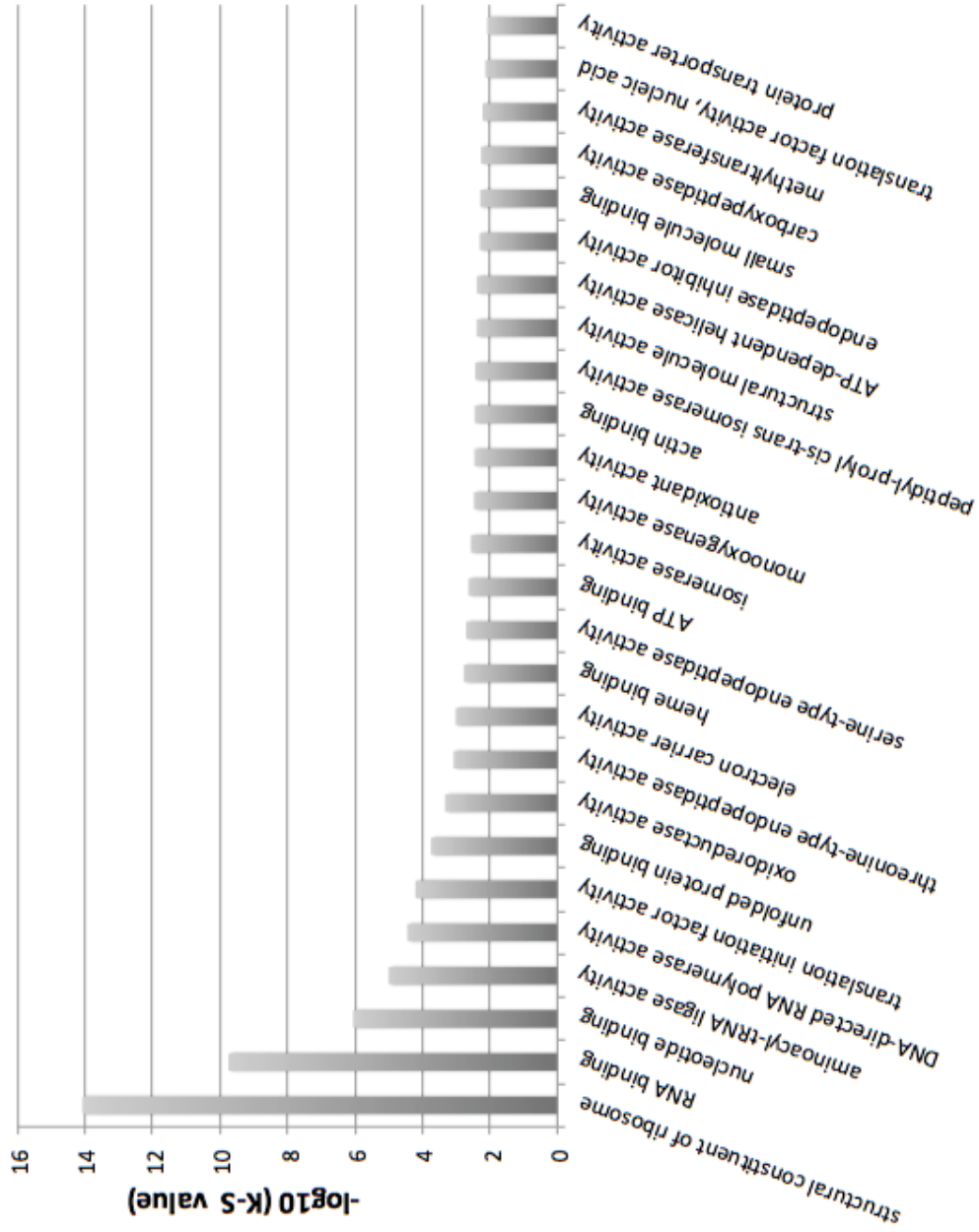


Figure A - 5 The enriched molecular function ontology terms in *sel^{S463}* mutants at statistical significance of K-S value less than 0.01 ($-\log_{10}(\text{K-S value})$ more than 2.0).

Enriched Biological Process Ontology Terms

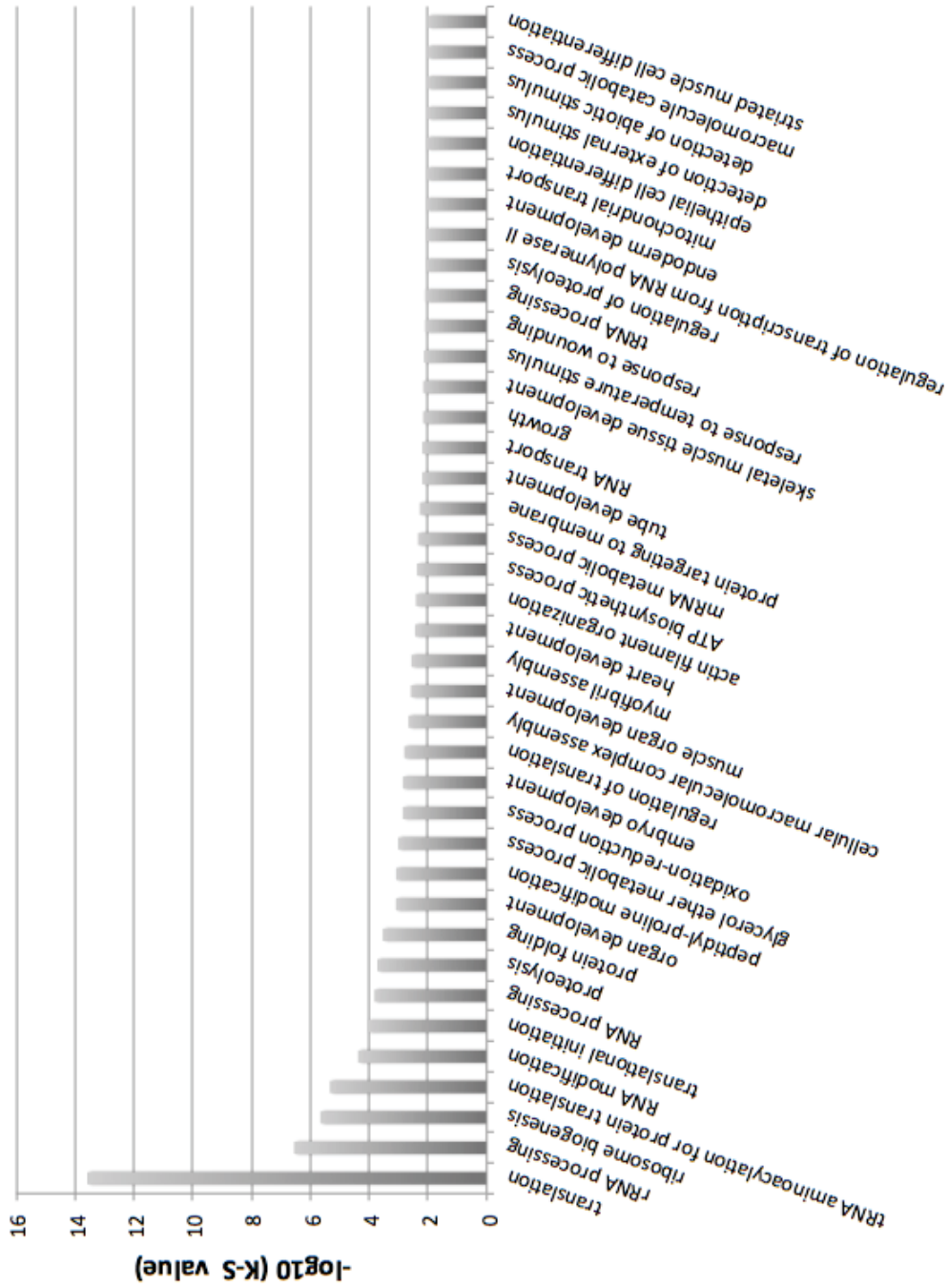


Figure A - 6 The enriched biological process ontology terms in *sc⁴⁵³* mutants at statistical significance of K-S value less than 0.01 ($-\log_{10}(\text{K-S value})$ more than 2.0)