

Supplementary Table S5**Organization of GO-Term, Transcription Factor and Transcription Module Correlations
Associated with Low or High Variation**

Cluster	Gene Set	Process/Function	$\overline{DM} \times \log_{10}(P)$	# genes
1	TM	Not annotated	-5.7	46
1	TM	Protein synthesis	-6	37
2	CC	Cytosolic large ribosomal subunit (sensu Eukaryota)	-8.1	66
3	CC	Ribonucleoprotein complex	-7.2	255
3	CC	Ribosome	-5	191
3	BP	Protein biosynthesis	-8.7	281
4	TM	Protein synthesis	-7.4	252
4	TM	Protein synthesis	-7.1	228
4	TM	Protein synthesis	-9.7	182
4	TM	Protein synthesis	-7.9	286
4	TM	Protein synthesis	-8.8	310
4	TM	Protein synthesis	-8.8	337
4	TM	Protein synthesis	-10.4	160
4	TM	Protein synthesis	-10.8	145
4	TM	Protein synthesis	-12.1	131
4	TM	Protein synthesis	-11.3	120
4	TM	Protein synthesis	-10.8	115
4	TM	Protein synthesis	-10.9	108
4	TM	Protein synthesis	-10.8	96
4	TF	FHL1	-11.7	119
4	CC	Cytosolic ribosome (sensu Eukaryota)	-11.7	119
4	TM	Protein synthesis	-10.1	85
4	TM	Protein synthesis	-11.1	89
4	TM	Protein synthesis	-9.2	76
4	TM	Protein synthesis	-8.6	60
4	TM	Protein synthesis	-9	70
4	TM	Protein synthesis	-7	48
4	TM	protein synthesis	-5	18
5	TF	RAP1	-4.5	91
6	CC	Cytosolic small ribosomal subunit (sensu Eukaryota)	-4.1	45
6	CC	Eukaryotic 48S initiation complex	-4.1	45
6	CC	Eukaryotic 43S preinitiation complex	-4.6	50
7	BP	Macromolecule biosynthesis	6.3	360
8	CC	Non-membrane-bound organelle	4.2	304
8	CC	Intracellular non-membrane-bound organelle	4.2	304
9	CC	Cytosol	6.3	248
10	BP	Protein metabolism	6.9	484
11	CC	Protein complex	10	592

Supplementary Table S5, continued.

Cluster	Gene Set	Process/Function	$\overline{DM} \times \log_{10}(P)$	# genes
12	MF	Nucleic acid binding	4.8	193
12	MF	Binding	6.2	375
13	CC	Intracellular	4.7	2020
13	CHR	TFIID	23.9	1857
14	BP	Translation	-4.5	65
14	MF	Translation factor activity, nucleic acid binding	-4.7	31
14	MF	Translation initiation factor activity	-5.7	21
14	BP	Translational initiation	-5	24
15	TM	Heat shock	4.8	11
15	TM	Not annotated	4.8	11
16	TM	Stress	6.5	11
16	TM	Stress	6.5	11
16	TM	Stress	9.3	17
17	TM	Stress	4.4	6
18	TM	Stress	10.1	22
18	TM	Stress	10.8	26
18	TM	Stress	12.6	32
18	TM	Stress	14.1	37
18	TM	Stress	16.4	46
18	TM	Stress	18.5	55
18	TM	Stress	17.4	50
18	TM	Stress	20.7	64
18	TM	Stress	21.9	72
18	TM	Stress	23.9	85
18	TM	Stress	26.6	95
19	MF	Oxidoreductase activity, acting on the aldehyde or oxo group of donors	4.7	13
20	CC	Mitochondrial matrix	7.9	87
21	BP	Tricarboxylic acid cycle intermediate metabolism	4.4	13
21	BP	Tricarboxylic acid cycle	5.3	10
22	BP	Energy pathways	9.5	92
22	BP	Energy derivation by oxidation of organic compounds	9.5	92
22	BP	Carbohydrate metabolism	5.5	85
22	BP	Main pathways of carbohydrate metabolism	4.8	39
23	CHR	Δ ino80	21.1	180
23	CHR	Δ ino80	21.1	180
24	CHR	SAGA	28.9	234
25	CHR	TATA	31.1	416

Supplementary Table S5, continued.

Cluster	Gene Set	Process/Function	$\overline{DM} \times \log_{10}(P)$	# genes
26	MF	Catalytic activity	6.2	795
27	MF	Oxidoreductase activity	22.4	127
28	MF	Oxidoreductase activity, acting on CH-OH group of donors	9.6	39
28	MF	Oxidoreductase activity, acting on the CHOH group of donors, NAD or NADP as acceptor	8.2	33
29	CHR	Δ snf2	9.3	29
30	TM	Proteolysis	-6.3	20
30	TM	Proteolysis	-5	22
30	TM	Proteosome subunits	-4.5	25
31	CC	COPI vesicle coat	-4.3	6
32	BP	Secretory pathway	-6.7	119
33	CC	Nucleus	4.6	745
34	CHR	Δ isw2 Δ rp3/WT	5.1	10
35	CHR	Δ isw2 Δ sin3/WT	4.1	6
36	CHR	Δ swr1	6.4	31
36	CHR	Δ swr1	6.4	31
37	CHR	Δ swi1	8.8	22
38	BP	Vacuolar acidification	-4.2	14
38	BP	pH reduction	-4.2	14
38	CC	Hydrogen-translocating V-type ATPase complex	-4.9	13
38	MF	Hydrogen-transporting ATPase activity, rotational mechanism	-4.5	12
38	MF	Cation-transporting ATPase activity	-4.9	13
39	TM	Amino-acid biosynthesis	4.9	44
39	TM	Amino-acid biosynthesis	4.6	43
39	TM	Amino-acid biosynthesis	4.4	42
39	TM	Amino-acid biosynthesis	5.5	53
39	TM	Amino-acid biosynthesis	5.8	48
39	TM	Amino-acid biosynthesis	5.3	46
39	TM	Amino-acid biosynthesis	5.4	55
39	TM	Amino-acid biosynthesis	4.8	58
39	TM	Amino-acid biosynthesis	4.3	61
39	TM	Amino-acid biosynthesis	4.9	64
39	TM	Amino-acid biosynthesis	5.5	70
39	TM	Amino-acid biosynthesis	5.3	77
39	TM	Amino-acid biosynthesis	7.7	94
39	TM	Amino-acid biosynthesis	7.1	91
39	TM	Amino-acid biosynthesis	5.8	82
39	TM	Amino-acid biosynthesis	8.6	101
39	TM	Amino-acid biosynthesis	8.7	99
39	TM	Amino-acid biosynthesis	8.9	108

Supplementary Table S5, continued.

Cluster	Gene Set	Process/Function	$\overline{DM} \times \log_{10}(P)$	# genes
40	BP	Organic acid metabolism	7.3	141
40	BP	Carboxylic acid metabolism	7.3	141
40	BP	Amine metabolism	4.5	109
40	BP	Amino acid and derivative metabolism	4.2	105
40	BP	Amine biosynthesis	4.2	69
41	BP	Glutamine family amino acid metabolism	4.8	18
42	BP	Ion transport	5.6	55
42	BP	Cation transport	4.6	42
43	BP	Nucleotide metabolism	5.5	59
43	BP	Nucleotide biosynthesis	4.3	36
44	BP	Coenzyme metabolism	7.8	49
45	BP	Purine nucleotide biosynthesis	4.3	34
45	BP	Ribonucleotide biosynthesis	4.2	25
45	BP	Purine ribonucleotide biosynthesis	4.6	24
45	BP	Purine ribonucleotide metabolism	4.2	25
46	BP	Coenzyme biosynthesis	4.7	26
46	BP	Cofactor biosynthesis	4.7	26
46	MF	Hydrogen-transporting ATP synthase activity, rotational mechanism	6.8	10
46	BP	Oxidative phosphorylation	12.6	24
46	BP	Monovalent inorganic cation transport	6.7	17
46	BP	Hydrogen transport	7.4	16
46	BP	Proton transport	7.4	16
46	BP	Nucleoside phosphate metabolism	7.5	14
46	BP	ATP biosynthesis	7.5	14
46	BP	Energy coupled proton transport, down electrochemical gradient	7.5	14
46	BP	ATP synthesis coupled proton transport	7.5	14
46	BP	ATP metabolism	7.5	14
46	CC	Proton-transporting ATP synthase complex (sensu Eukaryota)	7.5	14
46	CC	Proton-transporting two-sector ATPase complex	7.5	14
46	CC	Hydrogen-translocating F-type ATPase complex	7.5	14
46	CC	Proton-transporting ATP synthase complex	7.5	14
46	BP	Purine nucleoside triphosphate metabolism	7.4	16
46	BP	Purine nucleoside triphosphate biosynthesis	7.4	16
46	BP	Purine ribonucleoside triphosphate metabolism	7.4	16
46	BP	Purine ribonucleoside triphosphate biosynthesis	7.4	16
46	BP	Nucleoside triphosphate biosynthesis	6.7	17
46	BP	Ribonucleoside triphosphate metabolism	6.7	17
46	BP	Ribonucleoside triphosphate biosynthesis	6.7	17
46	BP	Nucleoside triphosphate metabolism	6.8	18
47	BP	Cofactor metabolism	8.4	65

Supplementary Table S5, continued.

Cluster	Gene Set	Process/Function	$\overline{DM} \times \text{Log}_{10}(P)$	# genes
48	CC	Mitochondrial membrane	9.4	66
49	TF	HAP4_YPD	11.3	31
50	MF	Monovalent inorganic cation transporter activity	5.8	38
50	MF	Hydrogen ion transporter activity	6.2	37
50	MF	Cation transporter activity	5.7	64
50	MF	Ion transporter activity	5.2	72
51	TM	Oxydative phosphorylation	14.7	26
51	TM	Oxydative phosphorylation	15.8	28
51	TM	Oxydative phosphorylation	16.3	29
51	TM	Oxydative phosphorylation	16.3	29
51	TM	Oxydative phosphorylation	16	31
51	TM	Oxydative phosphorylation	16.5	34
51	CC	Mitochondrial inner membrane	10.6	52
51	CC	Inner membrane	10.6	52
52	BP	Mitochondrial electron transport, ubiquinol to cytochrome c	4.5	8
52	MF	Ubiquinol-cytochrome-c reductase activity	4.5	8
52	MF	Oxidoreductase activity, acting on diphenols and related substances as donors	4.5	8
52	MF	Oxidoreductase activity, acting on diphenols and related substances as donors, cytochrome as acceptor	4.5	8
52	CC	Respiratory chain complex III (sensu Eukaryota)	5.1	9
52	CC	Respiratory chain complex III	5.1	9
52	CC	Mitochondrial electron transport chain	8.5	15
52	BP	ATP synthesis coupled electron transport	5.6	10
52	BP	ATP synthesis coupled electron transport (sensu Eukaryota)	5.6	10
52	BP	Electron transport	5.9	13
53	MF	Transporter activity	8.1	178
54	CC	Mitochondrion	23.4	386