STable 1. Sample output of screening co-expressed gene pairs based on Kendall correlation coefficient.

index1	index2	gene1	gene2	cor.list	p.list	q.list	lower	higher
971	972	HXT7	HXT6	0.965703	2.63E-09	0.000277	0.893359	1
266	356	RPL11B	GTT2	0.947368	5.22E-09	0.000277	0.834336	1
445	446	ERR1	ERR2	0.947368	5.22E-09	0.000277	0.84075	1
260	261	RPL9B	RPL9A	0.936842	7.69E-09	0.000277	0.821361	1
268	269	RPS23B	RPS23A	0.936842	7.69E-09	0.000277	0.827631	1
254	266	RPL24A	RPL11B	0.93404	8.52E-09	0.000277	0.829735	1
230	356	RPS6B	GTT2	0.926316	1.13E-08	0.000277	0.822449	1
239	301	RPS16B	YPL142C	0.926316	1.13E-08	0.000277	0.822449	1
247	334	RPS18A	ENT4	0.926316	1.13E-08	0.000277	0.755724	1
254	356	RPL24A	GTT2	0.923486	1.25E-08	0.000277	0.794477	1
275	348	YLL044W	SEC65	0.923486	1.25E-08	0.000277	0.797236	1
277	334	RPL42A	ENT4	0.923486	1.25E-08	0.000277	0.81526	1
230	266	RPS6B	RPL11B	0.91579	1.65E-08	0.000277	0.793336	1
233	313	RPL21A	RPS3	0.91579	1.65E-08	0.000277	0.812017	1
253	266	RPL24B	RPL11B	0.91579	1.65E-08	0.000277	0.799229	1
267	356	RPL11A	GTT2	0.91579	1.65E-08	0.000277	0.805438	1
294	295	RPL20B	RPL20A	0.91579	1.65E-08	0.000277	0.772159	1
300	302	RPL33B	RPL33A	0.91579	1.65E-08	0.000277	0.777149	1
249	250	RPL27A	RPL27B	0.912932	1.83E-08	0.000277	0.802223	1

Stable 2. List of "hub genes". The rank of each gene is the average rank over five networks. Each of five networks is constraint by a different pair of (FDR,MAS) criteria. Highest rank is the most connected and stable gene under varying constraints of (FDR,MAS).

Gene	Rank	Avg Rank
RPL42B	21	4.2
RPS16B	31	6.2
RPL14A	37	7.4
RPS3	37	7.4
GTT2	40	8
RPS4A	49	9.8
RPL33A	58	11.6
RPL23B	77	15.4
RPS7A	79	15.8
RPS4B	86	17.2
RPL27A	89	17.8
RPS18A	95	19
RPL26B	99	19.8
RPS9A	100	20
RPL33B	103	20.6
RPL21A	111	22.2
RPL23A	111	22.2

RPL9B	111	22.2
RPL11B	119	23.8
RPL20B	121	24.2
RPL43A	124	24.8
RPS6B	130	26
RPL24B	138	27.6
RPL14B	139	27.8
RPS11A	146	29.2
RPL20A	151	30.2
YPL142C	151	30.2
ENT4	152	30.4
RPL24A	155	31
RPS24A	161	32.2
YML014W	167	33.4
SEC65	168	33.6
RPS24B	169	33.8
RPL22A	171	34.2
RPS23B	180	36
RPS8B	186	37.2
YGL102C	193	38.6
YLL044W	197	39.4
RPL42A	201	40.2
RPS0A	202	40.4
RPL28	206	41.2
RPS17B	207	41.4
RPL21B	209	41.8
CAT5	210	42
MLC1	220	44
RPS0B	229	45.8
RPL9A	248	49.6
RPS23A	271	54.2
RPL11A	290	58
RPL6B	293	58.6
RPL27B	299	59.8
RPS28A	301	60.2
RPL8A	305	61
RPL12B	313	62.6
RPL7A	318	63.6
RPS10A	319	63.8
RPL18B	363	72.6
YDR417C	369	73.8
RPL17B	373	74.6
RPL10	397	79.4
MRPL24	407	81.4
RPS14B	449	89.8
YLR076C	485	97
RPL35A	499	99.8

RPL35B	526	105.2
RPS21A	611	122.2
RPS16A	640	128
HXT4	911	182.2
RPS13	921	184.2
ADE5,7	975	195
HXT3	995	199
HXT1	1033	206.6
HXT7	1070	214
HXT6	1101	220.2
SIK1	1169	233.8
HXT8	1237	247.4
MET6	1289	257.8
HOR2	1493	298.6
CBF5	1551	310.2
RHR2	1634	326.8
HXT9	1670	334
GCY1	1871	374.2
YGL068W	2077	415.4
YGL069C	2192	438.4
ERR1	2349	469.8
ERR2	2354	470.8
YOR121C	2421	484.2
PHO11	2464	492.8
PHO5	2470	494

STable 3. Clustering co-expressed genes with controlled FDR (5%) at a MAS level of 0.6 using "GAL10" as the "seed gene". Known genes in the pathway are in bold face. (a) Pearson correlation coefficient as metric

index1	index2	gene1	gene2	cor.list	p.list	q.list	lower	higher
2	2	GAL10	**GAL10**	1	0.00E+00	0.00E+00	1	1
2	1	GAL10	**GAL7**	0.925103	5.35E-09	2.67E-06	0.727108	0.981023
2	4	GAL10	**GCY1**	0.91733	1.27E-08	4.20E-06	0.701969	0.97899
2	3	GAL10	**GAL1**	0.905611	3.99E-08	9.95E-06	0.665053	0.975901
2	59	GAL10	**GAL2**	0.893609	1.12E-07	2.23E-05	0.628426	0.972709
2	5	GAL10	**YOR121C**	0.891345	1.34E-07	2.23E-05	0.621649	0.972104

(b) Kendall correlation coefficient as metric

index1	index2	gene1	gene2	cor.list	p.list	q.list	lower	higher
2	2	GAL10	**GAL10**	1	0.00E+00	0.00E+00	1	1
2	1	GAL10	**GAL7**	0.923399	5.35E-09	2.67E-06	0.727108	0.981023
2	4	GAL10	**GCY1**	0.916201	1.27E-08	4.20E-06	0.701969	0.97899
2	3	GAL10	**GAL1**	0.902109	3.99E-08	9.95E-06	0.665053	0.975901
2	59	GAL10	**GAL2**	0.890358	1.12E-07	2.23E-05	0.628426	0.972709
2	5	GAL10	YOR121C	0.888352	1.34E-07	2.23E-05	0.621649	0.972104

STable 4. Clustering co-expressed genes with controlled FDR (5%) at a MAS level of 0.5 using "GAL7" or "GAL1" as the "seed gene". Known genes in the pathway are in bold face. (a) Pearson correlation coefficient as metric

index1	index2	gene1	gene2	cor.list	p.list	q.list	lower	higher
1	1	GAL7	**GAL7**	1	0.00E+00	0.00E+00	1	1
1	2	GAL7	**GAL10**	0.925103	5.35E-09	2.67E-06	0.737186	0.980188
1	62	GAL7	**YMR318C**	0.892639	1.21E-07	4.03E-05	0.638563	0.971244
1	68	GAL7	YBR042C	0.882089	2.71E-07	5.84E-05	0.608213	0.968289
1	3	GAL7	**GAL1**	0.880999	2.93E-07	5.84E-05	0.605123	0.967982
1	70	GAL7	FAR1	0.864743	8.72E-07	1.45E-04	0.559998	0.963377
1	59	GAL7	**GAL2**	0.851884	1.88E-06	2.68E-04	0.525538	0.959693

(b) Kendall correlation coefficient as metric

index1	index2	gene1	gene2	cor.list	p.list	q.list	lower	higher
1	1	GAL7	**GAL7**	1	7.07E-10	7.05E-07	1	1
1	3	GAL7	**GAL1**	0.705263	1.38E-05	6.86E-03	0.442609	0.967917
1	2	GAL7	**GAL10**	0.652632	5.74E-05	1.88E-02	0.355487	0.949776

index1	index2	gene1	gene2	cor.list	p.list	q.list	lower	higher
3	3	GAL1	**GAL1**	1	0.00E+00	0.00E+00	1	1
3	2	GAL1	**GAL10**	0.905611	3.99E-08	1.99E-05	0.660385	0.976295
3	10	GAL1	**FKS1**	0.89891	7.22E-08	2.40E-05	0.639567	0.974545
3	1	GAL1	**GAL7**	0.880999	2.93E-07	7.30E-05	0.585731	0.969822