Supplementary Table 1. GO terms differentially associated with the network of raw GIs and GI profile correlations

GO Term	p_{raw}	p_{cor}	D	Size
structural constituent of ribosome	3.216e-06	5.366e-46	39.778	100
cytosolic small ribosomal subunit	4.779e-09	2.482e-33	24.285	42
maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA; 5.8S rRNA; LSU-rRNA)	7.094e-04	4.185e-26	22.229	37
piecemeal microautophagy of nucleus	3.355e-03	1.788e-24	21.273	31
90S preribosome	1.155e-05	4.105e-24	18.449	30
ribosome assembly	1.125e-02	7.359e-21	18.184	23
mRNA splicing; via spliceosome	1.053e-15	7.320e-34	18.158	48
mitotic sister chromatid cohesion	3.523e-12	4.467e-30	17.897	26
mitochondrial respiratory chain	2.741e-05	5.546e-23	17.694	20
ribosomal large subunit biogenesis	2.951e-06	2.614e-23	17.053	31
cytosolic large ribosomal subunit	7.900e-03	7.239e-19	16.038	54
nuclear replication fork	3.886e-11	2.012e-25	14.286	23
mitochondrial membrane organization	2.512e-08	1.370e-22	14.263	30
preribosome; large subunit precursor	1.311e-03	1.636e-17	13.904	22
cytoplasmic microtubule	6.969e-08	7.656e-20	11.959	21
cell division site part	1.060e-07	4.203e-19	11.402	21
rRNA binding	2.483e-02	1.390e-13	11.252	24
regulation of pH	3.710e-05	1.446e-15	10.409	21
tubulin binding	1.100e-13	1.015e-23	10.035	26
DNA-directed RNA polymerase II; holoenzyme	4.162e-08	4.636e-18	9.953	27
mating projection tip	1.541e-12	4.720e-22	9.514	74
U2-type spliceosomal complex	6.987e-08	2.973e-17	9.371	20
CVT pathway	8.063e-04	1.262e-12	8.805	33
oxidative phosphorylation	2.683e-03	5.283e-12	8.706	20
maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA; 5.8S rRNA; LSU-rRNA)	3.070e-05	8.746e-14	8.545	27
cellular component movement	1.423e-07	1.887e-15	7.878	21
pre-autophagosomal structure	9.734e-02	2.004e-09	7.686	27
spindle pole body	2.412e-10	2.444e-17	6.994	49
mitochondrial translation	9.621e-09	1.086e-15	6.947	22
small nuclear ribonucleoprotein complex	1.698e-10	2.651e-17	6.807	25
regulation of DNA-dependent DNA replication	1.436e-06	2.339e-13	6.788	22
incipient cellular bud site	4.199e-06	9.896e-13	6.628	41
transcription initiation from RNA polymerase II promoter	1.816e-05	5.915e-12	6.487	22
protein-DNA complex assembly	1.461e-14	1.451e-20	6.003	51
DNA replication initiation	1.331e-10	1.628e-16	5.912	27
mitotic recombination	3.332e-05	7.137e-11	5.669	25
proteasome complex	6.895e-04	1.790e-09	5.586	23
endosome membrane	2.454e-04	6.674e-10	5.566	65
protein complex localization	3.506e-04	1.505e-09	5.367	29
establishment of organelle localization	1.340e-12	1.693e-17	4.898	58
cleavage involved in rRNA processing	3.091e-06	4.239e-11	4.863	24
ER-associated protein catabolic process	1.047e-05	2.565e-10	4.611	36
protein-DNA complex	1.216e-08	3.838e-13	4.501	29
protein heterodimerization activity	9.517e-08	3.372e-12	4.451	23
macroautophagy	2.331e-05	1.906e-09	4.087	40
late endosome to vacuole transport via multivesicular body sorting pathway	4.135e-05	3.701e-09	4.048	21
ER to Golgi vesicle-mediated transport	2.683e-09	3.078e-13	3.940	62
protein import into nucleus	1.322e-10	2.760e-14	3.680	34
chromatin binding	1.425e-08	5.731e-12	3.396	57
condensed nuclear chromosome kinetochore	3.116e-11	2.051e-14	3.182	29
transcription cofactor activity	2.315e-07	2.091e-10	3.044	32
double-strand break repair via homologous recombination	1.100e-11	1.267e-14	2.938	31
nuclear pore	3.408e-10	5.525e-13	2.790	38
intracellular protein transmembrane import	7.411e-07	1.878e-09	2.596	43
regulation of cytoskeleton organization	5.515e-08	1.593e-10	2.539	36
nucleosome organization	6.464e-10	1.995e-12	2.511	45
tRNA wobble uridine modification	2.115e-08	1.493e-10	2.151	20
histone acetyltransferase complex	3.795e-11	3.027e-13	2.098	31
chromatin assembly	7.977e-08	5.181e-09	1.187	30
nuclear chromatin	3.243e-11	4.395e-12	0.868	100
cellular bud tip	2.527e-08	3.858e-09	0.816	77
mRNA export from nucleus	1.050e-09	2.789e-10	0.576	36
spindle organization	2.786e-09	1.666e-09	0.223	22
transcription elongation from RNA polymerase II promoter	1.244e-10	9.306e-10	-0.874	36
cellular response to heat	7.232e-09	4.009e-07	-1.744	29
protein transporter activity	2.648e-09	2.604e-07	-1.993	38
nuclear membrane	8.396e-09	1.825e-05	-3.337	52

Only those GO terms that associate strongly ($p < 1 \times 10^{-8}$) with either or both networks are listed. $D = log_{10}(p_{raw}) - log_{10}(p_{correlation})$. If $D < 0$, then the GO term associates more strongly with the network of raw GIs. If $D > 0$, then the GO term associates more strongly with the network of GI profile correlations. The set size is the number of network genes annotated with the GO term.