Supplementary Table 3. GO terms differentially associated with the untreated and UV-treated GI networks

GO Term	$p_{untreated}$	$p_{treated}$	D	Size
meiosis I	5.920e-01	2.616e-06	5.355	50
recombinational repair	5.895e-01	3.124e-06	5.276	20
DNA recombination	6.899e-01	4.236e-06	5.212	26
double-strand break repair	1.603e-01	1.090e-06	5.168	87
structure-specific DNA binding	2.033e-01	4.251e-06	4.680	77
transcription factor binding transcription factor activity	1.721e-02	5.523e-06	3.494	61
meiosis	5.581e-01	2.432e-04	3.361	52
nucleotide-excision repair	5.063e-02	2.581e-05	3.293	20
DNA-dependent ATPase activity	9.435e-02	4.940e-05	3.281	31
double-strand break repair via homologous recombination	4.662e-01	2.507e-04	3.269	32
meiotic cell cycle	5.048e-01	5.004e-04	3.004	32
ATPase activity, coupled	1.488e-01	2.004e-04	2.871	48
double-stranded DNA binding	9.225e-03	2.018e-05	2.660	67
transcription cofactor activity	1.744e-01	7.149e-04	2.387	34
helicase activity	9.320e-02	6.406e-04	2.163	41
protein-DNA complex subunit organization	2.031e-03	2.535e-05	1.904	76
SWI/SNF superfamily-type complex	1.056e-03	2.970e-05	1.551	46
negative regulation of transcription from RNA polymerase II promoter	4.932e-03	1.627e-04	1.482	46
protein binding transcription factor activity	1.932e-02	8.910e-04	1.336	24
chromatin remodeling	1.536e-04	5.720e-05	0.429	36
transcription from RNA polymerase I promoter	8.148e-04	4.306e-04	0.277	50
covalent chromatin modification	4.643e-04	6.167e-04	-0.123	90
DNA-dependent transcription, elongation	5.615e-04	1.514e-03	-0.431	37
nucleosome organization	1.041e-05	7.832e-05	-0.877	35
chromatin assembly	8.163e-04	1.174e-02	-1.158	39
histone modification	8.095e-05	2.599e-03	-1.507	77
endosomal transport	9.833e-04	3.323e-02	-1.529	70
DNA packaging	1.223e-05	7.683e-03	-2.798	70
nuclear chromatin	1.772e-09	1.310e-06	-2.869	26
establishment of protein localization to vacuole	1.871e-05	2.347e-02	-3.099	28
chromatin silencing at telomere	1.559e-08	3.392e-05	-3.337	39
vacuolar transport	4.349e-06	2.051e-02	-3.674	76
protein targeting to vacuole	2.582e-06	1.363e-02	-3.722	55
chromatin silencing at silent mating-type cassette	9.137e-07	2.088e-02	-4.359	44
negative regulation of gene expression, epigenetic	6.990e-09	4.060e-04	-4.764	76
chromatin	1.499e-13	1.943e-08	-5.113	93
protein localization to vacuole	5.691e-08	1.360e-02	-5.378	32
chromatin silencing	8.118e-11	2.587e-04	-6.503	71
gene silencing	4.754e-12	2.388e-04	-7.701	37
regulation of gene expression, epigenetic	2.138e-14	4.675e-05	-9.340	36

Only those GO terms that associate strongly ($p < 0.001$) with either or both networks are listed.
$D = log_{10}(p_{untreated}) - log_{10}(p_{treated})$. If $D < 0$, then the GO term associates more strongly with the untreated network. If $D > 0$, then the GO term associates more strongly with the UV-treated network. The set size is the number of network genes annotated with the GO term.