Supplementary Table 2. GO terms differentially associated with the untreated and MMS-treated GI networks

GO Term	$p_{untreated}$	$p_{treated}$	D	Size
DNA repair	1.030e-19	1.714e-31	11.7787	25
response to DNA damage stimulus	1.558e-17	6.604e-29	11.3728	57
covalent chromatin modification	6.059e-06	8.203e-14	7.8684	53
histone modification	2.047e-06	1.852e-13	7.0435	25
chromosome organization	6.043e-26	5.830e-30	4.0155	49
chromatin organization	5.586e-19	6.981e-22	2.9032	45
cell cycle checkpoint	8.511e-02	1.556e-04	2.7378	35
DNA replication	1.080e-09	7.740e-12	2.1447	68
regulation of cell cycle process	3.428e-04	2.481e-06	2.1403	70
regulation of cell cycle phase transition	1.136e-01	9.341e-04	2.0852	25
negative regulation of cell cycle phase transition	1.146e-01	9.950e-04	2.0615	38
chromatin silencing at telomere	1.206e-05	1.834e-07	1.8179	60
negative regulation of cell cycle process	3.214e-02	4.984e-04	1.8094	21
meiotic cell cycle	9.129e-05	2.074e-06	1.6437	31
chromatin modification	1.021e-18	3.421e-20	1.4748	21
regulation of gene expression, epigenetic	4.536e-07	8.062e-08	0.7502	60
meiosis	2.510e-04	9.482e-05	0.4227	25
cell cycle process	5.551e-05	2.312e-05	0.3804	37
macromolecular complex subunit organization	1.993e-05	1.086e-05	0.2636	93
chromatin silencing	1.599e-07	1.172e-07	0.1348	92
negative regulation of gene expression, epigenetic	2.092e-08	1.945e-08	0.0317	47
negative regulation of nitrogen compound metabolic process	6.611e-05	1.718e-04	-0.4148	86
negative regulation of cellular biosynthetic process	1.626e-04	5.199e-04	-0.5049	31
negative regulation of gene expression	4.667e-04	1.818e-03	-0.5907	32
negative regulation of biosynthetic process	9.265e-05	4.724e-04	-0.7074	56
negative regulation of nucleobase-containing compound metabolic process	4.452e-05	2.416e-04	-0.7346	24
gene silencing	2.795e-07	1.698e-06	-0.7835	24
negative regulation of transcription, DNA-dependent	4.342e-04	3.159e-03	-0.8618	99
negative regulation of macromolecule biosynthetic process	8.533e-05	6.318e-04	-0.8695	93
negative regulation of cellular macromolecule biosynthetic process	3.925e-05	2.929e-04	-0.8729	87
negative regulation of RNA metabolic process	2.199e-04	2.581e-03	-1.0694	81
organelle fission	3.156e-04	3.704e-03	-1.0695	31
nuclear division	3.082e-04	4.218e-03	-1.1363	96
mitosis	1.761e-04	5.808e-03	-1.5183	96
chromatin remodeling	1.393e-10	2.229e-08	-2.2041	84
mitotic cell cycle	3.256e-07	3.155e-04	-2.9863	46
chromatin	1.402e-11	2.619e-08	-3.2712	61
protein-DNA complex subunit organization	1.957e-08	4.883e-05	-3.3970	98
chromosome	7.535e-21	2.076e-17	-3.4402	31
nuclear chromatin	1.881e-10	7.399e-07	-3.5947	52
intracellular non-membrane-bounded organelle	2.078e-21	9.921e-18	-3.6788	31
nucleoplasm part	1.691e-10	1.041e-06	-3.7894	84
nucleoplasm	2.737e-13	4.722e-09	-4.2368	88
intracellular organelle lumen	8.280e-25	2.281e-19	-5.4401	25
chromosomal part	1.017e-16	4.537e-11	-5.6496	20
nuclear chromosome	8.379e-18	6.611e-12	-5.8970	88
DNA metabolic process	6.428e-38	6.334e-32	-5.9936	84
membrane-enclosed lumen	6.189e-23	6.189e-17	-6.0000	74
nuclear chromosome part	3.722e-15	3.983e-09	-6.0295	39
organelle lumen	1.566e-24	2.673e-18	-6.2321	84
nuclear part	1.321e-27	4.292e-21	-6.5117	21
non-membrane-bounded organelle	1.024e-24	4.131e-18	-6.6057	26
nuclear lumen	6.551e-29	7.455e-21	-8.0561	26
regulation of DNA metabolic process	9.805e-15	1.875e-05	-9.2815	92

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 MMS-treated network. The set size is the number of network genes annotated with the GO term.