	Datasets	0->N	N->0	Fold	p-values ^{#1}	p-values #2
Back- ground	Ortholog-Poly	1,856	1,754	1.06		
	SNP-Poly	426	341	1.25		
CSM	Colon_Adenocarcinoma	1,819	617	2.95	9.16E-74	6.031E-24
	Ovarian_Serous_Cystadenocarcinoma	973	247	3.94	1.31E-67	1.156E-30
	Liver_Cancer	859	336	2.56	3.69E-35	1.087E-13
	Rectum_Adenocarcinoma	398	148	2.69	6.00E-21	1.453E-10
	Breast_Carcinoma	216	39	5.54	6.82E-25	6.931E-17
	Breast_Invasive_Carcinoma	203	31	6.55	8.25E-26	5.224E-18
	Pancreatic_Cancer	112	33	3.39	1.02E-09	1.104E-06
	Acute_Myeloid_Leukemia	90	15	6.00	3.99E-12	3.644E-09
	Lung_Adenocarcinoma	66	3	22.00	3.15E-13	8.857E-11
	Gastric_Cancer	57	35	1.63	0.045	0.241
	Glioblastoma_Multiforme	42	8	5.25	4.64E-06	8.093E-05
	Chronic_Lymphocytic_Leukemia	40	15	2.67	0.0016922	0.0129654
	Pediatric_Brain_Tumors	37	8	4.63	3.94E-05	0.0004417
	Breast_Cancer	26	5	5.20	0.000317	0.0018057
	Malignant_Lymphoma	22	10	2.20	0.050	0.140
	Colorectal_Cancer	16	9	-	-	-
	Prostate_Cancer	16	8	-	-	-
	Small_Cell_Lung_Carcinoma	11	1	-	-	-
	Malignant_Melanoma	7	2	-	-	-
	Lung_Squamous_Cell_Carcinoma	5	3	-	-	-
	Myeloproliferative_Disorders	2	0	-	-	-

The p-values^{#1} were obtained from the comparison in folds of O->N/N->O between the CSM and Ortholog-Poly, the p-values^{#2} were obtained from the comparison in folds of O->N/N->O between the CSM and SNP-Poly. The datasets with a total number of O->N and N->O larger than 30 were analyzed, the p-values \leq 0.05 were represented by red color and indicate significant higher number of O->N than N->O in CSM considering the distribution from the control datasets.