

Additional Table 1: The overlap between different methods for the yeast data

fdr	0.1%		1%		5%		10%		20%	
sam.only	113	0.19	172	0.11	234	0.09	310	0.09	207	0.04
samraw.only	129	0.21	123	0.08	59	0.02	56	0.02	22	0.00
ttest.only	100	0.17	138	0.09	108	0.04	85	0.03	58	0.01
lpe.only	236	0.39	399	0.26	484	0.18	485	0.15	573	0.11
inter.lpe.ttest	189	0.31	765	0.50	1771	0.65	2347	0.71	4299	0.84
inter.sam.ttest	314	0.52	990	0.64	1984	0.73	2492	0.75	4664	0.91
inter.ttest.samraw	383	0.64	1194	0.77	2400	0.88	3011	0.91	4986	0.97
inter.lpe.sam	317	0.53	984	0.64	1907	0.70	2382	0.72	4406	0.86
inter.lpe.samraw	188	0.31	784	0.51	1811	0.66	2388	0.72	4337	0.84
inter.sam.samraw	268	0.44	959	0.62	2006	0.73	2521	0.76	4681	0.91
total	603	1.00	1544	1.00	2731	1.00	3304	1.00	5140	1.00

This table lists the number and percentage of overlapped genes among different methods. For example, “sam.only” represents the number of genes selected by SAM only; “inter.lpe.ttest” represents the number of genes selected by both LPE and T-Test.