

Table S1  
 Size, normal distributed data (40 genes in a set),  
 for design D1-3

scenario	Cutoff P value	mean	msq	mean50	floormean
Up	0.001	0.001	0.0013	0.0007	0.0007
	0.005	0.0037	0.0033	0.0023	0.002
	0.01	0.0087	0.007	0.0053	0.0057
	0.03	0.0263	0.024	0.023	0.0217
	0.05	0.044	0.046	0.041	0.0403
Up cor 0.1	0.001	0.0013	0.0013	0.0013	0.0013
	0.005	0.006	0.0047	0.005	0.0047
	0.01	0.0113	0.0103	0.0107	0.0107
	0.03	0.032	0.032	0.0313	0.0327
	0.05	0.0527	0.0483	0.0527	0.052
Mix	0.001	0.0003	0.0003	0.0007	0.0007
	0.005	0.0023	0.0033	0.005	0.004
	0.01	0.0087	0.0087	0.0087	0.01
	0.03	0.027	0.03	0.0307	0.031
	0.05	0.0403	0.0503	0.051	0.0543
Mix cor 0.1	0.001	0.0007	0.001	0.001	0.0007
	0.005	0.0047	0.004	0.0047	0.0043
	0.01	0.009	0.01	0.01	0.01
	0.03	0.032	0.0317	0.031	0.039
	0.05	0.0507	0.0497	0.0483	0.047

2999 rotations were in ROAST. 3000 simulations were run.

Table S2  
 Size, exp distributed data (40 genes in a set),  
 for design D1-3

scenario	Cutoff P value	mean	msq	mean50	floormean
Up	0.001	0.0009	0.002	0.0009	0.0008
	0.005	0.0044	0.0089	0.0051	0.0044
	0.01	0.0091	0.0162	0.0099	0.0095
	0.03	0.0288	0.0422	0.0307	0.0301
	0.05	0.0502	0.068	0.0499	0.0483
Up cor0.1	0.001	0.0021	0.0021	0.0018	0.002
	0.005	0.0053	0.009	0.0072	0.0067
	0.01	0.0098	0.0158	0.013	0.0112
	0.03	0.0305	0.0399	0.0356	0.0319
	0.05	0.0495	0.0632	0.0538	0.0495
Mix	0.001	0.0014	0.0034	0.003	0.0036
	0.005	0.006	0.0126	0.0093	0.0112
	0.01	0.0106	0.0203	0.0169	0.0195
	0.03	0.0303	0.0484	0.0426	0.0478
	0.05	0.0483	0.0746	0.065	0.0739
Mix cor0.1	0.001	0.002	0.0032	0.0027	0.0025
	0.005	0.0078	0.0123	0.0102	0.0104
	0.01	0.0132	0.0226	0.0183	0.0199
	0.03	0.0408	0.0545	0.0482	0.0522
	0.05	0.0627	0.0813	0.0736	0.0795

2999 rotations were in ROAST. 3000 simulations were run.

Table S3  
 Power, normal distributed data (40 genes in a set),  
 for design D1-3

scenario	Cutoff P value	mean	msq	mean50	floormean
1	0.002	0.396	0.186	0.244	0.304
	0.005	0.542	0.320	0.383	0.451
	0.01	0.645	0.421	0.484	0.568
	0.03	0.804	0.610	0.693	0.738
	0.05	0.862	0.691	0.783	0.810
2	0.002	0.269	0.273	0.277	0.284
	0.005	0.416	0.415	0.430	0.431
	0.01	0.535	0.529	0.542	0.547
	0.03	0.708	0.695	0.697	0.709
	0.05	0.777	0.771	0.786	0.794
3	0.002	0.183	0.330	0.309	0.296
	0.005	0.278	0.464	0.432	0.412
	0.01	0.373	0.563	0.543	0.517
	0.03	0.554	0.725	0.707	0.694
	0.05	0.657	0.800	0.793	0.776
4	0.002	0.280	0.597	0.508	0.446
	0.005	0.407	0.728	0.657	0.595
	0.01	0.531	0.799	0.753	0.727
	0.03	0.708	0.891	0.878	0.860
	0.05	0.787	0.918	0.920	0.913
5	0.002	0.537	0.512	0.534	0.524
	0.005	0.683	0.651	0.664	0.650
	0.01	0.766	0.737	0.740	0.729
	0.03	0.872	0.854	0.864	0.844
	0.05	0.907	0.903	0.903	0.899
6	0.002	0.200	0.200	0.204	0.199
	0.005	0.316	0.320	0.317	0.323
	0.01	0.418	0.421	0.415	0.417
	0.03	0.596	0.583	0.593	0.584
	0.05	0.671	0.657	0.664	0.662
7	0.002	0.299	0.395	0.380	0.382
	0.005	0.425	0.512	0.504	0.504
	0.01	0.520	0.601	0.591	0.597
	0.03	0.695	0.760	0.744	0.740
	0.05	0.767	0.817	0.803	0.813
8	0.002	0.604	0.707	0.698	0.691
	0.005	0.728	0.804	0.804	0.806
	0.01	0.812	0.859	0.854	0.862
	0.03	0.897	0.925	0.917	0.918
	0.05	0.925	0.947	0.941	0.940

999 rotations were in ROAST. 1000 simulations were run.

Table S4  
 Size, norm distributed data (1000 genes in a set),  
 for design D1-3

scenario	Cutoff P value	mean	msq	mean50	floormean
Up	0.001	0.0023	0.0023	0.002	0.0017
	0.005	0.01	0.0086	0.0077	0.007
	0.01	0.014	0.0137	0.0157	0.017
	0.03	0.0333	0.035	0.0357	0.036
	0.05	0.0523	0.0557	0.0567	0.057
Up cor0.1	0.001	0.001	0.0013	0.0013	0.001
	0.005	0.0037	0.0033	0.0033	0.0037
	0.01	0.0009	0.0103	0.0103	0.01
	0.03	0.0277	0.027	0.0267	0.0273
	0.05	0.0527	0.0493	0.0517	0.051
Mix	0.001	0.0017	0.0013	0.0007	0.0007
	0.005	0.004	0.0053	0.004	0.0047
	0.01	0.0087	0.0087	0.0087	0.011
	0.03	0.026	0.032	0.029	0.03
	0.05	0.0437	0.0507	0.0493	0.0513
Mix cor0.1	0.001	0.0007	0.0007	0.0007	0.0007
	0.005	0.003	0.0033	0.003	0.003
	0.01	0.0077	0.007	0.0077	0.008
	0.03	0.0263	0.0273	0.0273	0.0277
	0.05	0.0453	0.0447	0.0437	0.045

2999 rotations were in ROAST. 3000 simulations were run.

Table S5  
 Power, normal distributed data (1000 genes in a set),  
 for design D1-3

scenario	Cutoff P value	mean	msq	mean50	floormean
1	0.002	0.356	0.126	0.212	0.227
	0.005	0.527	0.213	0.338	0.358
	0.01	0.639	0.294	0.445	0.47
	0.03	0.801	0.514	0.647	0.66
	0.05	0.857	0.623	0.755	0.763
2	0.002	0.364	0.395	0.401	0.384
	0.005	0.512	0.55	0.556	0.534
	0.01	0.639	0.67	0.684	0.661
	0.03	0.811	0.838	0.839	0.836
	0.05	0.873	0.895	0.896	0.893
3	0.002	0.258	0.148	0.199	0.214
	0.005	0.388	0.233	0.316	0.326
	0.01	0.51	0.329	0.453	0.465
	0.03	0.707	0.512	0.653	0.666
	0.05	0.787	0.625	0.735	0.742
4	0.002	0.303	0.364	0.346	0.338
	0.005	0.46	0.522	0.51	0.501
	0.01	0.577	0.641	0.625	0.62
	0.03	0.751	0.808	0.808	0.799
	0.05	0.832	0.864	0.859	0.858
5	0.002	0.219	0.222	0.231	0.213
	0.005	0.34	0.332	0.334	0.309
	0.01	0.435	0.433	0.443	0.414
	0.03	0.599	0.61	0.616	0.588
	0.05	0.7	0.681	0.698	0.663
6	0.002	0.318	0.326	0.327	0.329
	0.005	0.457	0.464	0.464	0.466
	0.01	0.558	0.56	0.563	0.566
	0.03	0.753	0.75	0.751	0.745
	0.05	0.838	0.835	0.837	0.835
7	0.002	0.119	0.111	0.117	0.104
	0.005	0.187	0.198	0.201	0.176
	0.01	0.256	0.288	0.284	0.275
	0.03	0.27	0.462	0.467	0.441
	0.05	0.536	0.555	0.559	0.542
8	0.002	0.289	0.298	0.299	0.295
	0.005	0.429	0.44	0.44	0.439
	0.01	0.547	0.546	0.549	0.548
	0.03	0.714	0.723	0.725	0.724
	0.05	0.793	0.787	0.797	0.788

999 rotations were in ROAST. 1000 simulations were run.

Table S6  
Power, normal distributed data, 1 factor (40 genes in a set),  
for design D1-5

scenario	Cutoff P value	mean	msq	mean50	floormean	GSEAlm
1	0.002	0.59	0.33	0.4	0.48	0.35
	0.005	0.72	0.47	0.58	0.63	0.35
	0.01	0.81	0.58	0.67	0.75	0.68
	0.03	0.9	0.73	0.83	0.85	0.88
	0.05	0.94	0.86	0.87	0.91	0.93
2	0.002	0.53	0.54	0.56	0.56	0.45
	0.005	0.72	0.7	0.7	0.74	0.45
	0.01	0.8	0.76	0.76	0.81	0.67
	0.03	0.94	0.92	0.94	0.92	0.86
	0.05	0.97	0.97	0.97	0.97	0.95
3	0.002	0.26	0.66	0.56	0.49	0.32
	0.005	0.39	0.73	0.71	0.63	0.32
	0.01	0.55	0.82	0.8	0.77	0.5
	0.03	0.76	0.91	0.92	0.9	0.72
	0.05	0.86	0.95	0.94	0.94	0.81
4	0.002	0.49	0.89	0.87	0.77	0.42
	0.005	0.7	0.94	0.9	0.89	0.42
	0.01	0.79	0.95	0.93	0.91	0.68
	0.03	0.92	0.99	0.98	0.96	0.82
	0.05	0.96	0.99	0.99	0.98	0.95

999 rotations were in ROAST. 125 permutations were in GSEAlm. 100 simulations were run.