

		Score	Correlation	Contrast	Gene coverage Number	Gene coverage Number	Mean number of exps.	
1	MAKrow(expr.)	0.441	0.91	2.70	0.02	1	0.0232	97.0
2	<i>QUBIC</i>	0.422	0.80	3.34	0.05	10	0.0052	34.9
3	MAKconst(expr.)	0.412	0.80	2.42	0.33	76	0.0043	41.2
4	MAKconst_col_row(expr.)	0.410	0.75	2.68	0.57	138	0.0041	27.7
5	MAKconst_col_row_checker(expr.)	0.409	0.78	2.42	0.61	321	0.0019	33.8
6	MAKchecker(expr.)	0.409	0.83	2.22	0.38	188	0.0020	41.6
7	MAKcol(expr.) w/ Pearson & complete linkage	0.406	0.64	2.97	0.47	167	0.0028	13.2
8	MAKcol(expr.) w/ Manhattan & Ward criterion	0.405	0.657	2.88	0.54	108	0.0050	12.2
9	MAKchecker(expr.+TF)	0.402	0.75	2.05	0.73	421	0.0017	38.3
10	<i>cMonkey2</i>	0.398	0.47	0.88	1.00	616	0.0016	326.7
11	<i>BicMix</i>	0.397	0.42	3.73	0.24	143	0.0017	9.8
12	<i>cMonkey</i>	0.390	0.62	1.12	0.45	255	0.0018	106.4
13	2D-HCL_Pearson & complete linkage > 1.0  expr.	0.390	0.70	1.70	0.58	167	0.0035	29.1
14	<i>ISA</i>	0.388	0.56	1.75	0.38	72	0.0053	35.6
15	<i>FABIA</i>	0.387	0.23	0.97	0.65	5	0.1300	174.2
16	2D-HCL_Manhattan & Ward criterion > 1.0  expr.	0.381	0.49	1.71	0.97	439	0.0022	26.5
17	MAKchecker(expr.+TF+PPI+ortho.)	0.376	0.96	1.23	0.22	1590	0.0001	10
18	<i>COALESCE</i>	0.375	0.42	1.41	0.31	183	0.0017	43.7