Report

Protein goodness of fit--sorted by PVE(Genotype)

Protein	Symbol	Entrez	Mixture	Genotype	BioFraction	Residuals
Q8C2E7	Washc5	223593	0.0004987	0.9130491	0.0442397	0.0422125
Q8VDD8	Washc1	68767	0.0070136	0.8808449	0.0436028	0.0685388
Q3UMB9	Washc4	319277	0.0133109	0.8722170	0.0489876	0.0654845
Q6PGL7	Washc2	28006	0.0000000	0.7646015	0.1685491	0.0668494
Q9CR27	Washc3	67282	0.0205066	0.6701031	0.0640885	0.2453017
Q19LI2	A1bg	117586	0.2186346	0.5170321	0.0000000	0.2643333

Evaluating Nakagawa goodness-of-fit, refitting modules...

Protein	Symbol	Entrez	Mixture	Genotype	BioFraction	Residuals	R2.fixef	R2.total
Q8C2E7	Washc5	223593	0.0004987	0.9130491	0.0442397	0.0422125	0.9744804	0.9762336
Q8VDD8	Washc1	68767	0.0070136	0.8808449	0.0436028	0.0685388	0.9232585	0.9298346
Q3UMB9	Washc4	319277	0.0133109	0.8722170	0.0489876	0.0654845	0.9353344	0.9494330
Q6PGL7	Washc2	28006	0.0000000	0.7646015	0.1685491	0.0668494	0.9409087	0.9409087
Q9CR27	Washc3	67282	0.0205066	0.6701031	0.0640885	0.2453017	0.7341464	0.7521275
Q19LI2	A1bg	117586	0.2186346	0.5170321	0.0000000	0.2643333	0.4804040	0.7027026
Protein	**Symbol**	**Entrez**	**Mixture**	**Genotype**	**BioFraction**	**Residuals**	**R2.fixef**	**R2.total**
P62908	Rps3	27050	0.0005153	0.0001460	0.9971205	0.0022183	0.9974401	0.9979517
Q8VDJ3	Hdlbp	110611	0.0001679	0.0000000	0.9968848	0.0029474	0.9965136	0.9966430
Q9D8E6	Rpl4	67891	0.0004759	0.0003769	0.9968231	0.0023241	0.9970994	0.9975514
Q6ZWN5	Rps9	76846	0.0000000	0.0000000	0.9968041	0.0031959	0.9967923	0.9967923
P62281	Rps11	27207	0.0001360	0.0001584	0.9968025	0.0029032	0.9970040	0.9971343
Q6ZQ08	Cnot1	234594	0.0001539	0.0001600	0.9967507	0.0029354	0.9964280	0.9965353

R2 threshold: 0.7

r2_threshold	out	percent	total	final
0.7	791	0.114	6910	6119

Number of proteins with poor fit: 791

WASHC* protein goodness-of-fit statistics:

Protein	Symbol	Entrez	Mixture	Genotype	BioFraction	Residuals	R2.fixef	R2.total
Q8C2E7	Washc5	223593	0.0004987	0.9130491	0.0442397	0.0422125	0.9744804	0.9762336
Q8VDD8	Washc1	68767	0.0070136	0.8808449	0.0436028	0.0685388	0.9232585	0.9298346
Q3UMB9	Washc4	319277	0.0133109	0.8722170	0.0489876	0.0654845	0.9353344	0.9494330
Q6PGL7	Washc2	28006	0.0000000	0.7646015	0.1685491	0.0668494	0.9409087	0.9409087
Q9CR27	Washc3	67282	0.0205066	0.6701031	0.0640885	0.2453017	0.7341464	0.7521275

Loading SwipProteomics
Warning message:
Removing 791 proteins with poor fit before building network.

samples	proteins
42	6119

Generating protein co-variation network.

Performing network enhancement.

Creating protein-protein interaction network.

PPI graph:

Edges	Nodes
93,573	6,119

Performing Leidenalg clustering utilizing the SurpriseVertexPartition method to find optimal partition(s).

Input graph: IGRAPH UNW- 6119 18350456 --

- attr: name (v), weight (e)
  Recursively splitting modules larger than 100 nodes with 'Surprise'.

Final partition: Clustering with 6119 elements and 502 clusters

Removing modules that contain less than 5 nodes.

Module statistic(s) used to evaluate module preservation:
avg.weight, avg.cor, avg.contrib.

Criterion for module preservation: strong.

Evaluating preservation of Swip modules in the Swip network...
... 296 of 329 Swip modules are preserved in the Swip network.

Loading SwipProteomics

nProts	kModules	pClustered	medSize
6,119	296	0.908	13

lmer fit to WASH complex (Washc1, Washc2, Washc3, Washc4, Washc5) proteins:

```
Abundance ~ 0 + Genotype:BioFraction + (1 | Mixture) + (1 | Protein)
```

Term	Estimate	SE	DF	Tvalue	Pvalue
Control:BioFractionF4	6.883	0.151	6.891	45.636	2.91e-09
Control:BioFractionF5	7.167	0.151	6.891	47.520	8.249e-10
Control:BioFractionF6	7.465	0.151	6.891	49.494	2.289e-09
Control:BioFractionF7	7.495	0.151	6.891	49.692	6.248e-10
Control:BioFractionF8	7.327	0.151	6.891	48.580	2.017e-09

Control:BioFractionF9	7.138	0.151	6.891	47.328	4.722e-10
Control:BioFractionF10	7.756	0.151	6.891	51.424	1.931e-09
Mutant:BioFractionF4	5.729	0.151	6.891	37.983	4.595e-10
Mutant:BioFractionF5	5.933	0.151	6.891	39.334	2.303e-09
Mutant:BioFractionF6	6.043	0.151	6.891	40.065	5.369e-10
Mutant:BioFractionF7	6.082	0.151	6.891	40.322	2.384e-09
Mutant:BioFractionF8	5.927	0.151	6.891	39.299	6.424e-10
Mutant:BioFractionF9	5.897	0.151	6.891	39.101	1.991e-09
Mutant:BioFractionF10	6.054	0.151	6.891	40.142	3.631e-10

R2m: Marginal; variation explained by fixed effects.
R2c: Conditional; total variation explained by the model.

R2m	R2c
0.7620866	0.8928053

Contrast	log2FC	percentControl	Pvalue	Tstatistic	SE	DF	nProteins
Mutant-Control	-1.366663	0.3877871	0	-36.94728	0.0369896	190	5

Assessing module-level contrasts with lmerTest.

Time to analyze 296 modules:
Time difference of 5.151603 secs
Warning message:
0 modules with singular fits will be removed.

Final number of modules : 296

Final percent clustered : 0.908

Final Median module size: 13

Washc4 assigned to module: M17

All significant (Padjust < 0.05) modules:

Module	Size	Contrast	log2FC	percentControl	Pvalue	Tstatistic	SE	
M17	48	Mutant-Control	-0.3985879	0.7586004	0.0000000	-18.709226	0.0213043	1953.0(
M4	83	Mutant-Control	-0.1438451	0.9051037	0.0000000	-15.184667	0.0094730	3388.0(
M7	79	Mutant-Control	0.1595391	1.1169303	0.0000000	14.686956	0.0108626	3224.0(
M24	25	Mutant-Control	0.2504315	1.1895629	0.0000000	15.096616	0.0165886	1010.0(
M279	16	Mutant-Control	-0.2169742	0.8603680	0.0000000	-13.397911	0.0161946	641.0(
M3	89	Mutant-Control	0.1086236	1.0781991	0.0000000	12.384638	0.0087708	3634.0(
M241	15	Mutant-Control	0.2354806	1.1772988	0.0000000	11.458696	0.0205504	599.9(
		Mutant-						

M13	54	Control	0.1092996	1.0787045	0.0000000	9.896849	0.0110439	2199.0(
M174	16	Mutant-Control	0.1166477	1.0842126	0.0000000	10.025043	0.0116356	641.0(
M72	50	Mutant-Control	0.0822838	1.0586926	0.0000000	9.060332	0.0090818	2034.9(
M255	16	Mutant-Control	-0.1594672	0.8953557	0.0000000	-8.882048	0.0179539	641.0(
M182	18	Mutant-Control	0.0909614	1.0650797	0.0000000	8.252542	0.0110222	723.0(
M210	7	Mutant-Control	-0.1683780	0.8898425	0.0000000	-8.317970	0.0202427	272.0(
M81	12	Mutant-Control	0.1722502	1.1268147	0.0000000	8.039982	0.0214242	477.0(
M56	24	Mutant-Control	-0.0742119	0.9498608	0.0000000	-7.789278	0.0095274	969.0(
M147	21	Mutant-Control	-0.0970266	0.9349580	0.0000000	-7.784268	0.0124644	846.0(
M12	70	Mutant-Control	-0.0667810	0.9547660	0.0000000	-7.509543	0.0088928	2855.0(
M137	13	Mutant-Control	-0.0976532	0.9345520	0.0000000	-7.472013	0.0130692	518.0(
M159	16	Mutant-Control	0.0804343	1.0573363	0.0000000	7.413569	0.0108496	643.0(
M282	10	Mutant-Control	-0.1141203	0.9239455	0.0000000	-7.420852	0.0153783	395.0(
M106	29	Mutant-Control	0.0873664	1.0624290	0.0000000	6.973643	0.0125281	1174.0(
M198	17	Mutant-Control	-0.0939789	0.9369352	0.0000000	-6.992657	0.0134397	682.0(
M63	19	Mutant-Control	0.0717607	1.0509986	0.0000000	6.701930	0.0107075	764.0(
M117	10	Mutant-Control	-0.1107639	0.9260976	0.0000000	-6.658643	0.0166346	394.9(
M181	18	Mutant-Control	-0.0559994	0.9619279	0.0000000	-6.556877	0.0085406	723.0(
M161	12	Mutant-Control	0.0821982	1.0586298	0.0000000	6.524080	0.0125992	477.0(
M169	26	Mutant-Control	0.0604462	1.0427882	0.0000000	6.281167	0.0096234	1051.0(
M52	44	Mutant-Control	-0.0377619	0.9741650	0.0000000	-5.969982	0.0063253	1789.0(
M201	10	Mutant-Control	-0.1131815	0.9245469	0.0000000	-5.931925	0.0190801	395.0(
M265	5	Mutant-Control	-0.1972569	0.8722074	0.0000000	-5.953803	0.0331313	190.0(
M277	19	Mutant-Control	-0.0805182	0.9457179	0.0000000	-5.599560	0.0143794	764.0(

M6	79	Mutant-Control	-0.0687009	0.9534962	0.0000001	-5.313393	0.0129298	3223.9
M168	7	Mutant-Control	0.1046860	1.0752604	0.0000001	5.432184	0.0192714	272.0
M78	15	Mutant-Control	0.1174665	1.0848281	0.0000002	5.303767	0.0221477	599.9
M149	20	Mutant-Control	0.0660064	1.0468149	0.0000002	5.275002	0.0125131	805.0
M116	10	Mutant-Control	0.1162645	1.0839247	0.0000002	5.303923	0.0219205	395.0
M171	19	Mutant-Control	0.0606489	1.0429347	0.0000004	5.100238	0.0118914	764.0
M261	8	Mutant-Control	-0.0979199	0.9343792	0.0000006	-5.081877	0.0192685	313.0
M11	74	Mutant-Control	-0.0599055	0.9593269	0.0000007	-4.961416	0.0120743	3019.0
M163	10	Mutant-Control	-0.0847780	0.9429296	0.0000007	-5.031845	0.0168483	395.0
M283	10	Mutant-Control	-0.1296409	0.9140589	0.0000009	-4.999590	0.0259303	395.0
M119	46	Mutant-Control	0.0325016	1.0227840	0.0000011	4.888339	0.0066488	1871.0
M14	52	Mutant-Control	-0.0285712	0.9803907	0.0000017	-4.797911	0.0059549	2117.0
M146	24	Mutant-Control	-0.0409499	0.9720148	0.0000019	-4.794732	0.0085406	969.0
M281	13	Mutant-Control	-0.0945717	0.9365503	0.0000021	-4.795044	0.0197228	520.0
M115	11	Mutant-Control	-0.0793267	0.9464993	0.0000035	-4.697742	0.0168861	436.0
M264	7	Mutant-Control	-0.1191097	0.9207557	0.0000083	-4.544002	0.0262125	272.0
M199	12	Mutant-Control	0.0692216	1.0491504	0.0000128	4.410040	0.0156964	477.0
M32	84	Mutant-Control	-0.0480767	0.9672249	0.0000198	-4.273263	0.0112506	3428.9
M76	21	Mutant-Control	0.0639064	1.0452923	0.0000209	4.279123	0.0149345	846.0
M244	10	Mutant-Control	0.0841350	1.0600520	0.0000243	4.271913	0.0196949	395.0
M77	15	Mutant-Control	0.0636485	1.0451055	0.0000446	4.112605	0.0154764	600.0
M293	14	Mutant-Control	-0.0820756	0.9446975	0.0000536	-4.070705	0.0201625	559.0
M123	17	Mutant-Control	-0.0476856	0.9674872	0.0000691	-4.004202	0.0119089	682.0
M200	11	Mutant-Control	-0.0910132	0.9388632	0.0000694	-4.017211	0.0226558	436.0

M82	10	Mutant-Control	0.0779740	1.0555347	0.0000819	3.980233	0.0195903	395.0(
M25	20	Mutant-Control	0.1019540	1.0732260	0.0000856	3.948235	0.0258227	805.0(
M269	13	Mutant-Control	0.0678655	1.0481648	0.0000976	3.927139	0.0172812	517.9(
M266	5	Mutant-Control	0.1048497	1.0753823	0.0001174	3.933192	0.0266577	190.0(
M110	13	Mutant-Control	0.0399568	1.0280831	0.0001390	3.838701	0.0104089	518.0(
M132	16	Mutant-Control	-0.0650143	0.9559358	0.0001513	-3.811658	0.0170567	640.9(

Modules with greater than 10% change:

Module	Size	Contrast	log2FC	percentControl	Pvalue	Tstatistic	SE	DF
M17	48	Mutant-Control	-0.3985879	0.7586004	0	-18.709226	0.0213043	1953.0001
M4	83	Mutant-Control	-0.1438451	0.9051037	0	-15.184667	0.0094730	3388.0000
M7	79	Mutant-Control	0.1595391	1.1169303	0	14.686956	0.0108626	3224.0001
M24	25	Mutant-Control	0.2504315	1.1895629	0	15.096616	0.0165886	1010.0000
M279	16	Mutant-Control	-0.2169742	0.8603680	0	-13.397911	0.0161946	641.0000
M241	15	Mutant-Control	0.2354806	1.1772988	0	11.458696	0.0205504	599.9999
M255	16	Mutant-Control	-0.1594672	0.8953557	0	-8.882048	0.0179539	641.0000
M210	7	Mutant-Control	-0.1683780	0.8898425	0	-8.317970	0.0202427	272.0000
M81	12	Mutant-Control	0.1722502	1.1268147	0	8.039982	0.0214242	477.0000
M265	5	Mutant-Control	-0.1972569	0.8722074	0	-5.953803	0.0331313	190.0000

Number of significant modules (Bonferroni<0.05): 61

Evaluating goodness-of-fit of modules.
There were problems fitting 0 models.

Partition Quality: 2.14995 (mean module quality).

Module goodness-of-fit statistics.

The Columns BioFraction Genotype, Mixture, Protein, and Residuals describe the percent variance attributable to that term for the mixed-effect model fit to each module. R2.fixef is the overall variance explained by fixed effects.

R2.total is the overall variance explained by the model.
An intuitive measure of module quality is the ratio of variance explained by fixed effects and Protein. We wish to maximize the variance explained by fixed effects and minimize the random effect of Protein. An ideal module is a perfect summary of its protein constituents and thus PVE(Protein) = 0.

Module	Size	BioFraction	Genotype	Mixture	Protein	Residuals	R2.fixef	R2.total
M17	48	0.0216617	0.0415596	0.0008295	0.8160543	0.1198949	0.0409535	0.8771333
M24	25	0.1314741	0.0311901	0.0025102	0.7629233	0.0719023	0.1334930	0.9253178
M241	15	0.1280015	0.0277853	0.0081698	0.7694517	0.0665917	0.1285660	0.9307107
M265	5	0.5897232	0.0269422	0.0277118	0.2741576	0.0814652	0.5780107	0.9097542
M279	16	0.3418061	0.0244443	0.0023630	0.5853643	0.0460223	0.3260224	0.9510732
M116	10	0.5779793	0.0181111	0.0112224	0.2539783	0.1387090	0.5564406	0.8465175
M147	21	0.5726301	0.0154422	0.0041287	0.2924704	0.1153286	0.5498122	0.8747705
M7	79	0.2328404	0.0130158	0.0042103	0.6486381	0.1012954	0.2157252	0.8953092
M81	12	0.2967085	0.0123043	0.0001344	0.6416136	0.0492392	0.2756188	0.9488616
M210	7	0.2539551	0.0116152	0.0025664	0.7066985	0.0251649	0.2348556	0.9738819
M255	16	0.2778746	0.0112541	0.0002575	0.6620496	0.0485641	0.2564124	0.9492165
M117	10	0.1969801	0.0106512	0.0043995	0.7368317	0.0511376	0.1814433	0.9467321
M13	54	0.1513912	0.0099165	0.0095336	0.7134511	0.1157078	0.1387734	0.8809406
M56	24	0.3882378	0.0096546	0.0064261	0.5138723	0.0818092	0.3605305	0.9133846
M212	6	0.5450760	0.0092811	0.0000000	0.3276511	0.1179918	0.5157196	0.8696313
M282	10	0.5337498	0.0090091	0.0002966	0.4222116	0.0347329	0.5034547	0.9620516
M168	7	0.6918632	0.0088963	0.0016179	0.2517004	0.0459223	0.6678516	0.9490732
M201	10	0.4105730	0.0085168	0.0011051	0.5275912	0.0522138	0.3816215	0.9443217
M4	83	0.1983507	0.0083097	0.0000793	0.7297366	0.0635237	0.1807533	0.9348751
M174	16	0.2590547	0.0079808	0.0018922	0.7037333	0.0273390	0.2367762	0.9719194
M264	7	0.4819222	0.0078682	0.0106603	0.4395910	0.0599583	0.4531917	0.9367273
M182	18	0.1256933	0.0075935	0.0059097	0.8173894	0.0434141	0.1154455	0.9563065
M244	10	0.3716234	0.0072922	0.0056826	0.5271670	0.0882347	0.3434991	0.9062753
M198	17	0.7858823	0.0072207	0.0016682	0.1514027	0.0538261	0.7664903	0.9392503
M234	7	0.5072770	0.0071915	0.0004464	0.3859305	0.0991546	0.4759352	0.8913667
M283	10	0.2375652	0.0068470	0.0059707	0.6898786	0.0597384	0.2168231	0.9379087
M3	89	0.2957935	0.0067690	0.0050456	0.6090538	0.0833380	0.2697639	0.9130464
M161	12	0.5826370	0.0060070	0.0029248	0.3706292	0.0378020	0.5522005	0.9601998
M261	8	0.2958547	0.0059063	0.0034959	0.6549222	0.0398209	0.2703239	0.9582420
M106	29	0.2148946	0.0058943	0.0095150	0.6895330	0.0801632	0.1991935	0.9219891
M200	11	0.7914888	0.0057515	0.0022620	0.1129827	0.0875151	0.7713972	0.9011754
M63	19	0.2556473	0.0055941	0.0026612	0.6851605	0.0509370	0.2320124	0.9471496
M25	20	0.0874851	0.0055666	0.0100296	0.7377398	0.1591790	0.0803290	0.8377160
M82	10	0.6733931	0.0051741	0.0101572	0.2385487	0.0727269	0.6442919	0.9191302
M137	13	0.2069492	0.0049569	0.0010490	0.7625964	0.0244484	0.1863607	0.9745316
M206	7	0.5993699	0.0047271	0.0025858	0.3208750	0.0724421	0.5680374	0.9207721
M78	15	0.2956709	0.0046305	0.0014072	0.6440202	0.0542712	0.2693362	0.9438003
M277	19	0.6477122	0.0044605	0.0005115	0.2888496	0.0584663	0.6163003	0.9353608
M187	6	0.6305066	0.0038261	0.0020300	0.3131974	0.0504400	0.6004021	0.9457933

M72	50	0.5550288	0.0037747	0.0004672	0.3907005	0.0500288	0.5213265	0.9468120
M281	13	0.3229230	0.0037682	0.0000000	0.6265848	0.0467240	0.2939221	0.9509553
M199	12	0.8576973	0.0032776	0.0014870	0.0928719	0.0446662	0.8415986	0.9490156
M49	7	0.7144505	0.0032766	0.0039382	0.1833725	0.0949622	0.6857961	0.8932786
M159	16	0.5308059	0.0032336	0.0000000	0.4454564	0.0205042	0.4958929	0.9781937
M163	10	0.3686403	0.0029876	0.0004004	0.6022631	0.0257086	0.3366532	0.9727716
M66	11	0.2230639	0.0029429	0.0008833	0.7217949	0.0513150	0.2008973	0.9470537
M132	16	0.5569132	0.0027917	0.0030417	0.3684854	0.0687680	0.5214581	0.9247629
M105	5	0.6638925	0.0025452	0.0043370	0.2839678	0.0452575	0.6319146	0.9488599
M160	14	0.3633678	0.0025368	0.0012151	0.5629673	0.0699131	0.3311831	0.9257319
M191	12	0.2418391	0.0024741	0.0080145	0.6549034	0.0927688	0.2180175	0.9035140
M266	5	0.2807532	0.0023171	0.0005841	0.7000298	0.0163158	0.2534192	0.9825393
M181	18	0.2454895	0.0022598	0.0008085	0.7311052	0.0203369	0.2200069	0.9789051
M152	11	0.1883745	0.0021988	0.0010014	0.7516619	0.0567634	0.1691226	0.9419314
M77	15	0.4181373	0.0021545	0.0012951	0.5350442	0.0433690	0.3844059	0.9546186
M149	20	0.1425876	0.0021003	0.0000841	0.8222748	0.0329531	0.1266240	0.9664117
M47	7	0.6126940	0.0020810	0.0002026	0.3332078	0.0518146	0.5798618	0.9440599
M6	79	0.4105335	0.0020806	0.0002475	0.4600131	0.1271253	0.3761048	0.8652790
M256	13	0.5720411	0.0020719	0.0000000	0.3791031	0.0467840	0.5365949	0.9490136
M110	13	0.5260370	0.0020473	0.0009945	0.4298444	0.0410768	0.4905309	0.9560079
M269	13	0.4122352	0.0018827	0.0000524	0.5503598	0.0354699	0.3776562	0.9621675
M202	9	0.4341718	0.0017620	0.0034130	0.5206784	0.0399748	0.3994855	0.9574522
M240	16	0.2863752	0.0015998	0.0007877	0.6579773	0.0532600	0.2585993	0.9450532
M29	14	0.1014855	0.0015360	0.0000000	0.8364532	0.0605253	0.0903560	0.9384929
M52	44	0.3838178	0.0015115	0.0007330	0.5732607	0.0406771	0.3498381	0.9573321
M190	13	0.1013782	0.0014788	0.0022587	0.8377922	0.0570921	0.0992183	0.9514015
M289	13	0.2647985	0.0013862	0.0050316	0.6727867	0.0559969	0.2379096	0.9415753
M31	7	0.2118394	0.0013598	0.0018360	0.7659437	0.0190211	0.1896134	0.9807426
M293	14	0.2389200	0.0013231	0.0005433	0.7343254	0.0248881	0.2135011	0.9741478
M162	12	0.3032783	0.0013049	0.0031119	0.5985812	0.0937237	0.2743638	0.9017857
M260	9	0.3797823	0.0012924	0.0008193	0.5641067	0.0539993	0.3462991	0.9422890
M146	24	0.0735848	0.0012883	0.0048038	0.8902177	0.0301054	0.0654128	0.9701351
M11	74	0.1224237	0.0011999	0.0001847	0.7971785	0.0790132	0.1078649	0.9196145
M171	19	0.1719410	0.0011641	0.0003347	0.8076588	0.0189012	0.1525271	0.9809496
M104	7	0.1758377	0.0011433	0.0009135	0.7994903	0.0226152	0.1563938	0.9766147
M76	21	0.2394704	0.0011196	0.0013741	0.7292819	0.0287540	0.2139897	0.9704559
M287	16	0.2365436	0.0011023	0.0037093	0.6836804	0.0749644	0.2114417	0.9219567
M65	12	0.2945638	0.0010751	0.0009594	0.6532916	0.0501100	0.2656390	0.9477315
M184	14	0.1331267	0.0010493	0.0008612	0.8362506	0.0287122	0.1189908	0.9721028
M173	18	0.2413338	0.0010355	0.0029827	0.7109924	0.0436556	0.2160609	0.9551334
M36	29	0.5983412	0.0010233	0.0008501	0.3293248	0.0704605	0.5630724	0.9238532
M68	8	0.1557715	0.0010018	0.0010151	0.8008340	0.0413775	0.1389348	0.9577887
M150	19	0.1293829	0.0008991	0.0008198	0.8333777	0.0355204	0.1141836	0.9638582
M259	11	0.4891734	0.0008716	0.0124064	0.4579168	0.0396318	0.4536329	0.9584676
M263	7	0.1948271	0.0008478	0.0037130	0.7823118	0.0183003	0.1736958	0.9814293

M209	7	0.7571146	0.0008421	0.0016842	0.1659895	0.0743696	0.7310265	0.9180045
M61	20	0.5180772	0.0007930	0.0014372	0.4301691	0.0495234	0.4812263	0.9469399
M59	21	0.1848031	0.0007767	0.0012782	0.7668738	0.0462682	0.1640648	0.9526630
M70	6	0.2826672	0.0007720	0.0018713	0.6814783	0.0332112	0.2544253	0.9647918
M43	11	0.8023529	0.0007396	0.0018022	0.1425300	0.0525754	0.7777648	0.9402683
M249	13	0.5218400	0.0007139	0.0021217	0.4397195	0.0356049	0.4845267	0.9612789
M27	17	0.0998633	0.0007058	0.0000000	0.8402017	0.0592292	0.0878856	0.9395099
M123	17	0.7013007	0.0007032	0.0000547	0.2812687	0.0166727	0.6690772	0.9814611
M75	33	0.5324063	0.0007006	0.0016420	0.3782247	0.0870265	0.4958525	0.9066571
M252	10	0.4022169	0.0006940	0.0000000	0.5702228	0.0268664	0.3670528	0.9712080
M193	10	0.2253947	0.0006900	0.0035743	0.7015580	0.0687830	0.2018349	0.9287258
M151	11	0.1619285	0.0006830	0.0017972	0.7951744	0.0404169	0.1441720	0.9591093
M14	52	0.0925937	0.0006759	0.0006168	0.8724695	0.0336440	0.0811323	0.9660182
M118	9	0.1087397	0.0006667	0.0012940	0.8748887	0.0144109	0.0957315	0.9853663
M23	30	0.0830124	0.0006559	0.0017500	0.8738296	0.0407521	0.0726711	0.9586271
M46	7	0.5124705	0.0006438	0.0004123	0.4272678	0.0592055	0.4764195	0.9359692
M215	14	0.3890193	0.0006195	0.0032454	0.5375325	0.0695833	0.3543644	0.9258018
M69	8	0.4762148	0.0006155	0.0001119	0.4624601	0.0605977	0.4403783	0.9349657
M124	17	0.8061934	0.0006033	0.0024644	0.1502916	0.0404473	0.7817735	0.9541317
M180	19	0.2824249	0.0005809	0.0028808	0.6570052	0.0571082	0.2535885	0.9405420
M207	7	0.6498028	0.0005663	0.0000000	0.3125678	0.0370631	0.6156409	0.9589433
M139	10	0.5473908	0.0005548	0.0000519	0.4134200	0.0385825	0.5104959	0.9580489
M32	84	0.7670252	0.0005462	0.0000081	0.1751688	0.0572518	0.7405097	0.9372365
M53	38	0.4928337	0.0005019	0.0000000	0.4459966	0.0606679	0.4562521	0.9357475
M285	25	0.2497124	0.0004996	0.0046456	0.6805631	0.0645794	0.2238271	0.9338643
M28	16	0.0269013	0.0004739	0.0111686	0.8912635	0.0701926	0.0243180	0.9291603
M170	20	0.3228941	0.0004603	0.0003336	0.6352886	0.0410234	0.2913748	0.9572359
M19	46	0.1307576	0.0004535	0.0013344	0.8100951	0.0573594	0.1148255	0.9415031
M5	81	0.1460117	0.0004414	0.0015653	0.7726662	0.0793154	0.1283785	0.9190198
M177	13	0.4636545	0.0004329	0.0000600	0.5076133	0.0282394	0.4274330	0.9703749
M296	6	0.3808841	0.0004197	0.0000262	0.6016100	0.0170599	0.3468102	0.9817142
M176	13	0.4654832	0.0004056	0.0031627	0.4231159	0.1078327	0.4295314	0.8846537
M55	26	0.3745907	0.0003848	0.0000000	0.5907783	0.0342461	0.3400936	0.9639400
M119	46	0.8521739	0.0003828	0.0005871	0.1306007	0.0162556	0.8322889	0.9816134
M74	34	0.2080460	0.0003771	0.0016323	0.7367145	0.0532300	0.1849810	0.9456294
M205	8	0.8413367	0.0003752	0.0012495	0.1183427	0.0386958	0.8201014	0.9555243
M120	20	0.7857645	0.0003703	0.0003837	0.1757969	0.0376845	0.7592888	0.9574792
M34	48	0.4044381	0.0003660	0.0004678	0.4846926	0.1100354	0.3691607	0.8836574
M80	12	0.5369564	0.0003528	0.0020346	0.3805178	0.0801384	0.4998514	0.9129467
M1	99	0.1776936	0.0003366	0.0004910	0.7583385	0.0631404	0.1571152	0.9356621
M99	15	0.5109403	0.0003296	0.0000000	0.4544215	0.0343086	0.4733323	0.9628568
M195	7	0.1873528	0.0003291	0.0056318	0.7610183	0.0456680	0.1665484	0.9522717
M108	22	0.1641361	0.0003263	0.0016731	0.8043305	0.0295340	0.1447623	0.9697483
M236	6	0.2176609	0.0003205	0.0007637	0.7606671	0.0205878	0.1938786	0.9783447
M130	9	0.8147983	0.0003190	0.0007977	0.1745690	0.0095160	0.7911267	0.9891339

M167	7	0.3502615	0.0003123	0.0000000	0.6158544	0.0335719	0.3180817	0.9647690
M204	9	0.4268501	0.0003036	0.0041771	0.5356451	0.0330240	0.3908374	0.9644818
M22	34	0.0474277	0.0003008	0.0001409	0.9302594	0.0218712	0.0413211	0.9779956
M140	9	0.3421511	0.0002902	0.0013139	0.6395109	0.0167338	0.3093101	0.9822176
M292	15	0.4060115	0.0002724	0.0000000	0.5598215	0.0338946	0.3703480	0.9638962
M143	7	0.2524578	0.0002697	0.0001441	0.7352821	0.0118463	0.2256150	0.9876448
M48	7	0.8076408	0.0002660	0.0007153	0.1689660	0.0224119	0.7841139	0.9752460
M273	9	0.2039009	0.0002617	0.0021050	0.7770816	0.0166508	0.1810018	0.9828066
M41	13	0.6128066	0.0002598	0.0064078	0.3347653	0.0457606	0.5776908	0.9508134
M225	6	0.1160615	0.0002575	0.0004720	0.8670964	0.0161127	0.1030020	0.9842548
M107	24	0.3277612	0.0002471	0.0006558	0.6353744	0.0359615	0.2956799	0.9625017
M213	6	0.3777880	0.0002425	0.0002151	0.6060425	0.0157119	0.3438166	0.9833305
M183	14	0.2162740	0.0002369	0.0003865	0.7349015	0.0482011	0.1936097	0.9512926
M94	29	0.6367490	0.0002239	0.0008345	0.3195680	0.0426246	0.6007910	0.9529479
M250	12	0.3593732	0.0002218	0.0007119	0.5931471	0.0465459	0.3257447	0.9505565
M38	22	0.4872586	0.0002152	0.0052341	0.4619255	0.0453665	0.4499773	0.9515641
M40	13	0.4808517	0.0002143	0.0038172	0.4113969	0.1037199	0.4439724	0.8883610
M157	24	0.3247600	0.0002096	0.0023075	0.6264730	0.0462499	0.2925142	0.9513433
M280	16	0.3348129	0.0001912	0.0013753	0.6166564	0.0469642	0.3020861	0.9503020
M238	24	0.1305376	0.0001741	0.0043953	0.8038658	0.0610272	0.1150837	0.9380234
M8	78	0.1606020	0.0001720	0.0002103	0.7375937	0.1014222	0.1414032	0.8962552
M254	5	0.2104008	0.0001710	0.0004595	0.7686476	0.0203211	0.1875563	0.9788092
M245	22	0.4380215	0.0001685	0.0003015	0.5422189	0.0192897	0.4010673	0.9794222
M154	8	0.0858146	0.0001598	0.0013569	0.8970620	0.0156067	0.0754454	0.9843521
M9	76	0.1892798	0.0001491	0.0005872	0.7563262	0.0536578	0.1673278	0.9451289
M33	51	0.3886397	0.0001439	0.0078923	0.5292003	0.0741239	0.3533027	0.9216482
M79	13	0.3932610	0.0001379	0.0005354	0.5590832	0.0469826	0.3582697	0.9501413
M251	10	0.2051723	0.0001226	0.0007035	0.7621177	0.0318839	0.1821142	0.9668398
M221	9	0.2058801	0.0001152	0.0006555	0.7648577	0.0284915	0.1828040	0.9703676
M141	8	0.5360515	0.0001111	0.0000000	0.3989919	0.0648455	0.4986822	0.9289200
M223	8	0.7282487	0.0001006	0.0022391	0.2250212	0.0443904	0.6972503	0.9498677
M64	12	0.1695569	0.0001006	0.0000000	0.8109388	0.0194037	0.1496813	0.9799894
M246	20	0.6913116	0.0000998	0.0004957	0.2844633	0.0236296	0.6579236	0.9737113
M84	33	0.2171742	0.0000872	0.0006934	0.7474101	0.0346351	0.1924264	0.9641689
M35	43	0.5371837	0.0000858	0.0064975	0.3836525	0.0725805	0.4994702	0.9216893
M156	27	0.3027363	0.0000776	0.0006054	0.6476294	0.0489513	0.2718391	0.9488436
M97	21	0.5839172	0.0000760	0.0007017	0.3720940	0.0432111	0.5465438	0.9527378
M257	11	0.2657441	0.0000682	0.0028898	0.6576873	0.0736106	0.2381006	0.9229073
M135	13	0.2836434	0.0000656	0.0005721	0.6953848	0.0203342	0.2539697	0.9786960
M268	21	0.5556708	0.0000617	0.0022339	0.3632499	0.0787838	0.5177997	0.9140934
M101	13	0.6829908	0.0000571	0.0002184	0.2818105	0.0349233	0.6491333	0.9609866
M21	42	0.3359543	0.0000527	0.0012301	0.5203375	0.1424255	0.3029555	0.8501234
M211	6	0.9136029	0.0000446	0.0019340	0.0436759	0.0407425	0.9023186	0.9545056
M2	97	0.0969774	0.0000310	0.0000000	0.8481688	0.0548229	0.0844439	0.9443624
M267	23	0.8273246	0.0000301	0.0002113	0.1375138	0.0349202	0.8043842	0.9603681

M58	21	0.4695862	0.0000218	0.0041975	0.4616354	0.0645590	0.4336745	0.9323018
M258	11	0.4581500	0.0000214	0.0010535	0.4790957	0.0616794	0.4213637	0.9336950
M121	17	0.5022977	0.0000204	0.0003589	0.4677743	0.0295486	0.4643203	0.9680115
M172	18	0.1068888	0.0000186	0.0019502	0.8624234	0.0287190	0.0939078	0.9711567
M85	25	0.1002778	0.0000158	0.0005874	0.8738443	0.0252748	0.0875439	0.9743373
M284	8	0.3290941	0.0000148	0.0003753	0.6545766	0.0159393	0.2974863	0.9837244
M247	19	0.6776965	0.0000135	0.0012863	0.2942380	0.0267657	0.6434581	0.9702284
M138	11	0.2490717	0.0000090	0.0012713	0.7161425	0.0335055	0.2221662	0.9649477
M166	7	0.1590568	0.0000079	0.0020822	0.8204552	0.0183980	0.1407015	0.9812557
M111	12	0.0871843	0.0000066	0.0000000	0.8940802	0.0187289	0.0761629	0.9809391
M179	35	0.5632740	0.0000049	0.0007797	0.3949181	0.0410233	0.5255737	0.9555860
M226	6	0.1417444	0.0000000	0.0245259	0.7322300	0.1014998	0.1267464	0.8944680
M262	8	0.5898813	0.0000000	0.0000000	0.3592937	0.0508250	0.5530164	0.9439229
M175	14	0.3259925	0.0000000	0.0113357	0.5429019	0.1197699	0.2942719	0.8736434
M228	29	0.4849625	0.0000000	0.0024055	0.4805447	0.0320873	0.4470102	0.9655135
M164	9	0.4719301	0.0000000	0.0004139	0.4839076	0.0437483	0.4350125	0.9528989
M235	7	0.2297265	0.0000000	0.0049595	0.7241910	0.0411230	0.2048420	0.9567778
M86	24	0.4838147	0.0000000	0.0006712	0.4472349	0.0682793	0.4458085	0.9262987
M216	13	0.3252211	0.0000000	0.0029218	0.6259188	0.0459383	0.2930823	0.9514240
M89	12	0.5617526	0.0000000	0.0021769	0.2911504	0.1449201	0.5278563	0.8453910
M185	7	0.3131257	0.0000000	0.0009576	0.6496732	0.0362435	0.2820013	0.9612509
M18	48	0.2104366	0.0000000	0.0009723	0.7254577	0.0631334	0.1863526	0.9349091
M71	6	0.1578410	0.0000000	0.0001230	0.8210064	0.0210296	0.1394237	0.9780659
M39	21	0.4339557	0.0000000	0.0070050	0.4901897	0.0688496	0.3976080	0.9268668
M271	11	0.4774339	0.0000000	0.0002014	0.4959383	0.0264264	0.4399846	0.9714744
M222	8	0.3546919	0.0000000	0.0000000	0.6086987	0.0366093	0.3213767	0.9609818
M237	6	0.2902040	0.0000000	0.0019589	0.6600103	0.0478269	0.2613522	0.9494175
M194	10	0.4527584	0.0000000	0.0000000	0.4401537	0.1070880	0.4158750	0.8842116
M125	14	0.7849357	0.0000000	0.0001695	0.1917688	0.0231260	0.7580469	0.9737784
M192	11	0.2478986	0.0000000	0.0010058	0.7078280	0.0432675	0.2211699	0.9547239
M274	9	0.5152631	0.0000000	0.0009832	0.4418547	0.0418989	0.4779483	0.9546165
M165	8	0.7673289	0.0000000	0.0003832	0.2025443	0.0297436	0.7392750	0.9663746
M103	8	0.1968517	0.0000000	0.0028767	0.7437437	0.0565279	0.1752806	0.9413107
M127	9	0.6711476	0.0000000	0.0009720	0.2879201	0.0399603	0.6367991	0.9552830
M131	28	0.5621818	0.0000000	0.0000000	0.4174636	0.0203546	0.5240943	0.9777609
M155	6	0.6019199	0.0000000	0.0000444	0.3267212	0.0713144	0.5670284	0.9223073
M93	31	0.4103158	0.0000000	0.0000000	0.5068635	0.0828207	0.3739625	0.9117472
M224	7	0.5529935	0.0000000	0.0004024	0.4181473	0.0284569	0.5158016	0.9687644
M51	6	0.6779052	0.0000000	0.0041717	0.2653571	0.0525659	0.6442925	0.9410007
M92	6	0.1498173	0.0000000	0.0007843	0.8286779	0.0207205	0.1324987	0.9787340
M16	49	0.0870255	0.0000000	0.1035694	0.6240134	0.1853917	0.0761056	0.8119291
M26	17	0.0909342	0.0000000	0.0318320	0.5918919	0.2853418	0.0816996	0.7101730
M30	12	0.1670058	0.0000000	0.0072517	0.6373354	0.1884070	0.1491117	0.8058814
M37	25	0.5283912	0.0000000	0.0000000	0.3768433	0.0947656	0.4906212	0.8975082
M42	11	0.7097856	0.0000000	0.0161304	0.1645134	0.1095706	0.6771667	0.8771762

M44	9	0.6879200	0.0000000	0.0070436	0.2304954	0.0745411	0.6545047	0.9166874
M50	6	0.8620551	0.0000000	0.0004030	0.0335888	0.1039531	0.8414831	0.8797768
M54	36	0.1016820	0.0000000	0.0000979	0.8592908	0.0389294	0.0886946	0.9604335
M57	21	0.2942685	0.0000000	0.0002167	0.6587448	0.0467700	0.2639174	0.9510922
M60	21	0.0666559	0.0000000	0.0000000	0.9099731	0.0233711	0.0579695	0.9763071
M62	20	0.1555989	0.0000000	0.0020719	0.7986963	0.0436329	0.1370152	0.9552823
M73	34	0.2981385	0.0000000	0.0005025	0.6740507	0.0273083	0.2676619	0.9719361
M83	65	0.5969629	0.0000000	0.0002778	0.3536440	0.0491152	0.5595175	0.9462652
M87	22	0.3918158	0.0000000	0.0007621	0.5224574	0.0849647	0.3566989	0.9100255
M90	11	0.0627564	0.0000000	0.0004987	0.9186205	0.0181244	0.0547106	0.9815487
M91	9	0.3545931	0.0000000	0.0002598	0.6190382	0.0261089	0.3209768	0.9721254
M95	25	0.5418272	0.0000000	0.0035567	0.3954216	0.0591945	0.5036736	0.9355497
M96	24	0.4788939	0.0000000	0.0021723	0.4743573	0.0445765	0.4411483	0.9521316
M98	17	0.4873429	0.0000000	0.0012967	0.4597510	0.0516094	0.4494873	0.9442153
M100	14	0.3755539	0.0000000	0.0003045	0.5312043	0.0929373	0.3411200	0.9011785
M102	11	0.3792341	0.0000000	0.0014815	0.5121758	0.1071086	0.3446047	0.8854783
M112	12	0.3537005	0.0000000	0.0105094	0.5096971	0.1260931	0.3260293	0.8718702
M114	11	0.4586250	0.0000000	0.0035258	0.4806273	0.0572219	0.4235901	0.9403837
M122	17	0.7496102	0.0000000	0.0006682	0.2298207	0.0199009	0.7198359	0.9775984
M128	9	0.7236437	0.0000000	0.0009154	0.2251717	0.0502691	0.6921504	0.9433264
M133	16	0.5180051	0.0000000	0.0001366	0.4571544	0.0247038	0.4798978	0.9731098
M134	15	0.5745390	0.0000000	0.0000000	0.3906588	0.0348023	0.5371357	0.9620782
M136	13	0.6478967	0.0000000	0.0002540	0.3107370	0.0411123	0.6124870	0.9543885
M142	8	0.7210807	0.0000000	0.0022275	0.2372762	0.0394157	0.6897080	0.9556871
M145	6	0.1657019	0.0000000	0.0008719	0.8150265	0.0183997	0.1465009	0.9808564
M153	9	0.1628896	0.0000000	0.0010120	0.8020233	0.0340752	0.1448350	0.9657334
M158	19	0.8159574	0.0000000	0.0017773	0.1483822	0.0338831	0.7922679	0.9619708
M178	6	0.3884940	0.0000000	0.0086006	0.5402677	0.0626377	0.3547175	0.9329783
M186	7	0.1117135	0.0000000	0.0008750	0.8736207	0.0137907	0.0983971	0.9862428
M189	15	0.2213520	0.0000000	0.0011217	0.7310939	0.0464323	0.1968816	0.9520220
M196	6	0.1551876	0.0000000	0.0000000	0.8234602	0.0213522	0.1372276	0.9778898
M197	6	0.4548889	0.0000000	0.0160536	0.4353243	0.0937332	0.4190130	0.8983694
M203	9	0.7827457	0.0000000	0.0016080	0.1702314	0.0454148	0.7557457	0.9484703
M208	7	0.5444938	0.0000000	0.0012751	0.3147129	0.1395182	0.5071182	0.8467361
M217	12	0.3908710	0.0000000	0.0083009	0.5154299	0.0853982	0.3557425	0.9087219
M218	10	0.7813027	0.0000000	0.0010273	0.1812493	0.0364207	0.7540100	0.9585556
M219	10	0.8356415	0.0000000	0.0000000	0.1294867	0.0348718	0.8139108	0.9604893
M227	5	0.3343414	0.0000000	0.0005111	0.6408551	0.0242924	0.3025963	0.9741067
M229	23	0.3888587	0.0000000	0.0043284	0.5260896	0.0807234	0.3534611	0.9142257
M230	19	0.3409307	0.0000000	0.0005464	0.6319148	0.0266081	0.3076632	0.9719484
M231	13	0.3781763	0.0000000	0.0003130	0.5992949	0.0222157	0.3431861	0.9762679
M232	10	0.2521928	0.0000000	0.0018959	0.6940618	0.0518495	0.2252659	0.9455969
M233	9	0.3953039	0.0000000	0.0047533	0.5318033	0.0681395	0.3600593	0.9267554
M239	18	0.3289730	0.0000000	0.0000000	0.6265046	0.0445224	0.2965671	0.9532065
M242	13	0.3151307	0.0000000	0.0022315	0.6005767	0.0820610	0.2842946	0.9138791

M253	6	0.7871255	0.0000000	0.0000000	0.1574632	0.0554113	0.7603116	0.9365864
M270	12	0.6924278	0.0000000	0.0009703	0.2712540	0.0353480	0.6589716	0.9603615
M276	5	0.6217963	0.0000000	0.0000000	0.2920519	0.0861518	0.5854554	0.9030880
M278	18	0.4106706	0.0000000	0.0016807	0.5001733	0.0874753	0.3747525	0.9067415
M286	17	0.1262455	0.0000000	0.0008316	0.8317525	0.0411705	0.1107921	0.9578818
M290	23	0.3482915	0.0000000	0.0001256	0.6302991	0.0212839	0.3144629	0.9774731
M295	7	0.7304699	0.0000000	0.0006389	0.2314241	0.0374671	0.6996987	0.9576994

Number of modules with something interesting going on: 116

Significant Modules with significant gse:
(23 of 61 significant modules.)

Module	TopPathway	moduleSize	n	N	FE	Padjust
M25	CORUM: Class C Vps complex (hVPS11, hVPS18, hVPS16, rVPS33a)	20	4	4	277.650000	0.0000000
M24	CORUM: Fibrinogen complex	25	3	3	222.120000	0.0000239
M171	CORUM: SNARE complex (Stx5, Gosr2, Sec22b, Bet1)	19	3	4	219.236842	0.0000401
M181	CORUM: Arp2/3 protein complex	18	3	7	132.238095	0.0002938
M17	CORUM: WASH complex	48	5	5	115.687500	0.0000000
M14	CORUM: EARP complex	52	4	4	106.788461	0.0000020
M119	CORUM: Ribosome, cytoplasmic	46	29	72	48.718599	0.0000000
M13	CORUM: Endocytic coat complex (11 subunits)	54	4	10	41.133333	0.0004756
M277	Takamori et al., 2006: Signalling molecules	19	4	33	35.457735	0.0011101
M201	Uezu et al., 2016: ePSD	10	5	114	24.438596	0.0002258
M3	LopitDC: LYSOSOME	89	17	60	17.729026	0.0000000
M12	LopitDC: PEROXISOME	70	7	33	16.851515	0.0000360
M81	LopitDC: ER	12	7	248	13.200269	0.0000587
M72	LopitDC: ER	50	25	248	11.314516	0.0000000
M199	LopitDC: PM	12	7	302	10.921082	0.0002154
M110	LopitDC: CYTOSOL	13	8	359	9.739876	0.0000678
M32	LopitDC: MITOCHONDRION	84	64	450	9.618624	0.0000000
M52	LopitDC: CYTOSOL	44	25	359	8.992783	0.0000000
M76	LopitDC: ER	21	8	248	8.620584	0.0004748
M11	Uezu et al., 2016: ePSD	74	13	114	8.586534	0.0000006
M174	LopitDC: ER	16	6	248	8.485887	0.0114359
M6	LopitDC: MITOCHONDRION	79	29	450	4.634290	0.0000000
M123	LopitDC: NUCLEUS/CHROMATIN	17	13	1210	3.897472	0.0001928

Modules with significant LopitDC gse:

Top module for each LopitDC category

Pathway	TopModule	FE	Padjust

LopitDC: CYTOSOL	M52	8.992783	0.0000000
LopitDC: ER	M72	11.314516	0.0000000
LopitDC: GA	M285	54.540444	0.0000000
LopitDC: LYSOSOME	M3	17.729026	0.0000000
LopitDC: MITOCHONDRION	M32	9.618624	0.0000000
LopitDC: NUCLEUS/CHROMATIN	M97	4.368595	0.0000000
LopitDC: PEROXISOME	M239	74.895623	0.0000000
LopitDC: PM	M199	10.921082	0.0002154
LopitDC: PROTEASOME	M83	62.153846	0.0000000
LopitDC: RIBOSOME	M119	29.597031	0.0000000

NS modules with Significant GSE:

Module	TopPathway	moduleSize	n	N	FE	Padjust
M1	LopitDC: ER	99	14	248	3.200065	0.0291190
M2	CORUM: COG complex	97	5	8	35.792526	0.0000233
M5	CORUM: Vacuolar ATPase	81	5	13	26.396011	0.0002017
M8	CORUM: AMPA receptor complex (anti-GluA1-a)	78	4	20	14.251282	0.0434058
M9	Takamori et al., 2006: Small GTPases and related proteins	76	5	34	10.750774	0.0253404
M18	LopitDC: PM	48	13	302	5.070502	0.0002339
M29	CORUM: Exocyst complex	14	2	8	99.214286	0.0484528
M33	LopitDC: MITOCHONDRION	51	29	450	7.178606	0.0000000
M34	CORUM: 39S ribosomal subunit, mitochondrial	48	5	48	12.113715	0.0145942
M35	CORUM: 28S ribosomal subunit, mitochondrial	43	6	29	26.771452	0.0000183
M36	CORUM: Respiratory chain complex I (beta subunit) mitochondrial	29	4	16	47.905172	0.0003087
M37	LopitDC: MITOCHONDRION	25	12	450	6.059733	0.0000314
M38	LopitDC: MITOCHONDRION	22	13	450	7.459899	0.0000003
M39	LopitDC: MITOCHONDRION	21	13	450	7.815132	0.0000001
M40	LopitDC: MITOCHONDRION	13	8	450	7.768889	0.0003895
M41	CORUM: MIB complex	13	3	11	116.496504	0.0004844
M43	LopitDC: MITOCHONDRION	11	8	450	9.181414	0.0000576
M44	LopitDC: MITOCHONDRION	9	6	450	8.416296	0.0048372
M45	LopitDC: MITOCHONDRION	8	5	450	7.890278	0.0413656
M48	LopitDC: MITOCHONDRION	7	7	450	12.624444	0.0000055
M49	CORUM: 55S ribosome, mitochondrial	7	3	77	31.129870	0.0249864
M51	LopitDC: MITOCHONDRION	6	5	450	10.520370	0.0050713
M53	LopitDC: CYTOSOL	38	11	359	4.581586	0.0041585
M54	LopitDC: CYTOSOL	36	10	359	4.396472	0.0152765
M55	CORUM: Alpha-GDI-Hsp90 chaperone complex, ATP dependent	26	2	4	106.788461	0.0372282
M61	LopitDC: CYTOSOL	20	7	359	5.539554	0.0424031

M73	LopitDC: ER	34	17	248	11.314516	0.0000000
M74	LopitDC: ER	34	9	248	5.990038	0.0032689
M75	LopitDC: ER	33	14	248	9.600195	0.0000000
M80	LopitDC: ER	12	5	248	9.428763	0.0293992
M83	CORUM: 20S proteasome	65	10	14	61.021978	0.0000000
M84	CORUM: BBS-chaperonin complex	33	6	10	101.018182	0.0000000
M85	CORUM: CSA complex	25	3	11	60.600000	0.0038415
M86	CORUM: 20S proteasome	24	3	14	49.580357	0.0074103
M87	Takamori et al., 2006: Metabolic enzymes	22	4	32	31.596591	0.0018190
M88	CORUM: CSA complex	22	4	11	91.818182	0.0000177
M93	CORUM: TRAPP complex	31	7	14	89.612903	0.0000000
M94	CORUM: p54(nrb)-PSF-matrin3 complex	29	3	3	191.482759	0.0000379
M95	CORUM: Spliceosome	25	8	128	13.945000	0.0000142
M96	LopitDC: NUCLEUS/CHROMATIN	24	14	1210	2.973072	0.0093318
M97	CORUM: CDC5L complex	21	3	28	28.357143	0.0424332
M98	LopitDC: NUCLEUS/CHROMATIN	17	12	1210	3.597666	0.0021250
M101	CORUM: 17S U2 snRNP	13	9	30	128.238461	0.0000000
M102	LopitDC: NUCLEUS/CHROMATIN	11	9	1210	4.170022	0.0046578
M107	LopitDC: CYTOSOL	24	10	359	6.594708	0.0002339
M114	LopitDC: CYTOSOL	11	6	359	8.633072	0.0063635
M122	CORUM: Large Drosha complex	17	3	18	54.460784	0.0055910
M124	CORUM: EIF3 complex (EIF3A, EIF3B, EIF3G, EIF3I, EIF3C)	17	5	5	326.647059	0.0000000
M125	CORUM: Spliceosome	14	7	128	21.789062	0.0000025
M129	CORUM: 12S U11 snRNP	9	3	14	132.357143	0.0003135
M130	CORUM: DNA-PK-Ku-eIF2-NF90-NF45 complex	9	3	8	231.416667	0.0000486
M138	CORUM: BBS1-BBS4-BBS5-PKD1-TTC8 complex	11	2	5	201.963636	0.0105231
M142	CORUM: Gamma-tubulin complex	8	4	6	462.750000	0.0000000
M144	CORUM: BBS1-BBS4-BBS5-PKD1-TTC8 complex	6	2	5	370.266667	0.0028751
M156	LopitDC: PM	27	8	302	5.547216	0.0162586
M170	LopitDC: ER	20	6	248	6.788710	0.0476602
M172	LopitDC: ER	18	7	248	8.800179	0.0018757
M177	CORUM: SNARE complex (RINT1, ZW10, p31, Stx18)	13	2	4	213.576923	0.0089628
M179	CORUM: ARHGEF7-GIT2-PAK1 complex	35	2	3	105.771429	0.0341396
M180	CORUM: Epsin-clathrin complex	19	2	5	116.905263	0.0326346
M184	CORUM: c-Abl-CAS-Abi1 complex	14	2	3	264.428571	0.0052346
M187	CORUM: AP3 adaptor complex	6	2	7	264.523810	0.0060297
M190	CORUM: CCC complex	13	9	12	320.538461	0.0000000
M194	CORUM: Arf1-beta/delta-coat protein subcomplex	10	2	3	370.200000	0.0025898
	CORUM: HES1 promoter-Notch enhancer					

M196	complex	6	2	13	142.589744	0.0222837
M203	CORUM: Kif3-cadherin-catenin complex	9	2	5	246.800000	0.0068953
M205	Uezu et al., 2016: Arhgef9	8	3	74	28.216216	0.0356161
M208	CORUM: Exocyst complex	7	3	8	297.642857	0.0000203
M212	Uezu et al., 2016: ePSD	6	3	114	24.438596	0.0472190
M217	LopitDC: NUCLEUS/CHROMATIN	12	9	1210	3.822521	0.0153742
M222	CORUM: AFF4 super elongation complex (SEC)	8	2	11	126.386364	0.0292955
M230	CORUM: Cohesin-SA2 complex	19	2	4	146.157895	0.0196138
M239	LopitDC: PEROXISOME	18	8	33	74.895623	0.0000000
M242	LopitDC: PEROXISOME	13	3	33	38.888112	0.0154829
M245	CORUM: 5FMC (Friends of Methylated Chtop) complex	22	2	5	100.963636	0.0440376
M246	CORUM: CCR4-NOT complex	20	3	9	92.566667	0.0009796
M249	LopitDC: NUCLEUS/CHROMATIN	13	9	1210	3.528481	0.0412503
M250	CORUM: PAS (PIKfyve-ArPIKfyve-Sac3) complex	12	2	3	308.500000	0.0037974
M251	CORUM: Parvulin-associated pre-rRNP complex	10	3	59	28.266102	0.0382674
M252	CORUM: IGF2BP1 complex	10	2	9	123.422222	0.0308874
M253	CORUM: Spliceosome	6	4	128	29.052083	0.0011341
M258	LopitDC: PM	11	6	302	10.211920	0.0024080
M259	CORUM: GABA-A receptor (GABRA1, GABRB2, GABRD)	11	2	3	336.545455	0.0031649
M262	CORUM: GNAI1-GNB2-GNG12 complex	8	2	3	462.750000	0.0016118
M263	LopitDC: PM	7	5	302	13.372753	0.0023944
M267	CORUM: 40S ribosomal subunit, cytoplasmic	23	14	29	116.638681	0.0000000
M268	CORUM: Multisynthetase complex	21	10	10	264.428571	0.0000000
M272	CORUM: Ribosome, cytoplasmic	9	3	72	25.759259	0.0488652
M280	LopitDC: PM	16	6	302	7.020695	0.0332160
M284	CORUM: Calcineurin complex (Calna, Cna2, Gria1, Gria2, Cacng8)	8	2	5	277.650000	0.0053649
M285	CORUM: SNARE complex (Stx5, Gosr1, GS15)	25	2	3	148.080000	0.0172340
M290	CORUM: hASC-1 complex	23	2	4	120.739130	0.0289913
M294	CORUM: NELF complex (Negative elongation factor complex)	11	3	4	378.681818	0.0000068