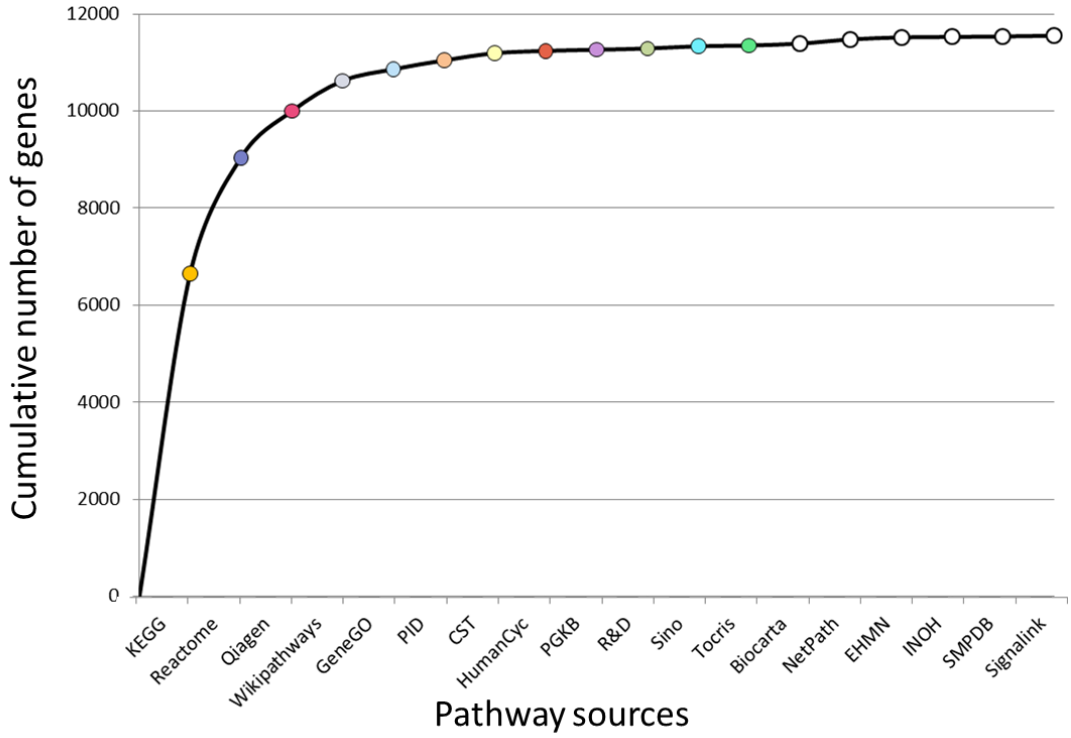


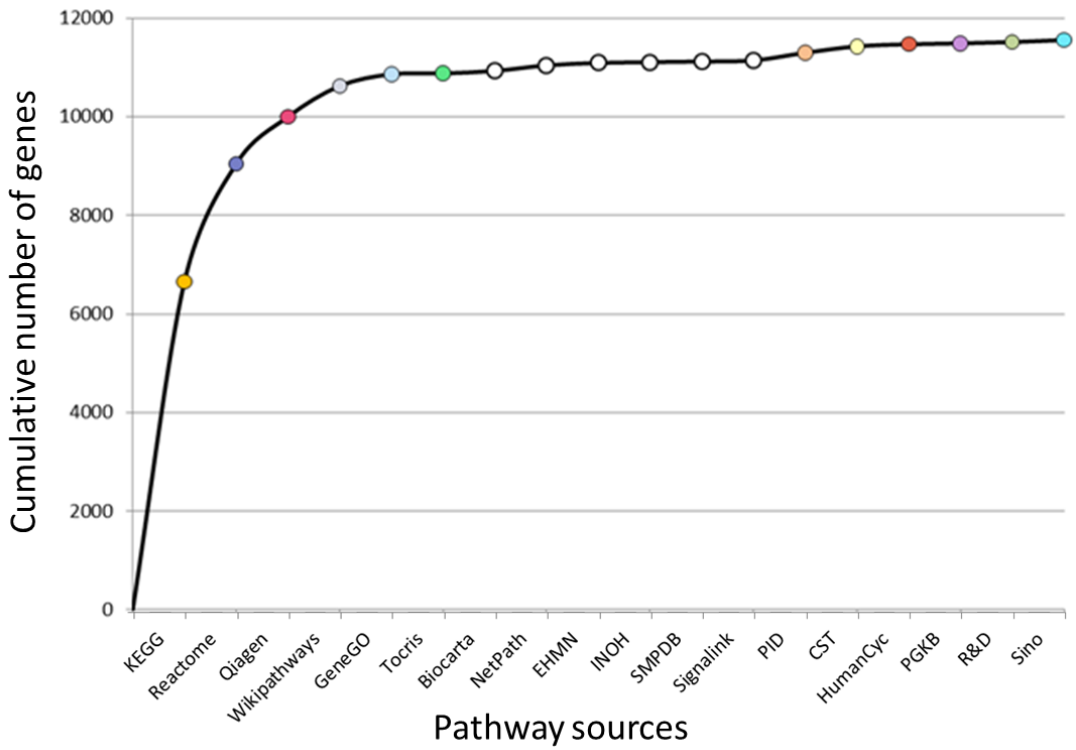


Figure S1. **(A)** Change of cumulative gene counts (removing duplicates) upon addition of pathway sources. Increase of total gene count by addition of sources approaches saturation after the first 12. The six additional sources (white) increase the total gene count by 2%. The order of source addition is based on the number of genes in each source and taking into account the popularity of the source, as reflected by the number of citations. **(B)** Switching the last 6 sources results in a very similar graph with increase of 4% in the total gene count.

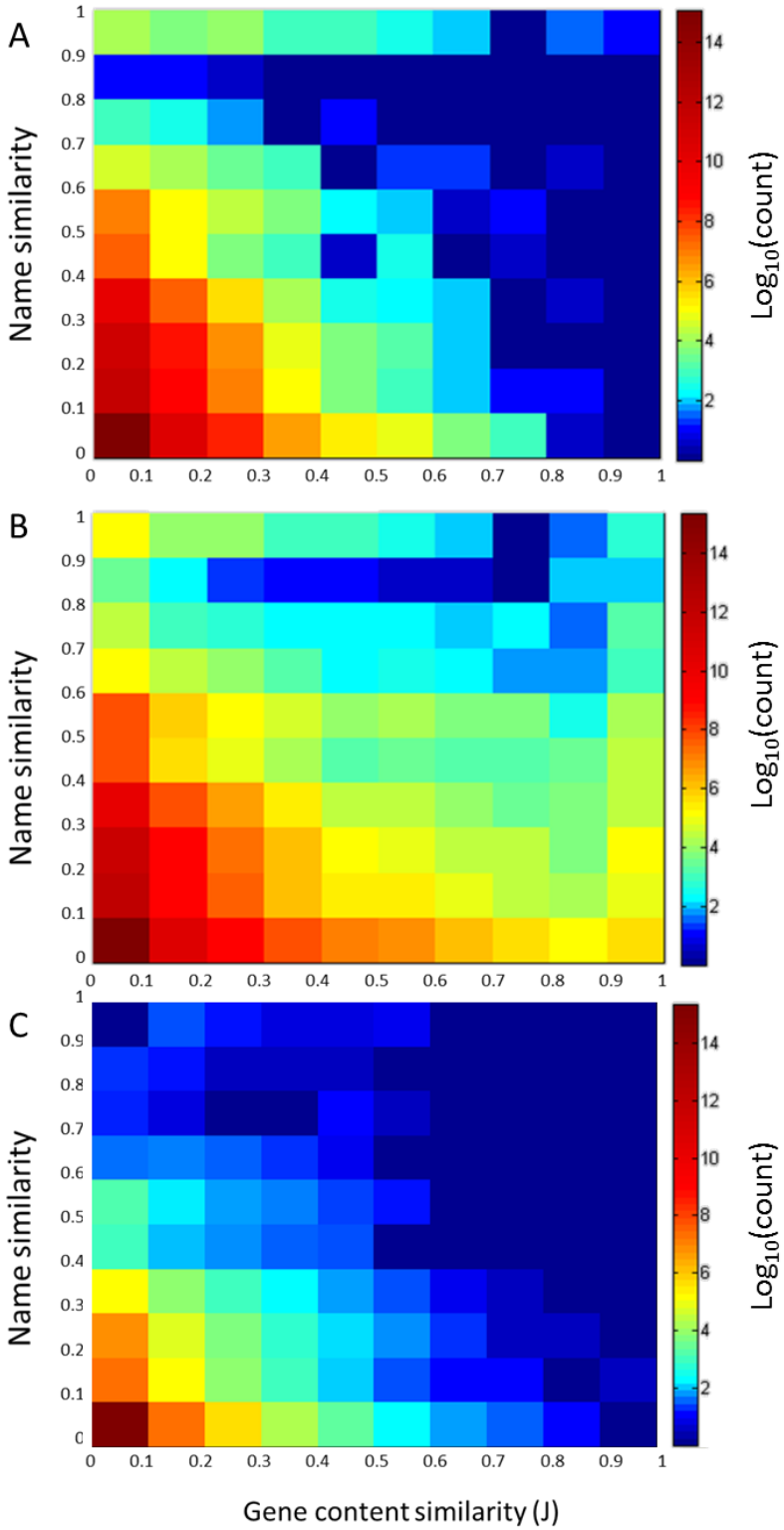
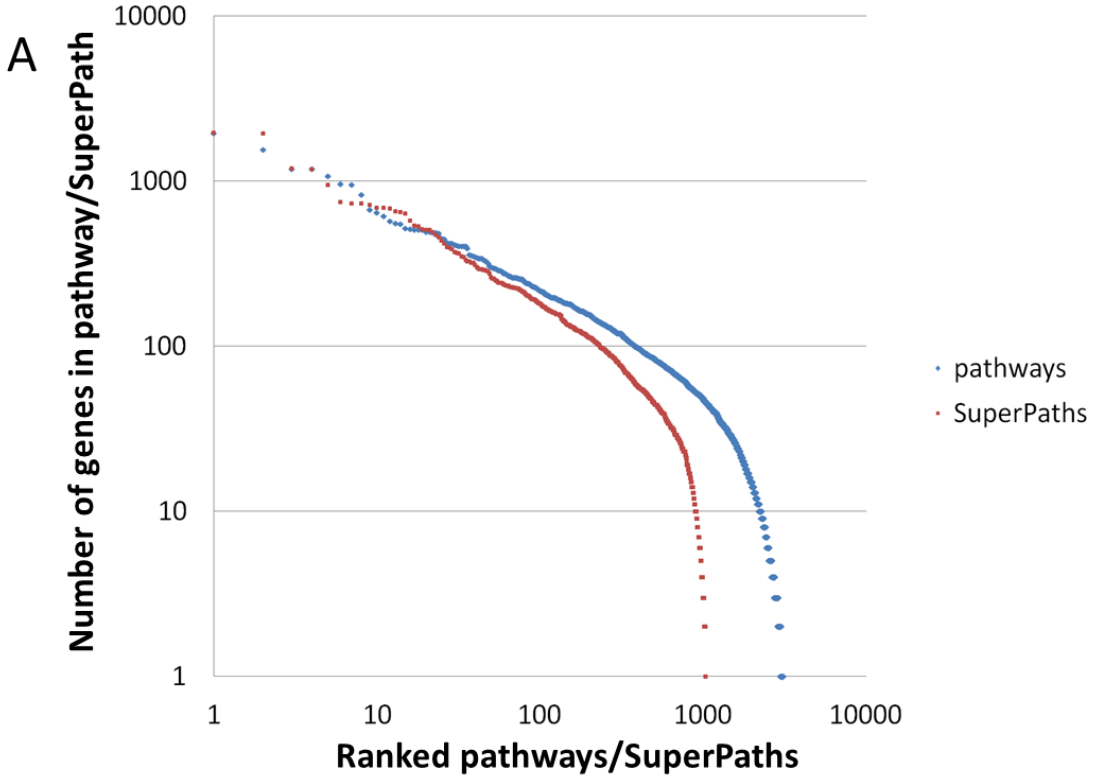


Figure S2. Name similarity vsersus gene-content similarity. **(A)** Name similarity *vs.* gene-content similarity in Pathway pairs where each pathway is from a different source. **(B)** Name similarity *vs.* gene-content similarity in all pathway pairs. **(C)** Name similarity *vs.* gene-content similarity in SuperPaths.



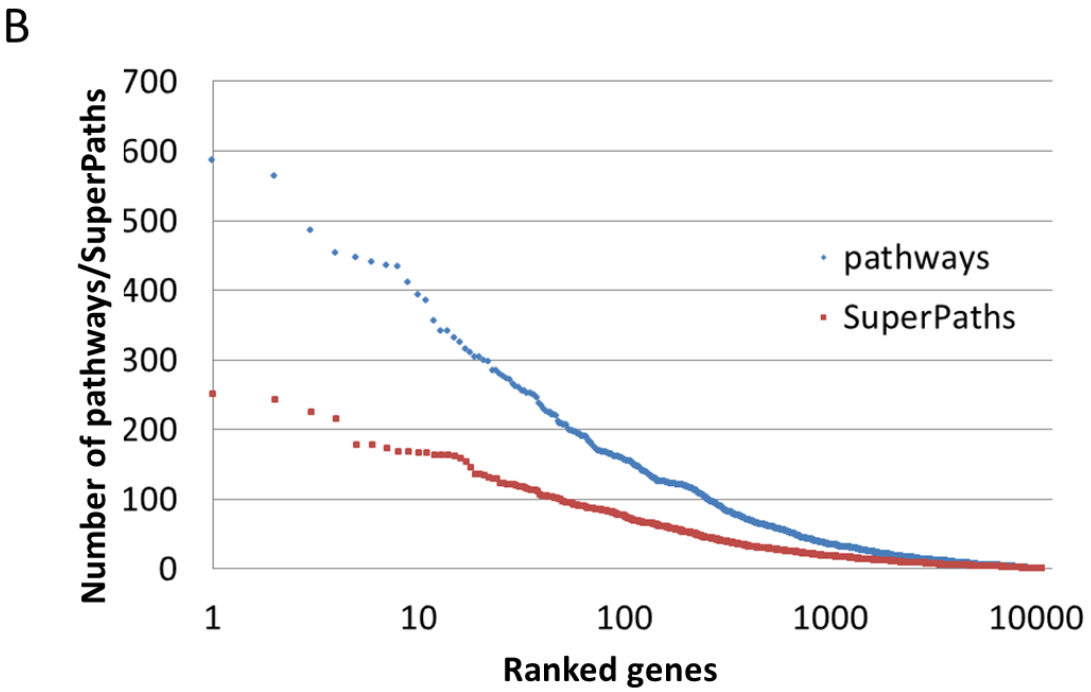


Figure S3. Genes vs. pathways and SuperPaths. **(A)** Number of genes in SuperPaths and Pathways. The pathways (blue) and SuperPaths (red) are ranked in descending order. The number of genes in pathways and SuperPaths have a similar shape indicating a similar distribution of gene count across pathways and SuperPaths. **(B)** The Number of pathways and SuperPaths across all ranked genes. Consolidation of pathways into SuperPaths reduces greatly the amount of pathway-related annotation per gene, especially for highly annotated genes.

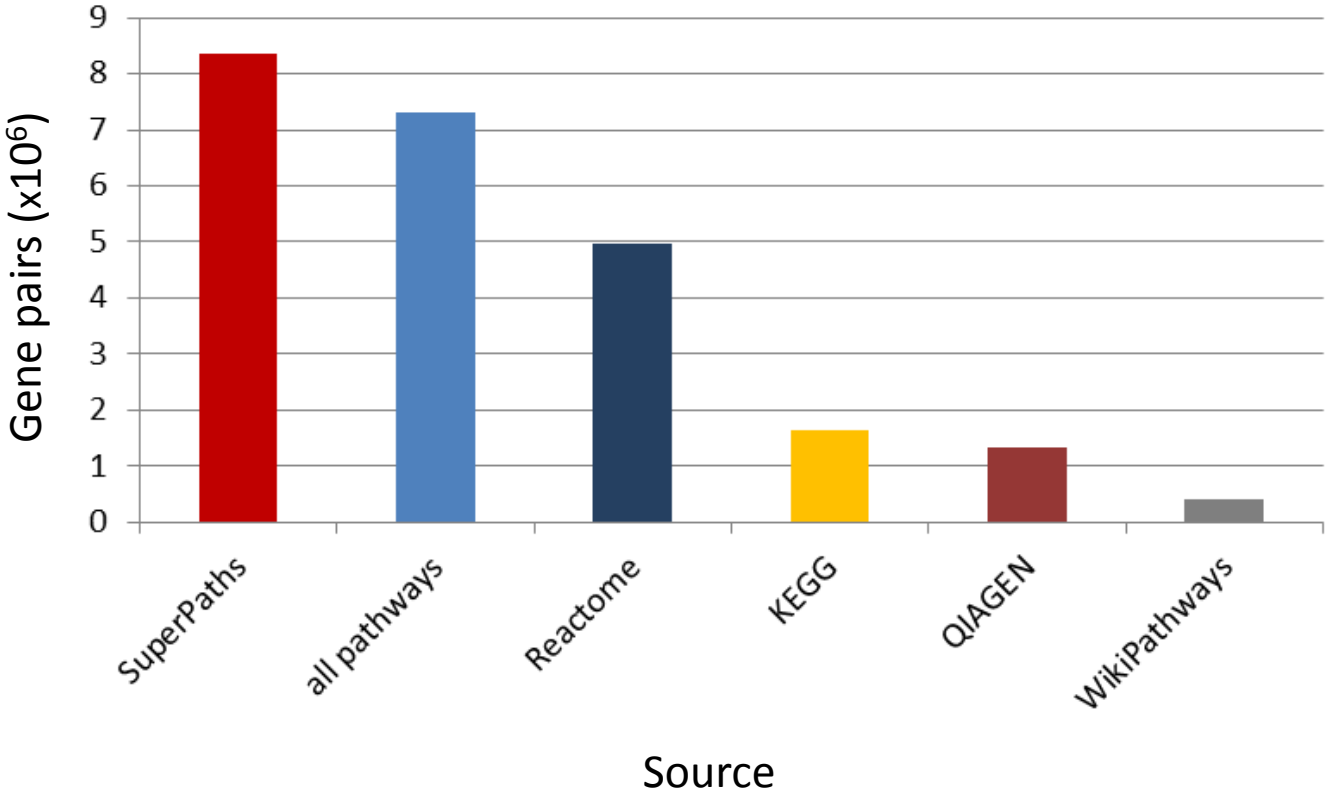


Figure S4. Enhancement of gene pair counts in SuperPaths. SuperPaths provide 14% more gene pairs than all pathway sources combined and x1.68 to x20 higher numbers than in the individual four largest pathway sources.

A

SuperPaths for SDHC *About* improved
See pathways by source

	SuperPath	Contained pathways *About*			
1	Citric acid cycle (TCA cycle)	Citric acid cycle (TCA cycle)	0.55	conversion of glucose to acetyl CoA and entry into the TCA cycle	0.43
		Citrate cycle (TCA cycle)	0.55	TCA Cycle	0.00
		Pyruvate metabolism and Citric Acid (TCA) cycle	0.49	TCA cycle	0.00
2	Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	0.81	Oxidative phosphorylation	0.64
		Respiratory electron transport	0.81	Parkinson's disease	0.57
		Electron Transport Chain	0.75	Huntington's disease	0.45
		The citric acid (TCA) cycle and respiratory electron transport	0.71	Non-alcoholic fatty liver disease (NAFLD)	0.41
3	Metabolism	Metabolism	0.38	Metabolic pathways	0.38
4	Alzheimer's disease	Alzheimer's disease	0.44		
5	Carbon metabolism	Carbon metabolism	0.38		

B

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LifeMap SCIENCES
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tca

Citric acid cycle (TCA cycle) SuperPath

Pathway network for *Citric acid cycle (TCA cycle)* SuperPath

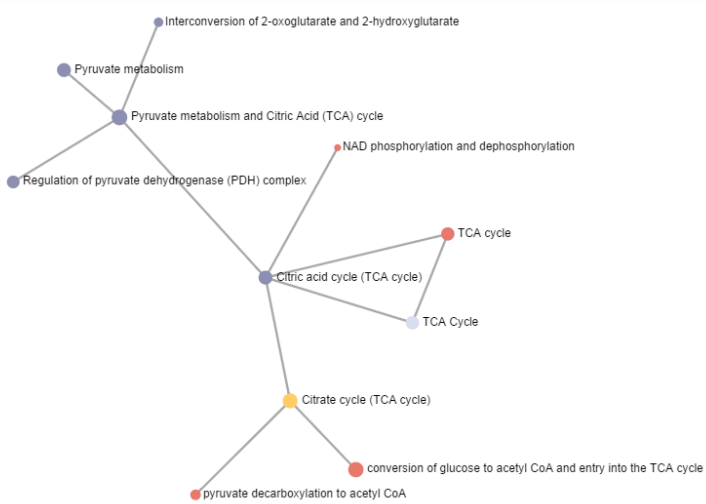

Figure S5. SuperPaths representation in GeneCards and PathCards.
(A) SuperPath representation in GeneCards for the SDHC gene. All the gene's SuperPaths are shown (left), each with its constituent source-specific individual pathways (right), affording an effective overview.
(B) SuperPath network representation in PathCards. The TCA cycle SuperPath is shown with 11 pathways from 4 sources, with connecting edges as defined in Fig. 3B.

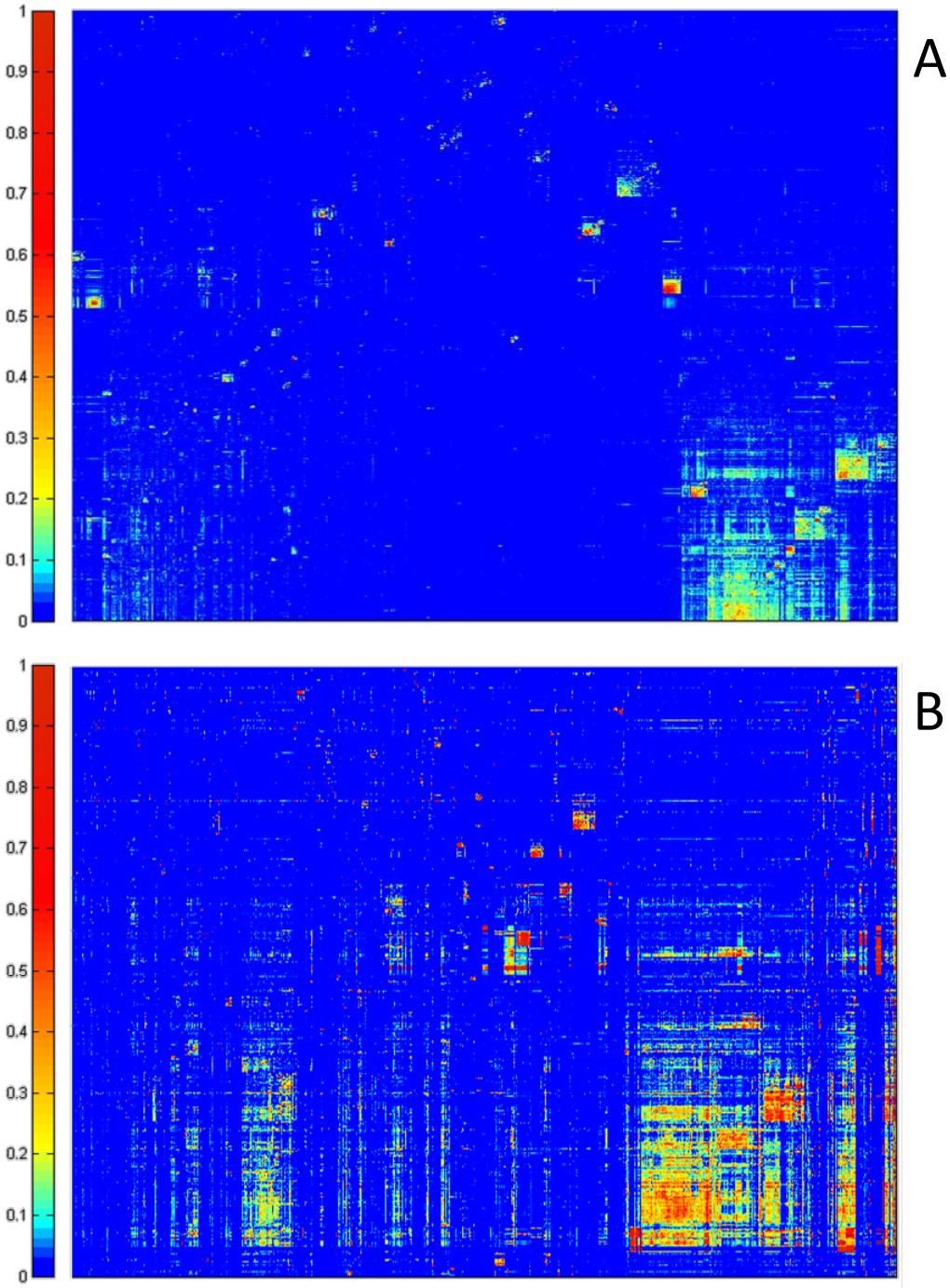

Figure S6. Pathway similarity. **(A)** All pairwise Jaccard incdex similarity clustered using the clustergram function **(B)** All pairwise percent similarity to the smaller pathway, clustered using the clustergram function.

Table S1. Pathway alignment significance vs. Jaccard similarity coeeficient

	Pathway1 (query in MetaPathwayHunter)	Pathway2	Jaccard coefficient	ALN P	# of ALN for query where P<0.01
1	yeast_de_novo_purine_nuc_biosynth (1)	yeast_super_histidine_purine_pyrimidine_biosynth	0.486486	<0.01	1
2	yeast_phenylalanine_tyrosine_tryptophan_biosynth (2)	yeast_chorismate_pathway (5)	0.533333	<0.01	1
3	yeast_folic_acid_biosynth (3)	yeast_chorismate_pathway (5)	0.387097	<0.01	1
4	yeast_super_phenylalanine_tyrosine_tryptophane_biosynth (4)	yeast_chorismate_pathway (5)	0.3	<0.01	2
5	yeast_super_phenylalanine_tyrosine_tryptophane_biosynth (4)	yeast_phenylalanine_tyrosine_tryptophan_biosynth	0.5625	<0.01	2
6	yeast_tryptophan_biosynth (6)	yeast_phenylalanine_tyrosine_tryptophan_biosynth	0.3125	<0.01	3
7	yeast_mevalonate_pathway (7)	yeast_ergosterol_biosynth	0.466667	<0.01	1
8	yeast_glycolysis (8)	yeast_glucose_fermentation	0.5	<0.01	1
9	yeast_aerobic_glycerol_catabolism (9)	yeast_glucose_fermentation	0.333333	<0.01	1
10	yeast_phosphatidic_biosynth (10)	yeast_phosphatidic_acid_phospholipid_biosynth	0.615385	<0.01	1
11	yeast_sulfate_assimilation_pathway2 (11)	yeast_sulfur_amino_acid_biosynth	0.454545	<0.01	2
12	yeast_ubiquinone_Q_prenylation (12)	yeast_ubiquinone_biosynth	0.555556	<0.01	1
13	yeast_hexaprenyl_diphosphate_biosynth (13)	yeast_ubiquinone_biosynth	0.444444	<0.01	2
14	yeast_deoxyribose_phosphate_metabolism (14)	yeast_ribose_deoxyribose_phosphate_metabolism	0.75	<0.01	1
15	yeast_ribose_catabolism (15)	yeast_ribose_deoxyribose_phosphate_metabolism	0.375	<0.01	4
16	yeast_tryptophan_biosynth (6)	yeast_super_phenylalanine_tyrosine_tryptophane_biosynth	0.555556	<0.01	3
17	yeast_super_phenylalanine_tyrosine_biosynth (16)	yeast_super_phenylalanine_tyrosine_tryptophane_biosynth	0.444444	<0.01	3
18	yeast_tyrosine_biosynth (17)	yeast_super_phenylalanine_tyrosine_tryptophane_biosynth	0.333333	<0.01	4
19	yeast_glycolysis (8)	yeast_aerobic_glycerol_catabolism	0.5	-	1
20	yeast_glutamate_degradation8 (18)	yeast_arginine_metabolism	0.625	<0.01	1
21	yeast_fatty_acid_elongation (19)	yeast_fatty_acid_biosynth	0.375	<0.01	1
22	yeast_salvage_pyrimidine_deoxyribonuc_pathway (20)	yeast_salvage_pyrimidine_ribonuc_pathway	0.3	<0.01	1
23	yeast_super_isoleucine_valine_biosynth2 (21)	yeast_super_leucine_isoleucine_valine_biosynth1	0.571429	<0.01	5
24	yeast_leucine_biosynth (22)	yeast_super_leucine_isoleucine_valine_biosynth1	0.571429	<0.01	2
25	yeast_valine_biosynth (23)	yeast_super_leucine_isoleucine_valine_biosynth1	0.571429	<0.01	5
26	yeast_isoleucine_biosynth (24)	yeast_super_leucine_isoleucine_valine_biosynth1	0.5	<0.01	3
27	yeast_super_isoleucine_valine_biosynth1 (25)	yeast_super_leucine_isoleucine_valine_biosynth1	0.5	<0.01	3
28	yeast_super_leucine_isoleucine_valine_biosynth2 (26)	yeast_super_leucine_isoleucine_valine_biosynth1	0.333333	<0.01	3
29	yeast_methionine_biosynth (27)	yeast_threonine_methionine_biosynth	0.75	<0.01	3
30	yeast_threonine_biosynth (28)	yeast_threonine_methionine_biosynth	0.625	<0.01	2

1) yeast_de_novo_purine_nuc_biosynth

Match results

Text File Name	Match Score	P-Value
yeast_de_novo_purine_nuc_biosynth.grp	0.0	0.0
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-55.3076	0.0
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-55.3076	0.0
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-57.0441	0.0
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-58.2822	0.0
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-61.3076	0.0

Click on a column name to sort table. Click on a row to view match.

2) yeast_phenylalanine_tyrosine_tryptophan_biosynth

Match results

Text File Name	Match Score	P-Value
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	0.0	0.0
yeast_chorismate_pathway.grp	0.0	0.0
yeast_chorismate_pathway.grp	-46.851	0.0
yeast_chorismate_pathway.grp	-81.7949	0.0
yeast_chorismate_pathway.grp	-83.7949	0.0
yeast_chorismate_pathway.grp	-115.568	0.05
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-133.677	0.92
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-133.677	0.92
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-134.021	0.97
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-135.011	0.97
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-136.473	1.0

Click on a column name to sort table. Click on a row to view match.

3) yeast_folic_acid_biosynth

Match results

Text File Name	Match Score	P-Value
yeast_folic_acid_biosynth.grp	0.0	0.0
yeast_chorismate_pathway.grp	-29.0899	0.0
yeast_chorismate_pathway.grp	-29.9647	0.0
yeast_chorismate_pathway.grp	-31.9647	0.0
yeast_chorismate_pathway.grp	-33.9647	0.0
yeast_chorismate_pathway.grp	-35.9647	0.0
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-96.4068	0.02
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-97.2834	0.02
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-98.4068	0.03
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-99.2834	0.05
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-100.84	0.06

Click on a column name to sort table. Click on a row to view match.

4) yeast_super_phenylalalnin_tyrosine_tryptophane_biosynth

Match results

Text File Name	Match Score	P-Value
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	0.0	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-7.76519	0.0
yeast_chorismate_pathway.grp	-7.76519	0.0
yeast_chorismate_pathway.grp	-24.1995	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-25.4135	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-25.4135	0.0
yeast_chorismate_pathway.grp	-25.4135	0.0
yeast_chorismate_pathway.grp	-25.4135	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-27.4135	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-27.4135	0.0
yeast_chorismate_pathway.grp	-27.4135	0.0
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-69.4023	0.34
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-71.4023	0.55
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-71.4666	0.56
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-72.0729	0.63
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-72.3647	0.7
yeast_de_novo_purine_nuc_biosynth.grp	-75.2948	0.9
yeast_de_novo_purine_nuc_biosynth.grp	-77.2948	0.95
yeast_de_novo_purine_nuc_biosynth.grp	-79.2948	1.0
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-79.6956	1.0
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-79.6956	1.0
yeast_folic_acid_biosynth.grp	-79.7197	1.0
yeast_folic_acid_biosynth.grp	-79.7197	1.0
yeast_de_novo_purine_nuc_biosynth.grp	-80.4193	1.0
yeast_de_novo_purine_nuc_biosynth.grp	-80.4817	1.0
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-80.9337	1.0
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-80.9337	1.0
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-80.9337	1.0
yeast_folic_acid_biosynth.grp	-81.7197	1.0
yeast_folic_acid_biosynth.grp	-81.7197	1.0
yeast_folic_acid_biosynth.grp	-83.7197	1.0

Click on a column name to sort table. Click on a row to view match.

5) yeast_chorismate_biosynth

Match results

Text File Name	Match Score	P-Value
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	0.0	0.0
yeast_chorismate_pathway.grp	0.0	0.0
yeast_chorismate_biosynth.grp	0.0	0.0
yeast_chorismate_pathway.grp	-37.6758	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-39.2454	0.0
yeast_chorismate_pathway.grp	-39.2454	0.0
yeast_chorismate_pathway.grp	-39.4951	0.01
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-40.1278	0.01
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-41.9471	0.02
yeast_chorismate_pathway.grp	-42.1304	0.04
yeast_chorismate_biosynth.grp	-44.3991	0.14
yeast_glucose_fermentation.grp	-45.438	0.24
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-45.893	0.29
yeast_heme_biosynth.grp	-46.4579	0.33
yeast_sulfur_amino_acid_biosynth.grp	-46.7048	0.36
yeast_serine_isocitrate_lyase_pathway.grp	-46.8299	0.37
yeast_glucose_fermentation.grp	-47.438	0.4
yeast_TCA_cycle_aerobic_respiration.grp	-47.4789	0.4
yeast_serine_isocitrate_lyase_pathway.grp	-47.5192	0.4
yeast_serine_isocitrate_lyase_pathway.grp	-47.7123	0.43
yeast_serine_isocitrate_lyase_pathway.grp	-48.1215	0.46
yeast_heme_biosynth.grp	-48.4579	0.47
yeast_glycolysis.grp	-48.7262	0.5
yeast_glucose_fermentation.grp	-48.7262	0.5
yeast_TCA_cycle_aerobic_respiration.grp	-48.7434	0.5
yeast_serine_isocitrate_lyase_pathway.grp	-48.8834	0.53
yeast_glucose_fermentation.grp	-49.1095	0.57
yeast_de_novo_purine_nuc_biosynth.grp	-49.2819	0.57
yeast_ergosterol_biosynth.grp	-49.3758	0.59
yeast_glucose_fermentation.grp	-49.438	0.59
yeast_ubiquinone_biosynth.grp	-49.5833	0.59
yeast_ergosterol_biosynth.grp	-49.5833	0.59
yeast_ergosterol_biosynth.grp	-49.9389	0.61
yeast_p_cymene_degradation.grp	-49.9814	0.63
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-50.1402	0.66
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-50.1642	0.67
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-50.1642	0.67
yeast_ergosterol_biosynth.grp	-50.2318	0.69
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-50.4795	0.7
yeast_folic_acid_biosynth.grp	-50.6838	0.72
yeast_ubiquinone_biosynth.grp	-50.7348	0.74
yeast_ergosterol_biosynth.grp	-50.7348	0.74
yeast_aerobic_glycerol_catabolism.grp	-51.1782	0.77
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-51.1852	0.77
yeast_de_novo_purine_nuc_biosynth.grp	-51.1852	0.77
yeast_de_novo_purine_nuc_biosynth.grp	-51.1852	0.77
yeast_de_novo_purine_nuc_biosynth.grp	-51.1852	0.77
yeast_phosphatidic_biosynth.grp	-51.2406	0.78
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-51.2406	0.78
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-51.2406	0.78
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-51.2406	0.78
yeast_de_novo_purine_nuc_biosynth.grp	-51.2819	0.8
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-51.3619	0.81
yeast_p_cymene_degradation.grp	-51.3619	0.81
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-51.3782	0.81
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-51.3782	0.81

Click on a column name to sort table. Click on a row to view match.

6) yeast_tryptophan_biosynth

Match results

Text File Name	Match Score	P-Value
yeast_tryptophan_biosynth.grp	0.0	0.0
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	0.0	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	0.0	0.0
yeast_chorismate_pathway.grp	0.0	0.0
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-2.0	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-2.0	0.0
yeast_chorismate_pathway.grp	-2.0	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-4.0	0.0
yeast_chorismate_pathway.grp	-4.0	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-6.0	0.0
yeast_chorismate_pathway.grp	-6.0	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-8.0	0.0
yeast_chorismate_pathway.grp	-8.0	0.0
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-17.9824	0.0
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-27.4582	0.04
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-27.828	0.04
yeast_tryptophan_biosynth.grp	-27.9647	0.04
yeast_serine_isocitrate_lyase_pathway.grp	-28.1663	0.05
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-28.7184	0.07
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-28.855	0.07
yeast_hestidine_biosynth.grp	-28.855	0.07
yeast_serine_isocitrate_lyase_pathway.grp	-30.1663	0.17
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-30.8343	0.24
yeast_deoxyribose_phosphate_metabolism.grp	-30.8343	0.24
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-30.855	0.24
yeast_hestidine_biosynth.grp	-30.855	0.24
yeast_heme_biosynth.grp	-31.0411	0.28
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-31.6006	0.34
yeast_serine_isocitrate_lyase_pathway.grp	-31.7506	0.35
yeast_p_cymene_degradation.grp	-31.8726	0.35
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-31.9519	0.38
yeast_deoxyribose_phosphate_metabolism.grp	-31.9519	0.38
yeast_serine_isocitrate_lyase_pathway.grp	-31.9651	0.38
yeast_serine_isocitrate_lyase_pathway.grp	-32.1663	0.41
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-32.2069	0.41
yeast_hestidine_biosynth.grp	-32.2069	0.41
yeast_glucose_fermentation.grp	-32.4162	0.45
yeast_folic_acid_biosynth.grp	-32.4247	0.46
yeast_mevalonate_pathway.grp	-32.6346	0.48
yeast_ergosterol_biosynth.grp	-32.6346	0.48
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-32.855	0.51
yeast_glycolysis.grp	-32.8682	0.51
yeast_heme_biosynth.grp	-33.0411	0.56
yeast_de_novo_pyrimidine_ribonuc_biosynth.grp	-33.1452	0.56
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-33.2863	0.57
yeast_super_leucine_isoleucine_valine_biosynth2.grp	-33.3071	0.57
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-33.3202	0.59
yeast_deoxyribose_phosphate_metabolism.grp	-33.3202	0.59
yeast_chorismate_biosynth.grp	-33.6895	0.6
yeast_glucose_fermentation.grp	-33.7506	0.61
yeast_p_cymene_degradation.grp	-33.8726	0.62
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-33.9519	0.62
yeast_deoxyribose_phosphate_metabolism.grp	-33.9519	0.62
yeast_threonine_methionine_biosynth.grp	-34.0229	0.63
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-34.0452	0.64
yeast_mevalonate_pathway.grp	-34.0615	0.65

Click on a column name to sort table. Click on a row to view match.

7) yeast_mevalonate_pathway

Match results

Text File Name	Match Score	P-Value
yeast_mevalonate_pathway.grp	0.0	0.0
yeast_ergosterol_biosynth.grp	0.0	0.0
yeast_ergosterol_biosynth.grp	-38.6098	0.0
yeast_ergosterol_biosynth.grp	-41.3963	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-42.2995	0.02
yeast_chorismate_pathway.grp	-42.2995	0.02
yeast_mevalonate_pathway.grp	-42.6343	0.02
yeast_glycolysis.grp	-43.4268	0.05
yeast_glucose_fermentation.grp	-43.4268	0.05
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-44.2995	0.12
yeast_chorismate_pathway.grp	-44.2995	0.12
yeast_glycolysis.grp	-45.4268	0.22
yeast_glucose_fermentation.grp	-45.4268	0.22
yeast_serine_isocitrate_lyase_pathway.grp	-46.5481	0.36
yeast_glucose_fermentation.grp	-46.5818	0.36
yeast_glycolysis.grp	-46.6058	0.36
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-46.6758	0.36
yeast_chorismate_pathway.grp	-46.6758	0.36
yeast_ergosterol_biosynth.grp	-46.827	0.41
yeast_chorismate_pathway.grp	-47.0314	0.45
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-47.1278	0.46
yeast_chorismate_pathway.grp	-47.1278	0.46
yeast_phosphatidic_biosynth.grp	-47.2166	0.49
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-47.2166	0.49
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-47.2166	0.49
yeast_ergosterol_biosynth.grp	-47.2785	0.5
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-47.3025	0.5
yeast_glucose_fermentation.grp	-47.4268	0.51
yeast_glucose_fermentation.grp	-47.8198	0.59
yeast_glycolysis.grp	-47.8438	0.59
yeast_glycolysis.grp	-47.9063	0.59
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-47.9196	0.6
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-47.9298	0.6
yeast_serine_isocitrate_lyase_pathway.grp	-47.9447	0.6
yeast_serine_isocitrate_lyase_pathway.grp	-48.2064	0.63
yeast_serine_isocitrate_lyase_pathway.grp	-48.3069	0.63
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-48.3644	0.64
yeast_de_novo_purine_nuc_biosynth.grp	-48.3644	0.64
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-48.4546	0.64
yeast_serine_isocitrate_lyase_pathway.grp	-48.5481	0.65
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-49.1202	0.67
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-49.1202	0.67
yeast_folic_acid_biosynth.grp	-49.1202	0.67
yeast_pantothenate_coenzymeA_biosynth.grp	-49.1553	0.67
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-49.2303	0.67
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-49.2642	0.67
yeast_de_novo_purine_nuc_biosynth.grp	-49.6024	0.69
yeast_pantothenate_coenzymeA_biosynth.grp	-49.7074	0.71
yeast_pantothenate_coenzymeA_biosynth.grp	-49.7074	0.71
yeast_pantothenate_coenzymeA_biosynth.grp	-49.7483	0.71
yeast_fatty_acid_biosynth.grp	-49.9471	0.72
yeast_de_novo_purine_nuc_biosynth.grp	-49.9471	0.72
yeast_folic_acid_biosynth.grp	-50.0026	0.72
yeast_TCA_cycle_aerobic_respiration.grp	-50.3103	0.74
yeast_de_novo_purine_nuc_biosynth.grp	-50.3644	0.74

Click on a column name to sort table. Click on a row to view match.

8) yeast_glycolysis

Match results

Text File Name	Match Score	P-Value
yeast_glycolysis.grp	0.0	0.0
yeast_glucose_fermentation.grp	-3.49651	0.0
yeast_glucose_fermentation.grp	-5.49651	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-57.6027	0.13
yeast_chorismate_pathway.grp	-57.6027	0.13
yeast_ergosterol_biosynth.grp	-58.6231	0.15
yeast_chorismate_pathway.grp	-59.3068	0.21
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-59.6027	0.25
yeast_chorismate_pathway.grp	-59.6027	0.25
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-60.1855	0.28
yeast_chorismate_pathway.grp	-60.1855	0.28
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-60.1879	0.28
yeast_chorismate_pathway.grp	-60.1879	0.28
yeast_ergosterol_biosynth.grp	-61.6513	0.46
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-62.1855	0.52
yeast_ergosterol_biosynth.grp	-63.0004	0.58
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-63.7403	0.63
yeast_ergosterol_biosynth.grp	-65.0004	0.66
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-65.6538	0.7
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-65.7403	0.7
yeast_pantothenate_coenzymeA_biosynth.grp	-66.3234	0.72
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-66.8865	0.75
yeast_ergosterol_biosynth.grp	-67.0004	0.76
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-67.0712	0.78
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-67.1826	0.78
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-67.6538	0.82
yeast_de_novo_purine_nuc_biosynth.grp	-68.8265	0.83
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-68.8889	0.85
yeast_de_novo_purine_nuc_biosynth.grp	-69.6125	0.9
yeast_de_novo_purine_nuc_biosynth.grp	-70.0645	0.9
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-70.1269	0.9
yeast_folic_acid_biosynth.grp	-70.2645	0.9
yeast_folic_acid_biosynth.grp	-70.2645	0.9
yeast_de_novo_purine_nuc_biosynth.grp	-70.8265	0.93
yeast_de_novo_purine_nuc_biosynth.grp	-70.913	0.93
yeast_ubiquinone_biosynth.grp	-71.4785	0.95
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-71.4785	0.95
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-71.4785	0.95
yeast_folic_acid_biosynth.grp	-72.2645	0.97
yeast_ubiquinone_biosynth.grp	-73.4785	0.99
yeast_folic_acid_biosynth.grp	-73.9545	0.99
yeast_folic_acid_biosynth.grp	-73.9545	0.99

Click on a column name to sort table. Click on a row to view match.

9) yeast_aerobic_glycerol_catabolism

Match results

Text File Name	Match Score	P-Value
yeast_aerobic_glycerol_catabolism.grp	0.0	0.0
yeast_glucose_fermentation.grp	-32.8687	0.0
yeast_glucose_fermentation.grp	-57.6238	0.08
yeast_glucose_fermentation.grp	-57.6421	0.08
yeast_glucose_fermentation.grp	-59.6238	0.13
yeast_glucose_fermentation.grp	-60.8643	0.18
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-61.4097	0.2
yeast_chorismate_pathway.grp	-61.4097	0.2
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-61.7033	0.2
yeast_chorismate_pathway.grp	-61.7033	0.2
yeast_chorismate_pathway.grp	-63.0479	0.33
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-63.4097	0.41
yeast_chorismate_pathway.grp	-63.4097	0.41
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-63.7033	0.41
yeast_chorismate_pathway.grp	-63.7033	0.41
yeast_ergosterol_biosynth.grp	-63.8808	0.42
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-63.8822	0.42
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-63.9638	0.44
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-64.3484	0.47
yeast_serine_isocitrate_lyase_pathway.grp	-64.4969	0.49
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-64.5023	0.5
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-64.5332	0.5
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-64.8432	0.53
yeast_p_cymene_degradation.grp	-65.2262	0.63
yeast_ergosterol_biosynth.grp	-65.2299	0.63
yeast_serine_isocitrate_lyase_pathway.grp	-65.7373	0.64
yeast_serine_isocitrate_lyase_pathway.grp	-65.7373	0.64
yeast_aerobic_glycerol_catabolism.grp	-65.7373	0.64
yeast_serine_isocitrate_lyase_pathway.grp	-65.841	0.64
yeast_TCA_cycle_aerobic_respiration.grp	-66.0636	0.66
yeast_ergosterol_biosynth.grp	-66.3931	0.73
yeast_ergosterol_biosynth.grp	-66.4369	0.74
yeast_ergosterol_biosynth.grp	-66.4703	0.75
yeast_serine_isocitrate_lyase_pathway.grp	-66.4993	0.76
yeast_TCA_cycle_aerobic_respiration.grp	-66.5266	0.76
yeast_pantothenate_coenzymeA_biosynth.grp	-66.7686	0.76
yeast_de_novo_purine_nuc_biosynth.grp	-66.83	0.77
yeast_de_novo_purine_nuc_biosynth.grp	-66.9675	0.78
yeast_hestidine_biosynth.grp	-67.1021	0.8
yeast_p_cymene_degradation.grp	-67.2262	0.8
yeast_TCA_cycle_aerobic_respiration.grp	-67.2928	0.81
yeast_de_novo_purine_nuc_biosynth.grp	-67.475	0.82
yeast_phosphatidic_biosynth.grp	-67.5374	0.82
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-67.5374	0.82
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-67.5374	0.82
yeast_TCA_cycle_aerobic_respiration.grp	-67.6032	0.82
yeast_de_novo_purine_nuc_biosynth.grp	-67.6125	0.82
yeast_ubiquinone_biosynth.grp	-67.6395	0.82
yeast_hestidine_biosynth.grp	-67.8641	0.84
yeast_hestidine_biosynth.grp	-68.7819	0.88
yeast_de_novo_purine_nuc_biosynth.grp	-68.8265	0.89
yeast_p_cymene_degradation.grp	-68.9016	0.91
yeast_folic_acid_biosynth.grp	-68.9641	0.91
yeast_folic_acid_biosynth.grp	-68.9641	0.91

Click on a column name to sort table. Click on a row to view match.

10) yeast_phosphatidic_biosynth

Match results

Text File Name	Match Score	P-Value
yeast_phosphatidic_biosynth.grp	0.0	0.0
yeast_phosphatidic_acid_phospholipid_biosynth.grp	0.0	0.0
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-2.0	0.0
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-4.0	0.0
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-18.3744	0.0
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-20.3744	0.0
yeast_ergosterol_biosynth.grp	-59.9369	0.09
yeast_phosphatidic_biosynth.grp	-60.7853	0.15
yeast_ubiquinone_biosynth.grp	-62.4656	0.27
yeast_glucose_fermentation.grp	-62.965	0.29
yeast_ergosterol_biosynth.grp	-63.878	0.42
yeast_chorismate_pathway.grp	-64.0073	0.45
yeast_chorismate_pathway.grp	-64.2669	0.5
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-64.3954	0.51
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-64.3954	0.51
yeast_de_novo_purine_nuc_biosynth.grp	-64.4004	0.51
yeast_de_novo_purine_nuc_biosynth.grp	-64.45	0.53
yeast_ubiquinone_biosynth.grp	-64.4656	0.53
yeast_glucose_fermentation.grp	-65.0854	0.57
yeast_chorismate_pathway.grp	-65.1493	0.58
yeast_lipid_linked_oligosaccharide_biosynth.grp	-65.2884	0.6
yeast_lipid_linked_oligosaccharide_biosynth.grp	-65.2884	0.6
yeast_lipid_linked_oligosaccharide_biosynth.grp	-65.2884	0.6
yeast_lipid_linked_oligosaccharide_biosynth.grp	-65.2884	0.6
yeast_lipid_linked_oligosaccharide_biosynth.grp	-65.2884	0.6
yeast_chorismate_pathway.grp	-65.5049	0.6
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-65.5546	0.6
yeast_folic_acid_biosynth.grp	-65.5546	0.6
yeast_chorismate_pathway.grp	-65.5546	0.6
yeast_de_novo_purine_nuc_biosynth.grp	-65.6334	0.63
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-65.7469	0.65
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-65.7469	0.65
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-65.8108	0.68
yeast_ergosterol_biosynth.grp	-65.878	0.68
yeast_serine_isocitrate_lyase_pathway.grp	-66.2405	0.72
yeast_hestidine_biosynth.grp	-66.2574	0.73
yeast_ergosterol_biosynth.grp	-66.2994	0.75
yeast_ergosterol_biosynth.grp	-66.3825	0.75
yeast_de_novo_purine_nuc_biosynth.grp	-66.4004	0.75
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-66.4369	0.78
yeast_de_novo_purine_nuc_biosynth.grp	-66.4369	0.78
yeast_glucose_fermentation.grp	-66.4959	0.79
yeast_hestidine_biosynth.grp	-66.5008	0.79
yeast_ubiquinone_biosynth.grp	-66.5264	0.79
yeast_folic_acid_biosynth.grp	-66.9353	0.8
yeast_glucose_fermentation.grp	-67.0854	0.82
yeast_ubiquinone_biosynth.grp	-67.2884	0.82
yeast_aerobic_glycerol_catabolism.grp	-67.5374	0.84
yeast_serine_isocitrate_lyase_pathway.grp	-67.675	0.86
yeast_glucose_fermentation.grp	-67.675	0.86
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-67.7885	0.86
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-68.4369	0.91
yeast_pantothenate_coenzymeA_biosynth.grp	-68.7754	0.92
yeast_serine_isocitrate_lyase_pathway.grp	-68.8301	0.92
yeast_folic_acid_biosynth.grp	-68.8393	0.92
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-68.8889	0.92

Click on a column name to sort table. Click on a row to view match.

11) yeast_sulfate_assimilation_pathway2

Match results

Text File Name	Match Score	P-Value
yeast_sulfur_amino_acid_biosynth.grp	0.0	0.0
yeast_sulfate_assimilation_pathway2.grp	0.0	0.0
yeast_sulfur_degradation.grp	-19.9897	0.0
yeast_threonine_methionine_biosynth.grp	-28.3278	0.08
yeast_sulfur_amino_acid_biosynth.grp	-28.6916	0.1
yeast_threonine_methionine_biosynth.grp	-28.9787	0.13
yeast_methionine_biosynth.grp	-28.9787	0.13
yeast_sulfur_amino_acid_biosynth.grp	-29.5452	0.16
yeast_threonine_biosynth.grp	-30.0773	0.18
yeast_sulfur_amino_acid_biosynth.grp	-30.3926	0.22
yeast_sulfur_amino_acid_biosynth.grp	-30.3926	0.22
yeast_sulfur_degradation.grp	-31.7622	0.33
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-32.855	0.44
yeast_chorismate_pathway.grp	-32.855	0.44
yeast_chorismate_biosynth.grp	-32.855	0.44
yeast_sulfate_assimilation_pathway2.grp	-32.8687	0.44
yeast_de_novo_NAD_biosynth.grp	-33.0728	0.46
yeast_threonine_methionine_biosynth.grp	-33.4288	0.51
yeast_TCA_cycle_aerobic_respiration.grp	-33.8739	0.56
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-33.8853	0.56
yeast_chorismate_pathway.grp	-33.8853	0.56
yeast_mevalonate_pathway.grp	-33.9554	0.57
yeast_ergosterol_biosynth.grp	-33.9554	0.57
yeast_phosphatidic_biosynth.grp	-34.3222	0.59
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-34.3222	0.59
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-34.6063	0.62
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-34.6063	0.62
yeast_de_novo_purine_nuc_biosynth.grp	-34.6063	0.62
yeast_de_novo_purine_nuc_biosynth.grp	-34.6063	0.62
yeast_mevalonate_pathway.grp	-34.7439	0.64
yeast_ergosterol_biosynth.grp	-34.7439	0.64
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-34.8039	0.68
yeast_threonine_catabolism.grp	-34.8063	0.68
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-34.8063	0.68
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-34.855	0.69
yeast_chorismate_pathway.grp	-34.855	0.69
yeast_chorismate_biosynth.grp	-34.855	0.69
yeast_de_novo_NAD_biosynth.grp	-35.0728	0.71
yeast_TCA_cycle_aerobic_respiration.grp	-35.1744	0.71
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-35.1744	0.71
yeast_glutamate_degradation7.grp	-35.1744	0.71
yeast_fatty_acid_biosynth.grp	-35.1744	0.71
yeast_chorismate_pathway.grp	-35.1744	0.71
yeast_chorismate_biosynth.grp	-35.1744	0.71
yeast_threonine_methionine_biosynth.grp	-35.2445	0.71
yeast_threonine_biosynth.grp	-35.2445	0.71
yeast_salvage_pyrimidine_ribonuc_pathway.grp	-35.2559	0.72
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-35.2559	0.72
yeast_serine_isocitrate_lyase_pathway.grp	-35.3934	0.73
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-35.3934	0.73
yeast_chorismate_pathway.grp	-35.3934	0.73
yeast_phosphatidic_biosynth.grp	-35.4548	0.73
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-35.4548	0.73
yeast_glycolysis.grp	-35.8229	0.77
yeast_glucose_fermentation.grp	-35.8229	0.77
yeast_TCA_cycle_aerobic_respiration.grp	-35.8739	0.77

Click on a column name to sort table. Click on a row to view match.

12) yeast_ubiquinone_Q_prenylation

Match results

Text File Name	Match Score	P-Value
yeast_ubiquinone_Q_prenylation.grp	0.0	0.0
yeast_ubiquinone_biosynth.grp	0.0	0.0
yeast_ubiquinone_biosynth.grp	-2.0	0.0
yeast_ubiquinone_biosynth.grp	-4.0	0.0
yeast_ubiquinone_biosynth.grp	-6.0	0.0
yeast_ubiquinone_biosynth.grp	-8.0	0.0
yeast_ergosterol_biosynth.grp	-38.1796	0.31
yeast_carbon_monoxide_dehydrogenase.grp	-38.5474	0.32
yeast_sulfur_amino_acid_biosynth.grp	-39.2492	0.41
yeast_ergosterol_biosynth.grp	-40.1796	0.46
yeast_phosphatidic_biosynth.grp	-40.2901	0.46
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-40.2901	0.46
yeast_carbon_monoxide_dehydrogenase.grp	-40.5474	0.47
yeast_arginine_metabolism.grp	-41.1465	0.5
yeast_sulfur_amino_acid_biosynth.grp	-41.2492	0.5
yeast_ergosterol_biosynth.grp	-41.6788	0.53
yeast_methionine_degradation.grp	-41.7877	0.53
yeast_ergosterol_biosynth.grp	-42.1796	0.56
yeast_threonine_methionine_biosynth.grp	-42.2581	0.57
yeast_threonine_methionine_biosynth.grp	-42.2581	0.57
yeast_sulfur_amino_acid_biosynth.grp	-42.2581	0.57
yeast_methionine_biosynth.grp	-42.2581	0.57
yeast_phosphatidic_biosynth.grp	-42.2901	0.58
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-42.2901	0.58
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-42.2901	0.58
yeast_phosphatidic_biosynth.grp	-42.3205	0.58
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-42.3205	0.58
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-42.3205	0.58
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-42.3845	0.58
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-42.3845	0.58
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-42.3845	0.58
yeast_arginine_metabolism.grp	-42.3845	0.58
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-42.4805	0.59
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-42.4805	0.59
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-42.5177	0.59
yeast_ergosterol_biosynth.grp	-42.5177	0.59
yeast_chorismate_pathway.grp	-42.5177	0.59
yeast_chorismate_biosynth.grp	-42.5177	0.59
yeast_de_novo_pyrimidine_deoxynuc_biosynth.grp	-43.0201	0.68
yeast_chorismate_pathway.grp	-43.3757	0.7
yeast_carbon_monoxide_dehydrogenase.grp	-43.4961	0.7
yeast_phosphatidic_biosynth.grp	-43.5586	0.72
yeast_phosphatidic_biosynth.grp	-43.5586	0.72
yeast_folic_acid_biosynth.grp	-43.6225	0.72
yeast_folic_acid_biosynth.grp	-43.6225	0.72
yeast_chorismate_pathway.grp	-43.6225	0.72
yeast_de_novo_purine_nuc_biosynth.grp	-43.685	0.73
yeast_folic_acid_biosynth.grp	-43.7557	0.73
yeast_chorismate_pathway.grp	-43.7557	0.73
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-43.8181	0.74
yeast_folic_acid_biosynth.grp	-43.8181	0.74
yeast_chorismate_pathway.grp	-43.8181	0.74
yeast_p_cymene_degradation.grp	-43.8797	0.74
yeast_p_cymene_degradation.grp	-43.8797	0.74
yeast_de_novo_NAD_biosynth.grp	-44.2173	0.75

Click on a column name to sort table. Click on a row to view match.

13) yeast_hexaprenyl_diphosphate_biosynth

Match results

Text File Name	Match Score	P-Value
yeast_ubiquinone_biosynth.grp	0.0	0.0
yeast_hexaprenyl_diphosphate_biosynth.grp	0.0	0.0
yeast_ubiquinone_biosynth.grp	-11.9109	0.0
yeast_ubiquinone_biosynth.grp	-11.9109	0.0
yeast_ubiquinone_biosynth.grp	-13.9109	0.0
yeast_ergosterol_biosynth.grp	-15.1963	0.0
yeast_hexaprenyl_diphosphate_biosynth.grp	-15.8812	0.0
yeast_ergosterol_biosynth.grp	-17.1963	0.0
yeast_ubiquinone_biosynth.grp	-18.89	0.0
yeast_ergosterol_biosynth.grp	-19.1666	0.0
yeast_ergosterol_biosynth.grp	-19.1963	0.01
yeast_ergosterol_biosynth.grp	-19.9286	0.01
yeast_ubiquinone_Q_prenylation.grp	-22.1755	0.04
yeast_thiamine_biosynth.grp	-24.9077	0.21
yeast_thiamine_biosynth.grp	-24.9077	0.21
yeast_thiamine_biosynth.grp	-24.9077	0.21
yeast_thiamine_biosynth.grp	-24.9077	0.21
yeast_ubiquinone_Q_prenylation.grp	-26.1458	0.26
yeast_riboflavin_FMN_FAD_biosynth.grp	-26.1458	0.26
yeast_riboflavin_FMN_FAD_biosynth.grp	-26.1458	0.26
yeast_chorismate_pathway.grp	-26.3749	0.39
yeast_chorismate_pathway.grp	-26.3749	0.39
yeast_chorismate_pathway.grp	-27.1369	0.4
yeast_chorismate_pathway.grp	-27.1369	0.4
yeast_sulfur_amino_acid_biosynth.grp	-27.3838	0.4
yeast_sulfur_amino_acid_biosynth.grp	-27.3838	0.4
yeast_sulfur_amino_acid_biosynth.grp	-27.3838	0.4
yeast_sulfur_amino_acid_biosynth.grp	-27.3838	0.4
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-27.3838	0.4
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-27.3838	0.4
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-27.3838	0.4
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-27.3838	0.4
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-27.3838	0.4
yeast_methionine_degradation.grp	-27.3838	0.4
yeast_methionine_degradation.grp	-27.3838	0.4
yeast_folic_acid_biosynth.grp	-27.3838	0.4
yeast_folic_acid_biosynth.grp	-27.3838	0.4
yeast_folic_acid_biosynth.grp	-27.3838	0.4
yeast_folic_acid_biosynth.grp	-27.3838	0.4
yeast_folic_acid_biosynth.grp	-27.3838	0.4
yeast_chorismate_pathway.grp	-27.3838	0.4
yeast_chorismate_biosynth.grp	-27.3838	0.4
yeast_chorismate_biosynth.grp	-27.3838	0.4
yeast_chorismate_biosynth.grp	-27.3838	0.4
yeast_chorismate_biosynth.grp	-27.3838	0.4
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-27.9166	0.49
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-27.9166	0.49
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-27.9166	0.49
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-27.9166	0.49
yeast_lipid_linked_oligosaccharide_biosynth.grp	-27.9166	0.49
yeast_lipid_linked_oligosaccharide_biosynth.grp	-27.9166	0.49
yeast_lipid_linked_oligosaccharide_biosynth.grp	-27.9166	0.49
yeast_lipid_linked_oligosaccharide_biosynth.grp	-27.9166	0.49
yeast_lipid_linked_oligosaccharide_biosynth.grp	-27.9166	0.49

Click on a column name to sort table. Click on a row to view match.

14) yeast_deoxyribose_phosphate_metabolism

Match results

Text File Name	Match Score	P-Value
yeast_ribose_deoxyribose_phosphate_metabolism.grp	0.0	0.0
yeast_deoxyribose_phosphate_metabolism.grp	0.0	0.0
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-49.303	0.07
yeast_deoxyribose_phosphate_metabolism.grp	-49.303	0.07
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-50.4466	0.11
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-52.0718	0.14
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-52.6914	0.18
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-53.3628	0.2
yeast_hestidine_biosynth.grp	-53.3628	0.2
yeast_aerobic_glycerol_catabolism.grp	-54.1534	0.26
yeast_glucose_fermentation.grp	-54.6261	0.3
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-54.6914	0.31
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-54.9542	0.38
yeast_chorismate_pathway.grp	-54.9542	0.38
yeast_de_novo_purine_nuc_biosynth.grp	-55.042	0.41
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-55.0528	0.43
yeast_serine_isocitrate_lyase_pathway.grp	-55.2504	0.43
yeast_aerobic_glycerol_catabolism.grp	-55.3915	0.43
yeast_de_novo_purine_nuc_biosynth.grp	-55.6737	0.46
yeast_chorismate_pathway.grp	-55.6737	0.46
yeast_hestidine_biosynth.grp	-55.9691	0.47
yeast_chorismate_pathway.grp	-56.015	0.48
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-56.1475	0.48
yeast_chorismate_pathway.grp	-56.1475	0.48
yeast_aerobic_glycerol_catabolism.grp	-56.1534	0.48
yeast_hestidine_biosynth.grp	-56.2788	0.5
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-56.5479	0.55
yeast_chorismate_pathway.grp	-56.5479	0.55
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-56.7336	0.56
yeast_de_novo_purine_nuc_biosynth.grp	-57.042	0.58
yeast_serine_isocitrate_lyase_pathway.grp	-57.2504	0.6
yeast_glycolysis.grp	-57.3467	0.62
yeast_glucose_fermentation.grp	-57.3467	0.62
yeast_serine_isocitrate_lyase_pathway.grp	-57.3708	0.62
yeast_aerobic_glycerol_catabolism.grp	-57.3915	0.62
yeast_phosphatidic_biosynth.grp	-57.4013	0.62
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-57.4013	0.62
yeast_folic_acid_biosynth.grp	-57.606	0.63
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-57.8822	0.63
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-57.9717	0.64
yeast_serine_isocitrate_lyase_pathway.grp	-58.1328	0.64
yeast_hestidine_biosynth.grp	-58.2788	0.65
yeast_de_novo_purine_nuc_biosynth.grp	-58.4004	0.65
yeast_glycolysis.grp	-58.5847	0.66
yeast_glucose_fermentation.grp	-58.5847	0.66
yeast_ergosterol_biosynth.grp	-58.5995	0.66
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-58.6889	0.67
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-58.6889	0.67
yeast_lipid_linked_oligosaccharide_biosynth.grp	-59.1786	0.73
yeast_lipid_linked_oligosaccharide_biosynth.grp	-59.1786	0.73
yeast_lipid_linked_oligosaccharide_biosynth.grp	-59.1786	0.73
yeast_lipid_linked_oligosaccharide_biosynth.grp	-59.1786	0.73
yeast_lipid_linked_oligosaccharide_biosynth.grp	-59.1786	0.73
yeast_serine_isocitrate_lyase_pathway.grp	-59.2504	0.73
yeast_glucose_fermentation.grp	-59.3467	0.73

Click on a column name to sort table. Click on a row to view match.

15) yeast_ribose_catabolism

Match results

Text File Name	Match Score	P-Value
yeast_ribose_catabolism.grp	0.0	0.0
yeast_pentose_phosphate_pathway.grp	-10.2172	0.0
yeast_non_oxidative_branch_pentose_phosphate_pathw...	-10.2172	0.0
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-13.241	0.0
yeast_deoxyribose_phosphate_metabolism.grp	-13.241	0.0
yeast_pentose_phosphate_pathway.grp	-13.9489	0.01
yeast_non_oxidative_branch_pentose_phosphate_pathw...	-13.9489	0.01
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-13.9583	0.01
yeast_xylulose_monophosphate_cycle.grp	-15.1398	0.01
yeast_super_gluconate_utilization.grp	-15.1963	0.02
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-15.1963	0.02
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-15.241	0.06
yeast_deoxyribose_phosphate_metabolism.grp	-15.241	0.06
yeast_pentose_phosphate_pathway.grp	-15.9489	0.07
yeast_non_oxidative_branch_pentose_phosphate_pathw...	-15.9489	0.07
yeast_glycolysis.grp	-16.2384	0.07
yeast_glucose_fermentation.grp	-16.2384	0.07
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-16.4343	0.07
yeast_pentose_phosphate_pathway.grp	-16.4343	0.07
yeast_deoxyribose_phosphate_metabolism.grp	-16.4343	0.07
yeast_lactose_degradation.grp	-16.9798	0.09
yeast_galactose_metabolism.grp	-16.9798	0.09
yeast_galactose_metabolism.grp	-16.9798	0.09
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-17.0028	0.1
yeast_trehalose_anabolism.grp	-17.6306	0.14
yeast_sucrose_biosynth.grp	-17.6306	0.14
yeast_stratch_cellulose_biosynth.grp	-17.6306	0.14
yeast_mannose_GDP_mannose_degradation.grp	-17.6306	0.14
yeast_lactose_degradation.grp	-17.6306	0.14
yeast_galactose_metabolism.grp	-17.6306	0.14
yeast_colanic_acid_building_blocks_biosynth2.grp	-17.6306	0.14
yeast_sucrose_biosynth.grp	-17.6513	0.17
yeast_mannose_GDP_mannose_degradation.grp	-17.6513	0.17
yeast_pentose_phosphate_pathway.grp	-17.9489	0.17
yeast_serine_isocitrate_lyase_pathway.grp	-18.2178	0.18
yeast_galactose_metabolism.grp	-18.2178	0.18
yeast_glycolysis.grp	-18.2384	0.18
yeast_glucose_fermentation.grp	-18.2384	0.18
yeast_glucose_fermentation.grp	-18.2384	0.18
yeast_aerobic_glycerol_catabolism.grp	-18.2384	0.18
yeast_tryptophan_biosynth.grp	-18.2408	0.18
yeast_super_phenylalanine_tyrosine_tryptophane_biosyn...	-18.2408	0.18
yeast_sucrose_biosynth.grp	-18.2408	0.18
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-18.2408	0.18
yeast_hestidine_biosynth.grp	-18.2408	0.18
yeast_glycolysis.grp	-18.2408	0.18
yeast_glucose_fermentation.grp	-18.2408	0.18
yeast_colanic_acid_building_blocks_biosynth1.grp	-18.2408	0.18
yeast_chorismate_pathway.grp	-18.2408	0.18
yeast_aerobic_glycerol_catabolism.grp	-18.2408	0.18
yeast_aerobic_glycerol_catabolism.grp	-18.2408	0.18
yeast_mevalonate_pathway.grp	-18.3444	0.21
yeast_ergosterol_biosynth.grp	-18.3444	0.21
yeast_deoxyribose_phosphate_metabolism.grp	-18.4343	0.21
yeast_UDP_N_acetylglactosamine_biosynth.grp	-18.8687	0.21
yeast_UDP_N_acetylglactosamine_biosynth.grp	-18.8687	0.21

Click on a column name to sort table. Click on a row to view match.

16) yeast_super_phenylalanine_tyrosine_biosynth

Match results

Text File Name	Match Score	P-Value
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	0.0	0.0
yeast_super_phenylalanine_tyrosine_biosynth.grp	0.0	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	0.0	0.0
yeast_chorismate_pathway.grp	0.0	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-2.0	0.0
yeast_chorismate_pathway.grp	-2.0	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-12.7443	0.0
yeast_chorismate_pathway.grp	-12.7443	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-13.9824	0.0
yeast_chorismate_pathway.grp	-13.9824	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-14.7443	0.0
yeast_chorismate_pathway.grp	-14.7443	0.0
yeast_serine_isocitrate_lyase_pathway.grp	-29.4768	0.14
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-30.1981	0.19
yeast_ergosterol_biosynth.grp	-31.2247	0.25
yeast_serine_isocitrate_lyase_pathway.grp	-31.4768	0.25
yeast_glycolysis.grp	-31.4797	0.25
yeast_glucose_fermentation.grp	-31.4797	0.25
yeast_aerobic_glycerol_catabolism.grp	-31.4797	0.25
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-31.496	0.26
yeast_deoxyribose_phosphate_metabolism.grp	-31.496	0.26
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-31.4985	0.26
yeast_glycolysis.grp	-32.1792	0.34
yeast_glucose_fermentation.grp	-32.1792	0.34
yeast_aerobic_glycerol_catabolism.grp	-32.1792	0.34
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-32.2457	0.35
yeast_hestidine_biosynth.grp	-32.2457	0.35
yeast_UDP_N_acetylglactosamine_biosynth.grp	-32.4835	0.37
yeast_UDP_N_acetylglactosamine_biosynth.grp	-32.4835	0.37
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-32.6135	0.37
yeast_serine_isocitrate_lyase_pathway.grp	-32.7177	0.38
yeast_glycolysis.grp	-32.9412	0.41
yeast_glucose_fermentation.grp	-32.9412	0.41
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.0077	0.41
yeast_hestidine_biosynth.grp	-33.0077	0.41
yeast_ergosterol_biosynth.grp	-33.1028	0.41
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-33.2234	0.42
yeast_ergosterol_biosynth.grp	-33.2247	0.42
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-33.3929	0.42
yeast_super_leucine_isoleucine_valine_biosynth2.grp	-33.439	0.43
yeast_super_isoleucine_valine_biosynth1.grp	-33.439	0.43
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.439	0.43
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.439	0.43
yeast_isoleucine_biosynth.grp	-33.439	0.43
yeast_hestidine_biosynth.grp	-33.439	0.43
yeast_heme_biosynth.grp	-33.8352	0.47
yeast_de_novo_pyrimidine_ribonuc_biosynth.grp	-33.8515	0.48
yeast_threonine_methionine_biosynth.grp	-33.9364	0.49
yeast_sulfur_amino_acid_biosynth.grp	-33.9364	0.49
yeast_stratch_cellulose_biosynth.grp	-33.948	0.49
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-33.948	0.49
yeast_deoxyribose_phosphate_metabolism.grp	-33.948	0.49
yeast_arginine_ornithine_proline_interconversion.grp	-33.9521	0.49
yeast_arginine_ornithine_proline_interconversion.grp	-33.9521	0.49
yeast_aerobic_glycerol_catabolism.grp	-34.1161	0.49
yeast_aerobic_glycerol_catabolism.grp	-34.1161	0.49

Click on a column name to sort table. Click on a row to view match.

17) yeast_tyrosine_biosynth

Match results

Text File Name	Match Score	P-Value
yeast_tyrosine_biosynth.grp	0.0	0.0
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	0.0	0.0
yeast_super_phenylalanine_tyrosine_biosynth.grp	0.0	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	0.0	0.0
yeast_chorismate_pathway.grp	0.0	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-2.0	0.0
yeast_chorismate_pathway.grp	-2.0	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-4.0	0.0
yeast_chorismate_pathway.grp	-4.0	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-6.0	0.0
yeast_chorismate_pathway.grp	-6.0	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-8.0	0.0
yeast_chorismate_pathway.grp	-8.0	0.0
yeast_ergosterol_biosynth.grp	-16.0284	0.09
yeast_UDP_N_acetylglactosamine_biosynth.grp	-16.0492	0.09
yeast_arginine_ornithine_proline_interconversion.grp	-16.2173	0.09
yeast_tyrosine_biosynth.grp	-16.4343	0.1
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-16.4343	0.1
yeast_super_phenylalanine_tyrosine_biosynth.grp	-16.4343	0.1
yeast_phenylalanine_degradation.grp	-16.4343	0.1
yeast_ergosterol_biosynth.grp	-16.6684	0.12
yeast_serine_isocitrate_lyase_pathway.grp	-16.7487	0.13
yeast_arginine_ornithine_proline_interconversion.grp	-17.5177	0.16
yeast_fatty_acid_oxidation.grp	-17.9139	0.16
yeast_fatty_acid_oxidation.grp	-17.9139	0.16
yeast_ergosterol_biosynth.grp	-18.0284	0.18
yeast_arginine_ornithine_proline_interconversion.grp	-18.2173	0.18
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-18.4343	0.18
yeast_super_phenylalanine_tyrosine_biosynth.grp	-18.4343	0.18
yeast_ergosterol_biosynth.grp	-18.6684	0.2
yeast_serine_isocitrate_lyase_pathway.grp	-18.7487	0.2
yeast_trehalose_anabolism.grp	-18.7517	0.2
yeast_sucrose_biosynth.grp	-18.7517	0.2
yeast_stratch_cellulose_biosynth.grp	-18.7517	0.2
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-18.7517	0.2
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-18.7517	0.2
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-18.7517	0.2
yeast_mannose_GDP_mannose_degradation.grp	-18.7517	0.2
yeast_glycolysis.grp	-18.7517	0.2
yeast_glycogen_catabolism.grp	-18.7517	0.2
yeast_glucose_fermentation.grp	-18.7517	0.2
yeast_galactose_metabolism.grp	-18.7517	0.2
yeast_deoxyribose_phosphate_metabolism.grp	-18.7517	0.2
yeast_deoxyribose_phosphate_metabolism.grp	-18.7517	0.2
yeast_aerobic_glycerol_catabolism.grp	-18.7517	0.2
yeast_super_gluconate_utilization.grp	-18.9197	0.22
yeast_aerobic_glycerol_catabolism.grp	-18.9197	0.22
yeast_aerobic_glycerol_catabolism.grp	-18.9197	0.22
yeast_methionine_degradation.grp	-19.2069	0.23
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-19.4105	0.24
yeast_lysine_biosynth.grp	-19.4105	0.24
yeast_lysine_biosynth.grp	-19.4105	0.24
yeast_leucine_biosynth.grp	-19.4105	0.24
yeast_glutamate_degradation8.grp	-19.4105	0.24
yeast_glutamate_degradation7.grp	-19.4105	0.24
yeast_ectoine_synth.grp	-19.4105	0.24

Click on a column name to sort table. Click on a row to view match.

18) yeast_glutamate_degradation8

Match results

Text File Name	Match Score	P-Value
yeast_glutamate_degradation8.grp	0.0	0.0
yeast_arginine_metabolism.grp	0.0	0.0
yeast_glutamate_degradation8.grp	-24.158	0.0
yeast_arginine_metabolism.grp	-24.158	0.0
yeast_glycolysis.grp	-30.0415	0.13
yeast_glucose_fermentation.grp	-30.0415	0.13
yeast_glycolysis.grp	-31.2795	0.17
yeast_glucose_fermentation.grp	-31.2795	0.17
yeast_aerobic_glycerol_catabolism.grp	-31.2795	0.17
yeast_arginine_metabolism.grp	-31.6307	0.19
yeast_serine_isocitrate_lyase_pathway.grp	-32.0173	0.22
yeast_glycolysis.grp	-32.0415	0.23
yeast_glucose_fermentation.grp	-32.0415	0.23
yeast_aerobic_glycerol_catabolism.grp	-32.0415	0.23
yeast_arginine_metabolism.grp	-32.3926	0.25
yeast_glucose_fermentation.grp	-32.8035	0.28
yeast_sulfur_amino_acid_biosynth.grp	-32.8405	0.29
yeast_mevalonate_pathway.grp	-32.8405	0.29
yeast_ergosterol_biosynth.grp	-32.8405	0.29
yeast_triglyceride_biosynth.grp	-33.0237	0.34
yeast_threonine_catabolism.grp	-33.6132	0.38
yeast_fatty_acid_biosynth.grp	-33.6132	0.38
yeast_fatty_acid_biosynth.grp	-33.6132	0.38
yeast_aerobic_glycerol_catabolism.grp	-34.0415	0.41
yeast_glycolysis.grp	-34.1156	0.43
yeast_glucose_fermentation.grp	-34.1156	0.43
yeast_aerobic_glycerol_catabolism.grp	-34.1156	0.43
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-34.141	0.43
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-34.141	0.43
yeast_sulfur_amino_acid_biosynth.grp	-34.192	0.45
yeast_mevalonate_pathway.grp	-34.192	0.45
yeast_ergosterol_biosynth.grp	-34.192	0.45
yeast_triglyceride_biosynth.grp	-34.3752	0.46
yeast_glycolysis.grp	-34.5358	0.48
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-34.6693	0.5
yeast_stratch_cellulose_biosynth.grp	-34.7822	0.53
yeast_phosphatidic_biosynth.grp	-34.7822	0.53
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-34.7822	0.53
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-34.7822	0.53
yeast_ergosterol_biosynth.grp	-34.7822	0.53
yeast_triglyceride_biosynth.grp	-34.8512	0.55
yeast_triglyceride_biosynth.grp	-34.8512	0.55
yeast_fatty_acid_biosynth.grp	-35.4301	0.59
yeast_fatty_acid_biosynth.grp	-35.4301	0.59
yeast_carbon_monoxide_dehydrogenase.grp	-35.4301	0.59
yeast_carbon_monoxide_dehydrogenase.grp	-35.4301	0.59
yeast_sulfur_amino_acid_biosynth.grp	-35.4925	0.6
yeast_sulfur_amino_acid_biosynth.grp	-35.4925	0.6
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-35.4925	0.6
yeast_aerobic_glycerol_catabolism.grp	-35.7738	0.64
yeast_lysine_biosynth.grp	-35.8449	0.66
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-35.9073	0.66
yeast_hestidine_biosynth.grp	-35.9073	0.66
yeast_threonine_methionine_biosynth.grp	-35.9578	0.68
yeast_threonine_methionine_biosynth.grp	-35.9578	0.68
yeast_threonine_biosynth.grp	-35.9578	0.68

Click on a column name to sort table. Click on a row to view match.

19) yeast_fatty_acid_elongation

Match results

Text File Name	Match Score	P-Value
yeast_fatty_acid_elongation.grp	0.0	0.0
yeast_fatty_acid_biosynth.grp	-2.0	0.0
yeast_fatty_acid_biosynth.grp	-4.0	0.0
yeast_fatty_acid_biosynth.grp	-6.0	0.0
yeast_fatty_acid_biosynth.grp	-8.0	0.0
yeast_fatty_acid_elongation.grp	-16.4343	0.06
yeast_fatty_acid_biosynth.grp	-16.4343	0.06
yeast_fatty_acid_oxidation.grp	-17.3448	0.11
yeast_threonine_methionine_biosynth.grp	-17.5887	0.11
yeast_threonine_catabolism.grp	-17.5887	0.11
yeast_methionine_biosynth.grp	-17.5887	0.11
yeast_TCA_cycle_aerobic_respiration.grp	-17.9899	0.12
yeast_glutamate_degradation7.grp	-17.9899	0.12
yeast_threonine_methionine_biosynth.grp	-18.8892	0.16
yeast_threonine_catabolism.grp	-18.8892	0.16
yeast_fatty_acid_oxidation.grp	-18.8892	0.16
yeast_TCA_cycle_aerobic_respiration.grp	-18.9333	0.18
yeast_sulfur_amino_acid_biosynth.grp	-18.9333	0.18
yeast_glutamate_degradation3.grp	-18.9333	0.18
yeast_fatty_acid_oxidation.grp	-19.3448	0.2
yeast_toluene_via_catechol_degradation.grp	-19.4105	0.2
yeast_p_cymene_degradation.grp	-19.4105	0.2
yeast_p_cymene_degradation.grp	-19.4105	0.2
yeast_ergosterol_biosynth.grp	-19.4105	0.2
yeast_threonine_biosynth.grp	-19.468	0.2
yeast_super_hexitol_degradation.grp	-19.468	0.2
yeast_pantothenate_coenzymeA_biosynth.grp	-19.468	0.2
yeast_glucuronate_degradation.grp	-19.468	0.2
yeast_threonine_methionine_biosynth.grp	-19.5887	0.22
yeast_threonine_catabolism.grp	-19.5887	0.22
yeast_methionine_biosynth.grp	-19.5887	0.22
yeast_heme_biosynth.grp	-19.8067	0.23
yeast_heme_biosynth.grp	-19.8067	0.23
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-19.8691	0.23
yeast_de_novo_pyrimidine_ribonuc_biosynth.grp	-19.8691	0.23
yeast_TCA_cycle_aerobic_respiration.grp	-19.9899	0.27
yeast_glutamate_degradation7.grp	-19.9899	0.27
yeast_sulfur_amino_acid_biosynth.grp	-20.2338	0.28
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-20.2338	0.28
yeast_phosphatidic_acid_biosynth.grp	-20.2338	0.28
yeast_mevalonate_pathway.grp	-20.2338	0.28
yeast_glutamate_degradation8.grp	-20.2338	0.28
yeast_glutamate_degradation8.grp	-20.2338	0.28
yeast_glutamate_degradation7.grp	-20.2338	0.28
yeast_ergosterol_biosynth.grp	-20.2338	0.28
yeast_ectoine_synth.grp	-20.2338	0.28
yeast_carbon_monoxide_dehydrogenase.grp	-20.2338	0.28
yeast_carbon_monoxide_dehydrogenase.grp	-20.2338	0.28
yeast_arginine_metabolism.grp	-20.2338	0.28
yeast_arginine_metabolism.grp	-20.2338	0.28
yeast_ureide_biosynth.grp	-20.706	0.33
yeast_ureide_biosynth.grp	-20.706	0.33
yeast_toluene_via_catechol_degradation.grp	-20.706	0.33

Click on a column name to sort table. Click on a row to view match.

20) yeast_salvage_pyrimidine_deoxyribonuc_pathway

Match results

Text File Name	Match Score	P-Value
yeast_salvage_pyrimidine_deoxyribonuc_pathway.grp	0.0	0.0
yeast_salvage_pyrimidine_ribonuc_pathway.grp	-19.9403	0.0
yeast_salvage_pyrimidine_ribonuc_pathway.grp	-21.9403	0.0
yeast_salvage_pyrimidine_ribonuc_pathway.grp	-25.3061	0.02
yeast_de_novo_pyrimidine_deoxynuc_biosynth.grp	-31.0857	0.23
yeast_de_novo_pyrimidine_deoxynuc_biosynth.grp	-31.7341	0.29
yeast_de_novo_pyrimidine_deoxynuc_biosynth.grp	-31.7838	0.29
yeast_de_novo_pyrimidine_deoxynuc_biosynth.grp	-31.7838	0.29
yeast_de_novo_pyrimidine_deoxynuc_biosynth.grp	-31.7838	0.29
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-32.0128	0.32
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.3005	0.43
yeast_thiamine_biosynth.grp	-33.3669	0.43
yeast_thiamine_biosynth.grp	-33.3669	0.43
yeast_thiamine_biosynth.grp	-33.3669	0.43
yeast_thiamine_biosynth.grp	-33.3669	0.43
yeast_NAD_salvage_pathway.grp	-33.4785	0.45
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.5946	0.45
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.5946	0.45
yeast_purine_fermentation.grp	-33.6752	0.46
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.7248	0.46
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-34.0178	0.5
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-34.0178	0.5
yeast_NAD_salvage_pathway.grp	-34.127	0.52
yeast_de_novo_purine_nuc_biosynth.grp	-34.3733	0.52
yeast_de_novo_purine_nuc_biosynth.grp	-34.9629	0.58
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-35.2392	0.61
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-35.2392	0.61
yeast_threonine_methionine_biosynth.grp	-35.2559	0.61
yeast_glycolysis.grp	-35.2559	0.61
yeast_glucose_fermentation.grp	-35.2559	0.61
yeast_ergosterol_biosynth.grp	-35.3694	0.67
yeast_de_novo_purine_nuc_biosynth.grp	-35.6113	0.69
yeast_de_novo_purine_nuc_biosynth.grp	-35.9067	0.69
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-36.0178	0.74
yeast_stratch_cellulose_biosynth.grp	-36.0202	0.75
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-36.0202	0.75
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-36.0202	0.75
yeast_ergosterol_biosynth.grp	-36.0202	0.75
yeast_de_novo_purine_nuc_biosynth.grp	-36.3733	0.77
yeast_threonine_methionine_biosynth.grp	-36.6074	0.77
yeast_sulfur_amino_acid_biosynth.grp	-36.6074	0.77
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-36.6074	0.77
yeast_pantothenate_coenzymeA_biosynth.grp	-36.6074	0.77
yeast_chorismate_pathway.grp	-36.6074	0.77
yeast_ureide_degradation.grp	-36.6748	0.79
yeast_ureide_degradation.grp	-36.6748	0.79
yeast_ureide_degradation.grp	-36.6748	0.79
yeast_sucrose_biosynth.grp	-37.1875	0.79
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-37.2392	0.8
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-37.2392	0.8
yeast_chorismate_pathway.grp	-37.2392	0.8
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-37.2416	0.8
yeast_chorismate_pathway.grp	-37.2416	0.8
yeast_glycolysis.grp	-37.2559	0.82
yeast_glucose_fermentation.grp	-37.2559	0.82
yeast_chorismate_pathway.grp	-37.2583	0.82

Click on a column name to sort table. Click on a row to view match.

21) yeast_super_isoleucine_valine_biosynth2

Match results

Text File Name	Match Score	P-Value
yeast_valine_biosynth.grp	0.0	0.0
yeast_super_leucine_isoleucine_valine_biosynth1.grp	0.0	0.0
yeast_super_isoleucine_valine_biosynth2.grp	0.0	0.0
yeast_super_isoleucine_valine_biosynth1.grp	0.0	0.0
yeast_isoleucine_biosynth.grp	0.0	0.0
yeast_super_isoleucine_valine_biosynth1.grp	-2.0	0.0
yeast_isoleucine_biosynth.grp	-2.0	0.0
yeast_super_leucine_isoleucine_valine_biosynth2.grp	-4.89037	0.0
yeast_super_leucine_isoleucine_valine_biosynth2.grp	-5.76519	0.0
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-13.9824	0.0
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-19.3247	0.02
yeast_leucine_biosynth.grp	-19.3247	0.02
yeast_super_leucine_isoleucine_valine_biosynth2.grp	-19.7476	0.03
yeast_super_isoleucine_valine_biosynth1.grp	-19.7476	0.03
yeast_isoleucine_biosynth.grp	-19.7476	0.03
yeast_super_phenylalanine_tyrosine_tryptophane_bios...	-19.8951	0.03
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-20.4932	0.03
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-21.8951	0.11
yeast_chorismate_pathway.grp	-21.8951	0.11
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-22.1995	0.11
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-22.7699	0.13
yeast_chorismate_pathway.grp	-22.7699	0.13
yeast_lysine_biosynth.grp	-23.6014	0.23
yeast_mevalonate_pathway.grp	-23.6588	0.24
yeast_ergosterol_biosynth.grp	-23.6588	0.24
yeast_serine_isocitrate_lyase_pathway.grp	-23.8356	0.25
yeast_serine_isocitrate_lyase_pathway.grp	-24.4449	0.31
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-24.7699	0.34
yeast_chorismate_pathway.grp	-24.7699	0.34
yeast_serine_isocitrate_lyase_pathway.grp	-25.0899	0.35
yeast_serine_isocitrate_lyase_pathway.grp	-25.1906	0.36
yeast_super_phenylalanine_tyrosine_biosynth.grp	-25.2219	0.37
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-25.2219	0.37
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-25.2219	0.37
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-25.2219	0.37
yeast_hestidine_biosynth.grp	-25.2219	0.37
yeast_chorismate_pathway.grp	-25.2219	0.37
yeast_heme_biosynth.grp	-25.4724	0.4
yeast_glucuronate_degradation.grp	-25.6513	0.4
yeast_TCA_cycle_aerobic_respiration.grp	-25.6588	0.41
yeast_mevalonate_pathway.grp	-25.6588	0.41
yeast_ergosterol_biosynth.grp	-25.6588	0.41
yeast_sulfur_amino_acid_biosynth.grp	-25.8057	0.43
yeast_p_cymene_degradation.grp	-25.828	0.43
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-25.828	0.43
yeast_glucose_fermentation.grp	-25.828	0.43
yeast_chorismate_pathway.grp	-25.828	0.43
yeast_chorismate_biosynth.grp	-25.828	0.43
yeast_serine_isocitrate_lyase_pathway.grp	-25.8356	0.46
yeast_de_novo_purine_nuc_biosynth.grp	-25.8443	0.47
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-26.2832	0.5
yeast_hestidine_biosynth.grp	-26.2832	0.5
yeast_folic_acid_biosynth.grp	-26.3039	0.5
yeast_TCA_cycle_aerobic_respiration.grp	-26.5174	0.52
yeast_lysine_biosynth.grp	-26.5174	0.52

Click on a column name to sort table. Click on a row to view match.

22) yeast_leucine_biosynth

Match results

Text File Name	Match Score	P-Value
yeast_super_leucine_isoleucine_valine_biosynth1.grp	0.0	0.0
yeast_leucine_biosynth.grp	0.0	0.0
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-2.0	0.0
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-4.0	0.0
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-6.0	0.0
yeast_super_leucine_isoleucine_valine_biosynth2.grp	-16.2277	0.0
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-16.728	0.0
yeast_lysine_biosynth.grp	-17.2501	0.01
yeast_super_isoleucine_valine_biosynth1.grp	-19.1025	0.01
yeast_isoleucine_biosynth.grp	-19.1025	0.01
yeast_valine_biosynth.grp	-19.3247	0.02
yeast_super_isoleucine_valine_biosynth2.grp	-19.3247	0.02
yeast_super_isoleucine_valine_biosynth1.grp	-19.3247	0.02
yeast_isoleucine_biosynth.grp	-19.3247	0.02
yeast_TCA_cycle_aerobic_respiration.grp	-21.1906	0.06
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-21.8489	0.1
yeast_chorismate_pathway.grp	-21.8489	0.1
yeast_super_leucine_isoleucine_valine_biosynth2.grp	-22.1995	0.1
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-22.3009	0.11
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-22.8273	0.14
yeast_chorismate_pathway.grp	-22.8273	0.14
yeast_chorismate_biosynth.grp	-22.8273	0.14
yeast_TCA_cycle_aerobic_respiration.grp	-23.1906	0.15
yeast_serine_isocitrate_lyase_pathway.grp	-23.2425	0.16
yeast_serine_isocitrate_lyase_pathway.grp	-23.8356	0.22
yeast_p_cymene_degradation.grp	-23.8356	0.22
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-23.8519	0.23
yeast_folic_acid_biosynth.grp	-23.8519	0.23
yeast_chorismate_pathway.grp	-23.8519	0.23
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-23.945	0.23
yeast_chorismate_pathway.grp	-23.945	0.23
yeast_chorismate_biosynth.grp	-23.945	0.23
yeast_threonine_catabolism.grp	-24.0817	0.25
yeast_serine_isocitrate_lyase_pathway.grp	-24.4449	0.26
yeast_sulfur_amino_acid_biosynth.grp	-24.5052	0.28
yeast_serine_isocitrate_lyase_pathway.grp	-24.59	0.29
yeast_serine_isocitrate_lyase_pathway.grp	-25.0899	0.33
yeast_folic_acid_biosynth.grp	-25.0899	0.33
yeast_chorismate_pathway.grp	-25.0899	0.33
yeast_super_phenylalanine_tyrosine_biosynth.grp	-25.1757	0.33
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-25.1757	0.33
yeast_fatty_acid_oxidation.grp	-25.2793	0.36
yeast_fatty_acid_biosynth.grp	-25.2793	0.36
yeast_sulfur_amino_acid_biosynth.grp	-25.4724	0.37
yeast_methionine_degradation.grp	-25.4724	0.37
yeast_glucuronate_degradation.grp	-25.6513	0.39
yeast_sulfur_degradation.grp	-25.7433	0.39
yeast_sulfur_amino_acid_biosynth.grp	-25.7433	0.39
yeast_sulfur_degradation.grp	-25.8057	0.39
yeast_sulfur_amino_acid_biosynth.grp	-25.8057	0.39
yeast_heme_biosynth.grp	-25.828	0.39
yeast_p_cymene_degradation.grp	-25.8356	0.4
yeast_4_hydroxyproline_degradation.grp	-26.2414	0.42
yeast_mevalonate_pathway.grp	-26.3039	0.43
yeast_ergosterol_biosynth.grp	-26.3039	0.43
yeast_sulfur_degradation.grp	-26.5052	0.47

Click on a column name to sort table. Click on a row to view match.

23) yeast_valine_biosynth

Match results

Text File Name	Match Score	P-Value
yeast_valine_biosynth.grp	0.0	0.0
yeast_super_leucine_isoleucine_valine_biosynth1.grp	0.0	0.0
yeast_super_isoleucine_valine_biosynth2.grp	0.0	0.0
yeast_super_isoleucine_valine_biosynth1.grp	0.0	0.0
yeast_isoleucine_biosynth.grp	0.0	0.0
yeast_super_isoleucine_valine_biosynth1.grp	-2.0	0.0
yeast_isoleucine_biosynth.grp	-2.0	0.0
yeast_super_leucine_isoleucine_valine_biosynth2.grp	-4.89037	0.0
yeast_super_leucine_isoleucine_valine_biosynth2.grp	-5.76519	0.0
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-13.9824	0.0
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-19.3247	0.02
yeast_leucine_biosynth.grp	-19.3247	0.02
yeast_super_leucine_isoleucine_valine_biosynth2.grp	-19.7476	0.03
yeast_super_isoleucine_valine_biosynth1.grp	-19.7476	0.03
yeast_isoleucine_biosynth.grp	-19.7476	0.03
yeast_super_phenylalanine_tyrosine_tryptophane_bio...	-19.8951	0.03
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-20.4932	0.03
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-21.8951	0.11
yeast_chorismate_pathway.grp	-21.8951	0.11
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-22.1995	0.11
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-22.7699	0.13
yeast_chorismate_pathway.grp	-22.7699	0.13
yeast_lysine_biosynth.grp	-23.6014	0.23
yeast_mevalonate_pathway.grp	-23.6588	0.24
yeast_ergosterol_biosynth.grp	-23.6588	0.24
yeast_serine_isocitrate_lyase_pathway.grp	-23.8356	0.25
yeast_serine_isocitrate_lyase_pathway.grp	-24.4449	0.31
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-24.7699	0.34
yeast_chorismate_pathway.grp	-24.7699	0.34
yeast_serine_isocitrate_lyase_pathway.grp	-25.0899	0.35
yeast_serine_isocitrate_lyase_pathway.grp	-25.1906	0.36
yeast_super_phenylalanine_tyrosine_biosynth.grp	-25.2219	0.37
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-25.2219	0.37
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-25.2219	0.37
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-25.2219	0.37
yeast_hestidine_biosynth.grp	-25.2219	0.37
yeast_chorismate_pathway.grp	-25.2219	0.37
yeast_heme_biosynth.grp	-25.4724	0.4
yeast_glucuronate_degradation.grp	-25.6513	0.4
yeast_TCA_cycle_aerobic_respiration.grp	-25.6588	0.41
yeast_mevalonate_pathway.grp	-25.6588	0.41
yeast_ergosterol_biosynth.grp	-25.6588	0.41
yeast_sulfur_amino_acid_biosynth.grp	-25.8057	0.43
yeast_p_cymene_degradation.grp	-25.828	0.43
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-25.828	0.43
yeast_glucose_fermentation.grp	-25.828	0.43
yeast_chorismate_pathway.grp	-25.828	0.43
yeast_chorismate_biosynth.grp	-25.828	0.43
yeast_serine_isocitrate_lyase_pathway.grp	-25.8356	0.46
yeast_de_novo_purine_nuc_biosynth.grp	-25.8443	0.47
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-26.2832	0.5
yeast_hestidine_biosynth.grp	-26.2832	0.5
yeast_folic_acid_biosynth.grp	-26.3039	0.5
yeast_TCA_cycle_aerobic_respiration.grp	-26.5174	0.52
yeast_lysine_biosynth.grp	-26.5174	0.52

Click on a column name to sort table. Click on a row to view match.

24) yeast_isoleucine_biosynth

Match results

Text File Name	Match Score	P-Value
yeast_super_isoleucine_valine_biosynth1.grp	0.0	0.0
yeast_isoleucine_biosynth.grp	0.0	0.0
yeast_super_leucine_isoleucine_valine_biosynth2.grp	-11.5304	0.0
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-22.1995	0.0
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-25.0899	0.02
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-27.0899	0.06
yeast_chorismate_pathway.grp	-27.6603	0.07
yeast_super_leucine_isoleucine_valine_biosynth2.grp	-27.9647	0.08
yeast_super_isoleucine_valine_biosynth1.grp	-27.9647	0.08
yeast_isoleucine_biosynth.grp	-27.9647	0.08
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-28.1122	0.08
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-28.2584	0.08
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-28.5351	0.08
yeast_chorismate_pathway.grp	-28.5351	0.08
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-28.7104	0.11
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-30.1122	0.23
yeast_serine_isocitrate_lyase_pathway.grp	-30.2101	0.23
yeast_serine_isocitrate_lyase_pathway.grp	-30.9557	0.28
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-30.9871	0.29
yeast_chorismate_pathway.grp	-30.9871	0.29
yeast_heme_biosynth.grp	-31.2376	0.29
yeast_serine_isocitrate_lyase_pathway.grp	-31.7177	0.36
yeast_mevalonate_pathway.grp	-31.876	0.38
yeast_ergosterol_biosynth.grp	-31.876	0.38
yeast_serine_isocitrate_lyase_pathway.grp	-32.0527	0.4
yeast_chorismate_pathway.grp	-32.069	0.4
yeast_serine_isocitrate_lyase_pathway.grp	-32.2025	0.4
yeast_TCA_cycle_aerobic_respiration.grp	-32.2989	0.43
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-32.2989	0.43
yeast_chorismate_pathway.grp	-32.2989	0.43
yeast_chorismate_biosynth.grp	-32.2989	0.43
yeast_arginine_metabolism.grp	-32.3294	0.44
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-32.6231	0.46
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-32.8551	0.47
yeast_heme_biosynth.grp	-33.2784	0.49
yeast_threonine_methionine_biosynth.grp	-33.3778	0.51
yeast_super_phenylalanine_tyrosine_biosynth.grp	-33.439	0.51
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.439	0.51
yeast_hestidine_biosynth.grp	-33.439	0.51
yeast_lysine_biosynth.grp	-33.5369	0.52
yeast_sulfur_degradation.grp	-33.6434	0.57
yeast_sulfur_amino_acid_biosynth.grp	-33.6434	0.57
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.6975	0.58
yeast_de_novo_purine_nuc_biosynth.grp	-33.6975	0.58
yeast_p_cymene_degradation.grp	-33.7299	0.58
yeast_heme_biosynth.grp	-33.7299	0.58
yeast_folic_acid_biosynth.grp	-33.7299	0.58
yeast_glucuronate_degradation.grp	-33.8684	0.59
yeast_TCA_cycle_aerobic_respiration.grp	-33.876	0.59
yeast_heme_biosynth.grp	-33.999	0.59
yeast_p_cymene_degradation.grp	-34.0452	0.59
yeast_glucose_fermentation.grp	-34.0452	0.59
yeast_de_novo_purine_nuc_biosynth.grp	-34.0615	0.59
yeast_chorismate_biosynth.grp	-34.2825	0.6
yeast_mevalonate_pathway.grp	-34.2989	0.6
yeast_ergosterol_biosynth.grp	-34.2989	0.6

Click on a column name to sort table. Click on a row to view match.

25) yeast_isoleucine_biosynth

Match results

Text File Name	Match Score	P-Value
yeast_super_isoleucine_valine_biosynth1.grp	0.0	0.0
yeast_isoleucine_biosynth.grp	0.0	0.0
yeast_super_leucine_isoleucine_valine_biosynth2.grp	-11.5304	0.0
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-22.1995	0.0
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-25.0899	0.02
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-27.0899	0.06
yeast_chorismate_pathway.grp	-27.6603	0.07
yeast_super_leucine_isoleucine_valine_biosynth2.grp	-27.9647	0.08
yeast_super_isoleucine_valine_biosynth1.grp	-27.9647	0.08
yeast_isoleucine_biosynth.grp	-27.9647	0.08
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-28.1122	0.08
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-28.2584	0.08
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-28.5351	0.08
yeast_chorismate_pathway.grp	-28.5351	0.08
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-28.7104	0.11
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-30.1122	0.23
yeast_serine_isocitrate_lyase_pathway.grp	-30.2101	0.23
yeast_serine_isocitrate_lyase_pathway.grp	-30.9557	0.28
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-30.9871	0.29
yeast_chorismate_pathway.grp	-30.9871	0.29
yeast_heme_biosynth.grp	-31.2376	0.29
yeast_serine_isocitrate_lyase_pathway.grp	-31.7177	0.36
yeast_mevalonate_pathway.grp	-31.876	0.38
yeast_ergosterol_biosynth.grp	-31.876	0.38
yeast_serine_isocitrate_lyase_pathway.grp	-32.0527	0.4
yeast_chorismate_pathway.grp	-32.069	0.4
yeast_serine_isocitrate_lyase_pathway.grp	-32.2025	0.4
yeast_TCA_cycle_aerobic_respiration.grp	-32.2989	0.43
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-32.2989	0.43
yeast_chorismate_pathway.grp	-32.2989	0.43
yeast_chorismate_biosynth.grp	-32.2989	0.43
yeast_arginine_metabolism.grp	-32.3294	0.44
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-32.6231	0.46
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-32.8551	0.47
yeast_heme_biosynth.grp	-33.2784	0.49
yeast_threonine_methionine_biosynth.grp	-33.3778	0.51
yeast_super_phenylalanine_tyrosine_biosynth.grp	-33.439	0.51
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.439	0.51
yeast_hestidine_biosynth.grp	-33.439	0.51
yeast_lysine_biosynth.grp	-33.5369	0.52
yeast_sulfur_degradation.grp	-33.6434	0.57
yeast_sulfur_amino_acid_biosynth.grp	-33.6434	0.57
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.6975	0.58
yeast_de_novo_purine_nuc_biosynth.grp	-33.6975	0.58
yeast_p_cymene_degradation.grp	-33.7299	0.58
yeast_heme_biosynth.grp	-33.7299	0.58
yeast_folic_acid_biosynth.grp	-33.7299	0.58
yeast_glucuronate_degradation.grp	-33.8684	0.59
yeast_TCA_cycle_aerobic_respiration.grp	-33.876	0.59
yeast_heme_biosynth.grp	-33.999	0.59
yeast_p_cymene_degradation.grp	-34.0452	0.59
yeast_glucose_fermentation.grp	-34.0452	0.59
yeast_de_novo_purine_nuc_biosynth.grp	-34.0615	0.59
yeast_chorismate_biosynth.grp	-34.2825	0.6
yeast_mevalonate_pathway.grp	-34.2989	0.6

Click on a column name to sort table. Click on a row to view match.

26) yeast_super_isoleucine_valine_biosynth1

Match results

Text File Name	Match Score	P-Value
yeast_super_isoleucine_valine_biosynth1.grp	0.0	0.0
yeast_isoleucine_biosynth.grp	0.0	0.0
yeast_super_leucine_isoleucine_valine_biosynth2.grp	-11.5304	0.0
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-22.1995	0.0
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-25.0899	0.02
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-27.0899	0.06
yeast_chorismate_pathway.grp	-27.6603	0.07
yeast_super_leucine_isoleucine_valine_biosynth2.grp	-27.9647	0.08
yeast_super_isoleucine_valine_biosynth1.grp	-27.9647	0.08
yeast_isoleucine_biosynth.grp	-27.9647	0.08
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-28.1122	0.08
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-28.2584	0.08
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-28.5351	0.08
yeast_chorismate_pathway.grp	-28.5351	0.08
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-28.7104	0.11
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-30.1122	0.23
yeast_serine_isocitrate_lyase_pathway.grp	-30.2101	0.23
yeast_serine_isocitrate_lyase_pathway.grp	-30.9557	0.28
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-30.9871	0.29
yeast_chorismate_pathway.grp	-30.9871	0.29
yeast_heme_biosynth.grp	-31.2376	0.29
yeast_serine_isocitrate_lyase_pathway.grp	-31.7177	0.36
yeast_mevalonate_pathway.grp	-31.876	0.38
yeast_ergosterol_biosynth.grp	-31.876	0.38
yeast_serine_isocitrate_lyase_pathway.grp	-32.0527	0.4
yeast_chorismate_pathway.grp	-32.069	0.4
yeast_serine_isocitrate_lyase_pathway.grp	-32.2025	0.4
yeast_TCA_cycle_aerobic_respiration.grp	-32.2989	0.43
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-32.2989	0.43
yeast_chorismate_pathway.grp	-32.2989	0.43
yeast_chorismate_biosynth.grp	-32.2989	0.43
yeast_arginine_metabolism.grp	-32.3294	0.44
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-32.6231	0.46
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-32.8551	0.47
yeast_heme_biosynth.grp	-33.2784	0.49
yeast_threonine_methionine_biosynth.grp	-33.3778	0.51
yeast_super_phenylalanine_tyrosine_biosynth.grp	-33.439	0.51
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.439	0.51
yeast_hestidine_biosynth.grp	-33.439	0.51
yeast_lysine_biosynth.grp	-33.5369	0.52
yeast_sulfur_degradation.grp	-33.6434	0.57
yeast_sulfur_amino_acid_biosynth.grp	-33.6434	0.57
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.6975	0.58
yeast_de_novo_purine_nuc_biosynth.grp	-33.6975	0.58
yeast_p_cymene_degradation.grp	-33.7299	0.58
yeast_heme_biosynth.grp	-33.7299	0.58
yeast_folic_acid_biosynth.grp	-33.7299	0.58
yeast_glucuronate_degradation.grp	-33.8684	0.59
yeast_TCA_cycle_aerobic_respiration.grp	-33.876	0.59
yeast_heme_biosynth.grp	-33.999	0.59
yeast_p_cymene_degradation.grp	-34.0452	0.59
yeast_glucose_fermentation.grp	-34.0452	0.59
yeast_de_novo_purine_nuc_biosynth.grp	-34.0615	0.59
yeast_chorismate_biosynth.grp	-34.2825	0.6
yeast_mevalonate_pathway.grp	-34.2989	0.6
yeast_ergosterol_biosynth.grp	-34.2989	0.6

Click on a column name to sort table. Click on a row to view match.

27) yeast_methionine_biosynth

Match results

Text File Name	Match Score	P-Value
yeast_threonine_methionine_biosynth.grp	0.0	0.0
yeast_methionine_biosynth.grp	0.0	0.0
yeast_threonine_methionine_biosynth.grp	-16.4343	0.0
yeast_sulfur_amino_acid_biosynth.grp	-28.9787	0.0
yeast_sulfur_degradation.grp	-29.6782	0.0
yeast_arginine_metabolism.grp	-36.3794	0.09
yeast_glucose_fermentation.grp	-37.0207	0.13
yeast_sulfur_degradation.grp	-37.3334	0.16
yeast_arginine_metabolism.grp	-38.3794	0.22
yeast_TCA_cycle_aerobic_respiration.grp	-39.2506	0.34
yeast_aerobic_glycerol_catabolism.grp	-39.4967	0.37
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-39.7551	0.41
yeast_glucose_fermentation.grp	-39.8807	0.44
yeast_glycolysis.grp	-40.0284	0.44
yeast_glucose_fermentation.grp	-40.0284	0.44
yeast_glycolysis.grp	-40.618	0.55
yeast_glucose_fermentation.grp	-40.618	0.55
yeast_aerobic_glycerol_catabolism.grp	-40.618	0.55
yeast_sulfur_amino_acid_biosynth.grp	-40.7396	0.58
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-41.1066	0.65
yeast_pantothenate_coenzymeA_biosynth.grp	-41.6559	0.69
yeast_phosphatidic_biosynth.grp	-41.7551	0.7
yeast_phosphatidic_biosynth.grp	-41.7551	0.7
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-41.7551	0.7
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-41.7551	0.7
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-41.7551	0.7
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-41.8365	0.73
yeast_de_novo_pyrimidine_ribonuc_biosynth.grp	-41.8365	0.73
yeast_chorismate_pathway.grp	-41.8365	0.73
yeast_lysine_biosynth.grp	-41.856	0.73
yeast_glucose_fermentation.grp	-41.8807	0.74
yeast_glycolysis.grp	-42.0284	0.74
yeast_aerobic_glycerol_catabolism.grp	-42.0284	0.74
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-42.1025	0.74
yeast_chorismate_pathway.grp	-42.1025	0.74
yeast_de_novo_pyrimidine_deoxynuc_biosynth.grp	-42.1446	0.77
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-42.1535	0.77
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-42.1535	0.77
yeast_hestidine_biosynth.grp	-42.1535	0.77
yeast_phosphatidic_biosynth.grp	-42.207	0.77
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-42.2194	0.77
yeast_ubiquinone_Q_prenylation.grp	-42.2581	0.77
yeast_ubiquinone_biosynth.grp	-42.2581	0.77
yeast_threonine_catabolism.grp	-42.3327	0.78
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-42.3784	0.78
yeast_de_novo_purine_nuc_biosynth.grp	-42.3784	0.78
yeast_de_novo_purine_nuc_biosynth.grp	-42.3784	0.78
yeast_threonine_catabolism.grp	-42.4092	0.78
yeast_ergosterol_biosynth.grp	-42.4919	0.78
yeast_aerobic_glycerol_catabolism.grp	-42.618	0.79
yeast_glucuronate_degradation.grp	-42.768	0.79
yeast_serine_isocitrate_lyase_pathway.grp	-42.809	0.79
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-42.968	0.81
yeast_chorismate_pathway.grp	-42.968	0.81
yeast_chorismate_biosynth.grp	-42.968	0.81
yeast_glutamate_degradation7.grp	-42.9746	0.81

Click on a column name to sort table. Click on a row to view match.

28) yeast_threonine_biosynth

Match results

Text File Name	Match Score	P-Value
yeast_threonine_methionine_biosynth.grp	0.0	0.0
yeast_threonine_biosynth.grp	0.0	0.0
yeast_methionine_biosynth.grp	-8.07776	0.0
yeast_threonine_methionine_biosynth.grp	-16.4343	0.0
yeast_aerobic_glycerol_catabolism.grp	-27.3941	0.04
yeast_glycolysis.grp	-28.0391	0.05
yeast_glucose_fermentation.grp	-28.0391	0.05
yeast_sulfur_degradation.grp	-28.7768	0.06
yeast_glucose_fermentation.grp	-29.6612	0.1
yeast_glucose_fermentation.grp	-30.0391	0.12
yeast_arginine_metabolism.grp	-30.0415	0.12
yeast_sulfur_amino_acid_biosynth.grp	-30.0773	0.12
yeast_sulfate_assimilation_pathway2.grp	-30.0773	0.12
yeast_TCA_cycle_aerobic_respiration.grp	-31.0335	0.25
yeast_aerobic_glycerol_catabolism.grp	-31.2795	0.26
yeast_glucose_fermentation.grp	-31.6612	0.35
yeast_arginine_metabolism.grp	-32.0415	0.39
yeast_sulfur_amino_acid_biosynth.grp	-32.5224	0.46
yeast_serine_isocitrate_lyase_pathway.grp	-32.5894	0.47
yeast_pantothenate_coenzymeA_biosynth.grp	-32.6744	0.47
yeast_threonine_methionine_biosynth.grp	-32.8687	0.52
yeast_threonine_biosynth.grp	-32.8687	0.52
yeast_methionine_biosynth.grp	-32.8687	0.52
yeast_threonine_catabolism.grp	-32.9016	0.52
yeast_TCA_cycle_aerobic_respiration.grp	-33.0335	0.53
yeast_glycolysis.grp	-33.0493	0.53
yeast_glucose_fermentation.grp	-33.0493	0.53
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-33.4548	0.61
yeast_mevalonate_pathway.grp	-33.5104	0.64
yeast_ergosterol_biosynth.grp	-33.5104	0.64
yeast_threonine_methionine_biosynth.grp	-33.6307	0.66
yeast_lysine_biosynth.grp	-33.6388	0.66
yeast_glycolysis.grp	-33.6388	0.66
yeast_aerobic_glycerol_catabolism.grp	-33.6388	0.66
yeast_lysine_biosynth.grp	-33.9148	0.68
yeast_aerobic_glycerol_catabolism.grp	-33.9329	0.68
yeast_sulfur_amino_acid_biosynth.grp	-34.0065	0.68
yeast_de_novo_purine_nuc_biosynth.grp	-34.1613	0.7
yeast_glucuronate_degradation.grp	-34.5508	0.71
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-34.7439	0.71
yeast_mevalonate_pathway.grp	-34.7439	0.71
yeast_ergosterol_biosynth.grp	-34.7439	0.71
yeast_chorismate_pathway.grp	-34.7439	0.71
yeast_chorismate_biosynth.grp	-34.7439	0.71
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-34.7484	0.72
yeast_chorismate_pathway.grp	-34.7484	0.72
yeast_chorismate_biosynth.grp	-34.7484	0.72
yeast_super_leucine_isoleucine_valine_biosynth2.grp	-34.7508	0.72
yeast_super_isoleucine_valine_biosynth1.grp	-34.7508	0.72
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-34.7508	0.72
yeast_isoleucine_biosynth.grp	-34.7508	0.72
yeast_chorismate_pathway.grp	-34.7508	0.72
yeast_chorismate_biosynth.grp	-34.7508	0.72
yeast_glutamate_degradation7.grp	-34.7575	0.74
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-34.8063	0.74

Click on a column name to sort table. Click on a row to view match.