

Functional Gene Network

Parameters of the query:

Server/Tool: <http://gtlinker.cnb.csic.es>

Raw results from functional enrichment and clustering (.txt): [\[Global overview\]](#) [\[Mg1\]](#) [\[Mg2\]](#) [\[Mg3\]](#) [\[Mg4\]](#) [\[Mg5\]](#) [\[Mg6\]](#) [\[Mg7\]](#) [\[Mg8\]](#) [\[Mg9\]](#)

Job ID: 1639610

Results:

Number of metagroups: 9

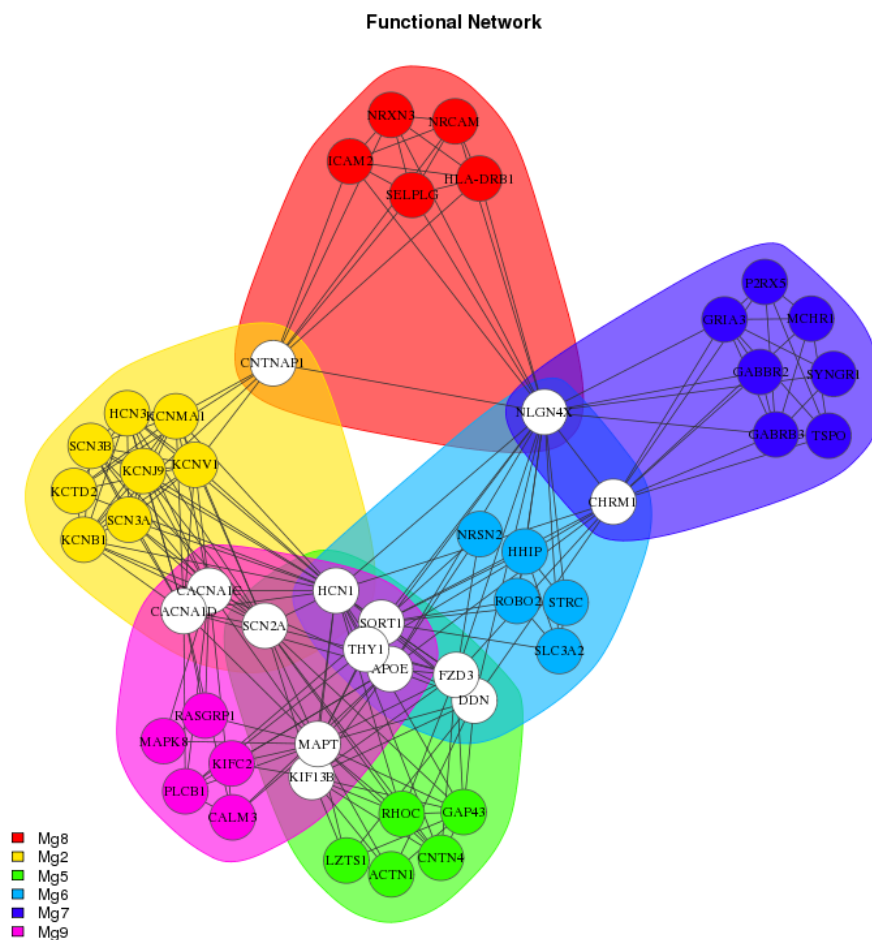
Number of genes included in all metagroups: 77

Filtered metagroup(s) (Silhouette Width < 0.2): Mg1, Mg3, Mg4

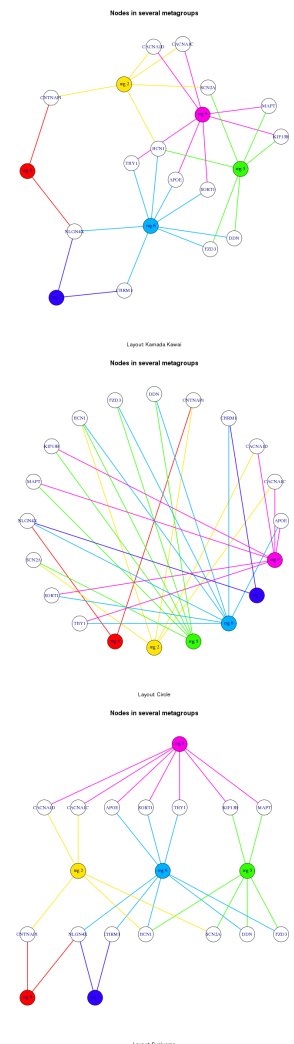
Number of genes included in non-filtered metagroups: 49

Functional network in other formats: [\[iGraph\]](#)

Simplified metagroup-terms table (shown below as legend): [\[Legend\]](#)



Nodes in several metagroups: (Different layouts)



Metagroups (sorted by Silhouette):

Metagroup 8	Silhouette: 0.68	P-value: 3e-06	Num genes: 7
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Cell adhesion molecules (CAMs)

Kegg

Metagroup 2	Silhouette: 0.53	P-value: 3.6e-12	Num genes: 13
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Voltage-gated ion channel activity (MF)

GO

Voltage-gated potassium channel activity (MF)

GO

Voltage-gated potassium channel complex (CC)

GO

[GO terms tree]

Metagroup 5 Silhouette: 0.37 P-value: 3.2e-08 Num genes: 11

Axon (CC)

GO

Cell projection (CC)

GO

[GO terms tree]

Metagroup 6 Silhouette: 0.36 P-value: 2.8e-07 Num genes: 13

Dendrite (CC)

GO

Neuronal cell body (CC)

GO

Cell surface (CC)

GO

[GO terms tree]

Metagroup 7 Silhouette: 0.28 P-value: 2.1e-06 Num genes: 9

Postsynaptic membrane (CC)

GO

Synapse (CC)

GO

Neuroactive ligand-receptor interaction

Kegg

[GO terms tree]

Metagroup 9 Silhouette: 0.27 P-value: 0.00035 Num genes: 12

Enzyme binding (MF)

GO

Microtubule (CC)

GO

Alzheimer's disease

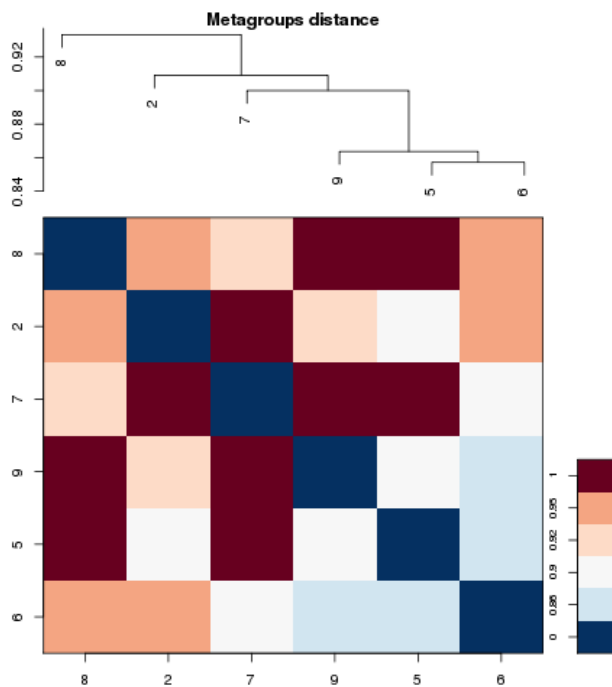
Kegg

MAPK signaling pathway

Kegg

[GO terms tree]

Distances between Metagroups:



Distance matrix:

	Mg8	Mg2	Mg7	Mg9	Mg5	Mg6
Mg8	0	0.95	0.93	1	1	0.95
Mg2	0.95	0	1	0.91	0.91	0.96
Mg7	0.93	1	0	1	1	0.9
Mg9	1	0.91	1	0	0.9	0.86
Mg5	1	0.91	1	0.9	0	0.86
Mg6	0.95	0.96	0.9	0.86	0.86	0