

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

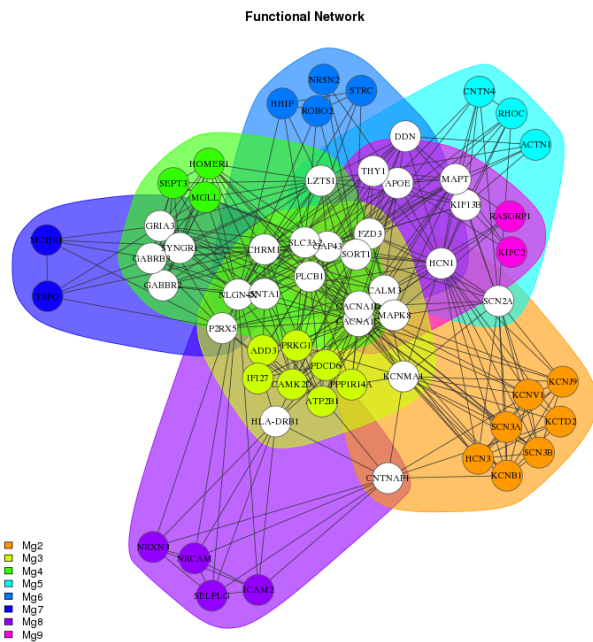
Number of genes included in all metagroups: 77

Filtered metagroup(s) (Silhouette Width < 0): Mg1

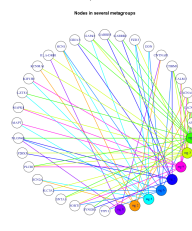
Number of genes included in non-filtered metagroups: 60

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

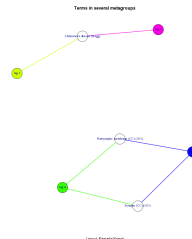
Simplified metagroup-terms table (shown below as legend): [\[Legend\]](#)



Genes in several metagroups:
(Different layouts)



Terms in several metagroups:
(Marked with * in the table)



Metagroups (sorted by Silhouette):

Metagroup 8	Silhouette: 0.68	P-value: 3e-06	Genes: 7
Cell adhesion molecules (CAMs) Kegg			
Metagroup 2	Silhouette: 0.53	P-value: 3.6e-12	Genes: 13
Voltage-gated ion channel activity (MF) GO			
Voltage-gated potassium channel activity (MF) GO			
Voltage-gated potassium channel complex (CC) GO			
<div>ACTN1, CNTN4, DDN, FZD3, GAP43, HCN1, KIF13B, LZTS1, MAPT, RHOC, SCN2A [GO tree]</div>			
Metagroup 5	Silhouette: 0.37	P-value: 3.2e-08	Genes: 11
Axon (CC) GO			
Cell projection (CC) GO			
Metagroup 6	Silhouette: 0.36	P-value: 2.8e-07	Genes: 13
Cell surface (CC) GO			
Dendrite (CC) GO			
Neuronal cell body (CC) GO			
[GO tree]			
Metagroup 7	Silhouette: 0.28	P-value: 2.1e-06	Genes: 9
Neuroactive ligand-receptor interaction Kegg			
Postsynaptic membrane (CC) * GO			
Synapse (CC) * GO			
[GO tree]			
Metagroup 9	Silhouette: 0.27	P-value: 0.00035	Genes: 12
Alzheimer's disease * Kegg			
Enzyme binding (MF) GO			
MAPK signaling pathway Kegg			
Microtubule (CC) GO			
[GO tree]			

