

Each column represents one gene in the input list. Each line stands for a functional term. Each table cell stands for one list/term association.

Cell colour and letter shows either evidence code (GO) or type of evidence (pathways, motifs, ...)

201852\_X\_AT  
211719\_X\_AT  
204114\_AT  
219773\_AT  
202363\_AT  
209325\_S\_AT  
211980\_AT  
213905\_X\_AT  
61734\_AT  
212354\_AT  
221729\_AT  
208782\_AT  
201438\_AT  
221731\_X\_AT  
202310\_S\_AT  
200665\_S\_AT  
212489\_AT  
202404\_S\_AT  
210511\_S\_AT

P-value T Q Q&T Q&T/Q Q&T/T term ID term domain and name

Fraction of genes in list with the functional term (a.k.a. precision)

Fraction of all functional genes detected in the list (a.k.a. recall)

											q					D	D	2.22e-06	26	19	3	0.158	0.115		GO:0018149	BP	peptide cross-linking (1)	
	M		q	e	e									A		e	D	D	9.98e-07	876	19	8	0.421	0.009		GO:0022610	BP	biological adhesion (1)
	M		q	e	e									A		e	D	D	9.89e-07	875	19	8	0.421	0.009		GO:0007155	BP	cell adhesion (1)
			q													e	D	D	2.16e-05	169	19	4	0.211	0.024		GO:0031589	BP	cell-substrate adhesion (2)
	e		q																1.82e-05	26	5	2	0.400	0.077		GO:0070206	BP	protein trimerization (1)
	e		q																3.37e-07	4	5	2	0.400	0.500		GO:0070208	BP	protein heterotrimerization (2)
M	M		M																5.45e-08	219	19	6	0.316	0.027		GO:0043062	BP	extracellular structure organization (1)
M	M		M			S													2.88e-09	134	19	6	0.316	0.045		GO:0030198	BP	extracellular matrix organization (2)
M	M		M			S													9.74e-11	31	19	5	0.263	0.161		GO:0030199	BP	collagen fibril organization (3)
M																			2.01e-05	7	19	2	0.105	0.286		GO:0043206	BP	fibril organization (3)

term name, left alignment and (#) according to depth in local hierarchy

Number of cells from the left shows optimal enrichment for an ordered input list.

Enrichment p-value. Significant values are usually shown.

# of genes in the list associated to functional term

click to visualise hierarchy of terms

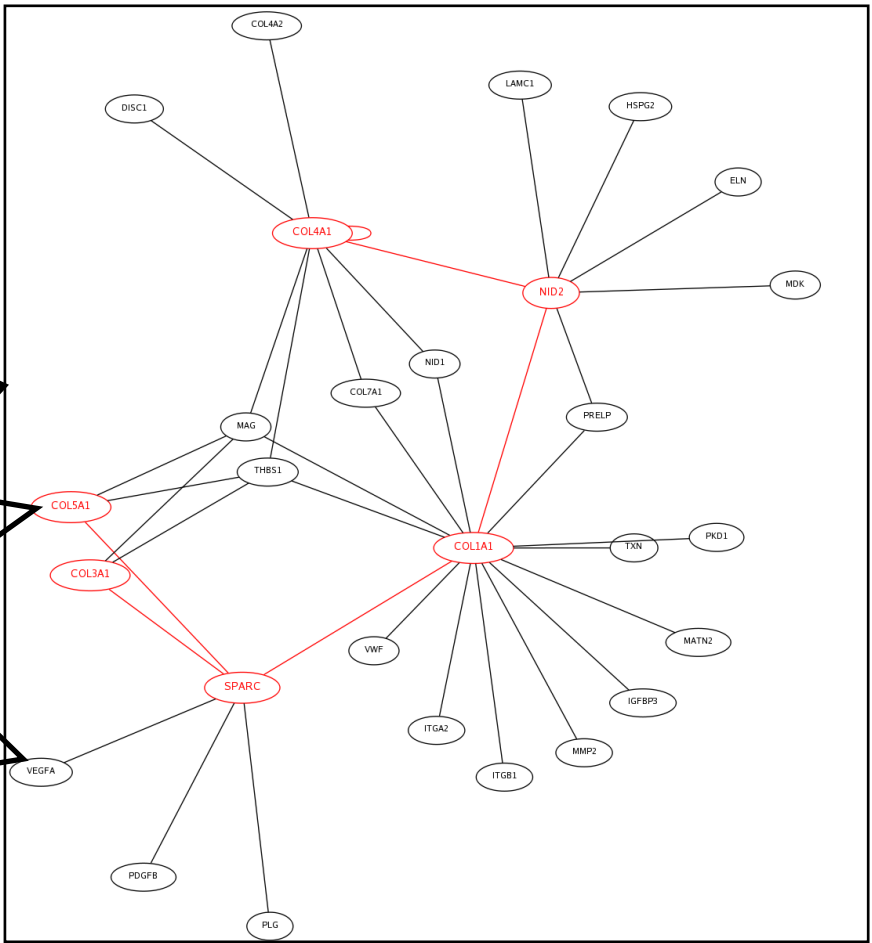
term type or GO domain

Multi-coloured cells have several sources of GO evidence.

Total # of genes associated to functional term

# of genes in input list. This varies when list is ordered and optimum list length is detected

term ID



Enriched protein-protein interaction modules in the input list

**RED:** genes from the input list that interact with one another (the core)

**BLACK:** direct interaction partners of the core that do not belong to the initial list (the neighbourhood)

Significance is tested with the hypergeometric test between  $k$ =core,  $n$ =input\_list and  $K$ =neighbourhood