

Pathway Result #47 — Analysis Report

Generated 2026-09-21 02:38:59 · 1 run(s) · CAT-G Data Analyzer

1. pathway (#47)

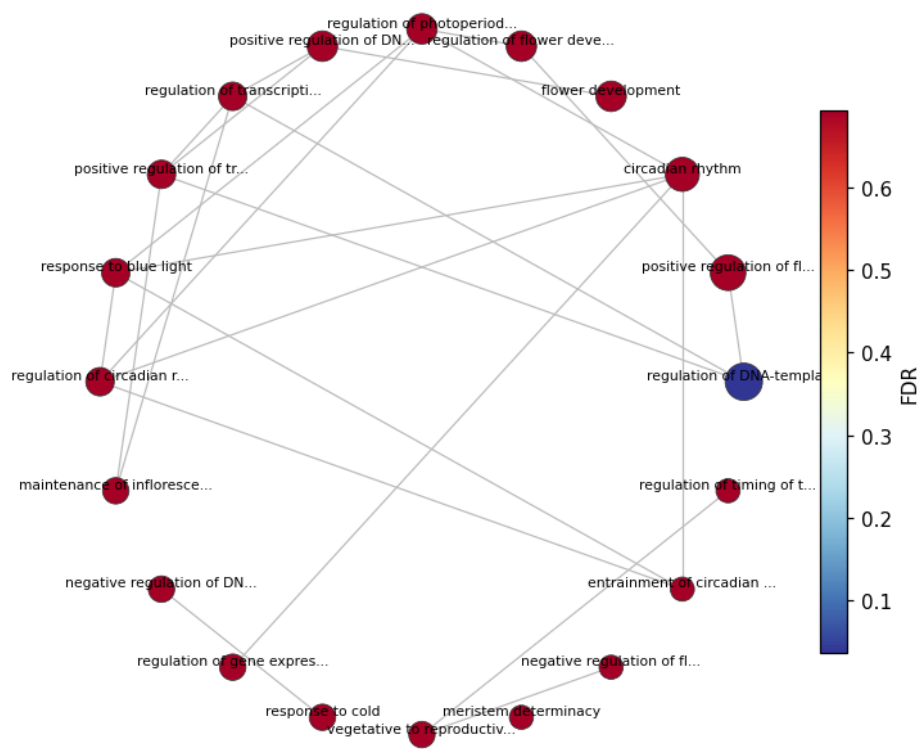
2026-09-21 02:17:58 · pathway · status: completed

Enrichment analysis found 125 significant term(s) across the queried databases.

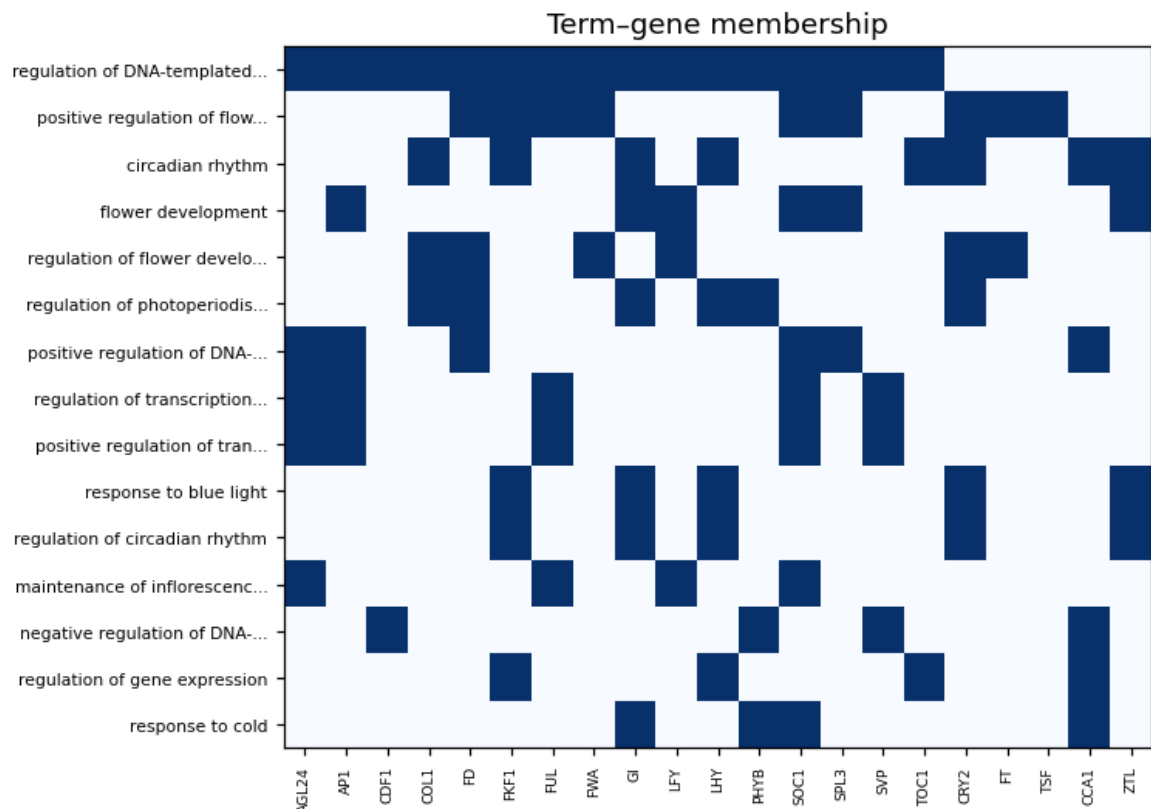
go

namespace	gene_count	bg_count	gene_ratio	bg_ratio	p_value	fdr	
biological_process	16	16	0.64	0.444444	0.00028	0.034945	['AGL24', 'AP1', 'CDF1', 'COL1', 'FD',
biological_process	9	9	0.36	0.25	0.021701	0.694444	['CRY2', 'F
biological_process	8	8	0.32	0.222222	0.035742	0.694444	['CCA1',
biological_process	6	6	0.24	0.166667	0.090923	0.694444	
biological_process	6	6	0.24	0.166667	0.090923	0.694444	
biological_process	6	6	0.24	0.166667	0.090923	0.694444	
biological_process	6	6	0.24	0.166667	0.090923	0.694444	
biological_process	5	5	0.2	0.138889	0.140931	0.694444	
biological_process	5	5	0.2	0.138889	0.140931	0.694444	
biological_process	5	5	0.2	0.138889	0.140931	0.694444	

Enrichment network (Jaccard >= 0.3)



enrichment network



term gene heatmap

Method & Provenance

method	Pathway enrichment — GO/KEGG/GSEA
engine	Python · scipy/gseapy 1.17.1
datasets	gallery — example_proteomics.csv
started	2026-09-21 02:17:58.014941
permanent link	https://cat-g-omxpert.wishartlab.com/pathway/results/by-token/fcbf2775619240969f9ae

Parameter	Value
organism	arabidopsis
namespace	biological_process
min_gene_count	1
n_input_genes	25
fdr_threshold	0.05

Command history

```
# python
# GO/KEGG enrichment: hypergeometric test per term

# python
from scipy.stats import hypergeom

# python
p = hypergeom.sf(k - 1, N_background, K_term, n_input)

# python
fdr = statsmodels.stats.multitest.multipletests(p_values, method='fdr_bh')
```

```
# python
# GSEA: gseapy.prerank(rnk=ranked_genes, gene_sets=gmt, seed=seed)
```