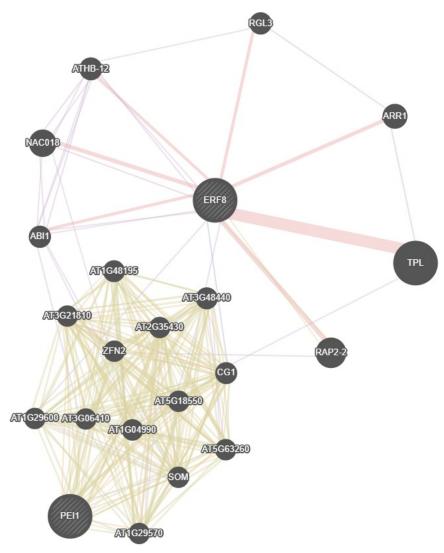
GeneMANIA report

Created on : 24 June 2020 21:04:32

Last database update : 13 March 2017 $00{:}00{:}00$

Application version : 3.6.0



Networks

- Physical Interactions
- Predicted
- Co-expression
- Shared protein domains
- Genetic Interactions
- Co-localization

Functions

N/A

Search parameters

Organism Arabidopsis thaliana (arabidopsis)

Genes ERF8, PEI1

Network Automatically selected weighting method

weighting

Networks

 $\mathbf{2}$

2011

 \mathbf{B}

Bassel-Cutler-2008-Dormant Seed Expression , Bassel-Cutler-2008-Germinating Seed Expression , BIOGRID-SMALL-SCALE-STUDIES , BIOGRID-SMALL-SCALE-STUDIES , Boruc-Russinova-2010 A , Boruc-Russinova-2010 B , Brady-Benfey-2007

 \mathbf{C}

Causier-Davies-2012 , Ceserani-Nelson-2009 , Chen-Rhee-2012 , Cutcliffe-Rashotte-2011

 \mathbf{D}

Danisman-Immink-2013 , de Folter-Angenent-2005 , Dean Rider-Ogas-2003 , Deeken-Hedrich-2006 A , Dinneny-Benfey-2008 D , Dortay-Heyl-2008 , Dreze-Vidal-2011-combined , Dreze-Vidal-2011-main , Dreze-Vidal-2011-repeat

 \mathbf{E}

Efroni-Wagner-2013, Elrouby-Coupland-2010

F,

Fujiwara-Fukao-2014

 \mathbf{G}

Gifford-Birnbaum-2008 , Goda-Shimada-2008 A , Goda-Shimada-2008 B

 \mathbf{H}

Hackbusch-Uhrig-2005, Hackenberg-Grimm-2012

T

 ${\it Igawa-Yanagawa-2009}~,~ {\it INTERPRO}~,~ {\it IREF-BIND}~,~ {\it IREF-BIOGRID}~,~ {\it IREF-INTACT}~,~ {\it IREF-SMALL-SCALE-STUDIES}~$

.]

Jones-Frommer-2014

 \mathbf{K}

Kim-Vierstra-2013 , Klopffleisch-Jones-2011 , Kram-Carter-2009 , Kuroda-Matsui-2012

Lalonde-Frommer-2010, Lee-Rhee-2010 AraNet, Lee-Rhee-2010 Co-citation worm2arabidopsis, Lee-Rhee-2010 Co-citation yeast2arabidopsis, Lee-Rhee-2010 co-expression human2arabidopsis, Lee-Rhee-2010 Co-expression worm2arabidopsis, Lee-Rhee-2010 Co-expression yeast2arabidopsis, Lee-Rhee-2010 Co-inheritance, Lee-Rhee-2010 Gene neighbourhoods, Lee-Rhee-2010 Genetic interactions worm2arabidopsis, Lee-Rhee-2010 Genetic interactions yeast2arabidopsis, Lee-Rhee-2010 Protein complexes human2arabidopsis, Lee-Rhee-2010 Protein complexes yeast2arabidopsis, Lee-Rhee-2010 Protein interactions, Lee-Rhee-2010 Protein interactions fly2arabidopsis, Lee-Rhee-2010 protein interactions from complexes yeast2arabidopsis, Lee-Rhee-2010 Protein interactions human2arabidopsis, Lee-Rhee-2010 Protein interactions worm2arabidopsis, Lee-Rhee-2010 protein interactions yeast2arabidopsis, Lee-Rhee-2010 Shared protein domains, Lee-Rhee-2010 shared protein domains human2arabidopsis, Lee-Rhee-2010 shared protein domains yeast2arabidopsis, Lee-Rhee-2010 Y2H human2arabidopsis, Lee-Rhee-2010 Y2H worm2arabidopsis, Lee-Rhee-2010 Y2H yeast2arabidopsis, Lumba-McCourt-2014

\mathbf{M}

Malitsky-Aharoni-2008 , Manzano-Del Pozo-2008 , Mirabella-Schuurink-2015 , Moreno-Risueno-Benfey-2015

N

Nozue-Maloof-2011

P

Pandey-Albert-2010 , PFAM , Piya-Hewezi-2014 , Popescu-Dinesh-Kumar-2007 , PPI-Predicted (Interologs)

\mathbf{Q}

Queval-Noctor-2012

\mathbf{R}

Risseeuw-Crosby-2003, Ronemus-Martienssen-2006

\mathbf{S}

Sako-Yamaguchi-2014 , Schmid-Lohmann-2003 A , Schmid-Lohmann-2003 B , Sozzani-Benfey-2010 , Swatek-Thelen-2011

\mathbf{T}

Tamura-Hara-Nishimura-2010

V

Van Leene-De Jaeger-2010, Vernoux-Traas-2011

\mathbf{W}

Waidmann-Jonak-2014

₹	

Yamaoka-Hara-Nishimura-2013

${f Z}$

Zuber-Gallardo-2010 A

Genes

Gene	Description	Rank
PEI1	Zinc finger CCCH domain-containing protein 54 [Source:UniProtKB/Swiss-Prot;Acc:O65036]	N/A
ERF8	Ethylene-responsive transcription factor 8 [Source:UniProtKB/Swiss-Prot;Acc:Q9MAI5]	N/A
TPL	Protein TOPLESS [Source:UniProtKB/Swiss-Prot;Acc:Q94AI7]	1
RAP2-2	Ethylene-responsive transcription factor RAP2-2 [Source:UniProtKB/Swiss-Prot;Acc:Q9LUM4]	2
NAC018	NAC domain-containing protein 18 [Source:UniProtKB/Swiss-Prot;Acc: Q9ZNU2]	3
ARR1	Two-component response regulator ARR1 [Source:UniProtKB/Swiss-Prot;Acc:Q940D0]	4
ATHB-12	Homeobox-leucine zipper protein ATHB-12 [Source:UniProtKB/Swiss-Prot;Acc:Q9M276]	5
RGL3	DELLA protein RGL3 [Source:UniProtKB/Swiss-Prot;Acc:Q9LF53]	6
ABI1	Protein phosphatase 2C 56 [Source:UniProtKB/Swiss-Prot;Acc:P49597]	7
AT3G48440	Zinc finger CCCH domain-containing protein 43 [Source:UniProtKB/Swiss-Prot;Acc:Q9STM4]	8
CG1	Zinc finger CCCH domain-containing protein 16 [Source:UniProtKB/Swiss-Prot;Acc:Q9FWS3]	9
AT1G48195	Zinc finger CCCH domain-containing protein 13 [Source:UniProtKB/Swiss-Prot;Acc:Q3ECU8]	10
AT1G04990	Zinc finger CCCH domain-containing protein 3 [Source:UniProtKB/Swiss-Prot;Acc:Q94AD9]	11
AT5G18550	Zinc finger CCCH domain-containing protein 58 [Source:UniProtKB/Swiss-Prot;Acc:Q6NPN3]	12
ZFN2	Zinc finger CCCH domain-containing protein 26 [Source:UniProtKB/Swiss-Prot;Acc:O48772]	13
AT1G29600	Putative zinc finger CCCH domain-containing protein 10 [Source: UniProtKB/Swiss-Prot;Acc:Q9C7P1]	14
AT2G35430	Zinc finger CCCH domain-containing protein 28 [Source:UniProtKB/Swiss-Prot;Acc:Q5PP65]	15
AT1G29570	Putative zinc finger CCCH domain-containing protein 9 [Source: UniProtKB/Swiss-Prot;Acc:Q9C7P4]	16
AT5G63260	Zinc finger CCCH domain-containing protein 67 [Source:UniProtKB/	17

Gene	Description	Rank
	Swiss-Prot;Acc:Q5RJC5]	
SOM	Zinc finger CCCH domain-containing protein 2 [Source:UniProtKB/Swiss-Prot;Acc:Q9ZWA1]	18
AT3G06410	Zinc finger CCCH domain-containing protein 34 [Source:UniProtKB/Swiss-Prot;Acc:Q9SQU4]	19
AT3G21810	Zinc finger CCCH domain-containing protein 40 [Source:UniProtKB/Swiss-Prot;Acc:Q93XW7]	20

Networks

Physical Interactions	66.87%
Cutcliffe-Rashotte-2011	12.88%
CRFs form protein-protein interactions with each other and with members of the cytokinin signalling pathway in Arabidopsis via the CRF domain. Cutcliffe et al (2011). $J Exp Bot$	
Physical Interactions with 68 interactions from BioGRID	
Sako-Yamaguchi-2014	12.06%
Proteomic analysis of the 26S proteasome reveals its direct interaction with transit peptides of plastid protein precursors for their degradation. Sako et al (2014) . J Proteome Res	
Physical Interactions with 187 interactions from BioGRID	
Danisman-Immink-2013	8.79%
Analysis of functional redundancies within the Arabidopsis TCP transcription factor family. Danisman et al (2013). $J \ Exp \ Bot$ Physical Interactions with 119 interactions from iRefIndex	
Causier-Davies-2012	4.47%
The TOPLESS interactome: a framework for gene repression in Arabidopsis. Causier et al (2012). <i>Plant Physiol</i> Physical Interactions with 110 interactions from BioGRID	
Kim-Vierstra-2013	4.09%
Advanced proteomic analyses yield a deep catalog of ubiquity lation targets in Arabidopsis. Kim et al (2013). Plant Cell Physical Interactions with 891 interactions from iRef Index	
Vernoux-Traas-2011	2.92%
The auxin signalling network translates dynamic input into robust patterning at the shoot apex. Vernoux et al (2011) . $Mol Syst$ $Biol$	
Physical Interactions with 404 interactions from iRefIndex	
IREF-DIP	2.28%
Physical Interactions with 339 interactions from iRefIndex	
Igawa-Yanagawa-2009	2.24%
Isolation and identification of ubiquitin-related proteins from Arabidopsis seedlings. Igawa et al (2009). $J Exp Bot$ Physical Interactions with 159 interactions from iRefIndex	
Boruc-Russinova-2010 B	2.05%
Functional modules in the Arabidopsis core cell cycle binary protein-protein interaction network. Boruc et al (2010). <i>Plant Cell</i> Physical Interactions with 27 interactions from BioGRID	
BIOGRID-SMALL-SCALE-STUDIES	1.77%
Physical Interactions with 5,720 interactions from BioGRID	
Fujiwara-Fukao-2014	1.73%
Interactomics of Qa-SNARE in Arabidopsis thaliana. Fujiwara et al (2014). Plant Cell Physiol Physical Interactions with 464 interactions from BioGRID	
Boruc-Russinova-2010 A	1.69%
Functional modules in the Arabidopsis core cell cycle binary protein-protein interaction network. Boruc et al (2010). Plant Cell Physical Interactions with 40 interactions from BioGRID	

Physical Interactions	66.87%
Piya-Hewezi-2014	1.63%
Protein-protein interaction and gene co-expression maps of ARFs and Aux/IAAs in Arabidopsis. Piya et al (2014). Front Plant Sci	
Physical Interactions with 142 interactions from BioGRID	
IREF-BIND	1.62%
Physical Interactions with 794 interactions from iRefIndex	
Lee-Rhee-2010 Protein interactions	1.59%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). $Nat\ Biotechnol$	
Physical Interactions with 751 interactions from supplementary material	
Lumba-McCourt-2014	1.01%
A mesoscale abscisic acid hormone interactome reveals a dynamic signaling landscape in Arabidopsis. Lumba et al (2014). Dev $Cell$	
Physical Interactions with 456 interactions from iRefIndex	
Manzano-Del Pozo-2008	0.85%
Identification of ubiquitinated proteins in Arabidopsis. Manzano et al (2008). Plant Mol Biol	
Physical Interactions with 170 interactions from iRefIndex	
Hackbusch-Uhrig-2005	0.66%
A central role of Arabidopsis thaliana ovate family proteins in networking and subcellular localization of 3-aa loop extension homeodomain proteins. Hackbusch et al (2005). <i>Proc Natl Acad Sci U S A</i>	
Physical Interactions with 169 interactions from iRefIndex	0.4007
Lalonde-Frommer-2010	0.48%
A membrane protein/signaling protein interaction network for Arabidopsis version AMPv2. Lalonde et al (2010). Front Physiol Physical Interactions with 282 interactions from BioGRID	
Yamaoka-Hara-Nishimura-2013	0.44%
Identification and dynamics of Arabidopsis adaptor protein-2 complex and its involvement in floral organ development. Yamaoka et al (2013). <i>Plant Cell</i>	
Physical Interactions with 150 interactions from iRefIndex	
Kuroda-Matsui-2012	0.35%
A comprehensive analysis of interaction and localization of Arabidopsis SKP1-like (ASK) and F-box (FBX) proteins. Kuroda et al (2012) . $PLoS\ One$	
Physical Interactions with 657 interactions from iRefIndex	
Van Leene-De Jaeger-2010	0.33%
Targeted interactomics reveals a complex core cell cycle machinery in Arabidopsis thaliana. Van Leene et al (2010). Mol Syst Biol	
Physical Interactions with 447 interactions from BioGRID	
IREF-INTACT	0.33%
Physical Interactions with 9,433 interactions from iRefIndex	
IREF-SMALL-SCALE-STUDIES	0.23%
Physical Interactions with 6,133 interactions from iRefIndex	
Chen-Rhee-2012	0.16%

Physical Interactions	66.87%
Chen-Rhee-2012	
Uncovering Arabidopsis membrane protein interactome enriched in transporters using mating-based split ubiquitin assays and classification models. Chen et al (2012). Front Plant Sci Physical Interactions with 486 interactions from iRefIndex	
Efroni-Wagner-2013	0.14%
Regulation of leaf maturation by chromatin-mediated modulation of cytokinin responses. Efroni et al (2013). Dev Cell Physical Interactions with 354 interactions from BioGRID	
Jones-Frommer-2014	0.05%
Border controla membrane-linked interactome of Arabidopsis. Jones et al (2014). Science Physical Interactions with 10,436 interactions from BioGRID	
Dreze-Vidal-2011-repeat	0.04%
Evidence for network evolution in an Arabidopsis interactome map. (2011). Science	
Physical Interactions with 1,015 interactions from supplementary material	
Predicted	14.02%
Lee-Rhee-2010 Co-citation worm2arabidopsis	1.70%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). $Nat\ Biotechnol$	
Predicted with 5,553 interactions from supplementary material	
Lee-Rhee-2010 Protein interactions human2arabidopsis	1.66%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). $Nat\ Biotechnol$	
Predicted with 102,798 interactions from supplementary material	
Lee-Rhee-2010 Co-citation yeast2arabidopsis	1.62%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). $Nat\ Biotechnol$	
Predicted with 52,241 interactions from supplementary material	
Lee-Rhee-2010 protein interactions from complexes yeast2arabidopsis	1.45%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). $Nat\ Biotechnol$	
Predicted with 10,826 interactions from supplementary material	
Lee-Rhee-2010 Gene neighbourhoods	1.32%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). $Nat\ Biotechnol$	
Predicted with 94,649 interactions from supplementary material	
Lee-Rhee-2010 Genetic interactions yeast2arabidopsis	0.78%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010) . Nat $Biotechnol$	
Predicted with 30,482 interactions from supplementary material	
Lee-Rhee-2010 Protein complexes human2arabidopsis	0.69%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010) . Nat $Biotechnol$	
Predicted with 2,153 interactions from supplementary material	

Predicted	14.02%
Lee-Rhee-2010 protein interactions yeast2arabidopsis	0.60%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010) . Nat $Biotechnol$	
Predicted with 25,127 interactions from supplementary material	
Lee-Rhee-2010 Protein complexes yeast2arabidopsis	0.59%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010) . Nat $Biotechnol$	
Predicted with 128,410 interactions from supplementary material	
Lee-Rhee-2010 Co-expression worm2arabidopsis	0.54%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). $Nat\ Biotechnol$	
Predicted with 92,935 interactions from supplementary material	
Lee-Rhee-2010 shared protein domains yeast2arabidopsis	0.52%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). $Nat\ Biotechnol$	
Predicted with 24,095 interactions from supplementary material	
Lee-Rhee-2010 Co-expression yeast2arabidopsis	0.45%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). $Nat\ Biotechnol$	
Predicted with 102,740 interactions from supplementary material	
Lee-Rhee-2010 Y2H worm2arabidopsis	0.35%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010) . Nat $Biotechnol$	
Predicted with 1,905 interactions from supplementary material	
PPI-Predicted (Interologs)	0.34%
A predicted interactome for Arabidopsis. Geisler-Lee et al (2007). Plant Physiol	
Predicted with 18,204 interactions from collaborator	
Lee-Rhee-2010 Protein interactions worm2arabidopsis	0.32%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). $Nat\ Biotechnol$	
Predicted with 1,806 interactions from supplementary material	
Lee-Rhee-2010 shared protein domains human2arabidopsis	0.29%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010) . Nat $Biotechnol$	
Predicted with 21,634 interactions from supplementary material	
Lee-Rhee-2010 Co-inheritance	0.28%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). Nat $Biotechnol$	
Predicted with 82,768 interactions from supplementary material	
Lee-Rhee-2010 AraNet	0.24%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010) . Nat $Biotechnol$	
Predicted with 735,927 interactions from supplementary material	

Predicted	14.02%
Lee-Rhee-2010 Protein interactions fly2arabidopsis	0.16%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010) . Nat $Biotechnol$	
Predicted with 7,978 interactions from supplementary material	
Lee-Rhee-2010 co-expression human2arabidopsis	0.11%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010) . Nat $Biotechnol$	
Predicted with 39,767 interactions from supplementary material	
Co-expression Co-expression	12.73%
Kram-Carter-2009	0.95%
Uncovering the Arabidopsis thaliana nectary transcriptome: investigation of differential gene expression in floral nectariferous tissues. Kram et al (2009) . $BMC\ Plant\ Biol$	
Co-expression with 672,038 interactions from GEO	
Ronemus-Martienssen-2006	0.94%
$\label{eq:microRNA-targeted} \begin{tabular}{l}{l}{MicroRNA-targeted and small interfering RNA-mediated mRNA degradation is regulated by argonaute, dicer, and RNA-dependent RNA polymerase in Arabidopsis. Ronemus et al (2006). Plant Cell \end{tabular}$	
Co-expression with 176,825 interactions from GEO	
Schmid-Lohmann-2003 B	0.86%
Dissection of floral induction pathways using global expression analysis. Schmid et al (2003). Development	
Co-expression with 134,679 interactions from GEO	
Bassel-Cutler-2008-Dormant Seed Expression	0.69%
Elucidating the germination transcriptional program using small molecules. Bassel et al (2008) . $Plant\ Physiol$	
Co-expression with 424,666 interactions from collaborator	
Nozue-Maloof-2011	0.66%
Genomic analysis of circadian clock-, light-, and growth-correlated genes reveals PHYTOCHROME-INTERACTING FACTOR5 as a modulator of auxin signaling in Arabidopsis. Nozue et al (2011). <i>Plant Physiol</i> Co-expression with 686,407 interactions from GEO	
Bassel-Cutler-2008-Germinating Seed Expression	0.66%
Elucidating the germination transcriptional program using small molecules. Bassel et al (2008). Plant Physiol	0.0070
Co-expression with 418,628 interactions from collaborator	
Dinneny-Benfey-2008 D	0.63%
Cell identity mediates the response of Arabidopsis roots to abiotic stress. Dinneny et al (2008). Science	
Co-expression with 709,273 interactions from GEO	
Goda-Shimada-2008 B	0.62%
The AtGenExpress hormone and chemical treatment data set: experimental design, data evaluation, model data analysis and data access. Goda et al (2008). $Plant\ J$	
Co-expression with 677,499 interactions from GEO	
Queval-Noctor-2012	0.62%
Day length is a key regulator of transcriptomic responses to both $CO(2)$ and $H(2)O(2)$ in Arabidopsis. Queval et al (2012). Plant Cell Environ	
Co-expression with 655,914 interactions from GEO	

The seed composition of Arabidopsis mutants for the group 3 sulface transporters indicates a role in sulfate translocation within reveloping seeds. Zuber et al (2010). Plant Physiol 10-respectation with 693,536 interactions from GEO Pandey-Albert-2010 Boolean modeling of transcripture data reveals navel modes of beterotrineric G-protein action. Pandey et al (2010). Mol Syst 56d Coopersonion with 693,557 interactions from GEO Goda-Shimada-2008 A 10.599 Goda-Shimada-2008 A 10.579 Goda-Shimada-2015 WikiYol and WikiYo act downstream of the green leaf volatile E-2-becenal in Arabidopsis. Mirabella et al (2015). Plant J 10. respection with 698,546 interactions from GEO Gifford-Bimbaum-2008 10.579 Goda-Ghimada-2008 A 10.579	Co-expression	12.73%
Comparison with 683,356 interactions from GEO	Zuber-Gallardo-2010 A	0.61%
Pandey-Albert-2010 Sonders modeling of transcriptome data reveals movel modes of heterotrimeric G protein action. Pandey et al (2010). Mol Syst Not Co-expression with 688-587 interactions from GEO Godds-Shiimada-2008 A The AtGenExpression with 688-587 interactions from GEO Godds-Shiimada-2008 A The AtGenExpression with 679-444 interactions from GEO Mirabella-Schuurink-2015 WRKY0 and WRKY6 act downstream of the green leaf volatile E-3-beavenal in Arabidopsis. Mirabella et al (2015). Plant J To expression with 595-546 interactions from GEO Gifford-Birnbaum-2008 Colleged responses meditate developmental plasticity. Gifford et al (2008). Proc Natl Acad Sci U S A Decken-Hedrich-2006 A In integrated view of gene expression and solute profiles of Arabidopsis tumors: a genome-wide approach. Decken et al (2006). Plant CM That CM To expression with 604.786 interactions from GEO Dean Rider-Ogas-2003 Conditator repression of regulators of embryonic identity by PICKLE during germination in Arabidopsis. Dean Rider et al (2003). Proc Natl Acad Sci U S A To expression with 116,036 interactions from GEO Malitsky-Aharoni-2008 The transcript and metabolite networks affected by the two clades of Arabidopsis glurosinolate biosynthesis regulators. Malitsky al (2008). Proc Natl Acad Sci U S A To expression with 155,045 interactions from GEO Moreno-Risueno-Benfey-2015 Transcriptional court of citiens form GEO Moreno-Risueno-Benfey-2015 Transcriptional court of citiens form GEO Moreno-Risueno-Benfey-2015 Transcriptional court of citiens form GEO Schmid-Lohmann-2003 A O.539 Solvetion of forml induction pathways using global expression analysis. Schmid et al (2003). Development To-expression with 625,625 interactions from GEO Schmid-Lohmann-2003 A O.539 Solvetion of forml induction pathways using global expression analysis. Schmid et al (2003). Development To-expression with 69,645 interactions from GEO Solvetion of forml induction pathways using global expression analysis. Schmid et al (2003). Developm	The seed composition of Arabidopsis mutants for the group 3 sulfate transporters indicates a role in sulfate translocation within developing seeds. Zuber et al (2010) . Plant Physiol	
boolean modeling of transcriptome data reveals novel modes of heterotrimeric G-protein action. Pasidey et al (2010). Mol Syst Not Coccupression with 686.557 interactions from GEO Goda-Shimada-2008 A The At-GenEygress hormone and chemical treatment data set: experimental design, data evaluation, model data analysis and data access. Goda et al (2008). Pasit J Coccupression with 679.444 interactions from GEO Wirabella-Schuurink-2015 Wirabella-Schuurink-2015 Wirabella-Schuurink-2015 Wirabella-Schuurink-2016 Wirabella-Schuurink-2018 O.579 Wirabella-Schuurink-2008 O.579 Coccupression with 698.788 interactions from GEO Cocken-Hodrich-2006 A Interaction from GEO Cocken-Hodrich-2006 A The integrated view of gene expression and solute profiles of Arabidopsis tumors: a genome-wide approach. Decken et al (2008). Pasit Cell Cocken-Hodrich-2006 A The integrated view of gene expression from GEO Cocken-Hodrich-2006 Cocken-Hodrich-2006 Cocken-Hodrich-2006 Cocken-Hodrich-2006 Cocken-Hodrich-2006 Cocken-Hodrich-2006 Cocken-Hodrich-2006 Cocken-Hodrich-2008 Coccupression with 694,796 interactions from GEO Cocken-Hodrich-2008 Coccupression with 694,796 interactions from GEO Cocken-Hodrich-2008 Cocken-Hodrich-2008 Coccupression with 694,796 interactions from GEO Cocken-Hodrich-2008 Malitsky-Aharoni-2008 Malitsky-Aharoni-2008 Moreno-Risueno-Benfey-2015 Transcriptional control of sissee formation throughout root development. Moreno-Risueno et al (2015). Science Coccupression with 648,813 interactions from GEO Moreno-Risueno-Benfey-2015 Transcriptional control of sissee formation throughout root development. Moreno-Risueno et al (2015). Science Coccupression with 625,025 interactions from GEO Moreno-Risueno-Benfey-2010 Cocken-Benfey-2010 Spatiotemporal regulation of cell-cycle genes by SHORTROOT links potterning and growth. Sozzani et al (2010). Nature Coccupression with 604,019 interactions from GEO Shared protein domains 3.008	Co-expression with 693,336 interactions from GEO	
Co-expression with 680,557 interactions from GEO Goda-Shimada-2008 A 0.599 De AtGmExpress hormone and chemical treatment data set: experimental design, data evaluation, model data analysis and data costs. Goda et al (2008). Plant J Desexpression with 670,444 interactions from GEO Mirabella-Schuurink-2015 WRKY 30 and WRKY 6 act downstream of the green leaf volatile E-2-hesenal in Arabidopsis. Mirabella et al (2015). Plant J Desexpression with 589,546 interactions from GEO Gifford-Birnbaum-2008 Co-expression with 680,788 interactions from GEO Decken-Hedrich-2006 A An integrated view of gene expression and solute profiles of Arabidopsis tumors: a genome-wide approach. Decken et al (2006): Plant General Co-expression with 604,796 interactions from GEO Dean Rider-Ogas-2003 Coordinate repression of regulators of embryonic identity by PICKLE during germination in Arabidopsis. Dean Rider et al (2003). Plant Physiol Desexpression with 116,036 interactions from GEO Malitsky-Aharoni-2008 Malitsky-Aharoni-2008 Malitsky-Aharoni-2005 Moreno-Risueno-Benfey-2015 Co-expression with 684,833 interactions from GEO Moreno-Risueno-Benfey-2015 Schmid-Lohmann-2003 A Desection of floral induction pathways using global expression analysis. Schmid et al (2003). Development Desexpression with 625,625 interactions from GEO Sozzani-Benfey-2010 Opatiotemporal regulation of cell-cycle genes by SHORTROOT links patterning and growth. Sozzani et al (2010). Nature Desexpression with 604,619 interactions from GEO Shared protein domains 3.007	Pandey-Albert-2010	0.60%
Codes-Shimada-2008 A O.599 The AtGenExpress hormone and chemical treatment data set: experimental design, data evaluation, model data analysis and data access. Coda et al (2008). Pant J Oespression with 679,444 interactions from GEO Mirabella-Schuurink-2015 WirKy40 and WRKY6 act downstream of the green leaf volatile E-2-hexenal in Arabidopsis. Mirabella et al (2015). Plant J Oespression with 598,546 interactions from GEO Gifford-Birnbaum-2008 O.579 Desken-Hedrich-2006 A Integrated view of gene expression and solute profiles of Arabidopsis tumors: a genome-wide approach. Desken et al (2006). Plant Cell Oespression with 604,796 interactions from GEO Dean Rider-Ogas-2003 Oespression with 604,796 interactions from GEO Dean Rider-Ogas-2003 Oespression with 116,036 interactions from GEO Malitsky-Aharoni-2008 The transcript and metabolite networks affected by the two clades of Arabidopsis glucosinolate biosynthesis regulators. Malitsky at al (2008). Plant Physical Oespression with 599,163 interactions from GEO Moreno-Risueno-Benfey-2015 Tennacriptional control of tissue formation throughout root development, Moreno-Risueno et al (2015). Science Oespression with 648,813 interactions from GEO Schmid-Lohmann-2003 A Descriptional control of tissue formation throughout root development, Moreno-Risueno et al (2015). Science Oespression with 648,813 interactions from GEO Schmid-Lohmann-2003 A Description of of floral induction pathways using global expression analysis. Schmid et al (2003). Development Description of floral induction pathways using global expression analysis. Schmid et al (2003). Development Description of of oespression with 625,625 interactions from GEO Sozzani-Benfey-2010 Description domains 3.008	Boolean modeling of transcriptome data reveals novel modes of heterotrimeric G-protein action. Pandey et al (2010) . $Mol Syst$ $Biol$	
The At GenExpress hormone and chemical treatment data set: experimental design, data evaluation, model data analysis and data coress. Goda et al (2008). Plant J To-expression with 679,444 interactions from GEO WirkP40 and WRKY6 act downstream of the green leaf volatile E-2-hexenal in Arabidopsis. Mirabella et al (2015). Plant J To-expression with 589,546 interactions from GEO Gifford-Birnbaum-2008 Co-expression with 699,788 interactions from GEO Decken-Hedrich-2006 A In integrated view of gene expression and solute profiles of Arabidopsis tumors: a genome-wide approach. Decken et al (2006). Plant Gell To-expression with 694,796 interactions from GEO Dean Rider-Ogas-2003 Co-expression with 116,036 interactions from GEO Malitsky-Aharoni-2008 The transcript and metabolic networks affected by the two clades of Arabidopsis glucosinolate biosynthesis regulators. Malitsky et al (2008). Plant Physiol To-expression with 599,163 interactions from GEO Moreno-Risueno-Benfey-2015 Transcriptional control of tissue formation throughout root development. Moreno-Risueno et al (2015). Science To-expression with 648,813 interactions from GEO Moreno-Risueno-Benfey-2015 Transcriptional control of tissue formation throughout root development. Moreno-Risueno et al (2015). Science To-expression with 648,813 interactions from GEO Schmid-Lohmann-2003 A Dissection of floral induction pathways using global expression analysis. Schmid et al (2003). Development To-expression with 659,625 interactions from GEO Sozzani-Benfey-2010 participation of cell-cycle genes by SHORTROOT links patterning and growth. Sozzani et al (2010). Nature To-expression with 604,619 interactions from GEO Shared protein domains 3.00°	Co-expression with 686,557 interactions from GEO	
Coespession with 679,444 interactions from GEO Wirabella-Schuurink-2015 WirKy 0 and WRKY 6 act downstream of the green leaf volatile E-2-hecenal in Arabidopsis. Mirabella et al (2015). Plant J Securpression with 598,546 interactions from GEO Coespression with 598,546 interactions from GEO Coespression with 699,788 interactions from GEO Coeken-Hedrich-2006 A An integrated view of gene expression and solute profiles of Arabidopsis tumors: a genome-wide approach. Decken et al (2006). Plant Cell Coexpression with 604,796 interactions from GEO Coeken-Hedrich-2006 A An integrated view of gene expression and solute profiles of Arabidopsis tumors: a genome-wide approach. Decken et al (2006). Plant Cell Coexpression with 604,796 interactions from GEO Coern Rider-Ogas-2003 Coordinate repression of regulators of embryonic identity by PICKLE during germination in Arabidopsis. Dean Rider et al (2003). Plant I J Coexpression with 116,036 interactions from GEO Malitsky-Aharoni-2008 Coexpression with 169,163 interactions from GEO Moreno-Risueno-Benfey-2015 Coexpression with 559,163 interactions from GEO Moreno-Risueno-Benfey-2015 Transcriptional control of tissue formation throughout root development. Moreno-Risueno et al (2015). Science Co-expression with 648,813 interactions from GEO Schmid-Lohmann-2003 A O.539 Dissection of floral induction pathways using global expression analysis. Schmid et al (2003). Development Coexpression with 625,625 interactions from GEO Sozzani-Benfey-2010 pantotemporal regulation of cell-cycle genes by SHORTROOT links patterning and growth. Sozzani et al (2010). Nature Co-expression with 604,619 interactions from GEO Scharce Protein domains 3.007 Scharce Protein domains 3.007	Goda-Shimada-2008 A	0.59%
Mirabella-Schuurink-2015 WRKY40 and WRKY6 act downstream of the green leaf volatile E-2-hexenal in Arabidopsis. Mirabella et al (2015). Plant J Ze-expression with 598,546 interactions from GEO Gifford-Birnbaum-2008 O.579 Zel-specific nitrogen responses mediate developmental plasticity. Gifford et al (2008). Proc Natl Acad Sci U S A Ze-expression with 668,788 interactions from GEO Decken-Hedrich-2006 A An integrated view of gene expression and solute profiles of Arabidopsis tumors: a genome-wide approach. Decken et al (2006). Plant Cell Ze-expression with 604,796 interactions from GEO Dean Rider-Ogas-2003 Coordinate repression of regulators of embryonic identity by PICKLE during germination in Arabidopsis. Dean Rider et al (2003). Plant I J Ze-expression with 116,036 interactions from GEO Malitsky-Aharoni-2008 Coexpression with 559,163 interactions from GEO Moreno-Risueno-Benfey-2015 Coexpression with 648,813 interactions from GEO Moreno-Risueno-Benfey-2015 Coexpression with 648,813 interactions from GEO Schmid-Lohmann-2003 A O.539 Schmid-Lohmann-2003 A O.539 Schmid-Lohmann-2003 A O.539 Schmid-Lohmann-2004 (2008). Plant induction pathways using global expression analysis. Schmid et al (2003). Development Co-expression with 625,025 interactions from GEO Schmid-Lohmann-2003 A O.539 Schmid-Lohmann-2003 A O.539 Schmid-Lohmann-2003 A O.539 Schmid-Lohmann-2004 O.519 Schmid-Lohmann-2005 Schmid-Lohmann-2006 Schmid-Lohmann-2007 O.519 Schmid-Lohmann-2008 O.519 Schmid-Lohmann-2008 O.539 Schmid-Lohmann-2008 O.549	The AtGenExpress hormone and chemical treatment data set: experimental design, data evaluation, model data analysis and data access. Goda et al (2008) . Plant J	
NRKY40 and WRKY6 act downstream of the green leaf volatile E-2-hexenal in Arabidopsis. Mirabella et al (2015). Plant J Co-expression with 598,546 interactions from GEO Occapression with 699,788 interactions from GEO Occapression with 699,788 interactions from GEO Occapression with 699,788 interactions from GEO Occapression with 694,796 interactions from GEO Occapression with 110,036 interactions from GEO Occapression with 110,036 interactions from GEO Malitsky-Aharoni-2008 Occapression with 110,036 interactions from GEO Moreno-Risueno-Benfey-2015 Occapression with 559,163 interactions from GEO Moreno-Risueno-Benfey-2015 Occapression with 648,813 interactions from GEO Occapression with 649,619 interactions from GEO Occapression with 640,619 interactions from GEO	Co-expression with 679,444 interactions from GEO	
Co-expression with 598,546 interactions from GEO Gifford-Birnbaum-2008 Cell-specific nitrogen responses mediate developmental plasticity. Gifford et al (2008). Proc Natl Acad Sci U S A Co-expression with 609,788 interactions from GEO Celeken-Hedrich-2006 A An integrated view of gene expression and solute profiles of Arabidopsis tumors: a genome-wide approach. Decken et al (2006). Co-expression with 604,796 interactions from GEO Co-expression with 604,796 interactions from GEO Co-expression with 116,036 interactions from GEO Malitsky-Aharoni-2008 Co-expression with 116,036 interactions from GEO Moreno-Risueno-Benfey-2015 Co-expression with 59,163 interactions from GEO Moreno-Risueno-Benfey-2015 Co-expression with 648,813 interactions from GEO Schmid-Lohmann-2003 A Dissection of floral induction pathways using global expression analysis. Schmid et al (2003). Development Co-expression with 625,625 interactions from GEO Sozzani-Benfey-2010 Sozzani-Benfey-2010 Sozzani-Benfey-2010 Sozzani-Benfey-2010 Sozzani-Benfey-2010 Sozzani-Benfey-2010 Sox Barded protein domains 3.009 Sockana Company of the sockana and solute profiles of Arabidopsis tumors: a genome-wide approach. Decken et al (2010). Nature Co-expression with 604,619 interactions from GEO Solutionerporal regulation of cell-cycle genes by SHORTROOT links patterning and growth. Sozzani et al (2010). Nature Co-expression with 604,619 interactions from GEO Scharded protein domains 3.009	Mirabella-Schuurink-2015	0.57%
Coll-specific nitrogen responses mediate developmental plasticity. Gifford et al (2008). Proc Natl Acad Sci U S A Coll-specific nitrogen responses mediate developmental plasticity. Gifford et al (2008). Proc Natl Acad Sci U S A Coll-specific nitrogen responses mediate developmental plasticity. Gifford et al (2008). Proc Natl Acad Sci U S A Coll-specific nitrogen responses mediate developmental plasticity. Gifford et al (2008). Plant Coll Coll-specific nitrogen responses mediate development genome-wide approach. Deeken et al (2006). Plant Coll Coll-specific nitrogen responses mediate development genome-wide approach. Deeken et al (2006). Plant Coll Coll-specific nitrogen responses mediate development. Deeken et al (2008). Plant Coll-specific nitrogen expression and solute profiles of Arabidopsis tumors: a genome-wide approach. Deeken et al (2008). Plant Coll-specific nitrogen profiles of Arabidopsis tumors: a genome-wide approach. Deeken et al (2003). Plant Coll-specific nitrogen germination in Arabidopsis. Dean Rider et al (2003). Plant J 116,036 interactions from GEO Malitsky-Aharoni-2008 Coll-specific nitrogen responses mediate development. Moreno-Risueno et al (2015). Science Coll-specific nitrogen profiles of the variety of the variet	WRKY40 and WRKY6 act downstream of the green leaf volatile E-2-hexenal in Arabidopsis. Mirabella et al (2015). $Plant\ J$ Co-expression with 598,546 interactions from GEO	
Co-expression with 669,788 interactions from GEO Decken-Hedrich-2006 A An integrated view of gene expression and solute profiles of Arabidopsis tumors: a genome-wide approach. Decken et al (2006). Plant Cell Co-expression with 604,796 interactions from GEO Dean Rider-Ogas-2003 Coordinate repression of regulators of embryonic identity by PICKLE during germination in Arabidopsis. Dean Rider et al (2003). Plant J Co-expression with 116,036 interactions from GEO Malitsky-Aharoni-2008 Che transcript and metabolite networks affected by the two clades of Arabidopsis glucosinolate biosynthesis regulators. Malitsky at al (2008). Plant Physiol Co-expression with 559,163 interactions from GEO Moreno-Risueno-Benfey-2015 Cranscriptional control of tissue formation throughout root development. Moreno-Risueno et al (2015). Science Co-expression with 648,813 interactions from GEO Schmid-Lohmann-2003 A Dissection of floral induction pathways using global expression analysis. Schmid et al (2003). Development Co-expression with 625,625 interactions from GEO Sozzani-Benfey-2010	Gifford-Birnbaum-2008	0.57%
Decken-Hedrich-2006 A Oeeken-Hedrich-2006 A On integrated view of gene expression and solute profiles of Arabidopsis tumors: a genome-wide approach. Decken et al (2006). Plant Cell Dean Rider-Ogas-2003 Ocordinate repression of regulators of embryonic identity by PICKLE during germination in Arabidopsis. Dean Rider et al (2003). Plant J Ocerpression with 116,036 interactions from GEO Malitsky-Aharoni-2008 Malitsky-Aharoni-2008 Moreno-Risueno-Benfey-2015 Coexpression with 559,163 interactions from GEO Moreno-Risueno-Benfey-2015 Coexpression with 648,813 interactions from GEO Schmid-Lohmann-2003 A Oissection of floral induction pathways using global expression analysis. Schmid et al (2003). Development Coexpression with 625,625 interactions from GEO Sozzani-Benfey-2010 Oispatiotemporal regulation of cell-cycle genes by SHORTROOT links patterning and growth. Sozzani et al (2010). Nature Coexpression with 604,619 interactions from GEO Shared protein domains 3.009	Cell-specific nitrogen responses mediate developmental plasticity. Gifford et al (2008). Proc Natl Acad Sci U S A	
An integrated view of gene expression and solute profiles of Arabidopsis tumors: a genome-wide approach. Decken et al (2006). **Polant Cell** Co-expression with 604,796 interactions from GEO **Dean Rider-Ogas-2003** Coordinate repression of regulators of embryonic identity by PICKLE during germination in Arabidopsis. Dean Rider et al (2003). **Polant J** Co-expression with 116,036 interactions from GEO **Malitsky-Aharoni-2008** Che transcript and metabolite networks affected by the two clades of Arabidopsis glucosinolate biosynthesis regulators. Malitsky et al (2008). **Polant Physiol** Co-expression with 559,163 interactions from GEO **Moreno-Risueno-Benfey-2015** Co-expression with 648,813 interactions from GEO **Schmid-Lohmann-2003 A** Co-expression with 648,813 interactions from GEO **Schmid-Lohmann-2003 A** Co-expression with 625,625 interactions from GEO **Sozzani-Benfey-2010** Co-expression with 625,625 interactions from GEO **Sozzani-Benfey-2010** Co-expression with 604,619 interactions from GEO **Schared protein domains** **3.009** **Schared protein domains** **3.009** **Application of cell-cycle genes by SHORTROOT links patterning and growth. Sozzani et al (2010). **Nature** Co-expression with 604,619 interactions from GEO **Schared protein domains**	Co-expression with 669,788 interactions from GEO	
Plant Cell Co-expression with 604,796 interactions from GEO Coan Rider-Ogas-2003 Coordinate repression of regulators of embryonic identity by PICKLE during germination in Arabidopsis. Dean Rider et al (2003). Plant J Co-expression with 116,036 interactions from GEO Malitsky-Aharoni-2008 Malitsky-Aharoni-2008 Co-expression with 519,163 interactions from GEO Moreno-Risueno-Benfey-2015 Co-expression with 559,163 interactions from GEO Moreno-Risueno-Benfey-2015 Co-expression with 648,813 interactions from GEO Schmid-Lohmann-2003 A Dissection of floral induction pathways using global expression analysis. Schmid et al (2003). Development Co-expression with 625,625 interactions from GEO Sozzani-Benfey-2010 Co-expression with 604,619 interactions from GEO Schared protein domains 3.009 Shared protein domains	Deeken-Hedrich-2006 A	0.54%
Dean Rider-Ogas-2003 Coordinate repression of regulators of embryonic identity by PICKLE during germination in Arabidopsis. Dean Rider et al (2003). Co-expression with 116,036 interactions from GEO Malitsky-Aharoni-2008 Co-expression with 259,163 interactions from GEO Moreno-Risueno-Benfey-2015 Co-expression with 648,813 interactions from GEO Co-expression with 625,625 interactions from GEO Co-expression with 604,619 interactions from GEO	An integrated view of gene expression and solute profiles of Arabidopsis tumors: a genome-wide approach. Deeken et al (2006). Plant Cell	
Coordinate repression of regulators of embryonic identity by PICKLE during germination in Arabidopsis. Dean Rider et al (2003). Coordinate repression of regulators of embryonic identity by PICKLE during germination in Arabidopsis. Dean Rider et al (2003). Coordinate repression with 116,036 interactions from GEO Malitsky-Aharoni-2008 Che transcript and metabolite networks affected by the two clades of Arabidopsis glucosinolate biosynthesis regulators. Malitsky et al (2008). Plant Physiol Coordinate repression with 559,163 interactions from GEO Moreno-Risueno-Benfey-2015 Coordinate repression with 559,163 interactions from GEO Coordinate repression with 648,813 interactions from GEO Coordinate re	Co-expression with 604,796 interactions from GEO	
Co-expression with 116,036 interactions from GEO Malitsky-Aharoni-2008 Co-expression with 2008 Co-expression with 559,163 interactions from GEO Moreno-Risueno-Benfey-2015 Co-expression with 648,813 interactions from GEO Schmid-Lohmann-2003 A Dissection of floral induction pathways using global expression analysis. Schmid et al (2003). Development Co-expression with 625,625 interactions from GEO Sozzani-Benfey-2010 Spatiotemporal regulation of cell-cycle genes by SHORTROOT links patterning and growth. Sozzani et al (2010). Nature Co-expression with 604,619 interactions from GEO Shared protein domains 3.009	Dean Rider-Ogas-2003	0.54%
Malitsky-Aharoni-2008 The transcript and metabolite networks affected by the two clades of Arabidopsis glucosinolate biosynthesis regulators. Malitsky et al (2008). Plant Physiol Co-expression with 559,163 interactions from GEO Moreno-Risueno-Benfey-2015 Cranscriptional control of tissue formation throughout root development. Moreno-Risueno et al (2015). Science Co-expression with 648,813 interactions from GEO Schmid-Lohmann-2003 A Dissection of floral induction pathways using global expression analysis. Schmid et al (2003). Development Co-expression with 625,625 interactions from GEO Sozzani-Benfey-2010 Spatiotemporal regulation of cell-cycle genes by SHORTROOT links patterning and growth. Sozzani et al (2010). Nature Co-expression with 604,619 interactions from GEO Shared protein domains 3.009	Coordinate repression of regulators of embryonic identity by PICKLE during germination in Arabidopsis. Dean Rider et al (2003). $Plant\ J$	
The transcript and metabolite networks affected by the two clades of Arabidopsis glucosinolate biosynthesis regulators. Malitsky et al (2008). Plant Physiol Co-expression with 559,163 interactions from GEO Moreno-Risueno-Benfey-2015 Cranscriptional control of tissue formation throughout root development. Moreno-Risueno et al (2015). Science Co-expression with 648,813 interactions from GEO Schmid-Lohmann-2003 A Dissection of floral induction pathways using global expression analysis. Schmid et al (2003). Development Co-expression with 625,625 interactions from GEO Sozzani-Benfey-2010 Spatiotemporal regulation of cell-cycle genes by SHORTROOT links patterning and growth. Sozzani et al (2010). Nature Co-expression with 604,619 interactions from GEO Shared protein domains 3.00%	Co-expression with 116,036 interactions from GEO	
tal (2008). Plant Physiol Co-expression with 559,163 interactions from GEO Moreno-Risueno-Benfey-2015 Cranscriptional control of tissue formation throughout root development. Moreno-Risueno et al (2015). Science Co-expression with 648,813 interactions from GEO Schmid-Lohmann-2003 A Dissection of floral induction pathways using global expression analysis. Schmid et al (2003). Development Co-expression with 625,625 interactions from GEO Sozzani-Benfey-2010 Spatiotemporal regulation of cell-cycle genes by SHORTROOT links patterning and growth. Sozzani et al (2010). Nature Co-expression with 604,619 interactions from GEO Shared protein domains 3.009	Malitsky-Aharoni-2008	0.53%
Moreno-Risueno-Benfey-2015 Cranscriptional control of tissue formation throughout root development. Moreno-Risueno et al (2015). Science Co-expression with 648,813 interactions from GEO Schmid-Lohmann-2003 A Dissection of floral induction pathways using global expression analysis. Schmid et al (2003). Development Co-expression with 625,625 interactions from GEO Sozzani-Benfey-2010 Spatiotemporal regulation of cell-cycle genes by SHORTROOT links patterning and growth. Sozzani et al (2010). Nature Co-expression with 604,619 interactions from GEO Schared protein domains 3.009	The transcript and metabolite networks affected by the two clades of Arabidopsis glucosinolate biosynthesis regulators. Malitsky et al (2008). <i>Plant Physiol</i>	
Co-expression with 648,813 interactions from GEO Schmid-Lohmann-2003 A Dissection of floral induction pathways using global expression analysis. Schmid et al (2003). Development Co-expression with 625,625 interactions from GEO Sozzani-Benfey-2010 Spatiotemporal regulation of cell-cycle genes by SHORTROOT links patterning and growth. Sozzani et al (2010). Nature Co-expression with 604,619 interactions from GEO Shared protein domains 3.009	Co-expression with 559,163 interactions from GEO	
Co-expression with 648,813 interactions from GEO Schmid-Lohmann-2003 A Dissection of floral induction pathways using global expression analysis. Schmid et al (2003). Development Co-expression with 625,625 interactions from GEO Sozzani-Benfey-2010 Spatiotemporal regulation of cell-cycle genes by SHORTROOT links patterning and growth. Sozzani et al (2010). Nature Co-expression with 604,619 interactions from GEO Shared protein domains 3.00%	Moreno-Risueno-Benfey-2015	0.53%
Dissection of floral induction pathways using global expression analysis. Schmid et al (2003). Development Co-expression with 625,625 interactions from GEO Sozzani-Benfey-2010 Spatiotemporal regulation of cell-cycle genes by SHORTROOT links patterning and growth. Sozzani et al (2010). Nature Co-expression with 604,619 interactions from GEO Shared protein domains 3.00%	Transcriptional control of tissue formation throughout root development. Moreno-Risueno et al (2015). Science Co-expression with 648,813 interactions from GEO	
Co-expression with 625,625 interactions from GEO Sozzani-Benfey-2010 Spatiotemporal regulation of cell-cycle genes by SHORTROOT links patterning and growth. Sozzani et al (2010). Nature Co-expression with 604,619 interactions from GEO Shared protein domains 3.00%	Schmid-Lohmann-2003 A	0.53%
Sozzani-Benfey-2010 Spatiotemporal regulation of cell-cycle genes by SHORTROOT links patterning and growth. Sozzani et al (2010). Nature Co-expression with 604,619 interactions from GEO Shared protein domains 3.00%	Dissection of floral induction pathways using global expression analysis. Schmid et al (2003). Development	
Spatiotemporal regulation of cell-cycle genes by SHORTROOT links patterning and growth. Sozzani et al (2010). Nature Co-expression with 604,619 interactions from GEO Shared protein domains 3.00%	Co-expression with 625,625 interactions from GEO	
Co-expression with 604,619 interactions from GEO Shared protein domains 3.00%	Sozzani-Benfey-2010	0.51%
•	Spatiotemporal regulation of cell-cycle genes by SHORTROOT links patterning and growth. Sozzani et al (2010). Nature Co-expression with 604,619 interactions from GEO	
1 700	Shared protein domains	3.00%
$2\mathrm{FAM}$	PFAM	1.76%

Shared protein domains	3.00%
PFAM	
Shared protein domains with 680,094 interactions from Pfam	
INTERPRO	1.23%
Shared protein domains with 743,516 interactions from InterPro	
Lee-Rhee-2010 Shared protein domains	0.01%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010) . Nat $Biotechnol$	
Shared protein domains with $50,665$ interactions from supplementary material	
Genetic Interactions	2.87%
BIOGRID-SMALL-SCALE-STUDIES	2.87%
Genetic Interactions with 219 interactions from BioGRID	
Co-localization	0.52%
Brady-Benfey-2007	0.52%
A high-resolution root spatiotemporal map reveals dominant expression patterns. Brady et al (2007). Science	
Co-localization with 831,109 interactions from GEO	