Table 1. GRNs built in this study.

net_type	study	note	sample_size	reference
tissue	stelpflug2016	B73	93	Stelpflug et al. 2016
	walley2016	B73	23	Walley et al. 2016
	briggs	B73	23	Briggs
		Mo17	23	Briggs
		BxM	23	Briggs
	leaf dev	leaf	40	Leaf Dev
	seed dev	embryo_endpsperm	61	Seed Dev
	dev atlas	combined	139	Dev Atlas
	root dev	root	50	Root Dev
genotype	eitchen2013	seedling_leaf3	62	Eitchen et al. 2013
	hirsch2014	seedling	503	Hirsch et al. 2014
	leiboff2015	SAM	383	Leiboff et al. 2015
	jin2016	kernel	368	Jin et al. 2016
	lin2017	ear	26	Lin et al. 2017
		root	27	Lin et al. 2017
		shoot	27	Lin et al. 2017
		tassel	26	Lin et al. 2017
		SAM	27	Lin et al. 2017
	kremling2018	GRoot	274	Kremling et al. 2018
		GShoot	280	Kremling et al. 2018
		Kern	231	Kremling et al. 2018
		L3Base	264	Kremling et al. 2018
		L3Tip	266	Kremling et al. 2018
		LMAD	204	Kremling et al. 2018
		LMAN	262	Kremling et al. 2018
	shaefer2018	root_GCN	48	Shaefer et al. 2018
	kaeppler2018	endosperm	89	Kaeppler et al. 2018
		internode	43	Kaeppler et al. 2018
		leaf	50	Kaeppler et al. 2018
		root	49	Kaeppler et al. 2018
		seedling	216	Kaeppler et al. 2018
		seedling inbred	166	Kaeppler et al. 2018
		seedling hybrid	50	Kaeppler et al. 2018
	biomap	endosperm	121	Biomap
		internode	77	Biomap
		leaf	84	Biomap
		root	84	Biomap
		seedling	84	Biomap
tissue*genotype	lin2017	5*27	133	Lin et al. 2017
	kremling2018	7*306	1781	Kremling et al. 2018
	kaeppler2018	5*96	447	Kaeppler et al. 2018
	briggs	3*23	73	Briggs
	biomap	5*121	450	Biomap
ril	li2013	SAM	107	Li et al. 2013
liftover	walley2016	mRNA	23	Walley et al. 2016
	huang2018	leaf	394	Huang et al. 2018
		root	176	Huang et al. 2018
		SAM	406	Huang et al. 2018
		seed	159	Huang et al. 2018

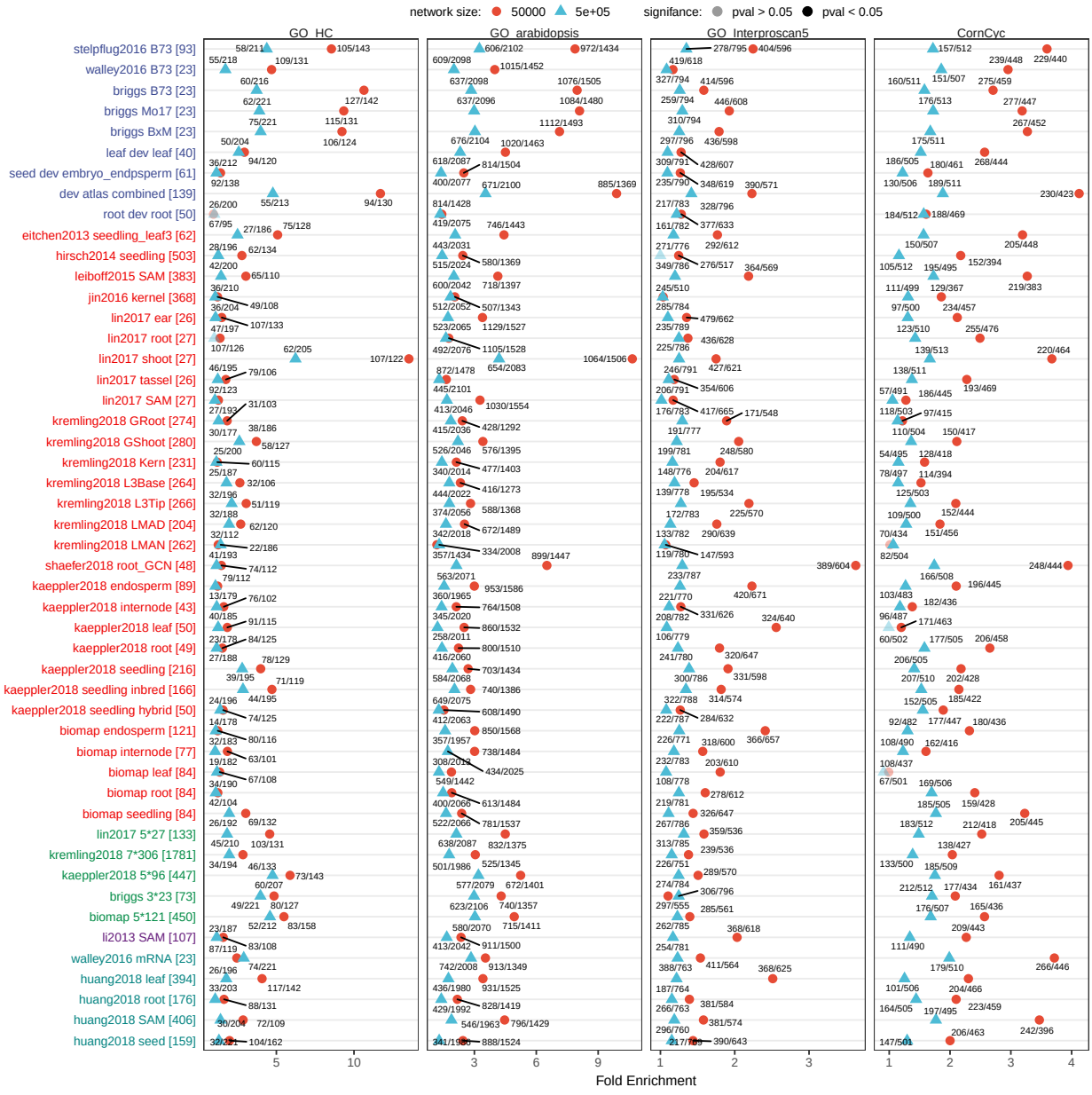

Fig 1

Fold enrichment in functional categories for networks of different sizes. For each functional classification (Gene Ontology or CornCyc metabolic pathway), the fold enrichment and significance of co-regulation in a given GRN was determined using permutation (comparing observation to the distribution of 100 permuted networks with the same size but functional labels shuffled, see Methods). Network of two different sizes (top 50,000 edges (red circles) or 500,000 edges (blue triangles)) were used in this analysis. Almost all enrichment is significant (i.e., having a P-value < 0.05), with rare insignificant ones shown in faded colors usually due to small sample size. Numbers in plot indicate the number of enriched / total functional terms for each evaluation.

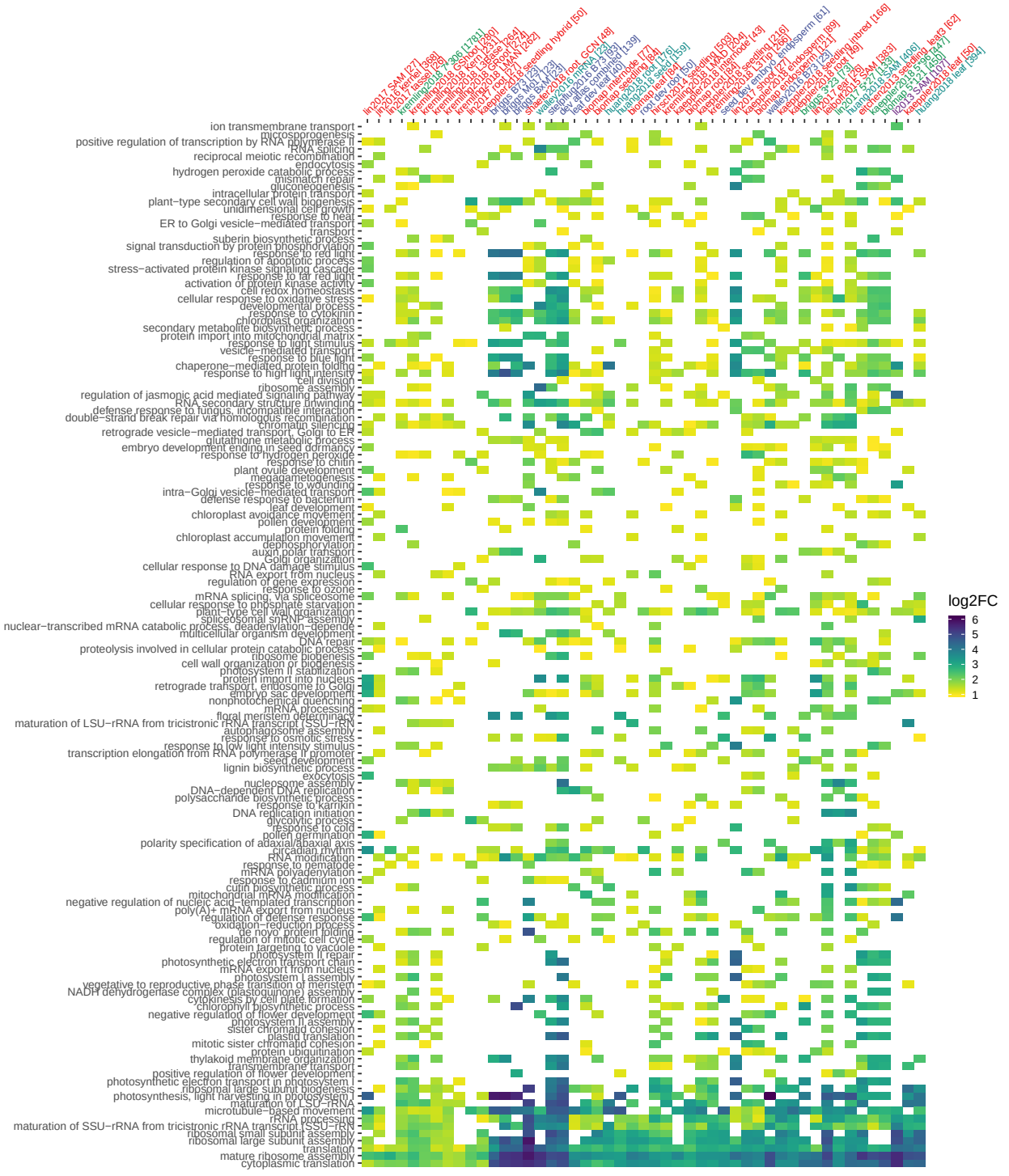

Fig 2

Heatmap of 140 GO (uniprot.plants) terms significantly enriched ($P < 0.05$) in at least 5 GRNs. Rows (GO terms) and columns (GRNs) are both clustered using hierarchical clustering (pearson correlation coefficient distant measure and "ward.D" clustering option).

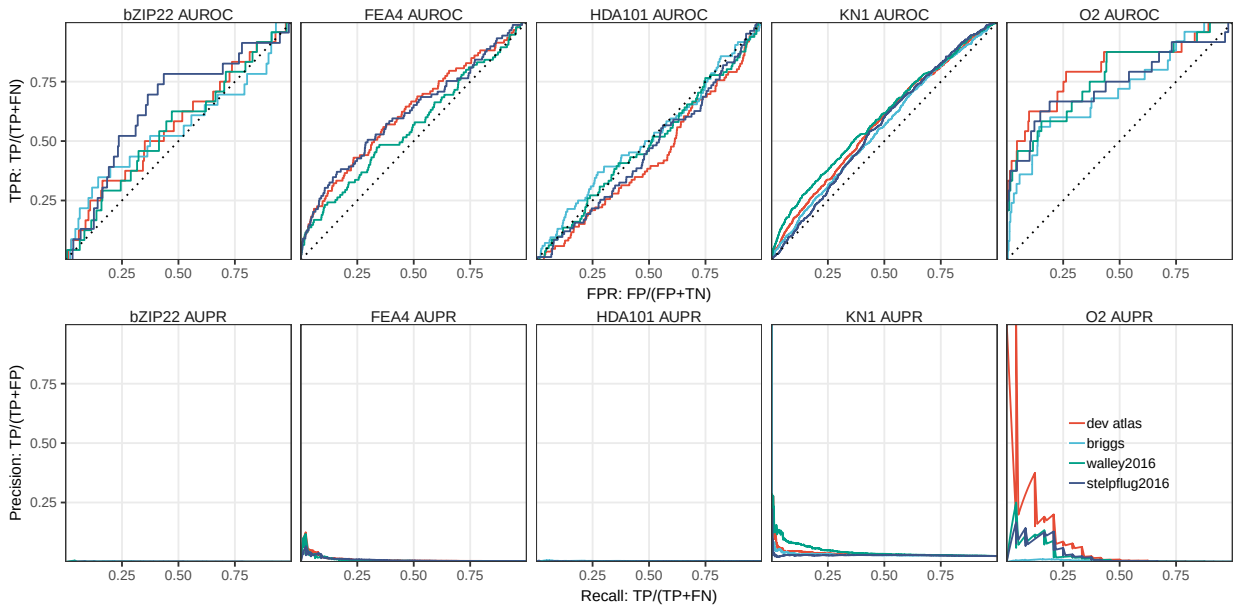

Fig S2

Area under receiver operating curves (AUROC) and area under precision-recall curve (AUPR) for GRNs built using different input datasets evaluated using experimentally (Chip-seq, mutant & wildtype RNA-Seq) determined transcription factor (TF) targets.


AUROC bZIP22
AUROC FEA4
AUROC HDA101
AUROC KN1
AUROC O2
AUROC RA1
stelpflug2016 B73 [93] .647 .618 .464 .560 .741
walley2016 B73 [23] .554 .562 .487 .597 .766
briggs B73 [23] .552 .516 .555 .709
briggs Mo17 [23] .536 .620 .479 .564 .699
briggs BxM [23] .487 .572 .438 .541 .712
leaf dev leaf [40] .474 .557 .521 .519
seed dev embryo_endpsperm [61] .591 .483 .581 .781
dev atlas combined [139] .567 .621 .434 .576 .803
root dev root [50] .611 .423 .483 .544
eitchen2013 seedling_leaf3 [62] .481
hirsch2014 seedling [503] .521 .544 .506
leiboff2015 SAM [383] .523 .564 .451 .513
jin2016 kernel [368] .521 .510 .415 .557 .866
lin2017 ear [26] .597 .541 .589 .502
lin2017 root [27] .502 .514 .454
lin2017 shoot [27] .560 .434 .459
lin2017 tassel [26] .495 .455 .523
lin2017 SAM [27] .436 .561 .531 .576
kremling2018 GRoot [274] .489 .478
kremling2018 GShoot [280] .432 .550
kremling2018 Kern [231] .582 .482 .515 .741
kremling2018 L3Base [264] .519
kremling2018 L3Tip [266] .440 .484 .532
kremling2018 LMAD [204] .483 .505
kremling2018 LMAN [262] .408 .530
shaefer2018 root_GCN [48] .511
kaeppler2018 endosperm [89] .503 .509 .571
kaeppler2018 internode [43] .555 .489
kaeppler2018 leaf [50] .468
kaeppler2018 root [49] .465
kaeppler2018 seedling [216] .507 .547
kaeppler2018 seedling inbred [166] .477 .547
kaeppler2018 seedling hybrid [50] .489 .535
biomap endosperm [121] .418 .466 .606
biomap internode [77] .560 .494
biomap leaf [84] .498
biomap root [84] .508 .461
biomap seedling [84] .483 .521
lin2017 5*27 [133] .515 .590 .448 .523
kremling2018 7*306 [1781] .442 .429 .800
kaeppler2018 5*96 [447] .566 .469 .526 .765
briggs 3*23 [73] .582 .621 .427 .570 .728
biomap 5*121 [450] .566 .440 .541 .768
li2013 SAM [107] .530 .447 .555
walley2016 mRNA [23] .493 .493 .500 .495
huang2018 leaf [394] .500
huang2018 root [176] .499
huang2018 SAM [406] .499 .505 .500
huang2018 seed [159] .525 .505 .500 .483
AUPR bZIP22
AUPR FEA4
AUPR HDA101
AUPR KN1
AUPR O2
AUPR RA1
stelpflug2016 B73 [93] .001 .009 .003 .028 .028
walley2016 B73 [23] .001 .008 .003 .045 .027
briggs B73 [23] .001 .004 .032
briggs Mo17 [23] .001 .008 .004 .035
briggs BxM [23] .001 .007 .003 .031
leaf dev leaf [40] .001 .005 .005 .027
seed dev embryo_endpsperm [61] .002 .003 .040
dev atlas combined [139] .001 .010 .003 .035 .092
root dev root [50] .001 .003 .003 .026
eitchen2013 seedling_leaf3 [62] .003
hirsch2014 seedling [503] .004 .004 .034
leiboff2015 SAM [383] .001 .005 .003 .028
jin2016 kernel [368] .001 .004 .002 .035 .044
lin2017 ear [26] .007 .003 .041 .008
lin2017 root [27] .003 .004 .018
lin2017 shoot [27] .005 .003 .020
lin2017 tassel [26] .001 .003 .024
lin2017 SAM [27] .001 .005 .003 .049
kremling2018 GRoot [274] .003 .023
kremling2018 GShoot [280] .002 .043
kremling2018 Kern [231] .001 .002 .029
kremling2018 L3Base [264] .003
kremling2018 L3Tip [266] .003 .021 .133
kremling2018 LMAD [204] .003 .022
kremling2018 LMAN [262] .002 .025
shaefer2018 root_GCN [48] .003
kaeppler2018 endosperm [89] .001 .002
kaeppler2018 internode [43] .003 .023
kaeppler2018 leaf [50] .003
kaeppler2018 root [49] .003
kaeppler2018 seedling [216] .003 .040
kaeppler2018 seedling inbred [166] .003 .038
kaeppler2018 seedling hybrid [50] .003 .032
biomap endosperm [121] .001 .002
biomap internode [77] .004 .024
biomap leaf [84] .003
biomap root [84] .005 .003
biomap seedling [84] .003 .030
lin2017 5*27 [133] .001 .007 .003 .031
kremling2018 7*306 [1781] .003 .024 .060
kaeppler2018 5*96 [447] .002 .003 .033
briggs 3*23 [73] .001 .008 .003 .035
biomap 5*121 [450] .001 .003 .034
li2013 SAM [107] .005 .003 .044
walley2016 mRNA [23] .001 .004 .027
huang2018 leaf [394] .004
huang2018 root [176] .004
huang2018 SAM [406] .001 .004 .028
huang2018 seed [159] .001 .005 .029

Fig S3

Barplot showing AUROC and AUPRs for all GRNs evaluated using each of the 6 known TFs.

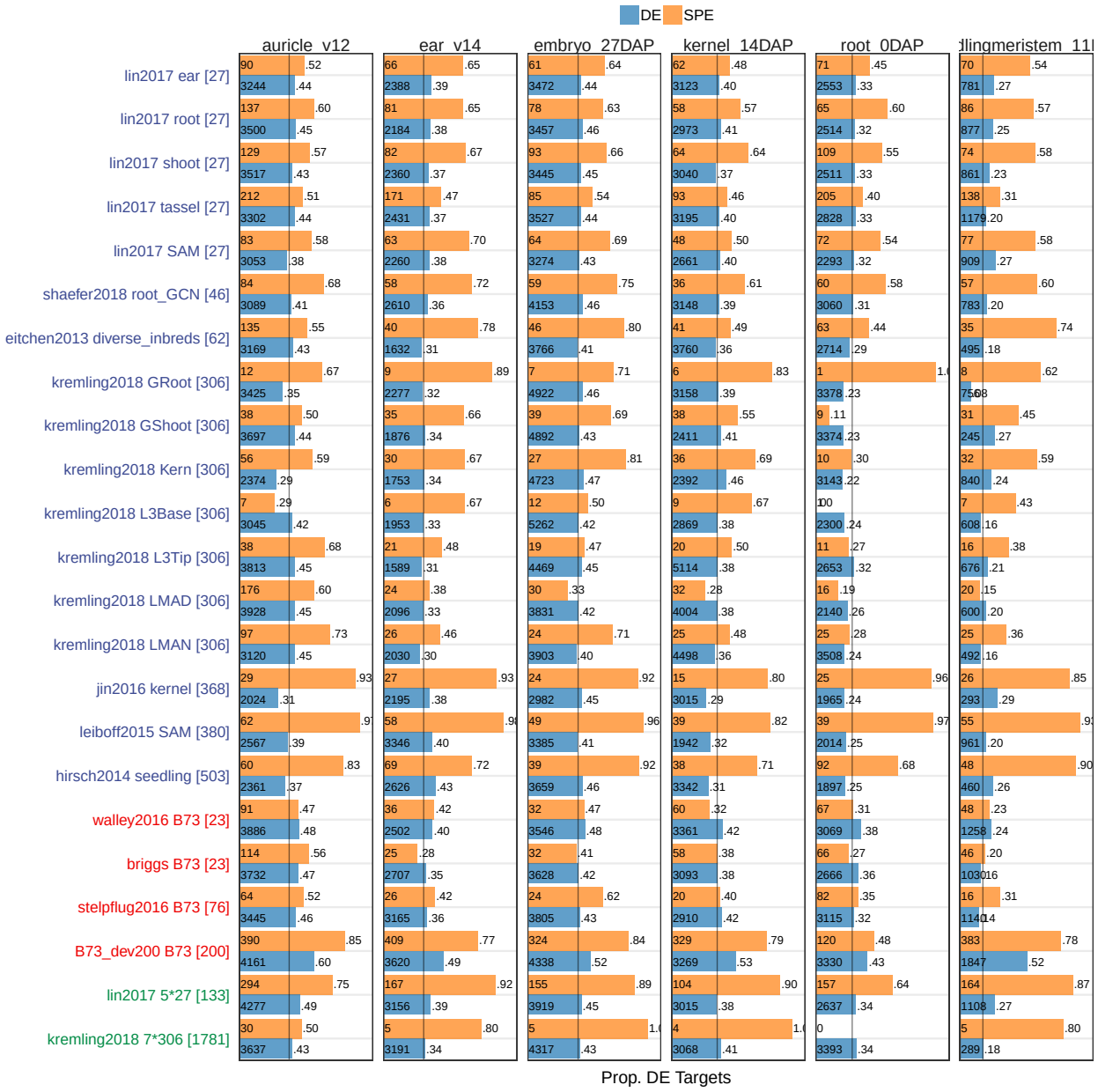

Fig S4

Enrichment of DE genes (using Briggs dataset) in predicted TF targets made by different GRNs. Only the top 10,000 strongest edges were taken from each GRN.

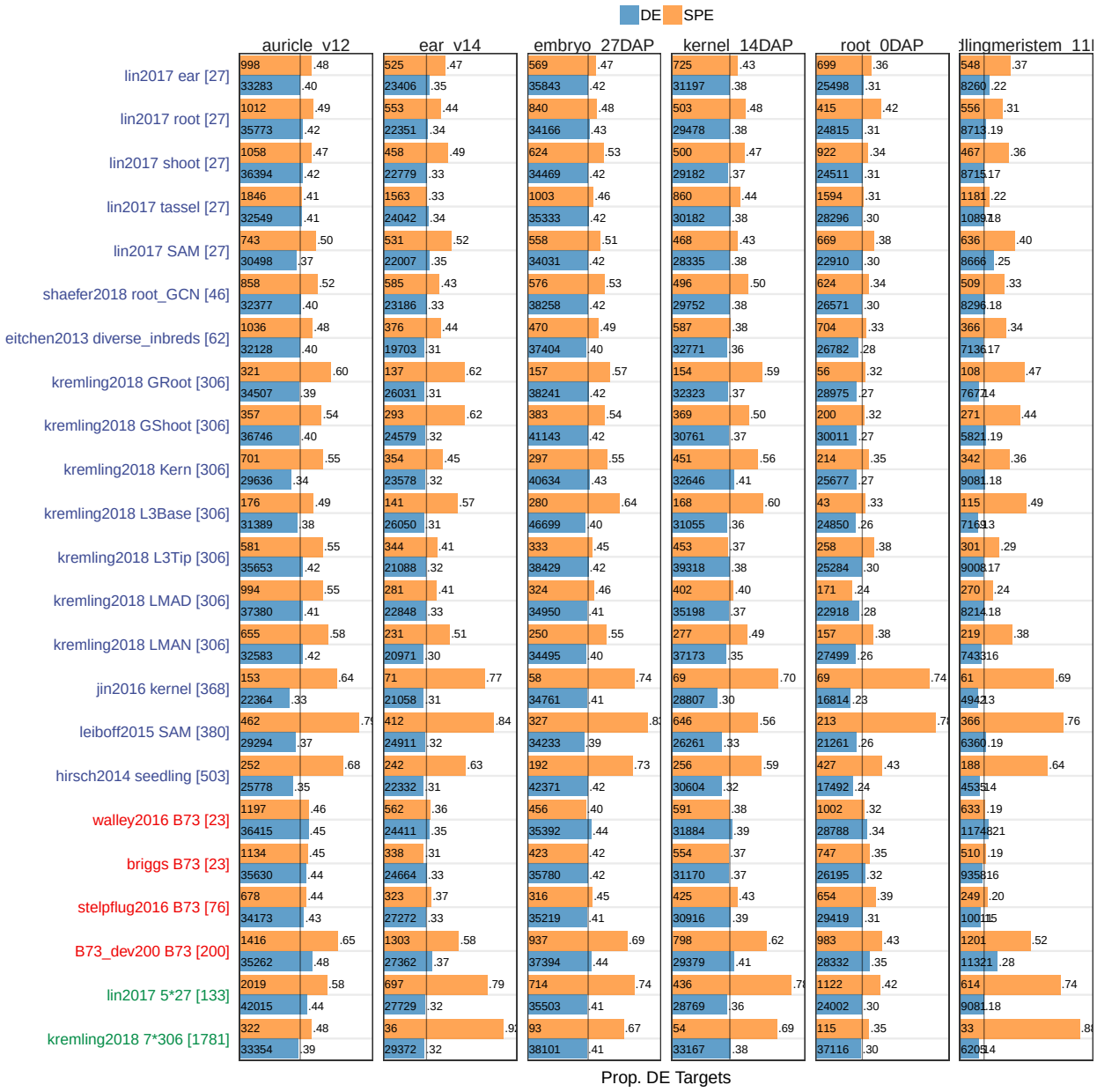

Fig S5

Enrichment of DE genes (using Briggs dataset) in predicted TF targets made by different GRNs. Only the top 100,000 strongest edges were taken from each GRN.

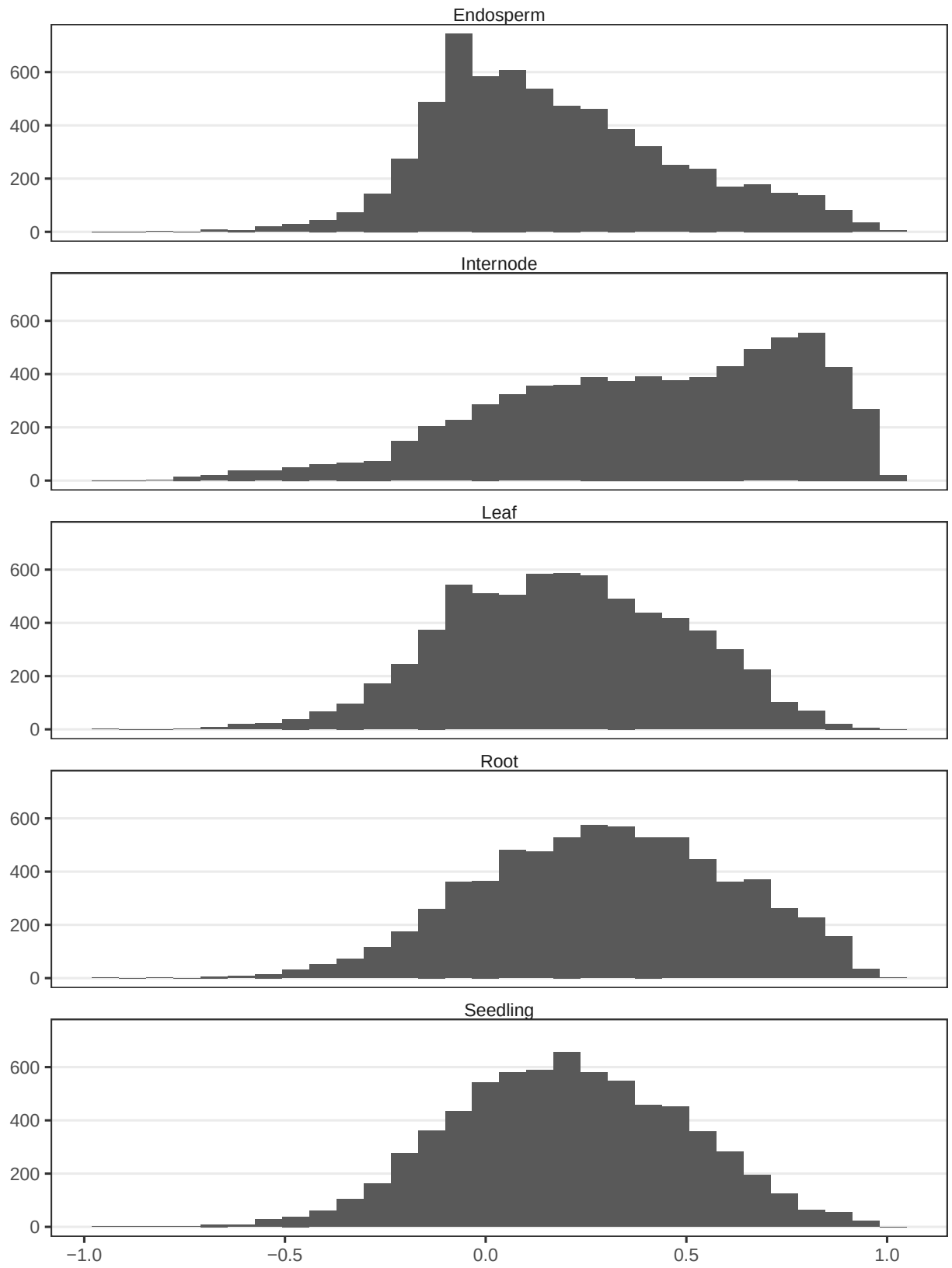
Endosperm
Internode
Leaf
Root
Seedling
600
400
200
0
−1.0
−0.5
0.0
0.5
1.0

Fig S6

Evaluation of GRN predictions using the bioMAP data containing ~200 genotypes (34 inbreds + 200 hybrids) in five tissues. The (Pearson) correlations between regulators and targets (as predicted by each GRN) were evaluated using the bioMAP expression matrix in each tissue, and shown as a boxplot for the top 10,000, 100,000 or 1,000,000 strongest edges in each network.