

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

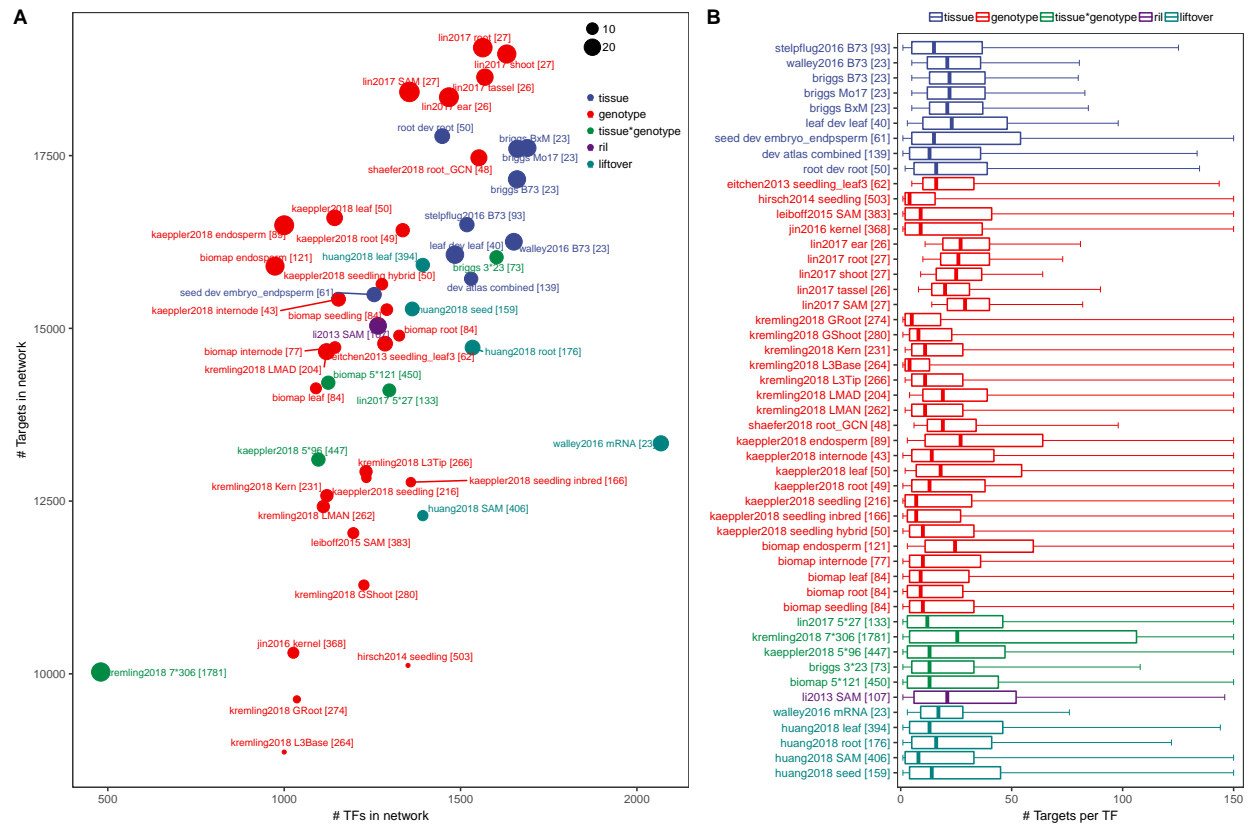


Fig SX

General network statistics.

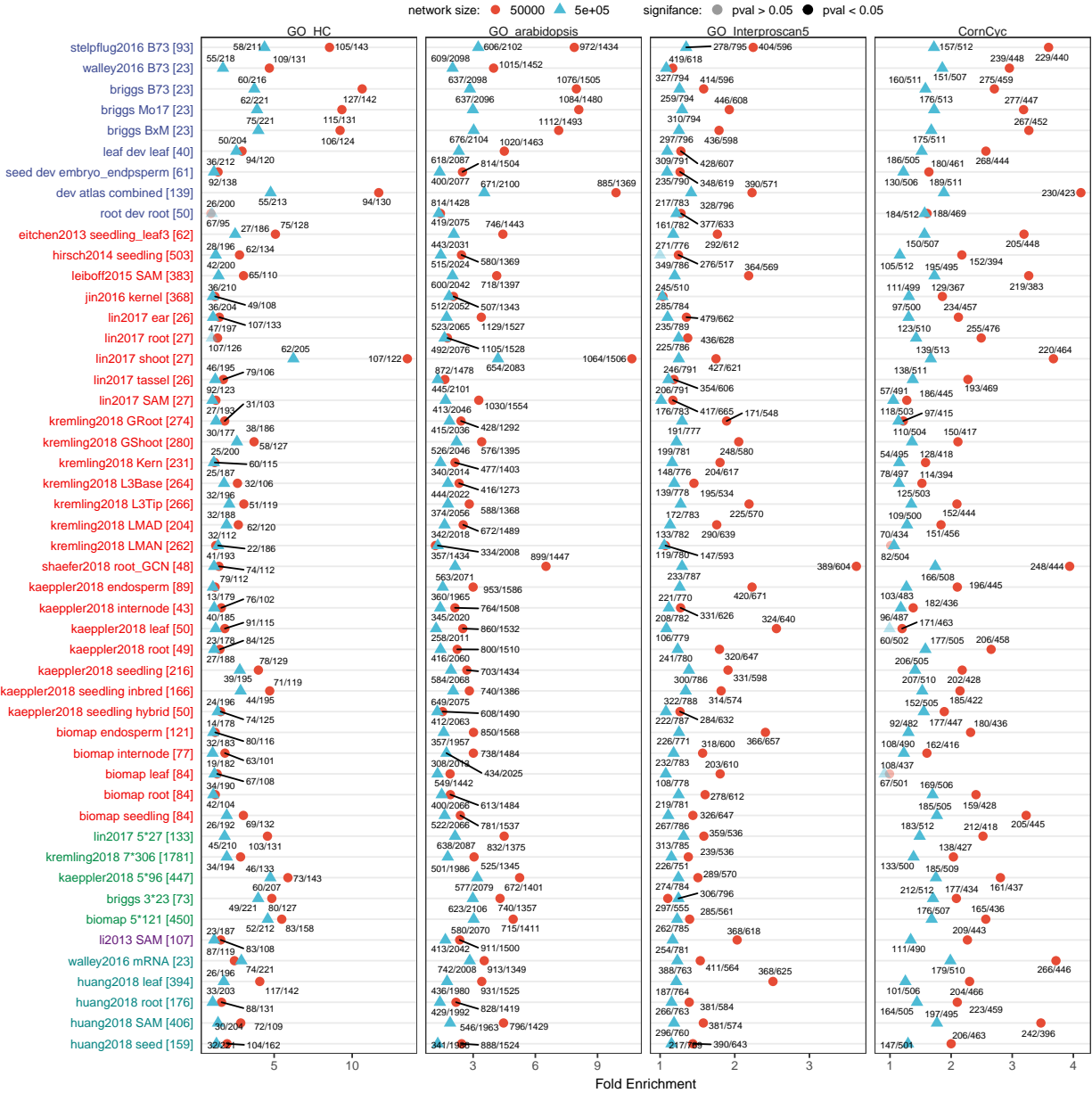


Fig 1

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.

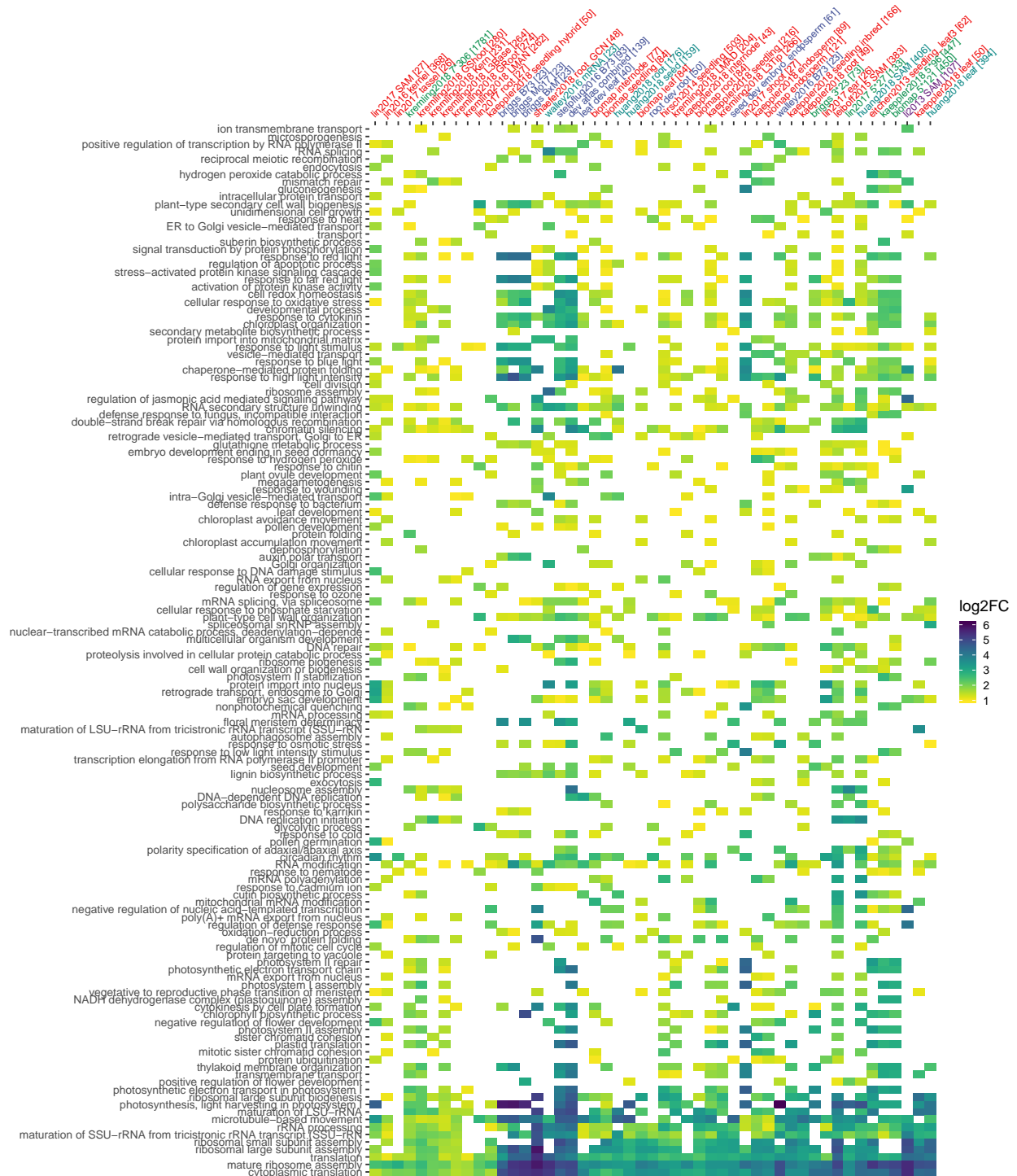


Fig 2

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).

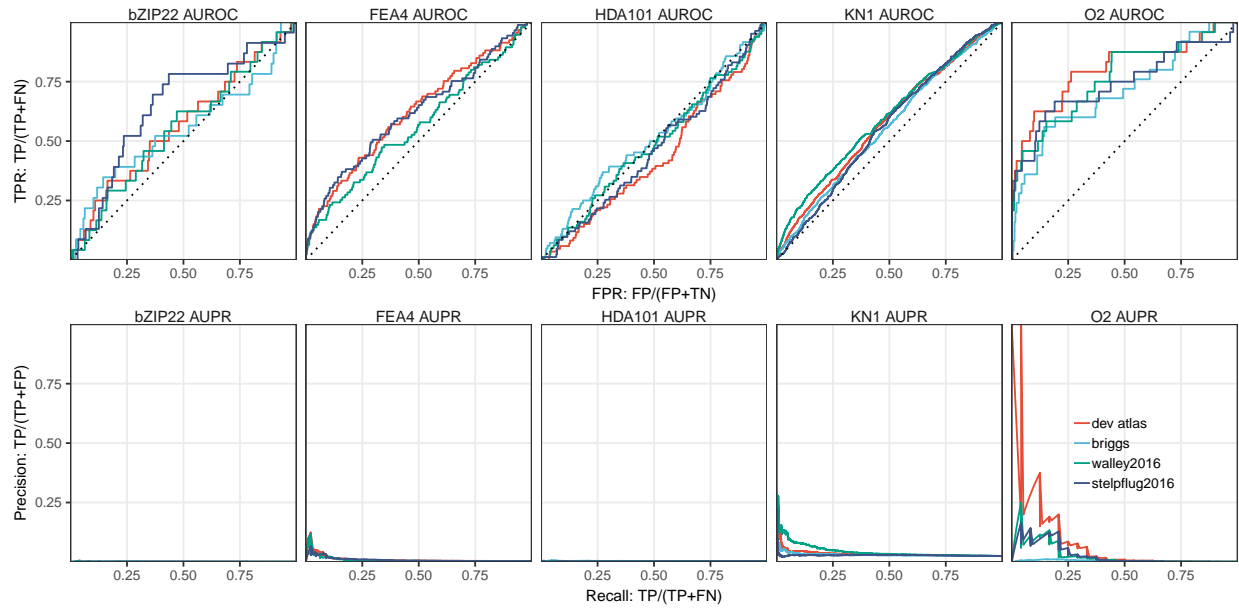


Fig S2

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.



Fig S3

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







Enrichment of DE genes (using Briggs dataset) in predicted TF targets made by different GRNs.

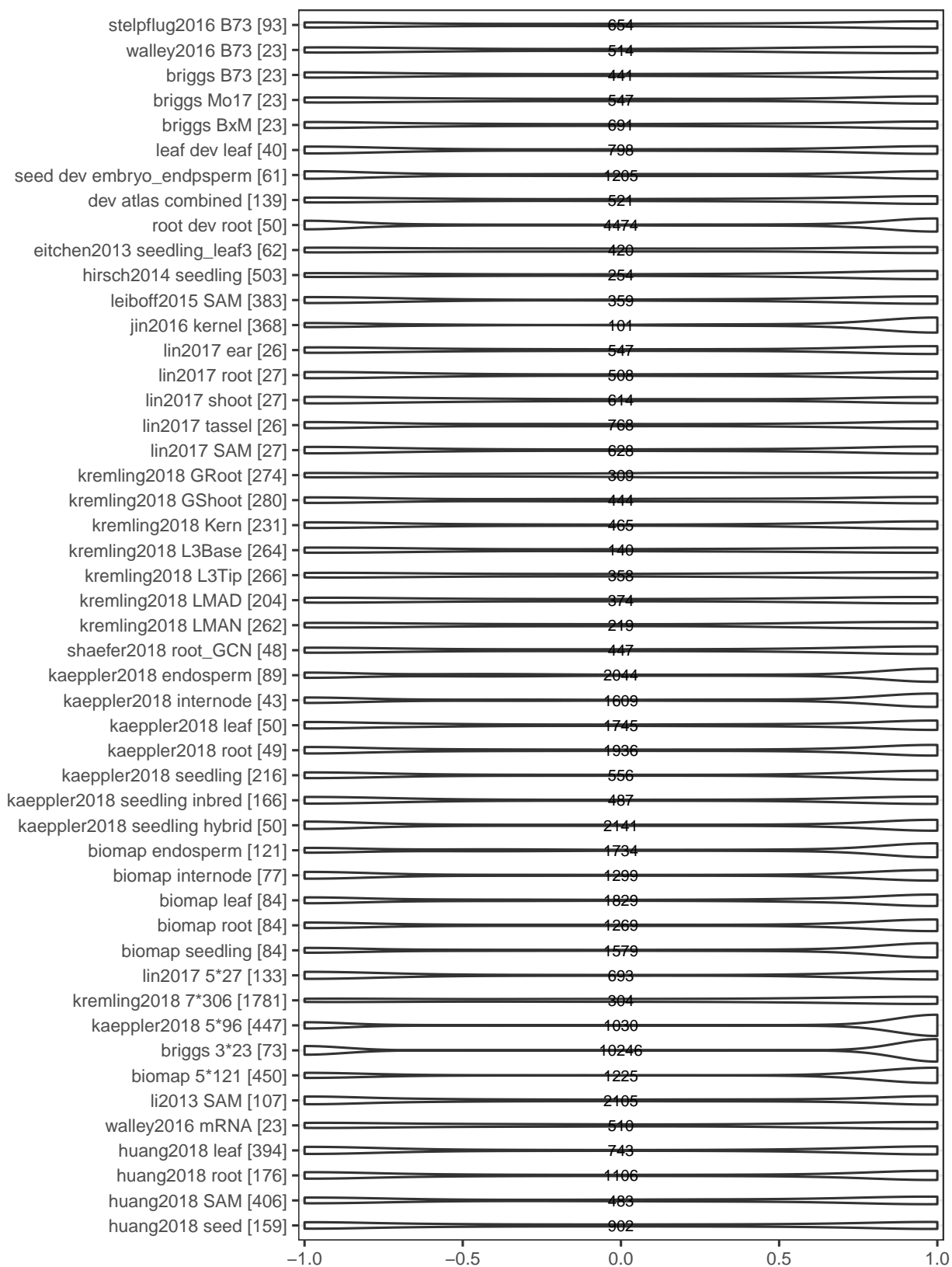


Fig SX

When a predicted TF/target pair is supported by at least 3 tissues of B73/Mo17 comparison (i.e., TF is DE4+ and target is DE), how often is the regulatory interaction consistent?

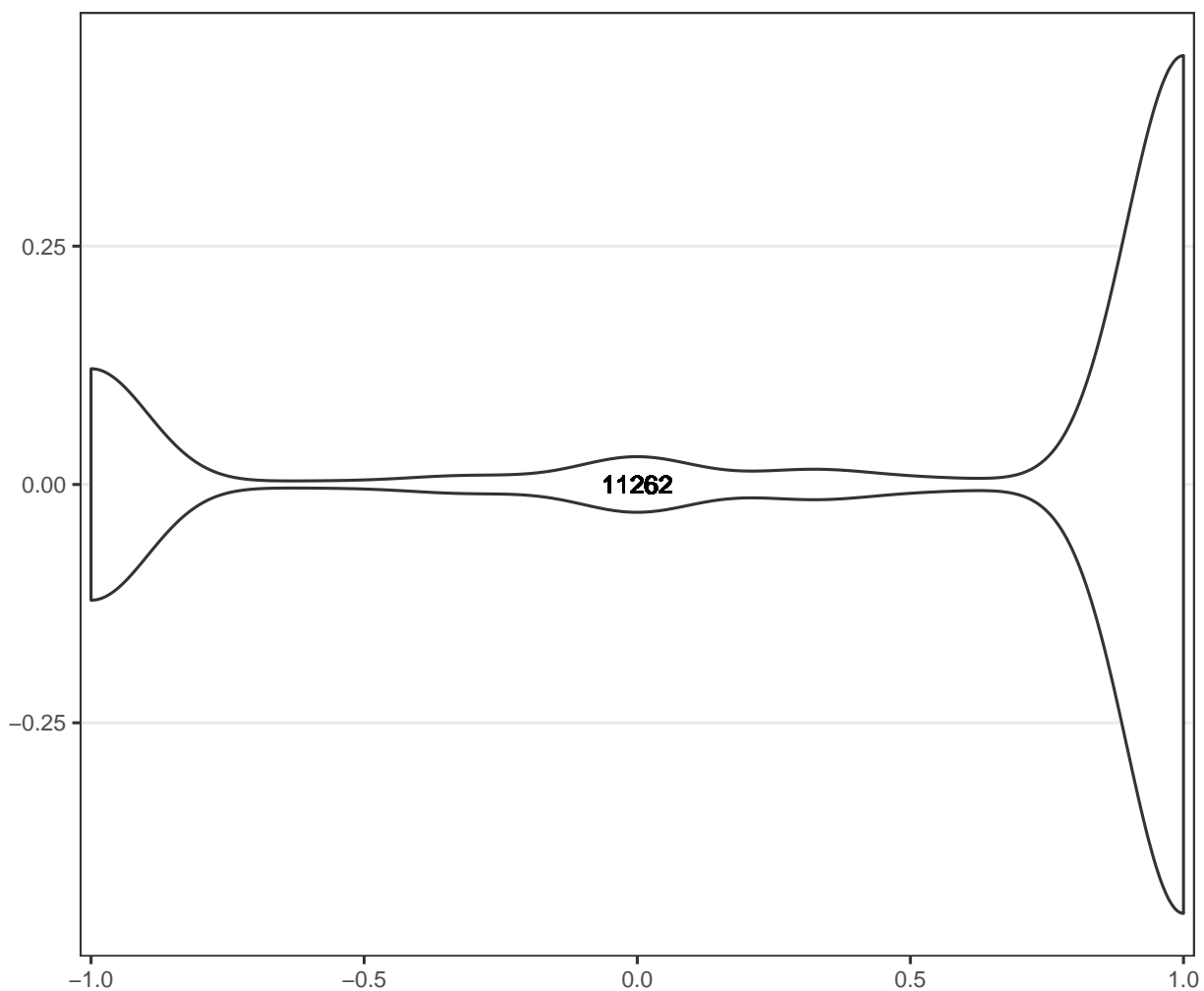


Fig SX

When a supported TF/target pair (in at least 1 tissues of B73/Mo17 comparison where TF is DE4+ and target is DE) is observed in multiple GRNs, how often is the regulatory interaction consistent?

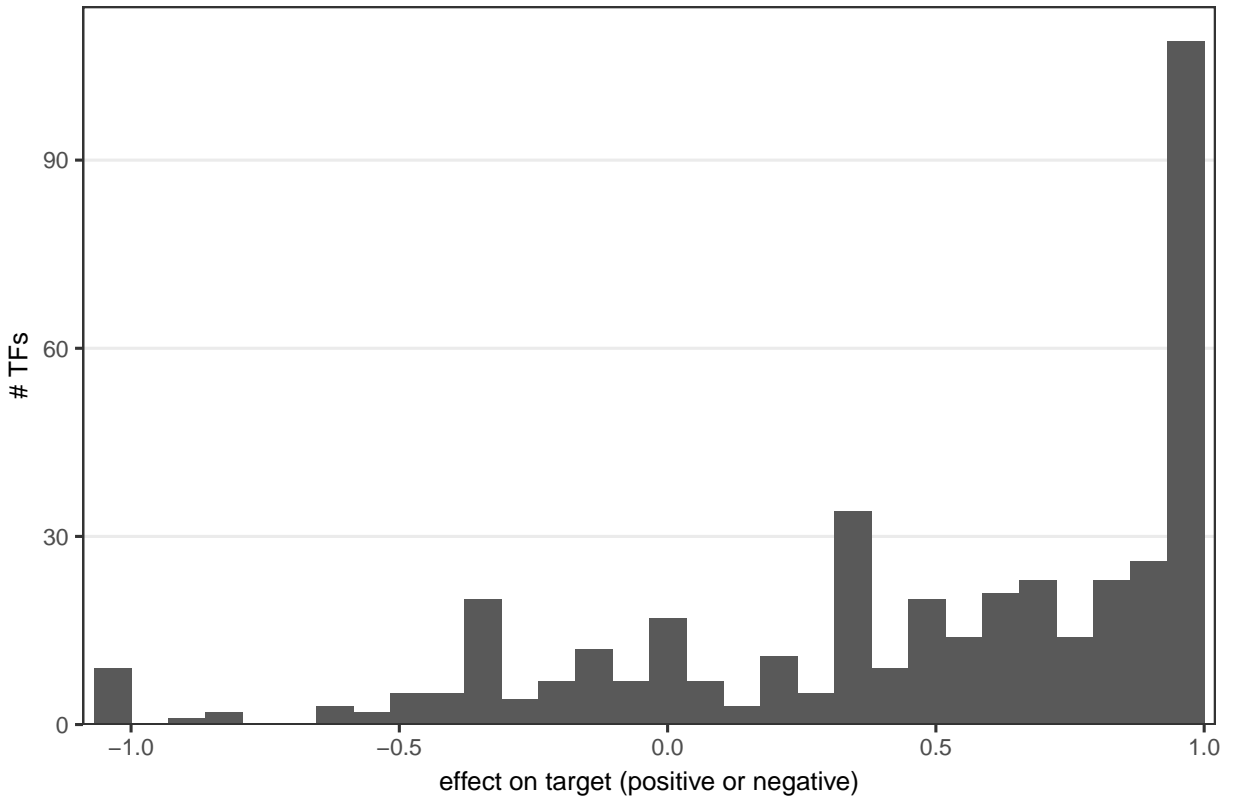


Fig SX

This is taking Briggs-supported TF/target pairs that are observed in at least 3 networks, filtered to TFs with at least 3 targets. Histogram shows the regulatory consistency among targets for each TF.

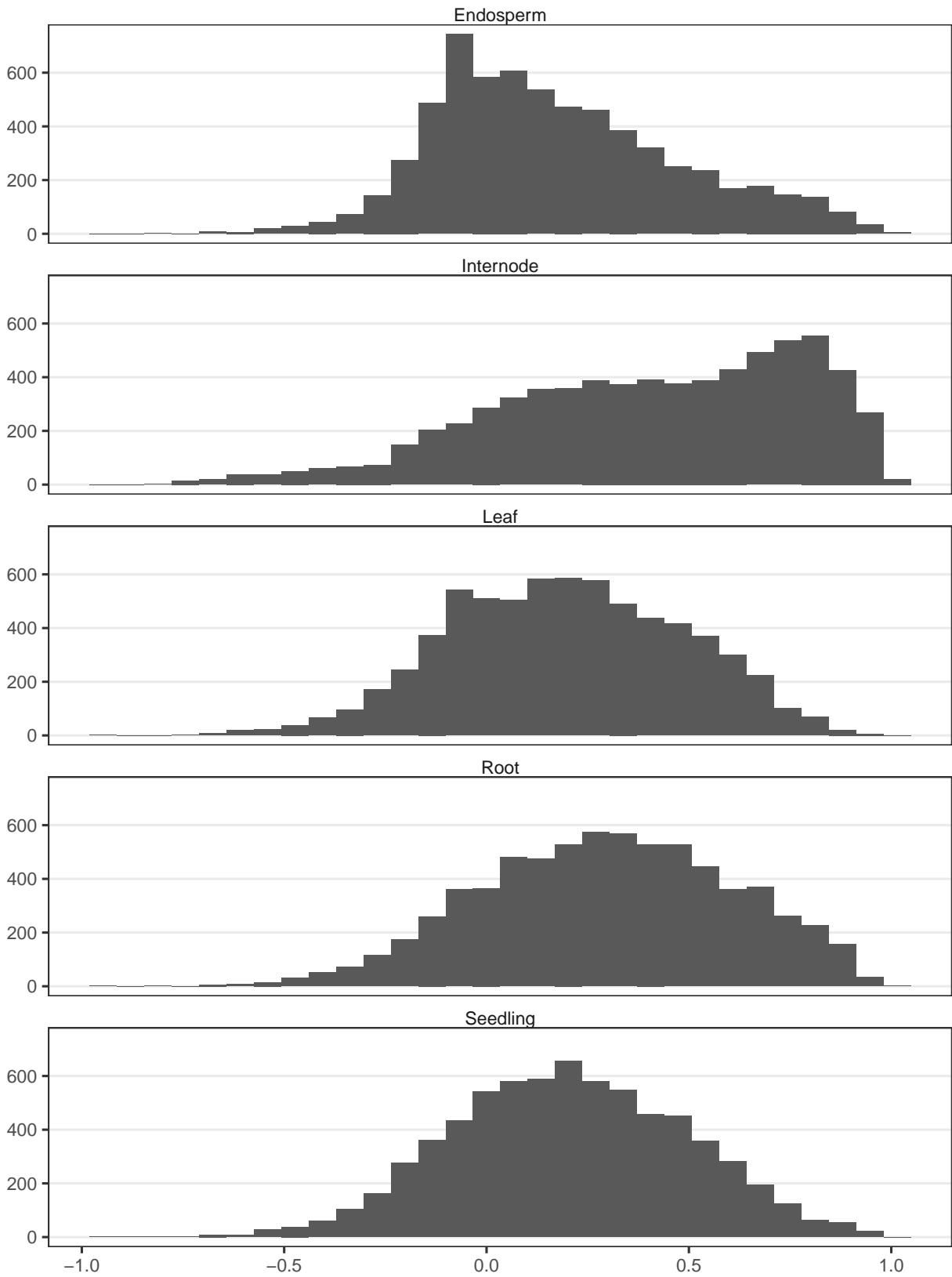


Fig SX

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.