Table 1. GRNs built in this study.

net_type	study	note	sample_size	reference
tissue	stelpflug2016	B73	93	
	walley2016	B73	23	
	briggs	B73	23	
	briggs	Mo17	23	
	briggs	BxM	23	
	leaf dev	leaf	40	
	seed dev	embryo_endpsperm	61	
	dev atlas	combined	139	
	root dev	root	50	
genotype	eitchen2013	seedling_leaf3	62	
	hirsch2014	seedling	503	
	leiboff2015	SAM	383	
	jin2016	kernel	368	
	lin2017	ear	26	
	lin2017	root	27	
	lin2017	shoot	27	
	lin2017	tassel	26	
	lin2017	SAM	27	
	kremling2018	GRoot	274	
	kremling2018	GShoot	280	
	kremling2018	Kern	231	
	kremling2018	L3Base	264	
	kremling2018	L3Tip	266	
	kremling2018	LMAD	204	
	kremling2018	LMAN	262	
	shaefer2018	root_GCN	48	
	kaeppler2018	endosperm	89	
	kaeppler2018	internode	43	
	kaeppler2018	leaf	50	
	kaeppler2018	root	49	
	kaeppler2018	seedling	216	
	kaeppler2018	seedling inbred	166	
	kaeppler2018	seedling hybrid	50	
	biomap	endosperm	121	
	biomap	internode	77	
	biomap	leaf	84	
	biomap	root	84	
	biomap	seedling	84	
tissue*genotype	lin2017	5*27	133	
	kremling2018	7*306	1,781	
	kaeppler2018	5*96	447	
	briggs	3*23	73	
	biomap	5*121	450	
ril	li2013	SAM	107	
liftover	walley2016	mRNA	23	
	huang2018	leaf	394	
	huang2018	root	176	
	huang2018	SAM	406	
	huang2018	seed	159	

Fig 1

Fold enrichment of GO and CornCyc categories for built networks (different sizes of top edges taken).

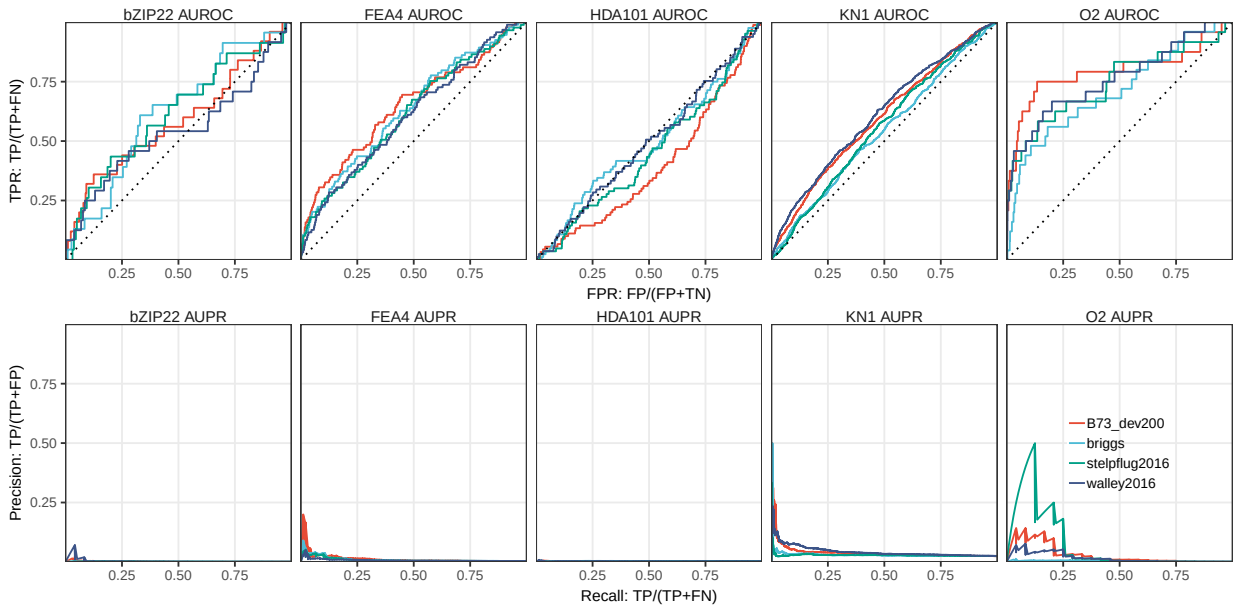

Fig SX

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.

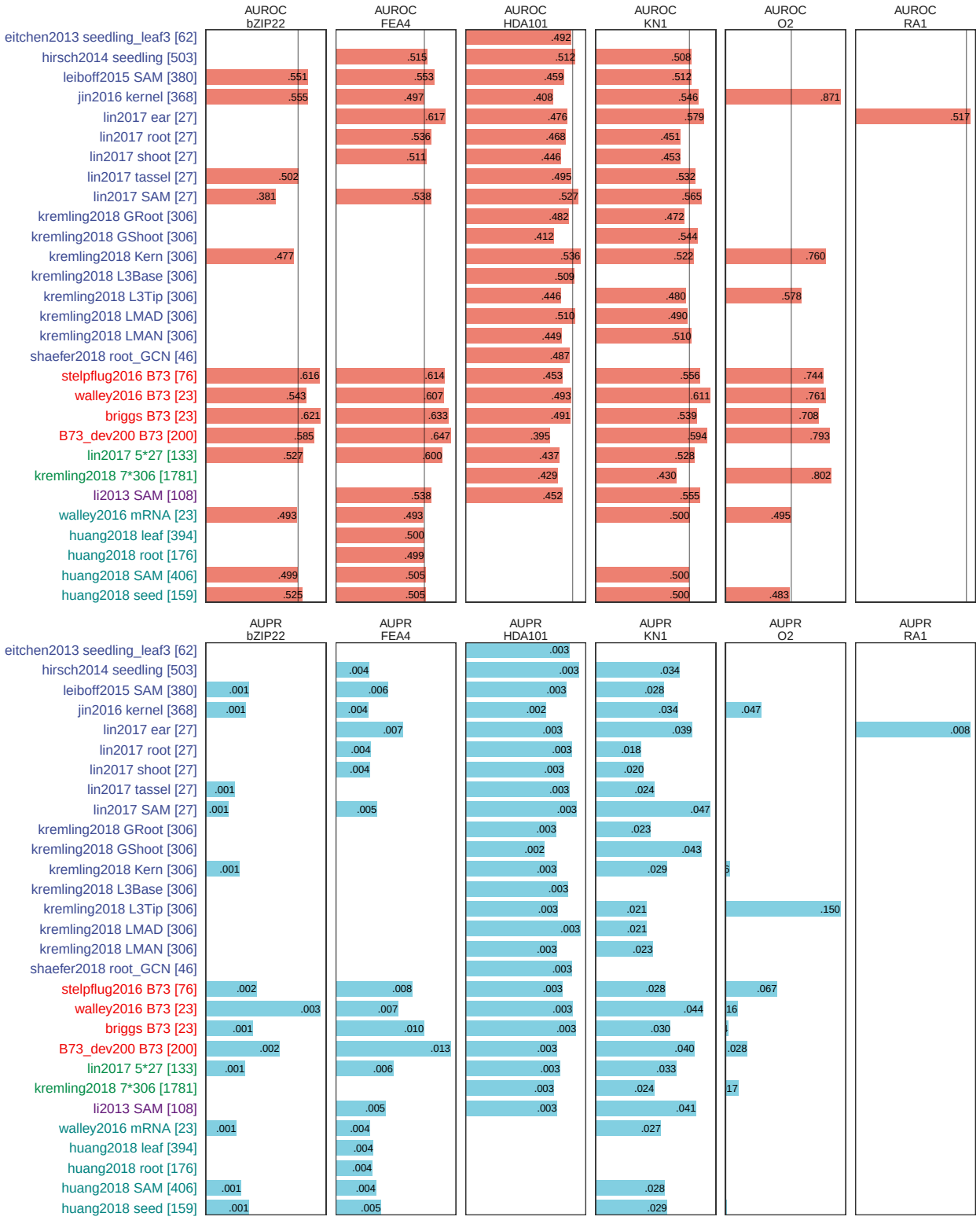

Fig SX

Barplot showing AUROC and AUPRs for lin2017 tissue-specific and pooled GRNs.

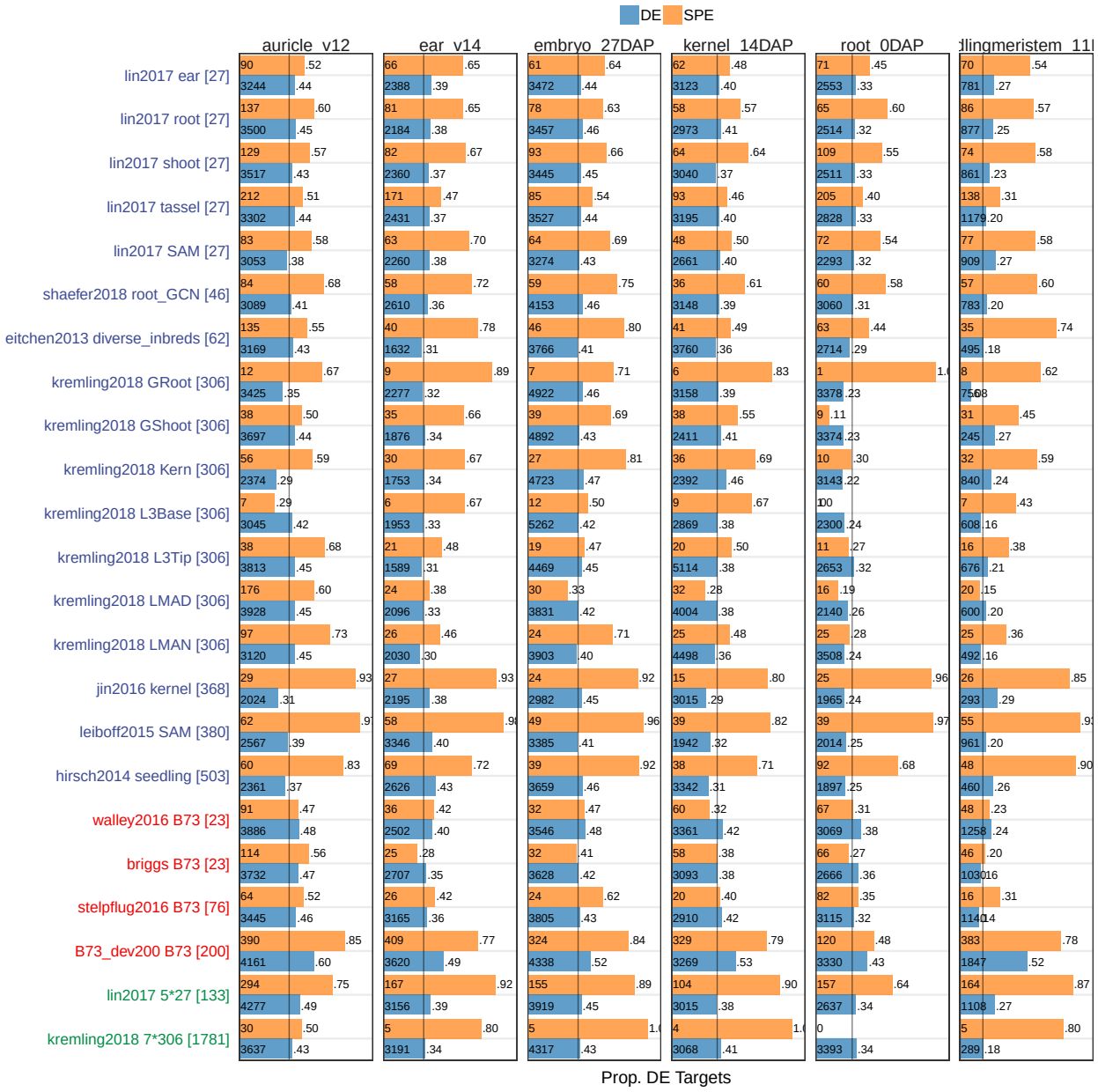

Fig SX

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.

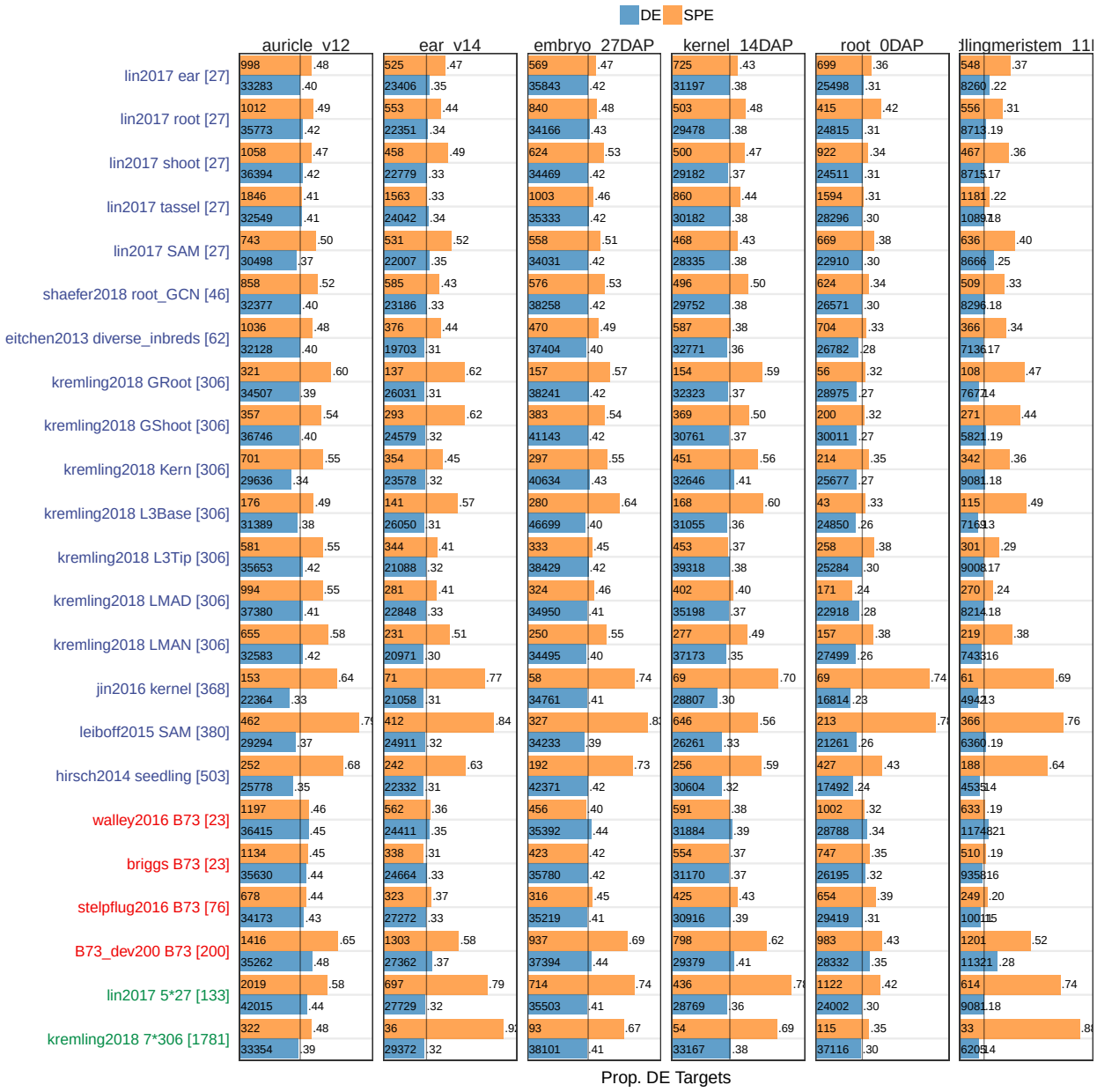

Fig SX

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.

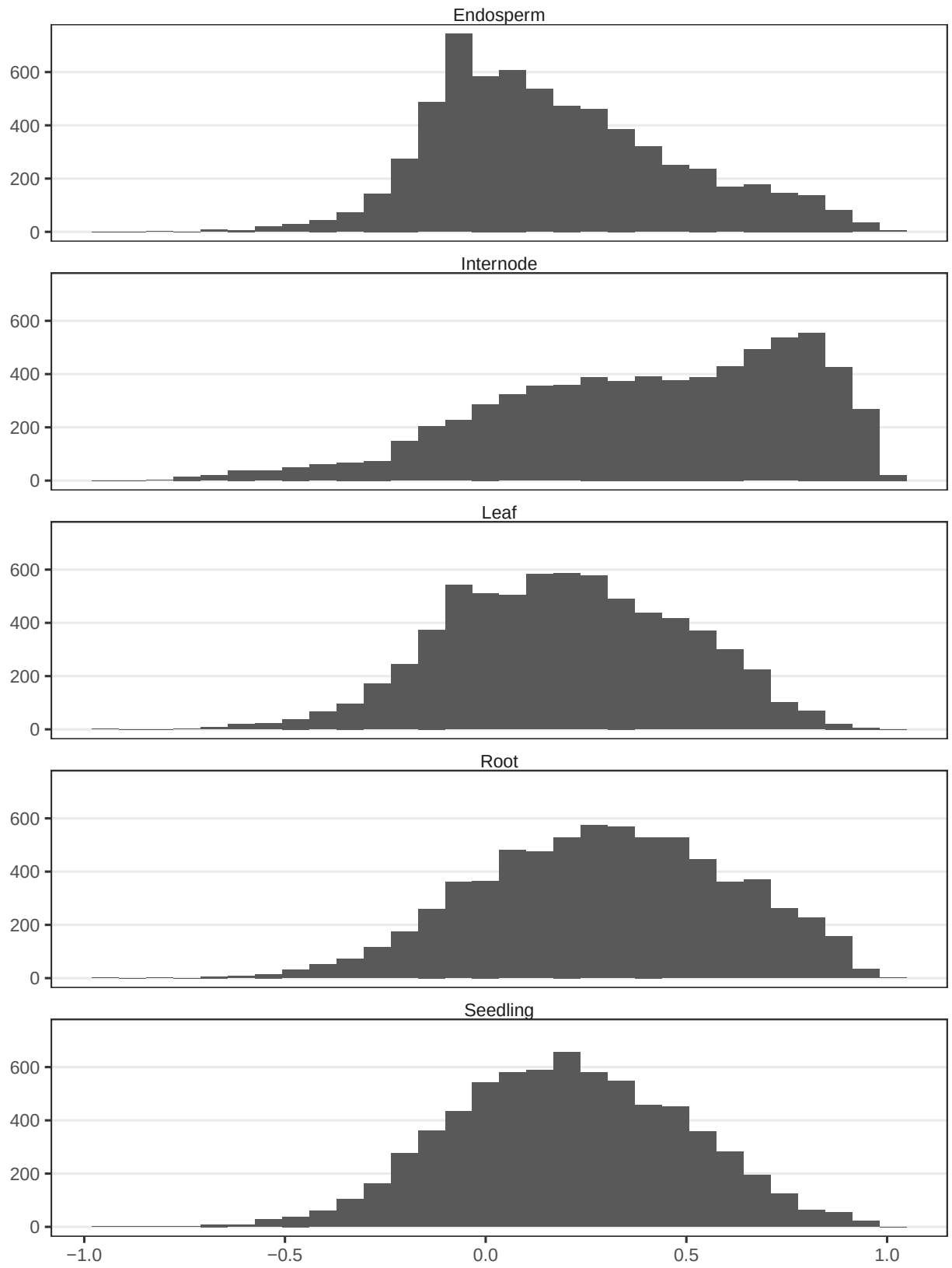
Endosperm
Internode
Leaf
Root
Seedling
600
400
200
0
−1.0
−0.5
0.0
0.5
1.0

Fig 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.