Table 1. GRNs built in this study.

net_type	nid	study	note	sample_size
genotype	n13c	eitchen2013	seedling_leaf3	62
	n14a	hirsch2014	seedling	503
	n15a	leiboff2015	SAM	380
	n16a	jin2016	kernel	368
	n17a_1	lin2017	ear	27
	n17a_2	lin2017	root	27
	n17a_3	lin2017	shoot	27
	n17a_4	lin2017	tassel	27
	n17a_5	lin2017	SAM	27
	n18a_1	kremling2018	GRoot	306
	n18a_2	kremling2018	GShoot	306
	n18a_3	kremling2018	Kern	306
	n18a_4	kremling2018	L3Base	306
	n18a_5	kremling2018	L3Tip	306
	n18a_6	kremling2018	LMAD	306
	n18a_7	kremling2018	LMAN	306
	n18d	shaefer2018	root_GCN	46
	n99a_1	kaeppler2018	inbred	170
	n99a_2	kaeppler2018	hybrid	299
liftover	np16_1	walley2016	mRNA	23
	np18_1	huang2018	leaf	394
	np18_2	huang2018	root	176
	np18_3	huang2018	SAM	406
	np18_4	huang2018	seed	159
ril	n13a	li2013	SAM	108
timeseries	n13b	liu2013	leaf	13
	n14b	li2014	endsperm	7
	n15b	yu2015	leaf	9
	nt01	leaf_22t	B73	22
tissue	n16b	stelpflug2016	B73	76
	n16c	walley2016	B73	23
	n99b_1	briggs	B73	23
	n99b_2	briggs	Mo17	23
	n99b_3	briggs	BxM	23
	nc01	B73_dev41	B73	41
	nc02	B73_dev64	B73	64
	nc03	B73_dev200	B73	200
tissue*genotype	n17a	lin2017	5*27	133
	n18a	kremling2018	7*306	1,781

Fig 1

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

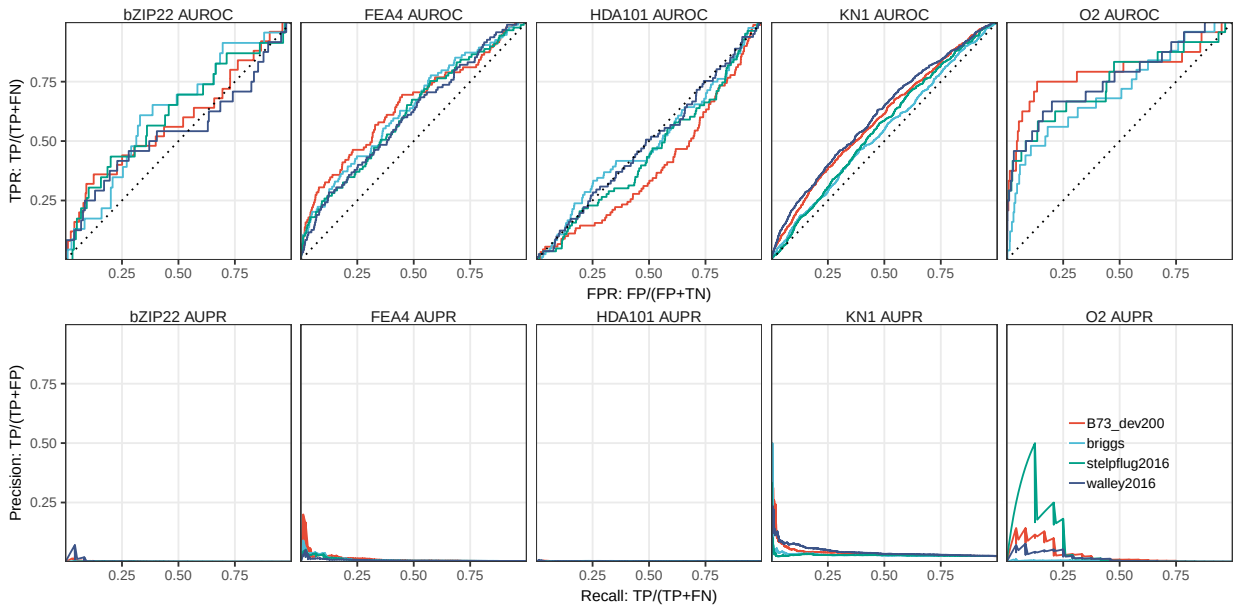

Fig SX

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.

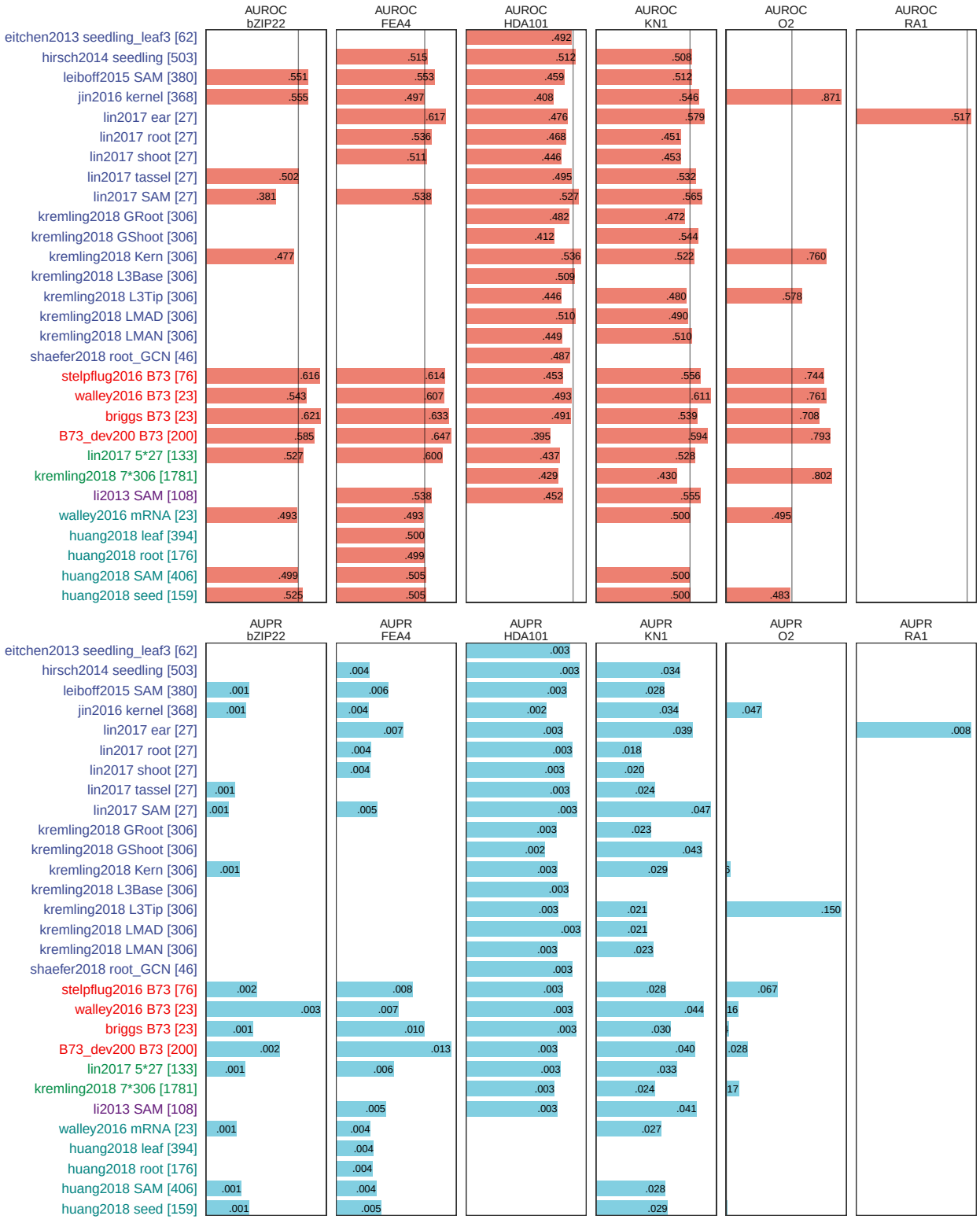

Fig SX

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

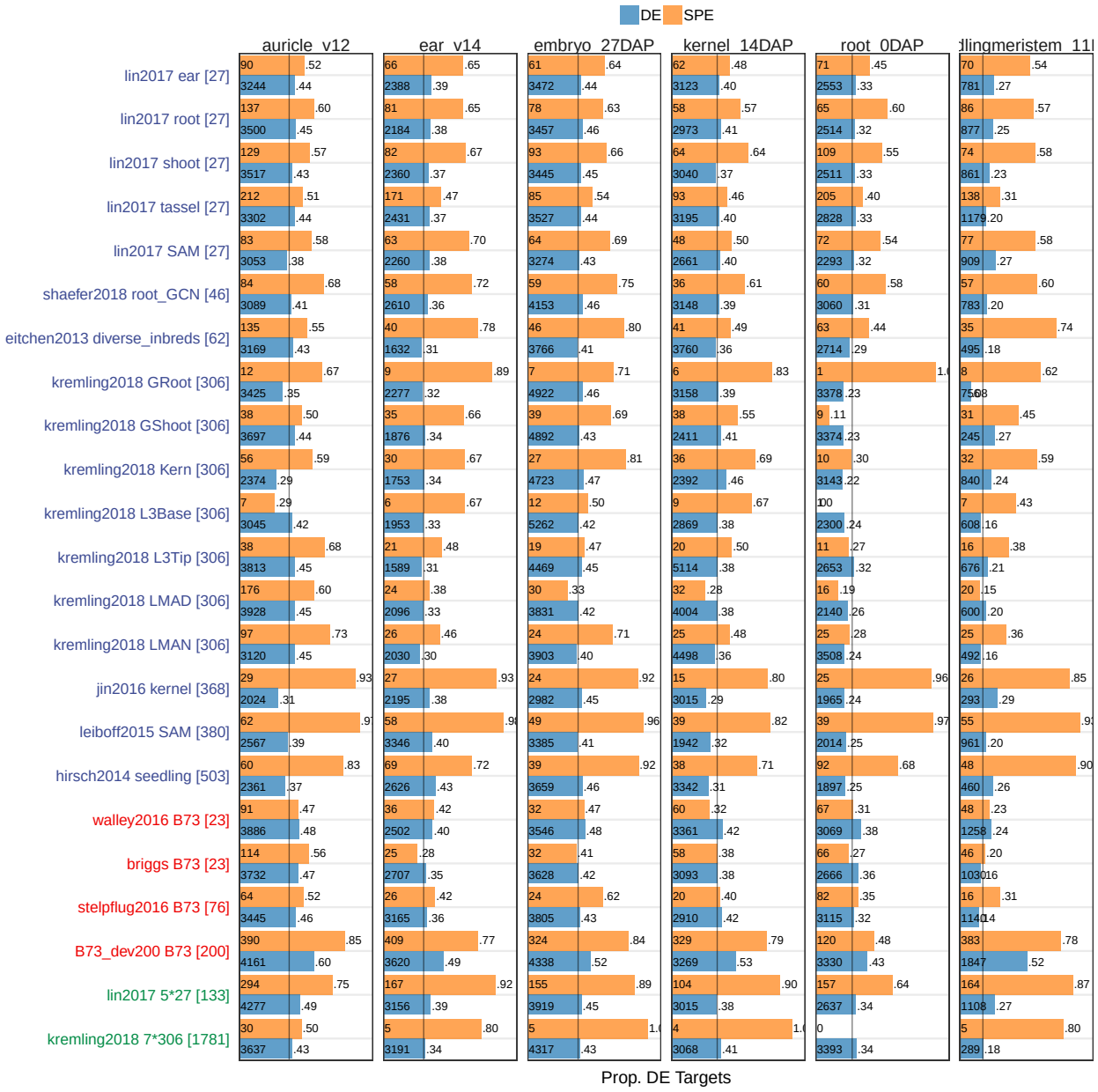

Fig SX

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.

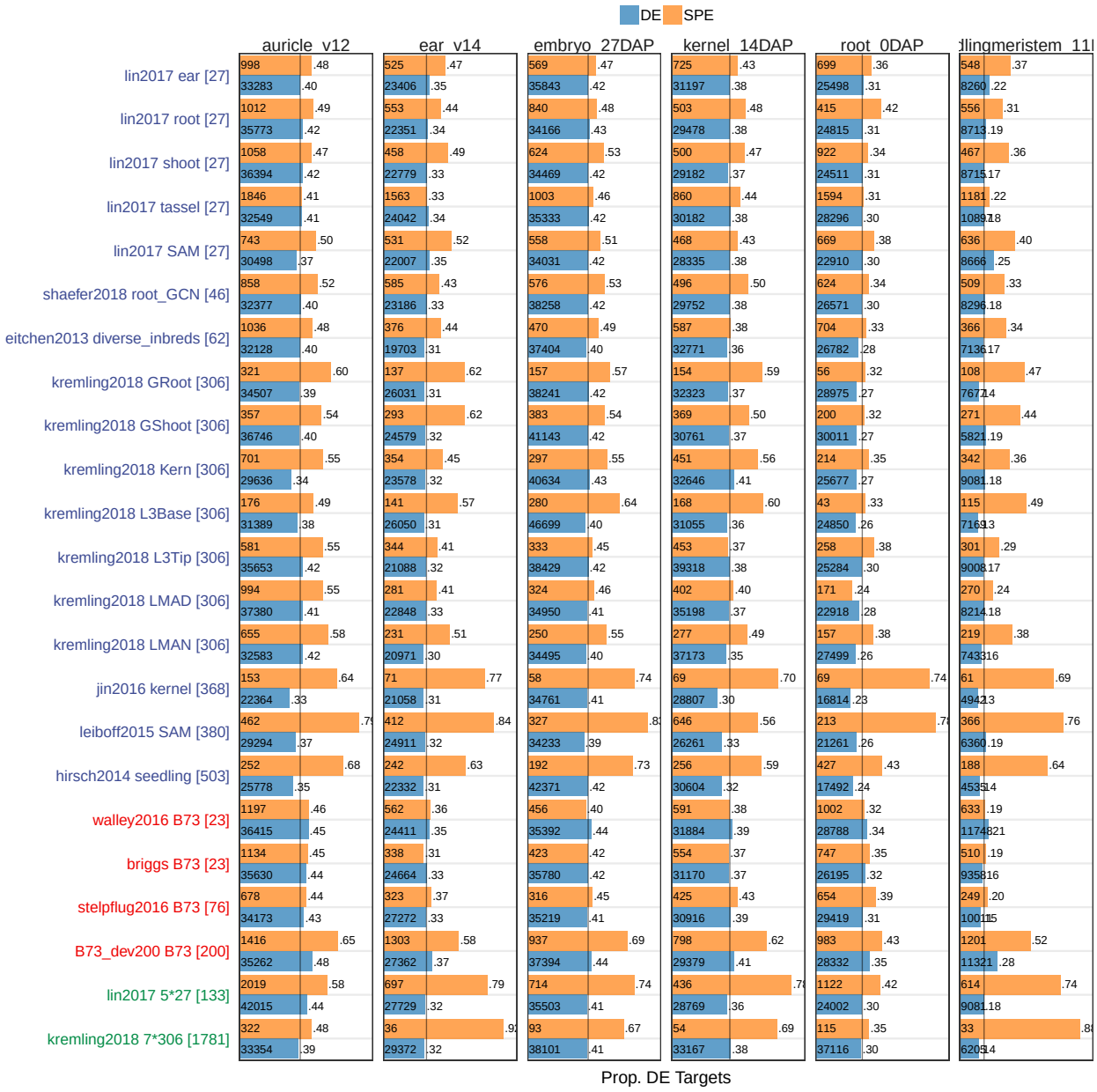

Fig SX

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.

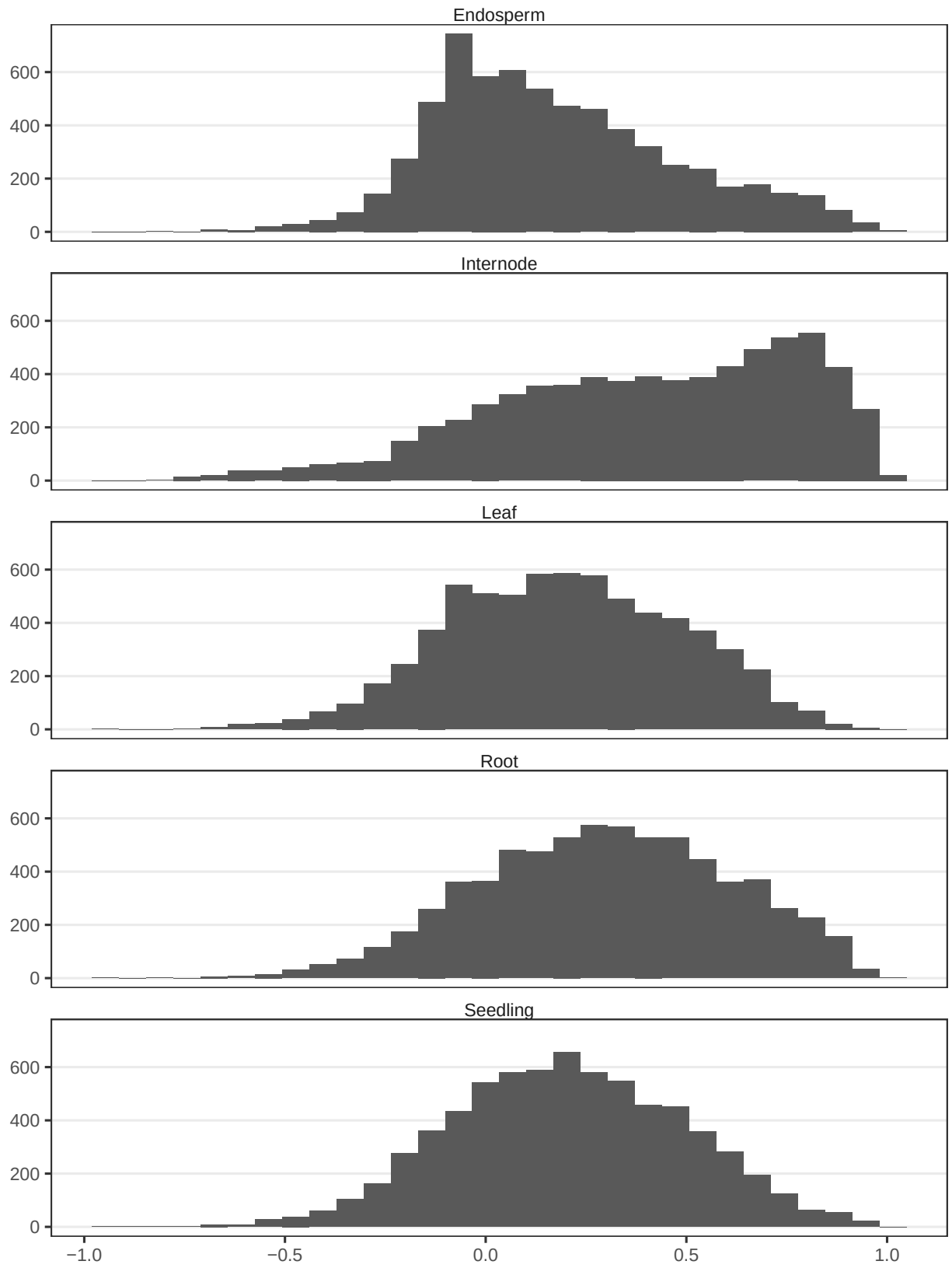
Endosperm
Internode
Leaf
Root
Seedling
600
400
200
0
−1.0
−0.5
0.0
0.5
1.0

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.