Table X. GRNs built in this study.

nid	mid	study	tag	note	net_type	sample_size
n13a	me13a	li2013		SAM	ril	108
n13b	me13b	liu2013		leaf	timeseries	13
n13c	me13c	eitchen2013		seedling_leaf3	genotype	62
n14a	me14a	hirsch2014		seedling	genotype	503
n14b	me14b	li2014		endsperm	timeseries	7
n15a	me15a	leiboff2015		SAM	genotype	380
n15b	me15b	yu2015		leaf	timeseries	9
n16a	me16a	jin2016		kernel	genotype	368
n16b	me16b	stelpflug2016		B73	tissue	76
n16c	me16c	walley2016		B73	tissue	23
n17a	me17a	lin2017		5*27	tissue*genotype	133
n17a_1	me17a	lin2017	ear	ear	genotype	27
n17a_2	me17a	lin2017	root	root	genotype	27
n17a_3	me17a	lin2017	shoot	shoot	genotype	27
n17a_4	me17a	lin2017	tassel	tassel	genotype	27
n17a_5	me17a	lin2017	SAM	SAM	genotype	27
n18a	me18a	kremling2018		7*306	tissue*genotype	1,781
n18a_1	me18a	kremling2018	GRoot	GRoot	genotype	306
n18a_2	me18a	kremling2018	GShoot	GShoot	genotype	306
n18a_3	me18a	kremling2018	Kern	Kern	genotype	306
n18a_4	me18a	kremling2018	L3Base	L3Base	genotype	306
n18a_5	me18a	kremling2018	L3Tip	L3Tip	genotype	306
n18a_6	me18a	kremling2018	LMAD	LMAD	genotype	306
n18a_7	me18a	kremling2018	LMAN	LMAN	genotype	306
n18d	me18d	shaefer2018	root	root_GCN	genotype	46
n99a_1	me99a	kaeppler2018	inbred	inbred	genotype	170
n99a_2	me99a	kaeppler2018	hybrid	hybrid	genotype	299
n99b_1	me99b	briggs	B73	B73	tissue	23
n99b_2	me99b	briggs	Mo17	Mo17	tissue	23
n99b_3	me99b	briggs	BxM	BxM	tissue	23
np16_1		walley2016	mRNA	mRNA	liftover	23
np18_1		huang2018	leaf	leaf	liftover	394
np18_2		huang2018	root	root	liftover	176
np18_3		huang2018	SAM	SAM	liftover	406
np18_4		huang2018	seed	seed	liftover	159
nc01	mec01	B73_dev41		B73	tissue	41
nc02	mec02	B73_dev64		B73	tissue	64
nc03	mec03	B73_dev200		B73	tissue	200
nt01	met01	leaf_22t		B73	timeseries	22
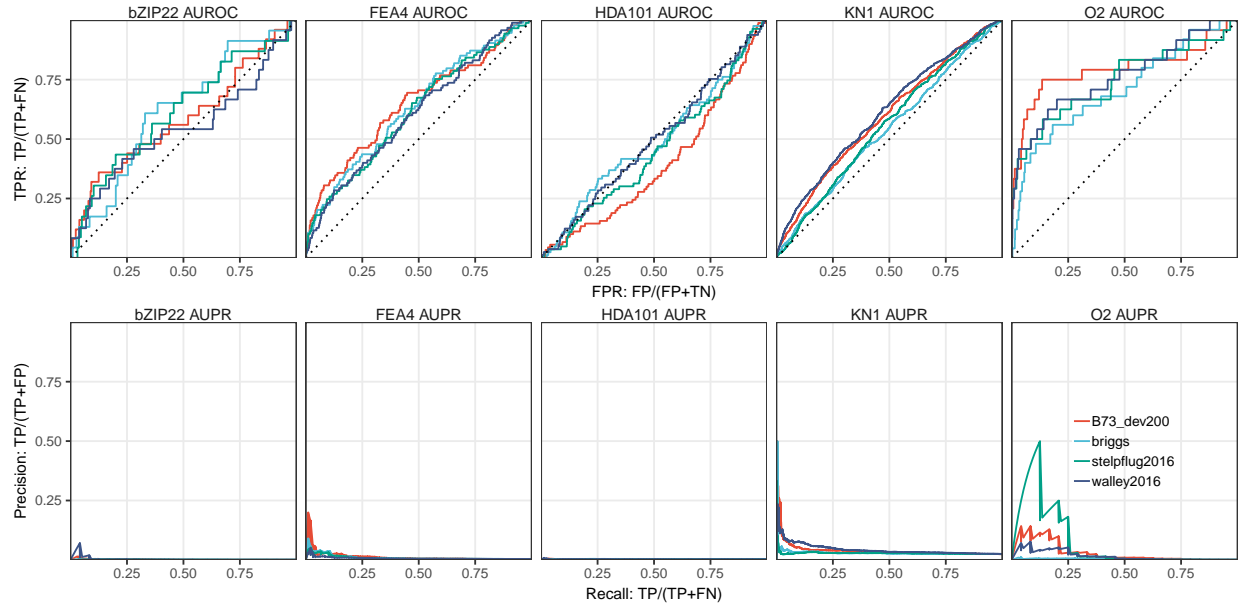
Fig 1

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 2

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

Fig 3

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

Fig 4a

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.

DE SPE

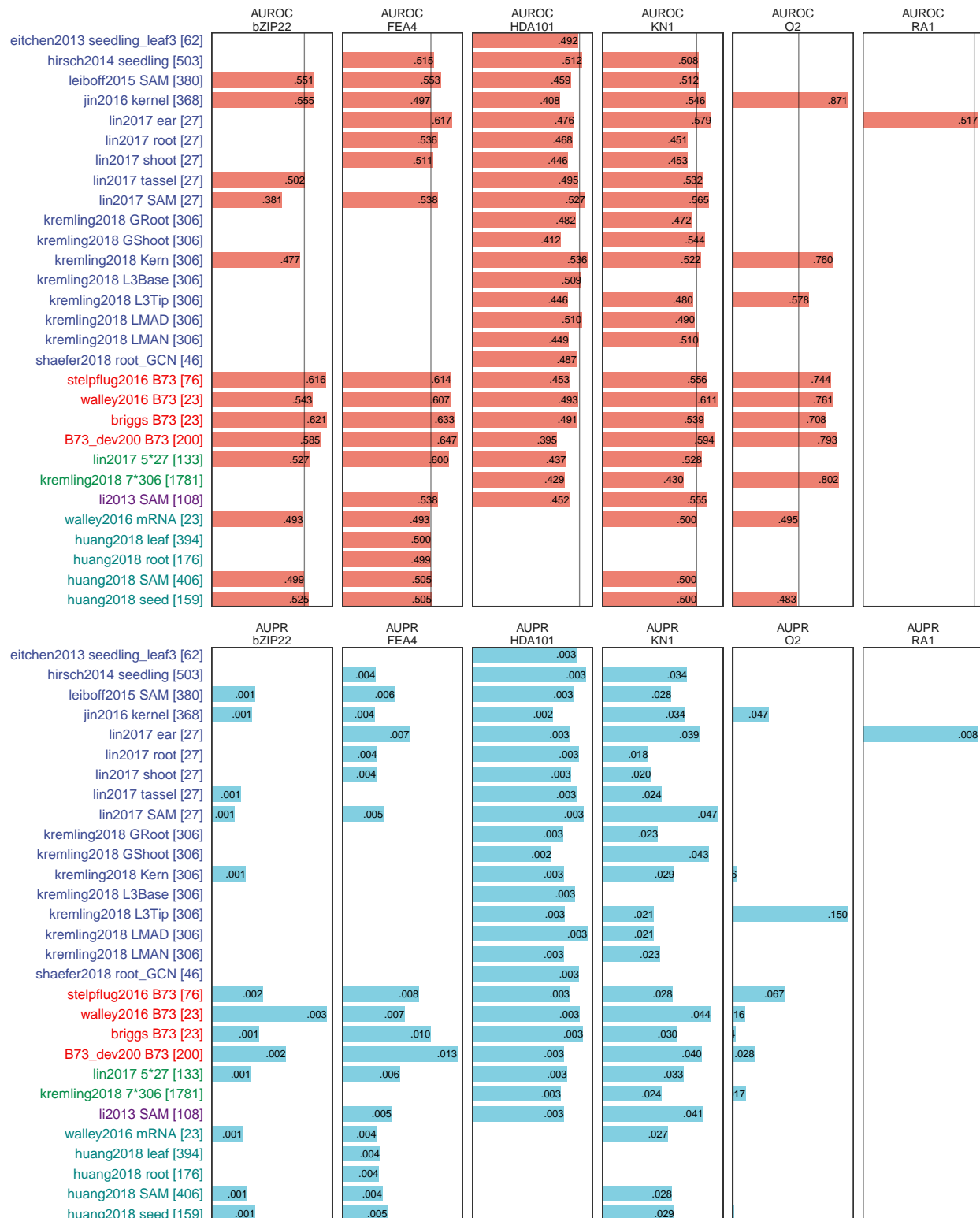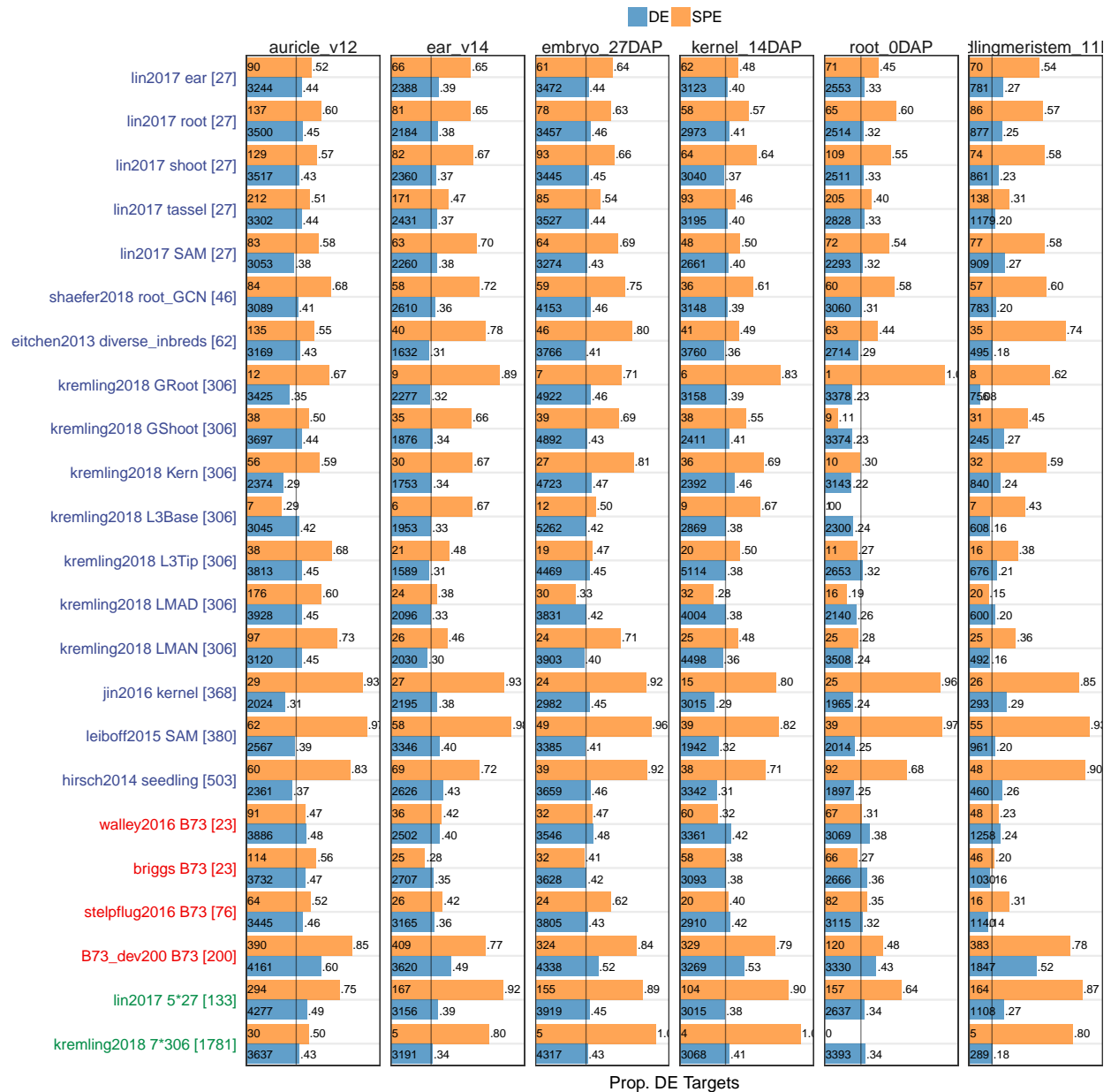|	auricle_v12	ear_v14	embryo_27DAP	kernel_14DAP	root_0DAP	dlingmeristem_11[
lin2017 ear [27]	998 .48 / 33283 .40	525 .47 / 23406 .35	569 .47 / 35843 .42	725 .43 / 31197 .38	699 .36 / 25498 .31	548 .37 / 8260 .22
lin2017 root [27]	1012 .49 / 35773 .42	553 .44 / 22351 .34	840 .48 / 34166 .43	503 .48 / 29478 .38	415 .42 / 24815 .31	556 .31 / 8713 .19
lin2017 shoot [27]	1058 .47 / 36394 .42	458 .49 / 22779 .33	624 .53 / 34469 .42	500 .47 / 29182 .37	922 .34 / 24511 .31	467 .36 / 8715 .17
lin2017 tassel [27]	1846 .41 / 32549 .41	1563 .33 / 24042 .34	1003 .46 / 35333 .42	860 .44 / 30182 .38	1594 .31 / 28296 .30	1181 .22 / 10897 .18
lin2017 SAM [27]	743 .50 / 30498 .37	531 .52 / 22007 .35	558 .51 / 34031 .42	468 .43 / 28335 .38	669 .38 / 22910 .30	636 .40 / 8666 .25
shaefer2018 root_GCN [46]	858 .52 / 32377 .40	585 .43 / 23186 .33	576 .53 / 38258 .42	496 .50 / 29752 .38	624 .34 / 26571 .30	509 .33 / 8296 .18
eitchen2013 diverse_inbreds [62]	1036 .48 / 32128 .40	376 .44 / 19703 .31	470 .49 / 37404 .40	587 .38 / 32771 .36	704 .33 / 26782 .28	366 .34 / 7136 .17
kremling2018 GRoot [306]	321 .60 / 34507 .39	137 .62 / 26031 .31	157 .57 / 38241 .42	154 .59 / 32323 .37	56 .32 / 28975 .27	108 .47 / 7677 .14
kremling2018 GShoot [306]	357 .54 / 36746 .40	293 .62 / 24579 .32	383 .54 / 41143 .42	369 .50 / 30761 .37	200 .32 / 30011 .27	271 .44 / 5821 .19
kremling2018 Kern [306]	701 .55 / 29636 .34	354 .45 / 23578 .32	297 .55 / 40634 .43	451 .56 / 32646 .41	214 .35 / 25677 .27	342 .36 / 9081 .18
kremling2018 L3Base [306]	176 .49 / 31389 .38	141 .57 / 26050 .31	280 .64 / 46699 .40	168 .60 / 31055 .36	43 .33 / 24850 .26	115 .49 / 7169 .13
kremling2018 L3Tip [306]	581 .55 / 35653 .42	344 .41 / 21088 .32	333 .45 / 38429 .42	453 .37 / 39318 .38	258 .38 / 25284 .30	301 .29 / 9008 .17
kremling2018 LMAD [306]	994 .55 / 37380 .41	281 .41 / 22848 .33	324 .46 / 34950 .41	402 .40 / 35198 .37	171 .24 / 22918 .28	270 .24 / 8214 .18
kremling2018 LMAN [306]	655 .58 / 32583 .42	231 .51 / 20971 .30	250 .55 / 34495 .40	277 .49 / 37173 .35	157 .38 / 27499 .26	219 .38 / 7743 .16
jin2016 kernel [368]	153 .64 / 22364 .33	71 .77 / 21058 .31	58 .74 / 34761 .41	69 .70 / 28807 .30	69 .74 / 16814 .23	61 .69 / 4942 .13
leiboff2015 SAM [380]	462 .79 / 29294 .37	412 .84 / 24911 .32	327 .83 / 34233 .39	646 .56 / 26261 .33	213 .7 / 21261 .26	366 .76 / 6360 .19
hirsch2014 seedling [503]	252 .68 / 25778 .35	242 .63 / 22332 .31	192 .73 / 42371 .42	256 .59 / 30604 .32	427 .43 / 17492 .24	188 .64 / 4535 .14
walley2016 B73 [23]	1197 .46 / 36415 .45	562 .36 / 24411 .35	456 .40 / 35392 .44	591 .38 / 31884 .39	1002 .32 / 28788 .34	633 .19 / 11748 .21
briggs B73 [23]	1134 .45 / 35630 .44	338 .31 / 24664 .33	423 .42 / 35780 .42	554 .37 / 31170 .37	747 .35 / 26195 .32	510 .19 / 9358 .16
stelpflug2016 B73 [76]	678 .44 / 34173 .43	323 .37 / 27272 .33	316 .45 / 35219 .41	425 .43 / 30916 .39	654 .39 / 29419 .31	249 .20 / 10011 .15
B73_dev200 B73 [200]	1416 .65 / 35262 .48	1303 .58 / 27362 .37	937 .69 / 37394 .44	798 .62 / 29379 .41	983 .43 / 28332 .35	1201 .52 / 11321 .28
lin2017 5*27 [133]	2019 .58 / 42015 .44	697 .79 / 27729 .32	714 .74 / 35503 .41	436 .7 / 28769 .36	1122 .42 / 24002 .30	614 .74 / 9081 .18
kremling2018 7*306 [1781]	322 .48 / 33354 .39	36 .9 / 29372 .32	93 .67 / 38101 .41	54 .69 / 33167 .38	115 .35 / 37116 .30	33 .8 / 6205 .14

Prop. DE Targets

Fig 4b

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.
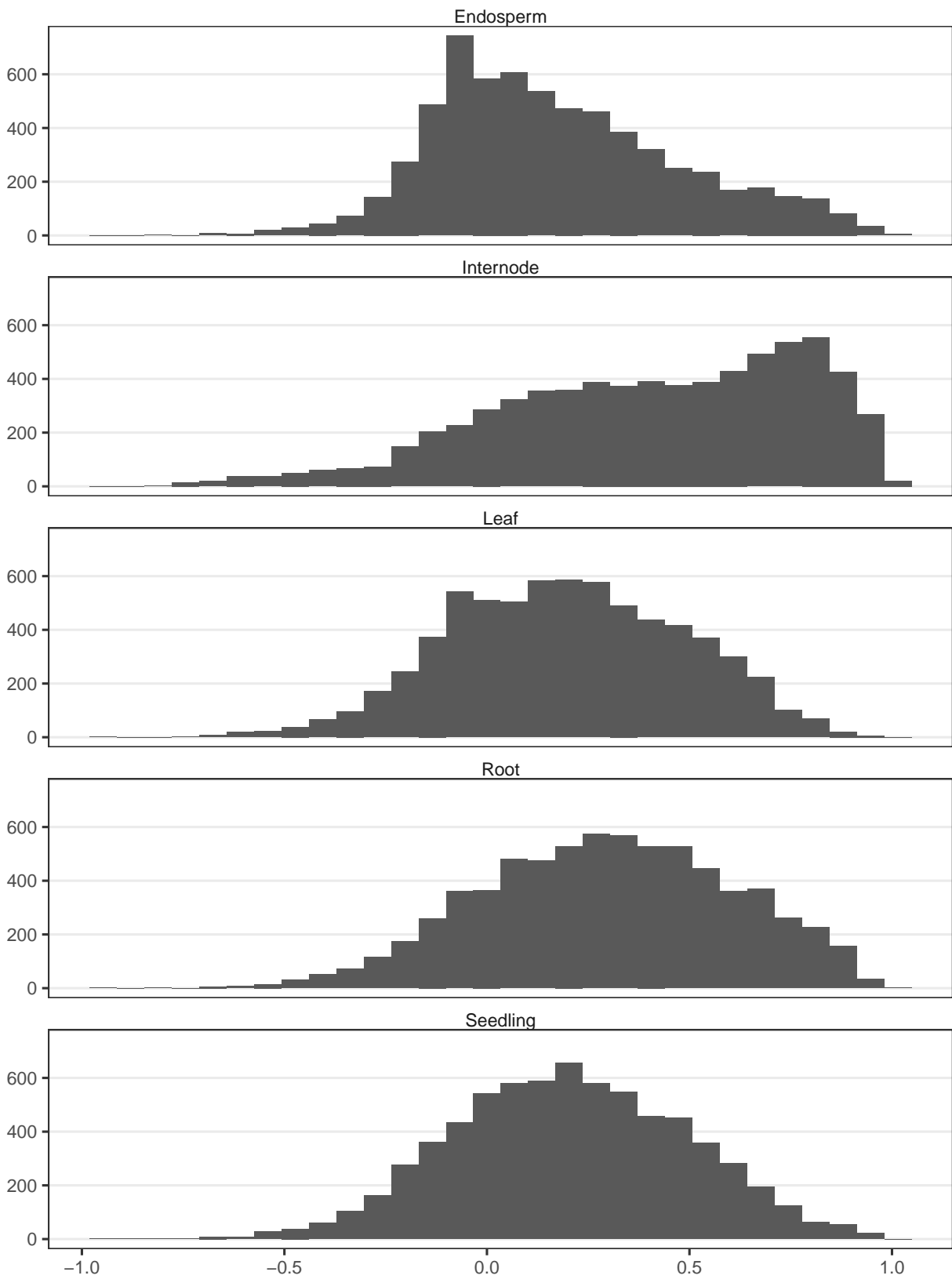
Fig X

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.