

Table X. GRNs built in this study.

nid	mid	study	tag	note	timeseries
n13a	me13a	li2013		SAM1	
n13b	me13b	liu2013		leaf_13t	TRUE
n14a	me14a	hirsch2014		seedling_503	
n14b	me14b	li2014		endsperm_7t	TRUE
n15a	me15a	leiboff2015		SAM_380	
n15b	me15b	yu2015		leaf_9t	TRUE
n16a	me16a	jin2016		kernel_368	
n16b	me16b	stelpflug2016		B73_76	
n16c	me16c	walley2016		B73_23	
n17a	me17a	lin2017		5_tissues	
n17a_1	me17a	lin2017	ear	ear	
n17a_2	me17a	lin2017	root	root	
n17a_3	me17a	lin2017	shoot	shoot	
n17a_4	me17a	lin2017	tassel	tassel	
n17a_5	me17a	lin2017	SAM	SAM	
n18a	me18a	kremling2018		7_tissues	
n18a_1	me18a	kremling2018	GRoot	GRoot	
n18a_2	me18a	kremling2018	GShoot	GShoot	
n18a_3	me18a	kremling2018	Kern	Kern	
n18a_4	me18a	kremling2018	L3Base	L3Base	
n18a_5	me18a	kremling2018	L3Tip	L3Tip	
n18a_6	me18a	kremling2018	LMAD	LMAD	
n18a_7	me18a	kremling2018	LMAN	LMAN	
n18d	me18d	shaefer2018	root	root GCN	
n99b_1	me99b	briggs	B73	B73	
n99b_2	me99b	briggs	Mo17	Mo17	
n99b_3	me99b	briggs	B73xMo17	B73xMo17	
nc01	mec01	B73_dev41			
nc02	mec02	B73_dev64			
nc03	mec03	B73_dev122			
nt01	met01	leaf_22t			TRUE

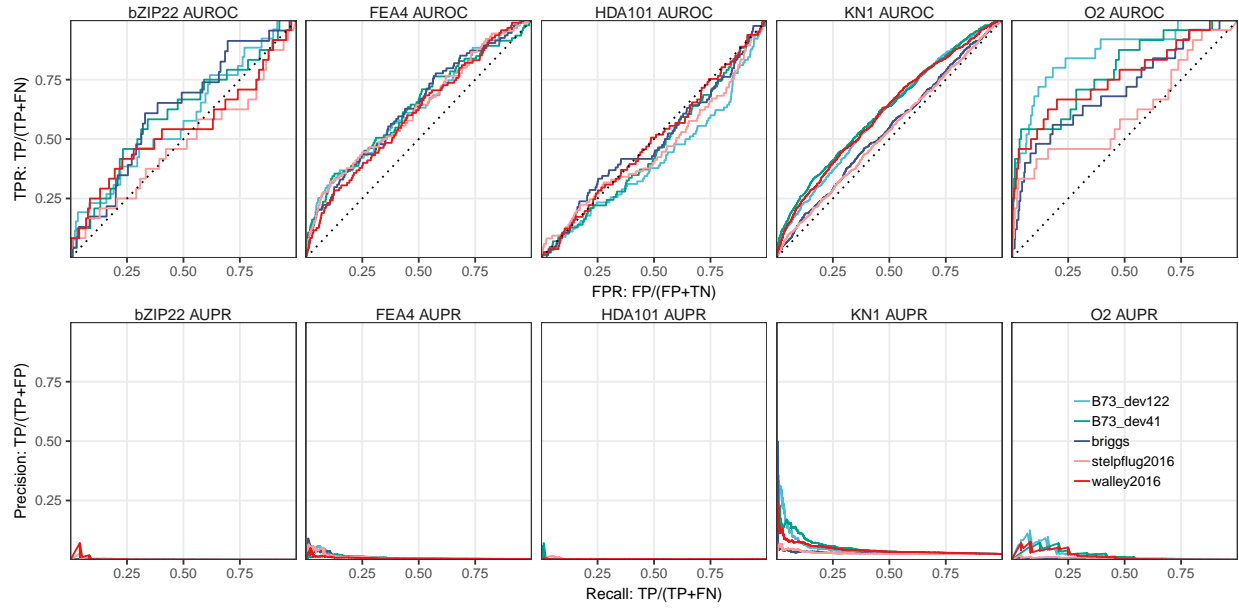


Fig 1

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.

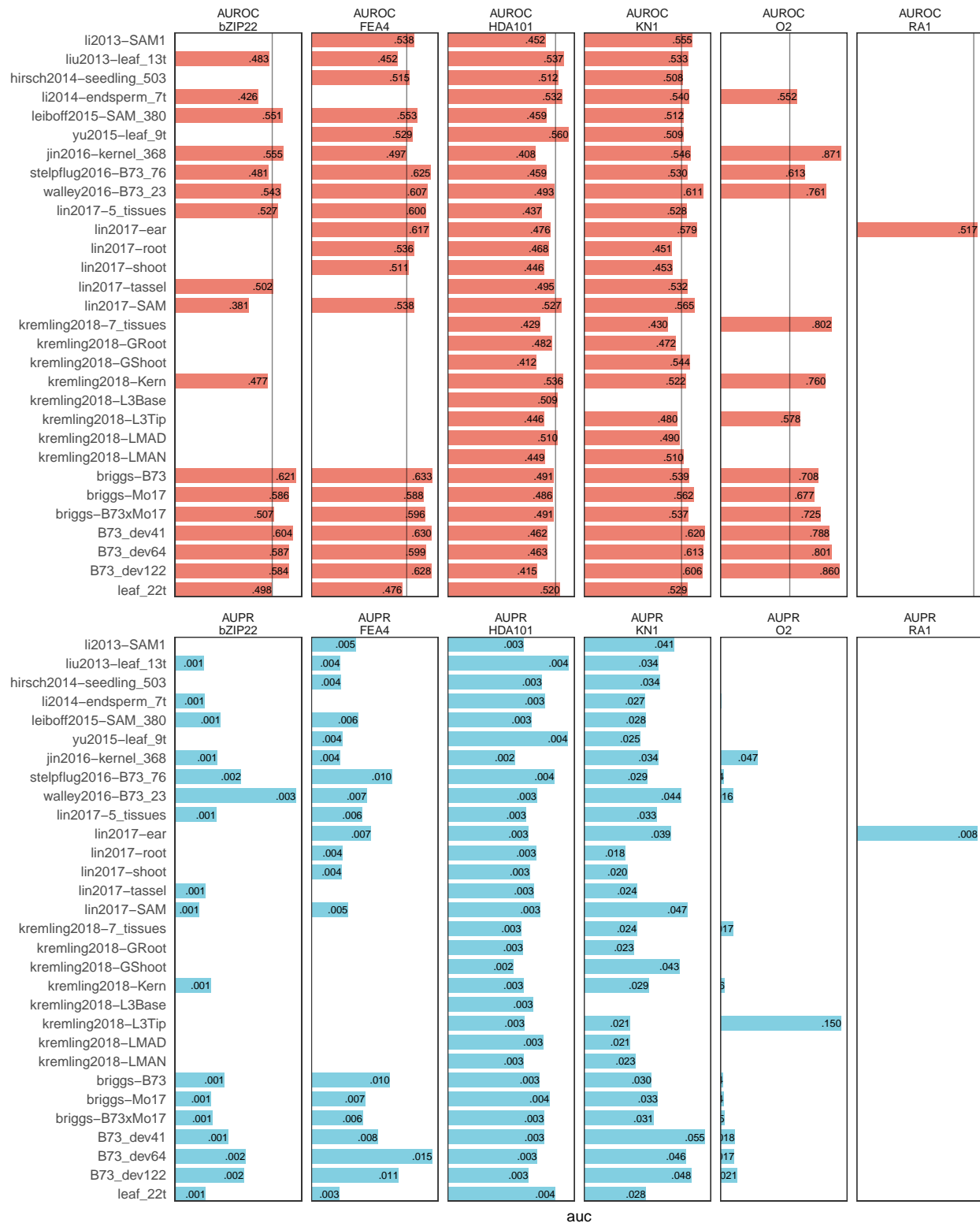


Fig 2

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

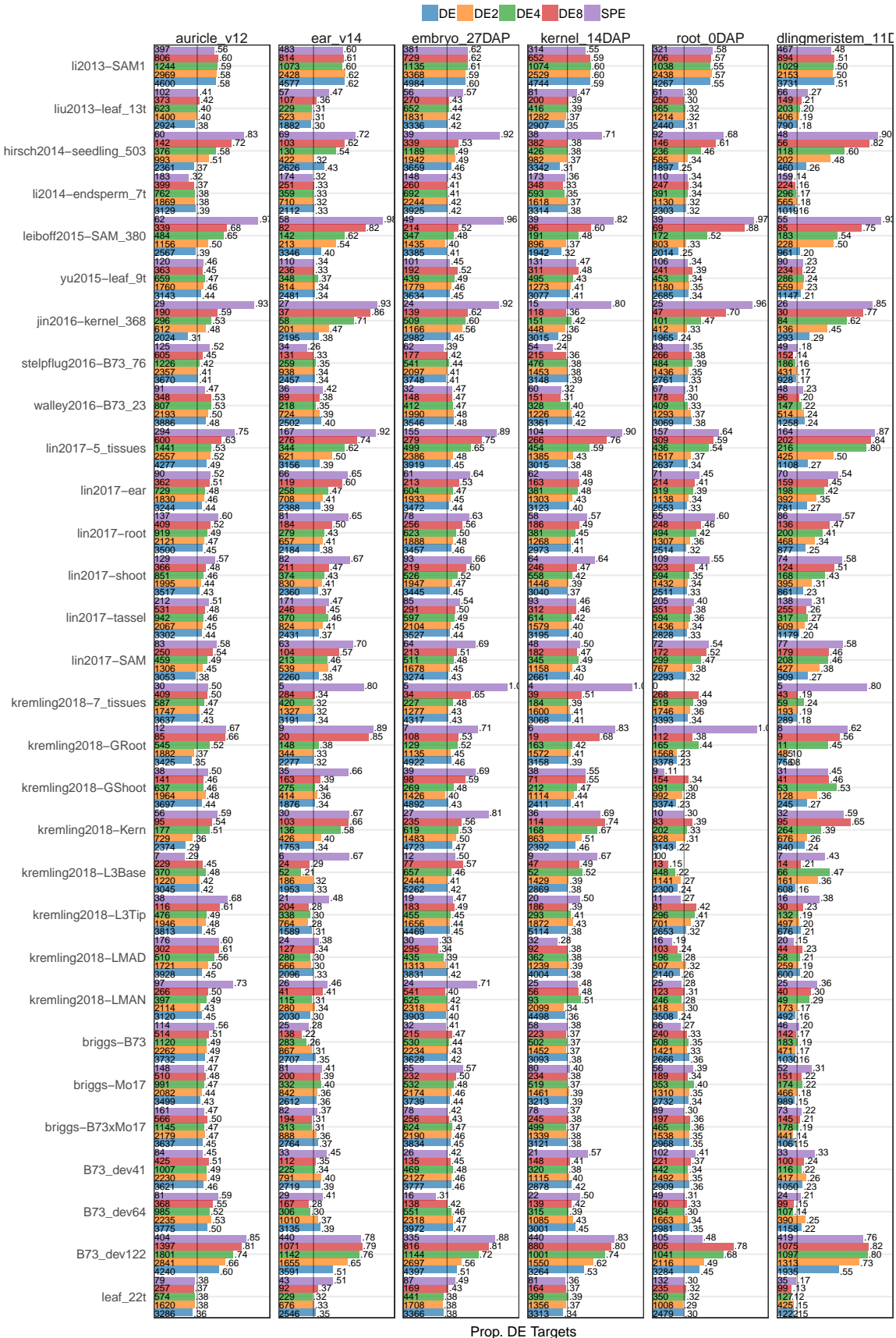
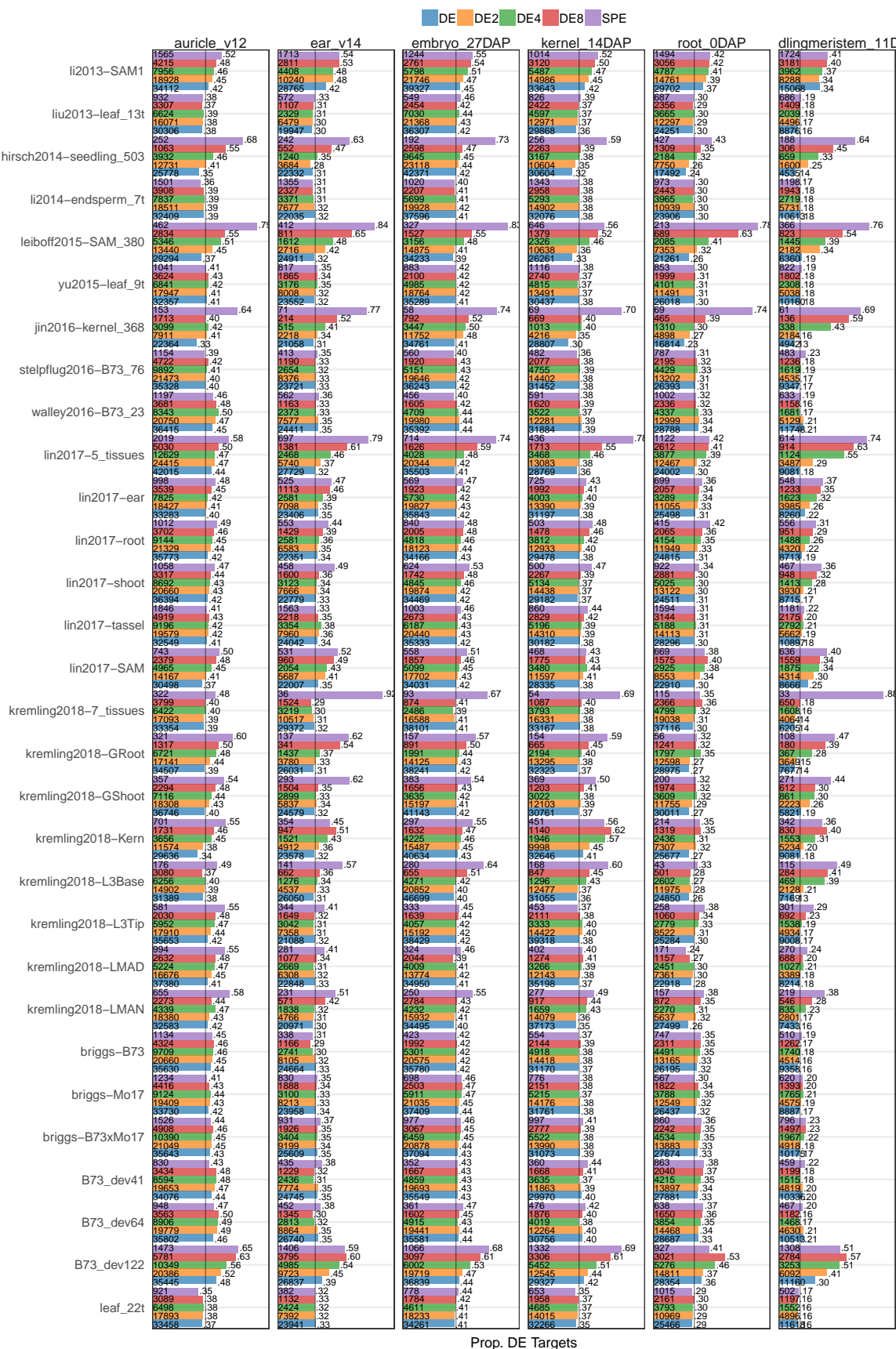
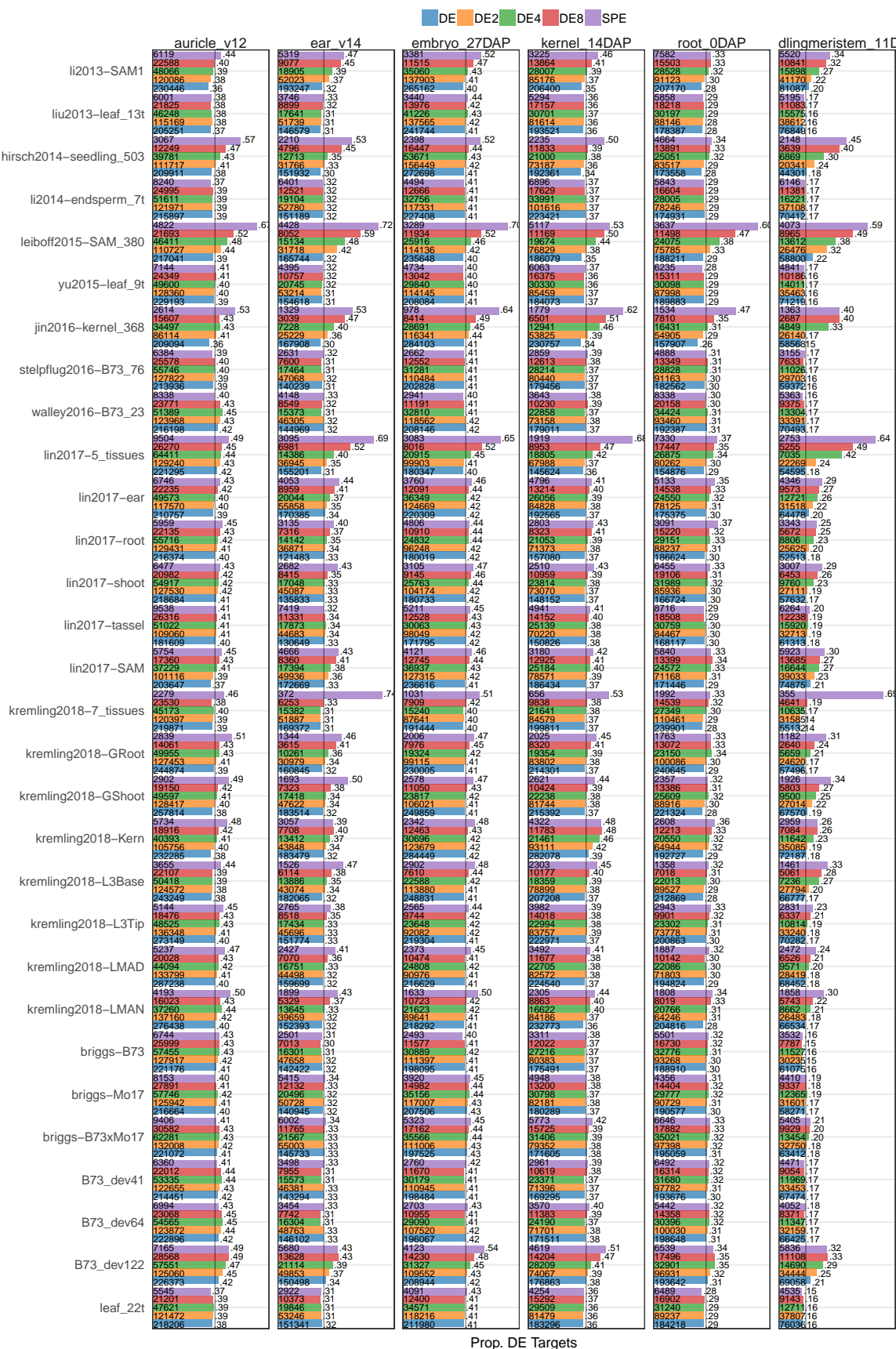


Fig 3a

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.



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.





Enrichment of DE genes (using Briggs dataset) in predicted TF targets made by different GRNs.  
Only the top 1,000,000 strongest edges were taken from each GRN.

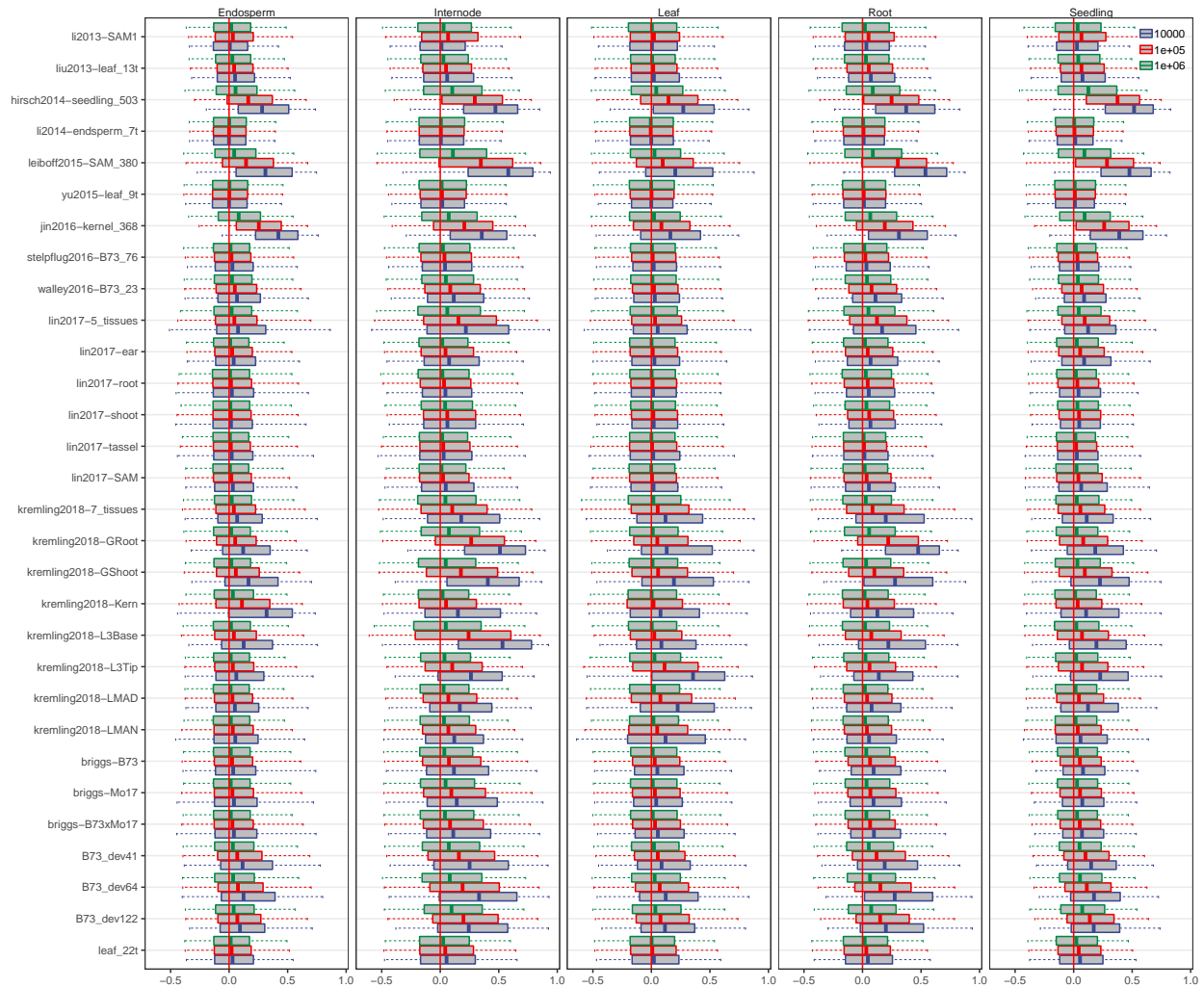


Fig 4a

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.

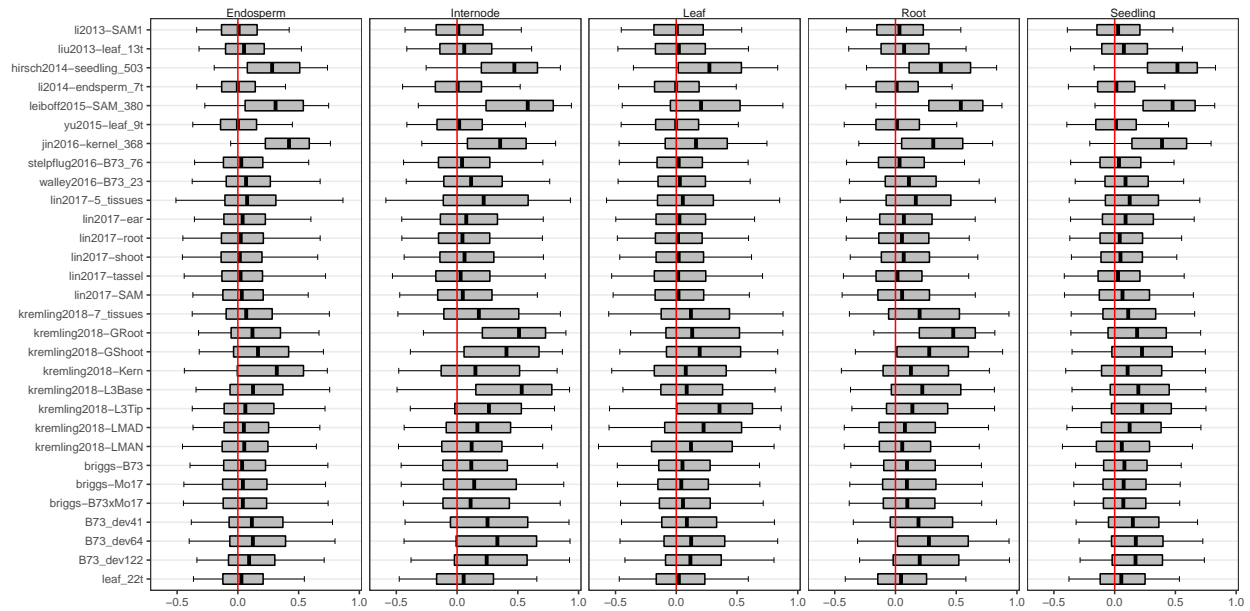


Fig 4b

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 strongest edges in each network.