Table X. GRNs built in this study.

| nid	study	tag
n01	li2013	SAM1
n02	li2013	SAM2
n11	hirsch2014	seedling_503
n21	leiboff2015	SAM_380
n31	jin2016	kernel_368
n41	stelpflug2016	B73_18
n42	walley2016	B73_23
n50	lin2017	5_tissues
n51	lin2017	ear
n52	lin2017	root
n53	lin2017	shoot
n54	lin2017	tassel
n55	lin2017	SAM
n58	lin2017	merge_addi
n59	lin2017	merge_multi
n60	kremling2018	7_tissues
n61	kremling2018	GRoot
n62	kremling2018	GShoot
n63	kremling2018	Kern
n64	kremling2018	L3Base
n65	kremling2018	L3Tip
n66	kremling2018	LMAD
n67	kremling2018	LMAN
n68	kremling2018	merge_addi
n69	kremling2018	merge_multi
n71	briggs	B73
n72	briggs	Mo17
n73	briggs	B73xMo17
n81	dev41	B73
n82	dev64	B73
np1	huang2018	leaf
np2	huang2018	root
np3	huang2018	sam
np4	huang2018	seed
np5	walley	rna
np6	walley	protein
np7	walley	all
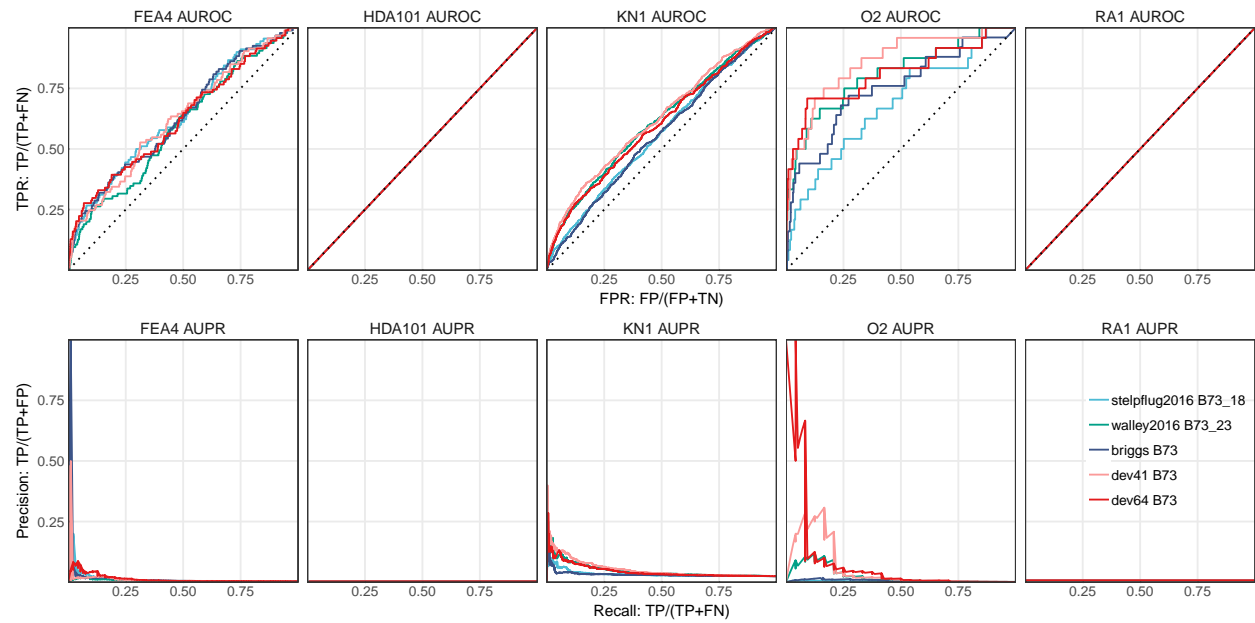
Fig 1

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.
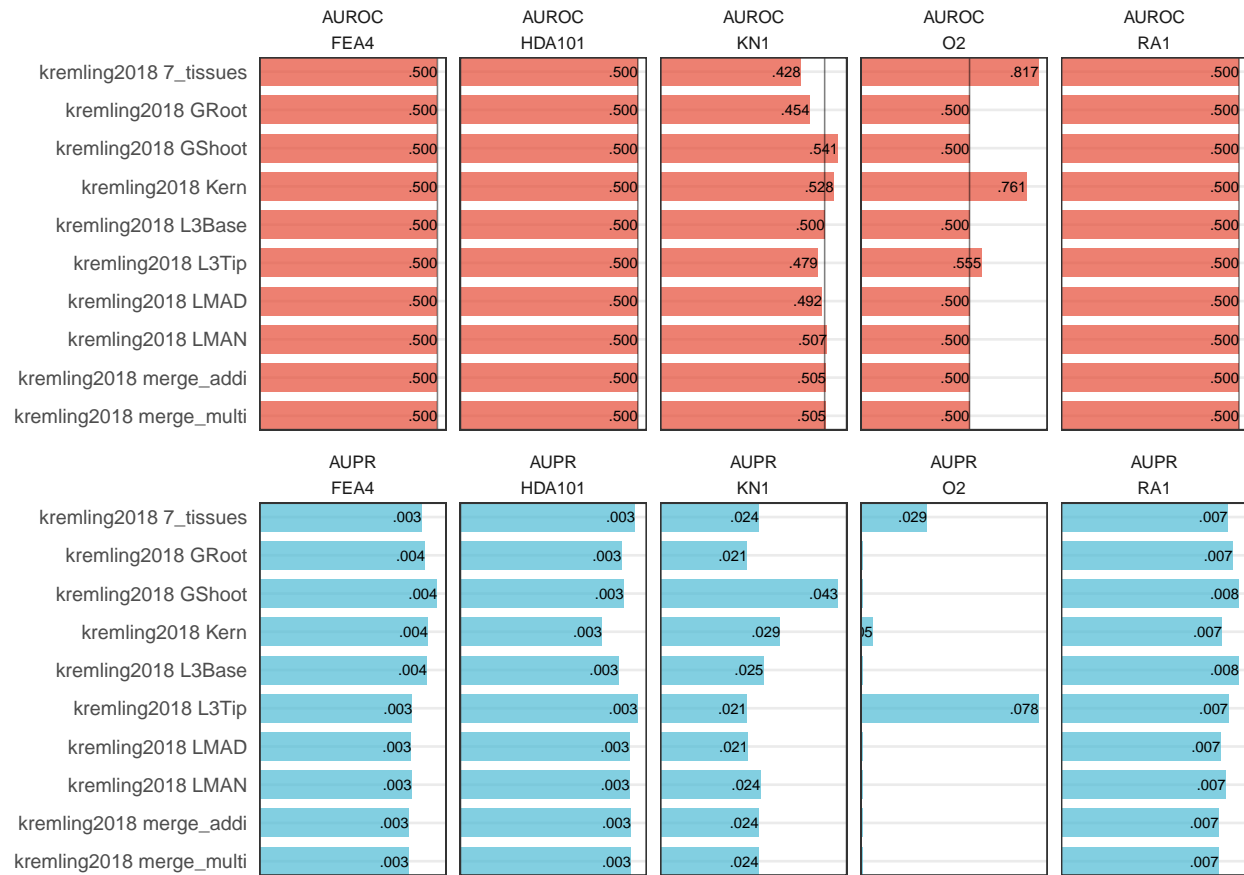
Fig 3

Barplot showing AUROC and AUPRs for kremling2018 tissue-specific and pooled GRNs.

	AUROC FEA4	AUROC KN1	AUROC O2
li2013 SAM1	.492	.546	
li2013 SAM2	.468	.557	
hirsch2014 seedling_503	.512	.502	
leiboff2015 SAM_380	.570	.503	
jin2016 kernel_368	.494	.543	.872
stelpflug2016 B73_18	.635	.561	.681
walley2016 B73_23	.594	.610	.809
briggs B73	.628	.557	.748
briggs Mo17	.559	.575	.708
briggs B73xMo17	.592	.553	.748
dev41 B73	.626	.624	.857
dev64 B73	.621	.599	.810
huang2018 leaf	.500		
huang2018 root	.504		
huang2018 sam	.505	.518	
huang2018 seed	.499	.540	.687
walley rna	.504	.508	.553
walley protein		.515	.739
walley all		.574	.822

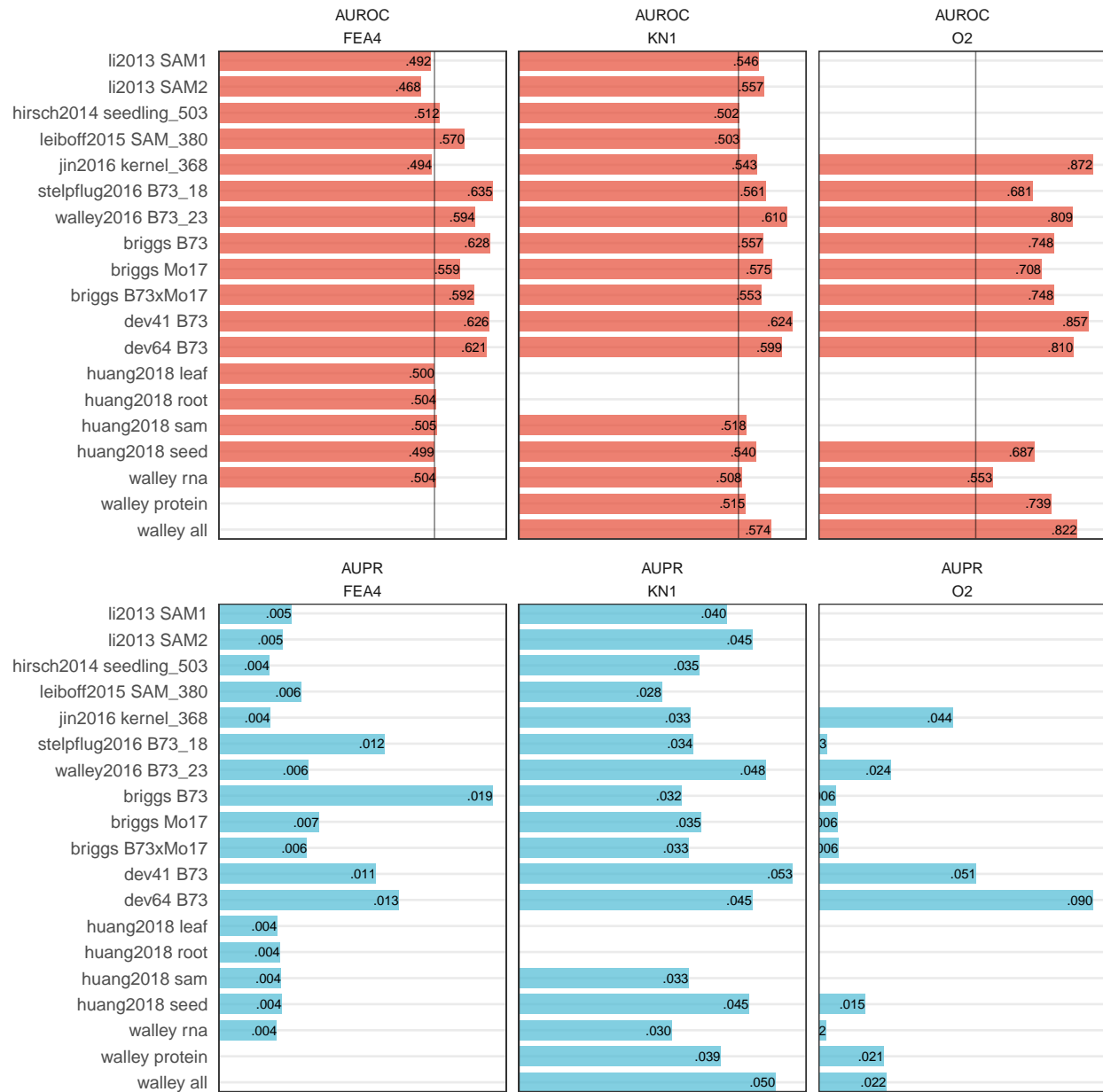|	AUPR FEA4	AUPR KN1	AUPR O2
li2013 SAM1	.005	.040	
li2013 SAM2	.005	.045	
hirsch2014 seedling_503	.004	.035	
leiboff2015 SAM_380	.006	.028	
jin2016 kernel_368	.004	.033	.044
stelpflug2016 B73_18	.012	.034	3
walley2016 B73_23	.006	.048	.024
briggs B73	.019	.032	06
briggs Mo17	.007	.035	006
briggs B73xMo17	.006	.033	006
dev41 B73	.011	.053	.051
dev64 B73	.013	.045	.090
huang2018 leaf	.004		
huang2018 root	.004		
huang2018 sam	.004	.033	
huang2018 seed	.004	.045	.015
walley rna	.004	.030	2
walley protein		.039	.021
walley all		.050	.022

Fig 4

Barplot showing AUROC and AUPRs for all GRNs.

Fig 5

Barplots showing AUROC and AUPRs for PCC-based TF-target prediction (ranked by PCC).

Fig 6

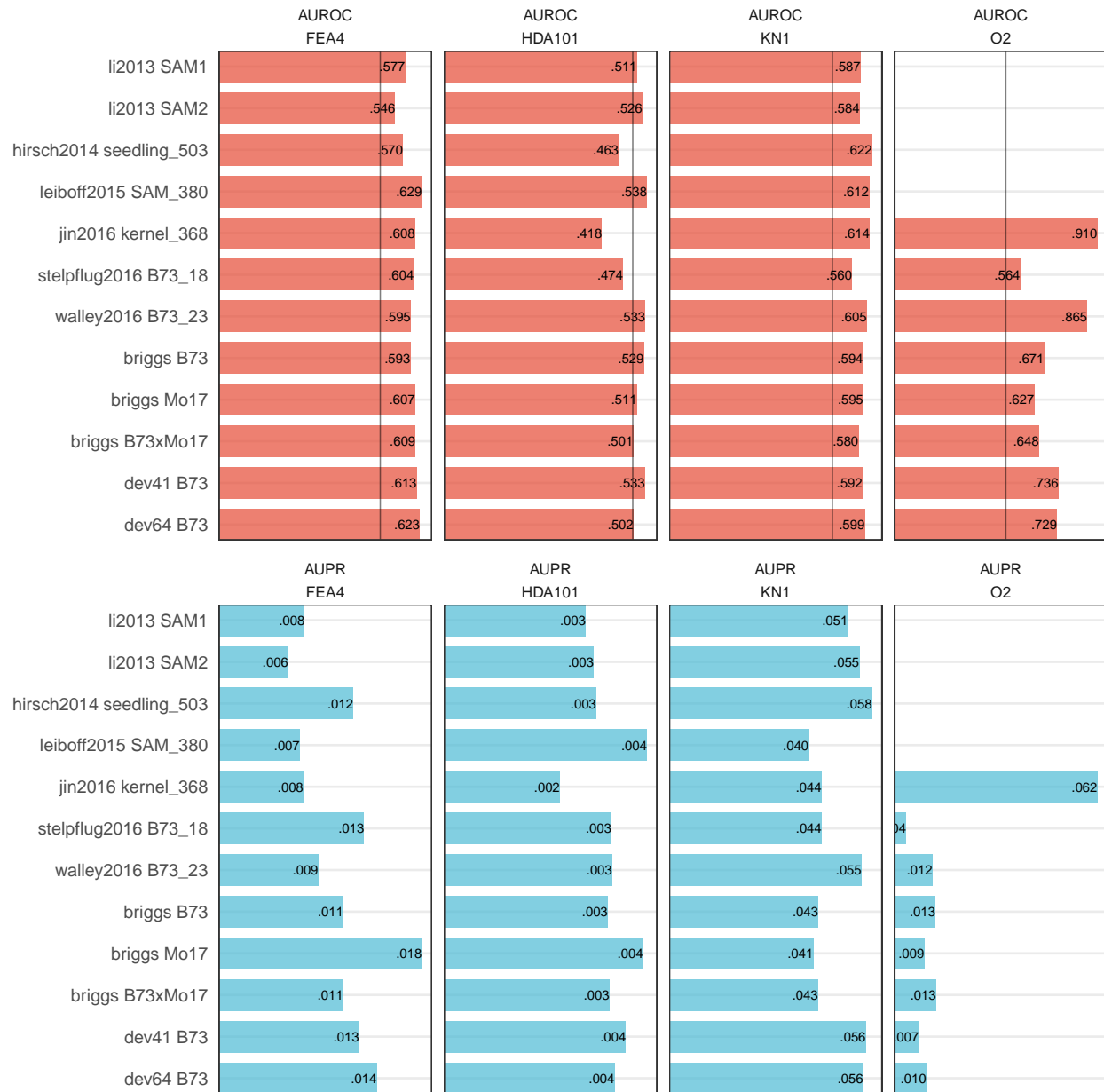Barplot showing AUROC and AUPRs for PCC-based TF-target prediction (ranked by PCC).

Fig 7

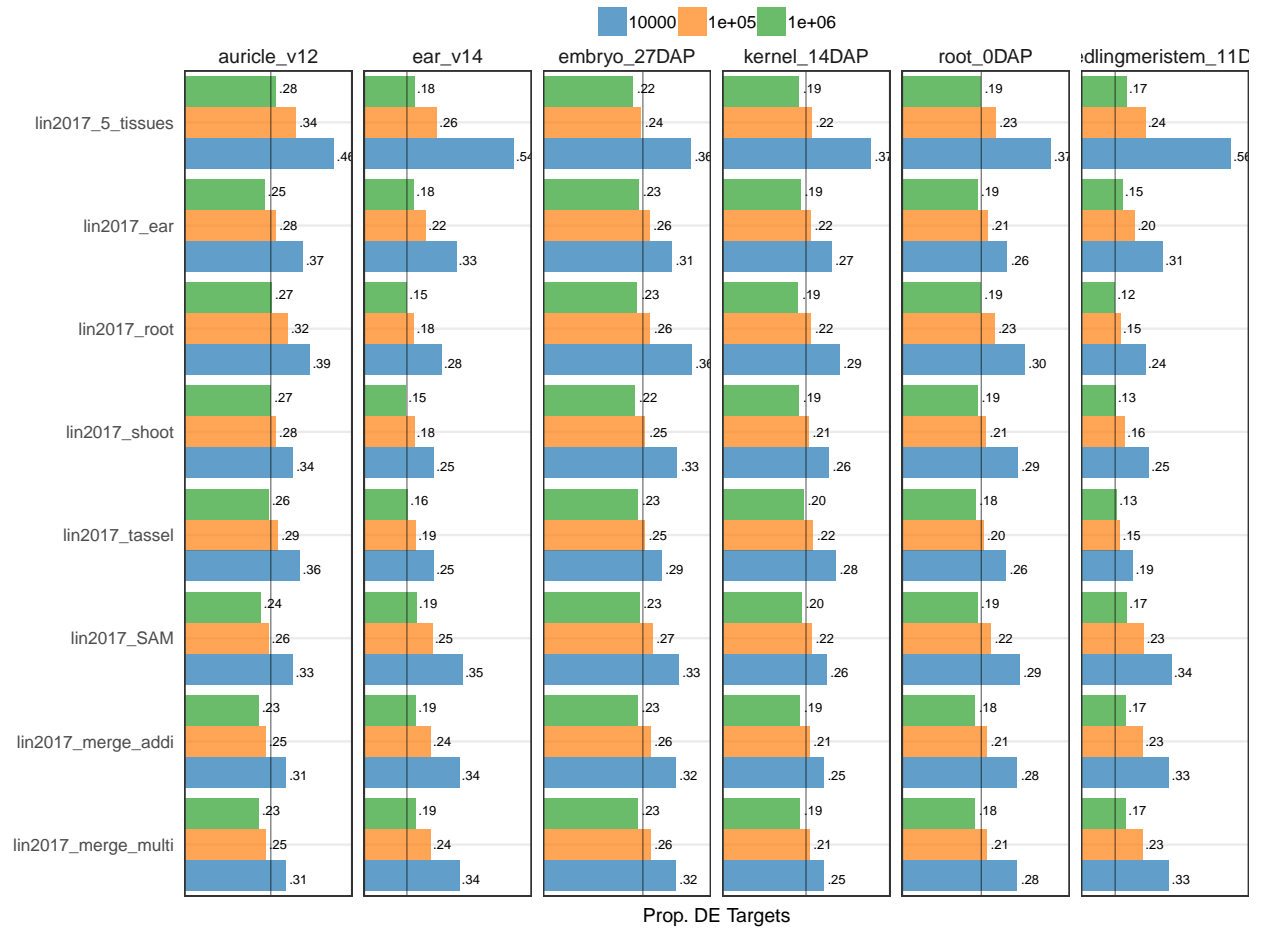Barplot showing AUROC and AUPRs for PCC-based TF-target prediction (ranked by PCC).

Fig 8

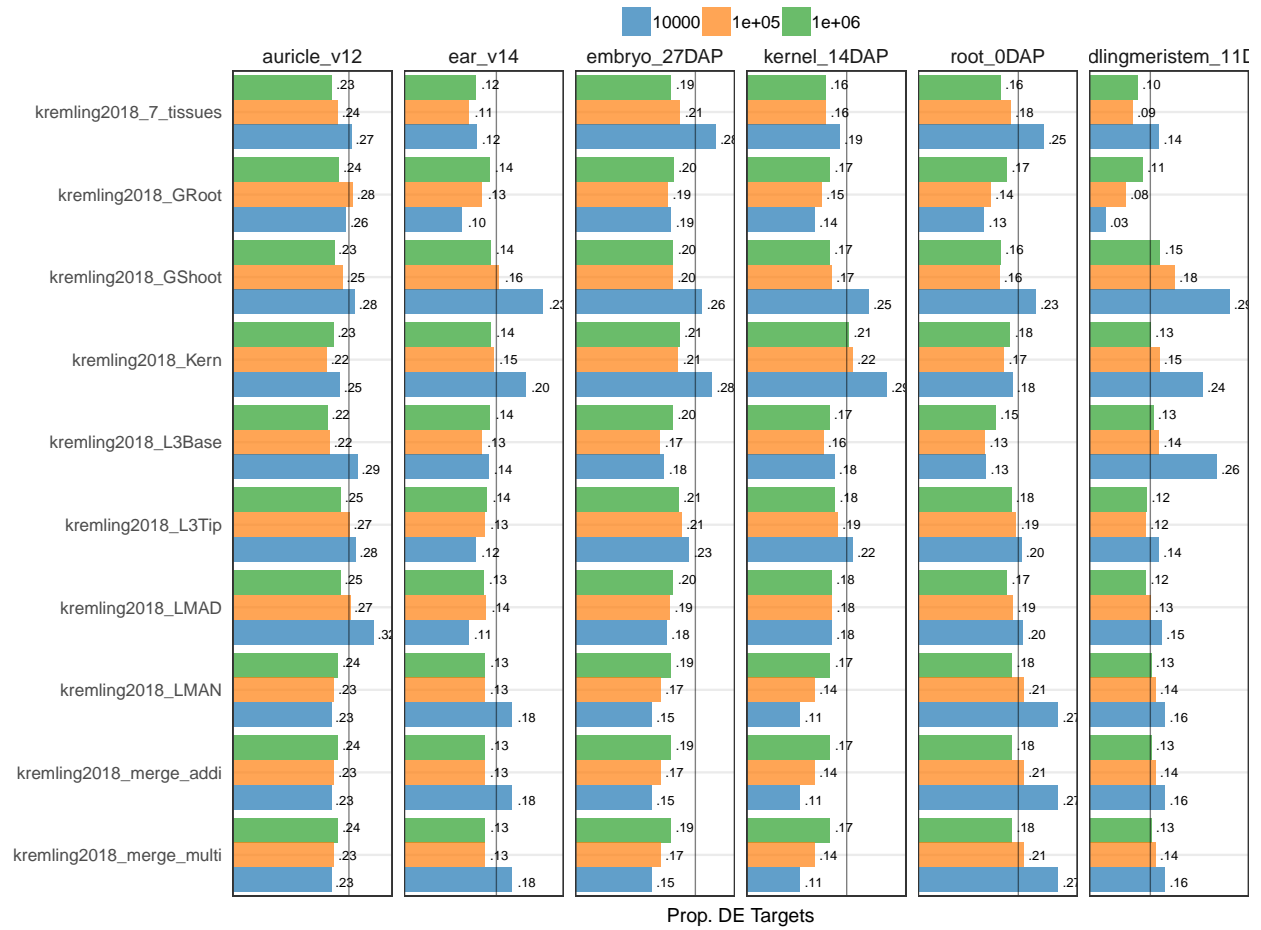Enrichment of DE genes (using Briggs dataset) in predicted TF targets made by different GRNs.

Fig 9

Enrichment of DE genes (using Briggs dataset) in predicted TF targets made by different GRNs.
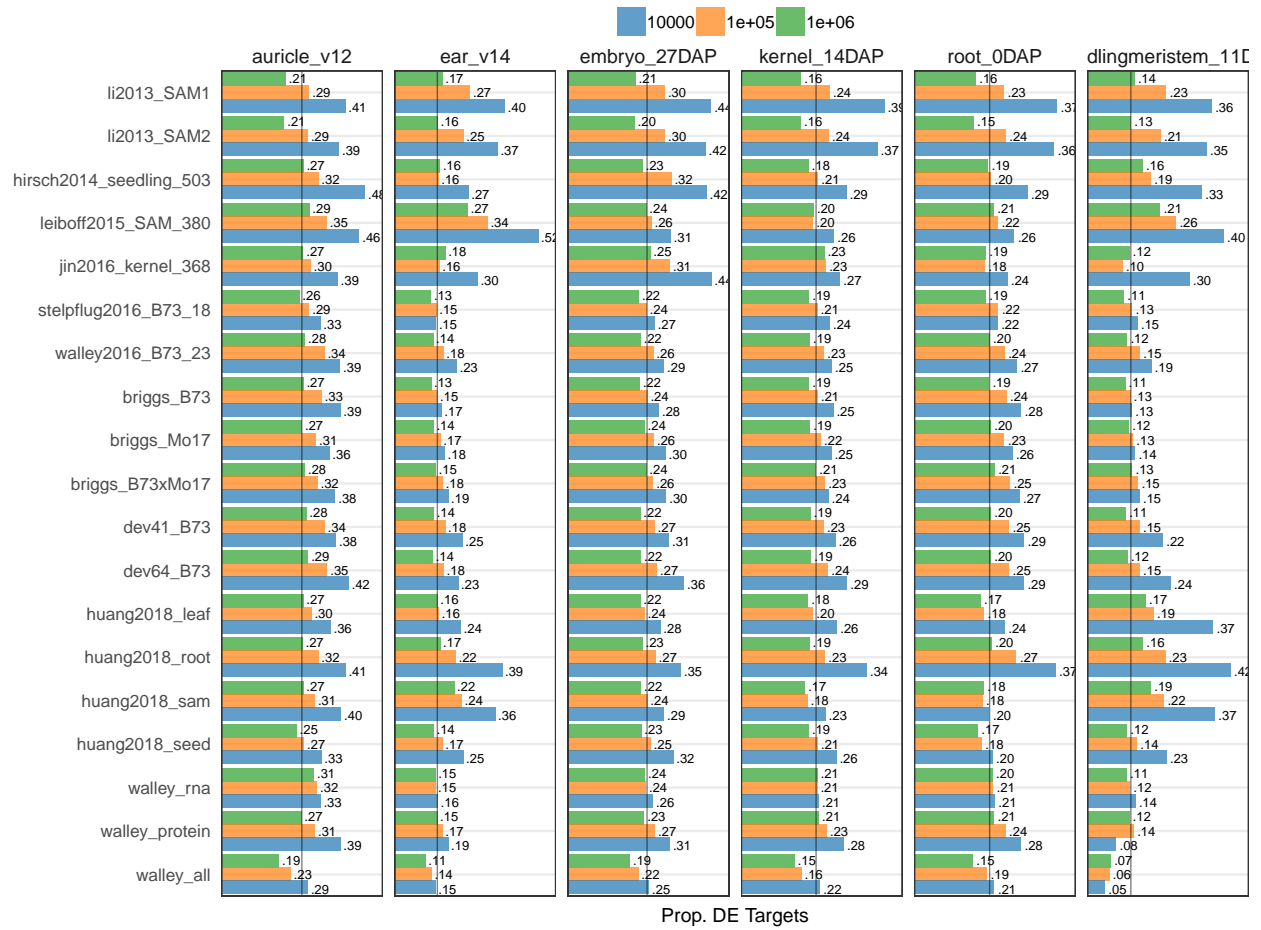
Fig 10

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