

Figure S1: QQplots of moderated t-statistics before and after additional normalization in CiA data set for representative chromosome arm (3L). Theoretical quantiles are based on t-statistic quantiles using the moderated t-statistic degrees of freedom for CiA (8.69). See Methods for details.

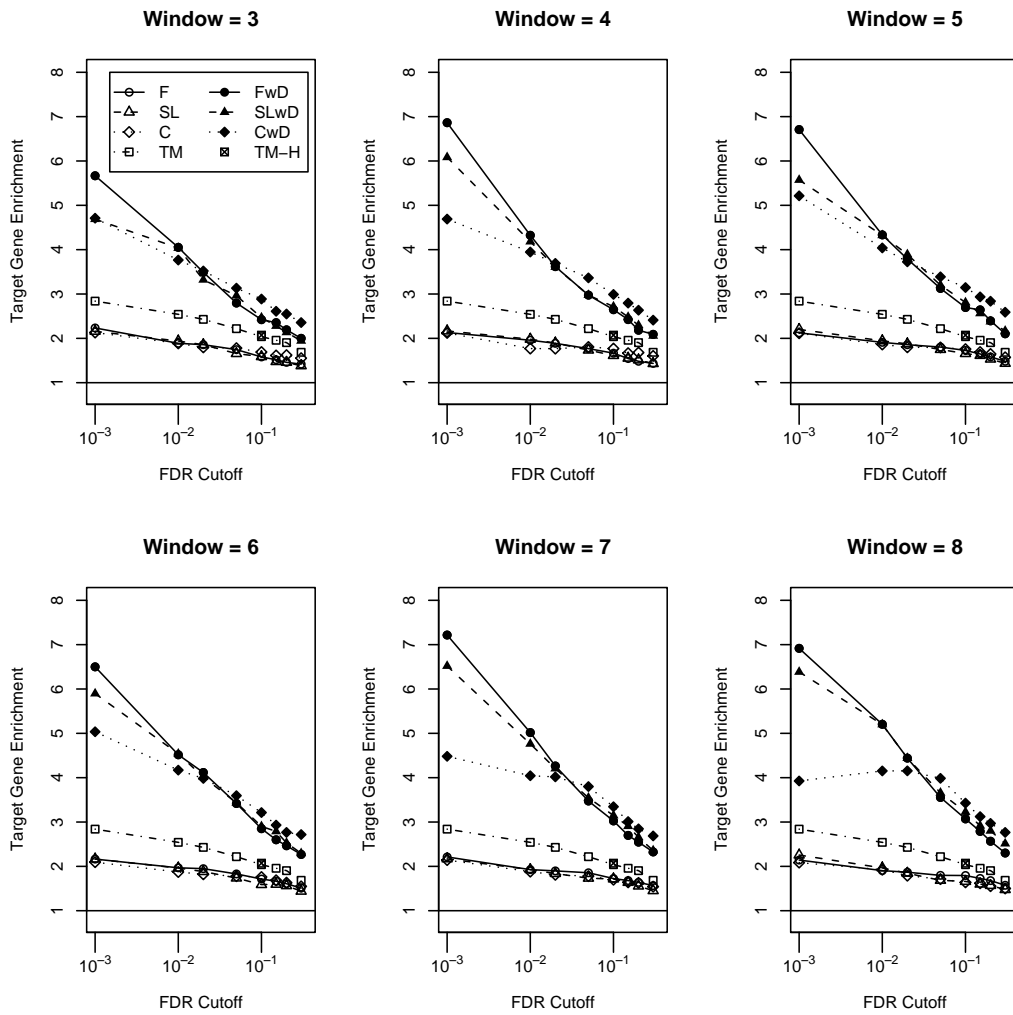


Figure S2: Target Gene Enrichment for All Window Sizes. See Figure 3 for details.

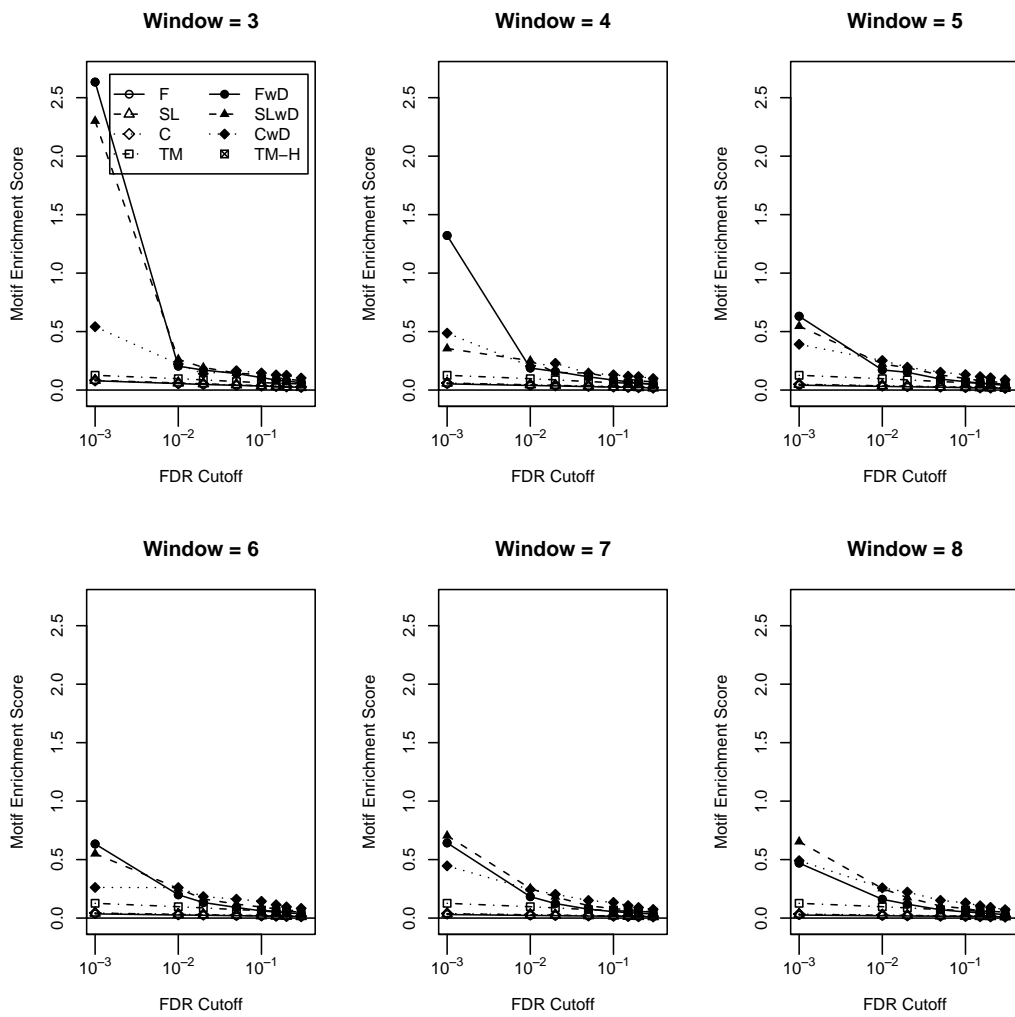


Figure S3: Motif Enrichment for All Window Sizes. See Figure 3 for details.

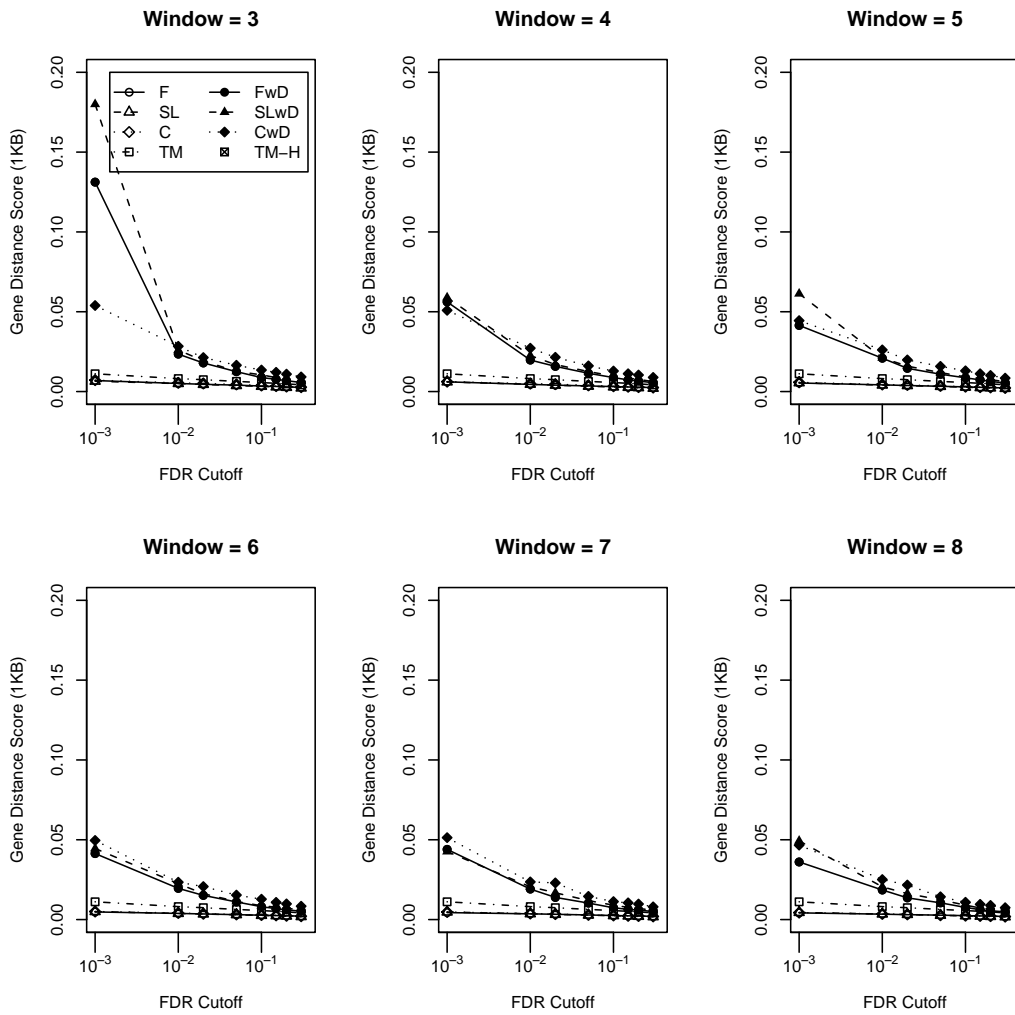


Figure S4: Gene Distance Score (1KB) for All Window Sizes. See Figure 4 for details.

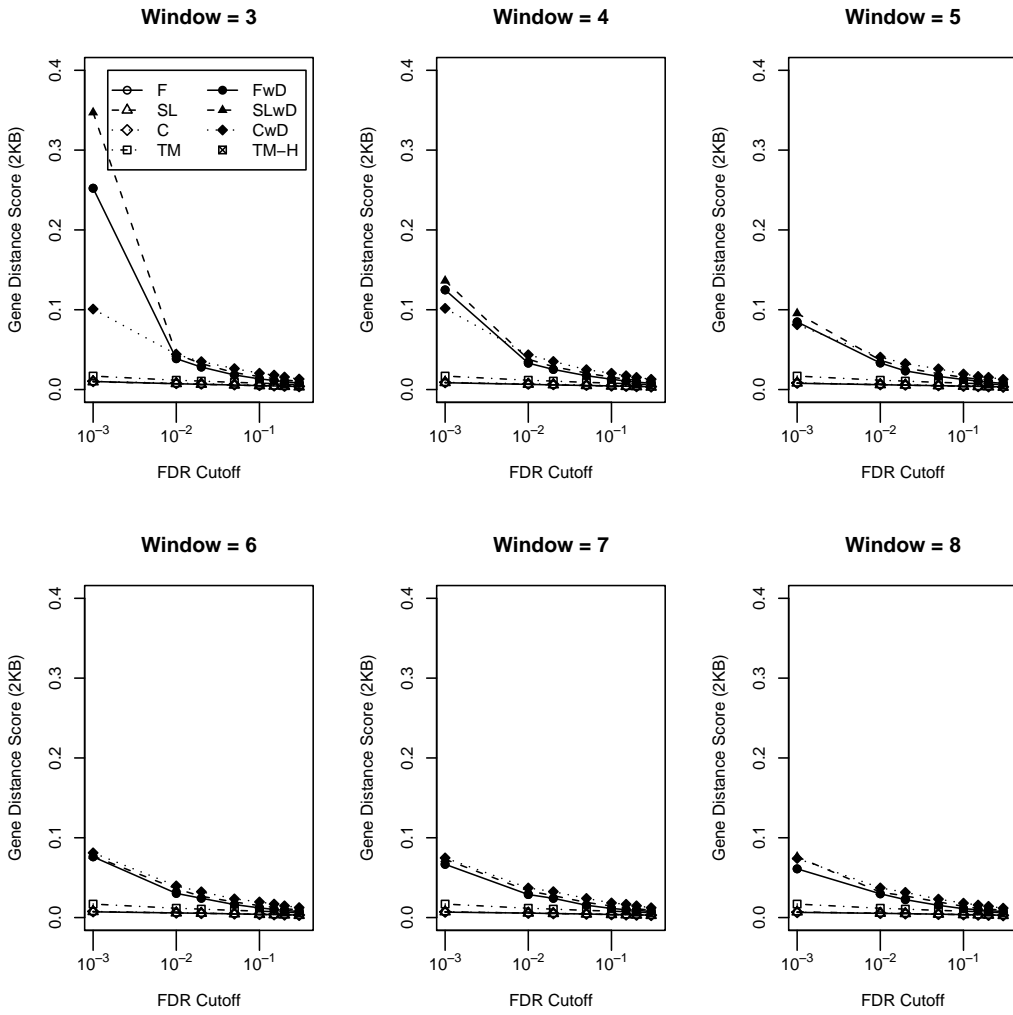


Figure S5: Gene Distance Score (2KB) for All Window Sizes. See Figure 4 for details.

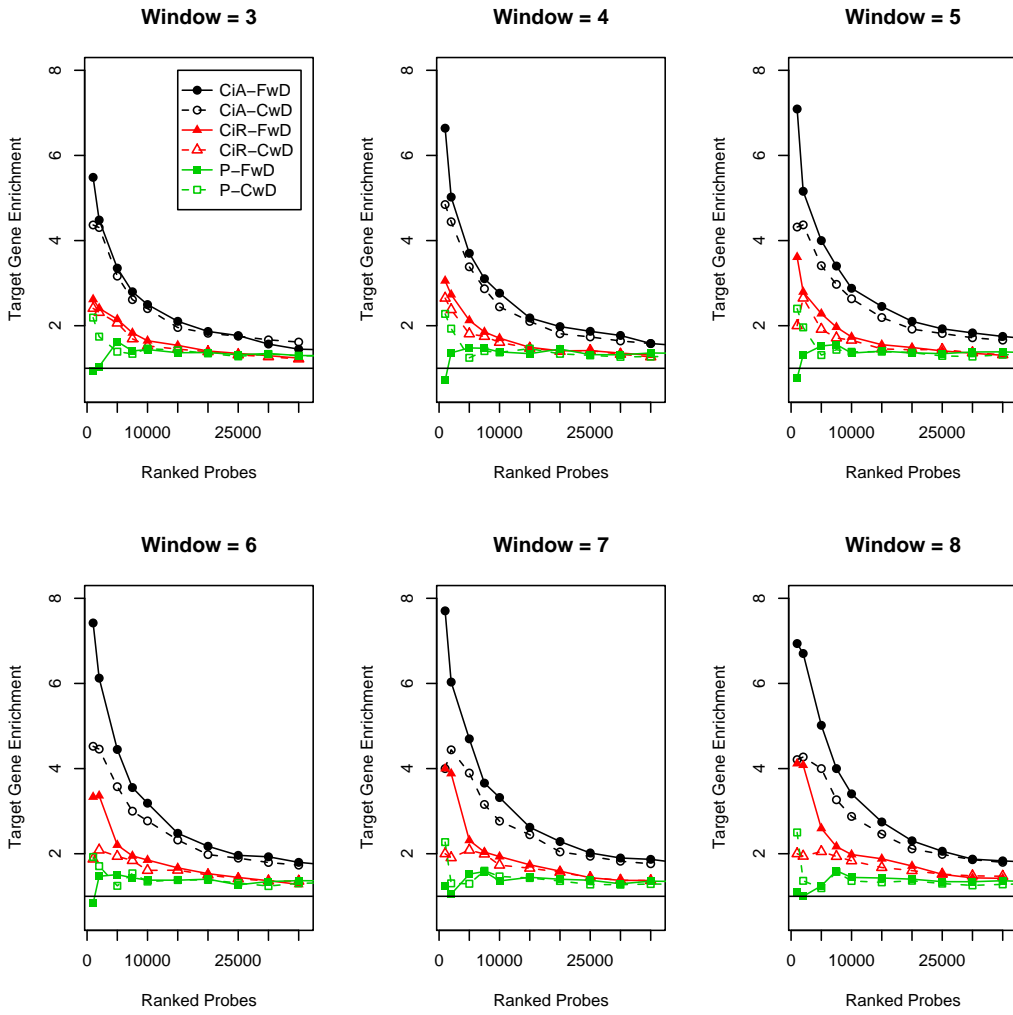


Figure S6: Target Gene for Top Predictions and All Window Sizes. See Figure 5 for details.

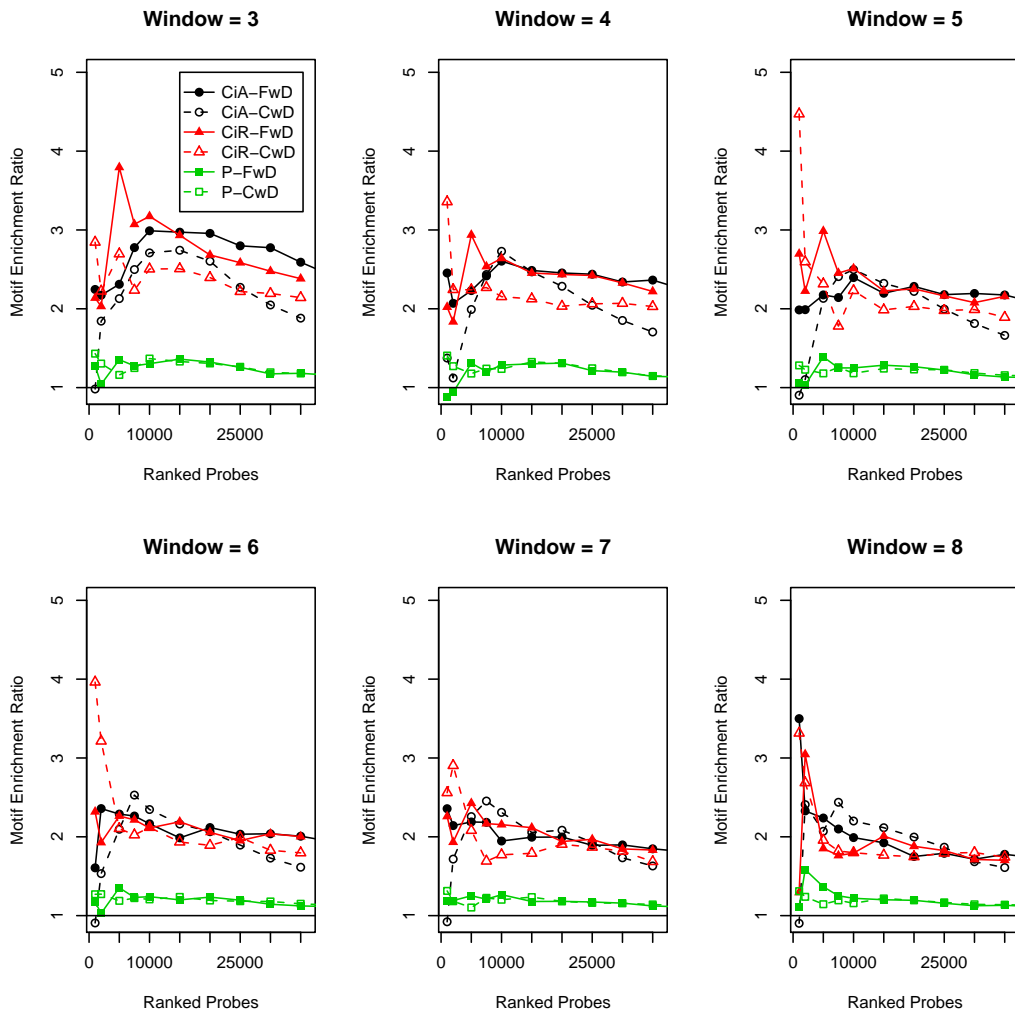


Figure S7: Motif Enrichment for Top Predictions and All Window Sizes. See Figure 5 for details.

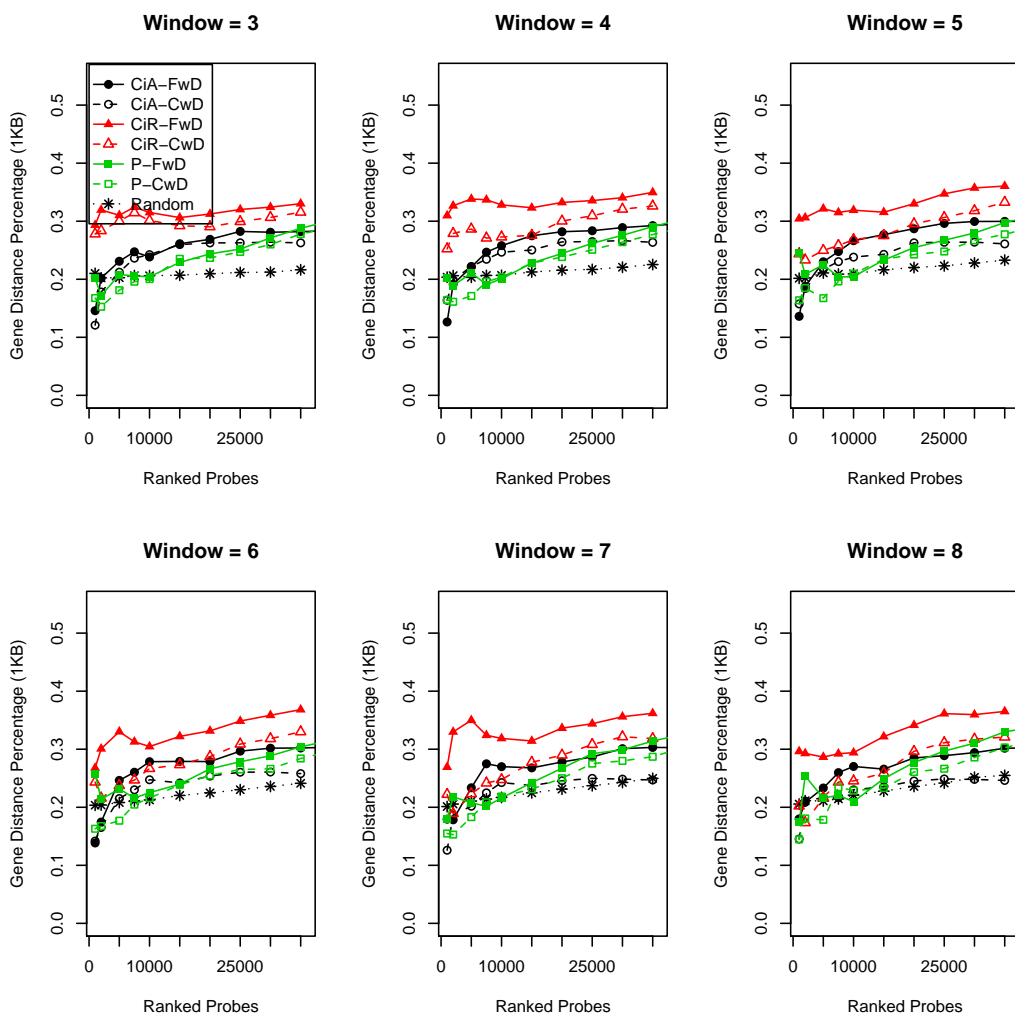


Figure S8: Gene Distance Score (1KB) for Top Predictions and All Window Sizes. See Figure 6 for details.



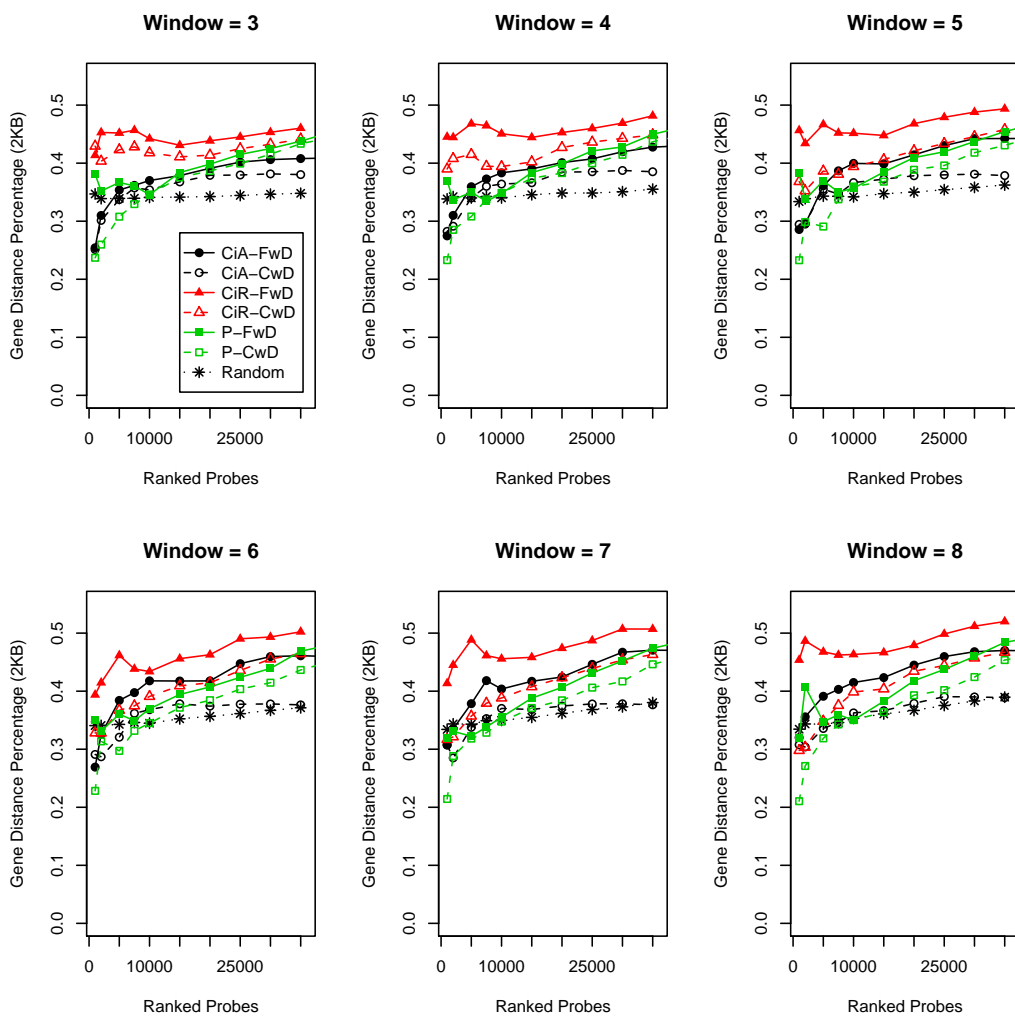


Figure S9: Gene Distance Score (2KB) for Top Predictions and All Window Sizes. See Figure 6 for details.

GO Term	# Gene List	# GO Term	Description
GO:0045165	56	227	cell fate commitment
GO:0003700	57	303	transcription factor activity
GO:0045449	76	523	regulation of transcription
GO:0048513	113	1101	organ development
GO:0006350	82	633	transcription
GO:0010468	78	595	regulation of gene expression
GO:0048731	125	1393	system development
GO:0019219	76	598	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
GO:0031323	79	649	regulation of cellular metabolic process
GO:0050794	101	1007	regulation of cellular process
GO:0019222	80	698	regulation of metabolic process
GO:0007399	69	565	nervous system development
GO:0048856	130	1685	anatomical structure development
GO:0003002	56	407	regionalization
GO:0050789	113	1353	regulation of biological process
GO:0007389	57	426	pattern specification process
GO:0048646	40	235	anatomical structure formation
GO:0003702	42	263	RNA polymerase II transcription factor activity
GO:0003677	69	632	DNA binding
GO:0065007	114	1459	biological regulation
GO:0007275	132	1905	multicellular organismal development
GO:0009790	59	532	embryonic development
GO:0005634	107	1420	nucleus
GO:0030154	90	1073	cell differentiation
GO:0006355	49	390	regulation of transcription, DNA-dependent
GO:0009653	97	1218	anatomical structure morphogenesis
GO:0048869	90	1105	cellular developmental process
GO:0009887	63	617	organ morphogenesis
GO:0048737	36	240	imaginal disc-derived appendage development
GO:0006351	54	483	transcription, DNA-dependent
GO:0032774	54	484	RNA biosynthetic process
GO:0007165	65	662	signal transduction
GO:0048736	36	243	appendage development
GO:0007154	75	856	cell communication
GO:0035114	35	237	imaginal disc-derived appendage morphogenesis
GO:0035107	35	240	appendage morphogenesis
GO:0032502	136	2243	developmental process
GO:0001709	37	118	cell fate determination
GO:0032501	140	2373	multicellular organismal process
GO:0007166	52	497	cell surface receptor linked signal transduction
GO:0006139	92	1303	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
GO:0022008	40	346	neurogenesis
GO:0001708	27	69	cell fate specification
GO:0048699	39	336	generation of neurons
GO:0007444	55	600	imaginal disc development
GO:0035220	31	233	wing disc development
GO:0007423	47	471	sensory organ development
GO:0006366	30	221	transcription from RNA polymerase II promoter
GO:0050793	28	199	regulation of developmental process
GO:0043231	126	2283	intracellular membrane-bound organelle

Table S1: Significant GO terms for genes associated with CiA-CiR ERs. Columns list the significant GO terms (p-value < 10<sup>-20</sup>), number of ER genes in the GO term, number of total genes in the GO term and GO term description.