Figure S10

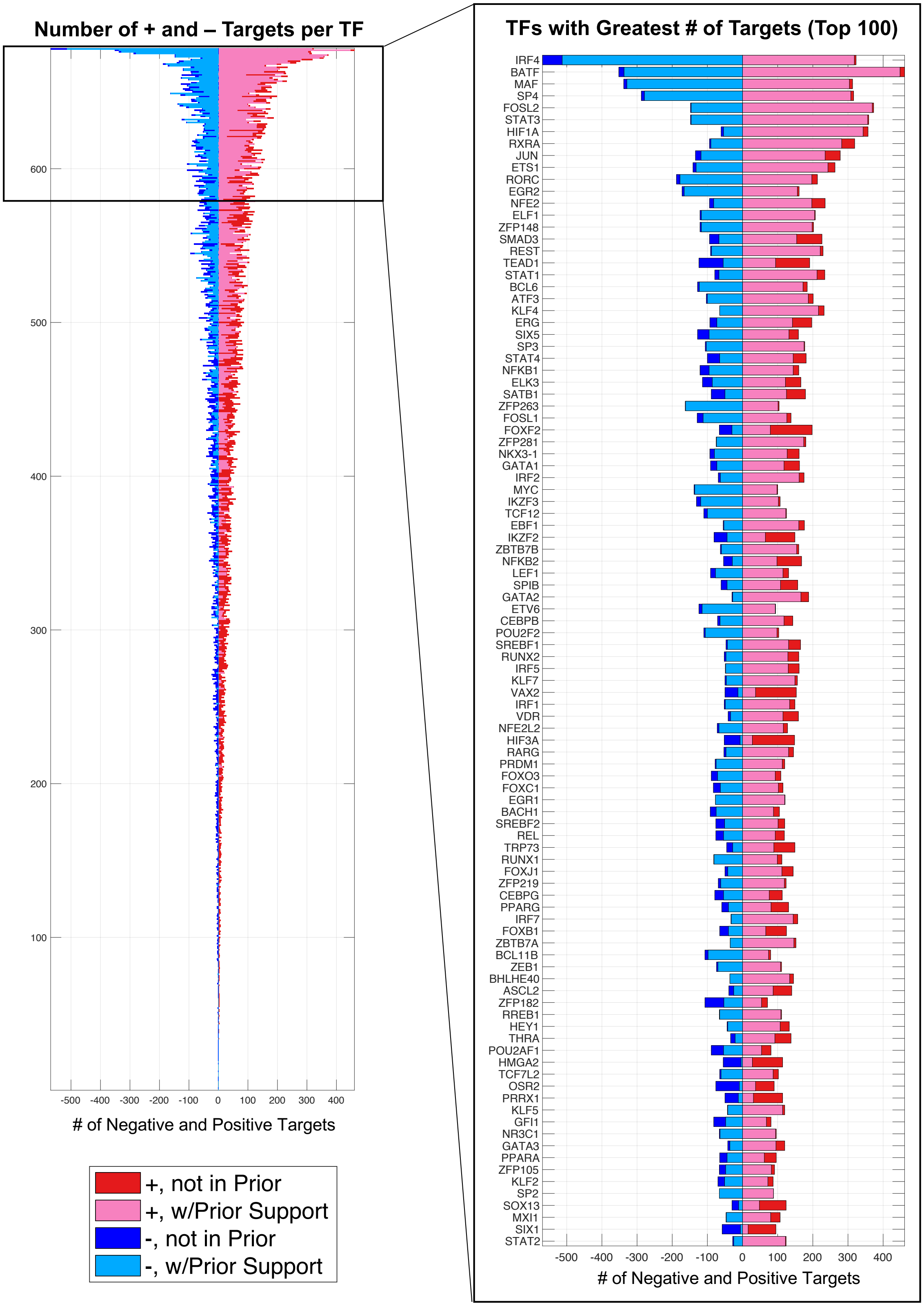

Figure S12. Distribution of targets per TF in final ChIP+KO+ATAC TRN. Network size was limited to mean 15 TFs per gene and network edges were further filter to remove any edge with absolute partial correlation < .01. TFs were ranked according to degree (total number of target genes) in the left panel, while the inset displays the Top 100 highest-degree TFs. TF target genes are colored according to interaction sign and whether the interaction was also in the prior (see key).