TF	Species	Raw Peaks	Filtered Peaks	Bound Windows	Frac. Bound	Accession ID
CTCF	Mouse	32006	28943	296117	0.71%	ENCSR000CBU
	Human	29067	26477	270100	0.55%	ENCSR911GFJ
CEBPA	Mouse	62636	48812	566945	1.35%	E-TABM-722
	Human	32243	28545	298066	0.61%	E-TABM-722
HNF4A	Mouse	44800	36540	415846	0.99%	E-TABM-722
	Human	42766	34714	387077	0.79%	E-TABM-722
RXRA	Mouse	46443	33751	404284	0.97%	GSM1299600
	Human	95085	71032	854289	1.75%	ENCSR098XMN

Table S5: For the primary experimental data used in this study, the following quantities are listed: the number of peaks called across the entire genome; the number of called peaks within the filtered window set, merged if within 500 bp of each other; the number of windows in the filtered window set labeled bound due to peak overlap; the fraction of the filtered window set labeled bound; and the database accession ID (ENCODE, GEO, or ArrayExpress). The size of the filtered window sets for the mouse and human genomes were 41883806 and 48742577, respectively.