Table S7: CTCF Binding divergence estimated by direct comparison

D. melanogaster centric

	Species B					
Species A		ı ıotai		Diverged with Species B	binding divergence	
D.mel	D.sim	2182	1424	758	34.74%	
D.mel	D.yak	2182	1483	699	32.03%	
D.mel	D.pse	2182	353	1829	83.82%	

non-D.melanogaster centric

	Species B					
Species A		Total	Conserved with Species B	Diverged with Species B	binding divergence	
D.sim	D.mel	2197	1381	816	37.14%	
D.yak	D.mel	2993	1497	1496	49.98%	
D.pse	D.mel	2332	388	1944	83.36%	

Note: for the "D. melanogaster centric" subtable, we mapped each non-D. melanogaster species binding sites back to D. melanogaster genome using LiftOver, and calculated the percentage of D. melanogaster binding sites that are not overlapping with any non-D. melanogaster LiftOver binding sites for each species pair as estimate of binding divergence. For the "non-D. melanogaster centric" subtable, we mapped the D. melanogaster binding sites to each non-D. melanogaster species genome using LiftOver, and calcualted the percentage of non-D. melanogaster binding sites that are not overlapping with any D. melanogaster LiftOver binding sites for each pair as estimate of binding divergence.