

# Figure S1

Enrichment profile correlations for regulatory elements in the ENCODE regions

**a**

Promoter		GM	K562	ES	dES
	HeLa	0.78	0.71	0.72	0.75
	GM		0.71	0.70	0.70
	K562			0.64	0.64
	ES				0.75

**b**

CTCF		GM	K562	ES	dES	IMR90
	HeLa	0.87	0.79	0.65	0.76	0.61
	GM		0.84	0.68	0.78	0.59
	K562			0.65	0.76	0.60
	ES				0.83	0.64
	dES					0.72

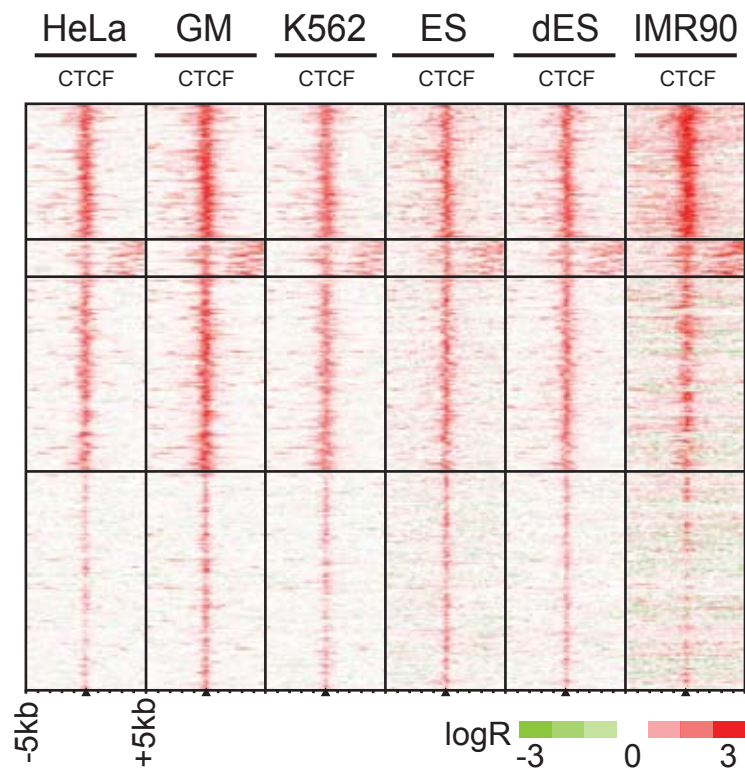
**c**

p300		p300 binding		chromatin	
		GM	K562	GM	K562
	HeLa	-0.20	-0.14	-0.20	-0.14
	GM		-0.20		-0.20

**d**

Enhancer		GM	K562	ES	dES
	HeLa	0.10	0.07	0.14	0.26
	GM		0.16	0.04	0.07
	K562			0.04	0.19
	ES				0.36

**e** CTCF binding at 729 predicted insulators is highly similar across cell types



**f** Chromatin modifications at 411 distal p300 binding sites are cell type-specific

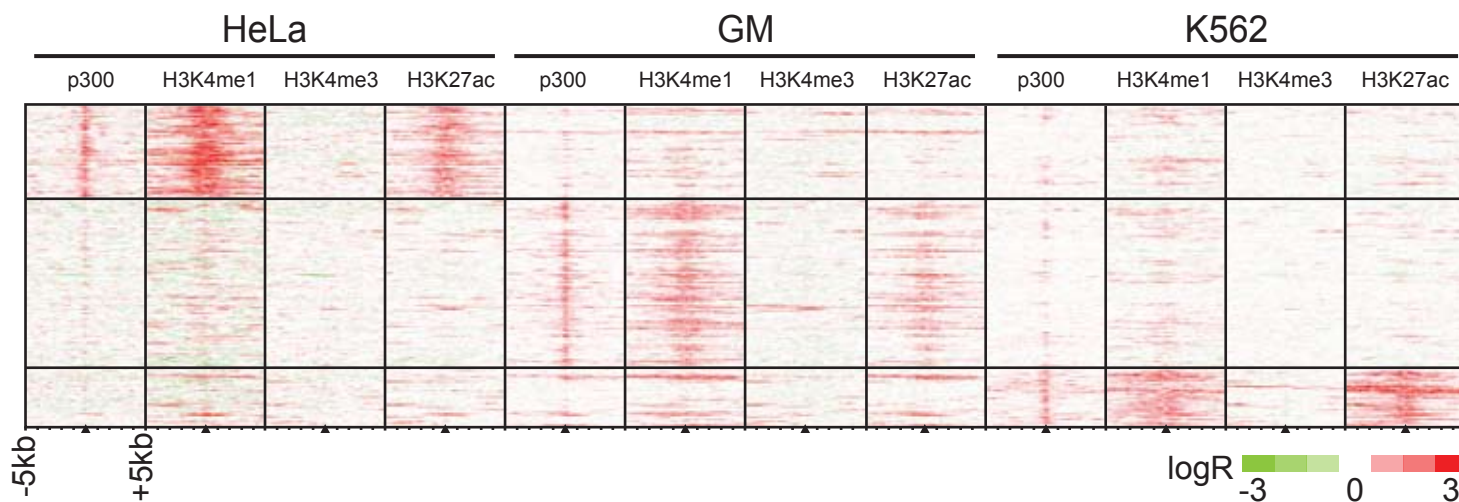
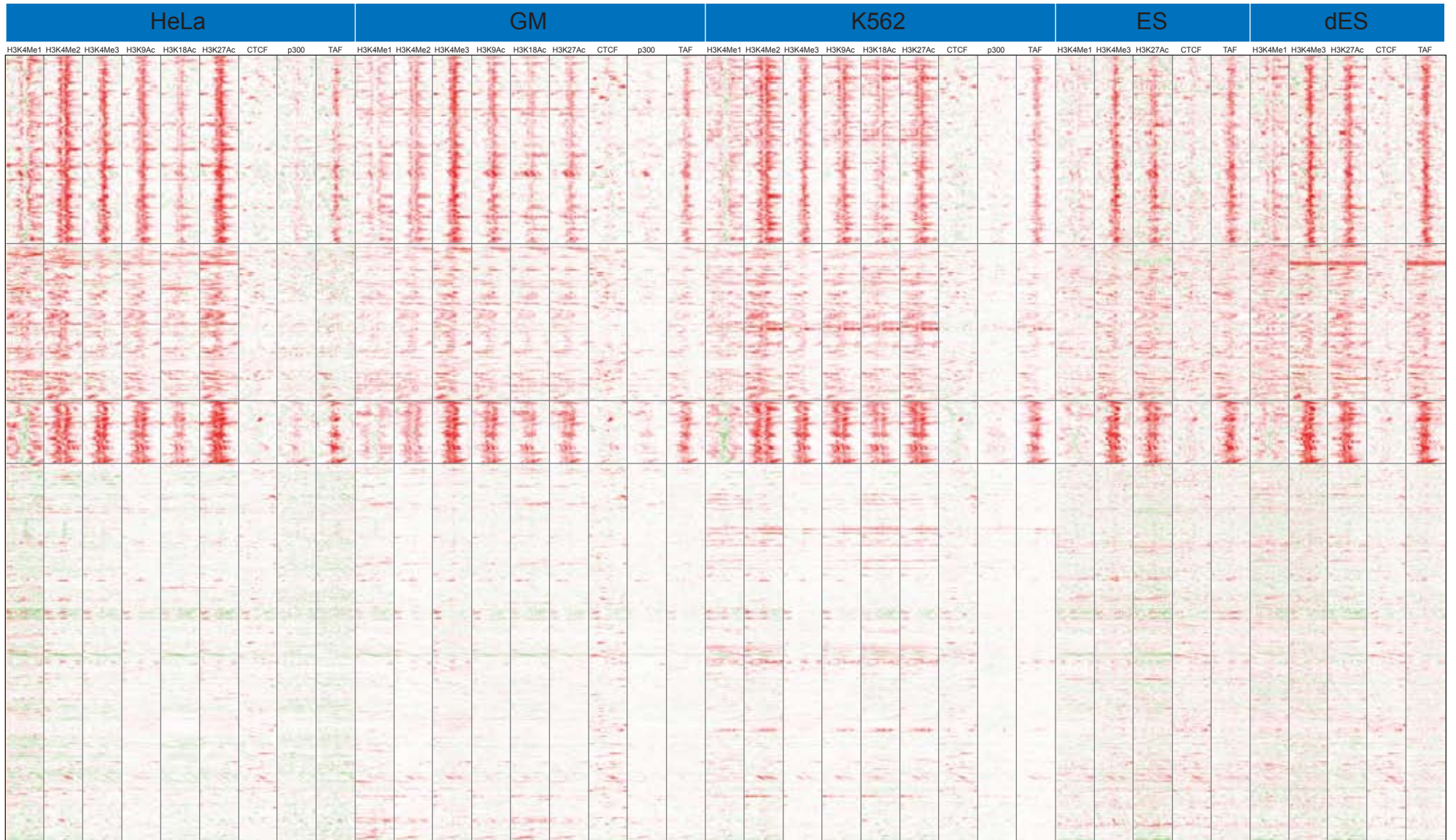


Figure S2: ChIP-chip enrichment profiles at TSS of Gencode genes



logR ■ ■ ■  
-3 0 3

Figure S3: ENCODE enhancer verification

DNase I hypersensitive sites

p300 sites

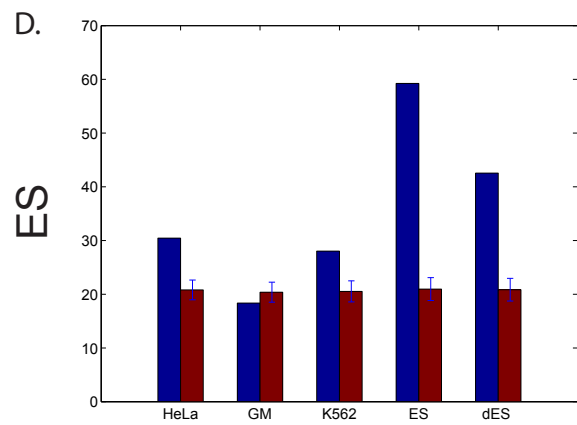
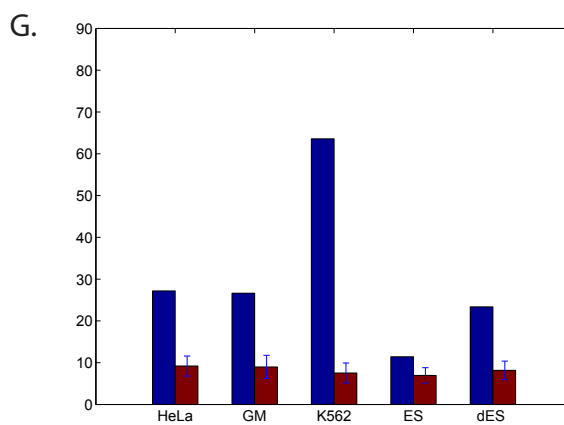
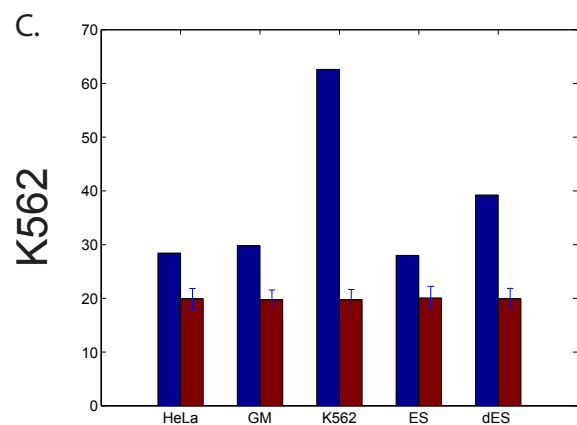
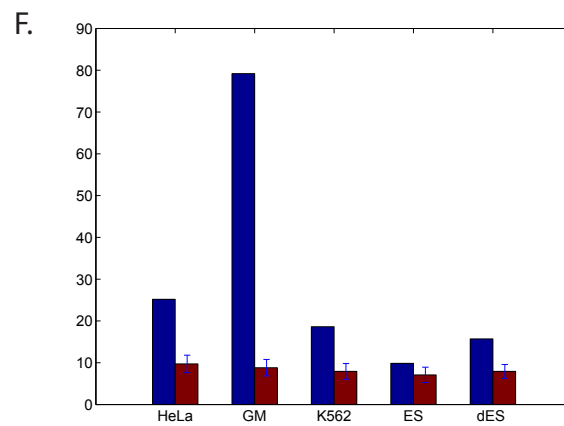
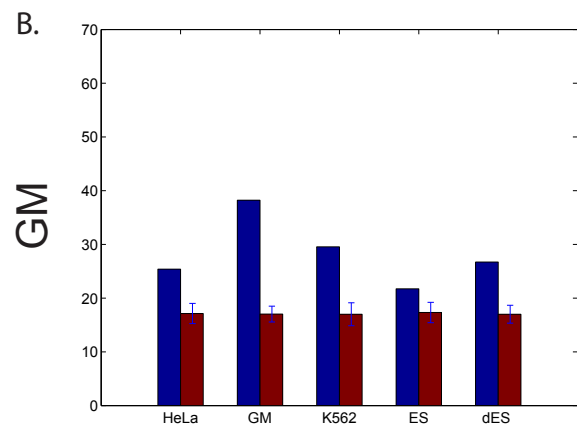
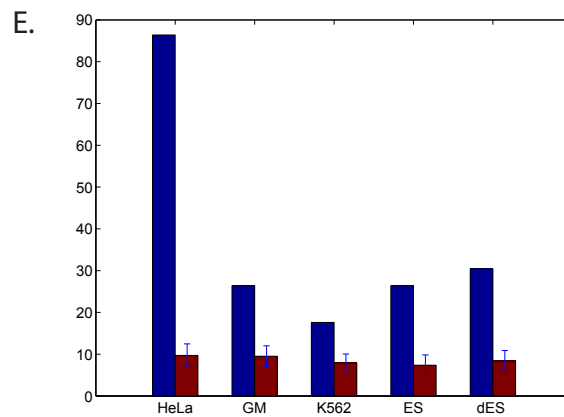
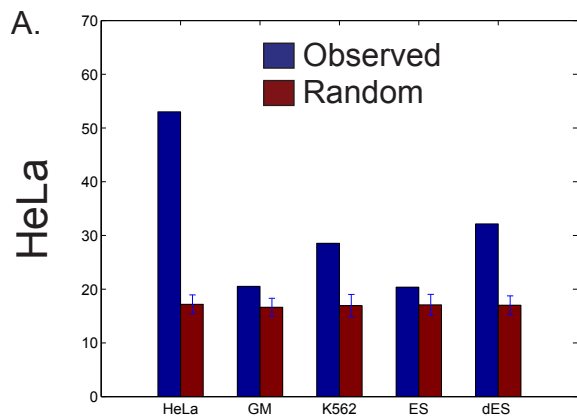
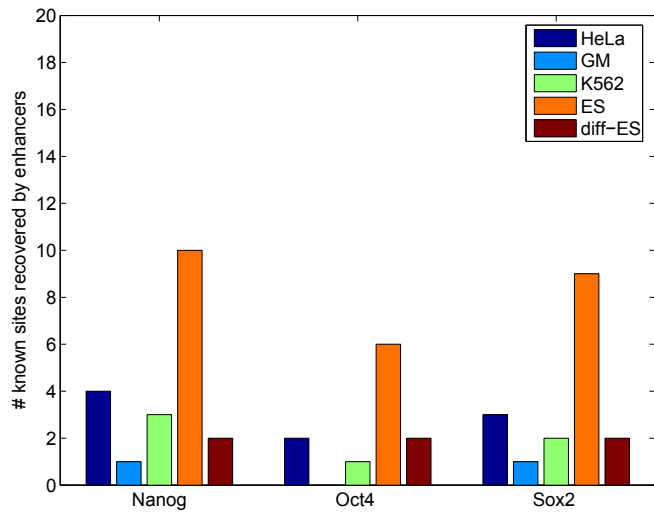
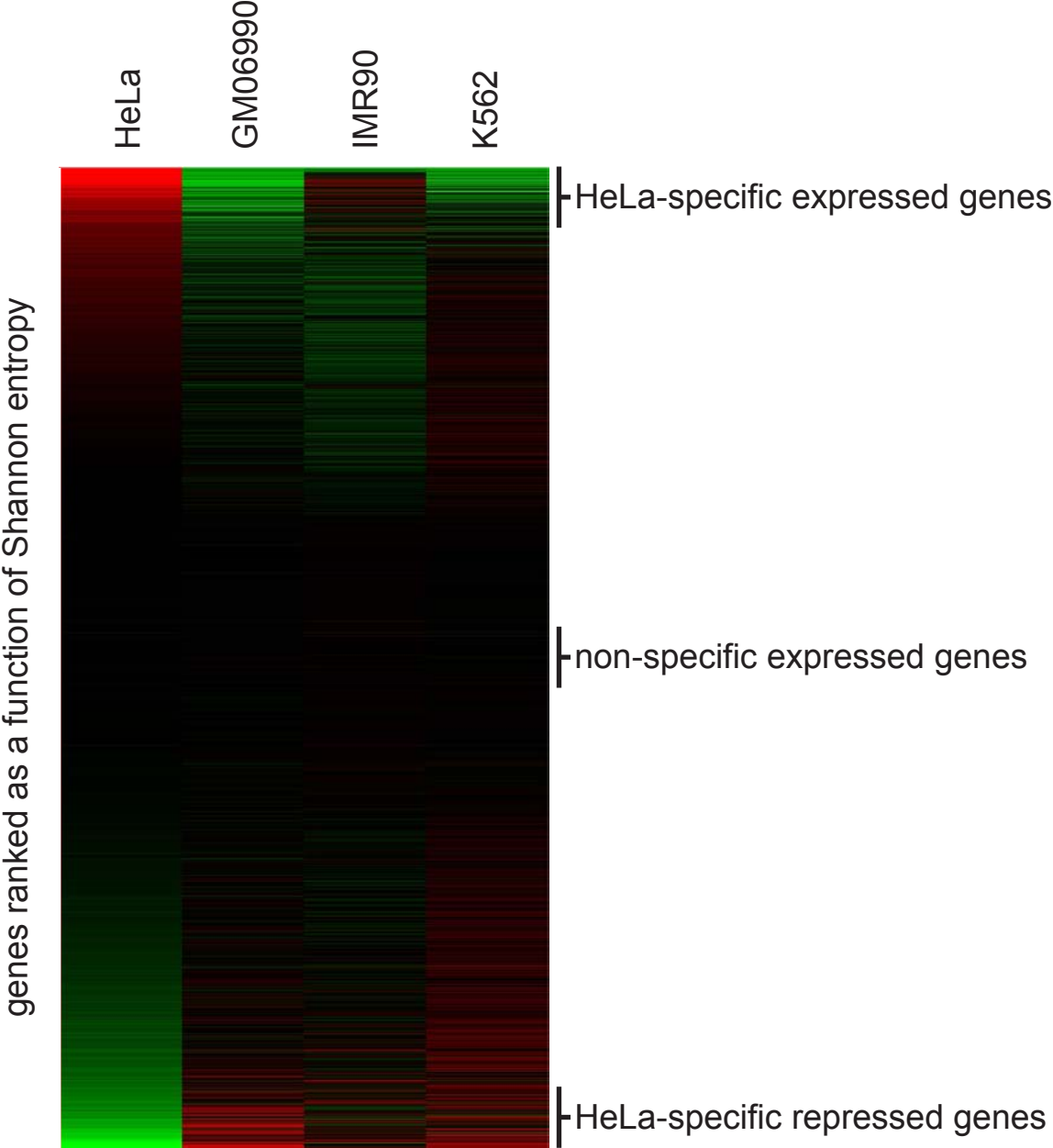


Figure S4 - ENCODE ES enhancer verification



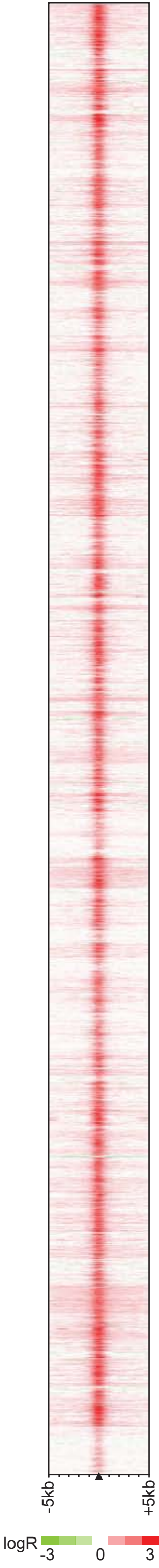
# FigureS5





# Figure S6

CTCF enrichment data in IMR90 cells at CTCF binding sites from IMR90, HeLa and CD4+ T cells



# FigureS7

