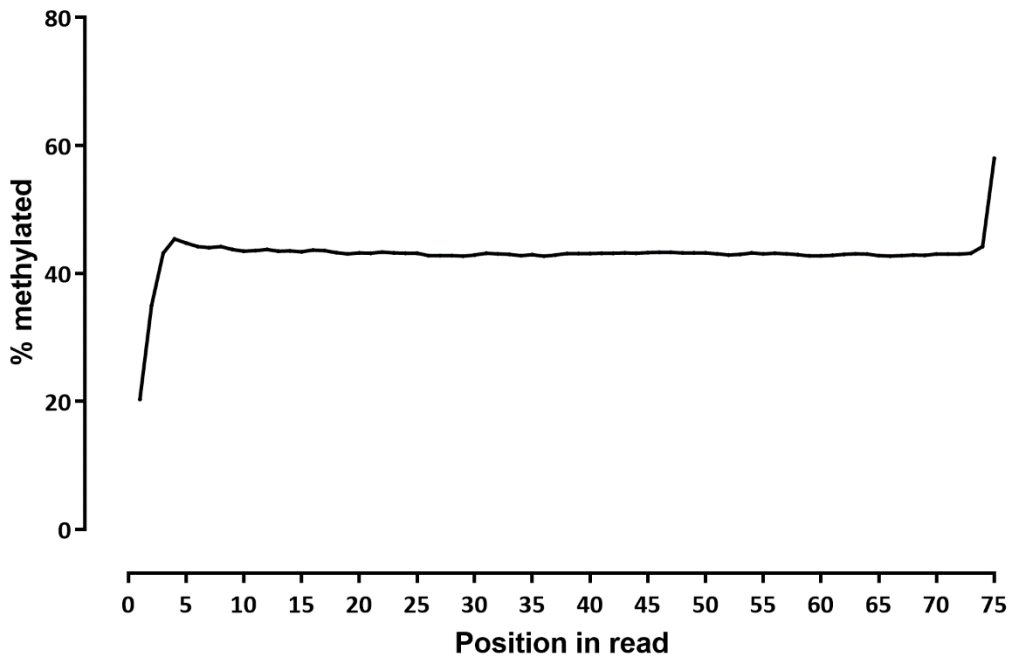


Mapping stats

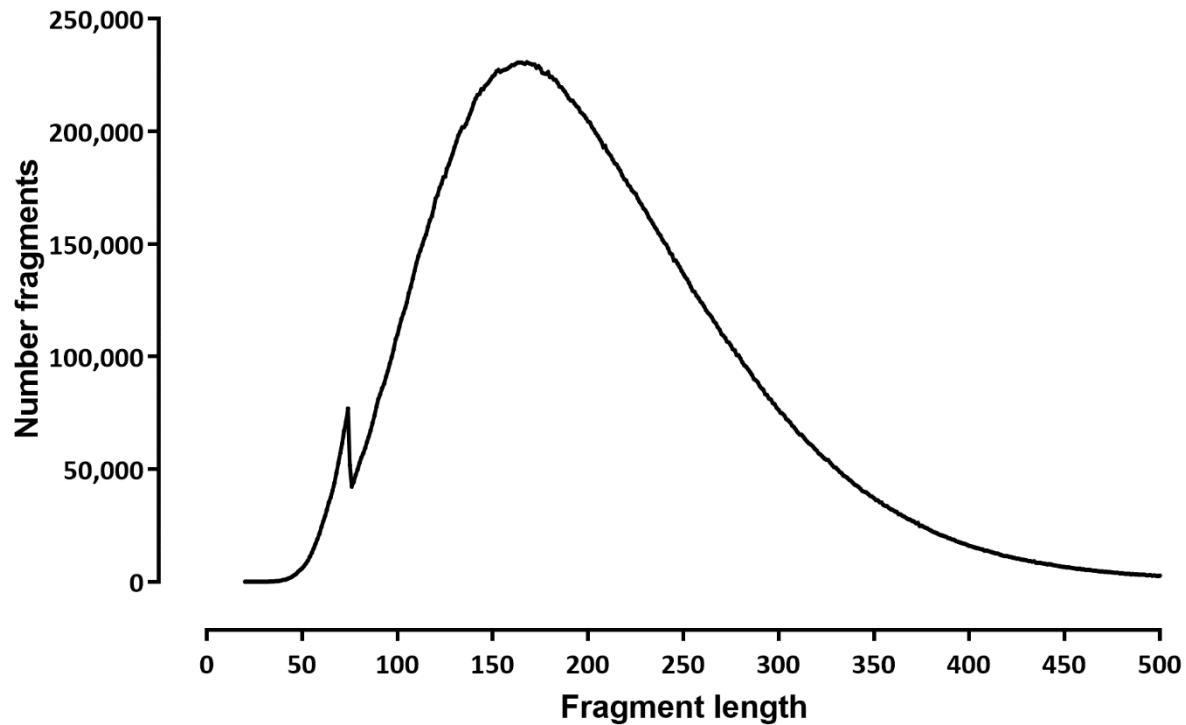
Species	#	CpG %	CHG%	CHH%	Complexity	Read Length	Mean alignment Length	Unique	Unique deduped	Multi	Raw fragments	Alignment fraction
<i>Homo sapiens</i> hg20-female	L575-GM12878_EM-seq	42.80%	10.10%	11.40%	0.97	2x75-trim	74.16	81,747,684			51,390,857	80.00%

L575-GM12878_EM-seq M-bias



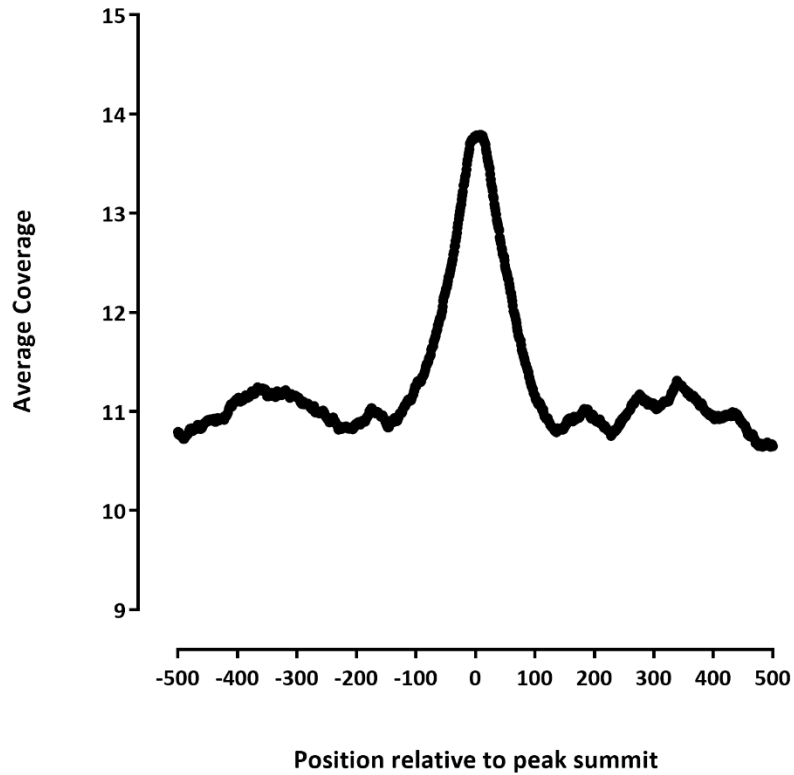
Insert Length Distribution

L575-GM12878_EM-seq

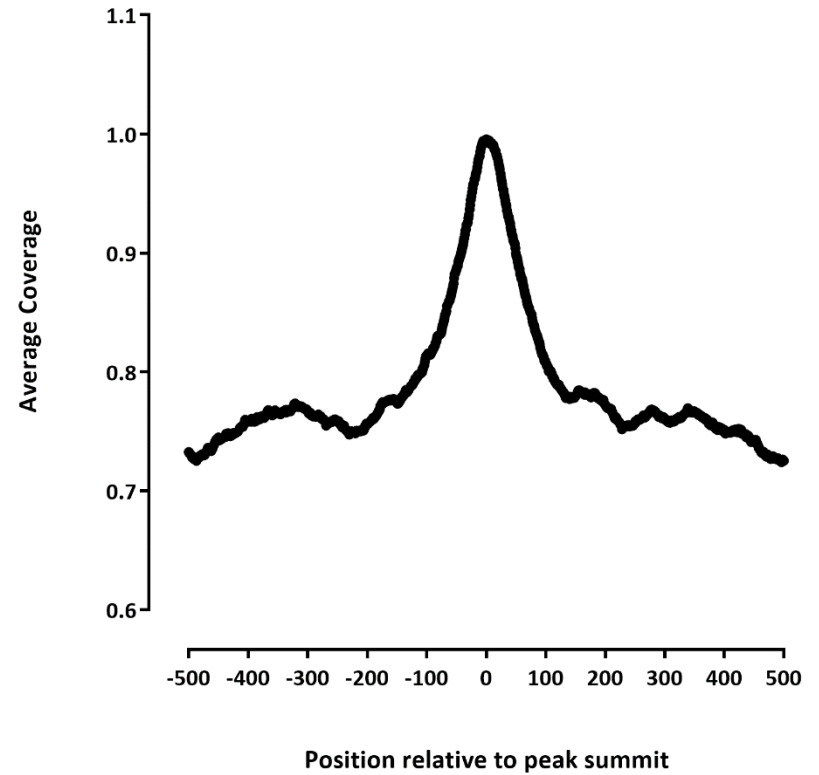


CTCF sites

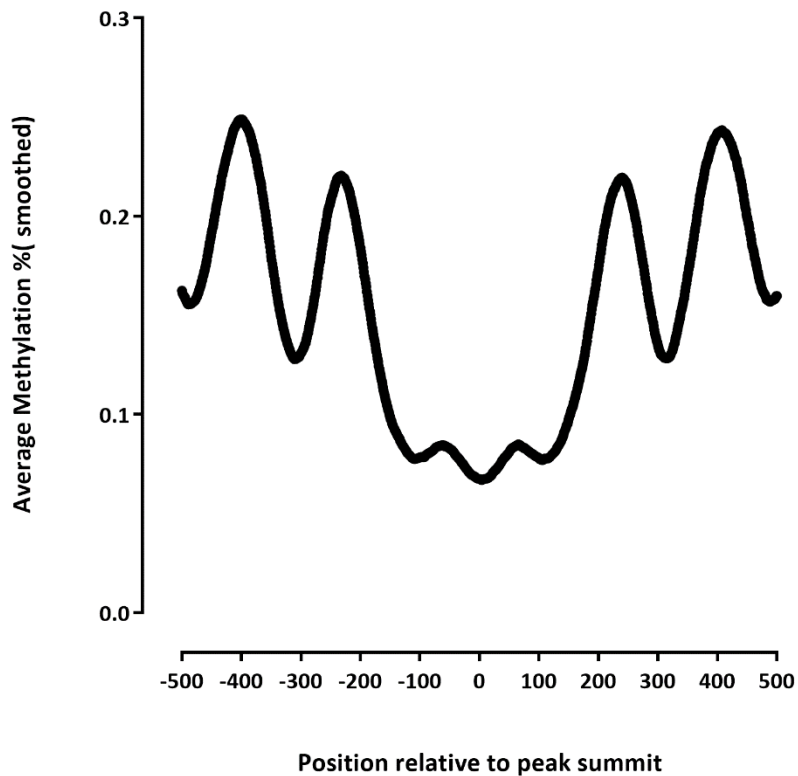
ENCODE GM12878 WGBS CTCF peaks coverage



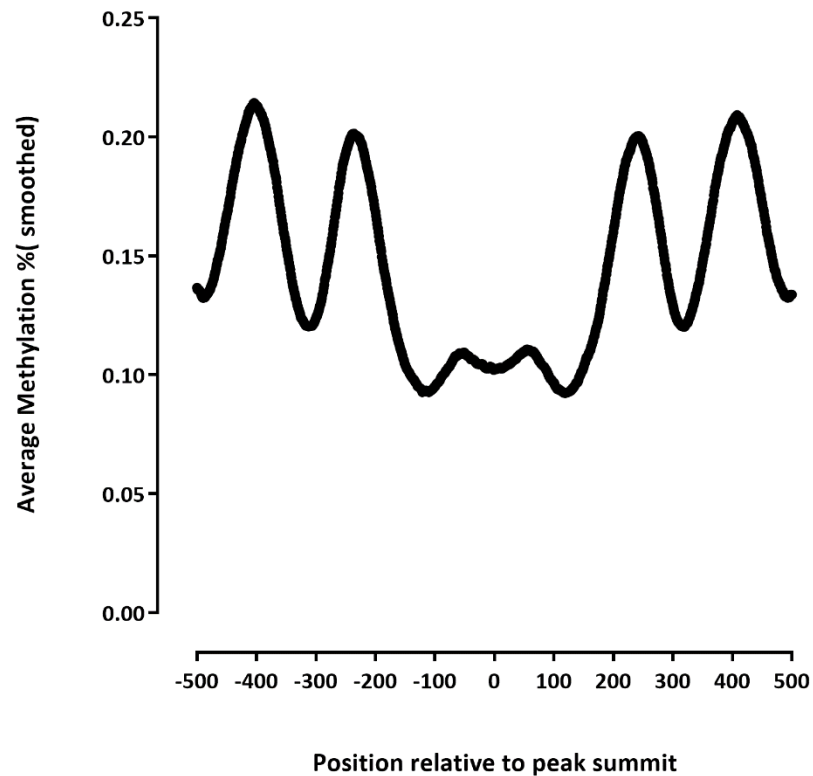
ENCODE GM12878 EM-seq CTCF peaks coverage



ENCODE GM12878 WGBS CTCF peaks methylation

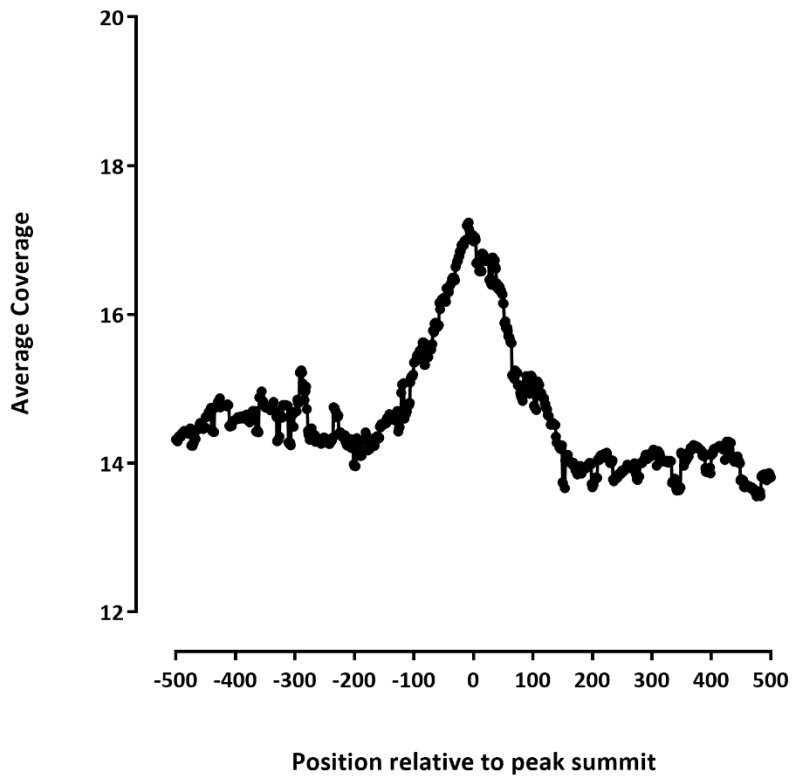


ENCODE GM12878 EM-seq CTCF peaks methylation

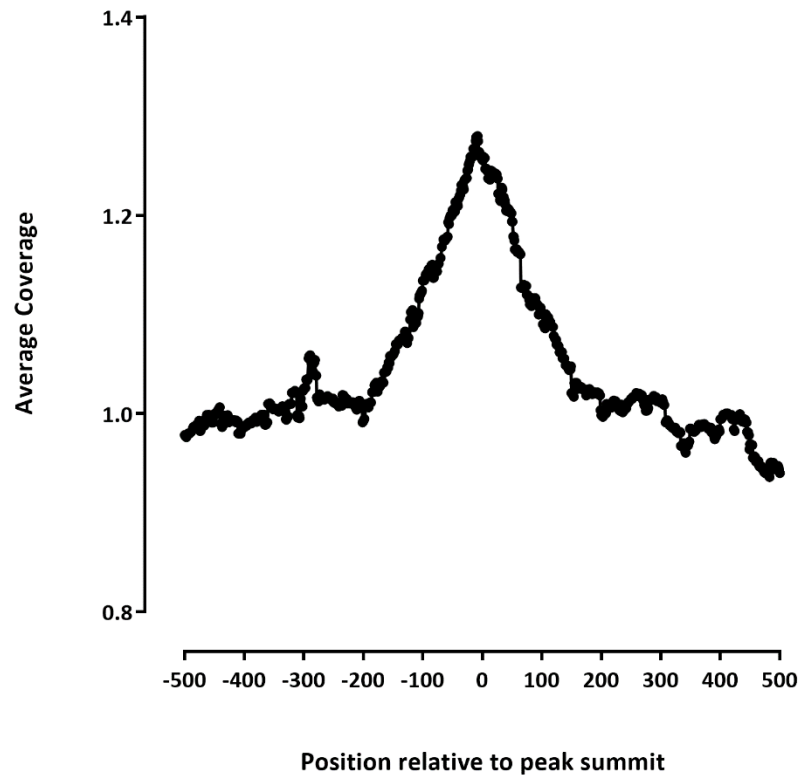


DNase peaks

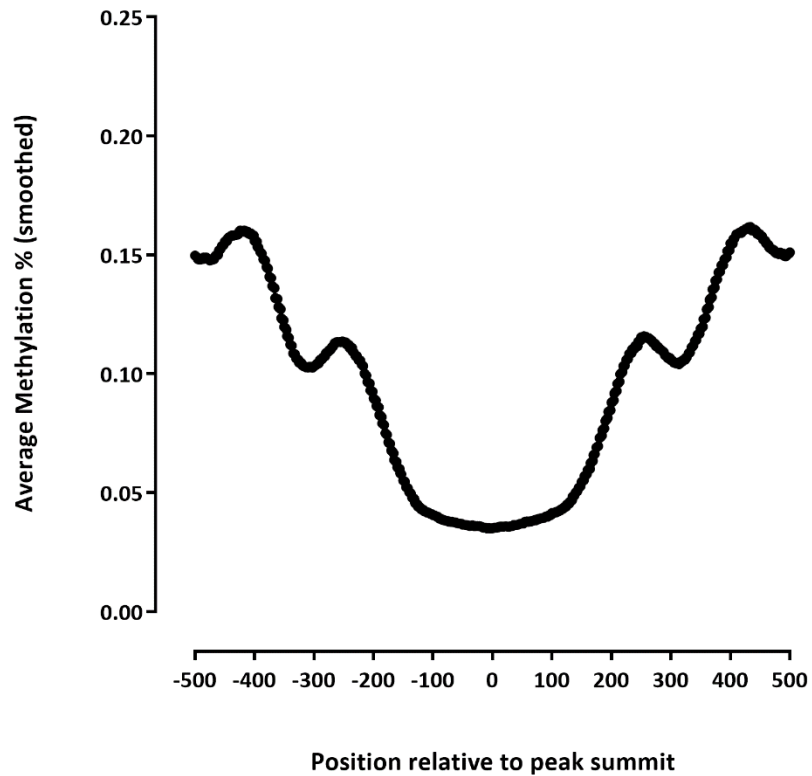
ENCODE GM12878 WGBS DNase peaks coverage



ENCODE GM12878 EM-seq DNase peaks coverage



ENCODE GM12878 WGBS DNase peaks methylation



ENCODE GM12878 EM-seq DNase peaks methylation

