

Table S3. Proportion of mapped regions overlapping with different functional regions in the genome.

Regions	Dnase I ¹ (%)	TFBS ² (%)	SEA SE ³ (%)	CAGE ⁴ (%)	
Mapped Regions (MR)	74.7	77.2	49.6	19.1	<p>max</p> <p>min</p>
— Proximal MR	97.9	99.0	37.8	55.5	
— Distal MR	68.7	71.9	54.8	8.0	
H3K27ac+ MR	93.3	94.6	59.3	36.3	
— Proximal MR	98.9	99.6	38.4	57.3	
— Distal MR	88.8	90.6	78.7	17.5	
H3K27ac- MR	57.7	61.3	40.7	3.5	
Random Regions	42.1	46.0	27.5	2.7	

¹ DNase I Hypersensitivity Peak Clusters from ENCODE (95 cell types)

² Transcription Factor ChIP-seq Clusters (340 factors, 129 cell types) from ENCODE 3

³ Super-enhancers from SEA database (<http://sea.edbc.org/>)

⁴ CAGE peaks from FANTOM5 project (<https://fantom.gsc.riken.jp/5/>)