


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

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

<sup>1</sup> DNase I Hypersensitivity Peak Clusters from ENCODE (95 cell types)

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

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

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