

**Table S1.** Proportion of mapped fragments of the studied DNA libraries that overlap with various functional sites in the genome

Dataset (N)	Dnase I <sup>1</sup>	TFBS <sup>2</sup>	SEA SE <sup>3</sup>	H3K27ac <sup>4</sup>	CAGE <sup>5</sup>	SE MIA PaCa-2 <sup>6</sup>	
L1 (6244)	75,3	77,9	49,7	48,4	20,3	8,8	max
L2 (5245)	74,6	76,9	49,8	48,4	18,6	8,9	
Mapped Regions (11264)	74,7	77,2	49,6	47,7	19,1	8,7	
Discarded Regions (11171)	62,8	65,7	41,5	31,9	13,0	5,9	
Random Regions (11264)	42,1	46,0	27,5	5,7	2,7	0,8	min

<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> H3K27ac ChIP-seq peaks in MIA PaCa-2 cell line (Diaferia et al., 2016)

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

<sup>6</sup> MIA PaCa-2 super-enhancers from SEdb 2.0 (<http://www.licpathway.net/sedb>)