

Table S3. Characterization of open chromatin regions in relation to gene annotations.

Genomic location	MK cells only	EB cells only	Both cell types
Intergenic	20.2%	39.3%	26.5%
Intronic	72.5%	45.8%	41.4%
Overlap 3'-UTR	0.9%	1.9%	1.9%
Overlap 5'-UTR	4.6%	5.6%	28.4%
Exonic	1.8%	7.5%	1.9%