Sample	Replicate	Clusters (Raw)	%PF Clusters	%Align	Correlation between replicates[a]
ESC FAIRE	**1**	**52,623,700**	75.58	68.29	**0. 999**
ESC FAIRE	**2**	**53,097,584**	75.2	68.33	
EpiSC FAIRE	**1**	**52,127,559**	75.05	78.83	**0.996**
EpiSC FAIRE	**2**	**42,797,368**	83.27	80.53	
NSC FAIRE	**1**	**55,226,119**	67.83	80.51	**0.994**
NSC FAIRE	**2**	**55,767,547**	72.25	81.17	
MEF FAIRE	**1**	**42,054,851**	84.8	79.56	**0.999**
MEF FAIRE	**2**	**42,276,672**	84.32	79.47	
Genomic DNA	**1**	**47,697,872**	79.83	68.15	**0.999**
Genomic DNA	**2**	**47,654,573**	78.03	68.11	

[a] The correlation coefficients for technical replicates were calculated by binning the genome into 1kbp windows and computing the Pearson correlation (*r*) of the genomic coverage between pairs. The calculation was done using an in-house Java code.

Supplemental Table S1 **Illumina sequencing summary of FAIRE samples.** Replicate samples of chromatin from each of the indicated cell lines were sonicated, subjected to FAIRE, and prepared for sequencing using the Illumina GAIIx genome analyzer as outlined in the Methods. FASTQ files were generated using CASAVA 1.8