A

correspondence with DNaseI	FAIRE peaks Enrichment Score	Number of sites
83%	all peaks	441855
95%	5	134864
98%	7.3	71587
99%	8.8	42754

B

	All Peaks	Peaks with enrichment ≥5	Clusters	Peaks in clusters	bp Coverage of FAIRE pks in clusters	% Genome[a]
ESC	441885	134864	74577	107742	99975258	3.68
EpiSC	387312	80214	36000	45276	40405716	1.49
NSC	555868	204234	81248	132646	99734444	3.67
MEF	431911	105515	43860	56270	34343092	1.26

[a]Mouse Genome = 2,716,965,481 bp

Table S4 Calibration of ESC FAIRE-seq data with respect to ESC DNaseI-seq (A) Enrichment scores and FDRs were calculated using the second method outlined above in the figure legend to Fig. S3. The degree of correspondence between the FAIRE and DNase sites was observed to be proportional to the FAIRE peak enrichment value (Fig. S4). For example, the "all FAIRE peaks" dataset displayed 83% correspondence with DNaseI-defined sites, whereas FAIRE peaks displaying an enrichment value of at least 5 showed greater than 95% correspondence with sites of open chromatin defined using DNaseI analysis. Thus open chromatin regions corresponding to FAIRE peaks with higher enrichment values were more likely to be detected using either method and represent high confidence regions of open chromatin. (It should be noted however, that correspondence between the two replicate DNaseI samples themselves was ~86%). While previous reports have noted that open regions defined using FAIRE or DNaseI largely overlap, each method was also observed to detect unique portions of the genome [6]. In our case, nearly identical FAIRE sites were observed for the replicate samples analyzed here, including those with lower enrichment values that did not overlap a DNaseI-defined site. Thus while the sites of open chromatin identified for ESC using FAIRE and DNaseI data are highly correlative, FAIRE peaks that do not correspond to DNaseI sites, or those with lower enrichment values, are nonetheless likely to be significant. **(B)** FAIRE peaks called for each of the four cell lines in the 'All Peaks' sample and using the threshold of enrichment value 5. Clusters of FAIRE peaks focus on those peaks which are likely to have the most relevance as regulatory regions [6] and defining these clusters in each cell line permits the a more focused analysis. The number of clusters defined using the enrichment ≥ datasets for each line, and the genomic coverage represented by the FAIRE clusters are shown.