

Table S1. **Summary of FAIRE-seq data sets in all the strains in this study.** Listed are the numbers of reads mapped uniquely to strain-specific reference genome, reads filtered for pairing and PCR duplicates, and total number of reproducible FAIRE peaks identified in each strains.

Strain	Sample	Total read x10 ⁶	Reads post filter x10 ⁶	FAIRE peak identified by F-seq & IDR
A/J	Rep1	13,836,220	12,331,312	29,914
	Rep2	14,323,695	12,159,127	
AKR/J	Rep1	25,120,508	21,888,481	29,923
	Rep2	27,067,431	23,766,117	
BALB/cJ	Rep1	19,185,543	12,556,928	30,077
	Rep2	20,374,839	13,877,891	
C57BL/6J	Rep1	22,484,699	20,942,285	30,598
	Rep2	24,519,376	23,343,598	
C3H/HeJ	Rep1	20,400,719	12,830,230	30,370
	Rep2	25,350,052	18,635,238	
CBA/J	Rep1	23,497,233	20,541,717	30,613
	Rep2	22,170,236	18,426,726	
DBA/2J	Rep1	16,778,315	15,883,801	26,769
	Rep2	20,831,992	19,808,014	
Average		21,138,633	17,642,248	29,752