

	Total reads	Uniquely mapped reads	Reproducibility rate between replicates
Total RNA-seq rep1	32,130,439 (pairs)	30,627,213 (pairs)	0.9890179
Total RNA-seq rep2	39,535,171 (pairs)	37,758,319 (pairs)	
Total RNA-seq rep3	33,858,047 (pairs)	31,956,451 (pairs)	
Total RNA-seq rep4	48,136,775 (pairs)	45,234,221 (pairs)	
ATAC-seq rep1	59,489,382 (pairs)	46,950,638 (pairs)	0.9924284
ATAC-seq rep2	47,851,401 (pairs)	37,473,435 (pairs)	
WGBS	524,986,745 (pairs)	354,206,959 (pairs)	-----
TAB-seq	535,459,250 (pairs)	355,482,726 (pairs)	-----
GRO-seq rep1	62,305,392	52,978,406	0.9983407
GRO-seq rep2	61,824,551	51,858,512	
ChIP-seq input rep1	21,237,153	13,482,321	0.9998723
ChIP-seq input rep2	40,212,234	24,506,028	
H3K36me3 rep1	40,256,311	26,268,964	0.994048
H3K36me3 rep2	144,135,649	97,632,459	
H3K4me3 rep1	124,632,769	80,774,272	0.9989464
H3K4me3 rep2	129,930,602	83,040,387	
H3K9me3 rep1	90,348,581	39,955,833	0.9997766
H3K9me3 rep2	53,961,724	23,678,180	
H3K79me2 rep1	127,133,235	92,216,556	0.9869342
H3K79me2 rep2	77,504,787	58,683,063	
H4K20me3 rep1	55,386,554	24,843,073	0.9990026
H4K20me3 rep2	98,059,498	51,028,097	

Supplemental Figure S1. Mapping statistics of the cortical sequencing data sets generated in this study. The reproducibility rate was calculated as the Pearson's correlation coefficient between the biological replicates.