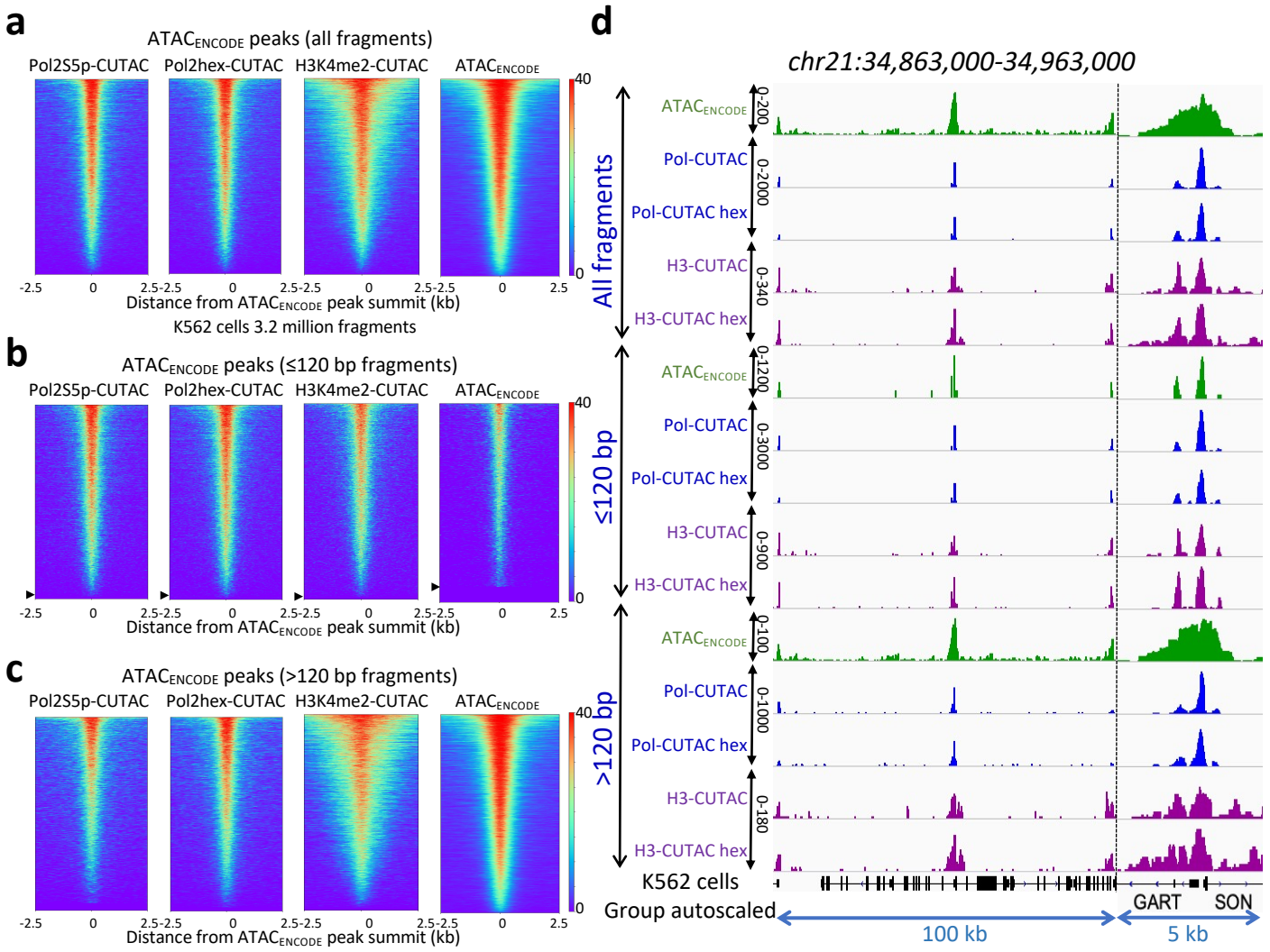

e

N=38155	ATAC_1	ATAC_2	H3-CUTAC	H3-CUTAC hex	Pol-CUTAC	Pol-CUTAC hex
ATAC_1	1	0.89	0.62	0.62	0.52	0.54
ATAC_2	0.89	1	0.61	0.62	0.52	0.53
H3-CUTAC	0.62	0.61	1	0.9	0.66	0.65
H3-CUTAC hex	0.62	0.62	0.9	1	0.58	0.58
Pol-CUTAC	0.52	0.52	0.66	0.58	1	0.96
Pol-CUTAC hex	0.54	0.53	0.65	0.58	0.96	1

R 0 0.5 1

Additional file 2: Close correspondences between CUTAC and ATAC-seq (**a**) Heatmaps showing alignments of Pol2S5p-CUTAC ±10% 1,6-hexanediol during tagmentation, H3K4me2-CUTAC and ATAC$_{ENCODE}$ data over peaks called on an ATAC$_{ENCODE}$ replicated dataset. (**b**) Same as (a) showing the ≤120-bp fragment subset, where arrowheads indicate the row where enrichment of signal over peaks ends: 98-99% for CUTAC and 93% for ATAC$_{ENCODE}$. (**c**) Same as (b) showing the >120 bp subset. Fragments were mapped to hg19, and 3.2 million fragments were randomly sampled from each dataset and used to make bedgraph tracks. **(d)** Tracks comparing Pol2S5p and H3K4me2 CUTAC to ATAC-seq using K562 cell data generated by the ENCODE project. The region around the GART-SON bidirectional promoter is shown at two different scales. (**e**) Correlation matrix of CUTAC and ATAC-seq datasets used in this analysis. ATAC_1 is the ENCODE dataset used to call peaks and ATAC_2 is a replicate of ATAC_1.