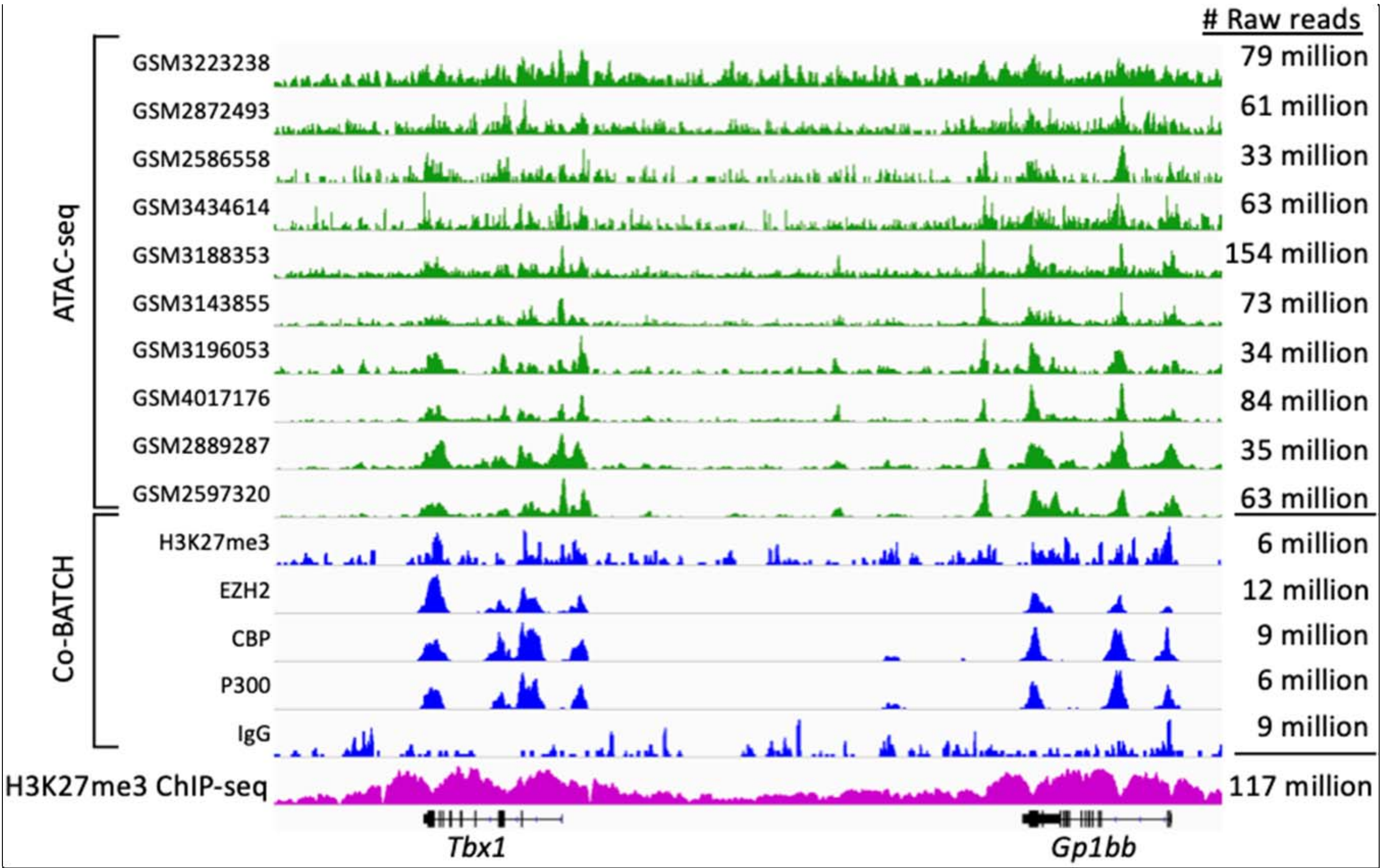

Supplementary Figure 1

CoBATCH datasets for EZH2, CBP and P300 reveal similar chromatin accessibility profiles with high signal-to-noise.

In contrast to CoBATCH profiles, ATAC-seq profiles from 8 different laboratories are relatively noisy with a wide signal-to-noise range, with 10-fold deeper sequencing than for low-background CoBATCH samples. Tracks are autoscaled. The region shown is the same as in 6, where track 8 is used for comparison.