



**Figure 4 – figure supplement 1. CUT&RUN consistency with high-Ca<sup>++</sup>/low salt digestion and total DNA extraction.** **A)** H3K4me2 CUT&RUN time points with digestions using either the standard protocol or the high-calcium/low-salt protocol with either supernatant or total DNA extraction. To construct the correlation matrix, all 8 H3K4me2 datasets were pooled and MACS2 was used to call peaks, which yielded 64,156 peaks. Peak positions were scored for each dataset and correlations (R<sup>2</sup> displayed with Java TreeView v.1.16r2, contrast = 1.25) were calculated between peak vectors. IgG and H3K27me3 (me3) negative controls were similarly scored. **B)** Same as Figure 4B. **C)** Same as Figure 4C.