



**Supplemental Fig. S12** – Comparison of peak calling consistency when using different sample sizes used for the subset used to estimate GC effects. We show results after sampling 5%, 15% and 25% of all genomic bins. We also compare to results obtained after taking five random samples of the same size and averaging the parameters (\*5 is used to denote these). The result showed here is based on the first replicate from UW for *CTCF* in HUVEC cell line.