

Figure S4

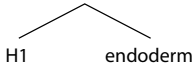
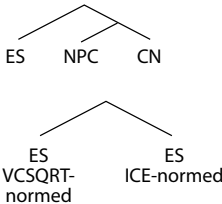
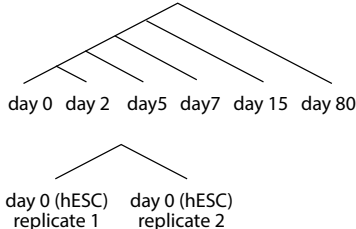
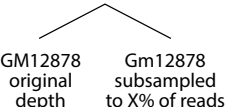
dataset	inputs/timepoints	tree structure	used in analysis
H1-endoderm (Reiff et al., 2022, Dekker et al., 2023)	H1 (hESC), definitive endoderm differentiated from H1		benchmarking: compartment -calling & differential compar- tment methods, DE analysis
mouse neural differentiation (Bonev et al., 2017)	ES (mESC), NPC (neural progenitors), CN (cortical neurons)		benchmarking: TAD stability to resolution, compartment histone mark charaterization, DE analysis benchmarking: TAD stability to normalization method
cardiomyocyte differentiation (Zhang et al., 2019)	day 0 (hESC), day 2 (mesoderm), day 5 (cardiac mesoderm), day 7 (cardiac progenitors), day 15 (primitive cardiomyocytes), day 80 (ventricular cardiomyocytes)		benchmarking: CTCF enrich- ment in TAD bondaries, DE analysis, SNP analysis benchmarking: TAD stability across biological replicates
GM12878 cell line (Rao et al.,2014)	GM12878 reads subsampled to 5, 10, 25, 50% of original depth		benchmarking: TAD stability to read depth

Figure S4. Overview of datasets used in benchmarking and analysis.