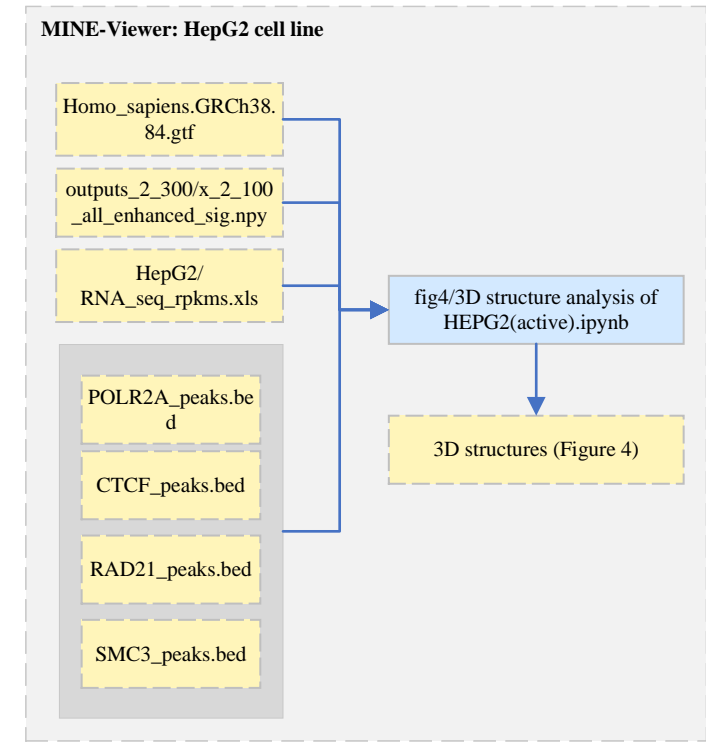
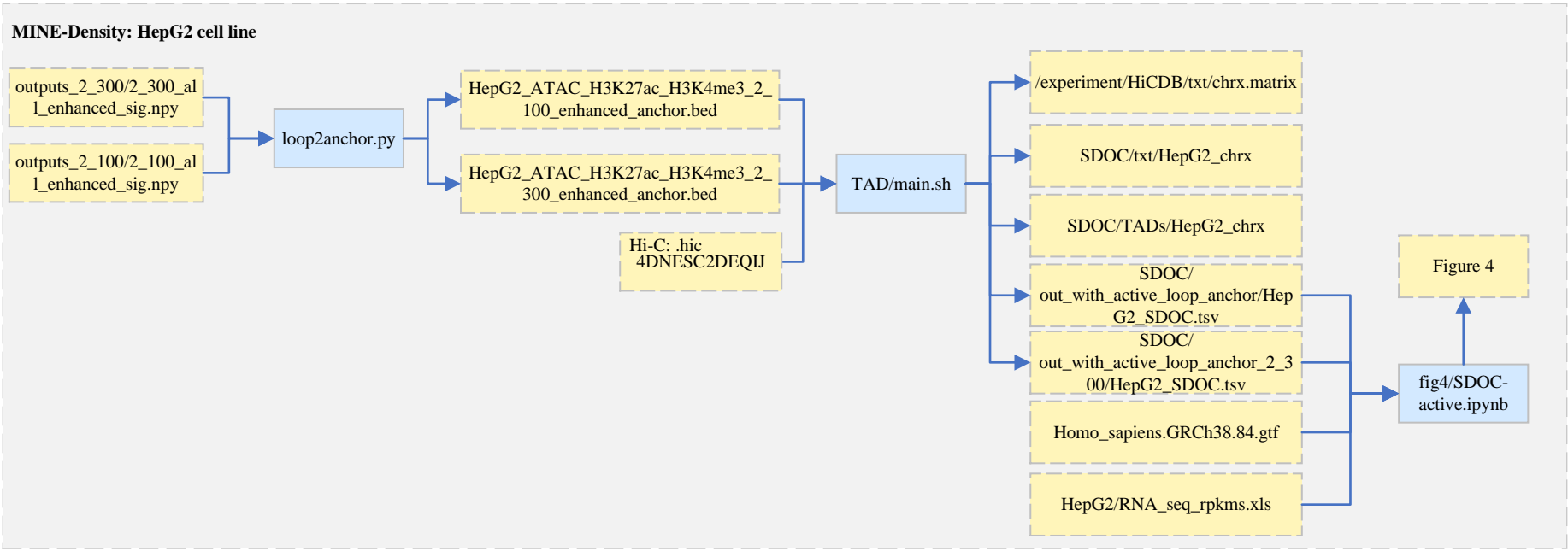
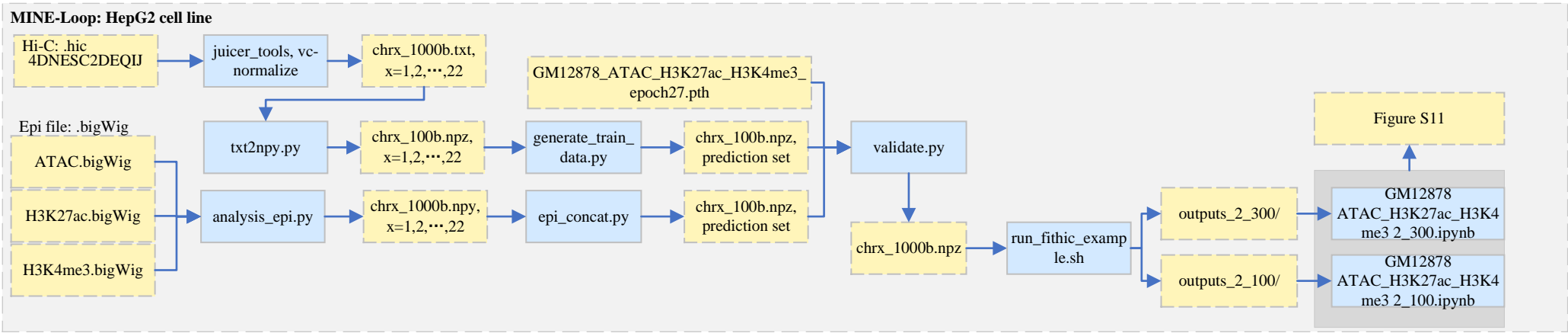
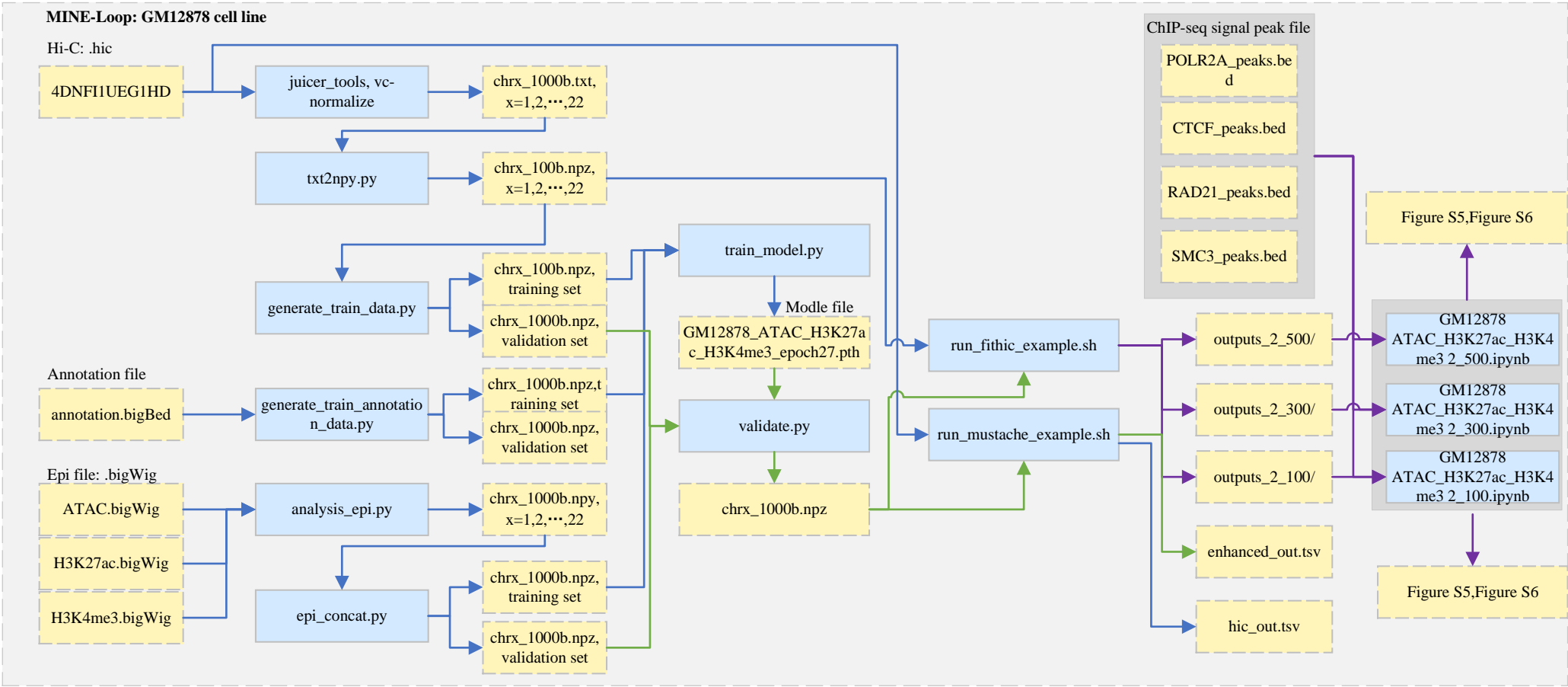
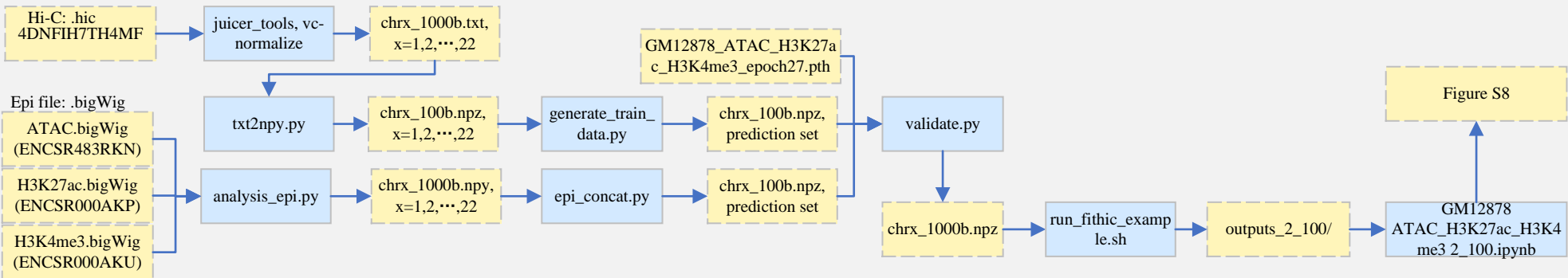


Train active MINE-Loop model using GM12878 cell line data , predict using GM12878 and HepG2 cell line

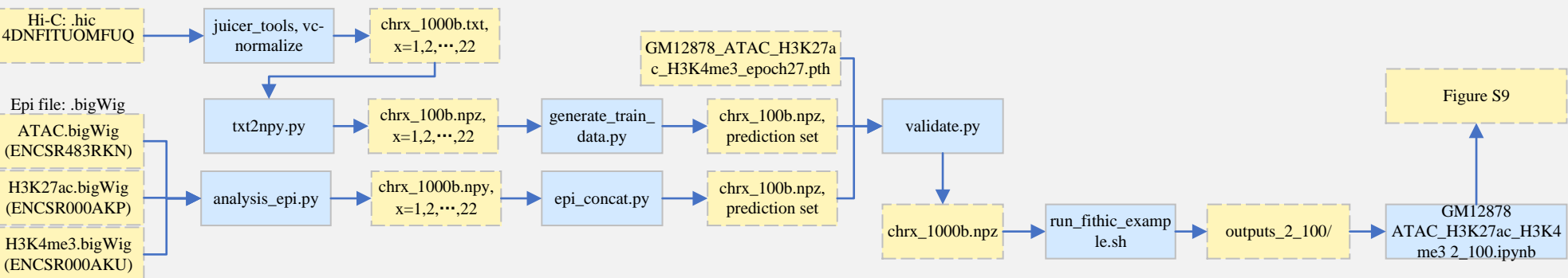


Prediction of different cell lines using active MINE-Loop model train using GM12878 cell line data

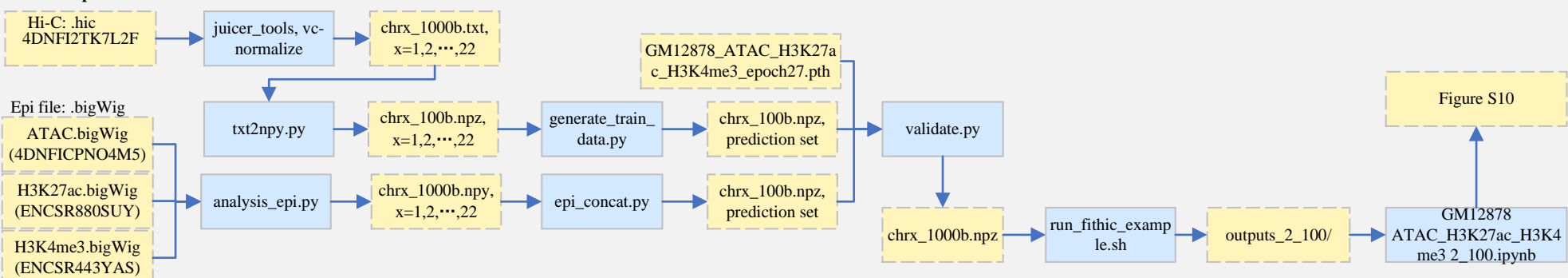
MINE-Loop: IMR90 cell line



MINE-Loop: K562 cell line

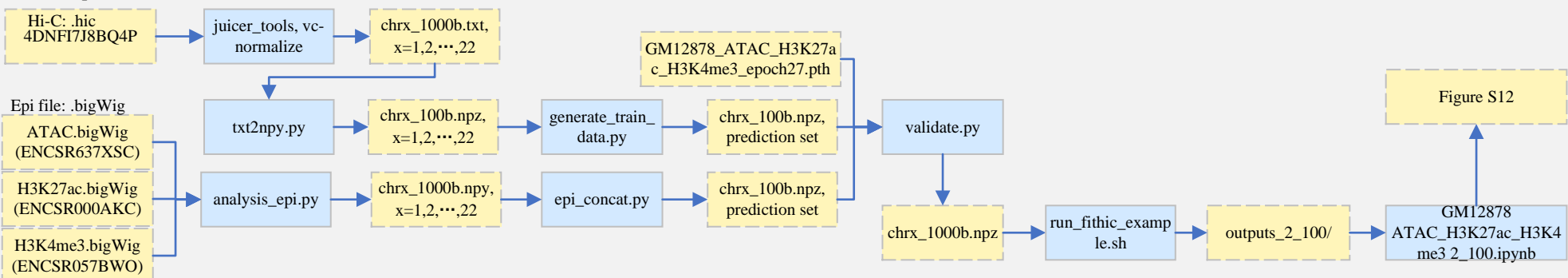


MINE-Loop: H1-hESC cell line

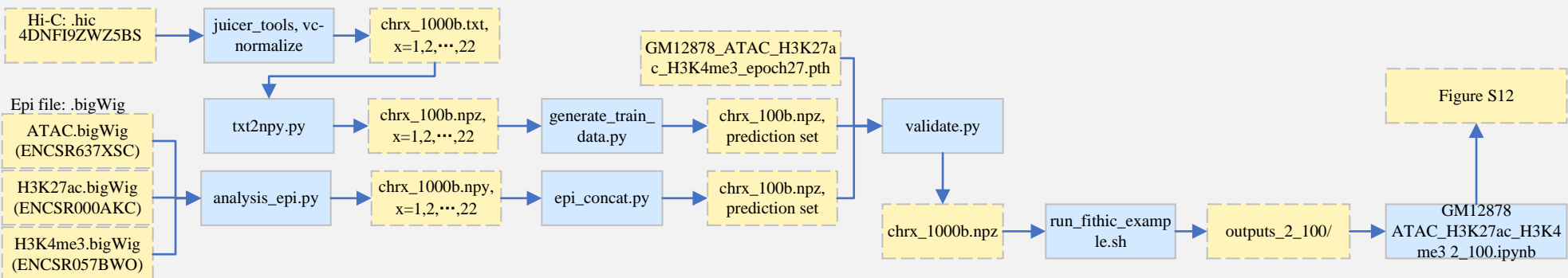


Prediction of GM12878 cell lines at different sequence depth using active MINE-Loop model train using GM12878 cell line data

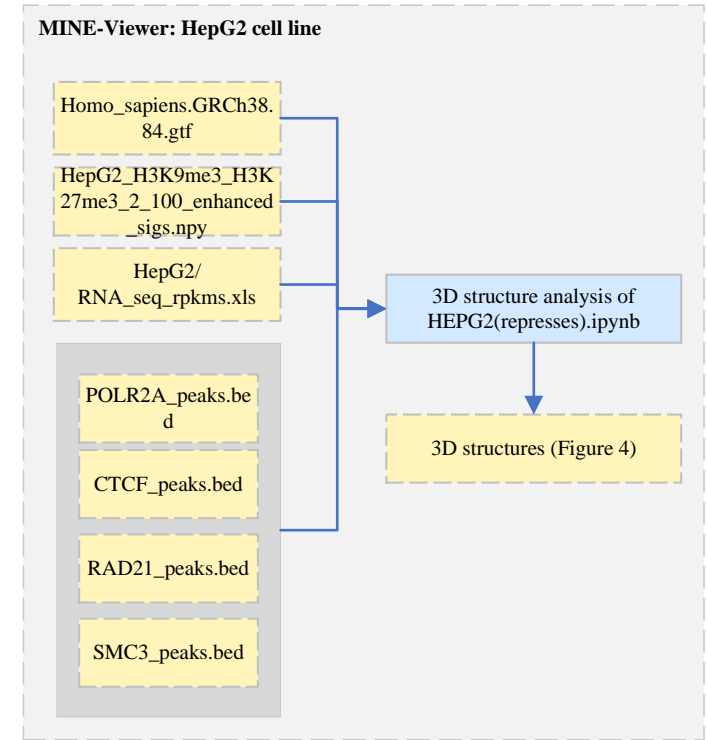
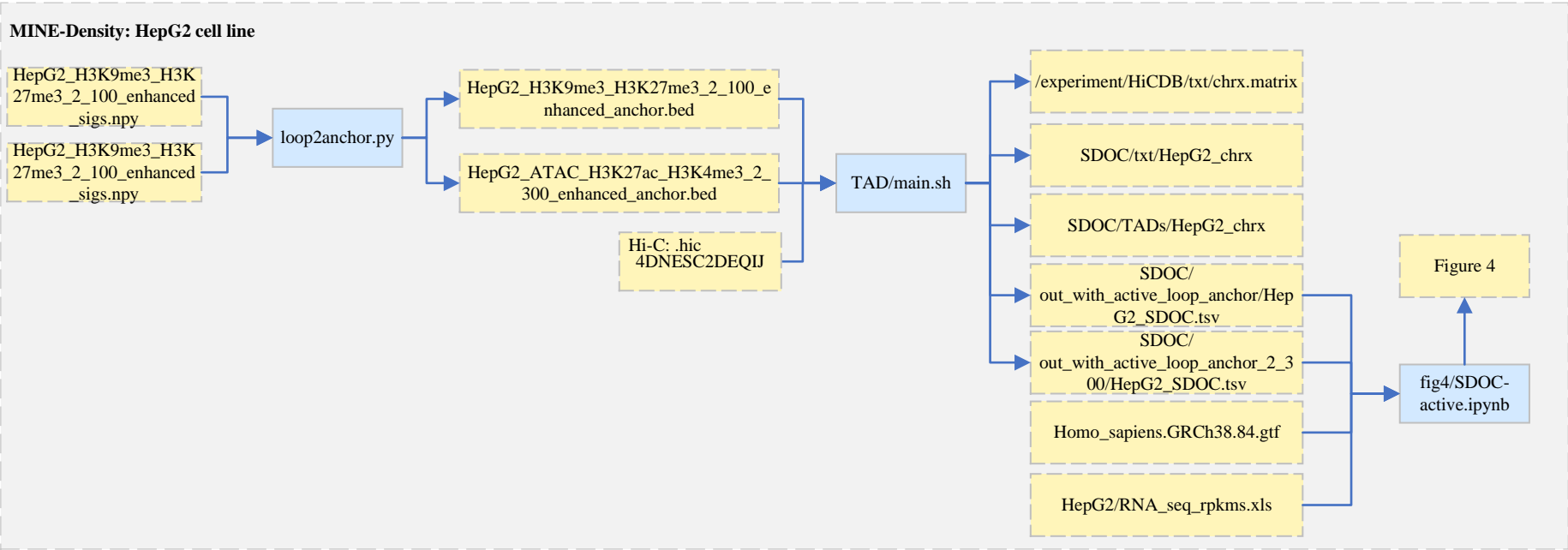
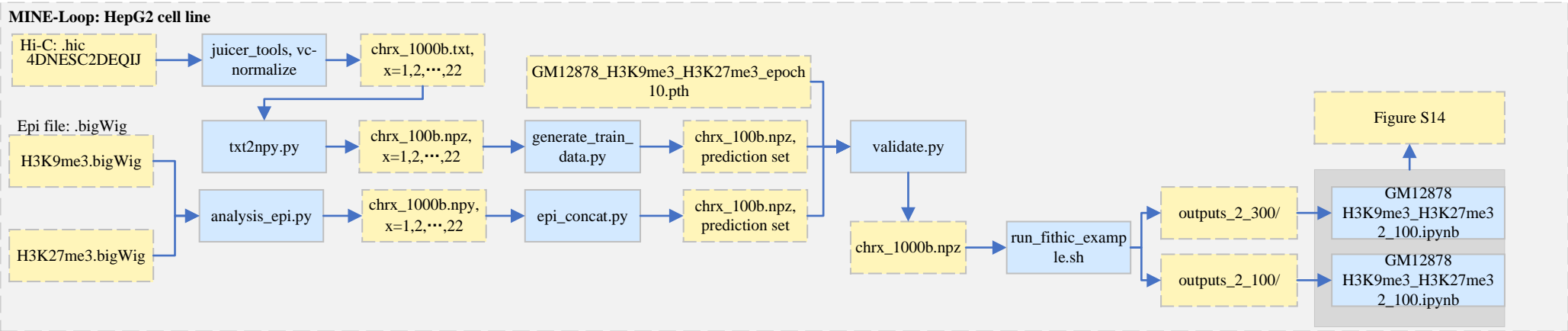
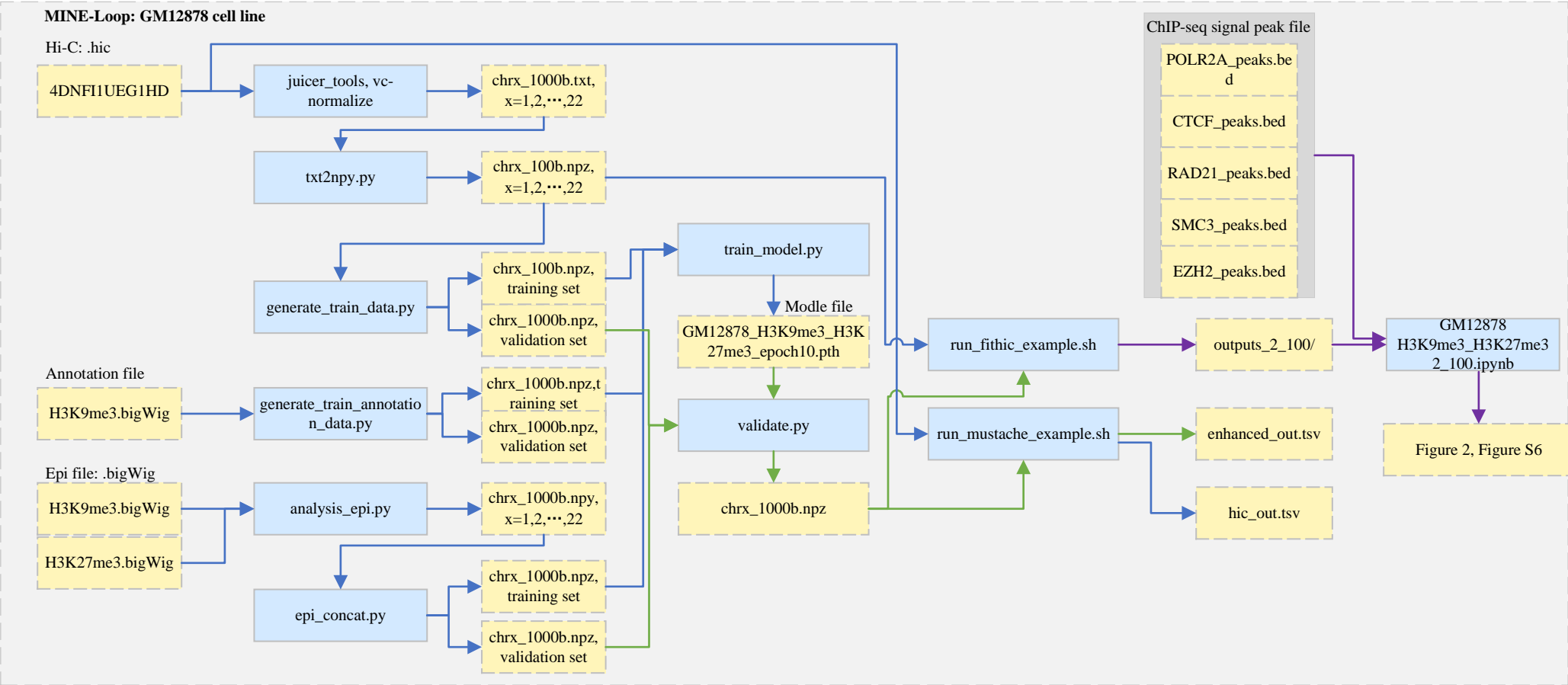
MINE-Loop: GM12878 cell line (601.74 million)



MINE-Loop: GM12878 cell line (421.77 million)

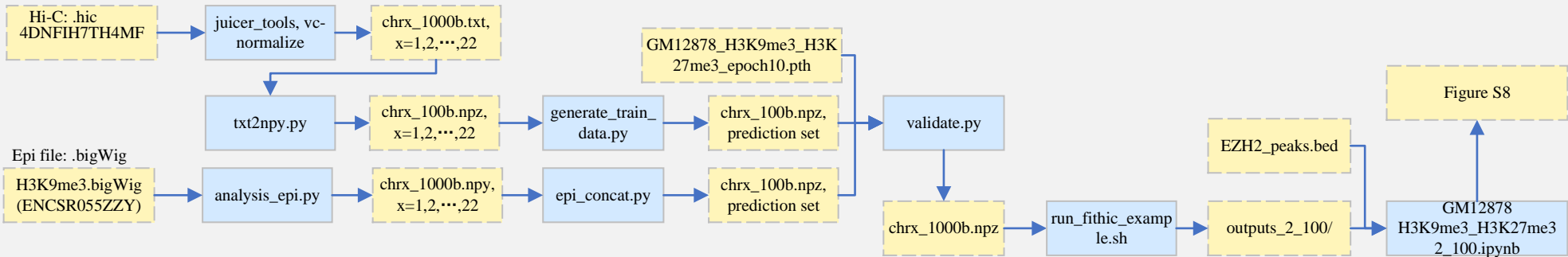


Train repressive MINE-Loop model using GM12878 cell line data, predict using GM12878 and HepG2 cell line

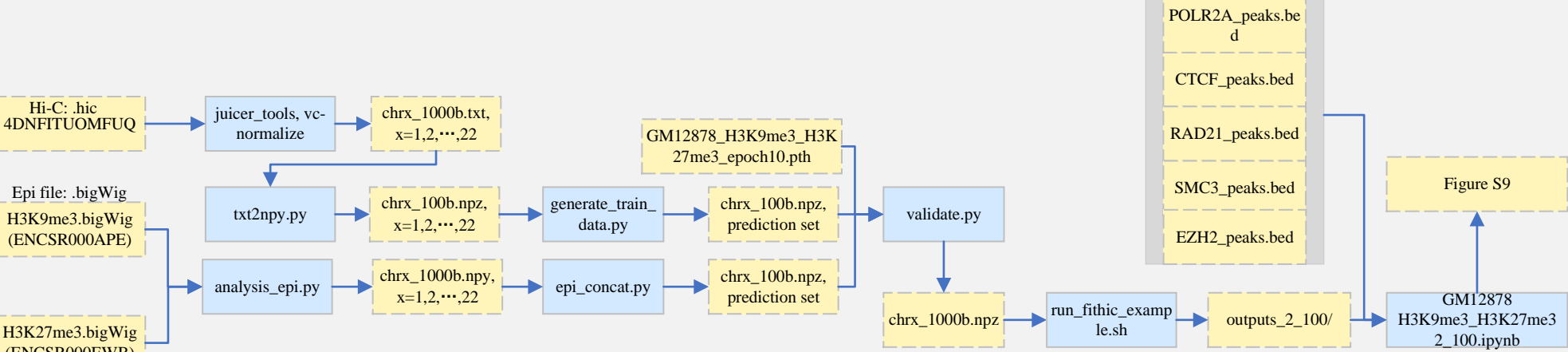


Prediction of different cell lines using repressive MINE-Loop model train using GM12878 cell line data

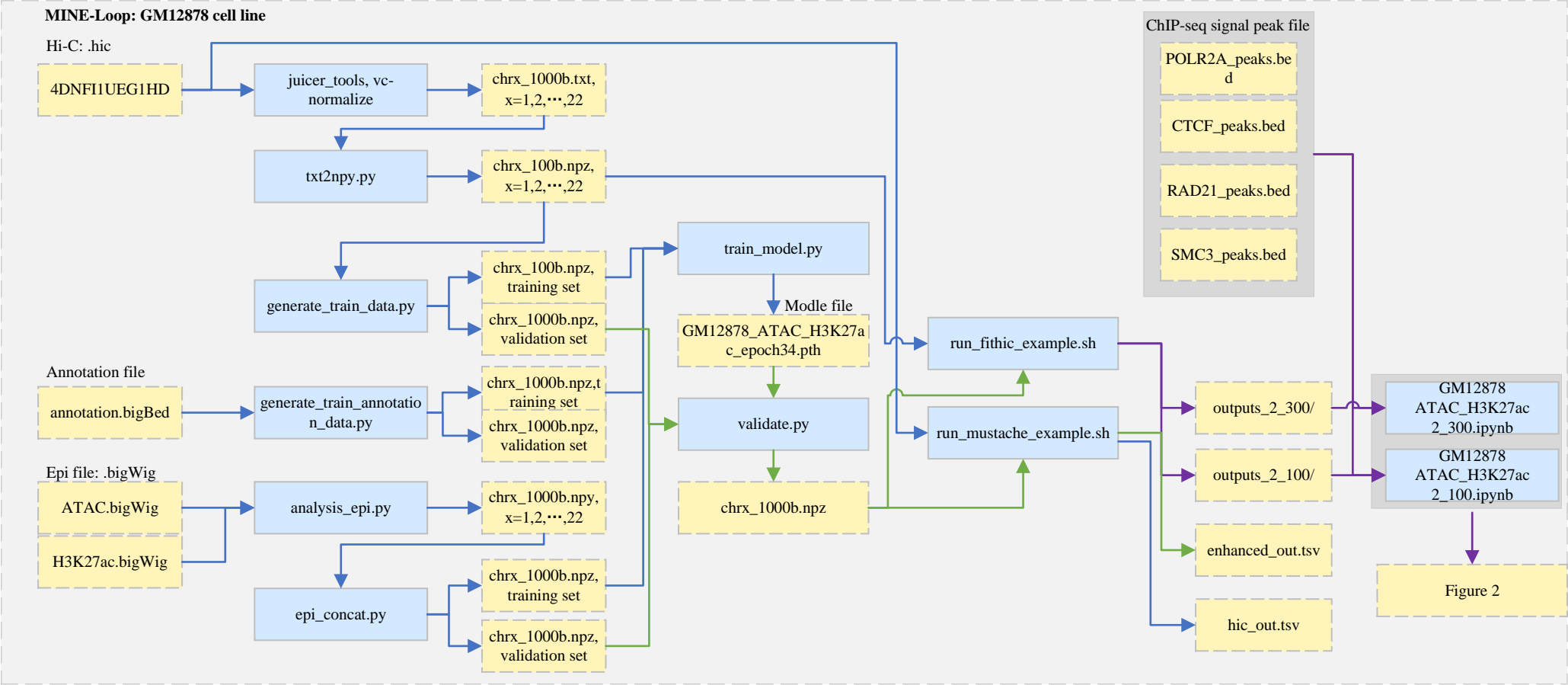
MINE-Loop: IMR90 cell line



MINE-Loop: K562 cell line



Train active MINE-Loop model using GM12878 cell line data and ATAC-seq, H3K27ac ChIP-seq , predict using GM12878 cell line



Train active MINE-Loop model using GM12878 cell line data and ATAC-seq, H3K4me3 ChIP-seq , predict using GM12878 cell line

