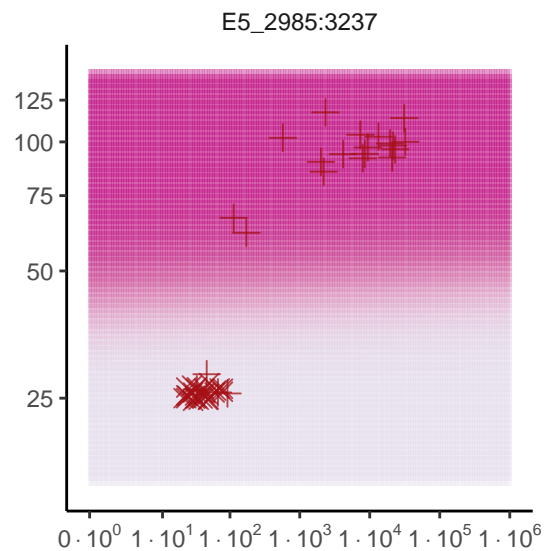
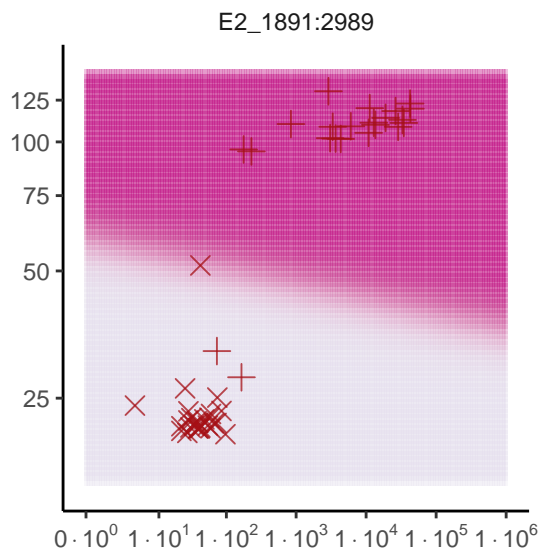
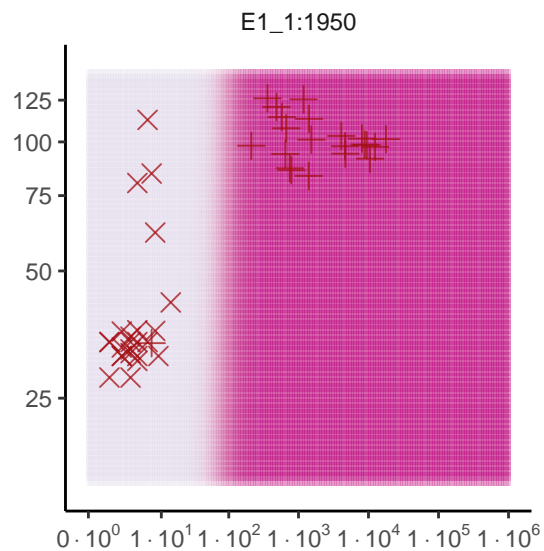


Mean Insert Size (bp)



ctDNA

+ve

-ve

Posterior
Probability

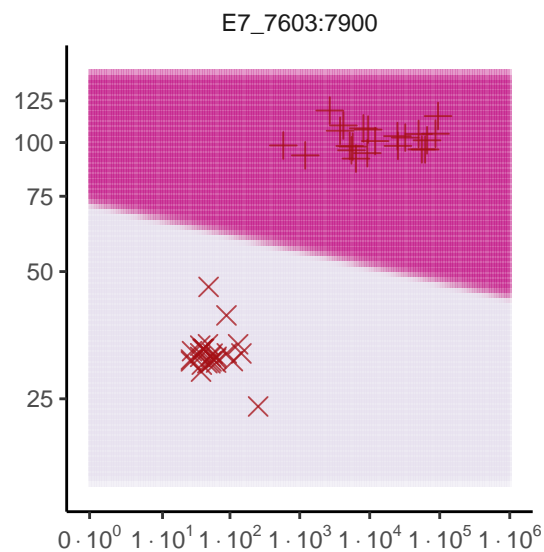
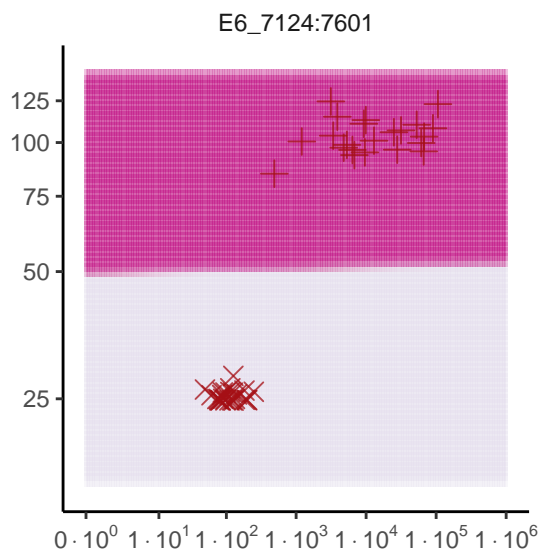
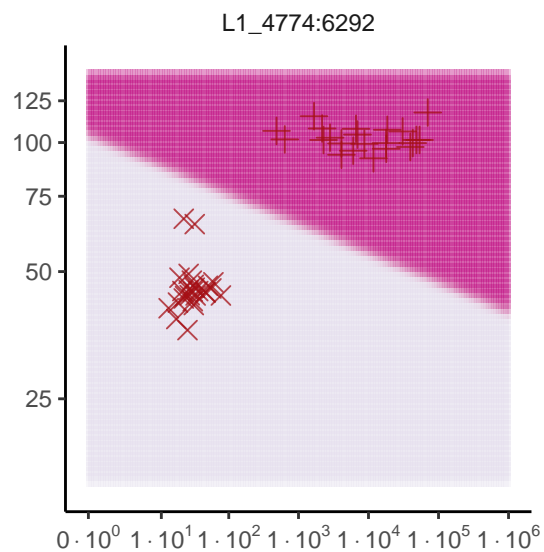
0.9

0.7

0.5

0.3

0.1



Number of Read Pairs Aligned