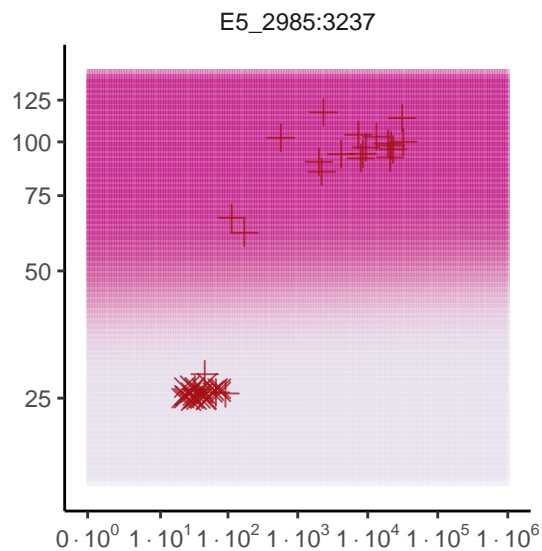
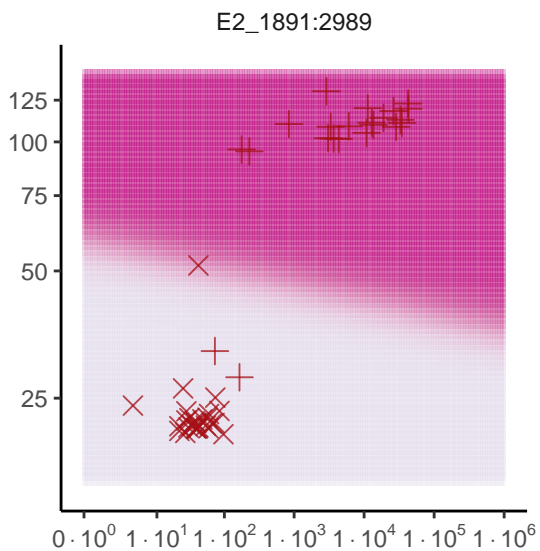
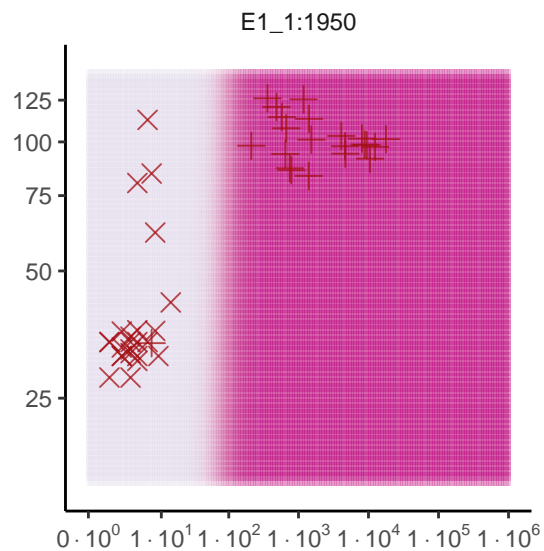


Mean Insert Size (bp)

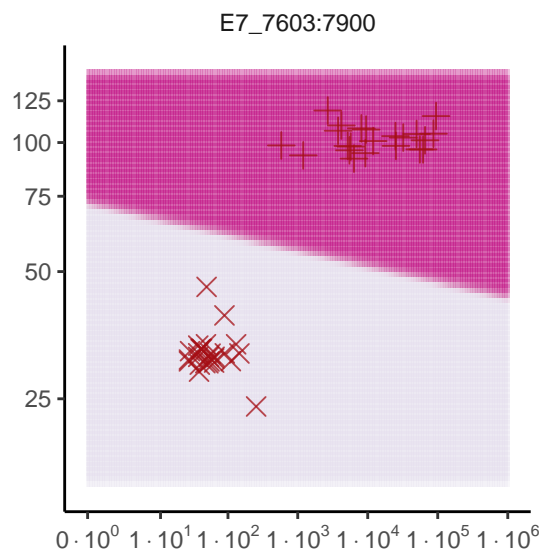
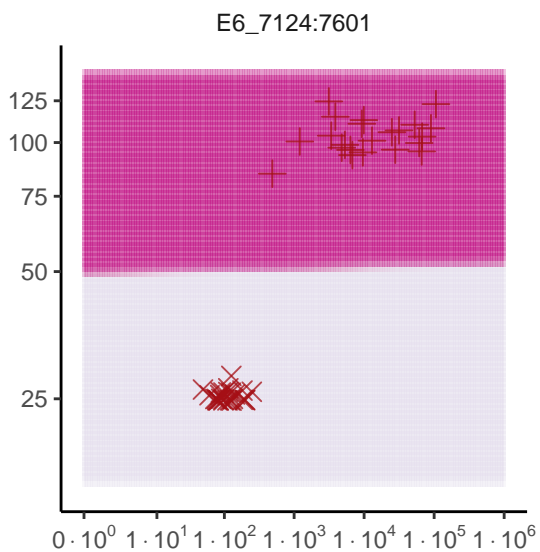
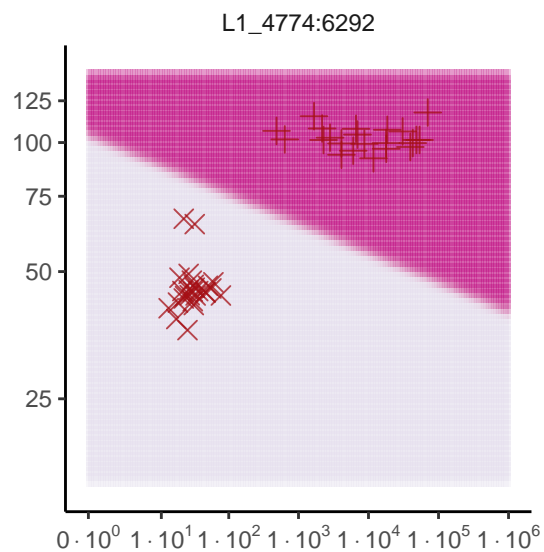
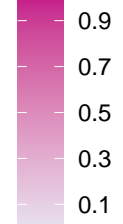


ctDNA

+ +ve

x -ve

Posterior  
Probability



Number of Read Pairs Aligned