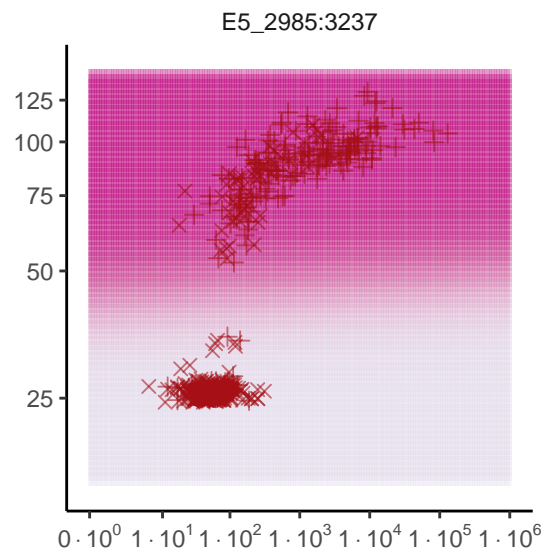
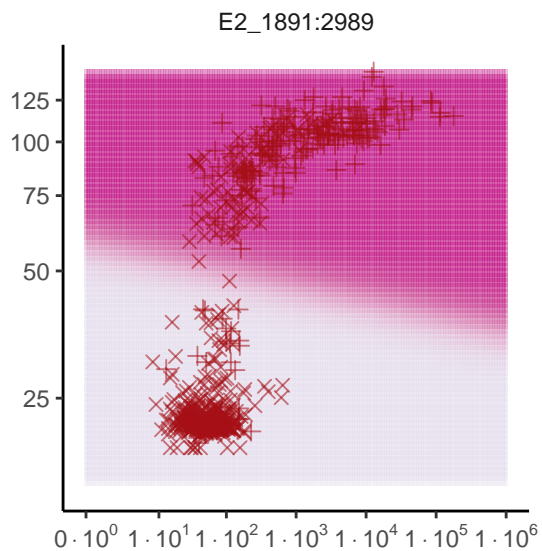
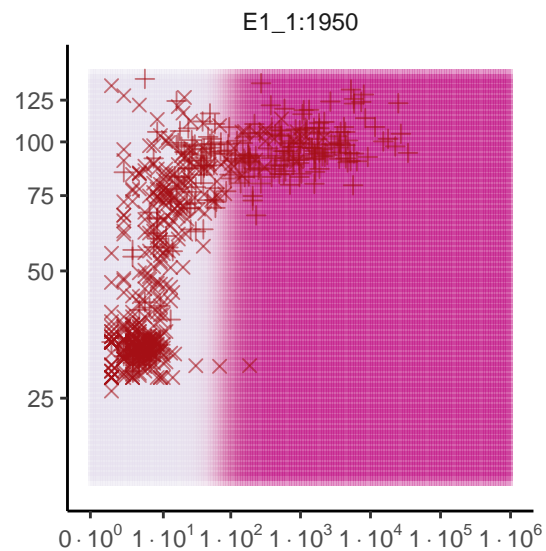


Mean Insert Size (bp)

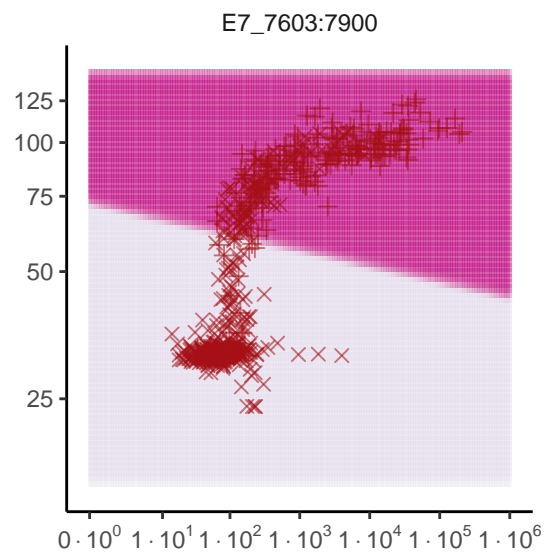
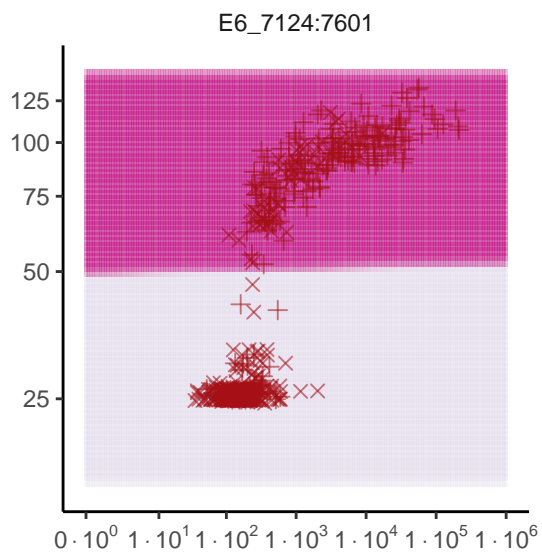
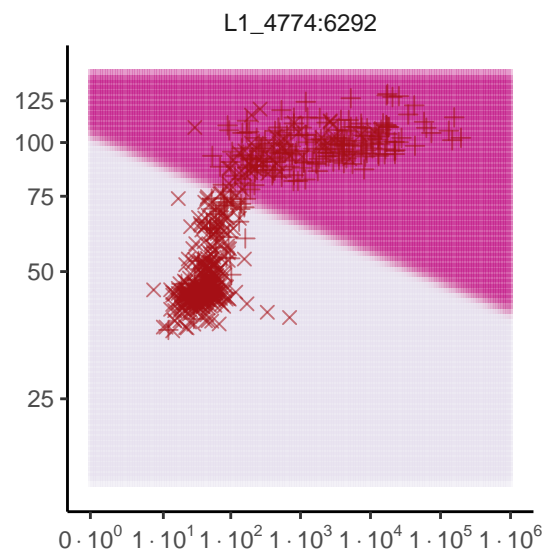
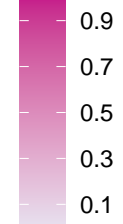


ctDNA

+ve

-ve

Posterior
Probability



Number of Aligned Read Pairs