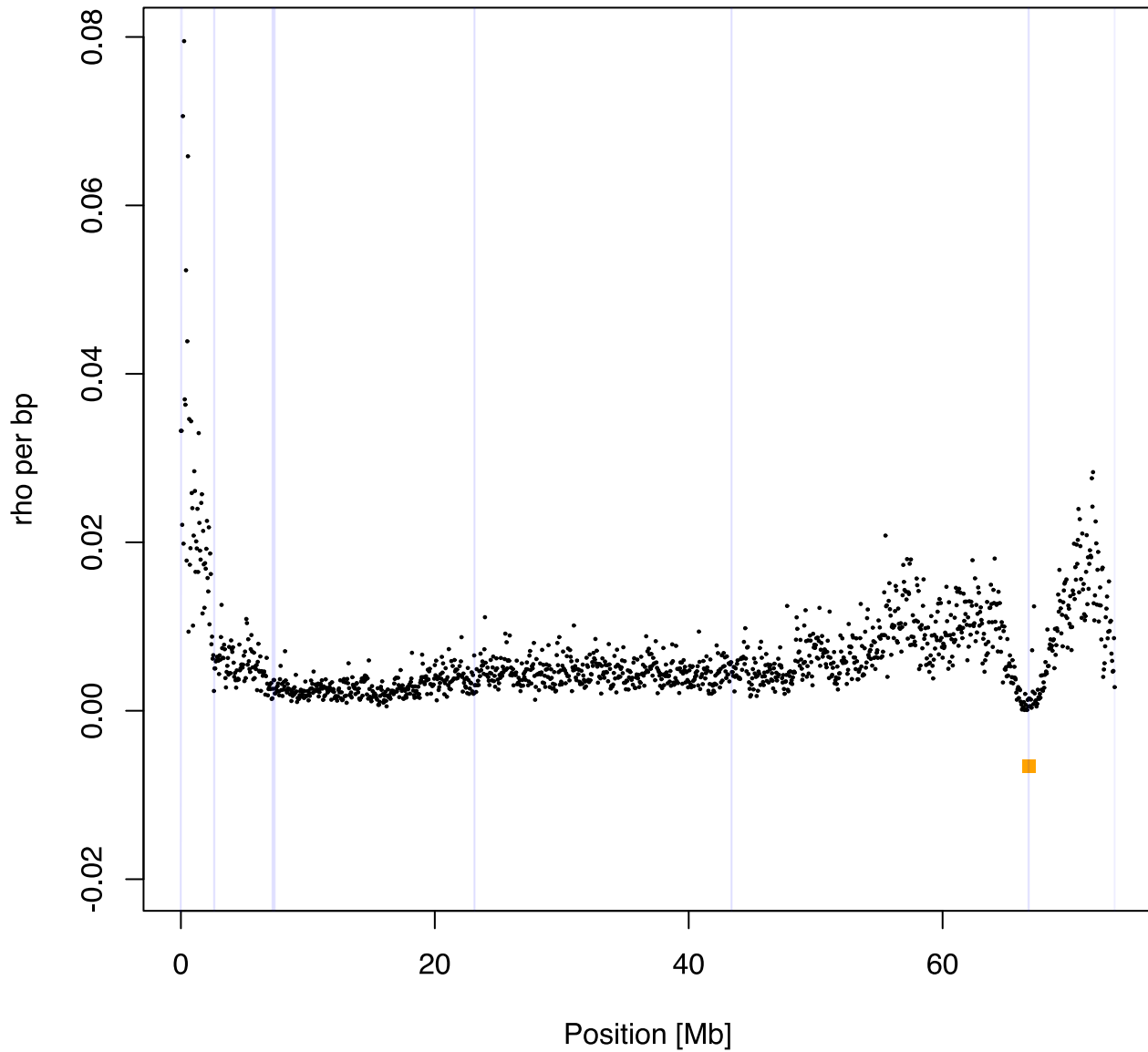
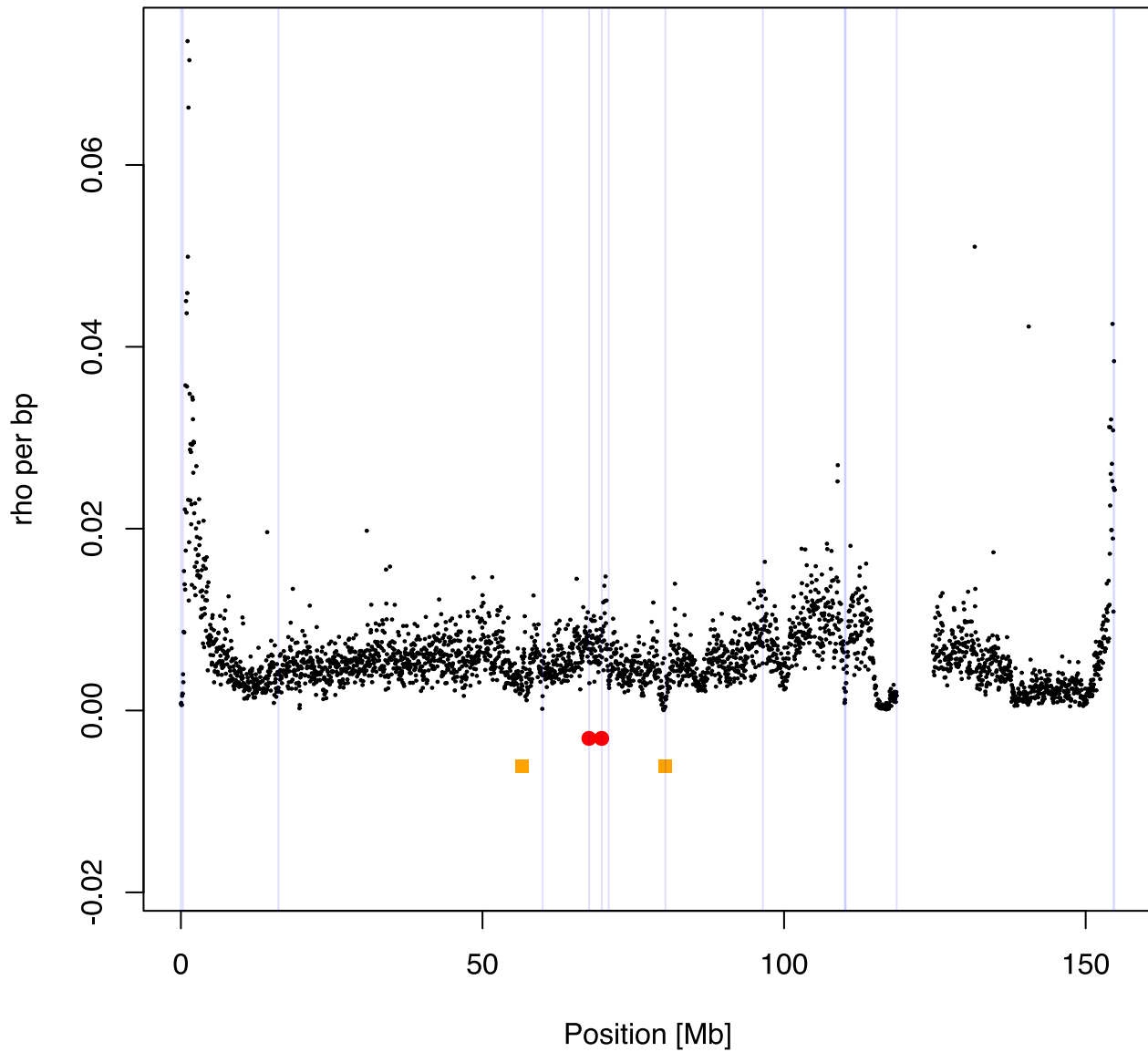


Supplemental Figure S5: Chromosome-level distribution of population-scaled recombination rate ρ and structural genome features. Black dots correspond to ρ /bp in 50-kb windows estimated from a Swedish hooded crow population. Grey lines indicate scaffold ends, red circles denote a repetitive anchored map (RAM), orange squares the occurrence of the crowSat1 satellite. Data is shown for all synteny-based chromosomal reconstructions >5 Mb except for those depicted in Fig. 3.

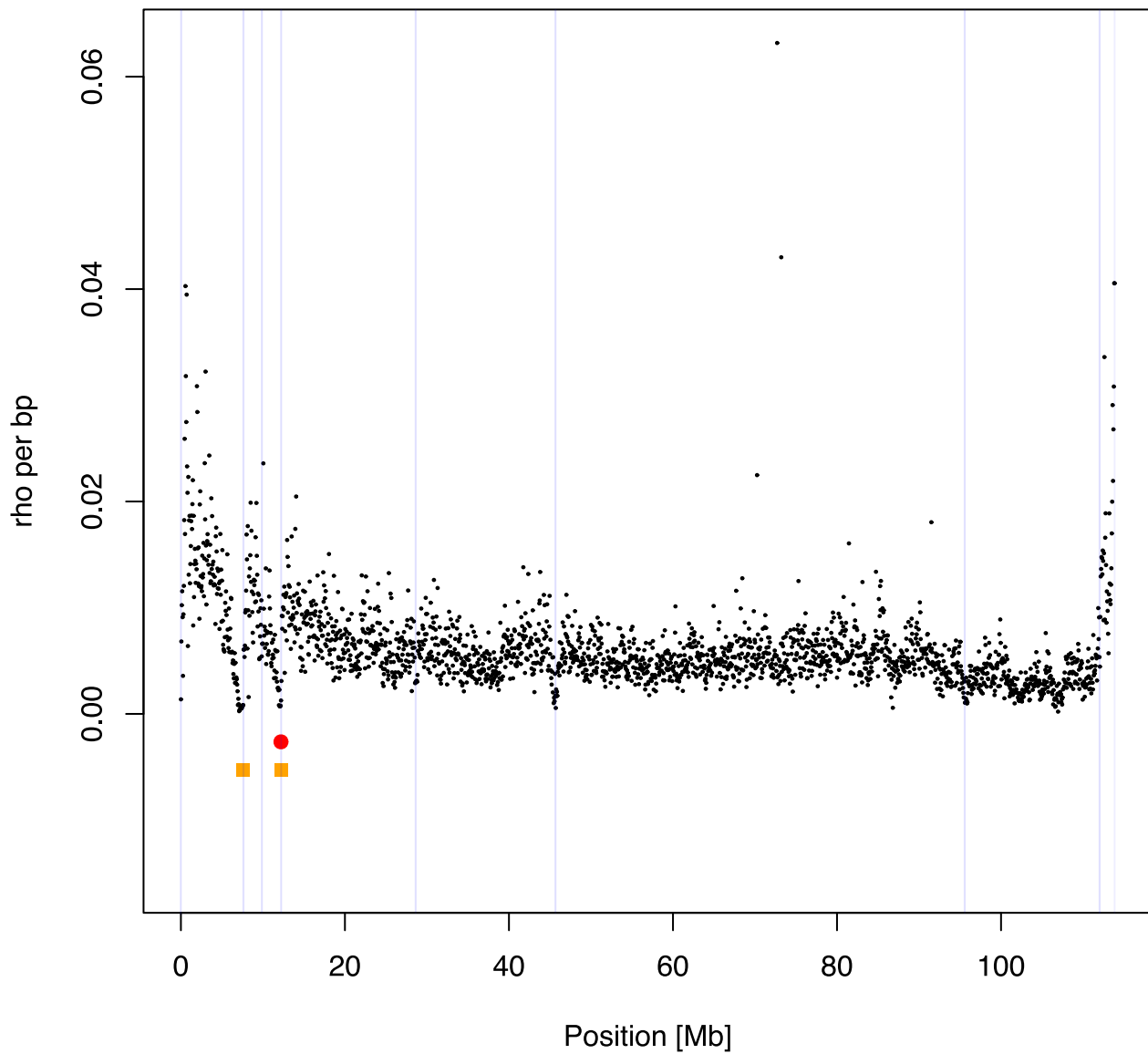
chr1A



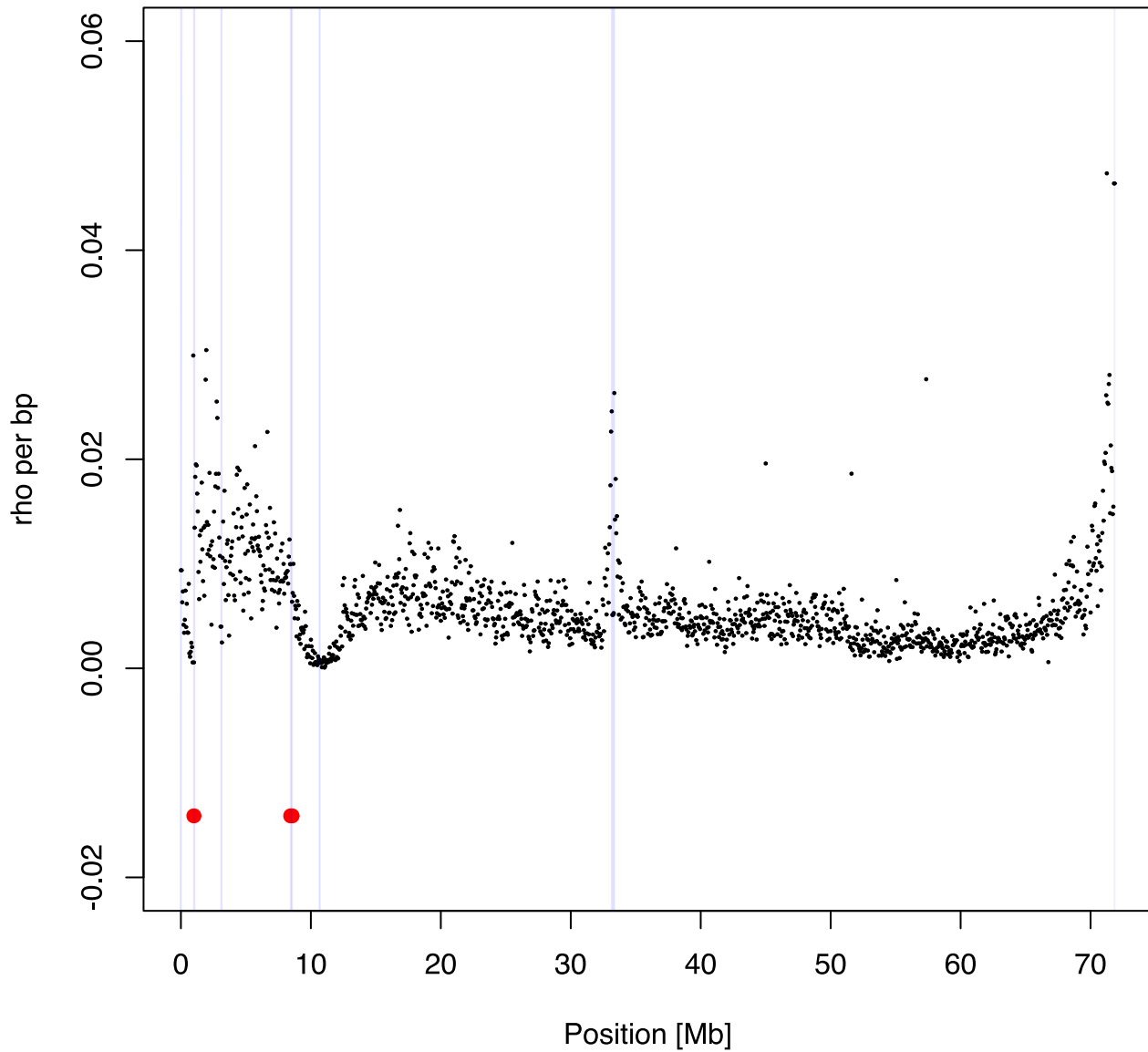
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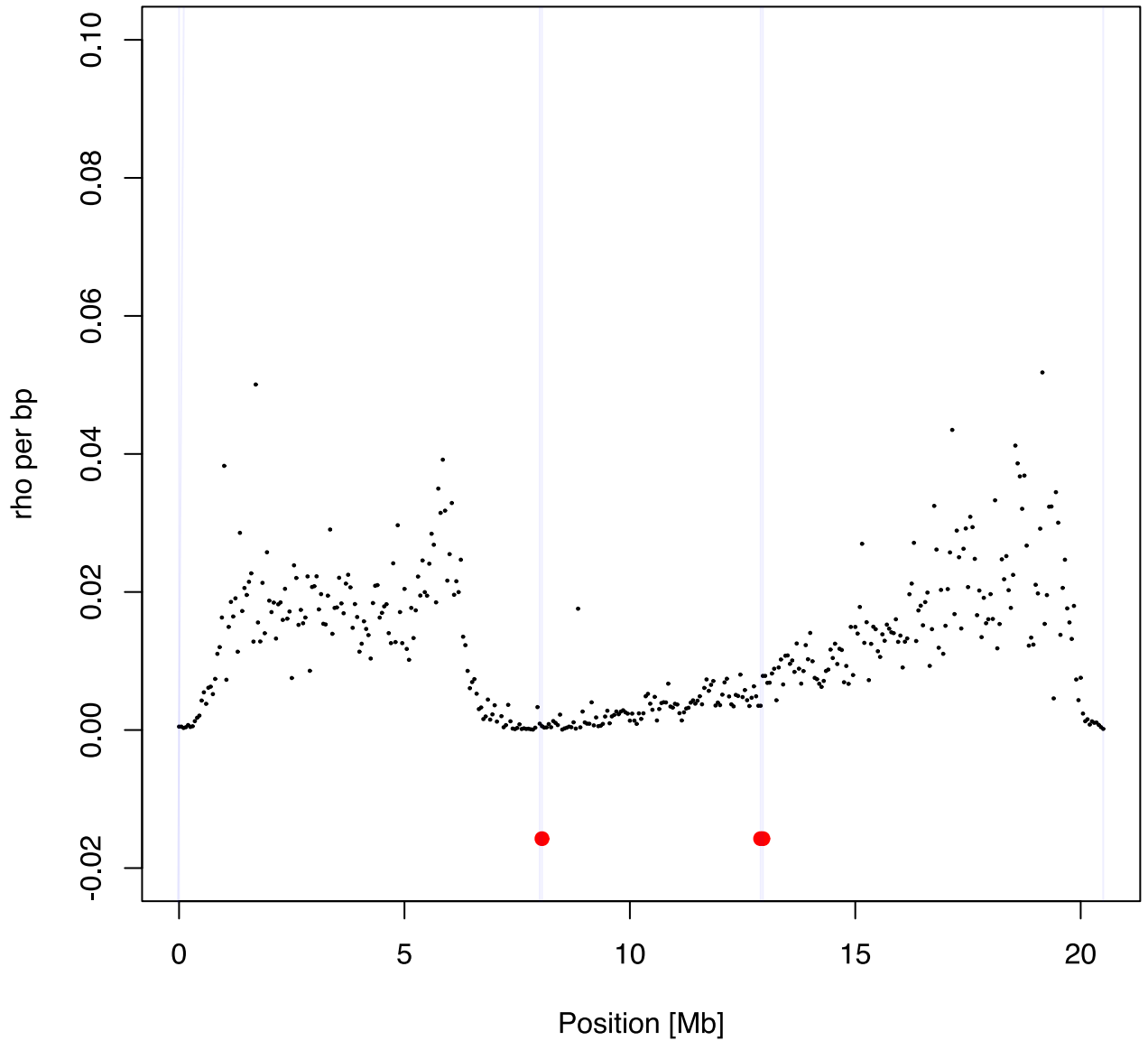
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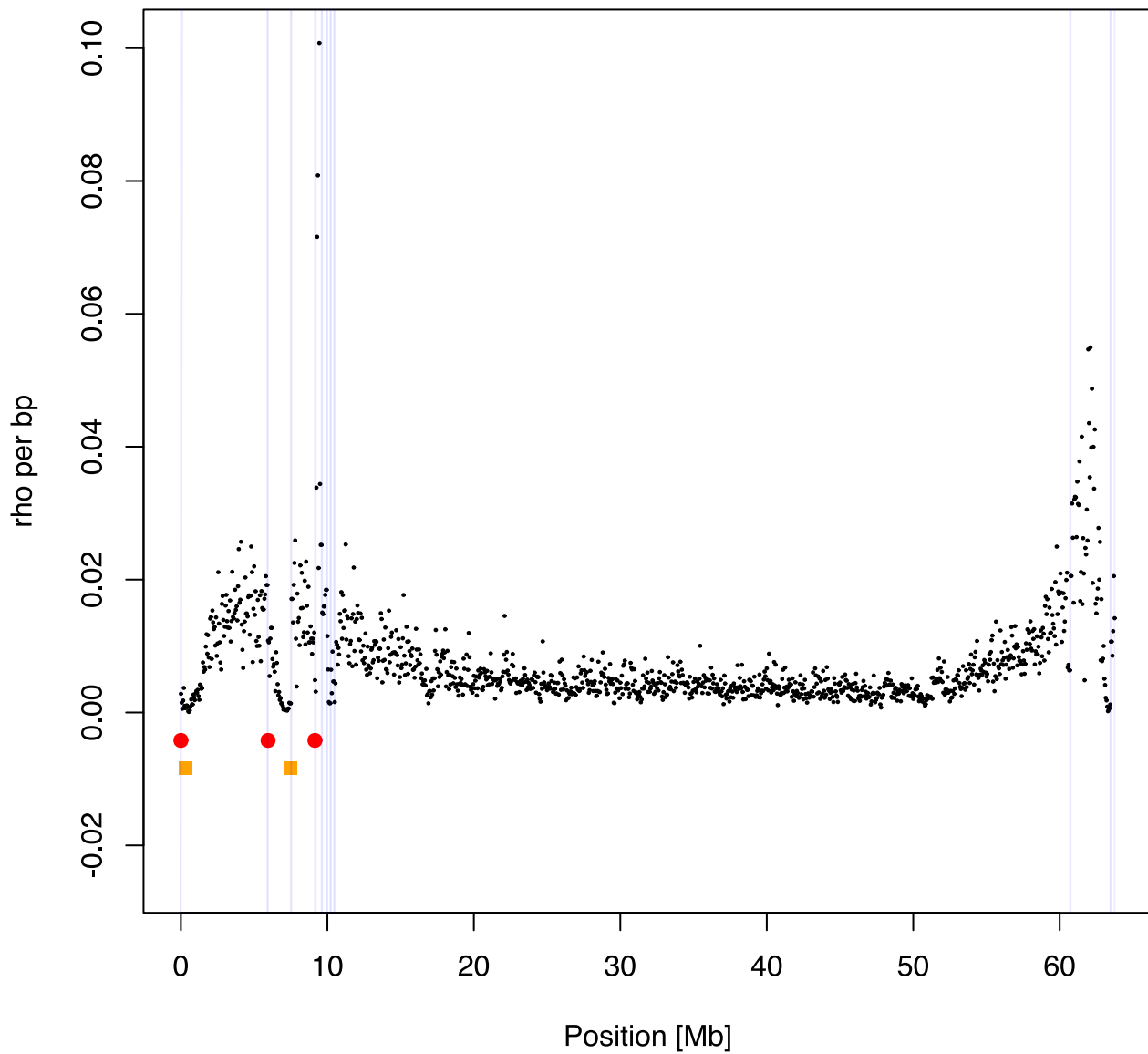
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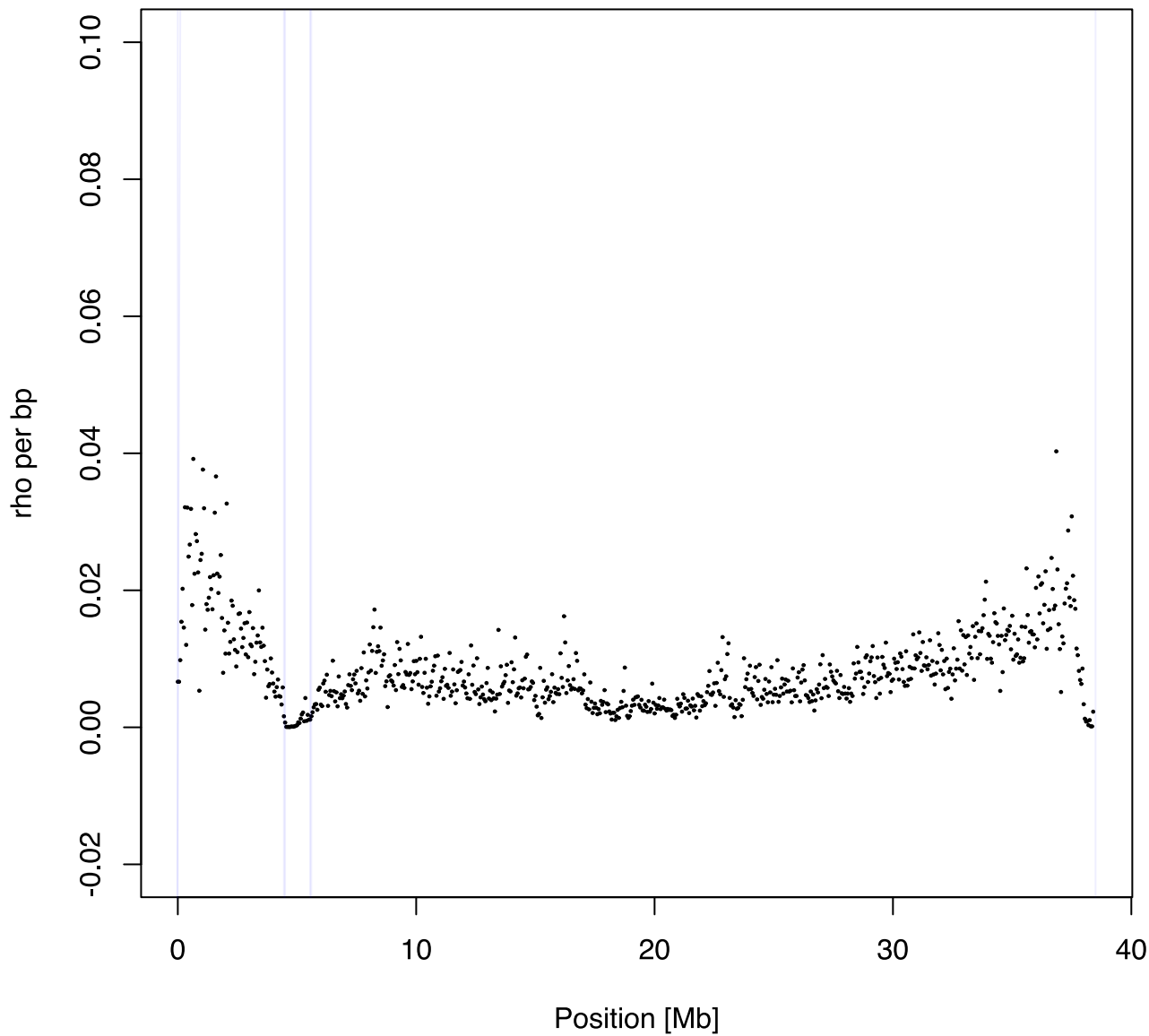
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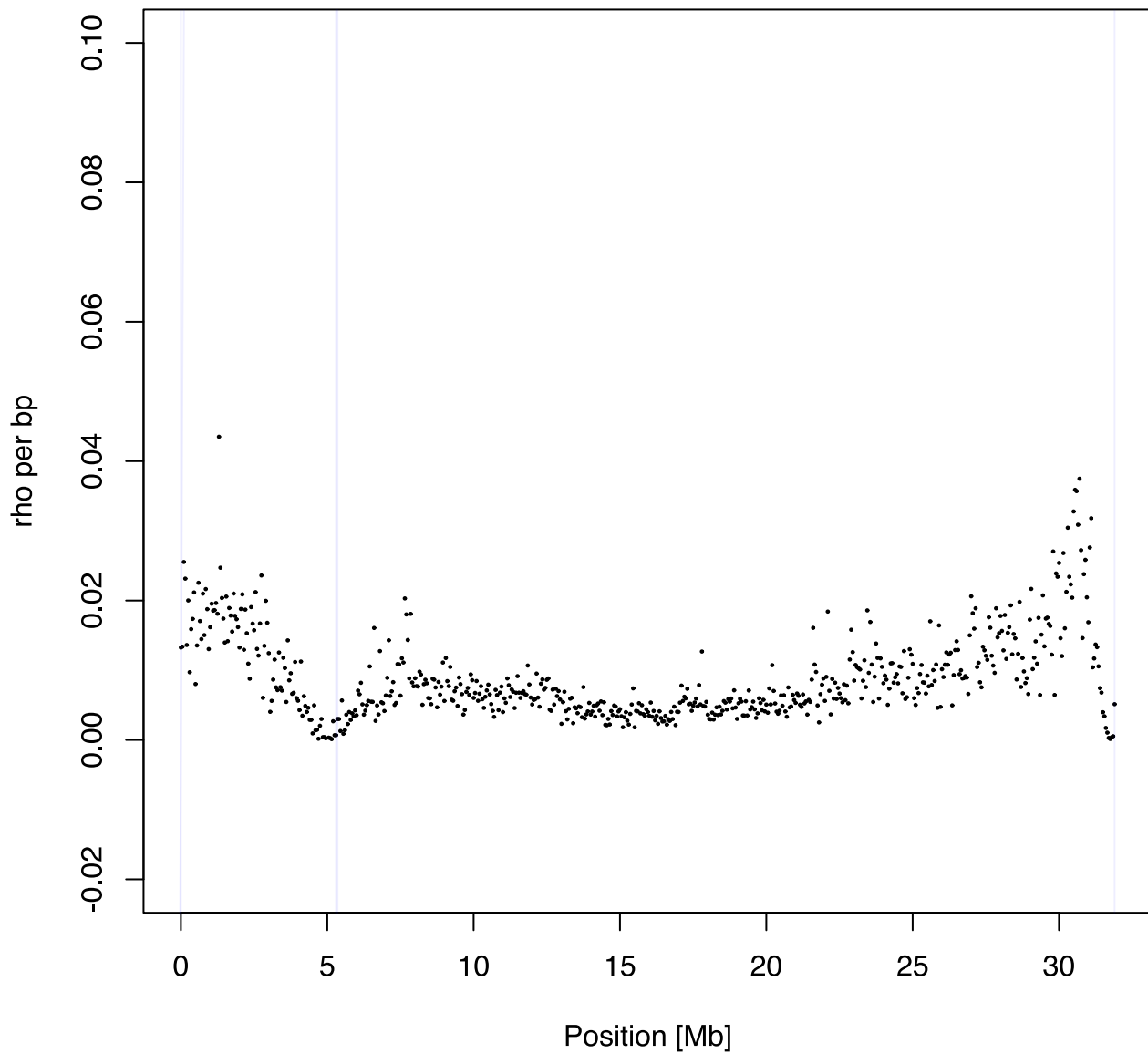
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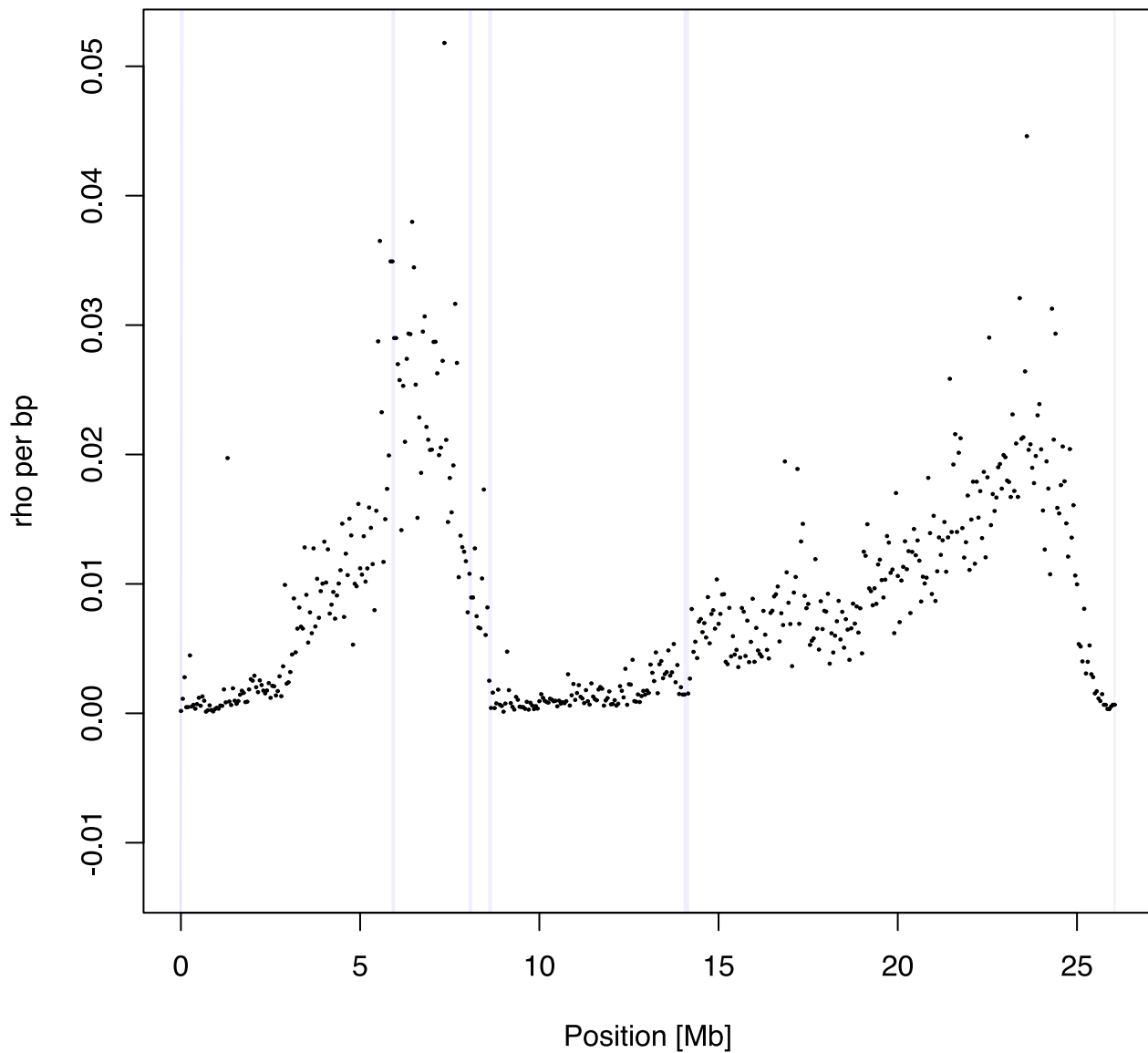
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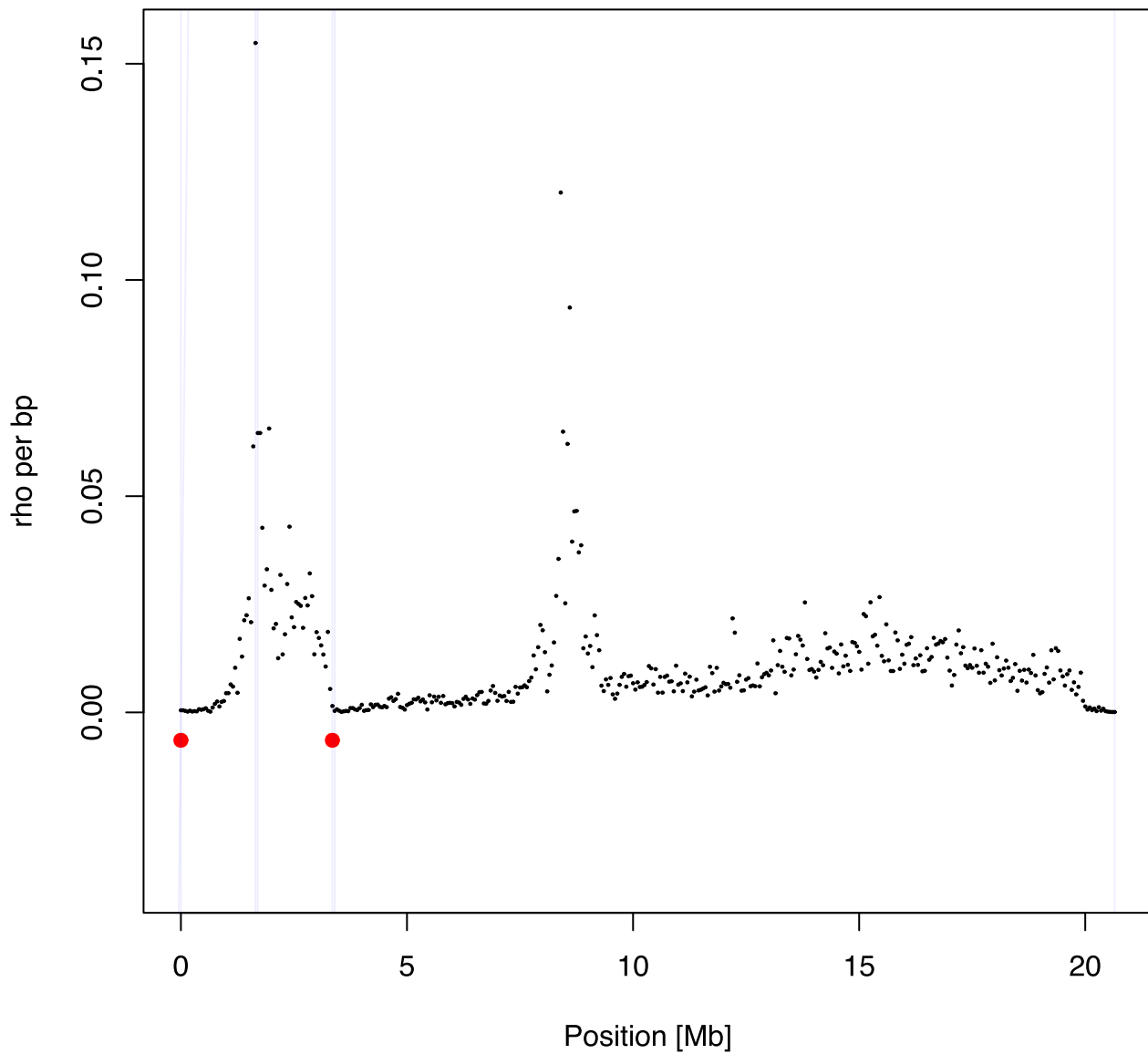
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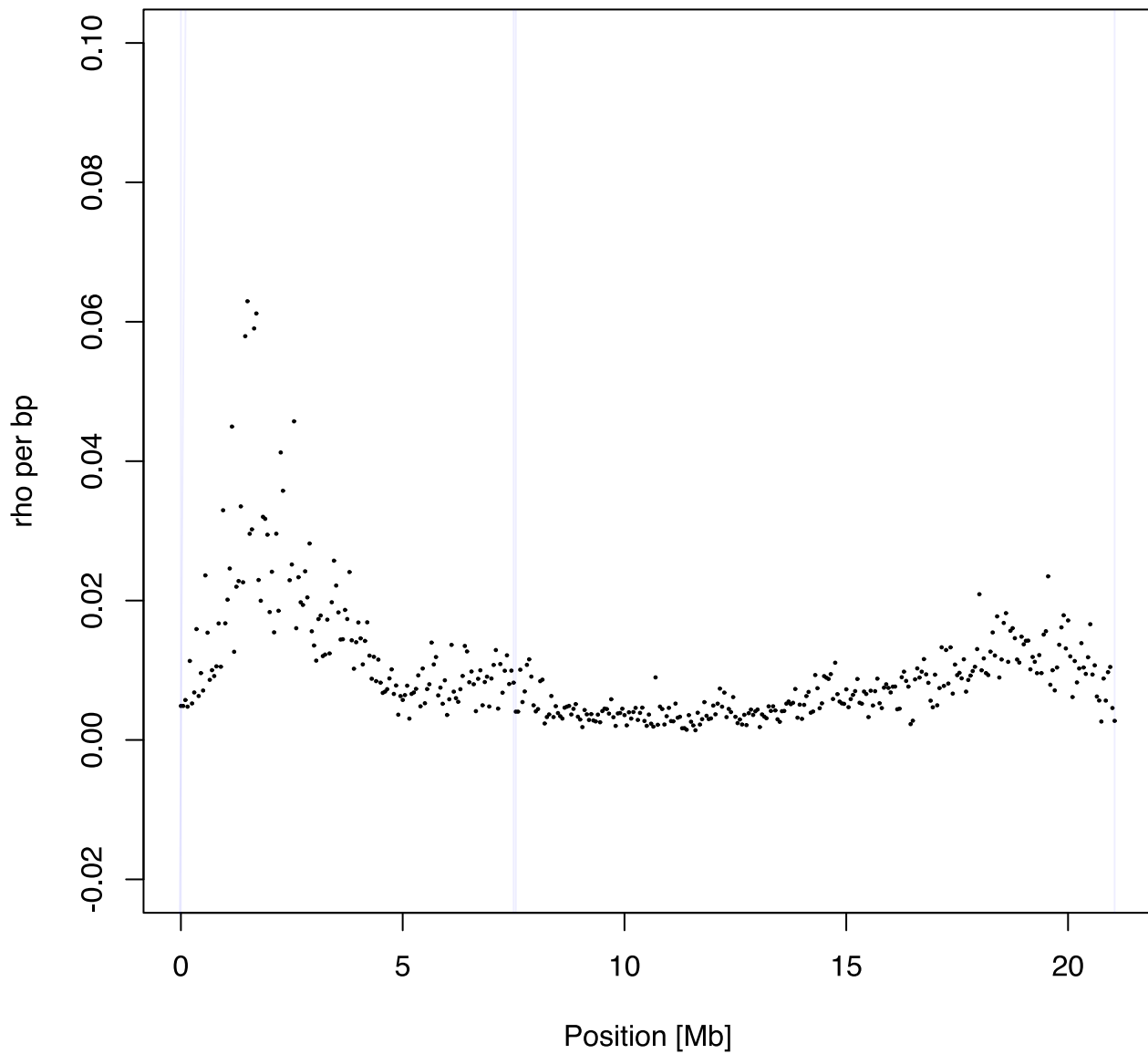
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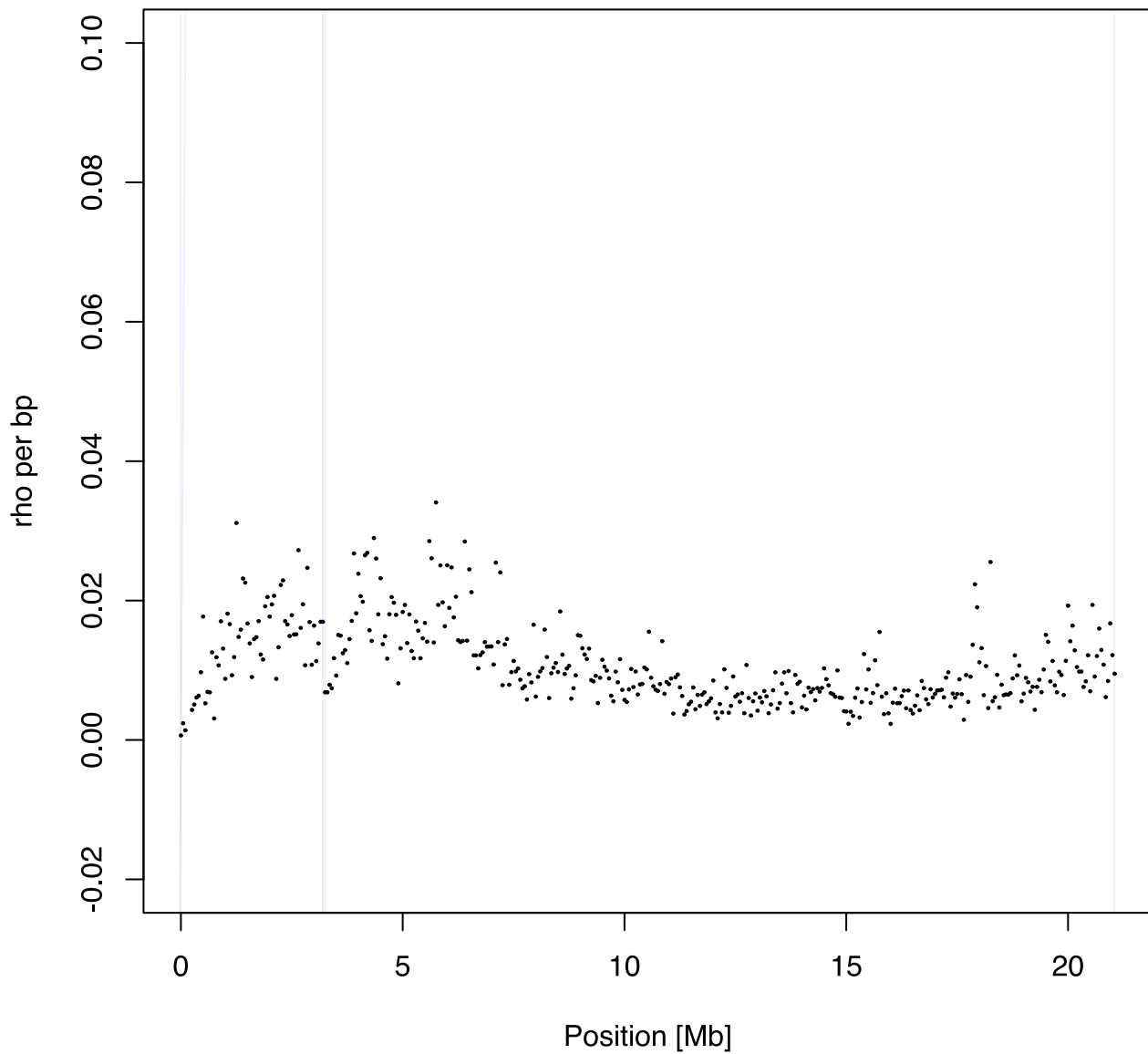
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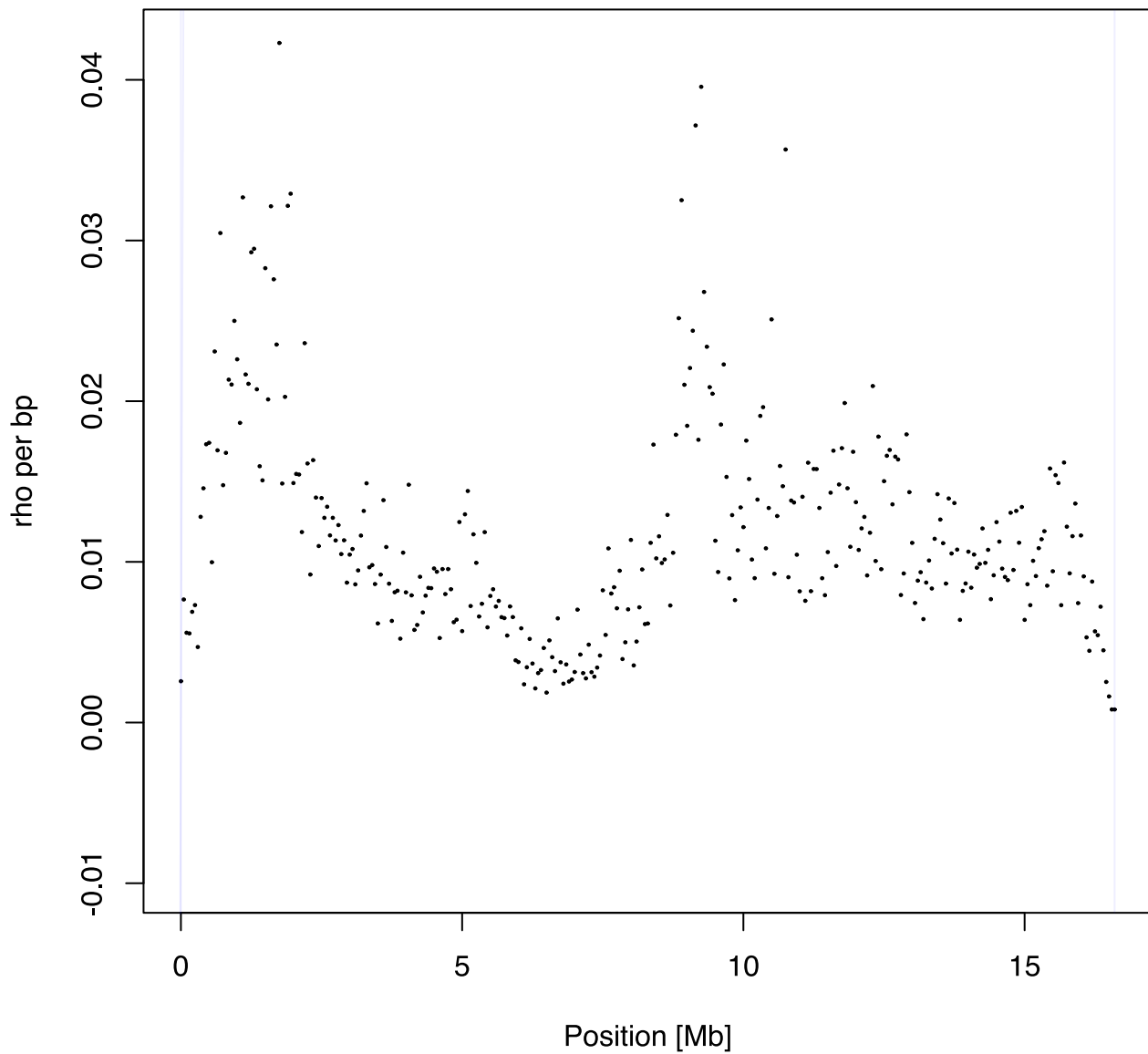
chr11



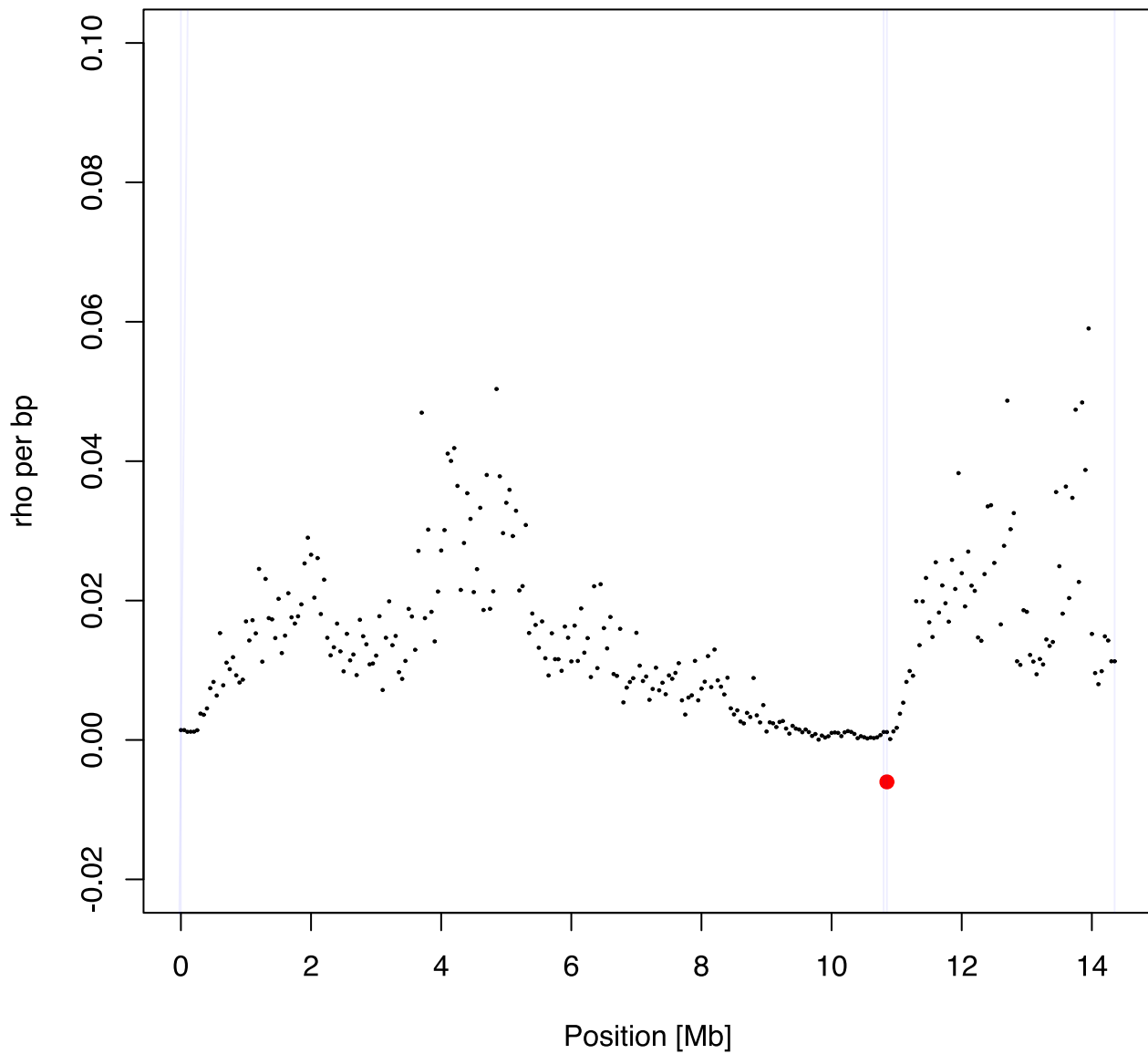
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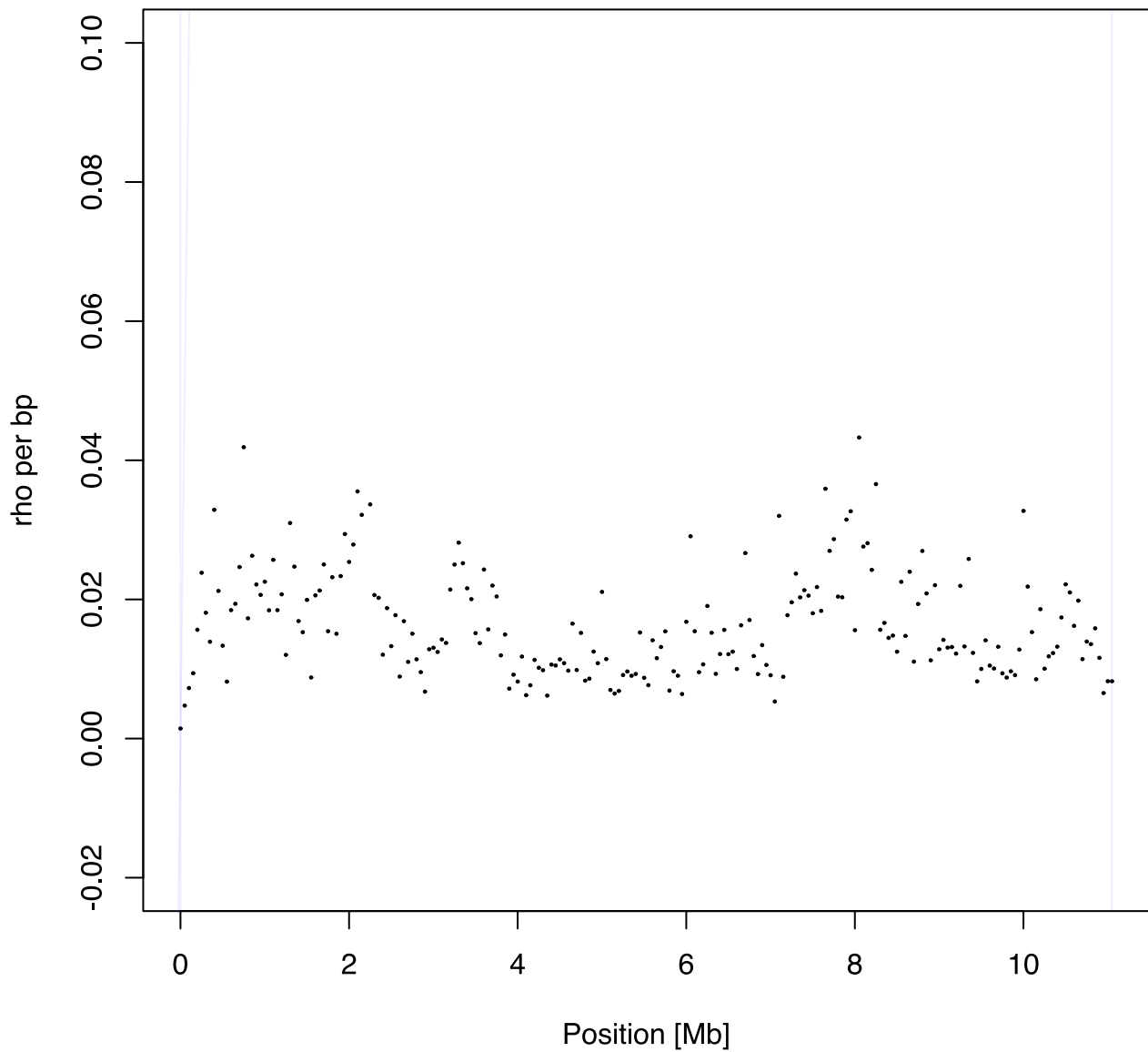
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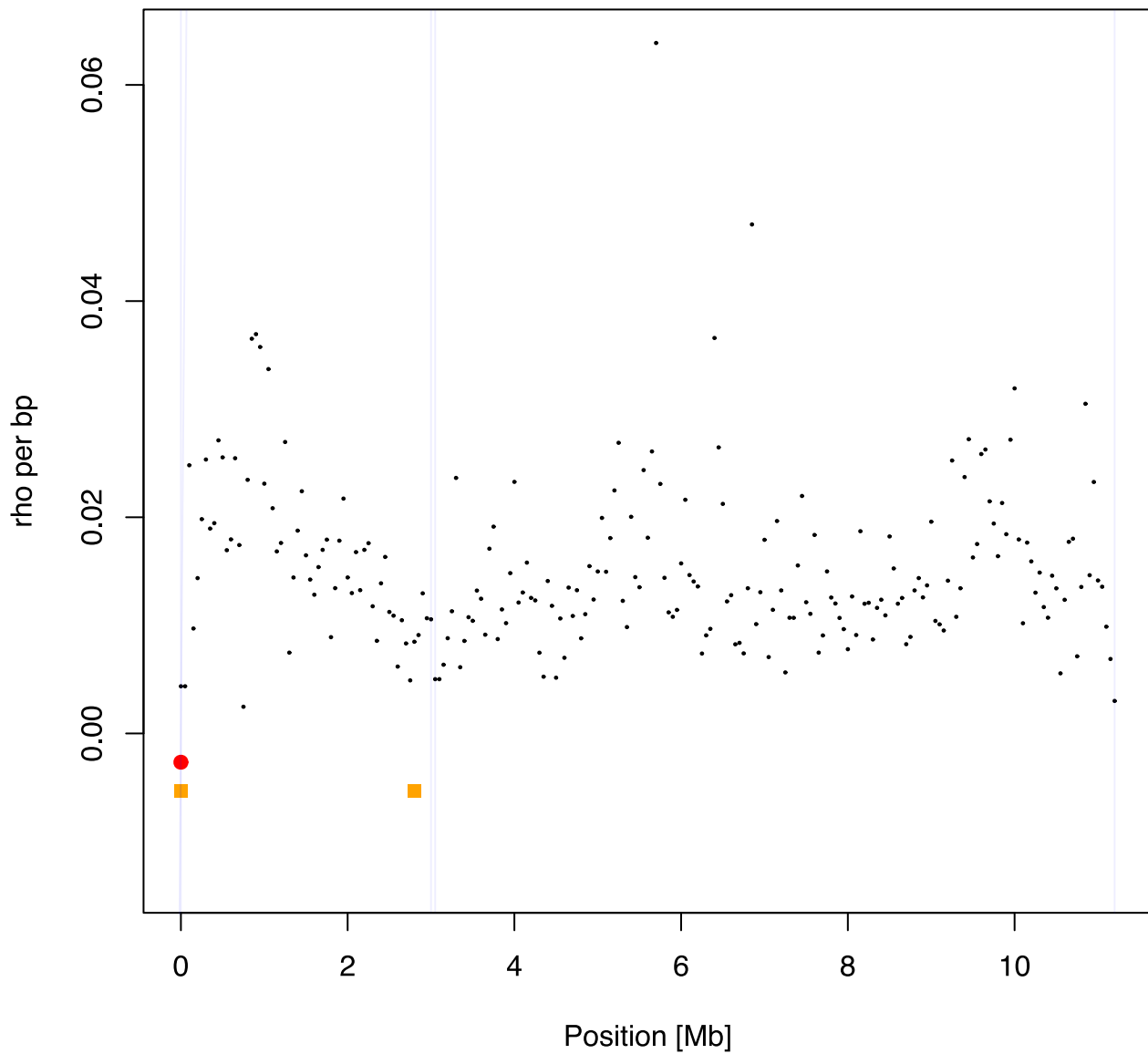
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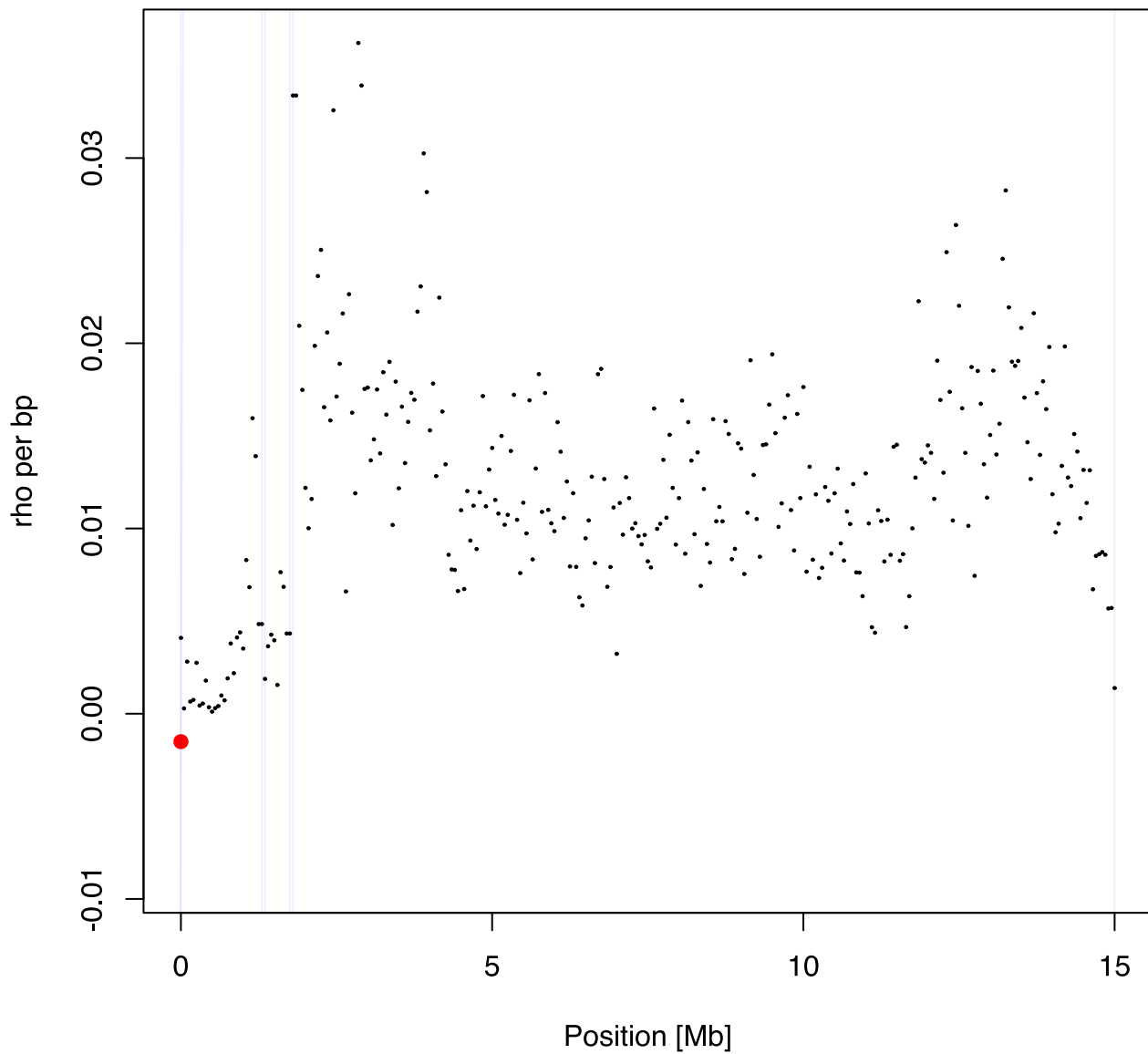
chr17



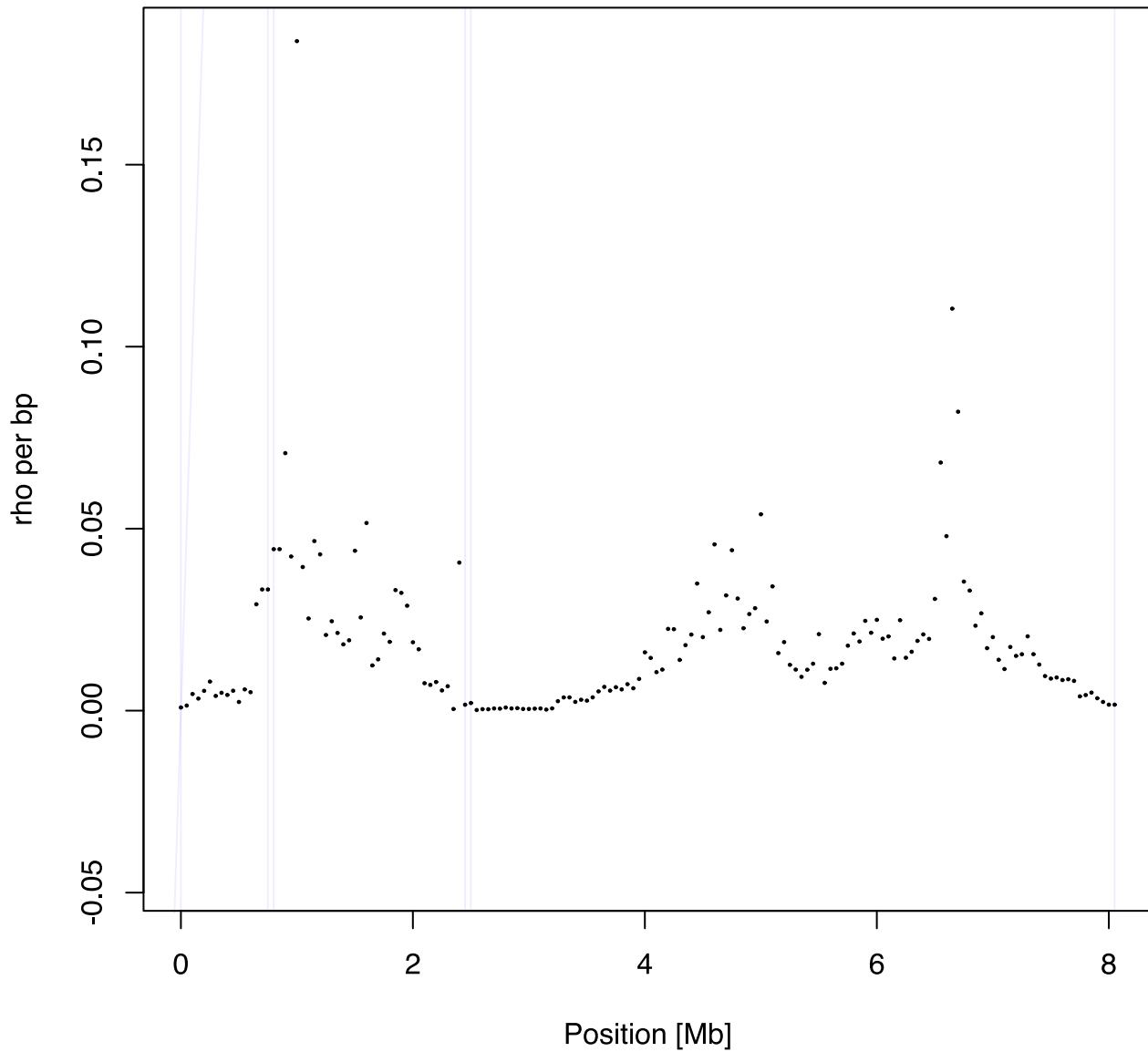
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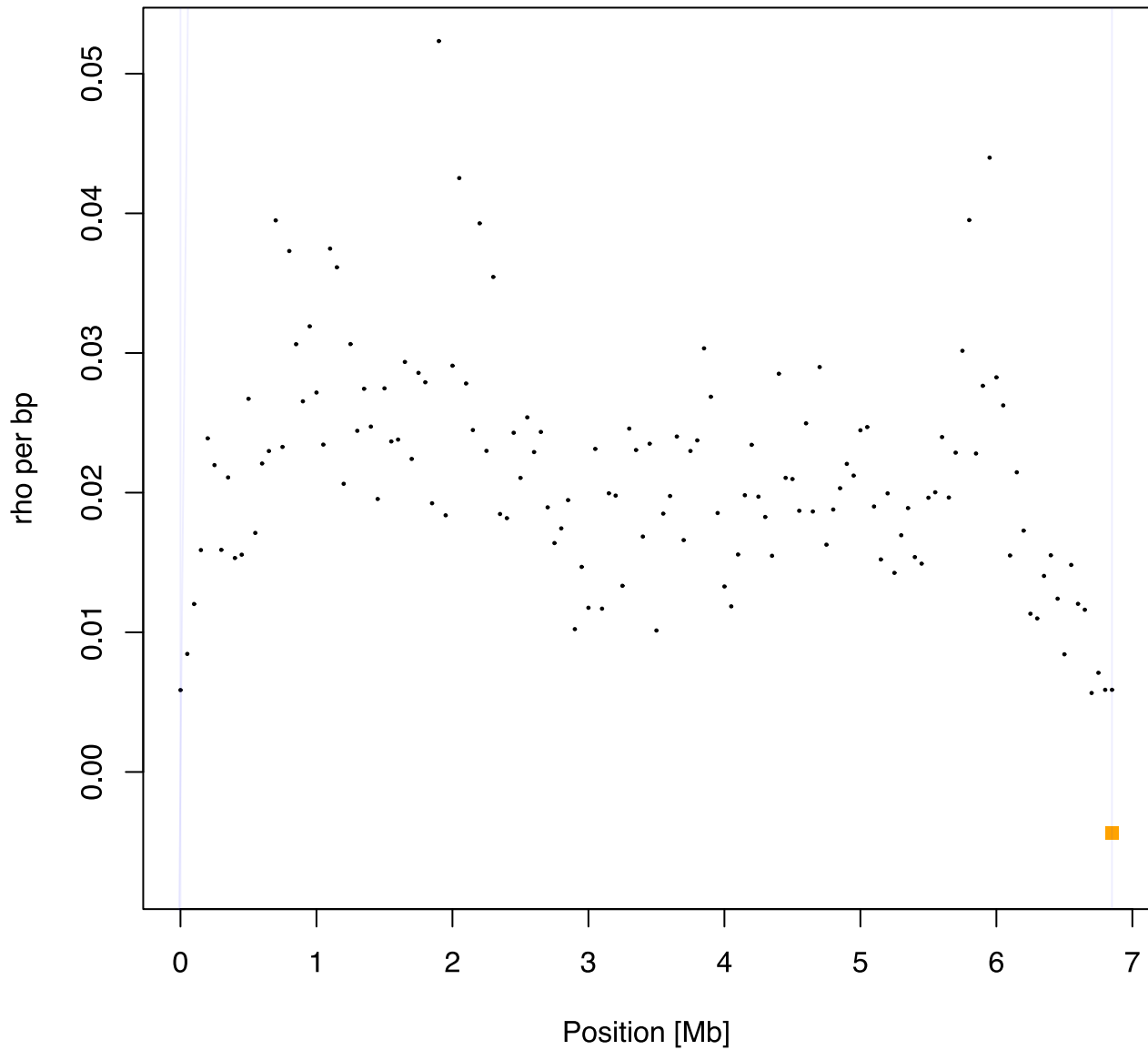
chr20



chr21



chr24



chr26

