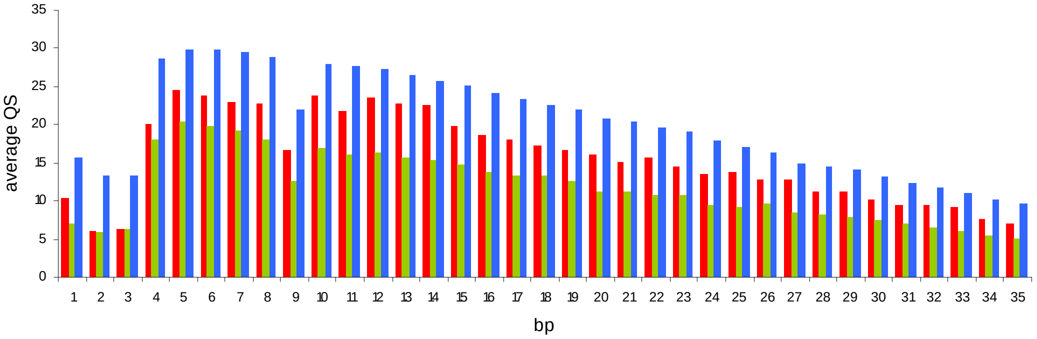
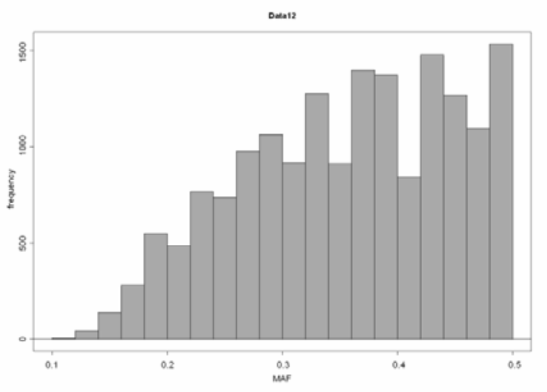
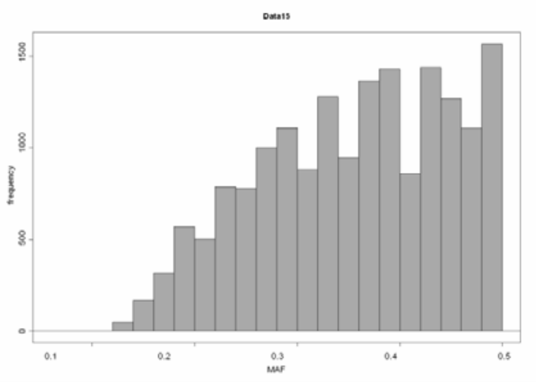
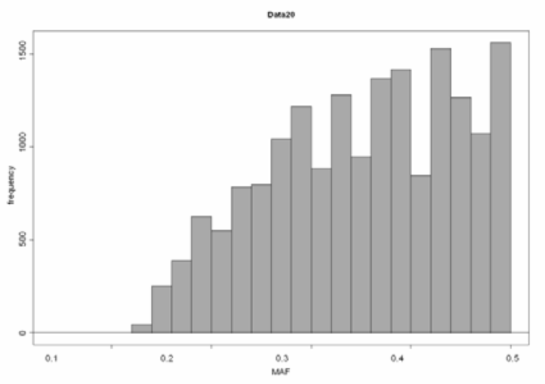
Supplemental Figure 1 - Average quality score per position on the sequence. Results are shown for several runs: Run 1 (red bars, 463,012 sequences), Run 2 (green bars, 14,827,185 sequences) and Run 3 (blue bars, 55,057,867 sequences). Sequences were trimmed at 35 bp.



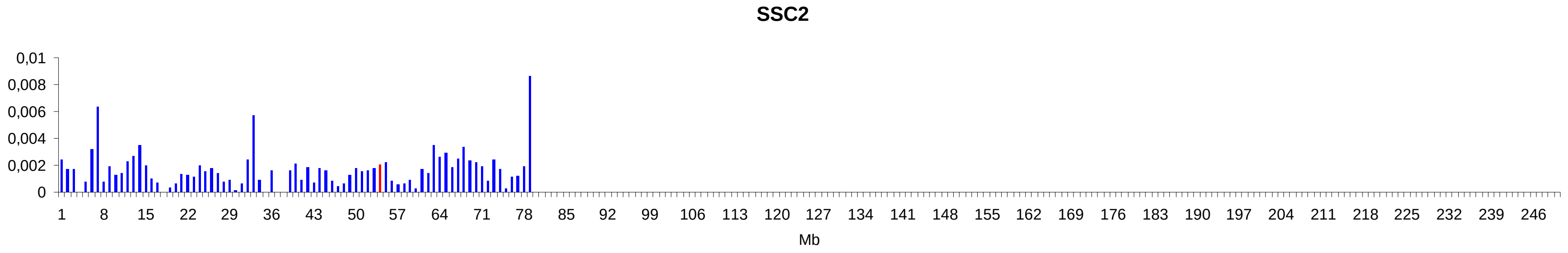
Supplemental Figure 2- Distribution of minor allele frequency for data sets: Data12, Data 15 and Data 20.

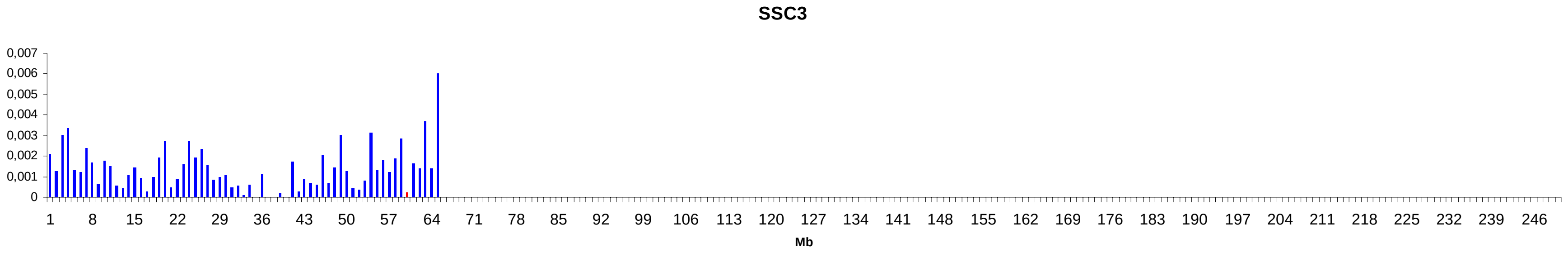


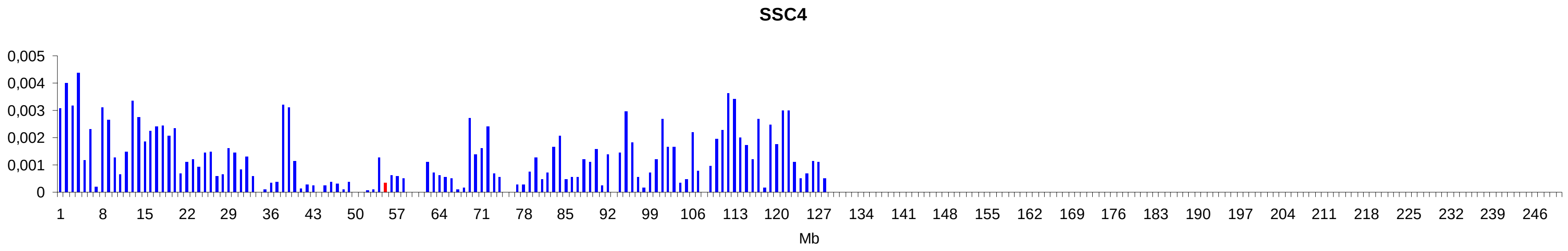




Supplemental Figure 3 - Nucleotide diversity along remaining porcine chromosomes. Each bar represents a window of 1Mb over the chromosome. Red bars indicate chromosome window containing the centromere.



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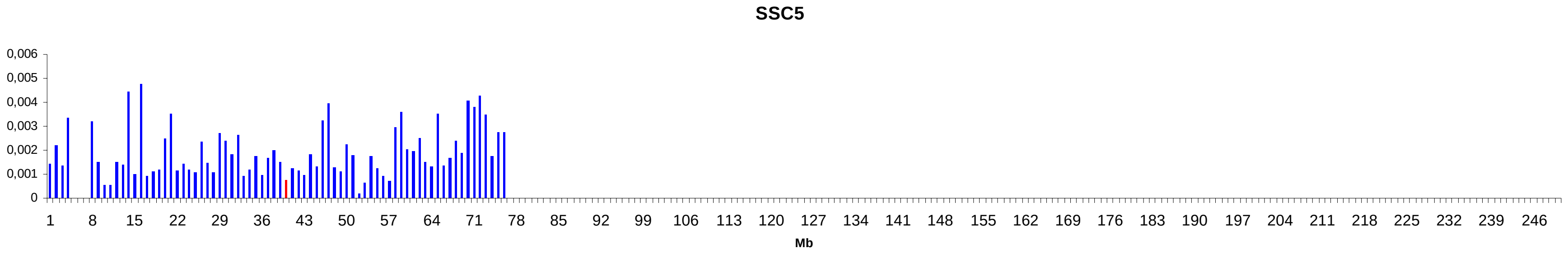
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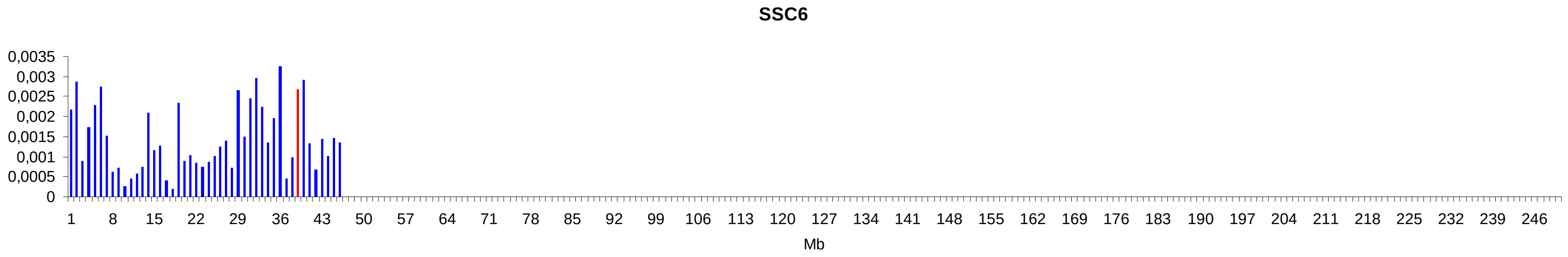
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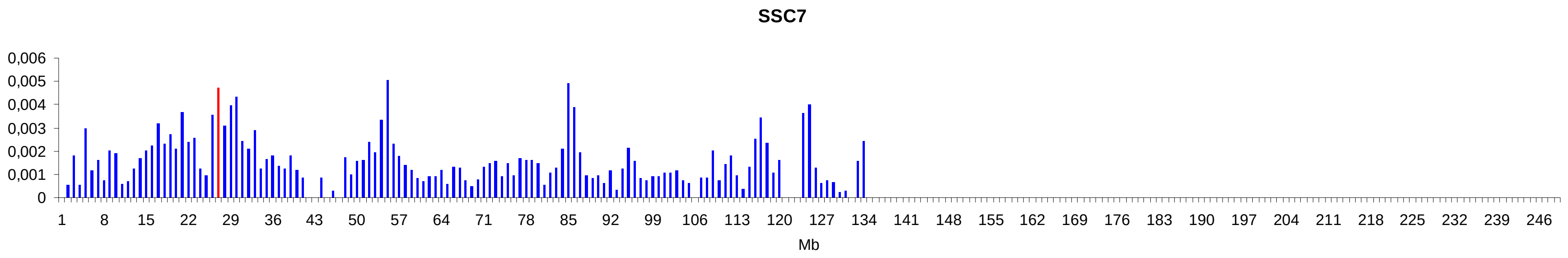
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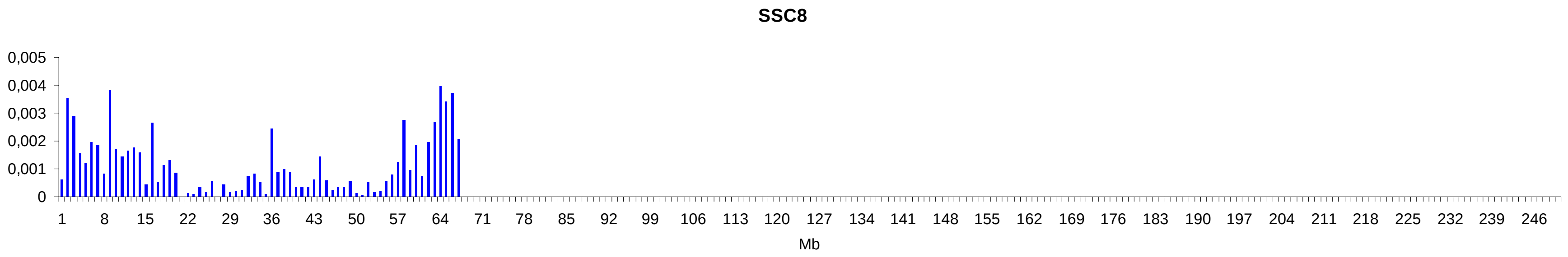
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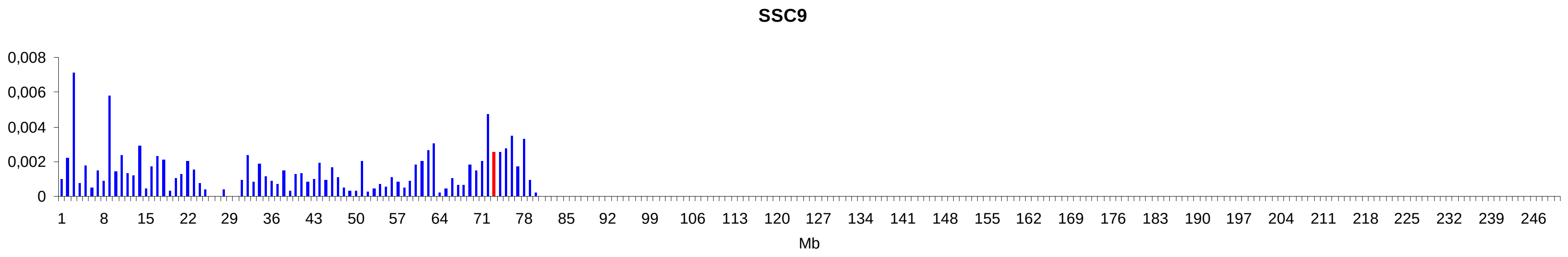
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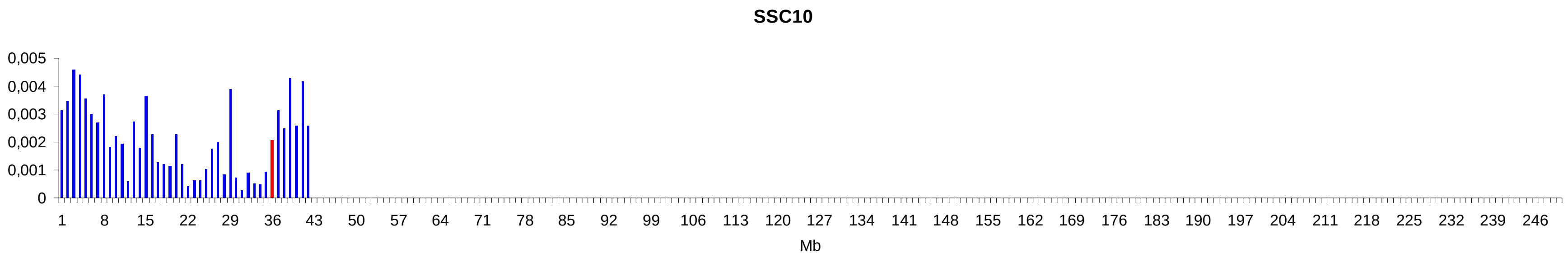
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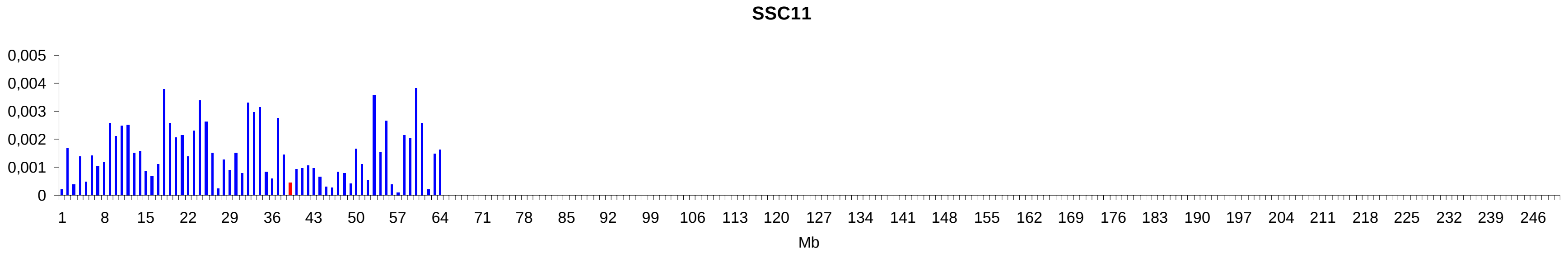
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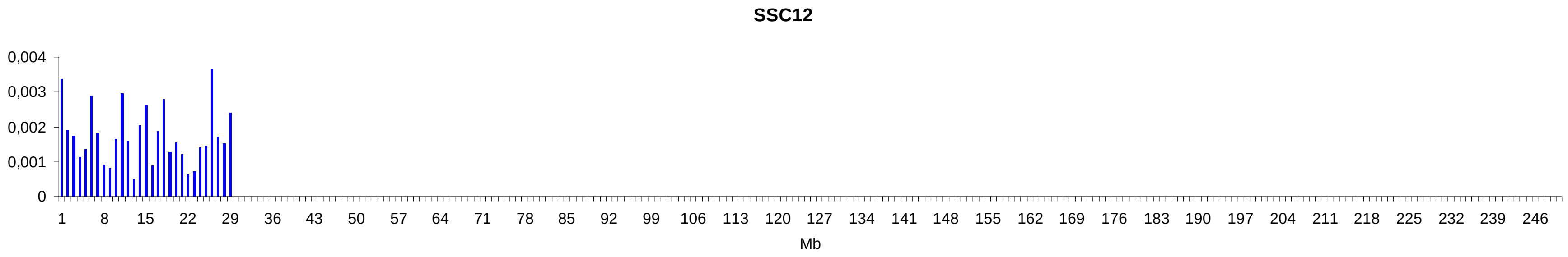
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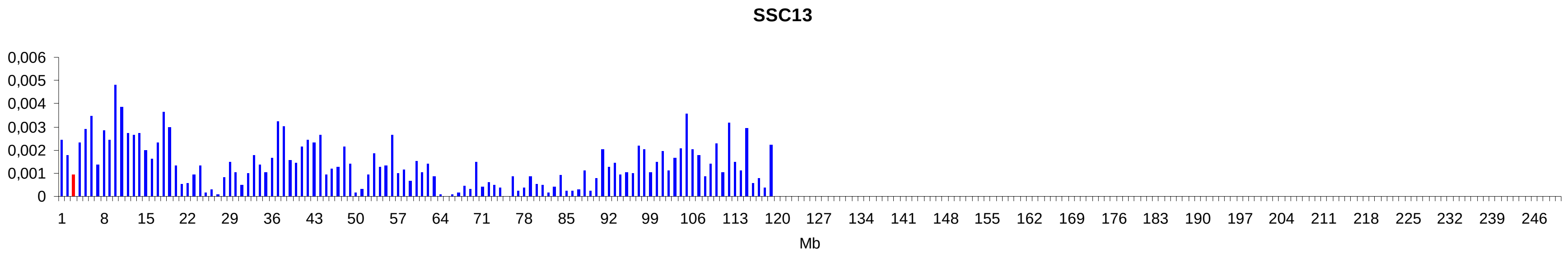
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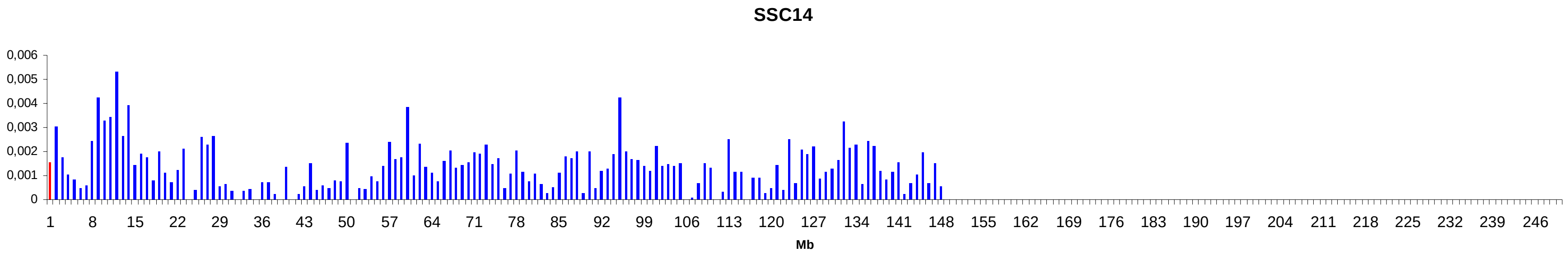
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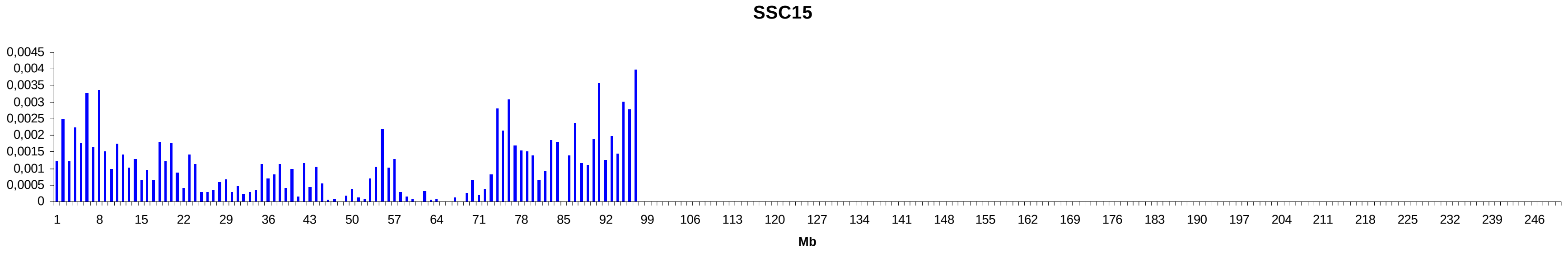
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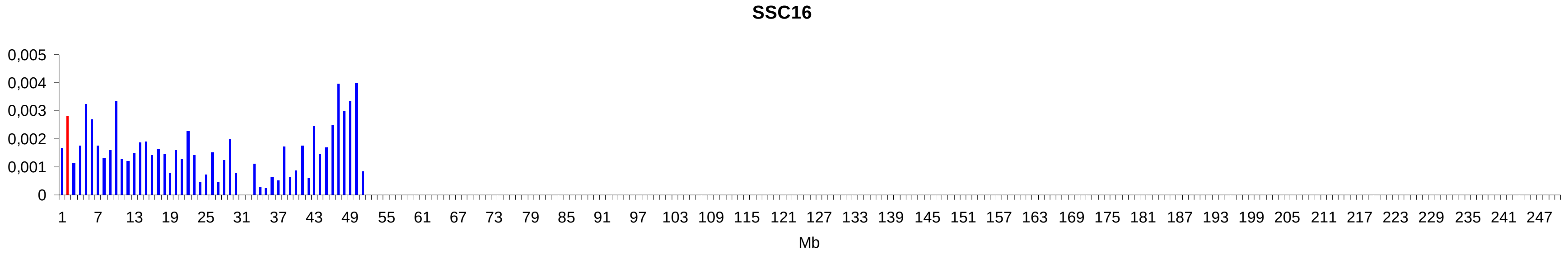
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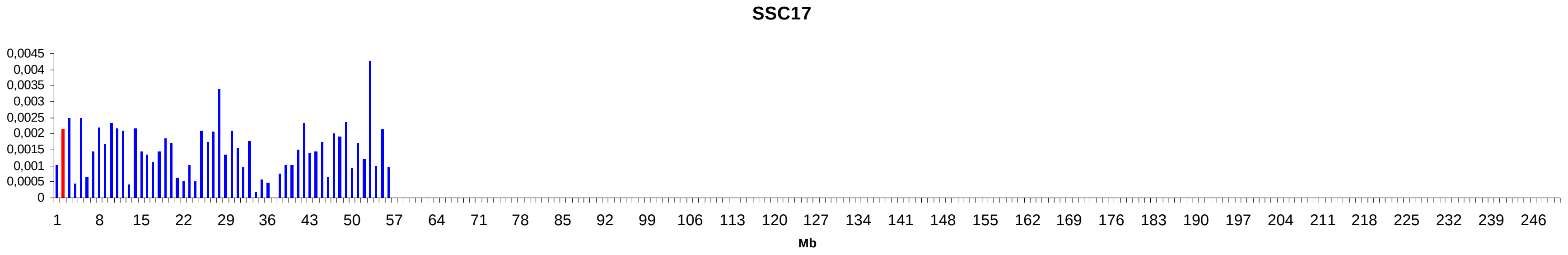
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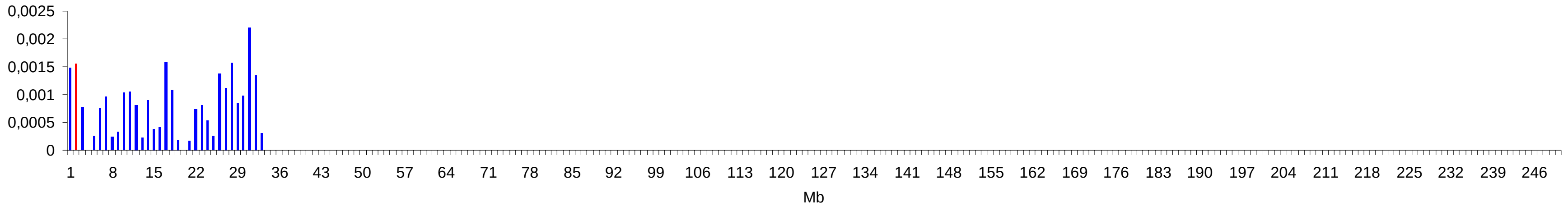
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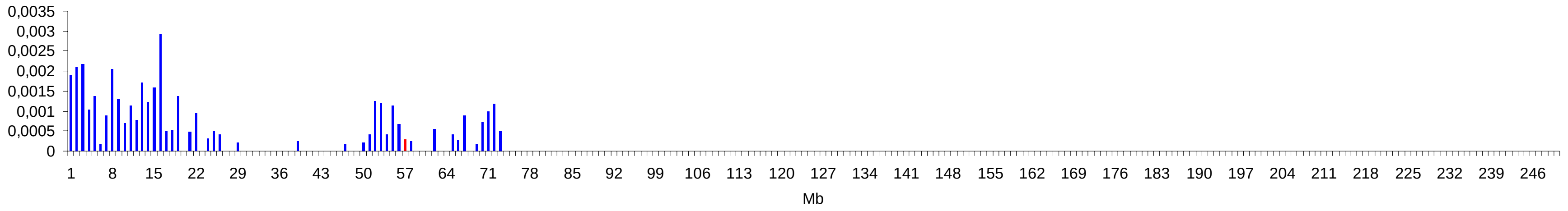
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