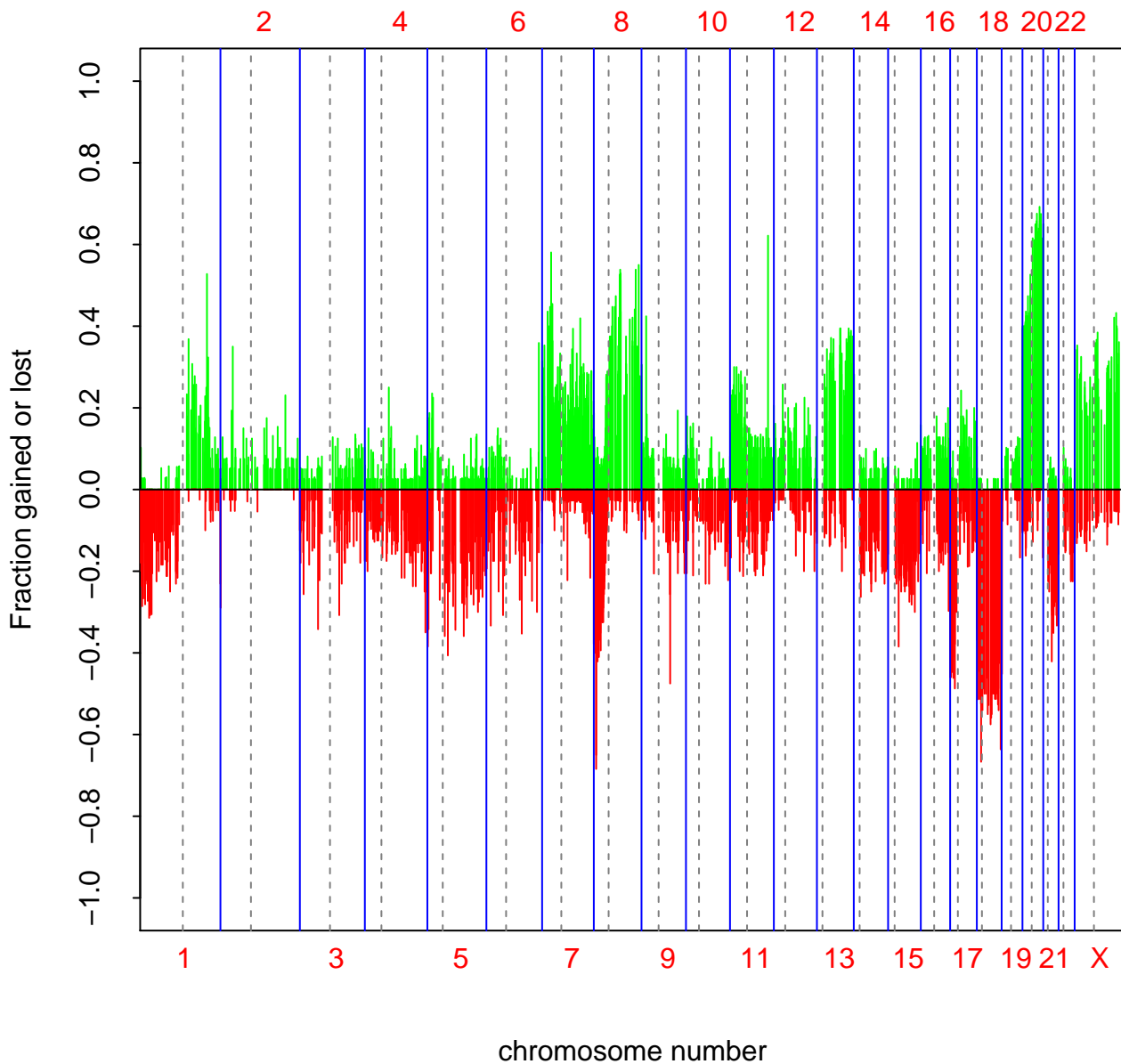
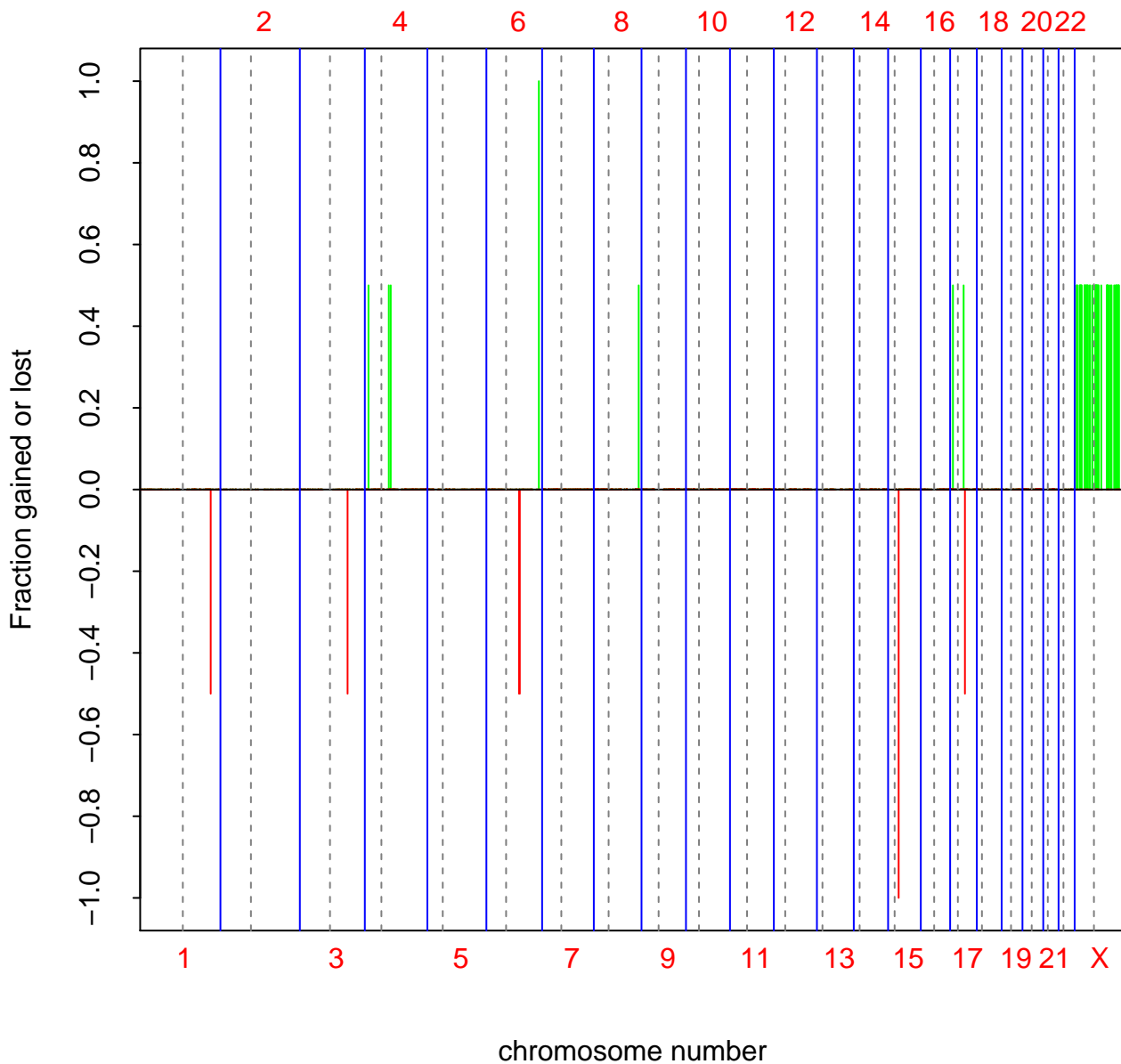


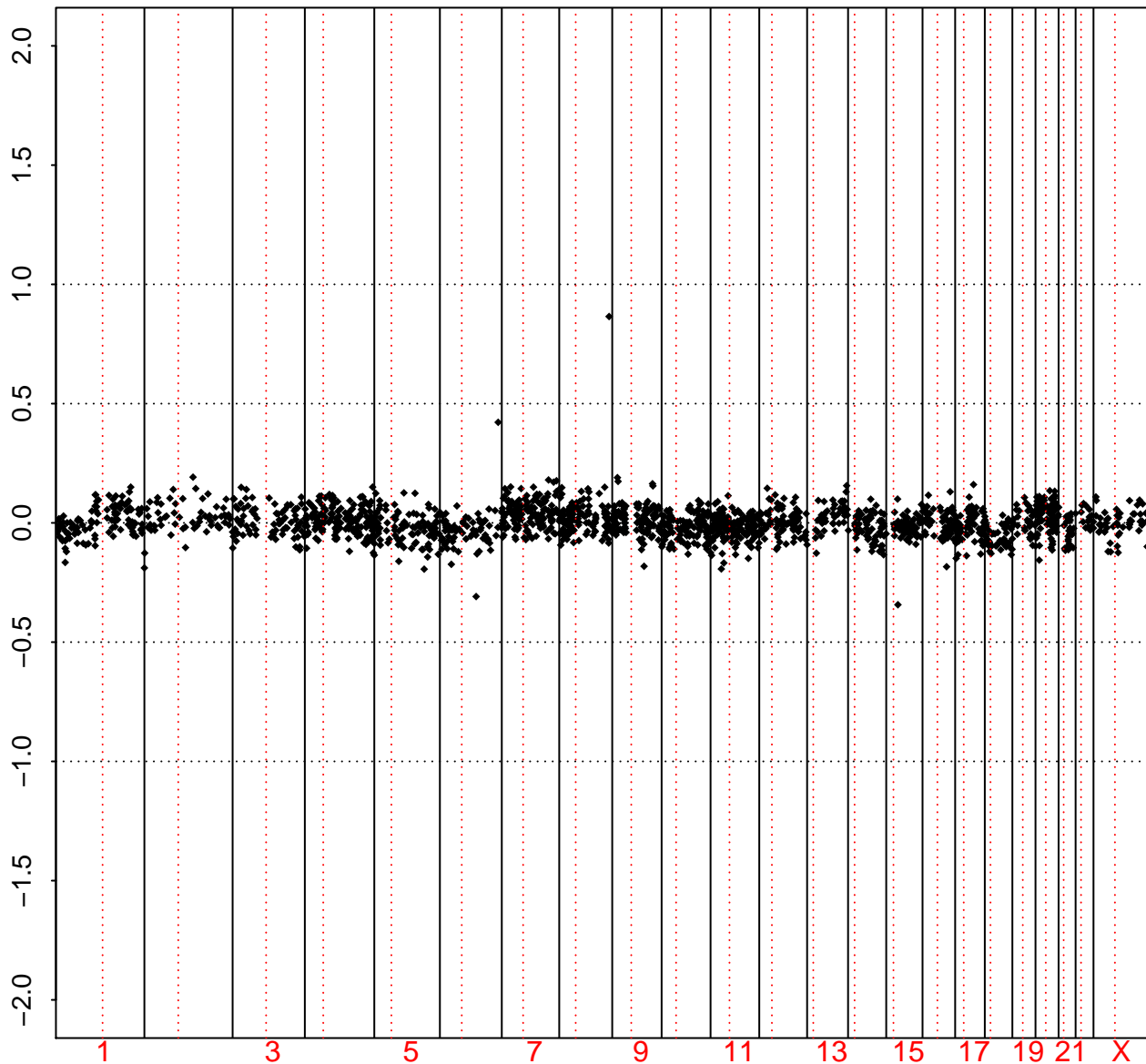
All Samples



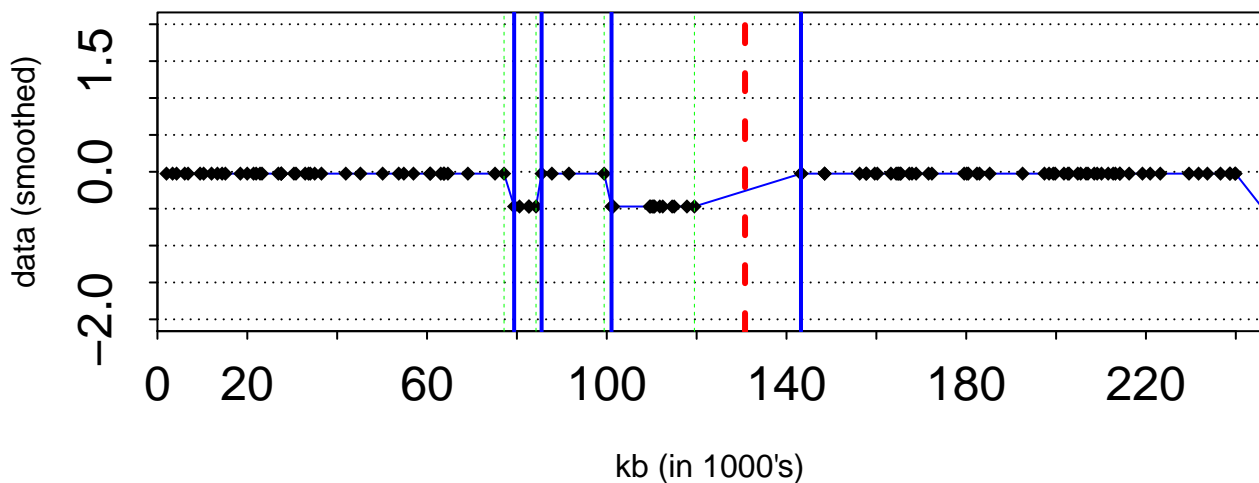
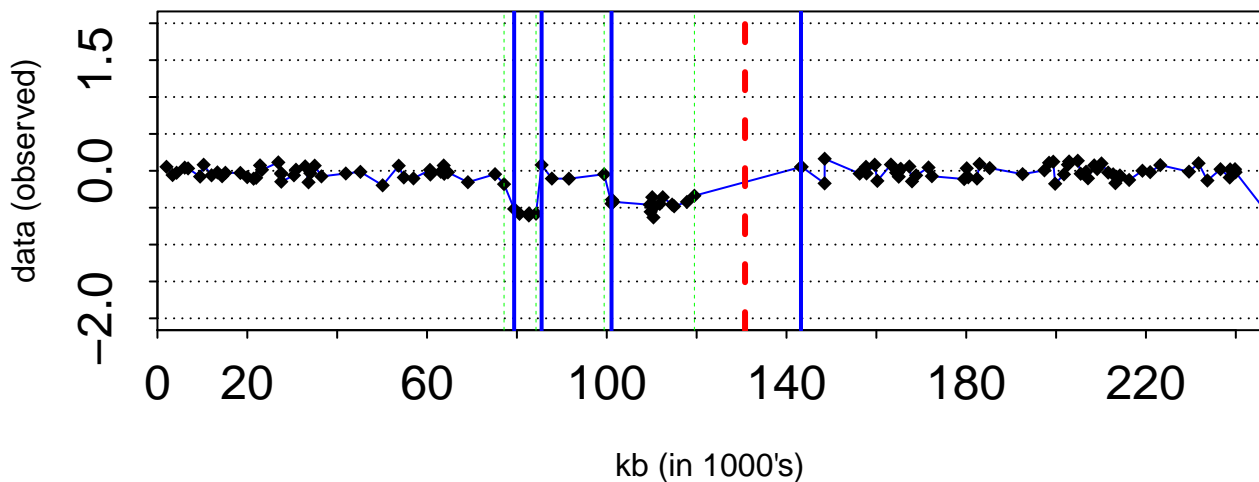
All Samples



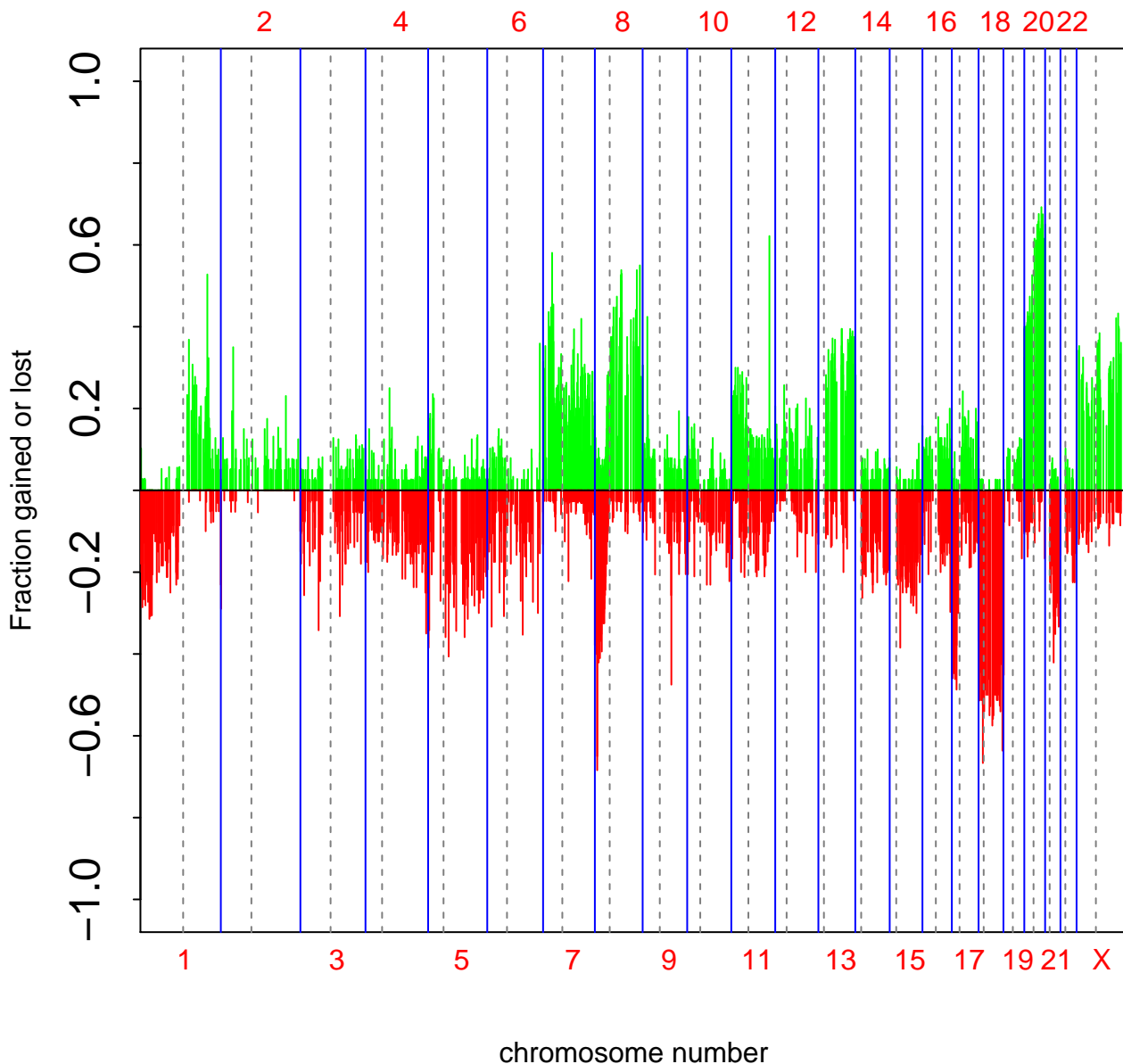
Log2Ratio

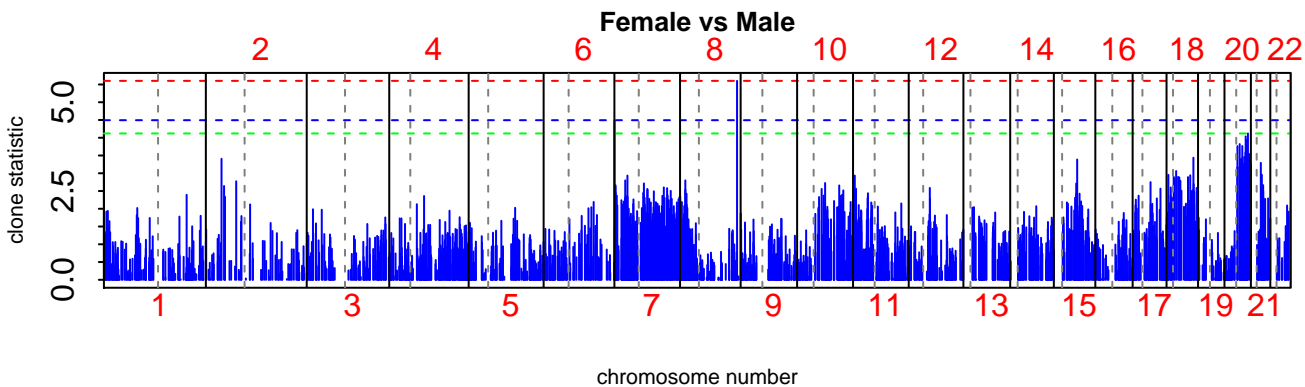
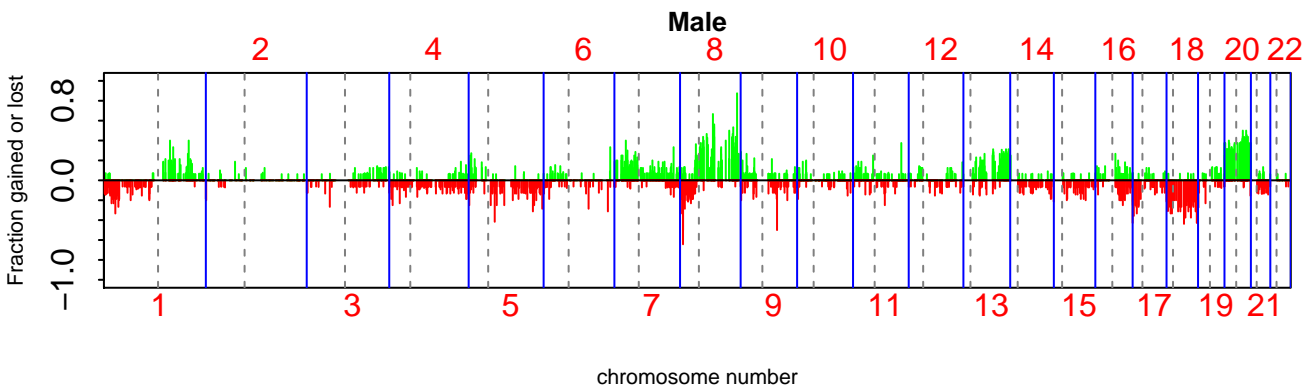
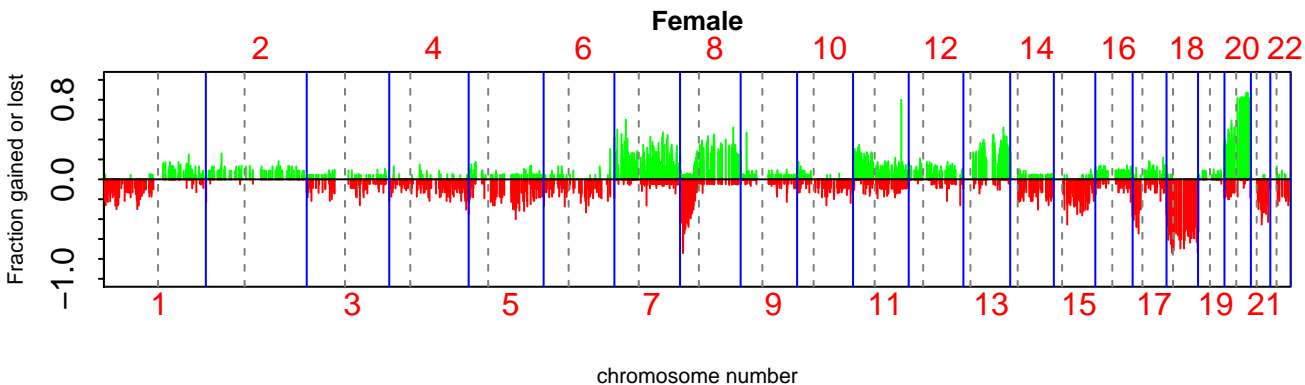


Sample 1 sprocCR31.txt – Chr 1 Number of states 2

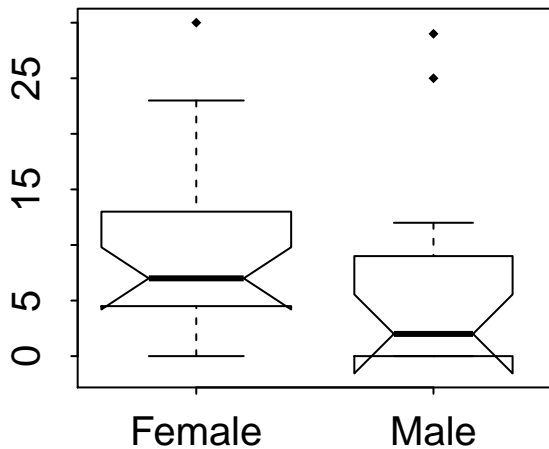


All Samples

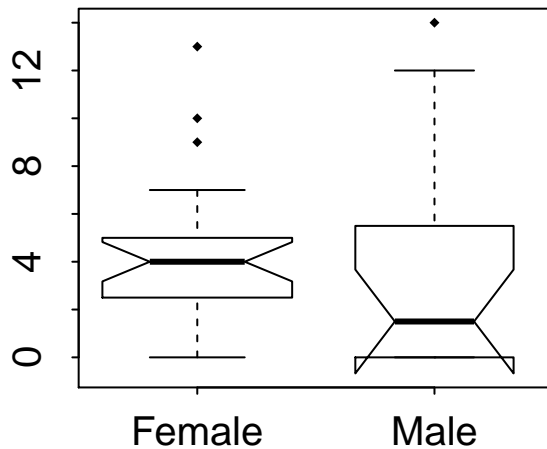




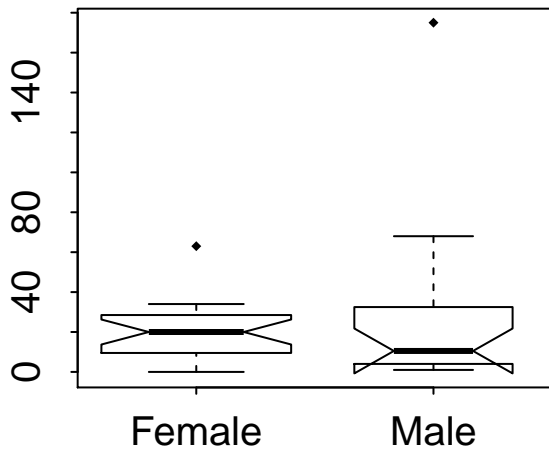
Number of Transitions 0.0950684



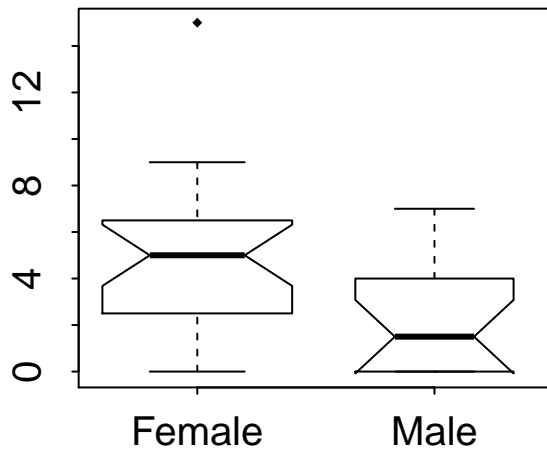
Number of Chrom containing Transitions 0.174915



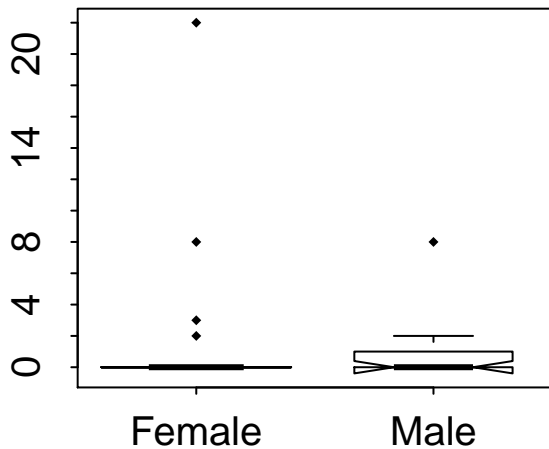
Number of Aberrations 0.841381



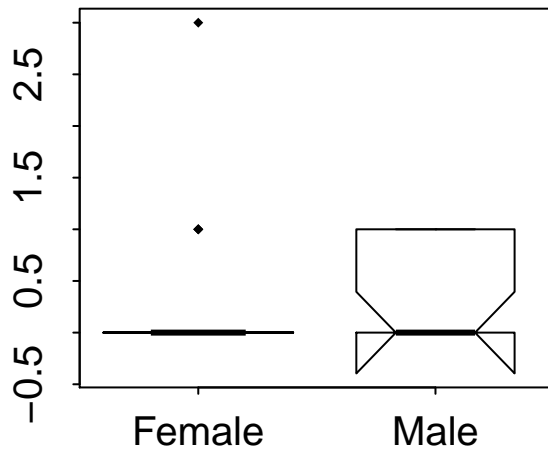
Number of Whole Chrom Changes 0.0174111



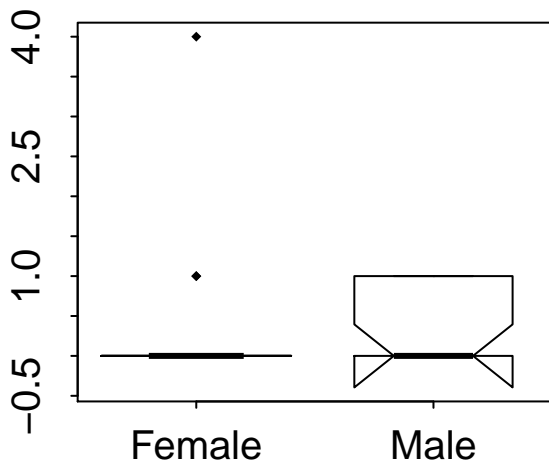
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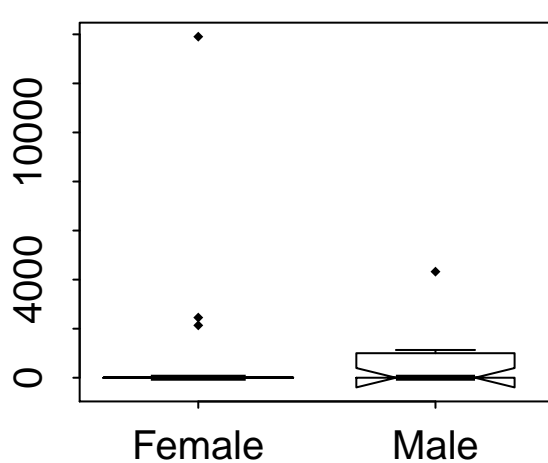
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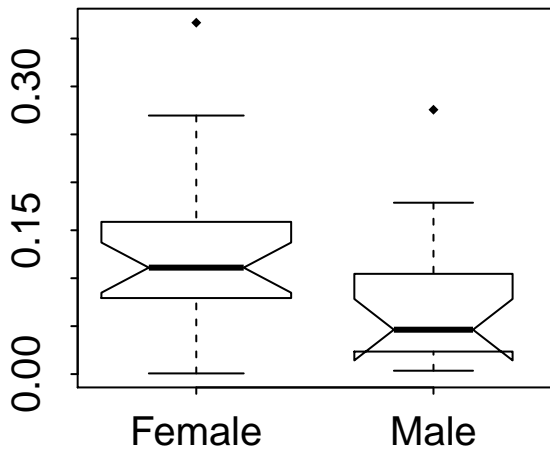
Number of Amplicons 0.207136



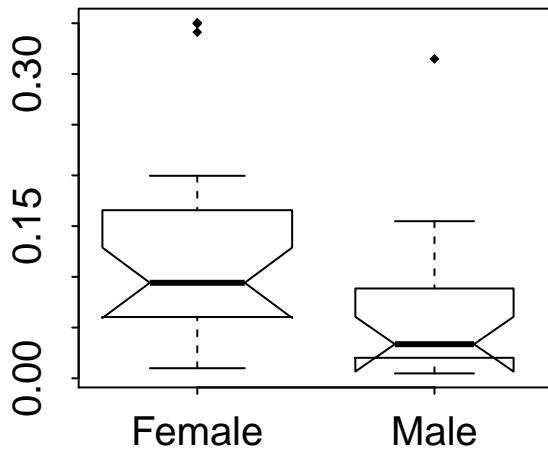
Amount of Genome Amplified 0.257209



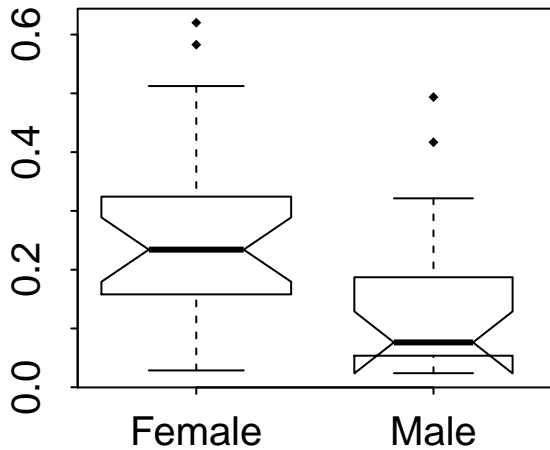
Fraction of Genome Gained 0.0300104

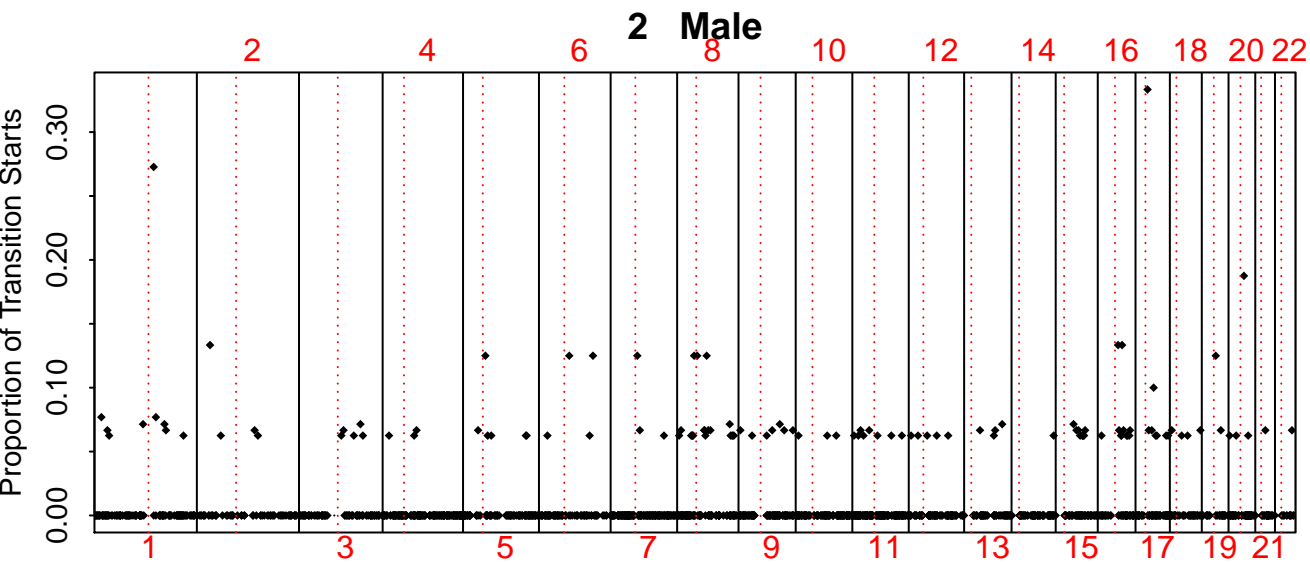
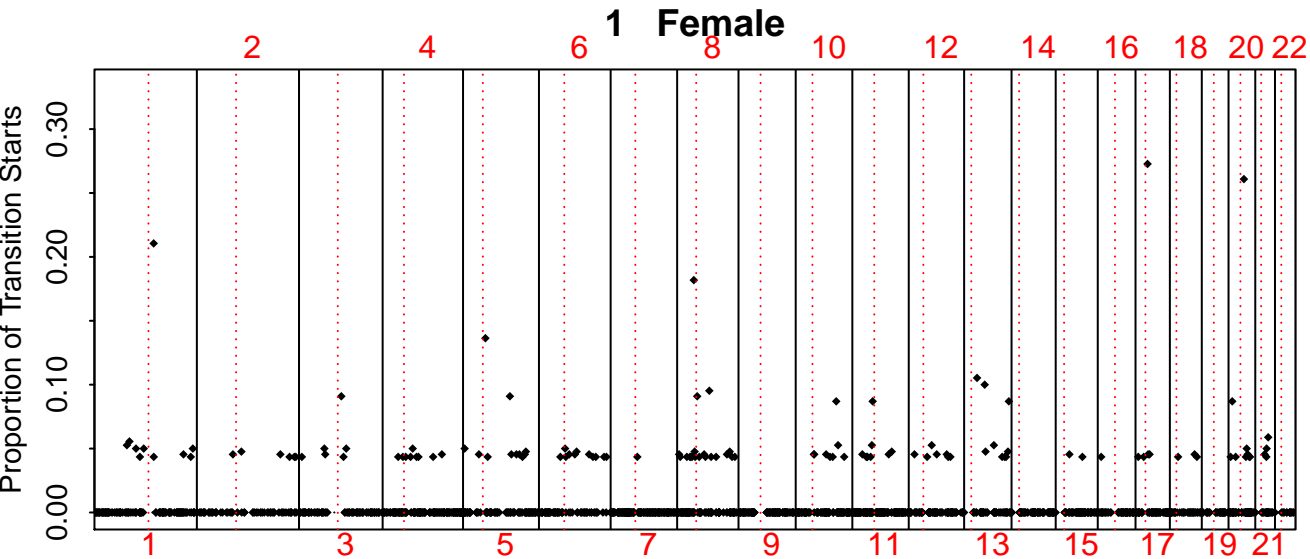


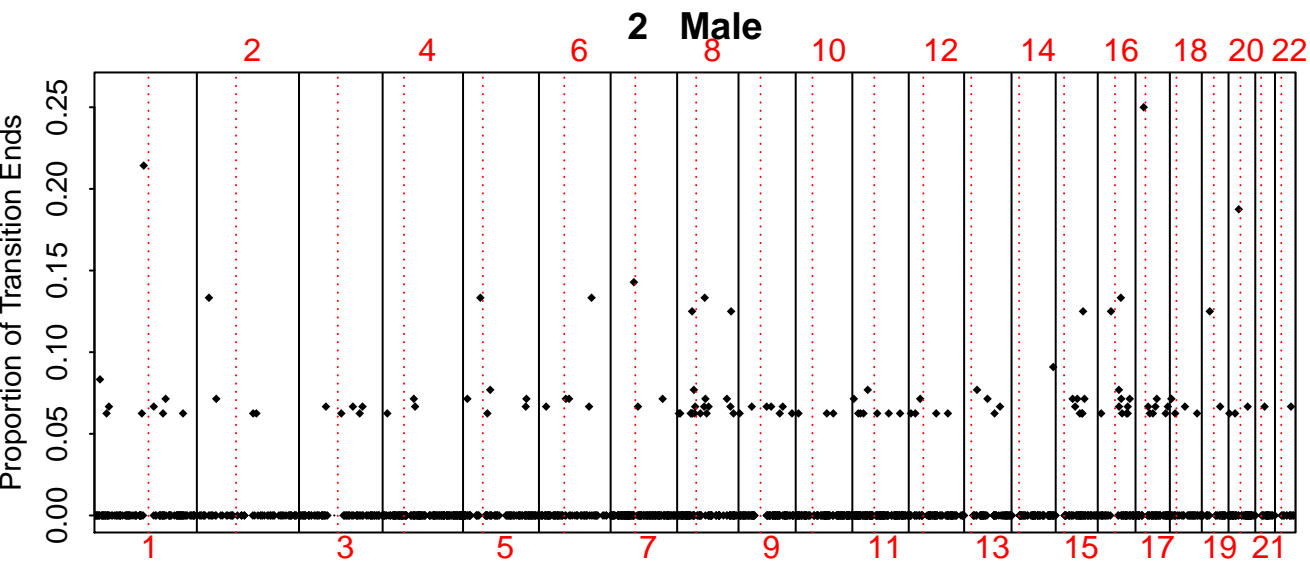
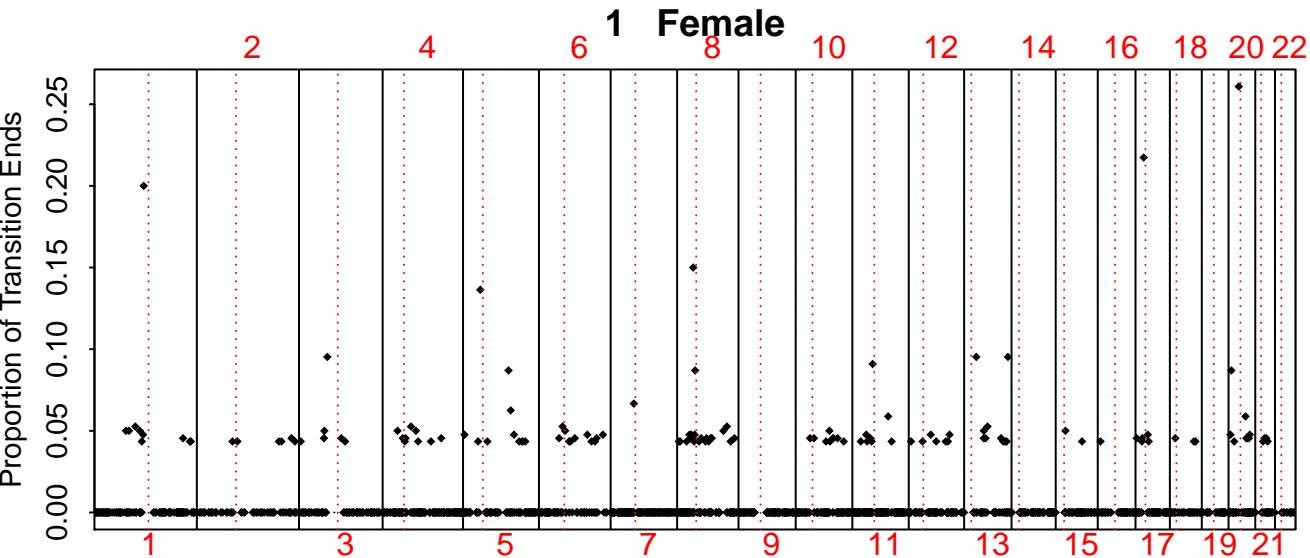
Fraction of Genome Lost 0.0300104



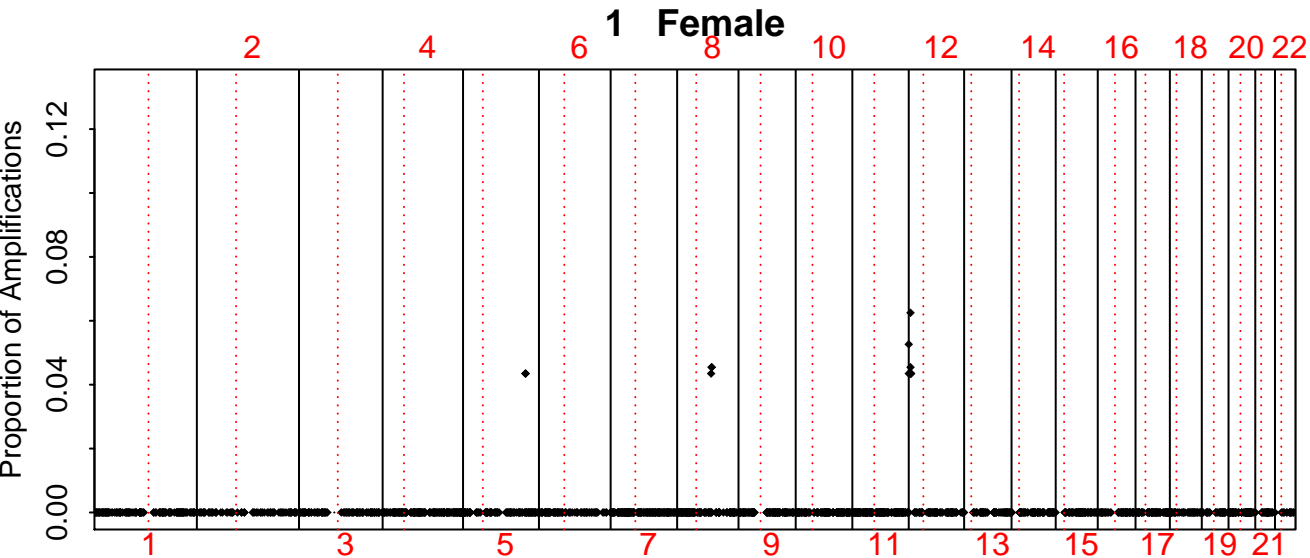
Fraction of Genome Altered 0.0240951



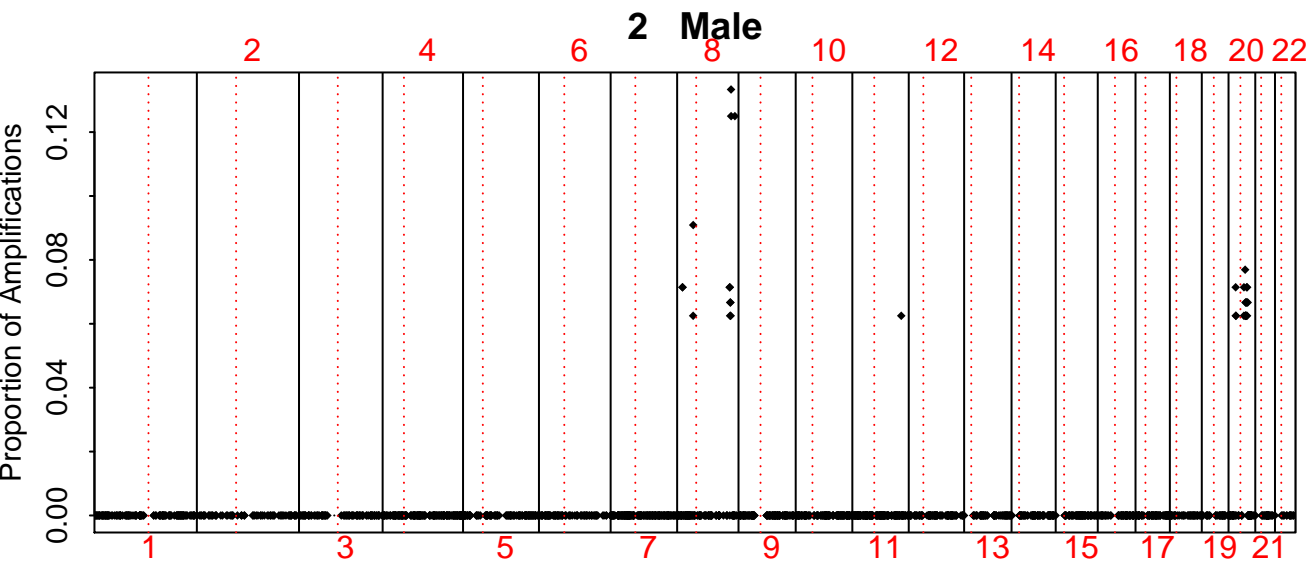




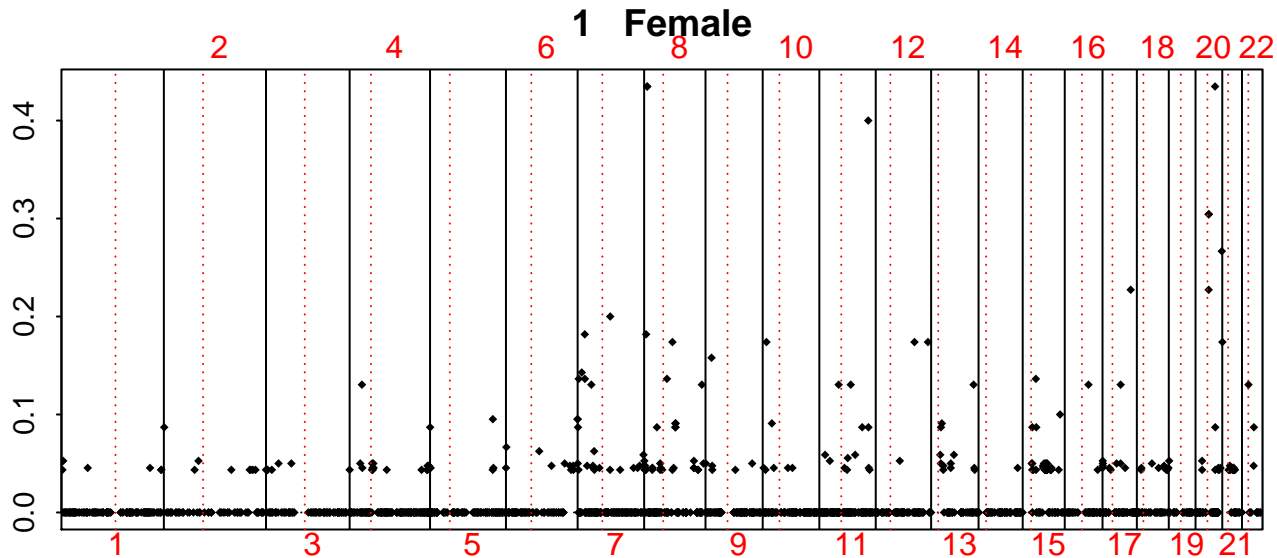
Proportion of Amplifications



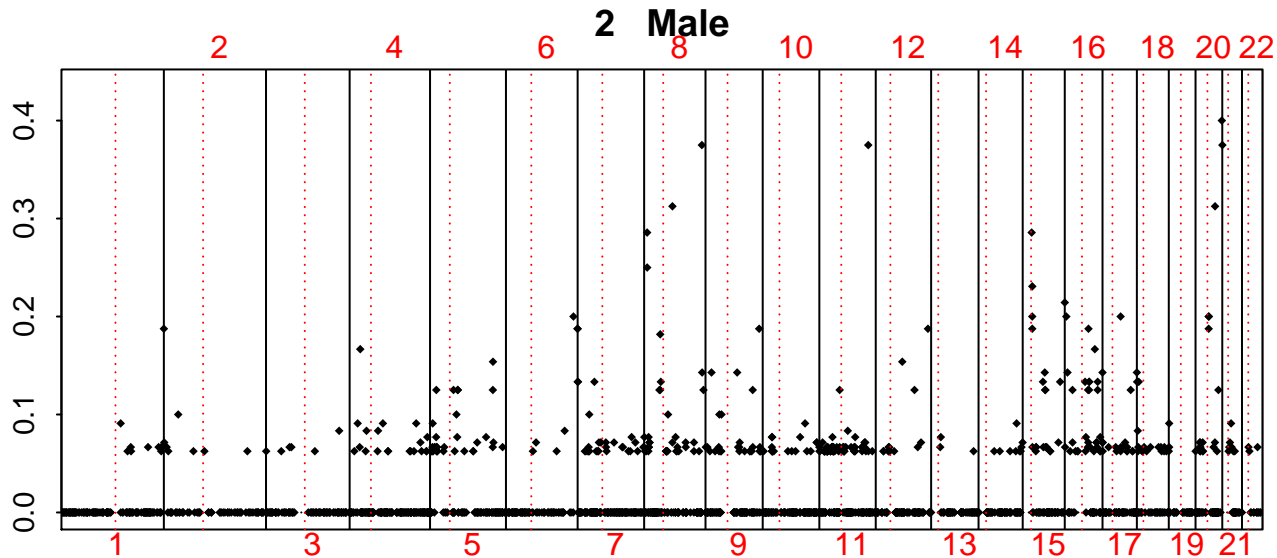
Proportion of Amplifications

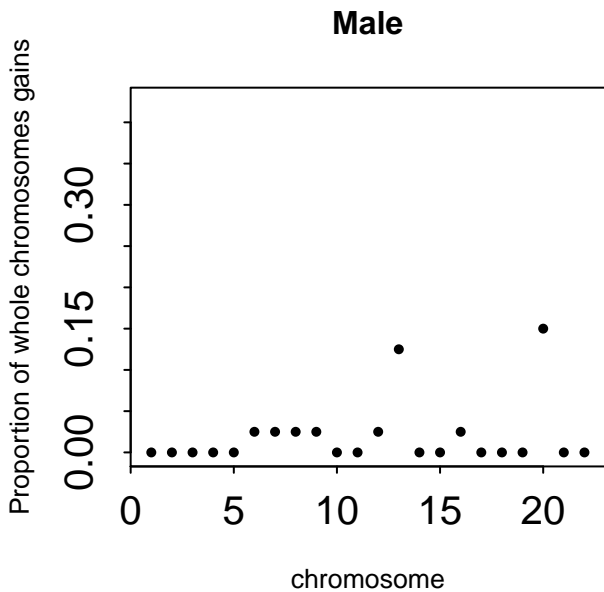
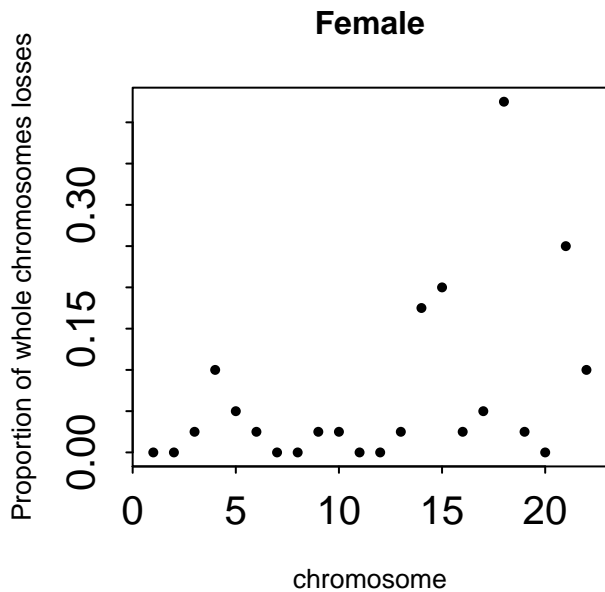
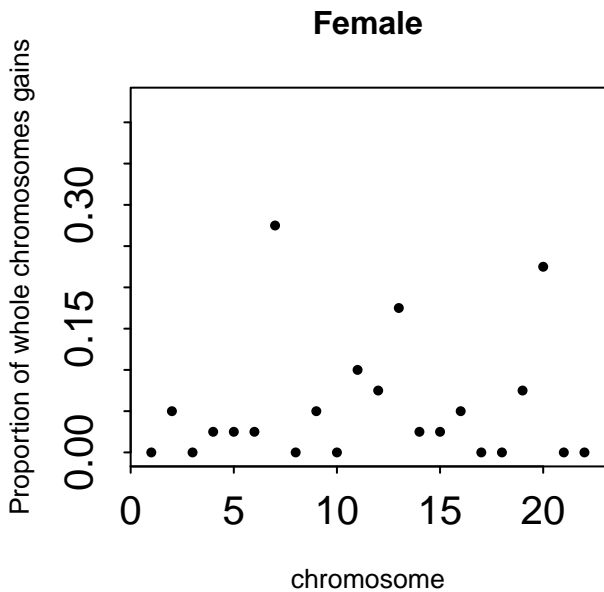


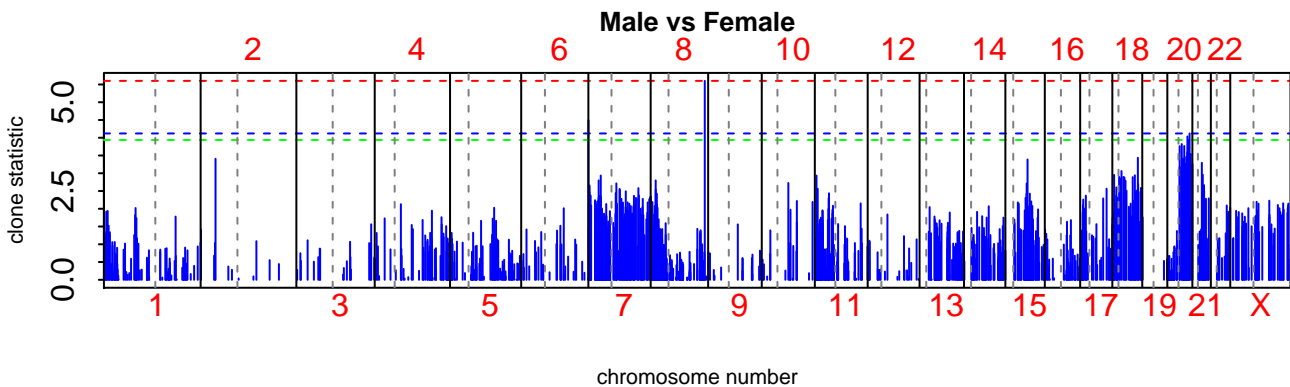
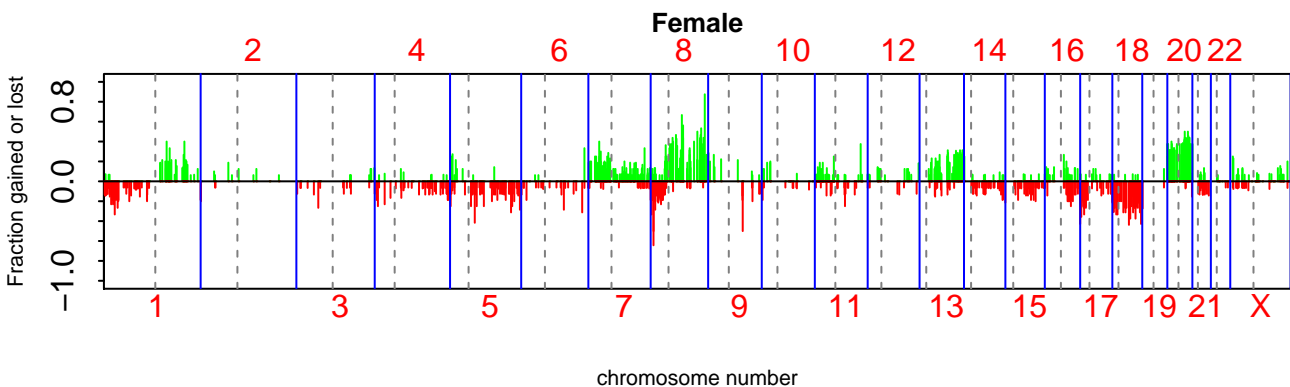
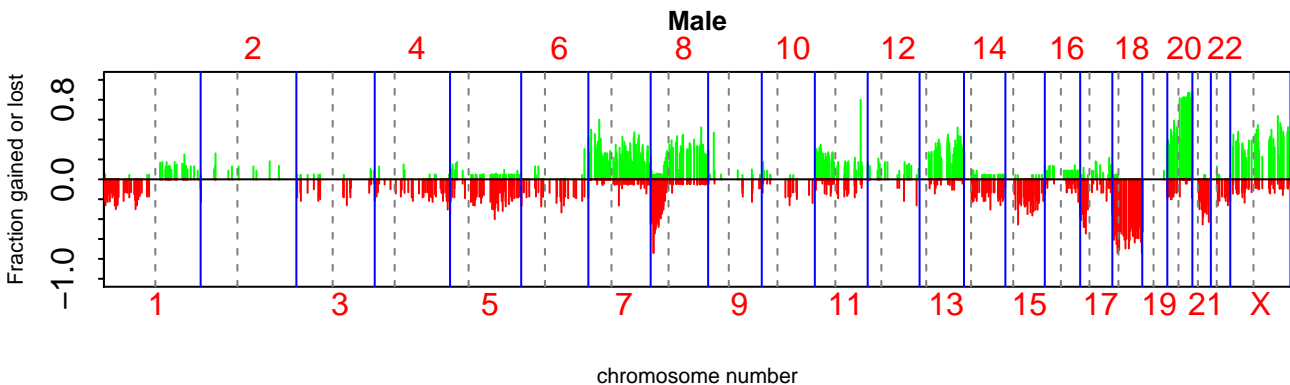
Proportion of Aberrations

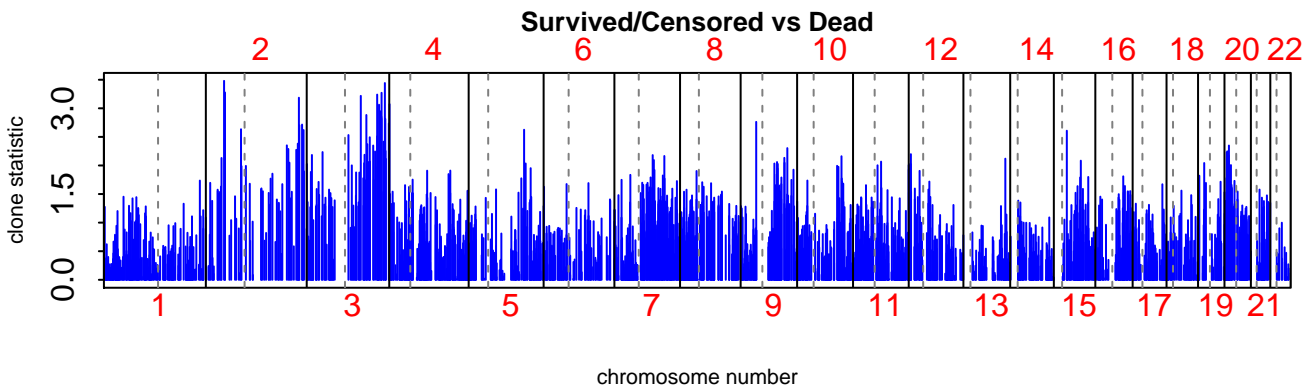
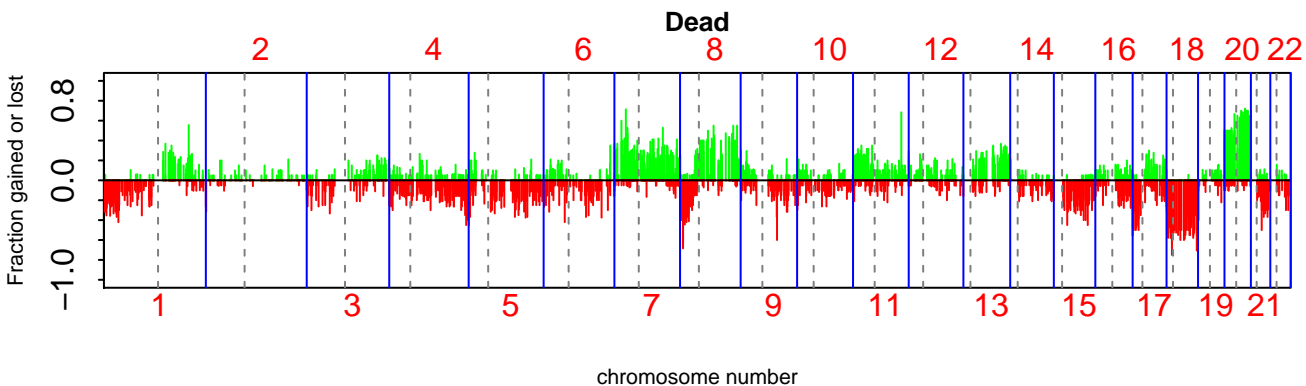
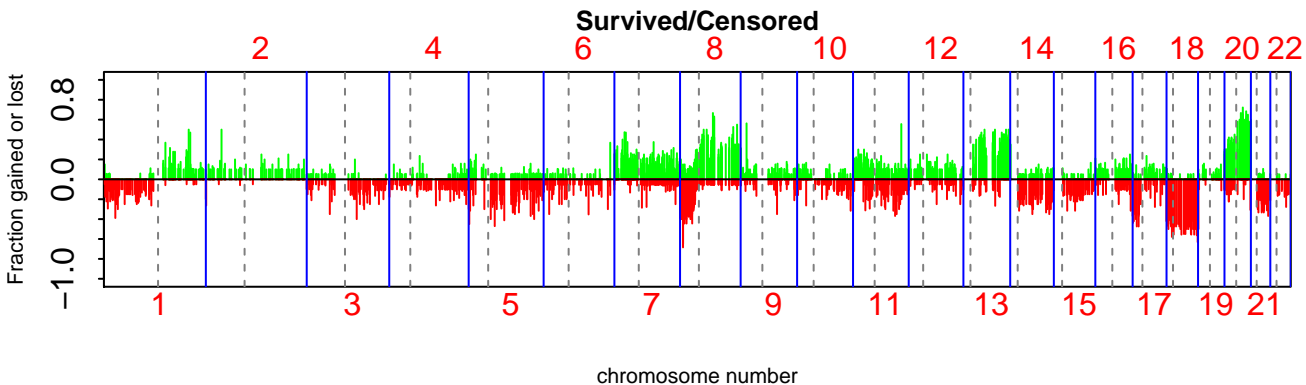


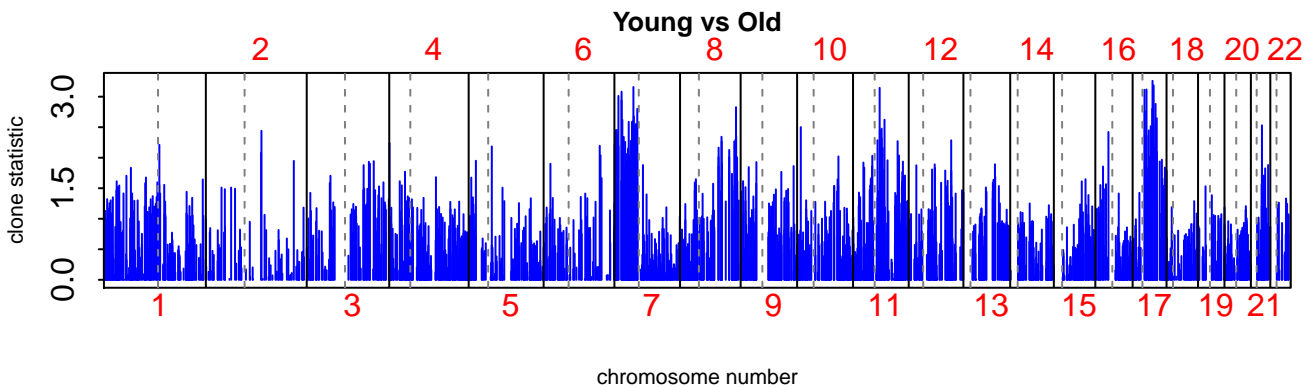
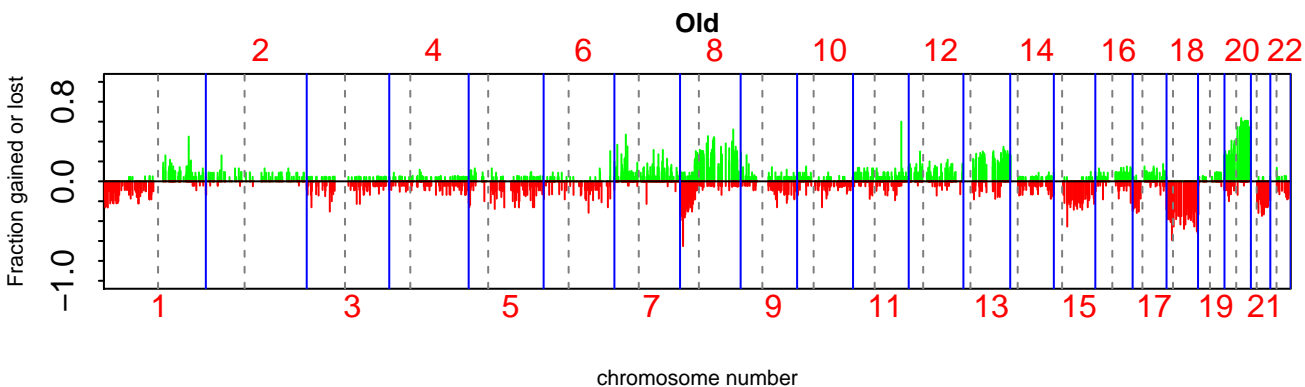
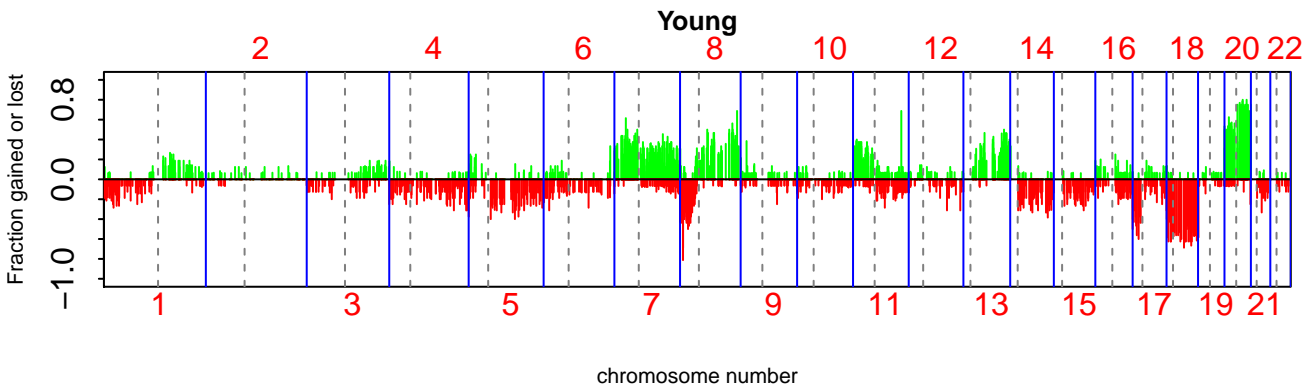
Proportion of Aberrations







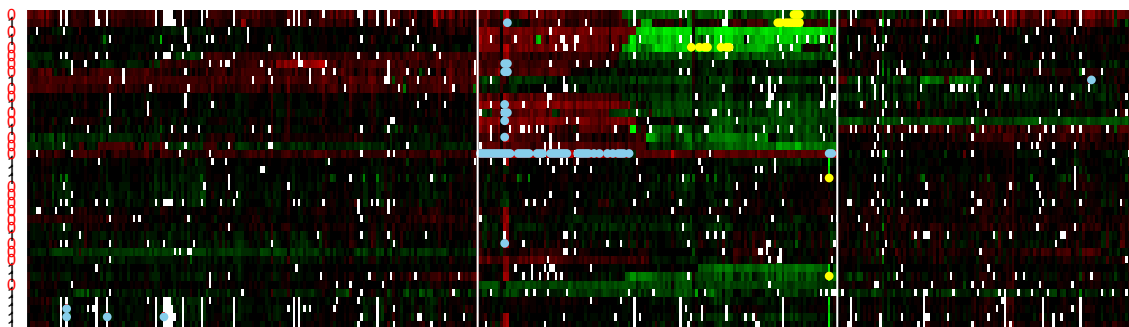




sample

Female
Male

8

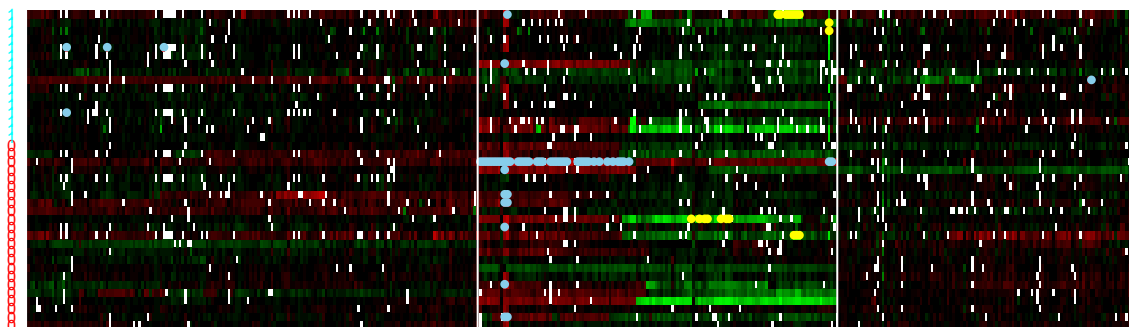


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sprocR210.0x
sprocR146.0x
sprocR170.0x
sprocR36.0x
sprocR135.0x
sprocR63.0x
sprocR169.0x
sprocR200.0x
sprocR152.0x
sprocR154.0x
sprocR161.0x
sprocR395.0x
sprocR340.0x
sprocR112.0x
sprocR183.0x
sprocR196.0x
sprocR100.0x
sprocR359.0x
sprocR193.0x
sprocR174.0x
sprocR218.0x
sprocR212.0x
sprocR232.0x

clone

Female
Male

8



sprocR210.0x
sprocR124.0x
sprocR36.0x
sprocR218.0x
sprocR212.0x
sprocR353.0x
sprocR174.0x
sprocR146.0x
sprocR245.0x
sprocR75.0x
sprocR227.0x
sprocR395.0x
sprocR73.0x
sprocR100.0x
sprocR148.0x
sprocR240.0x
sprocR196.0x
sprocR154.0x
sprocR112.0x
sprocR77.0x

sample

clone