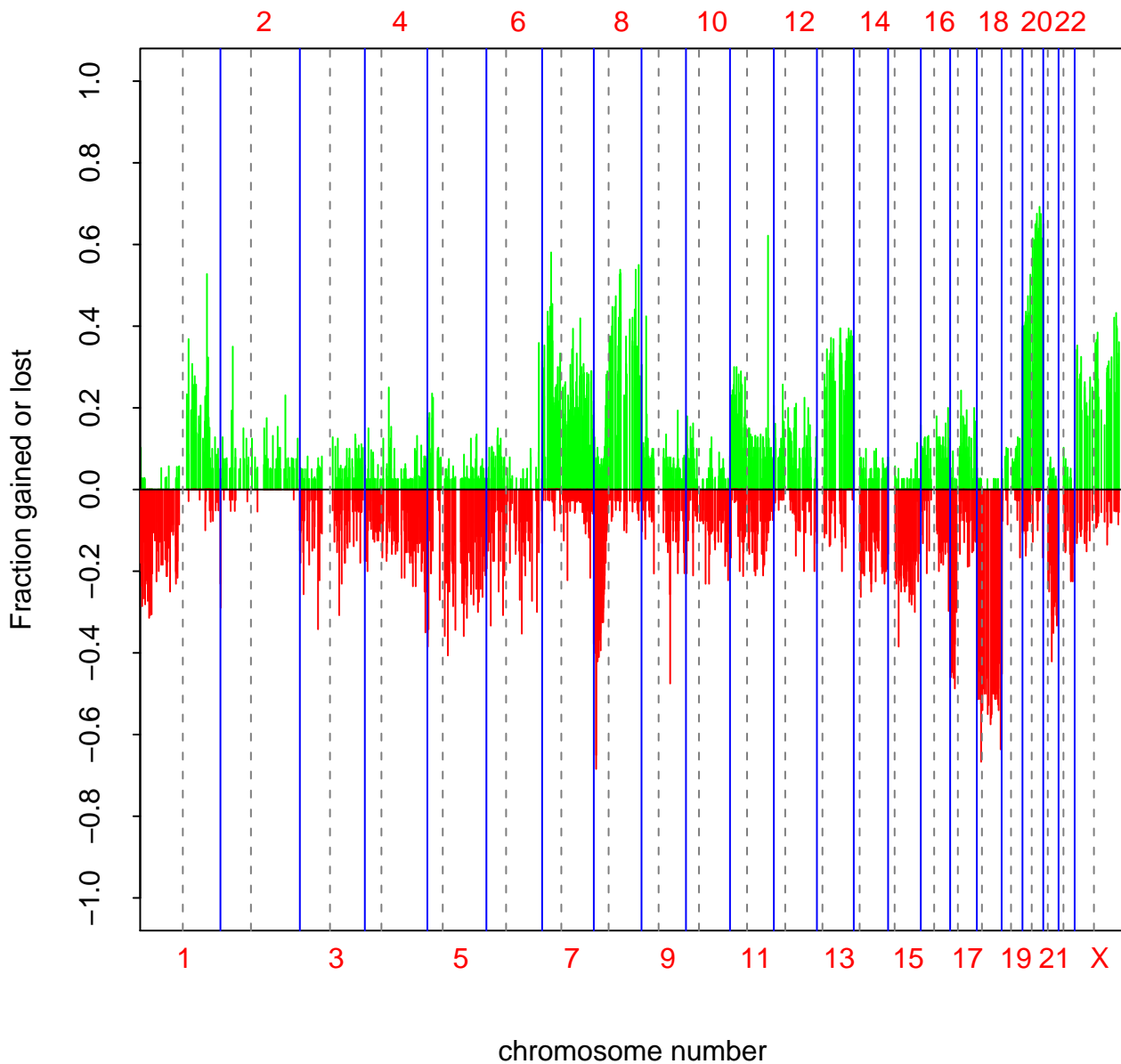
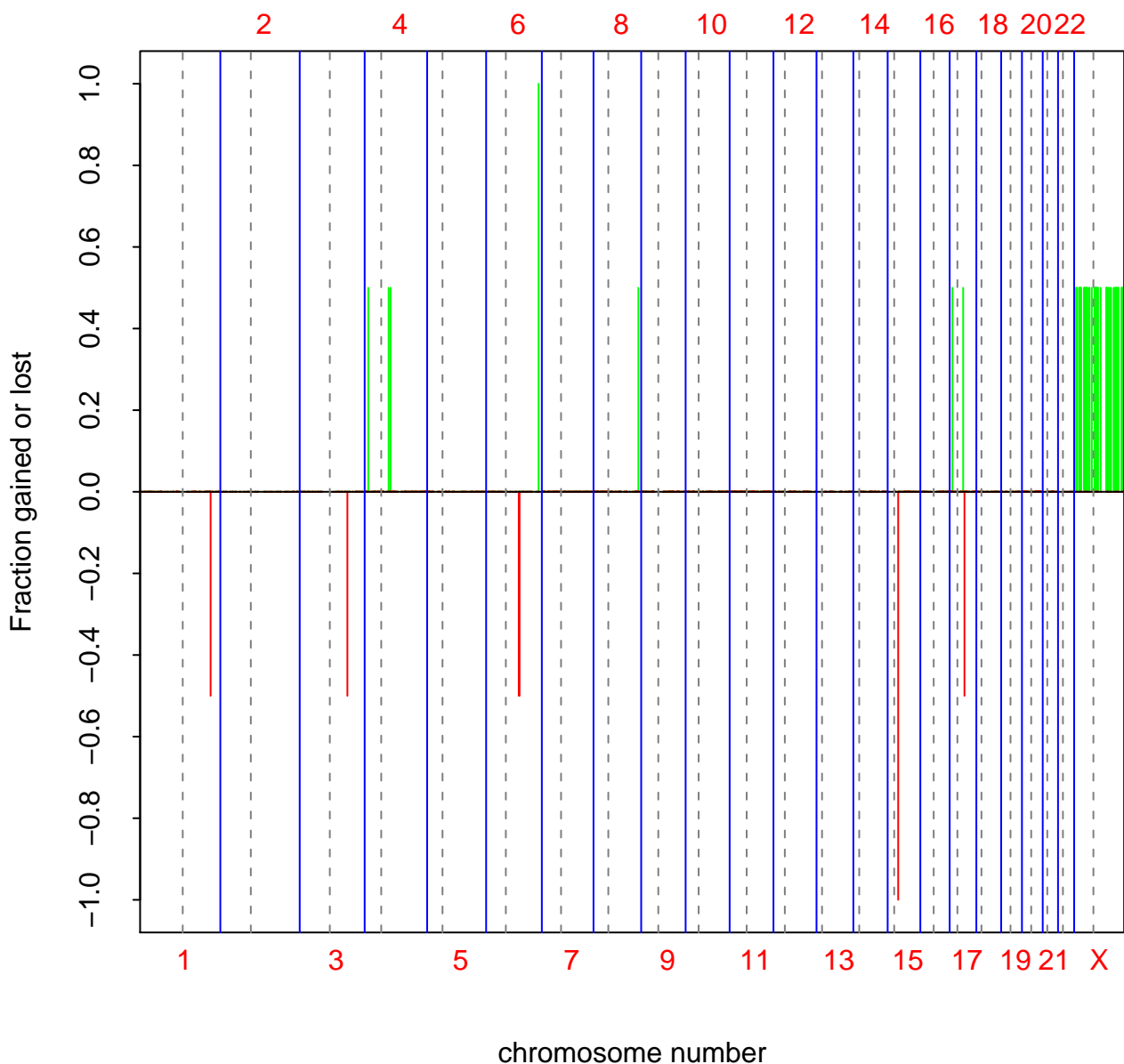


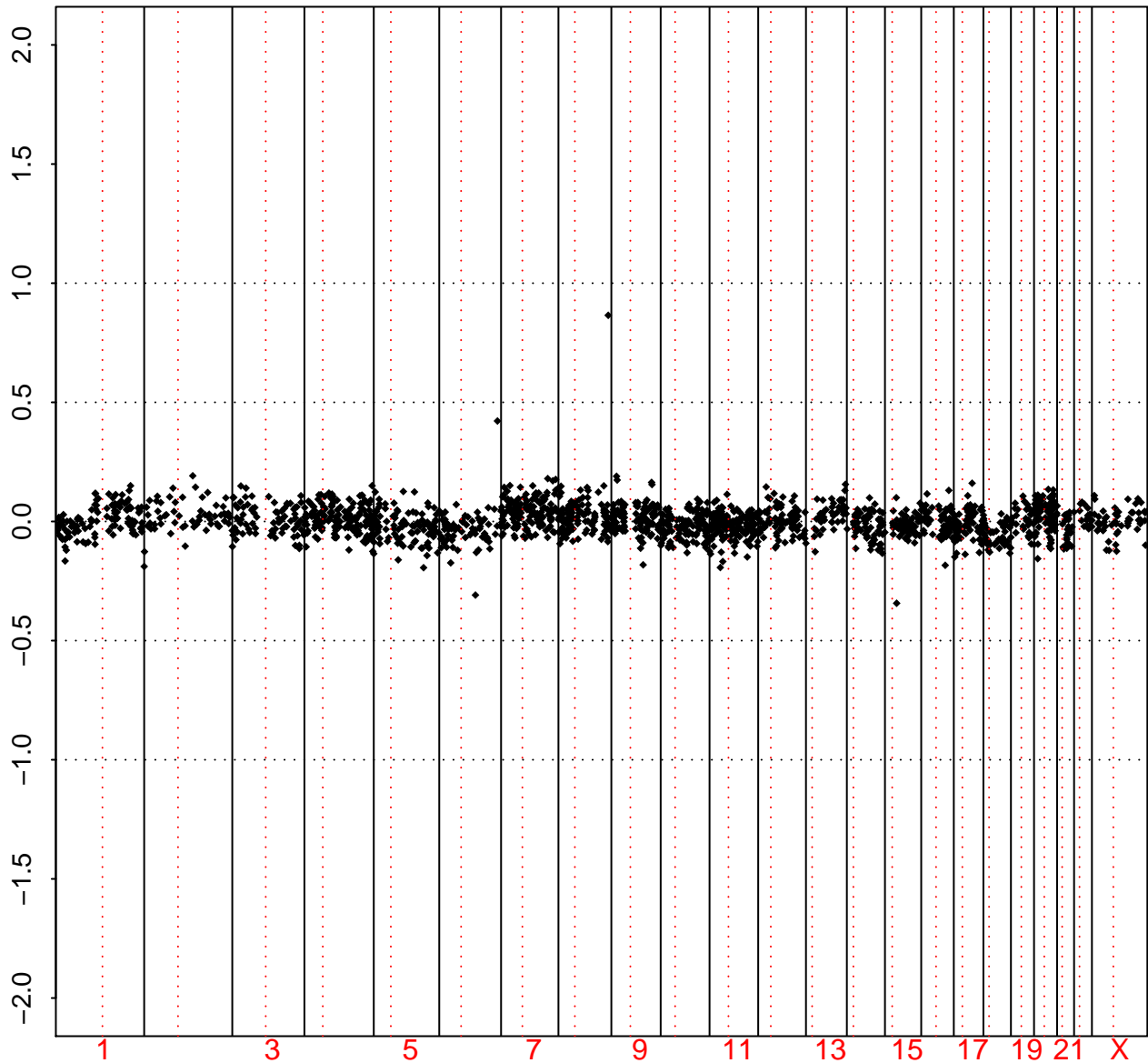
# All Samples



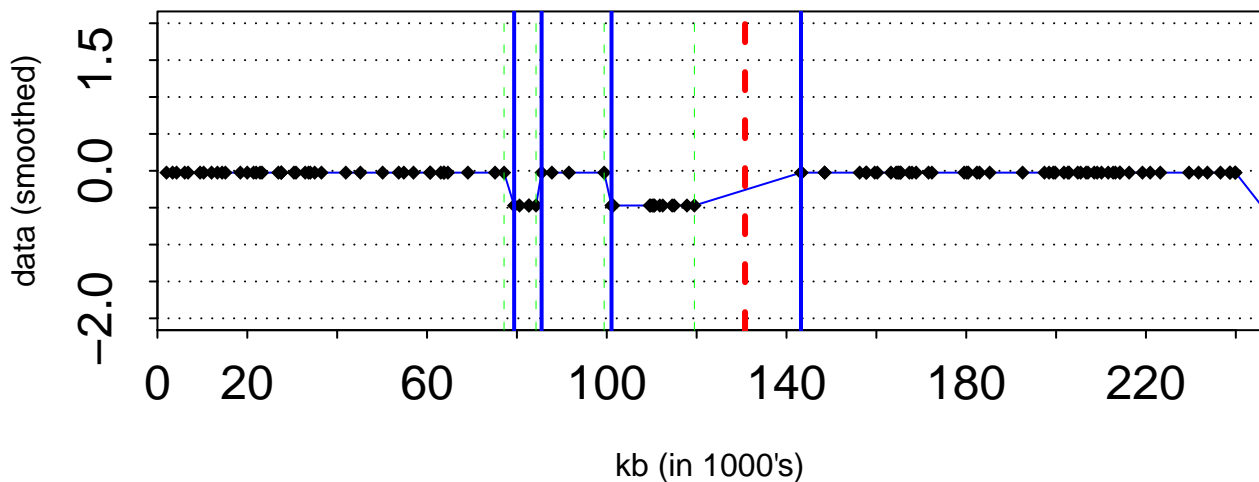
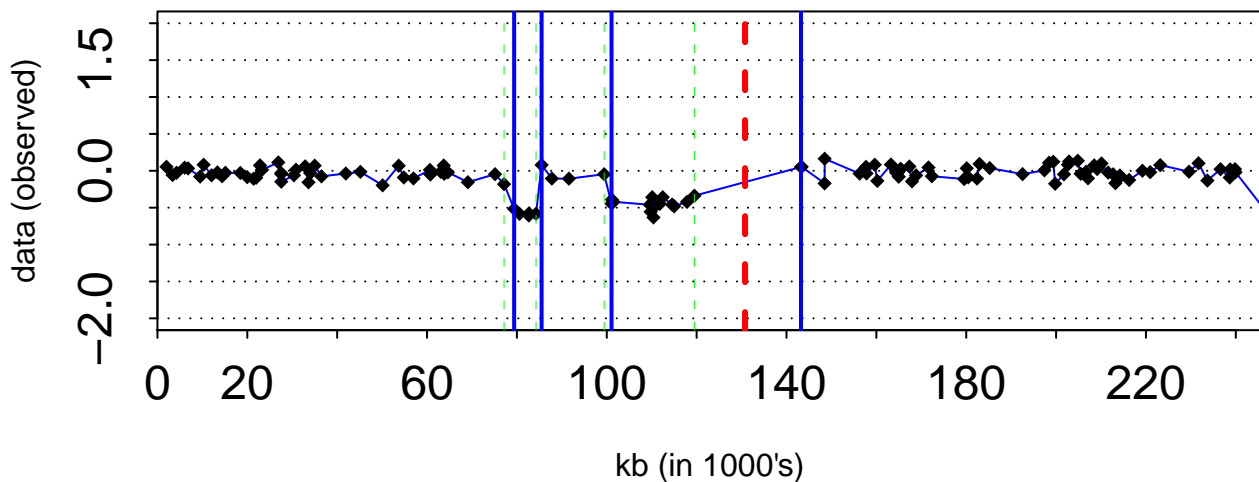
# All Samples



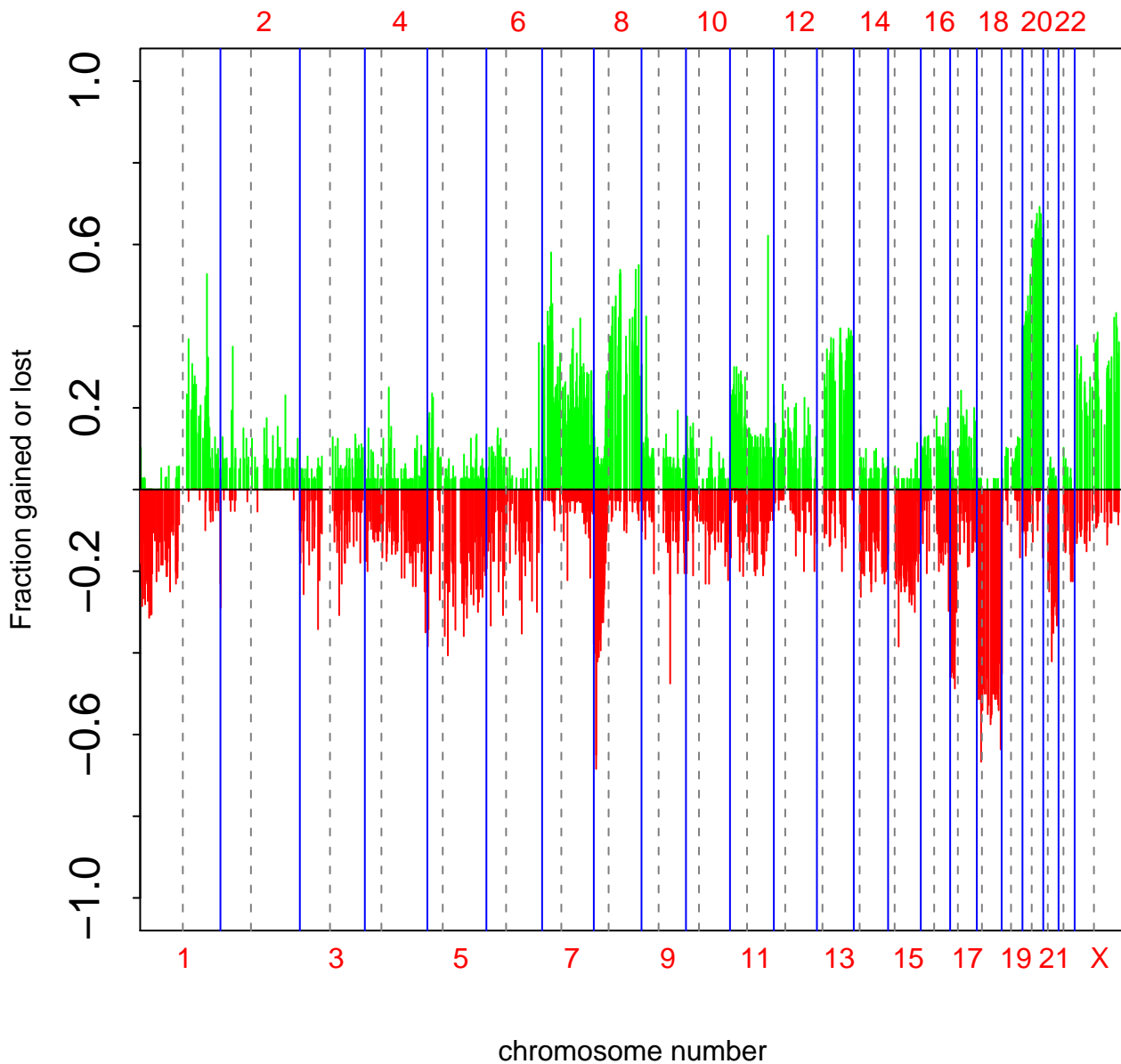
Log2Ratio

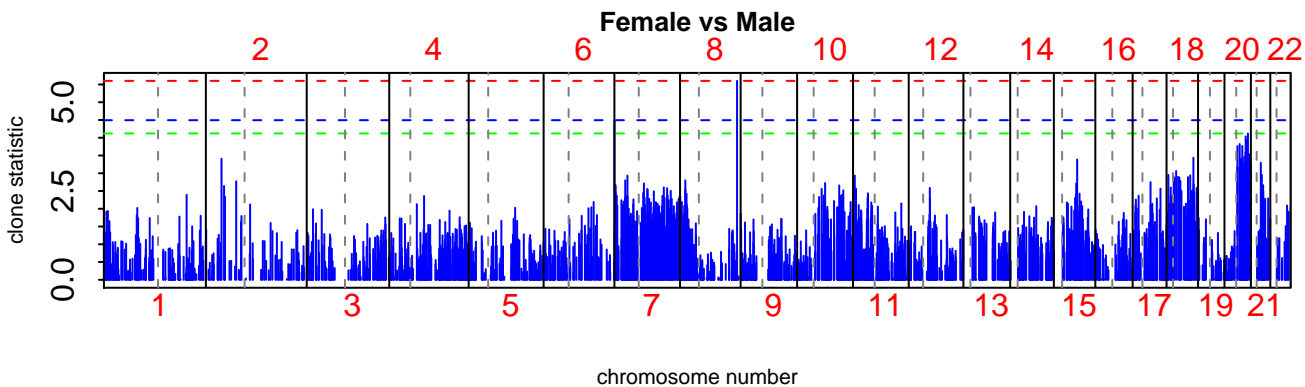
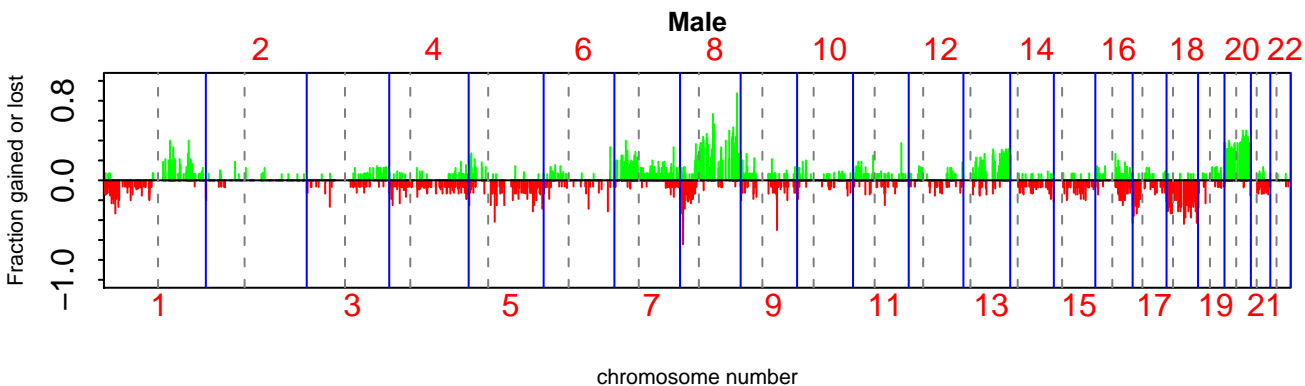
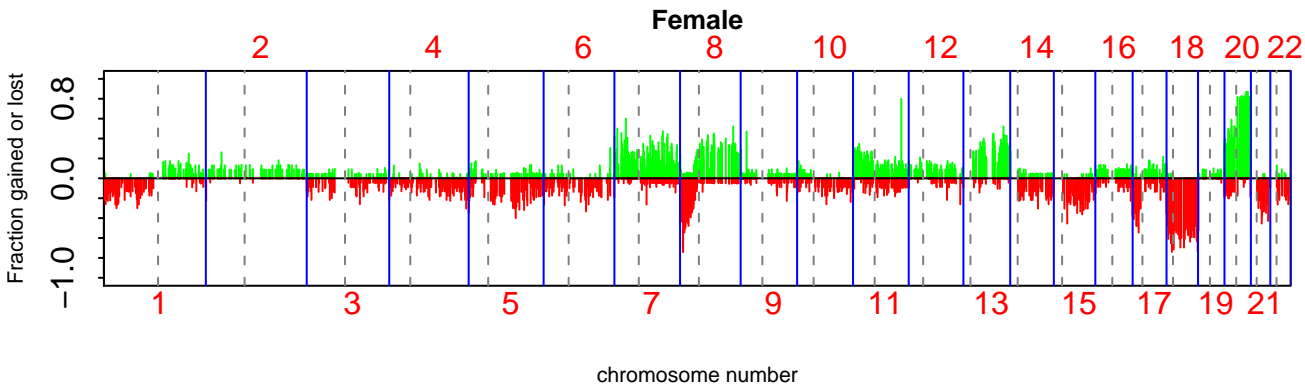


# Sample 1 sprocCR31.txt – Chr 1 Number of states 2

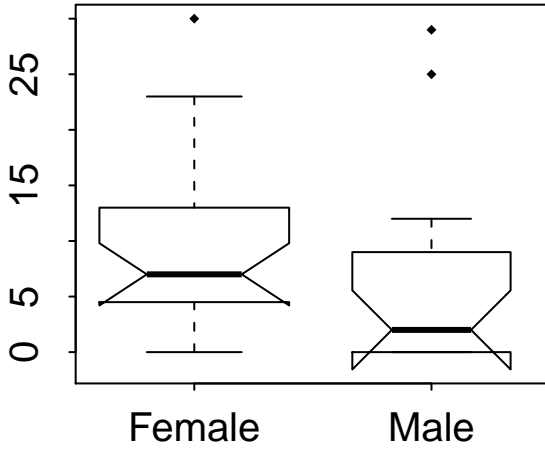


# All Samples

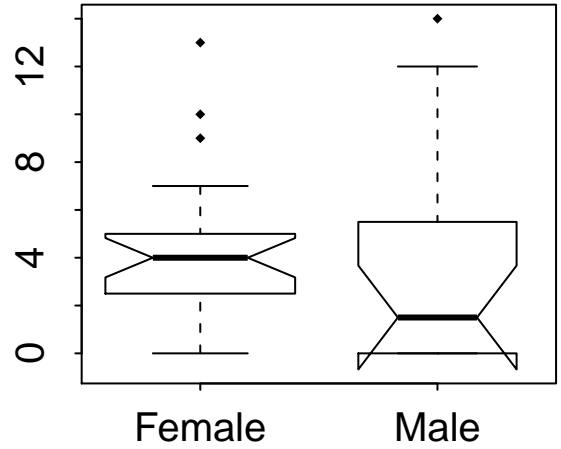




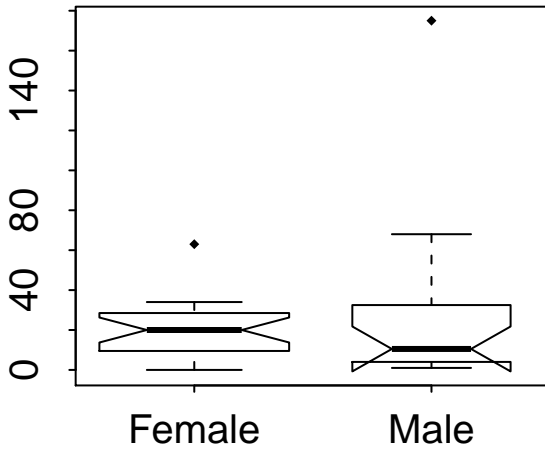
Number of Transitions 0.0950684



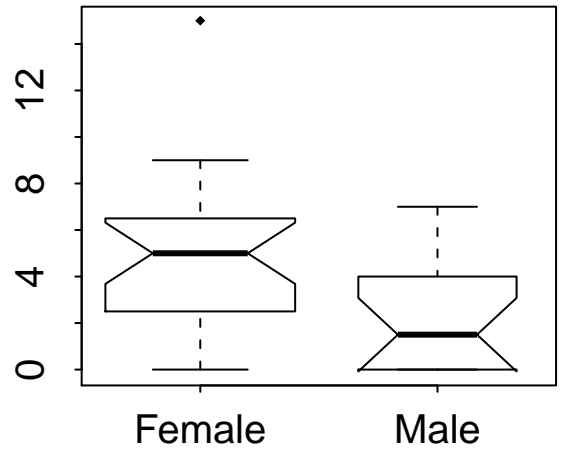
Number of Chrom containing Transitions 0.174915



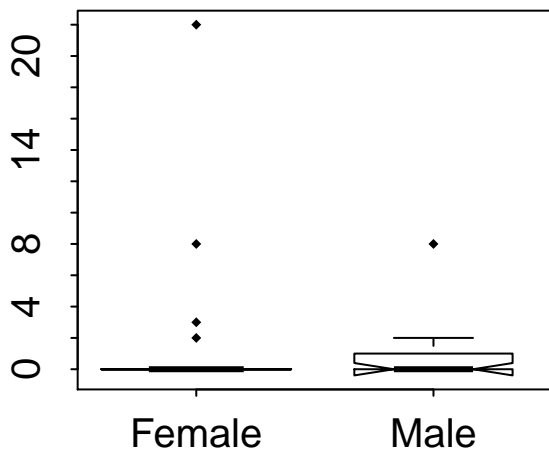
Number of Aberrations 0.841381



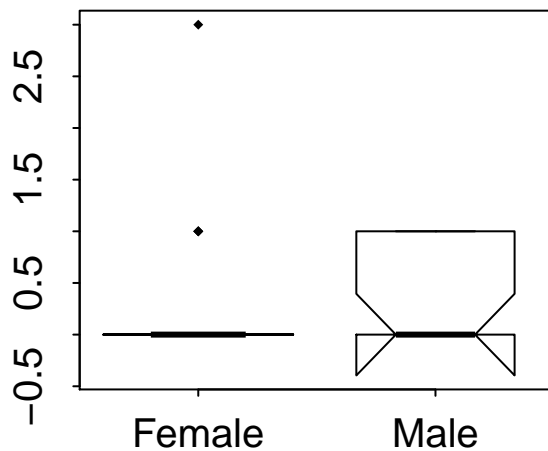
Number of Whole Chrom Changes 0.0174111



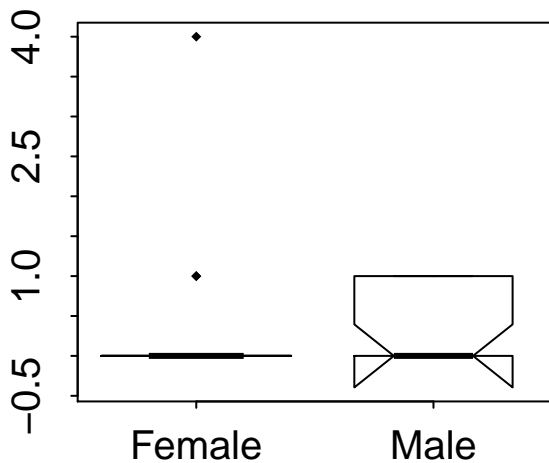
Number of Amplifications 0.462205



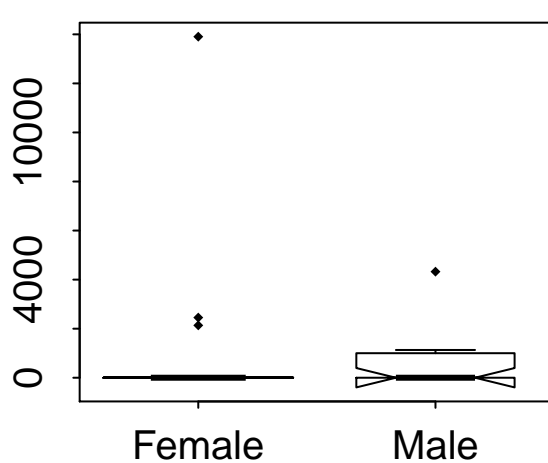
Number of Chrom containing Amplifications 0.369971



Number of Amplicons 0.207136

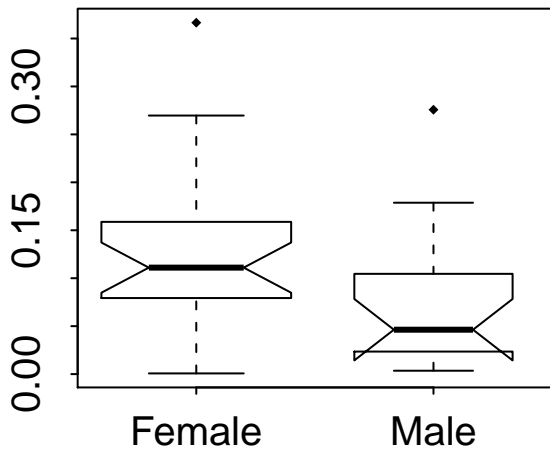


Amount of Genome Amplified 0.257209

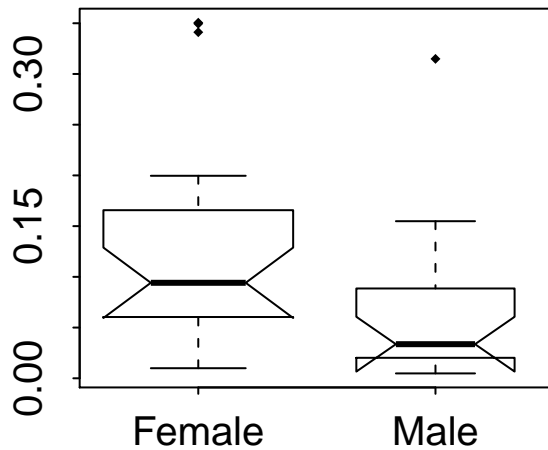




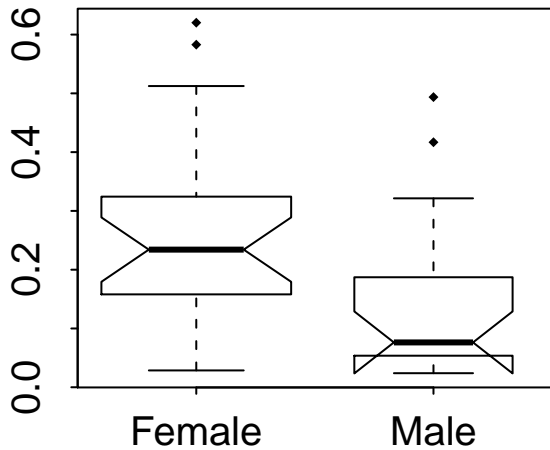
Fraction of Genome Gained 0.0300104

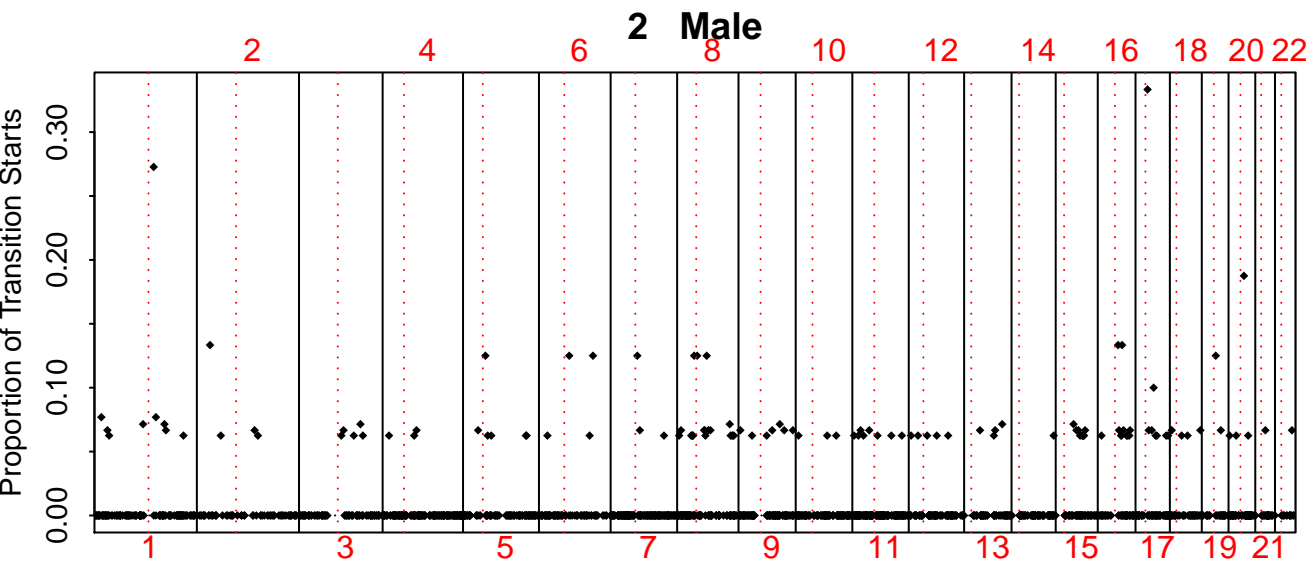
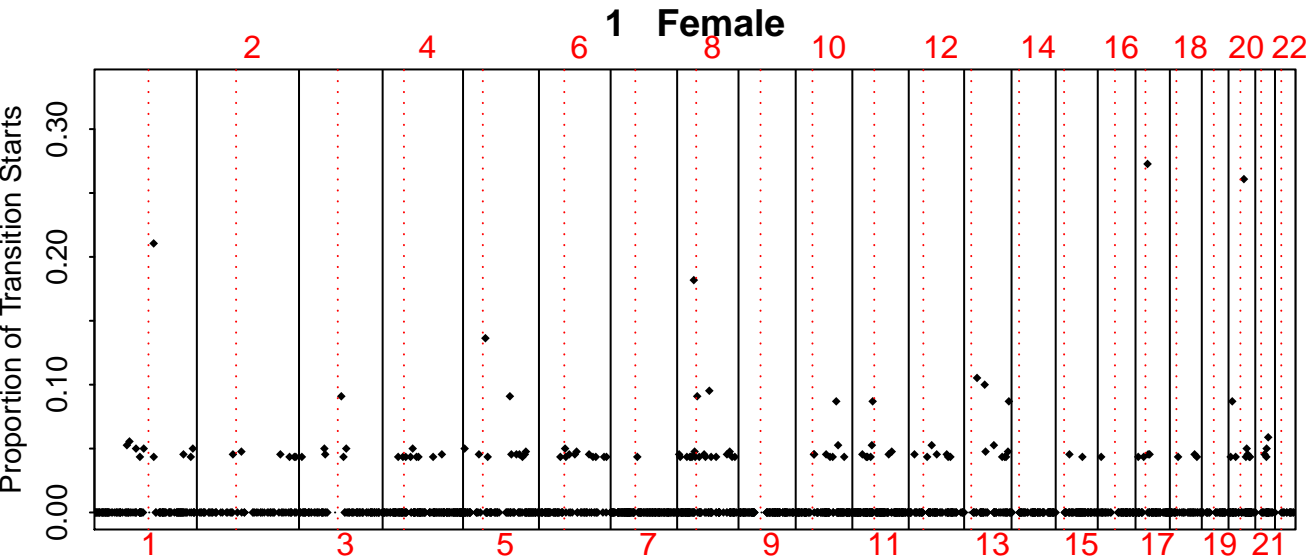


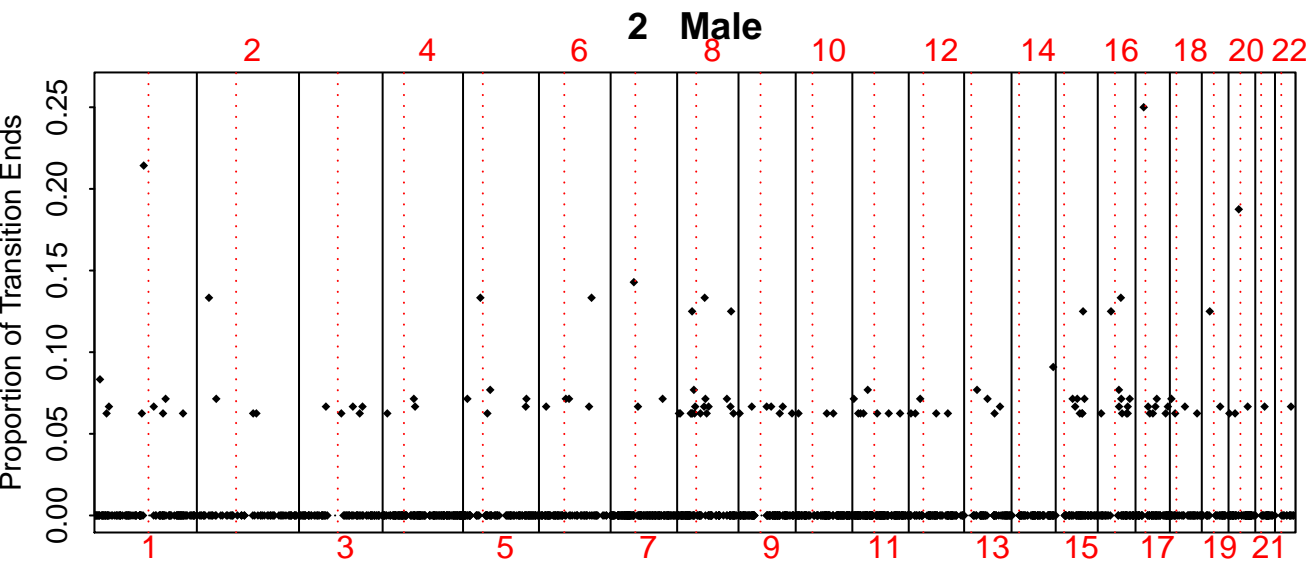
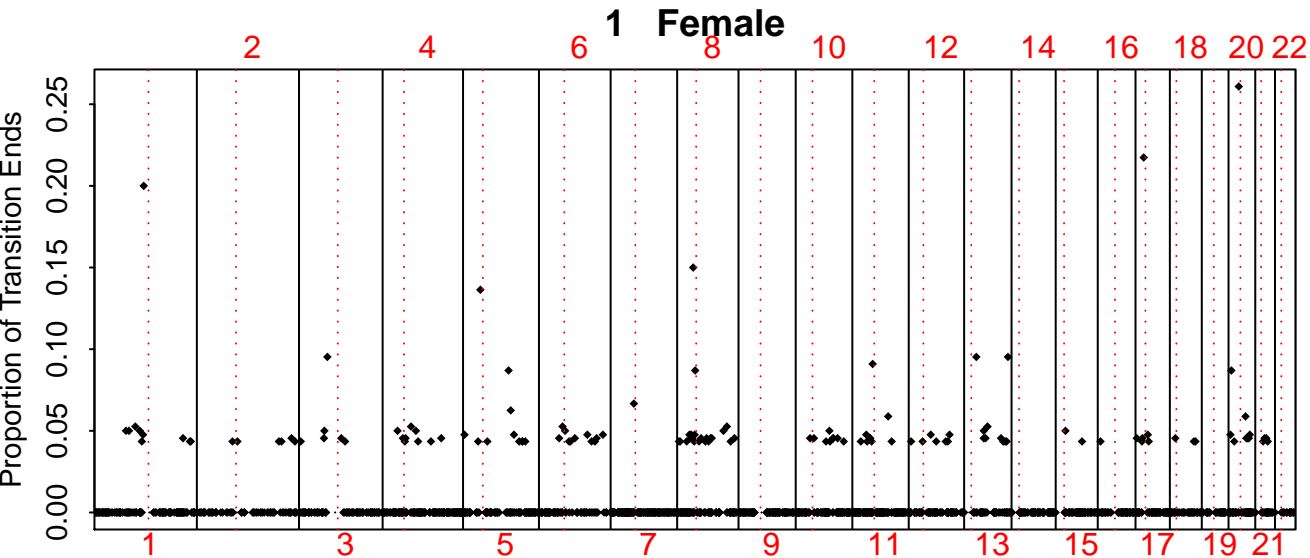
Fraction of Genome Lost 0.0300104



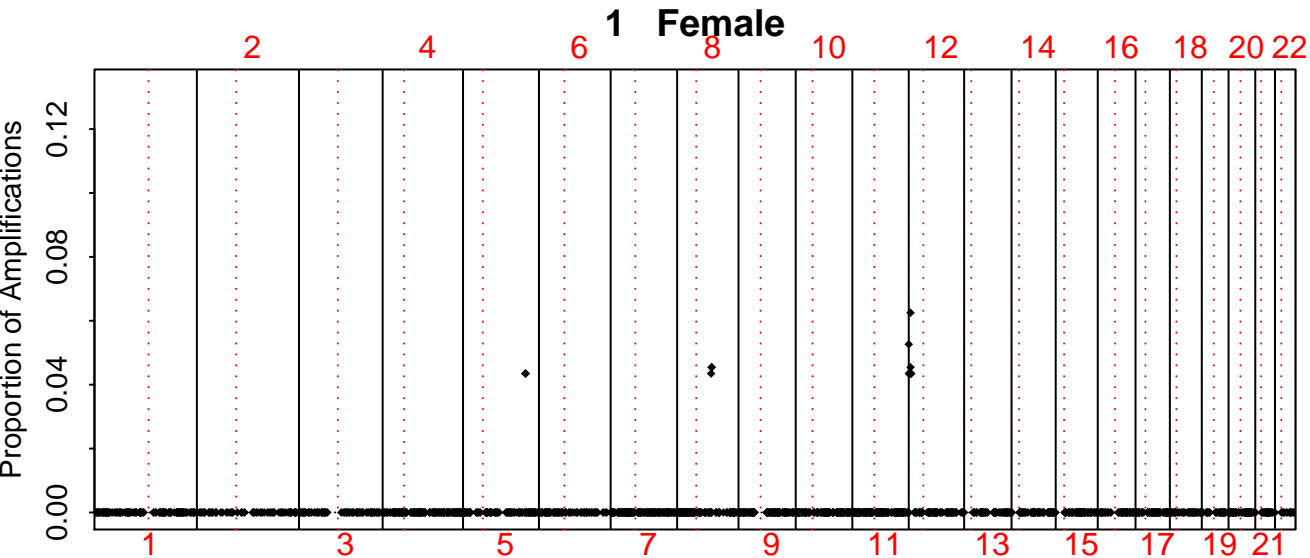
Fraction of Genome Altered 0.0240951



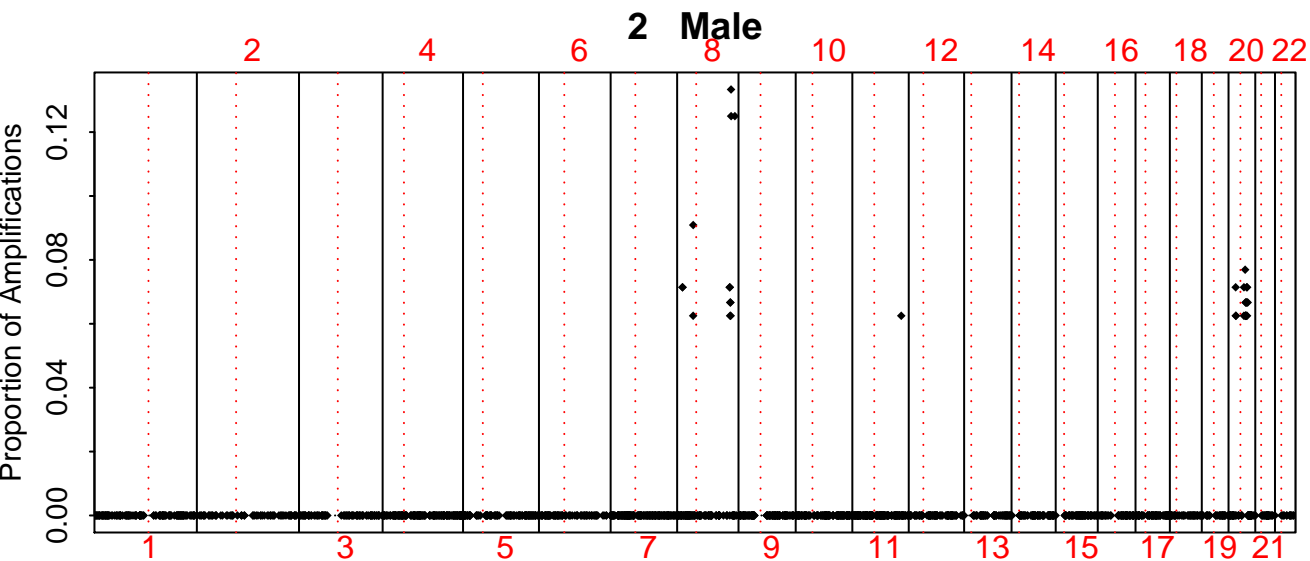




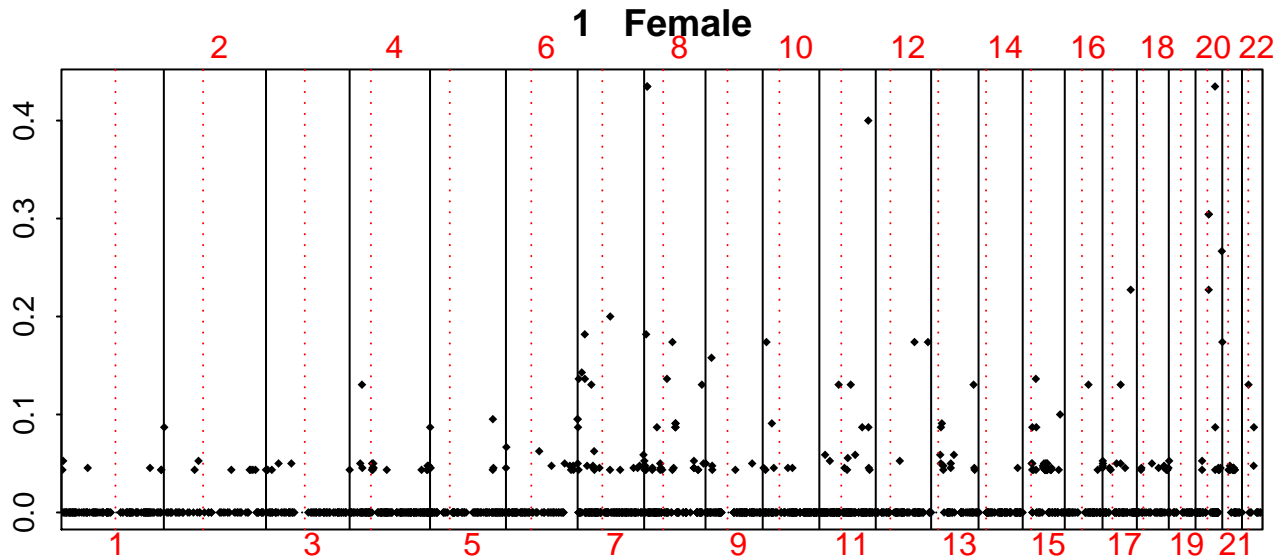
Proportion of Amplifications



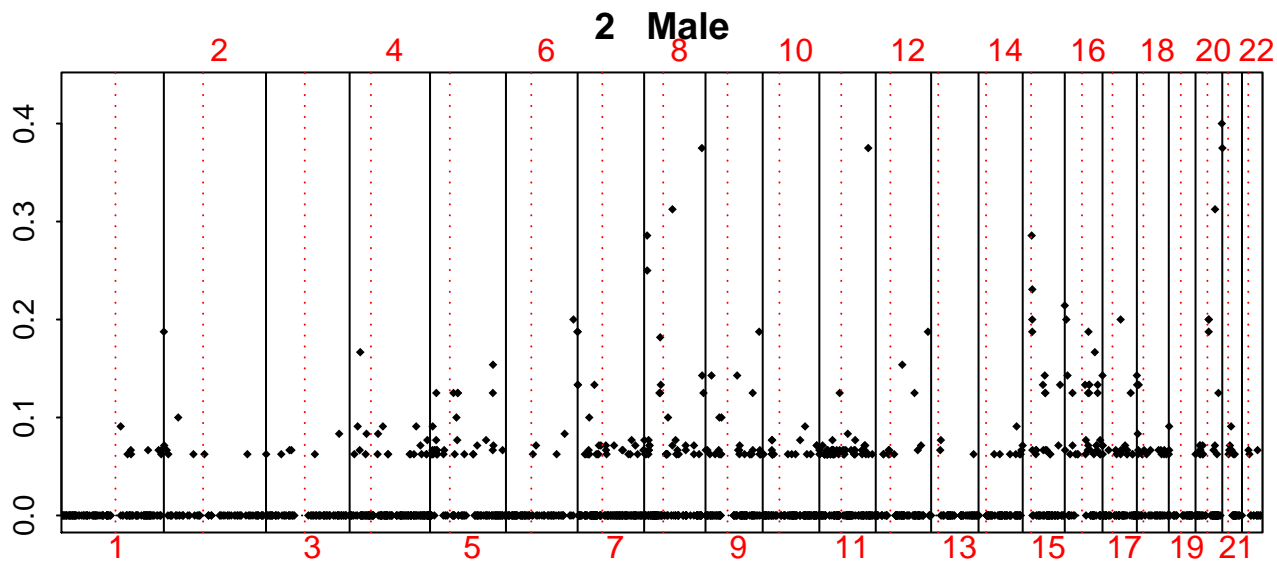
Proportion of Amplifications



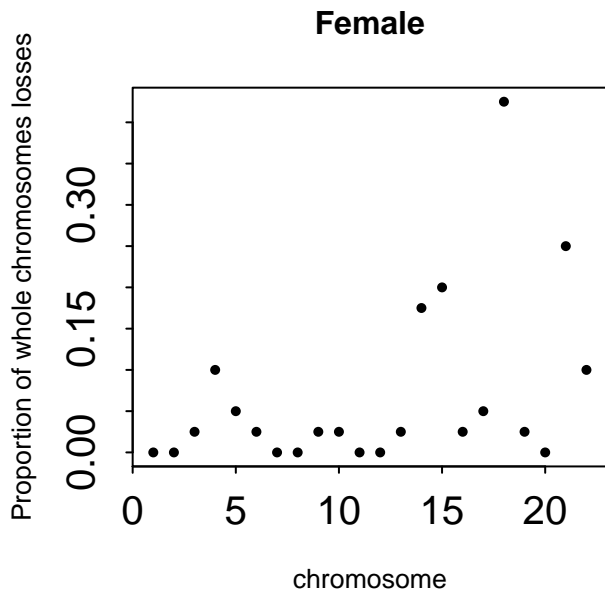
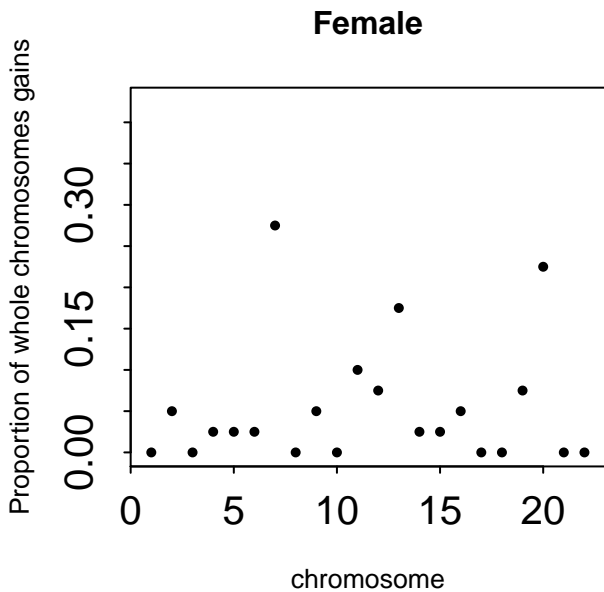
Proportion of Aberrations

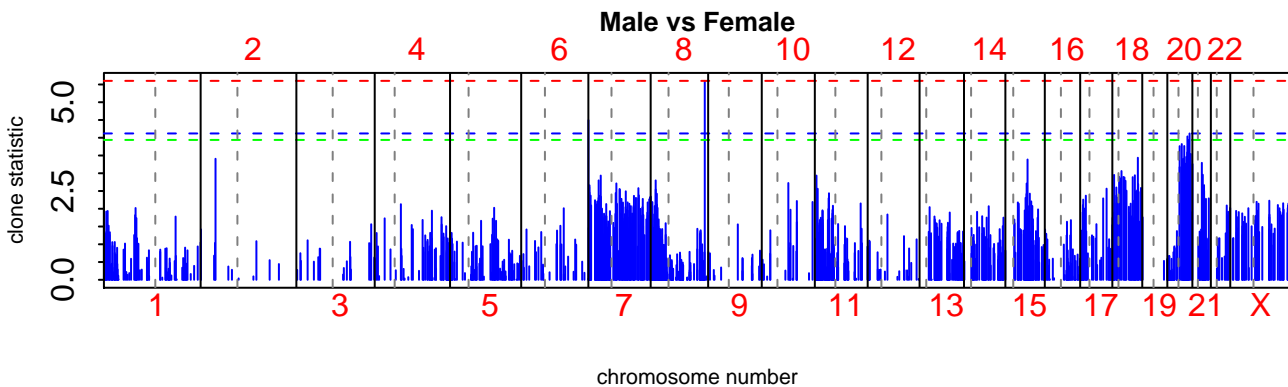
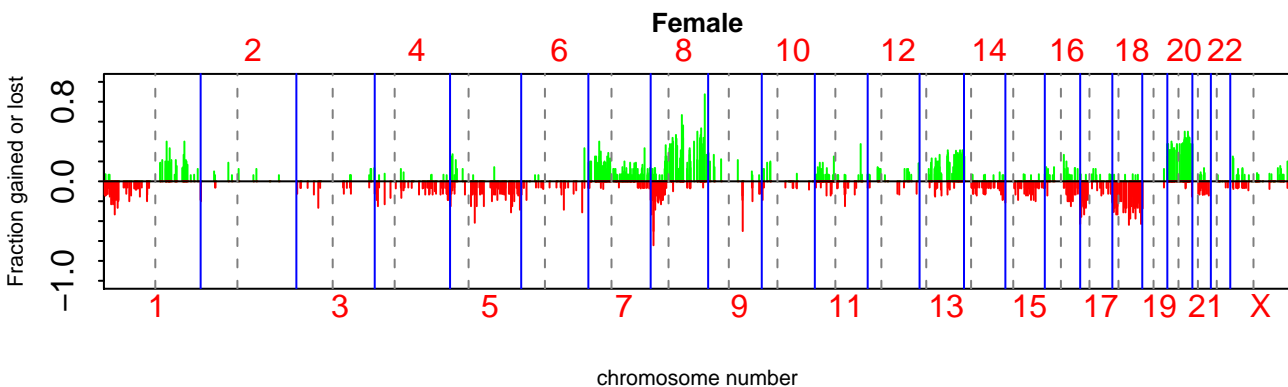
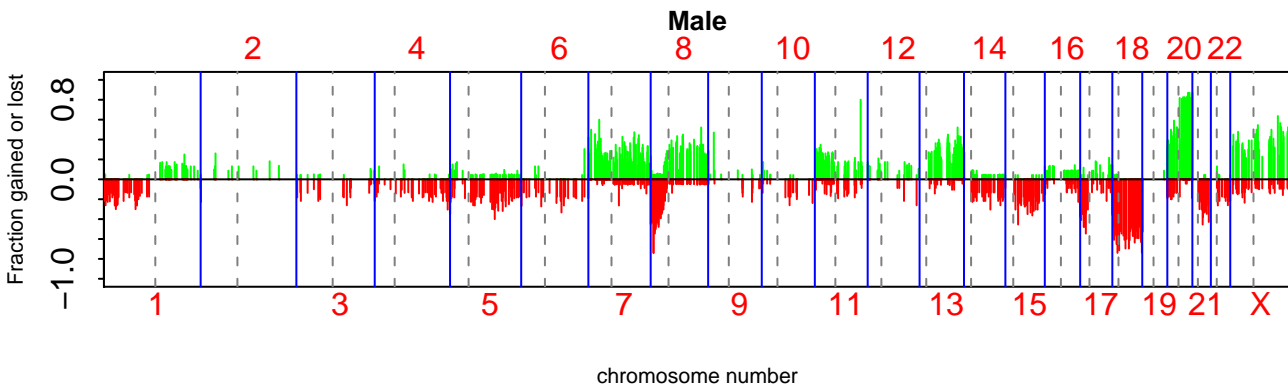


Proportion of Aberrations

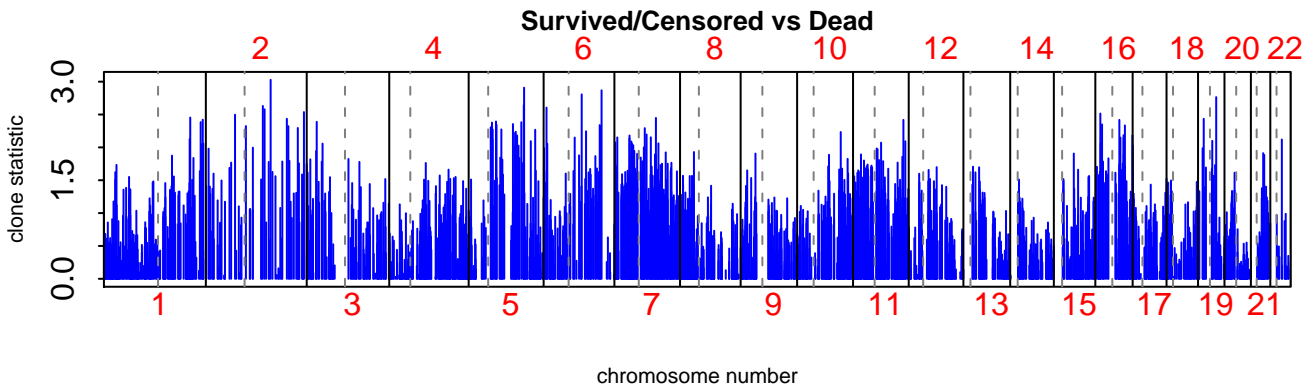
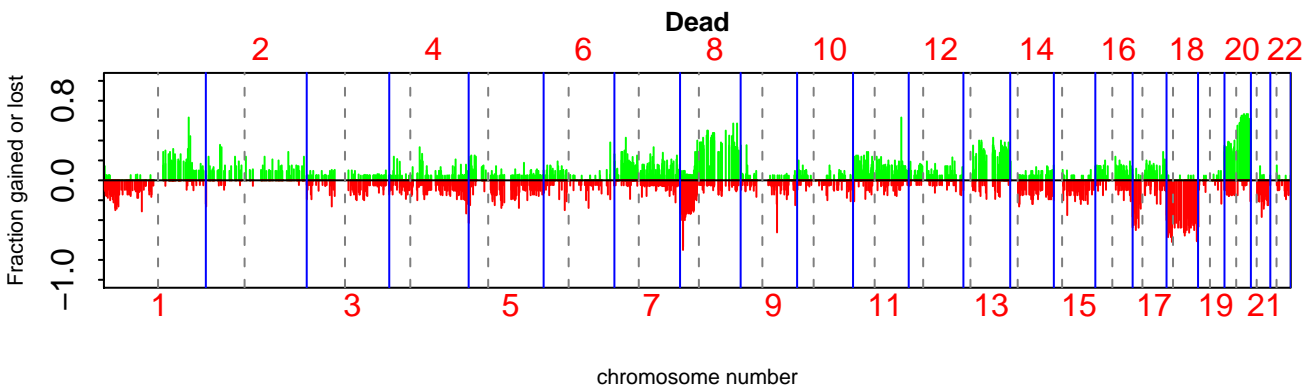
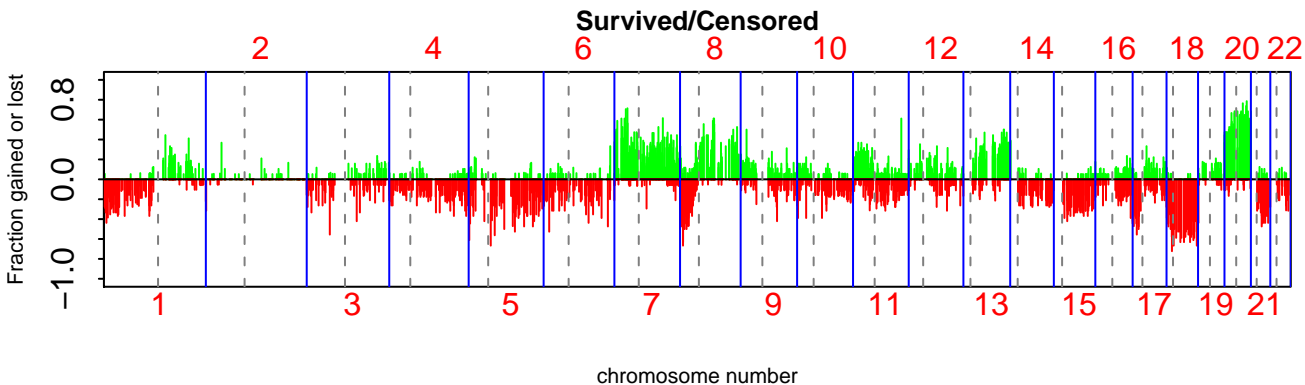


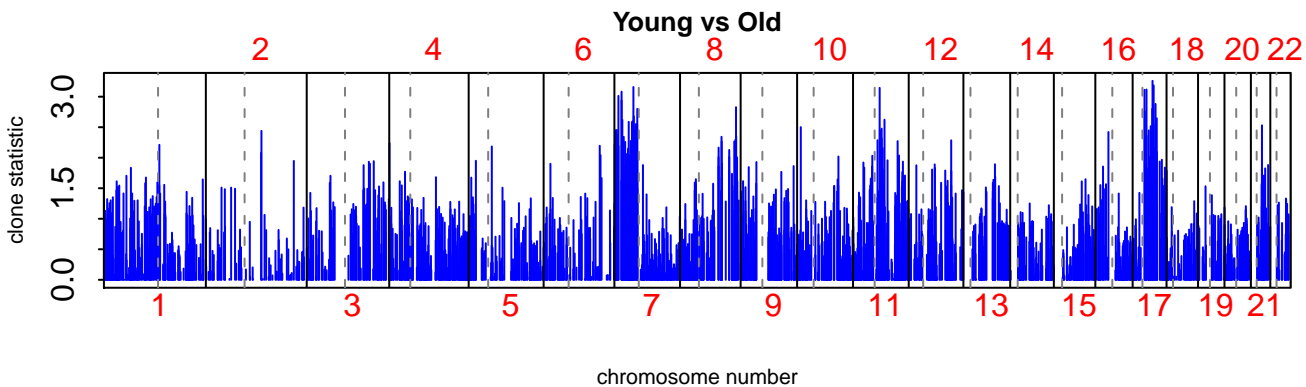
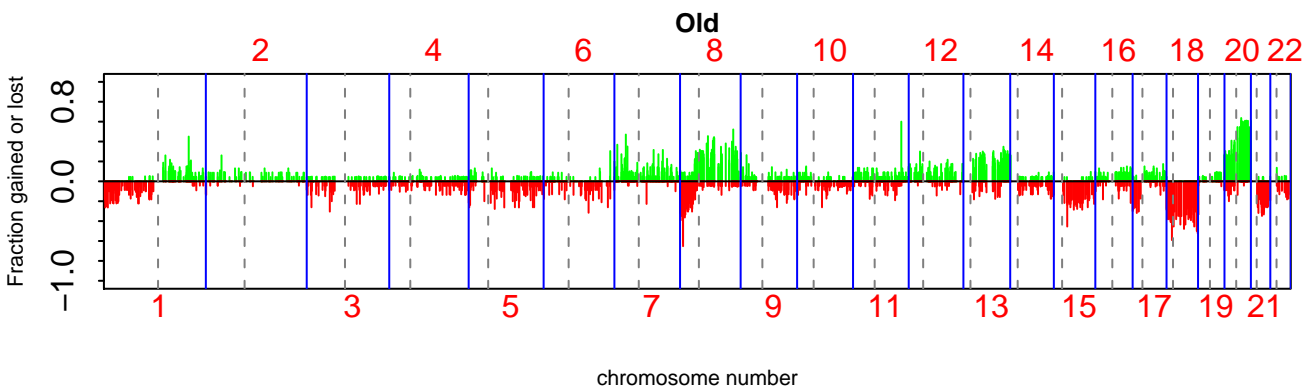
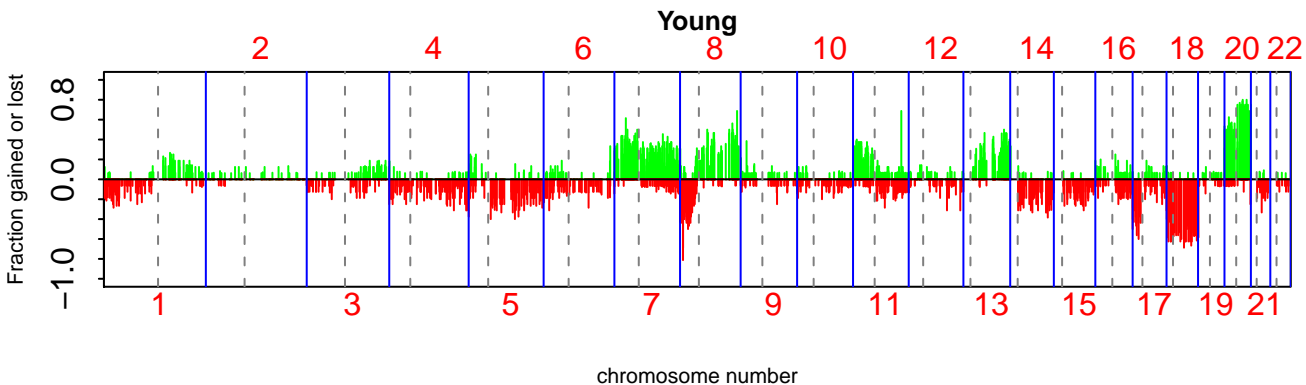








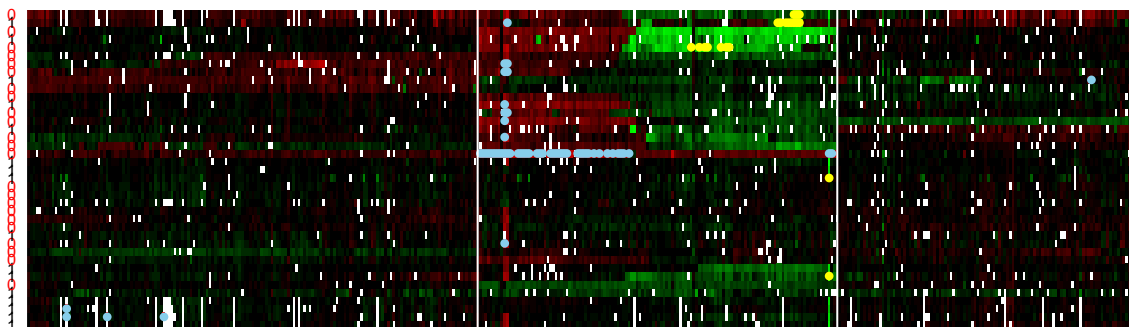




sample

Female  
Male

8



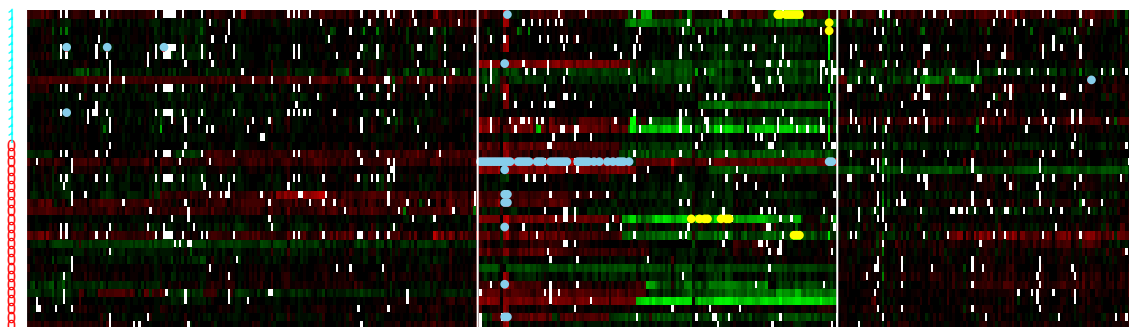
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sprocR63.0x  
sprocR169.0x  
sprocR200.0x  
sprocR152.0x  
sprocR154.0x  
sprocR161.0x  
sprocR395.0x  
sprocR340.0x  
sprocR112.0x  
sprocR177.0x  
sprocR196.0x  
sprocR100.0x  
sprocR359.0x  
sprocR193.0x  
sprocR174.0x  
sprocR218.0x  
sprocR212.0x  
sprocR217.0x  
sprocR232.0x

clone

Female  
Male

8

sample



sprocR210.0x  
sprocR124.0x  
sprocR36.0x  
sprocR210.0x  
sprocR217.0x  
sprocR353.0x  
sprocR174.0x  
sprocR174.0x  
sprocR218.0x  
sprocR146.0x  
sprocR245.0x  
sprocR75.0x  
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sprocR73.0x  
sprocR100.0x  
sprocR148.0x  
sprocR240.0x  
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sprocR154.0x  
sprocR112.0x  
sprocR77.0x

clone