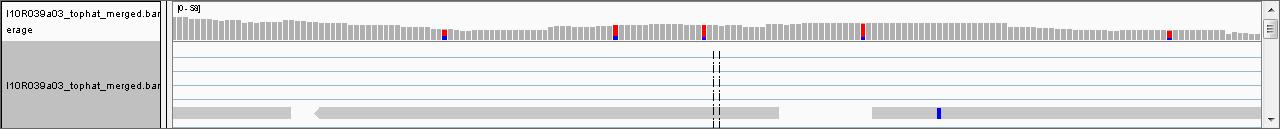
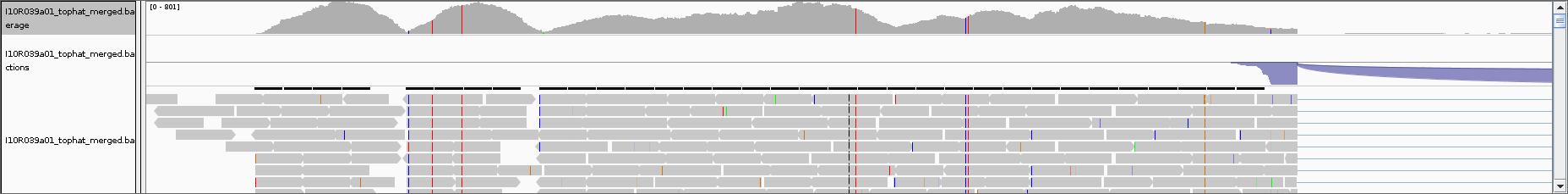
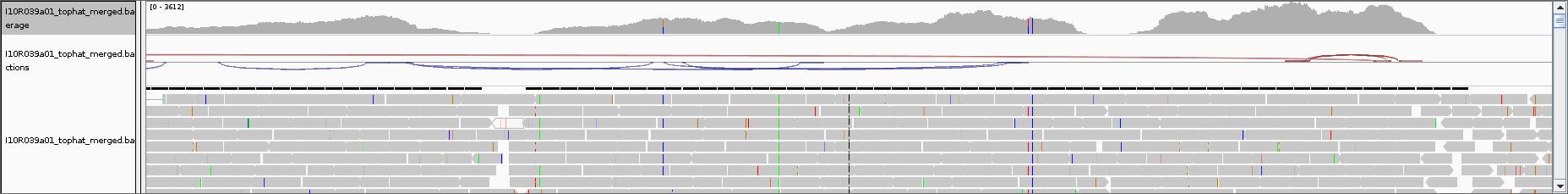
*EMC1:* MAF does not fit with our SNP frequency, besides new variant are created

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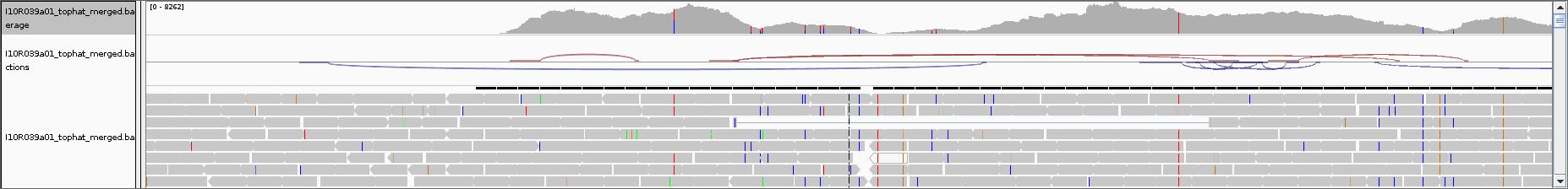
*CACNA2D4*: highly repetitive region at 3’UTR



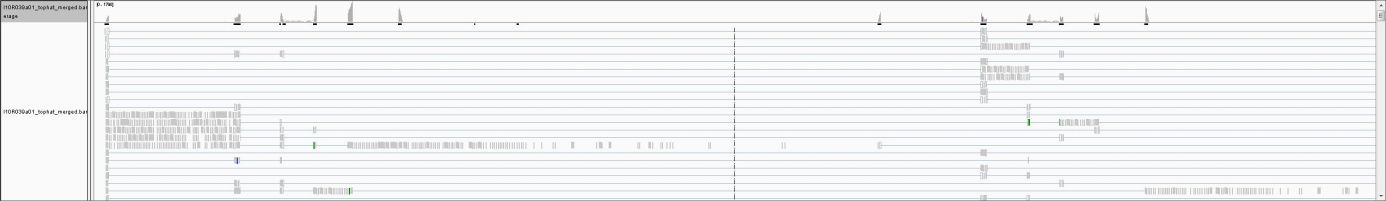
*CRX:* inconsistent mapping of reads leads to false splicing events

**

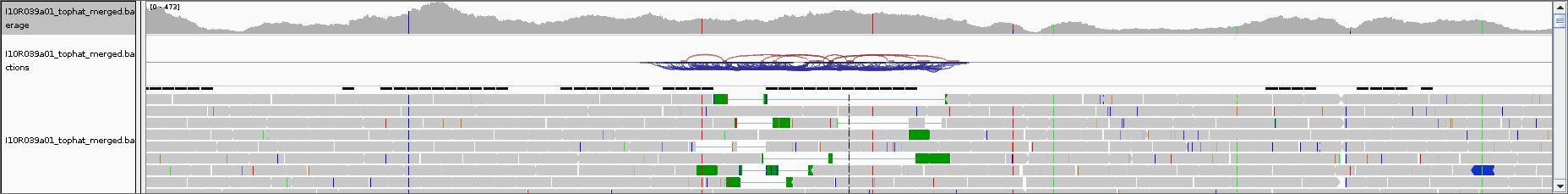
*PDE6A:* inconsistent mapping of reads leads to false splicing events

**

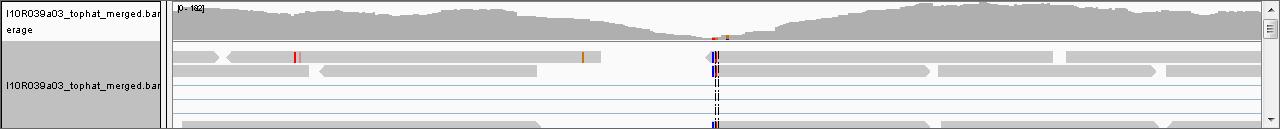
*OPN1LW/MW*: genes sharing high sequence identity results in misalignment, i.e. *OPN1LW* reads are mapped to *OPN1MW* and vice versa

**

*RP1L1:* inconsistent mapping of reads leads to false splicing events

**

*TUB:* SNP positioned in T-rich region (17 T in a row)

**

**Figure S2.** Integrative Genomics Viewer (IGV) visual inspection on candidate SNP regions.