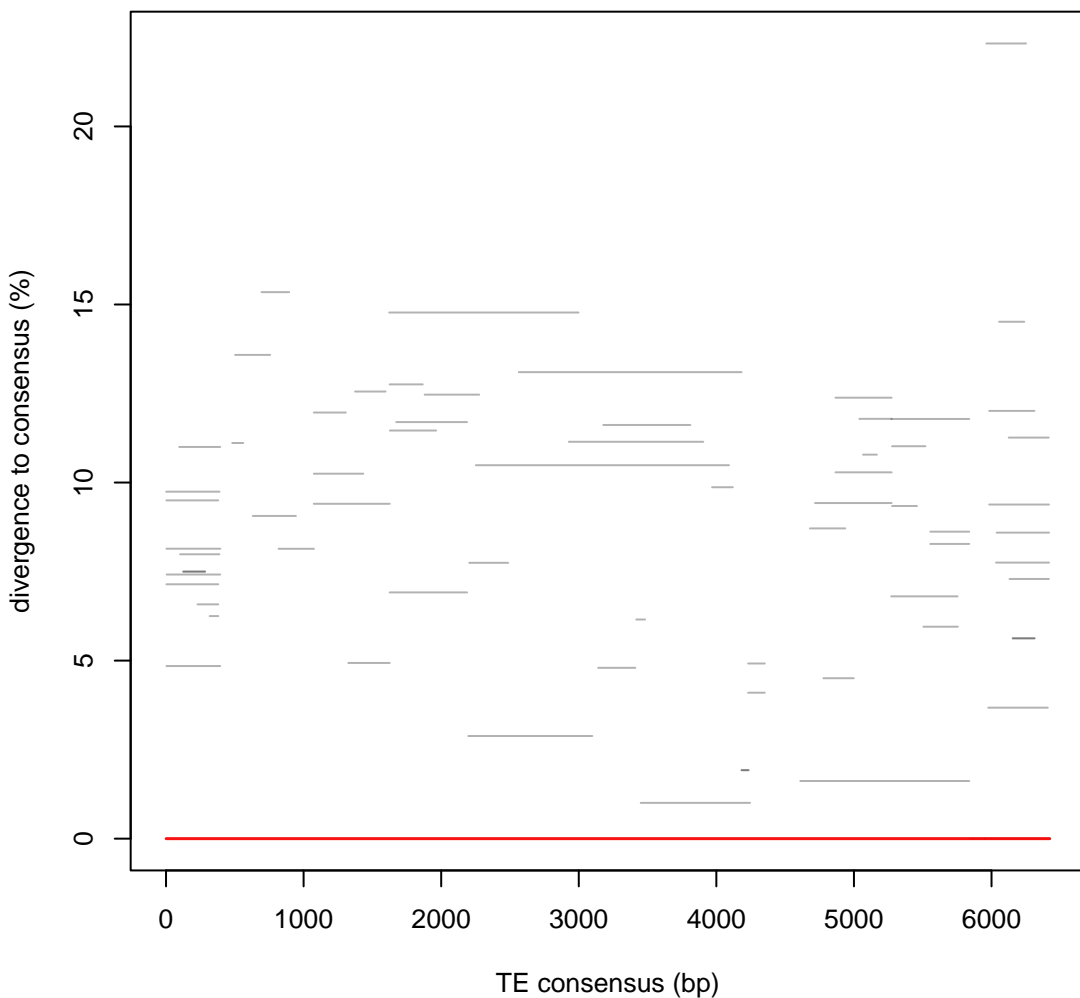
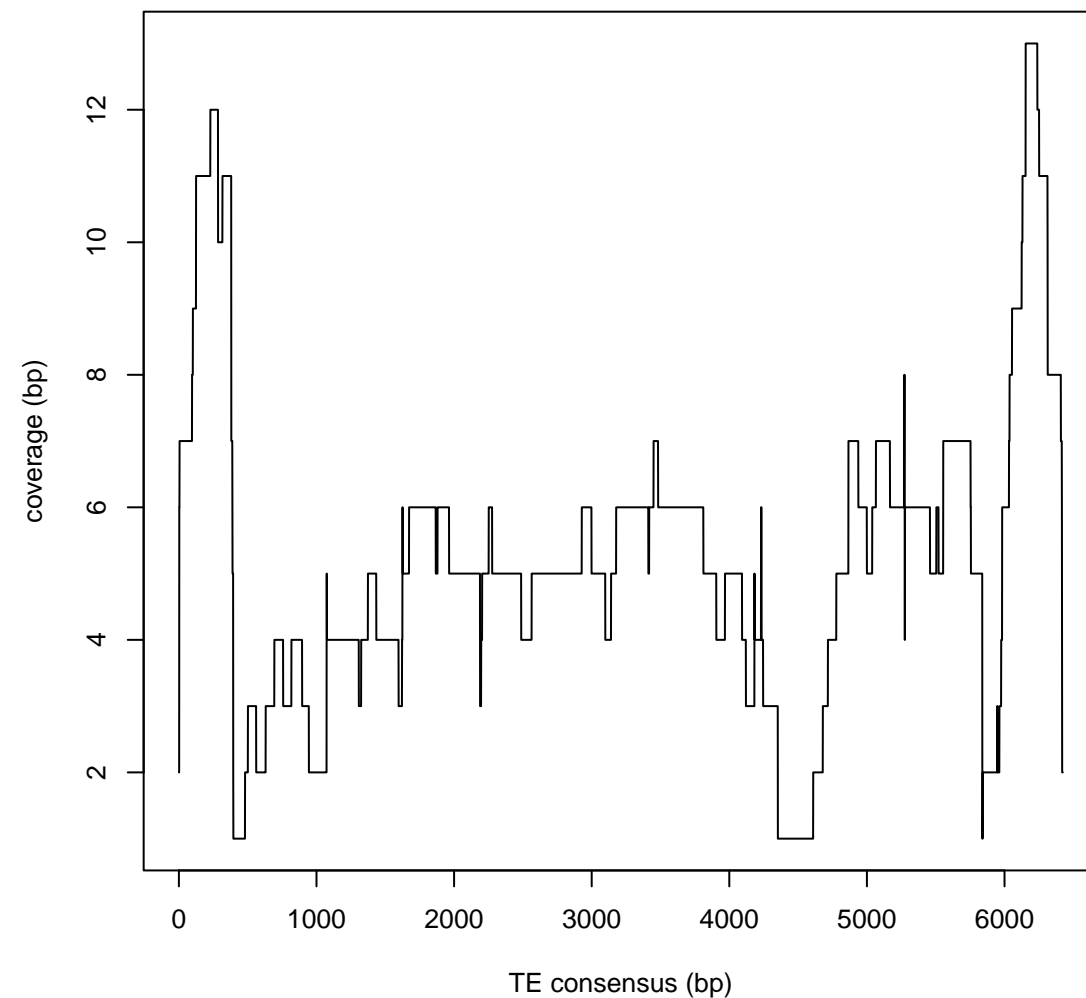


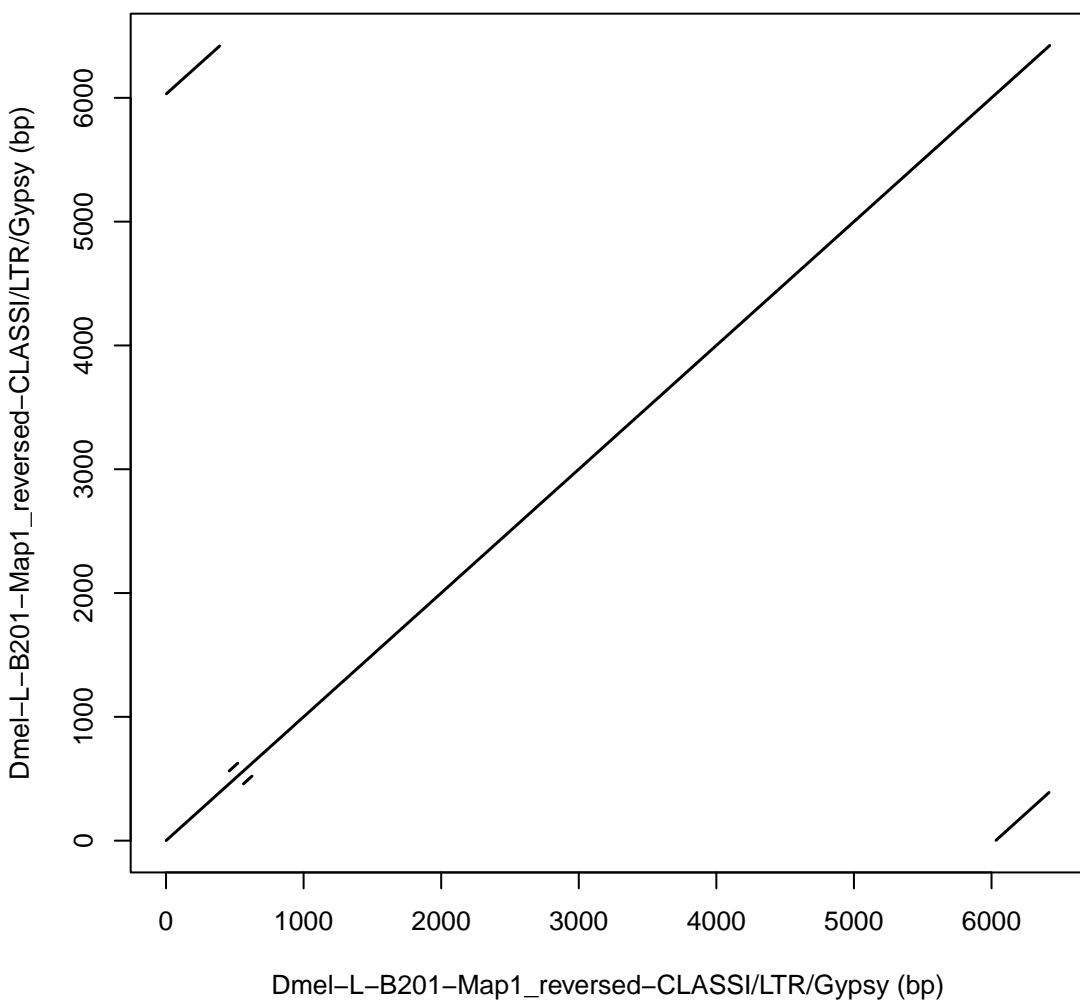
TE: Dmel-L-B201-Map1\_reversed-CLASSI/LTR/Gypsy  
consensus size: 6423bp; fragments: 71; full length: 1 (>=5780.7bp)



### TE consensus genomic coverage



### TE consensus self dotplot (blastn)



### TE consensus structure and protein hits

