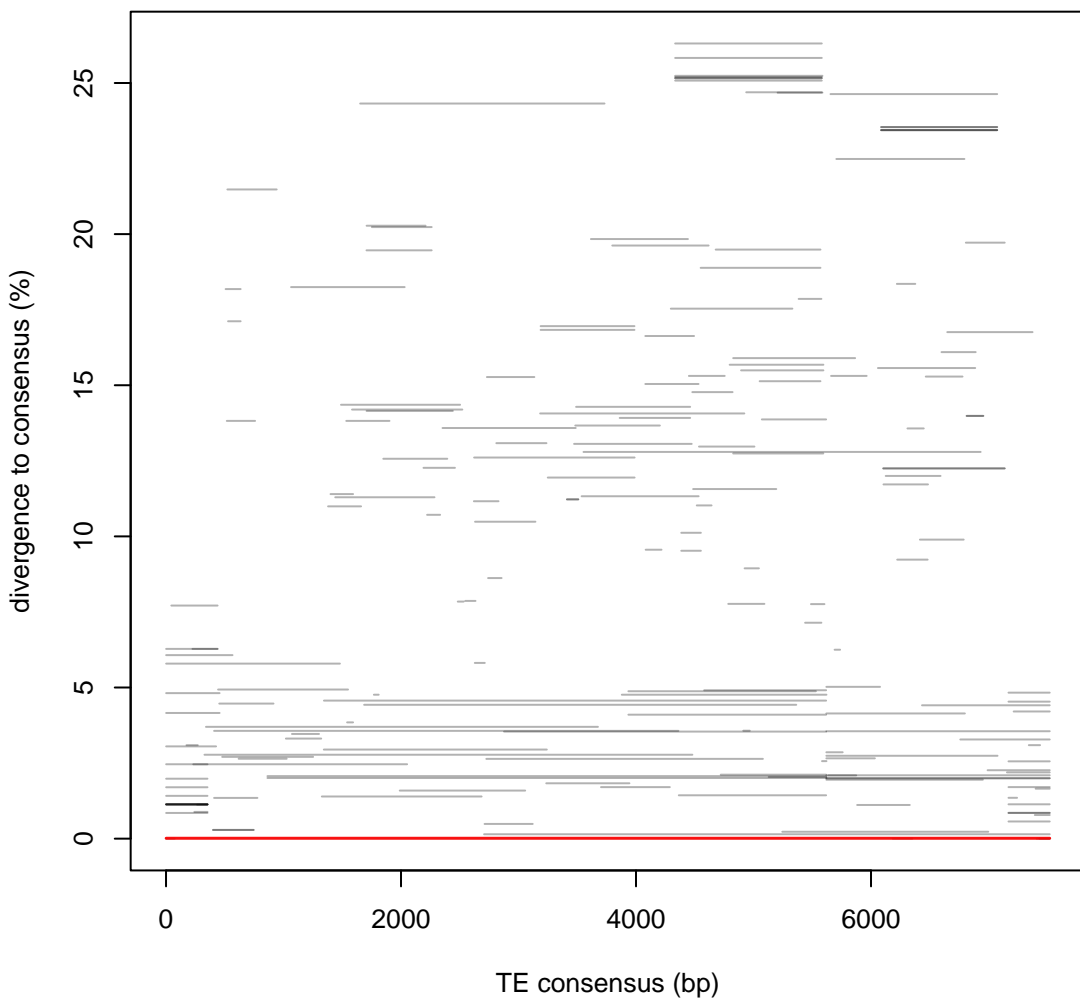
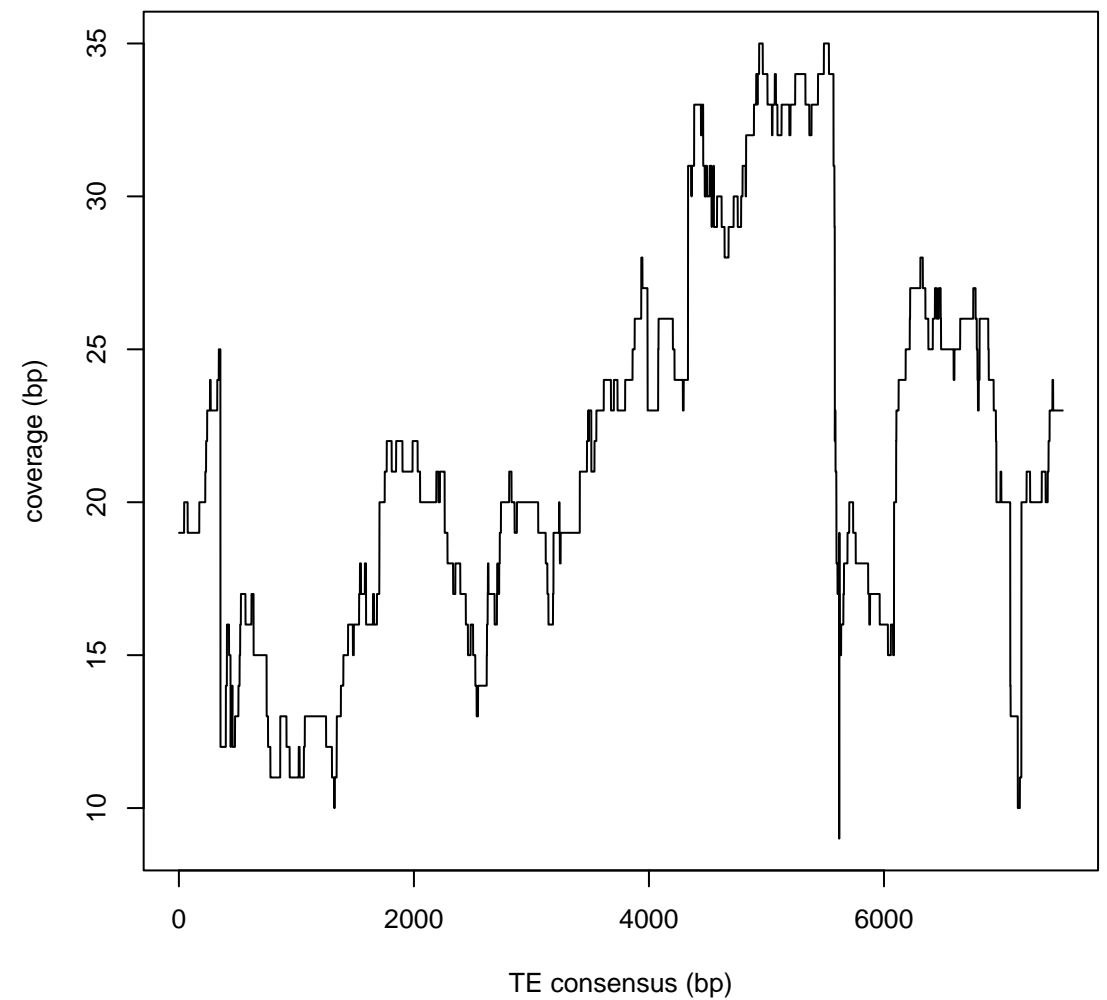


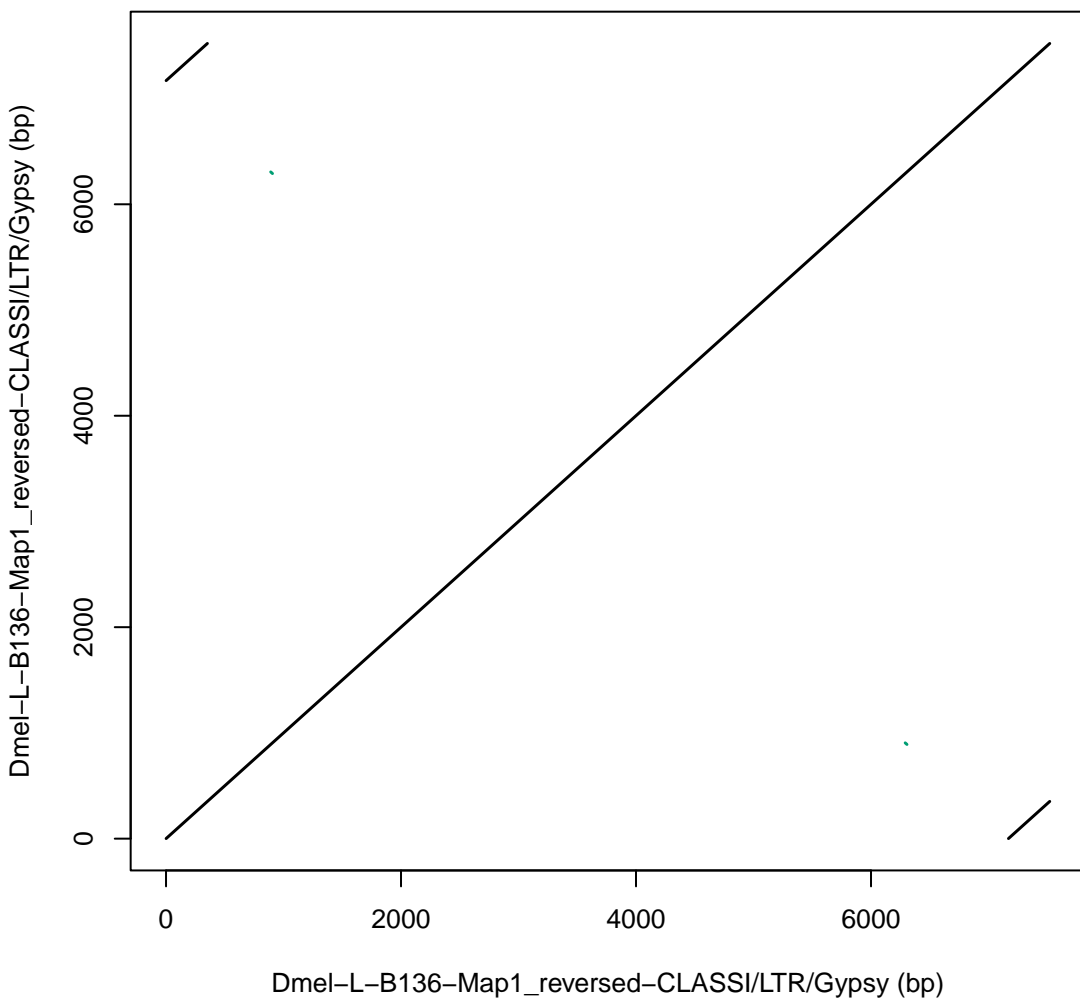
TE: Dmel-L-B136-Map1\_reversed-CLASSI/LTR/Gypsy  
consensus size: 7521bp; fragments: 194; full length: 1 (>=6768.9bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

