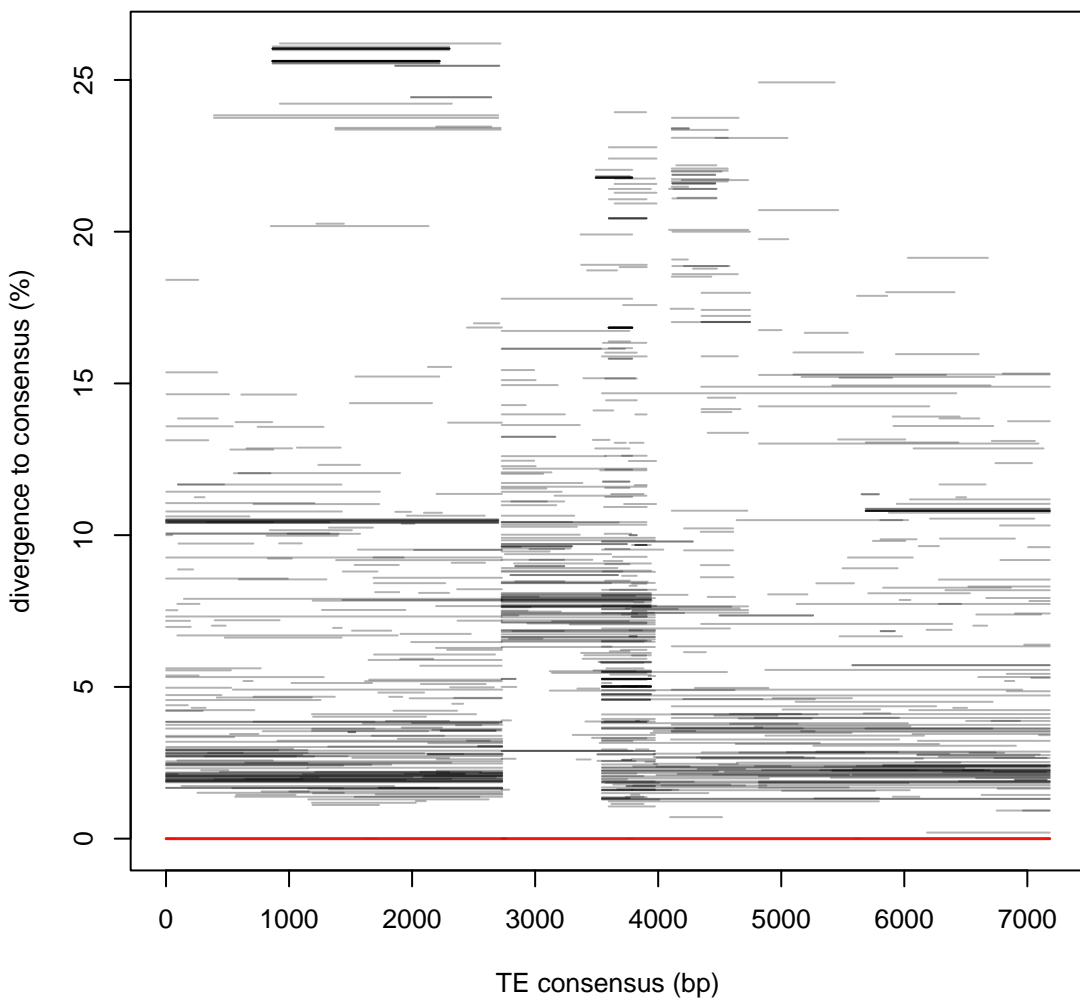
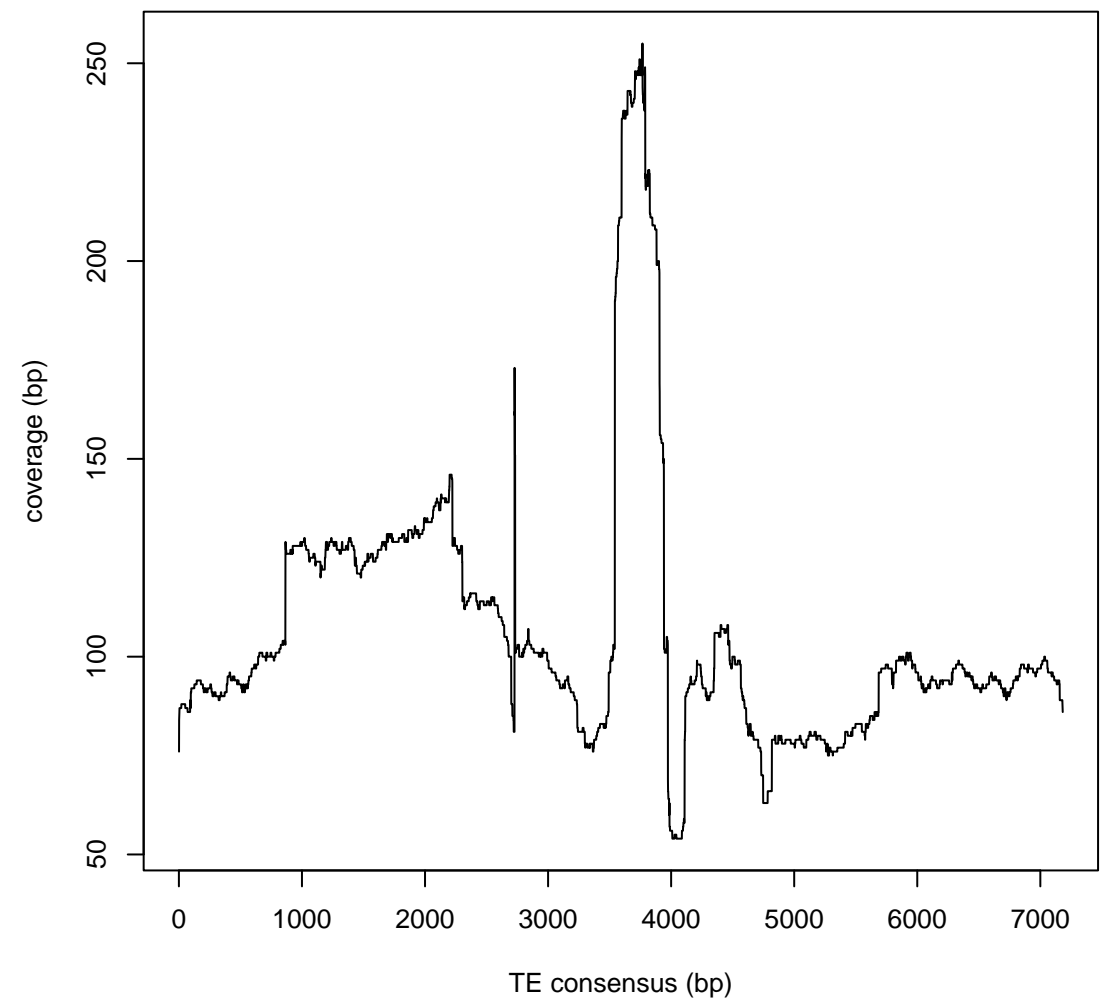


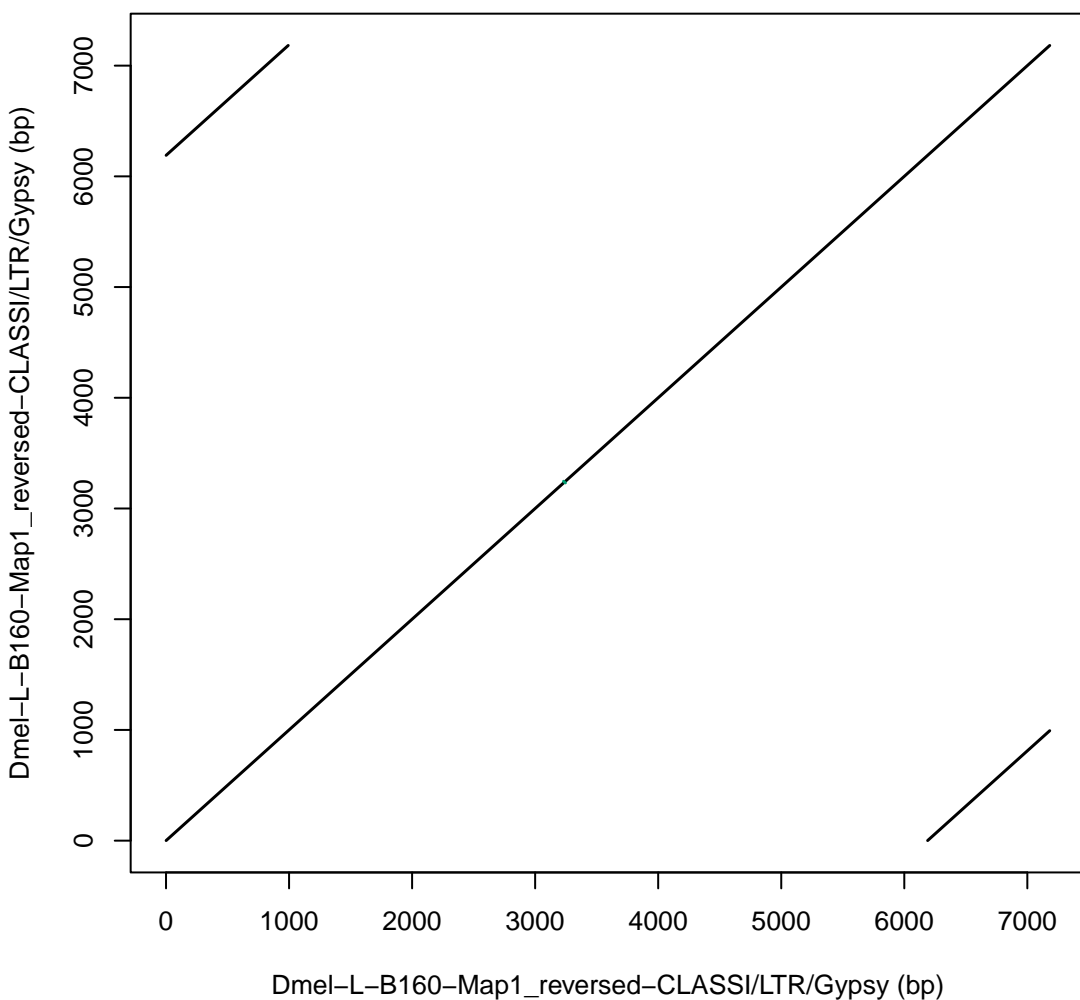
TE: Dmel-L-B160-Map1\_reversed-CLASSI/LTR/Gypsy  
consensus size: 7182bp; fragments: 865; full length: 1 (>=6463.8bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

