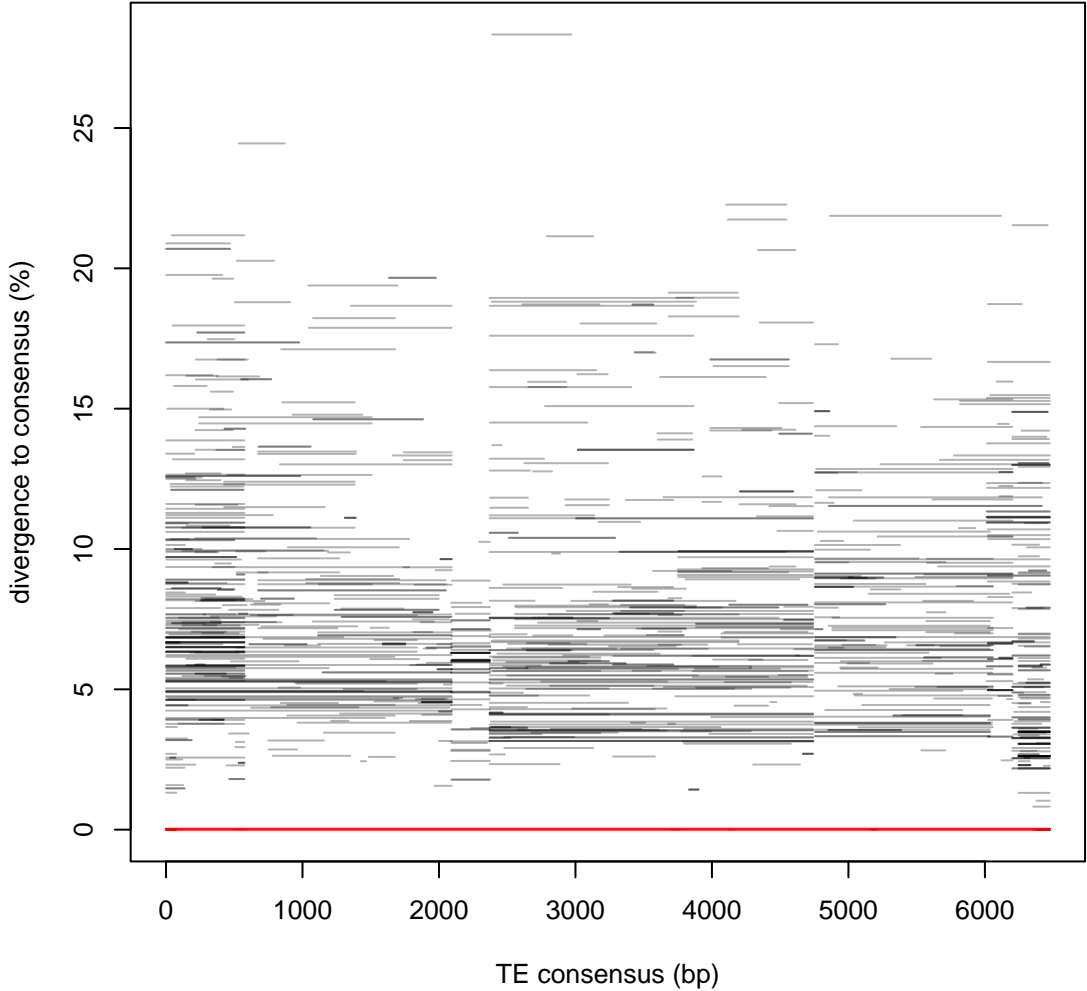
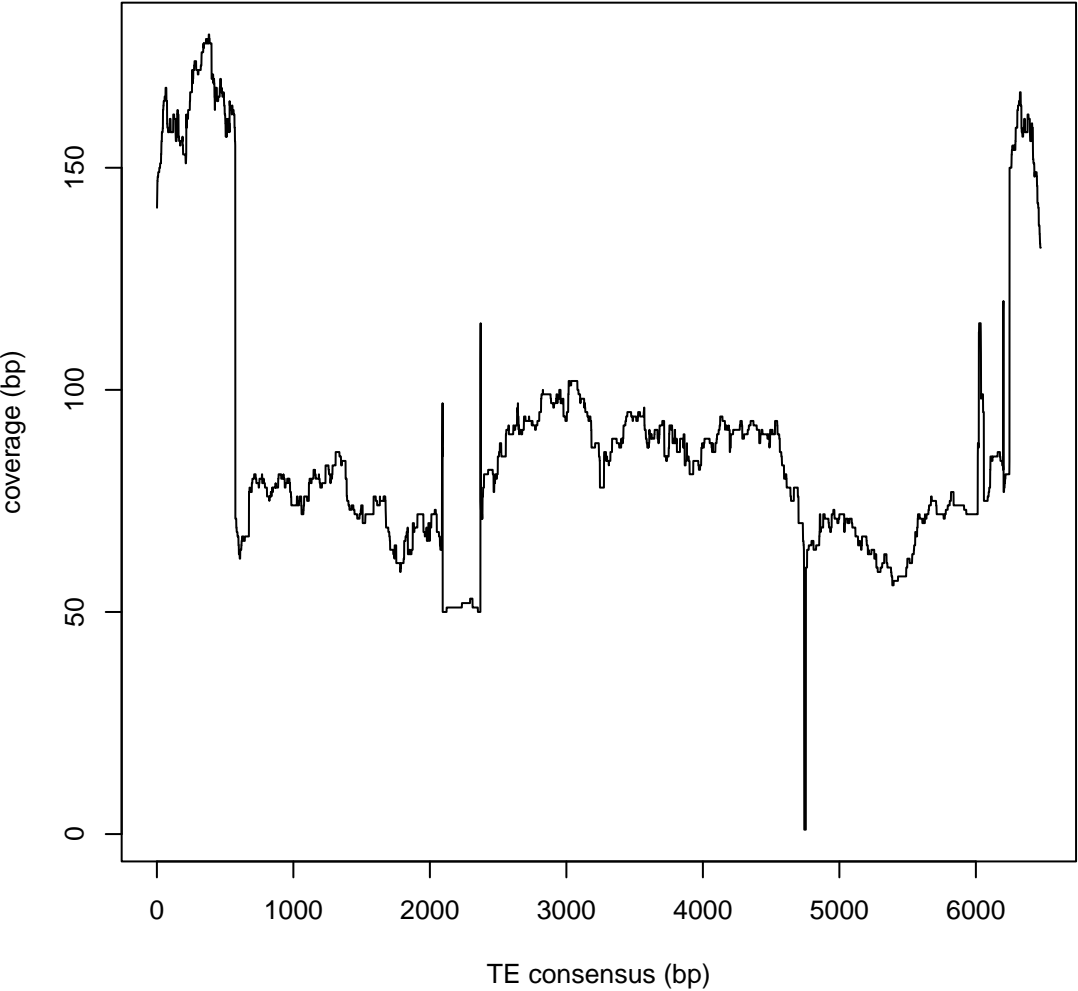


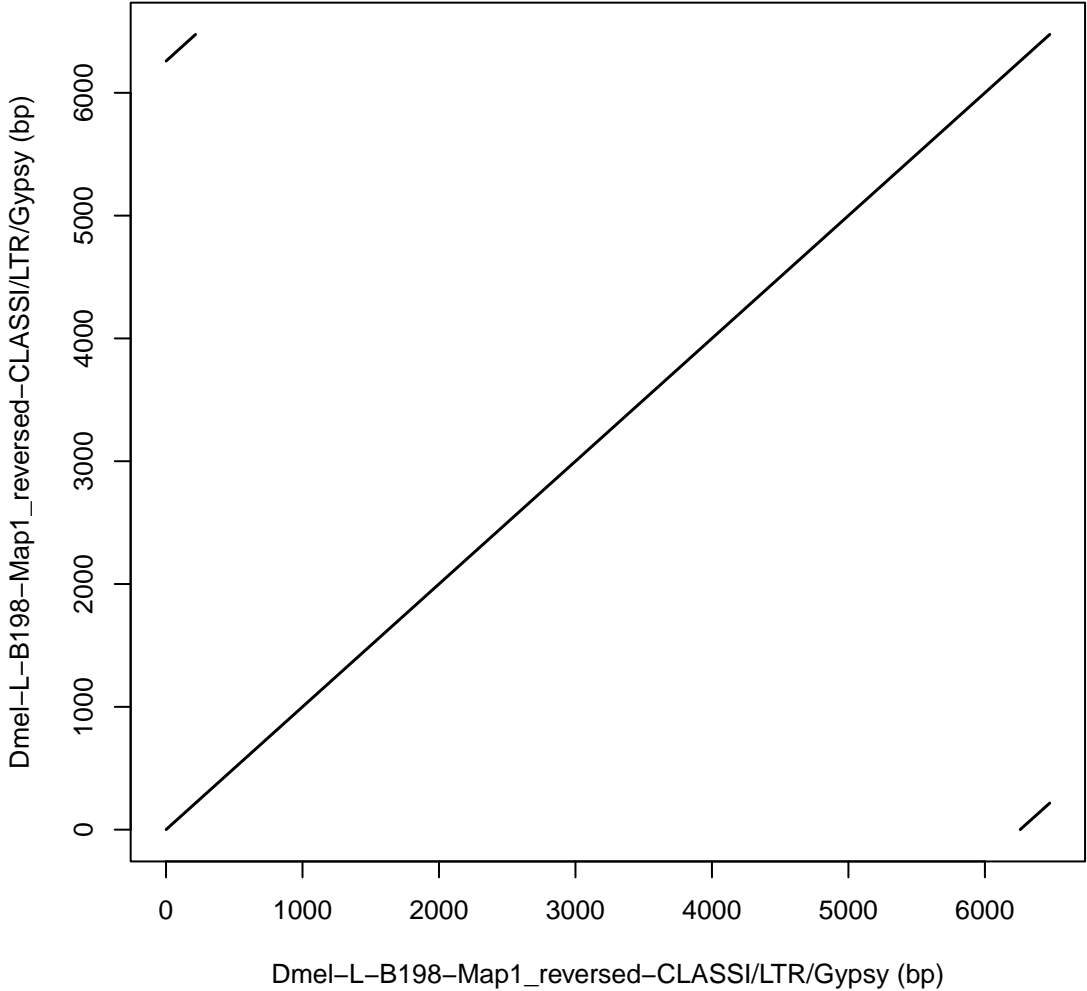
TE: Dmel-L-B198-Map1_reversed-CLASSI/LTR/Gypsy
consensus size: 6475bp; fragments: 1049; full length: 1 (>=5827.5bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

