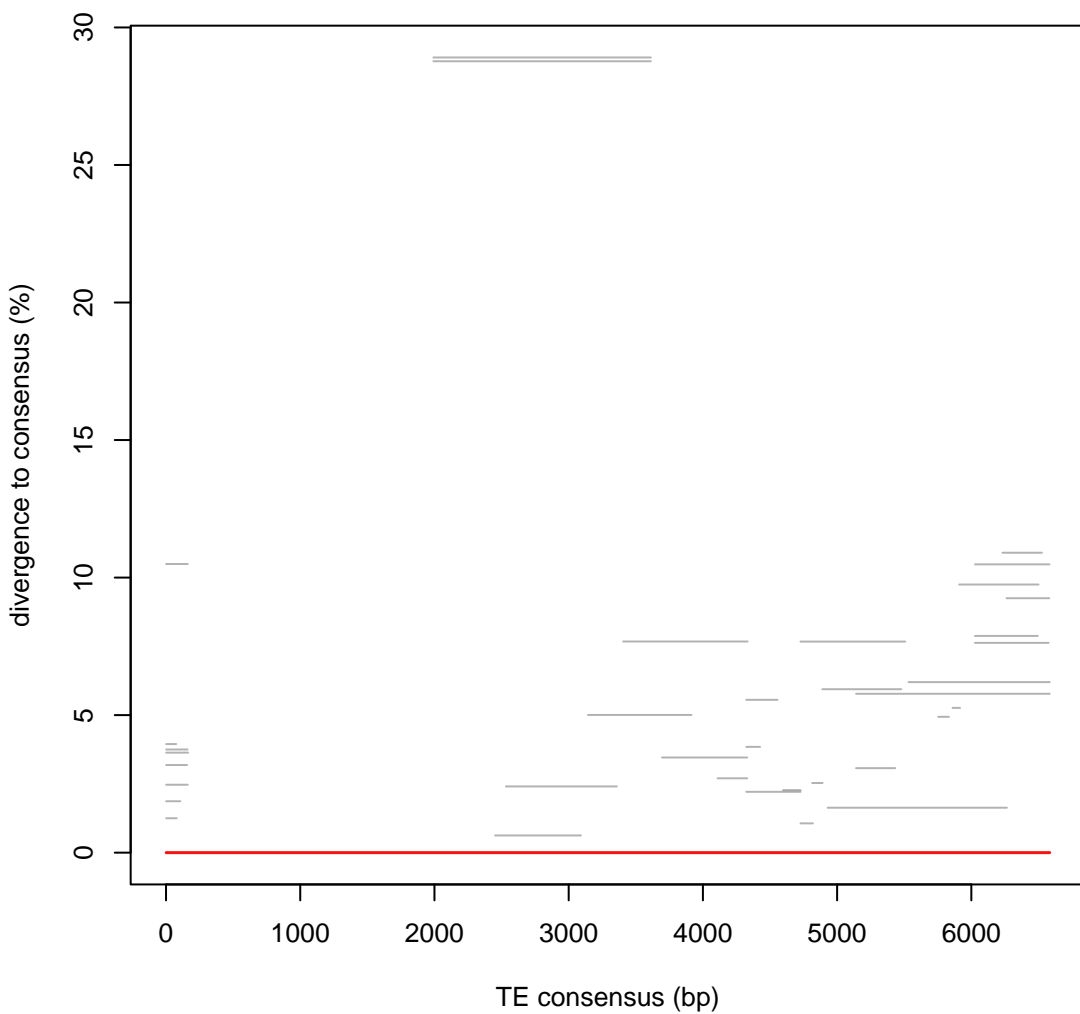
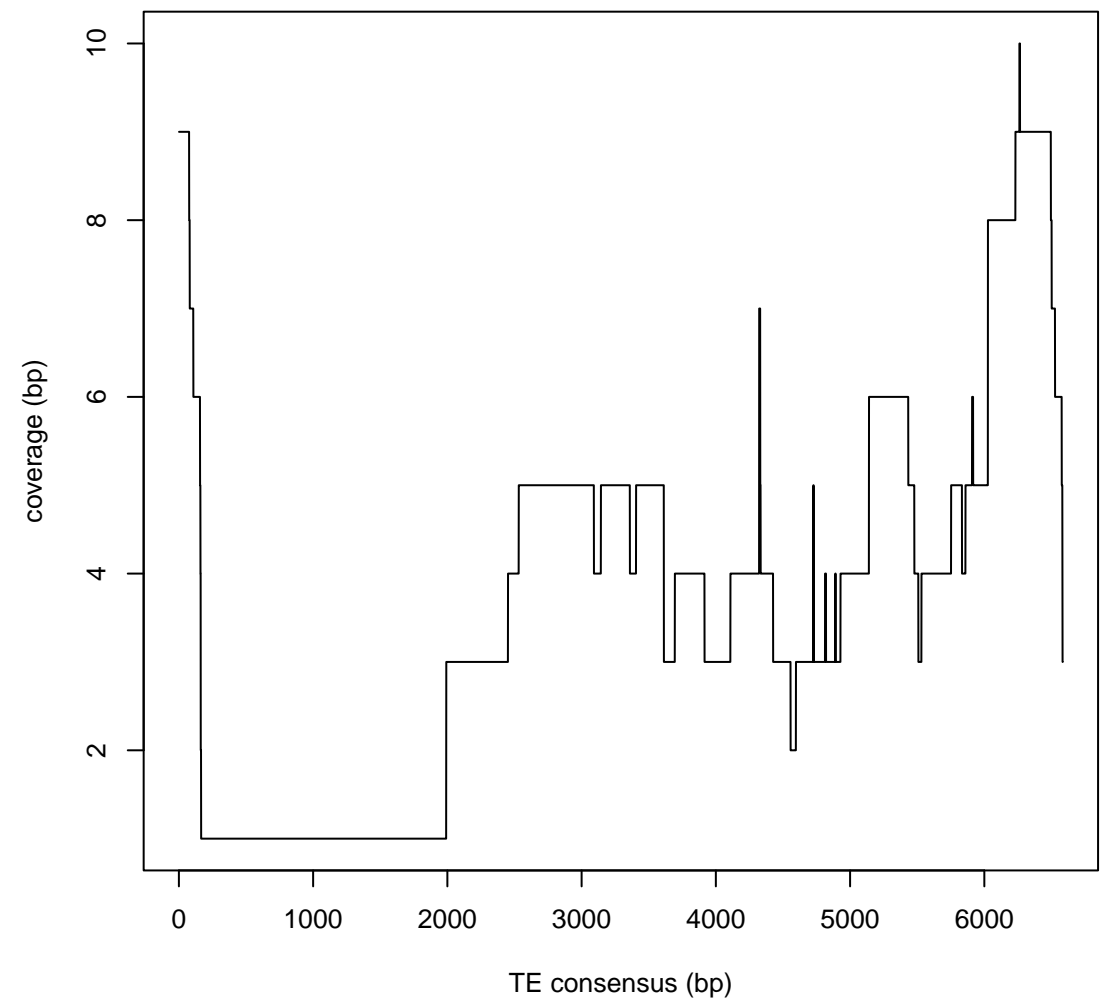


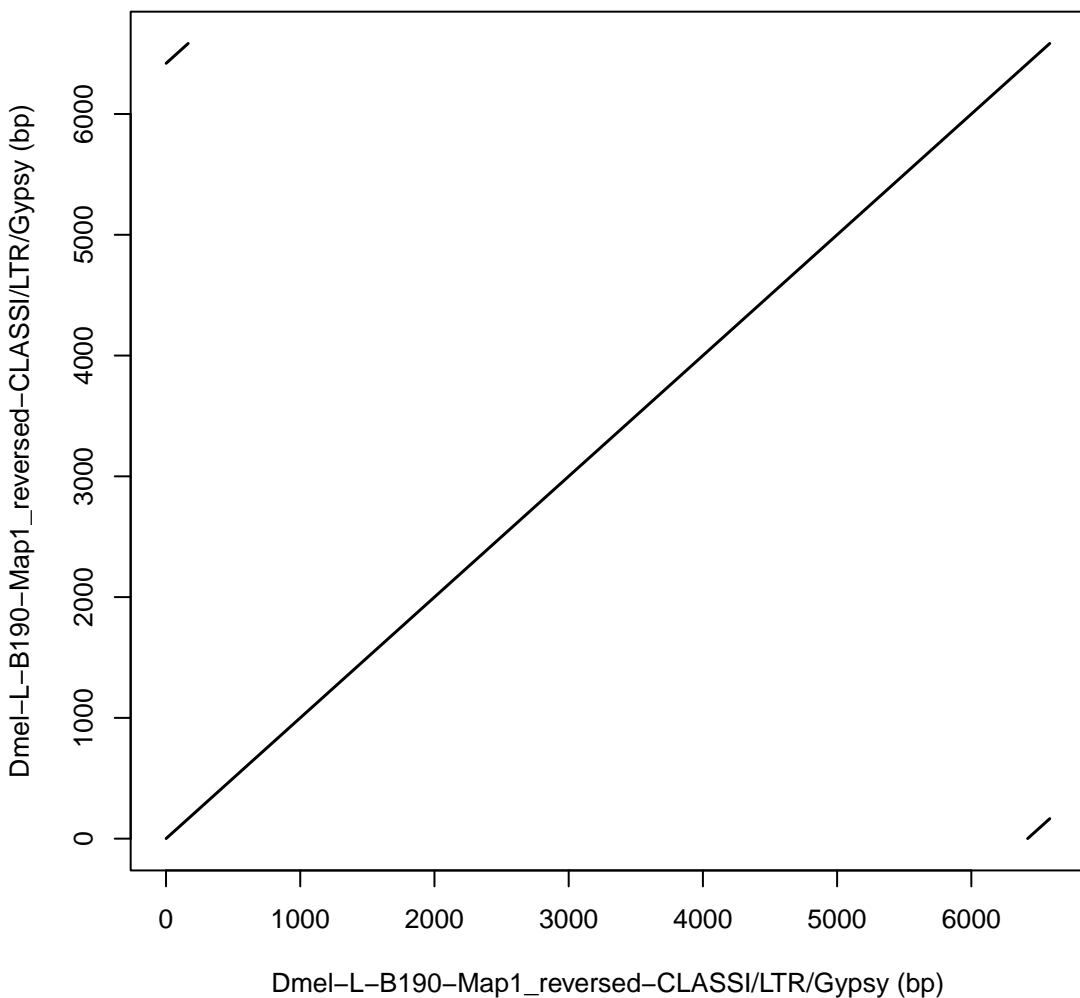
TE: Dmel-L-B190-Map1\_reversed-CLASSI/LTR/Gypsy  
consensus size: 6584bp; fragments: 37; full length: 1 (>=5925.6bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

