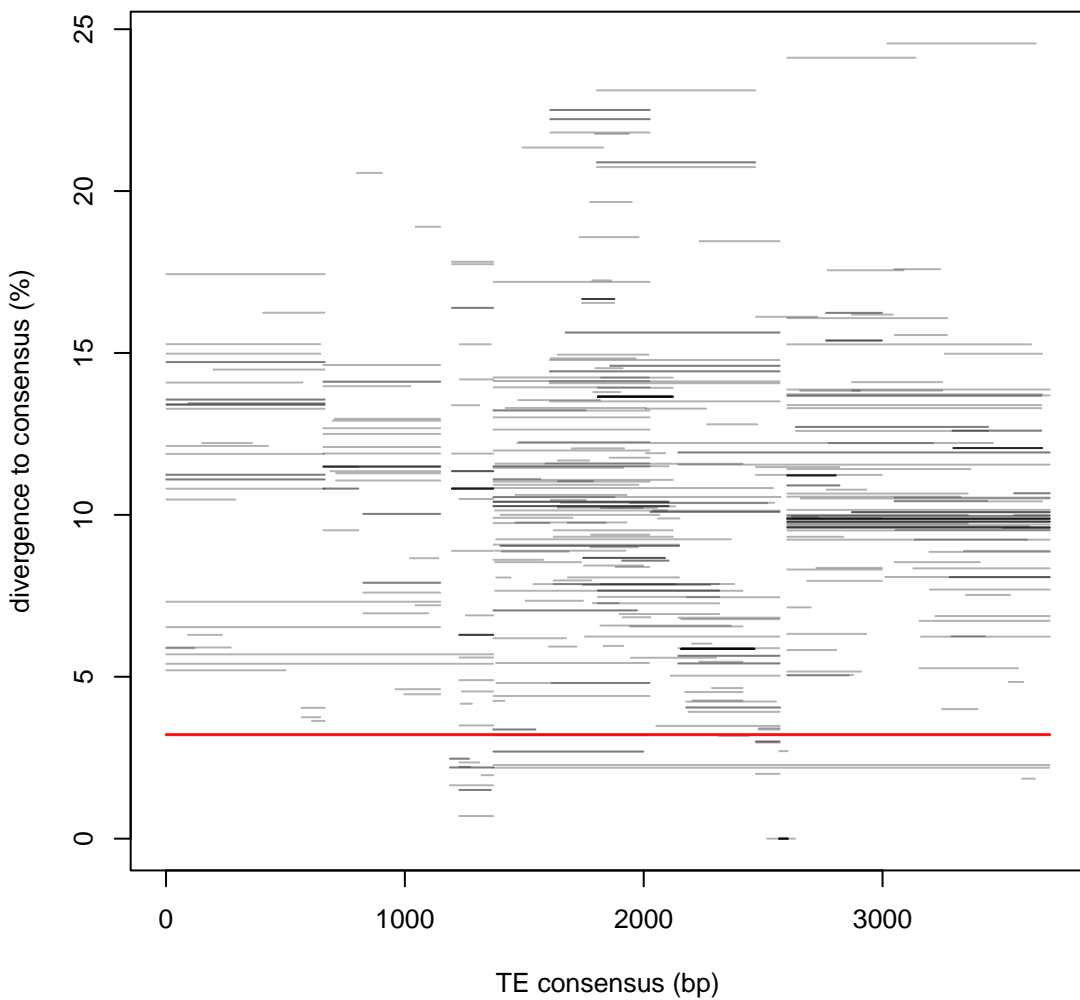
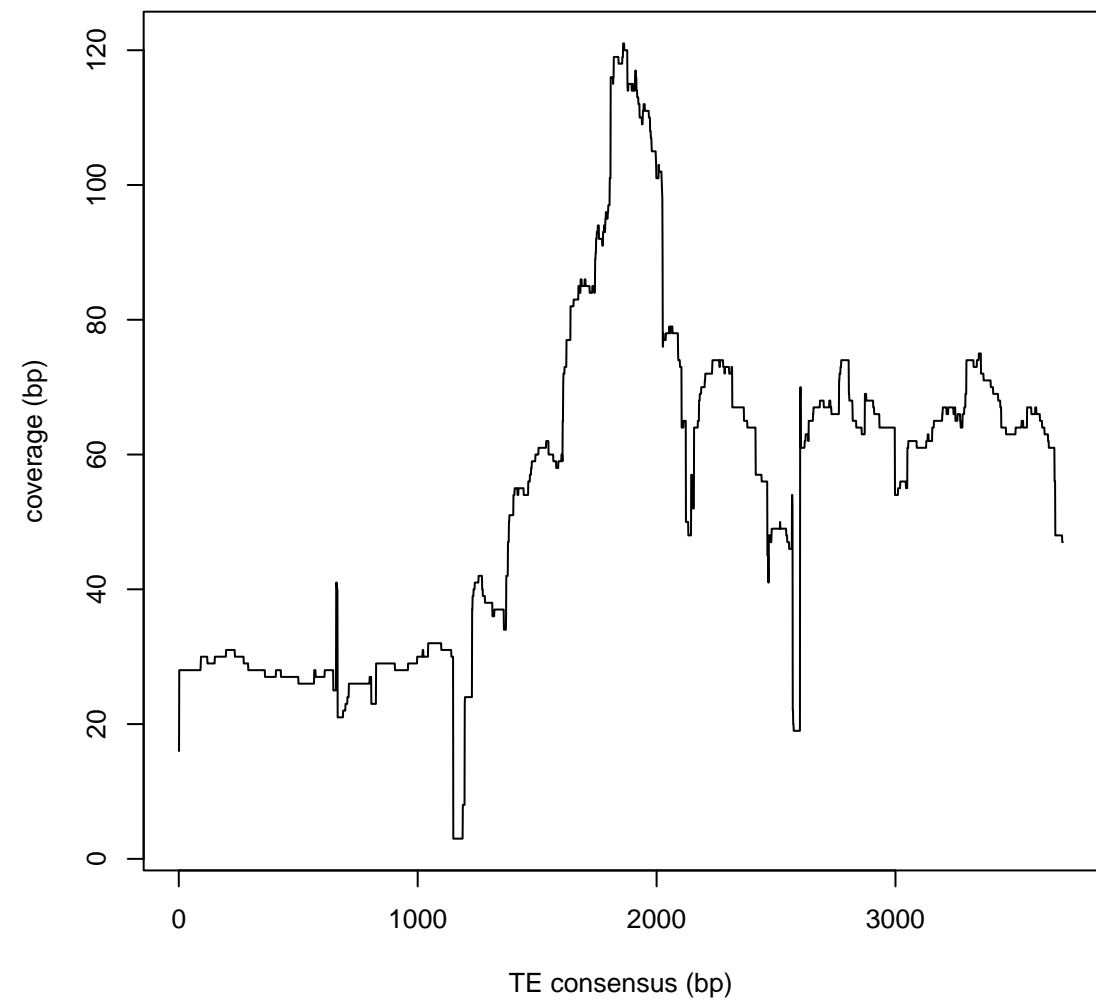


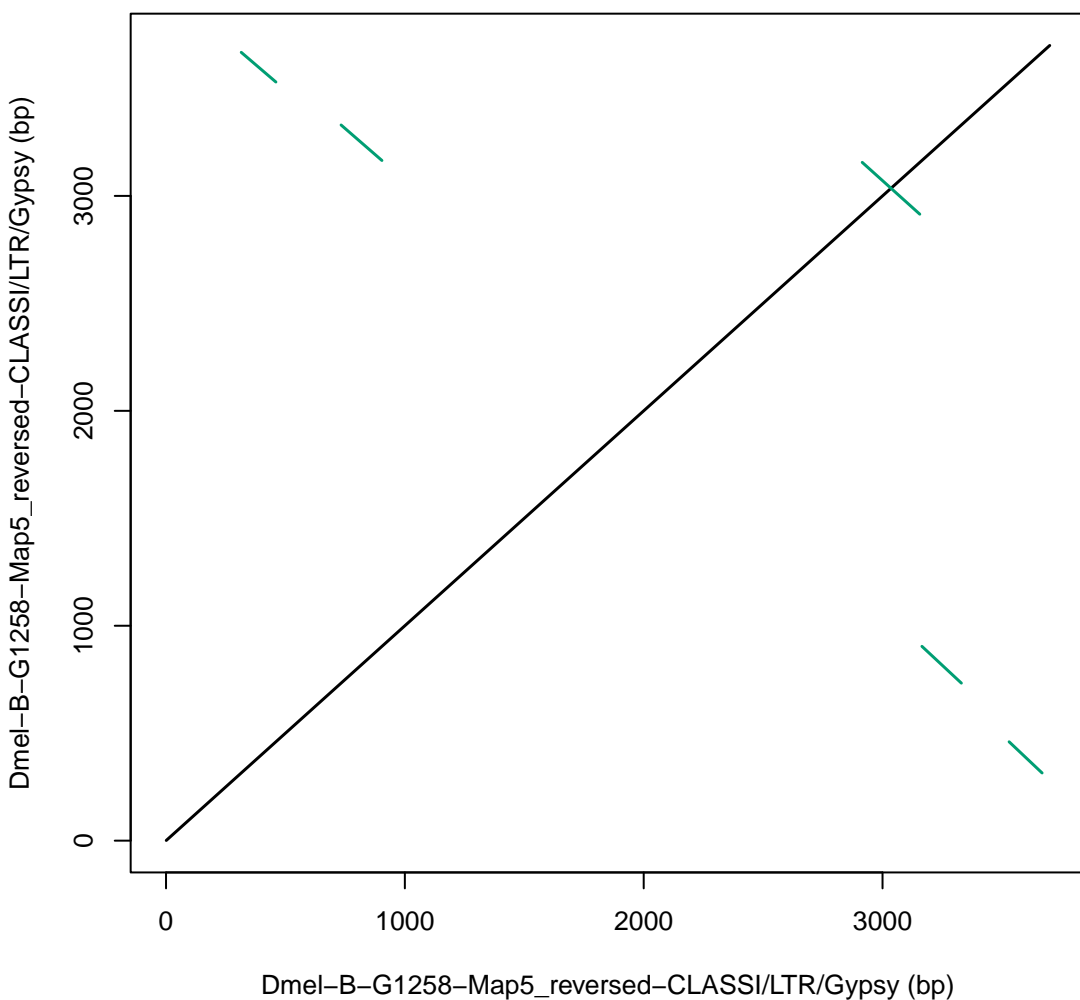
TE: Dmel-B-G1258-Map5_reversed-CLASSI/LTR/Gypsy
consensus size: 3700bp; fragments: 430; full length: 1 (>=3330bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

