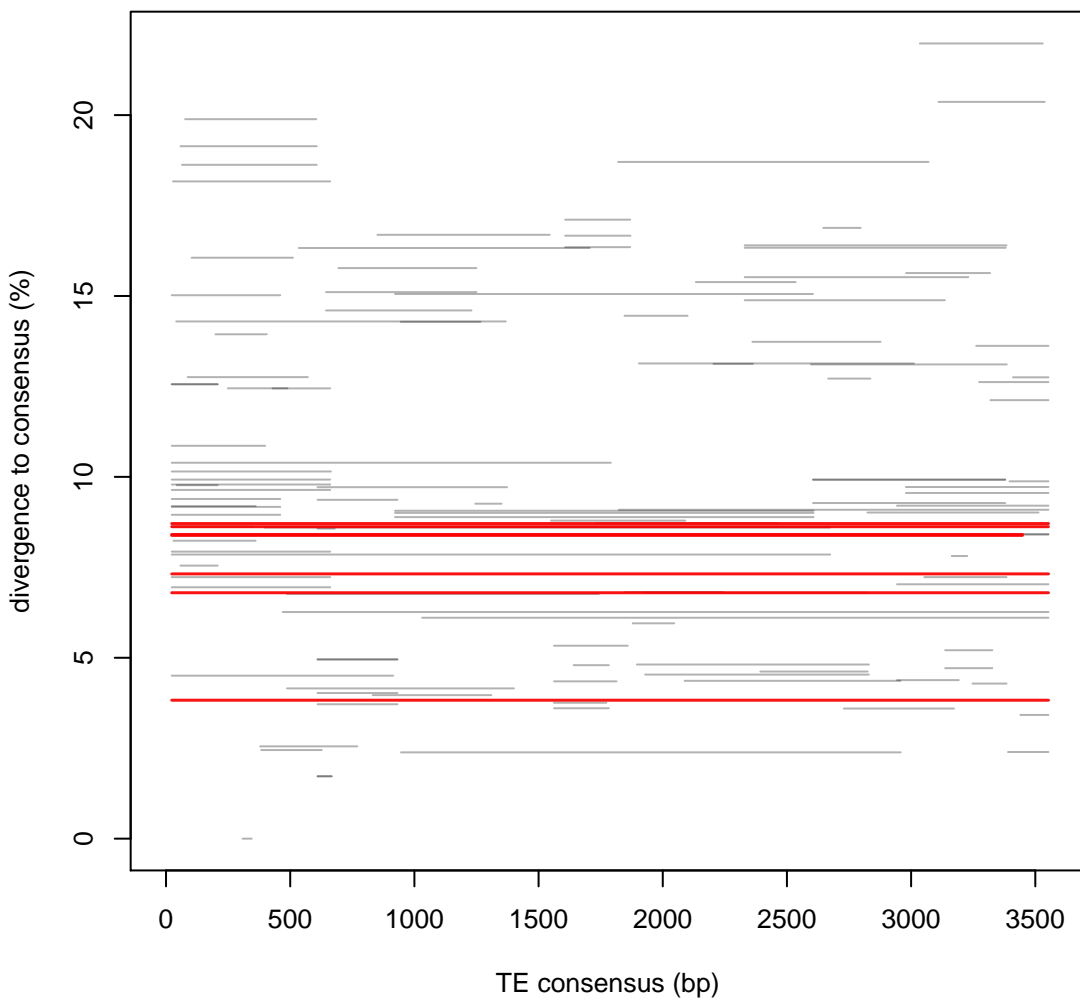
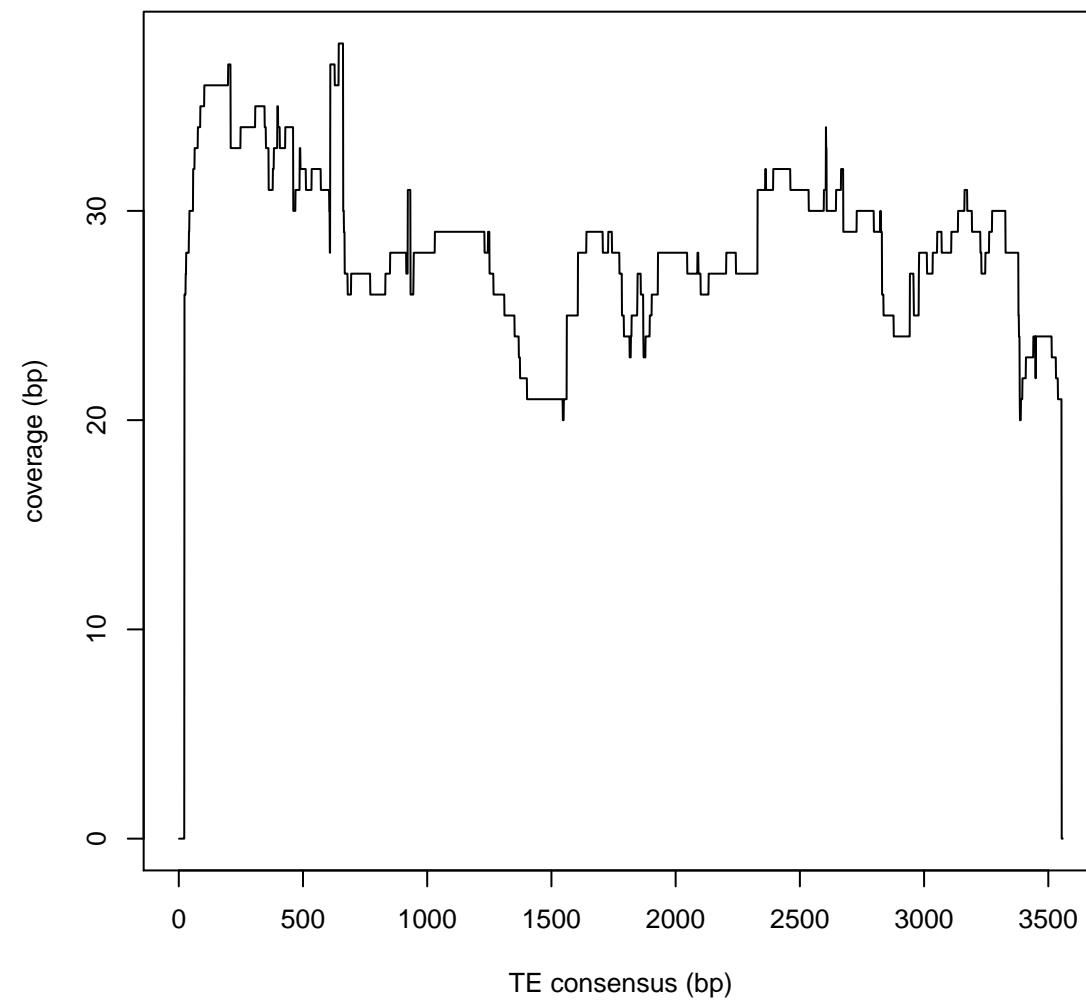


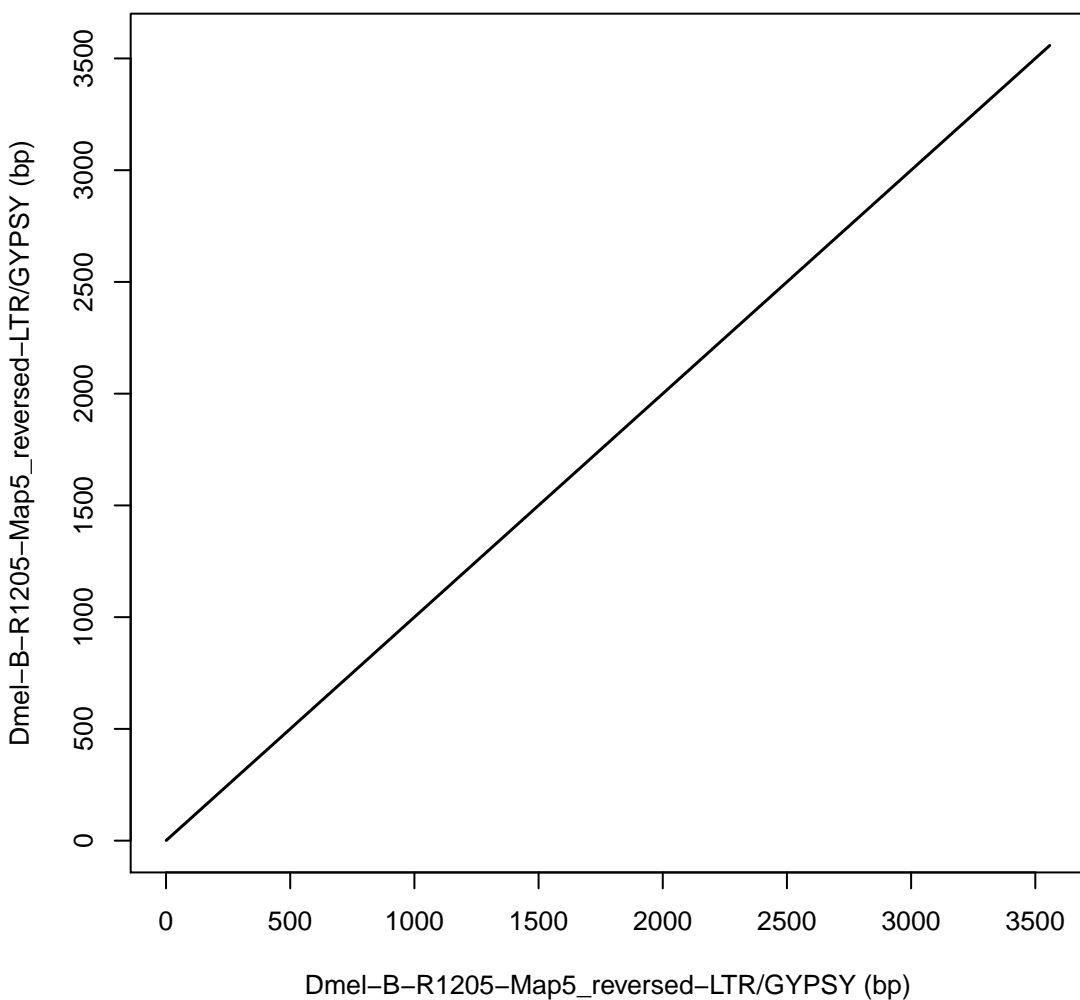
TE: Dmel-B-R1205-Map5_reversed-LTR/GYPSY
consensus size: 3558bp; fragments: 128; full length: 7 (>=3202.2bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

