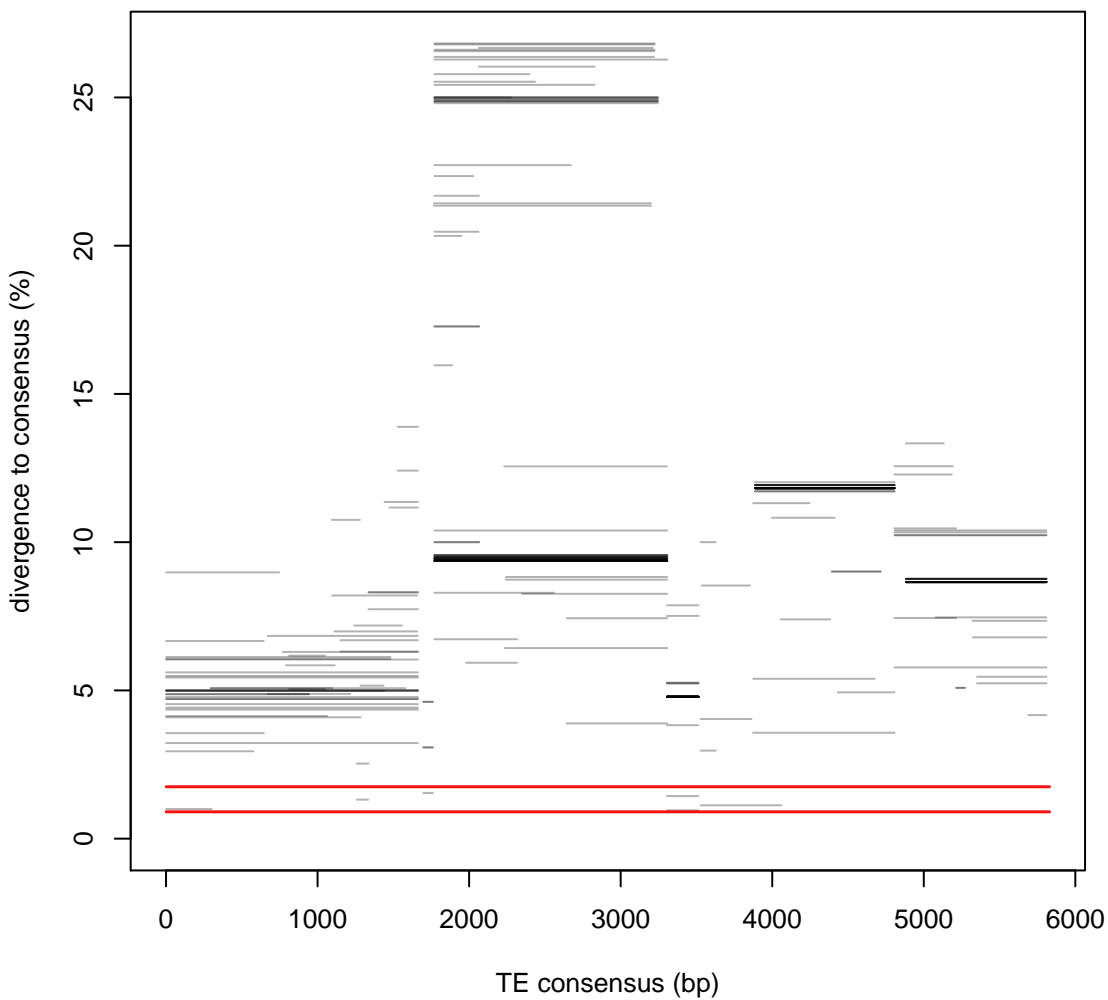
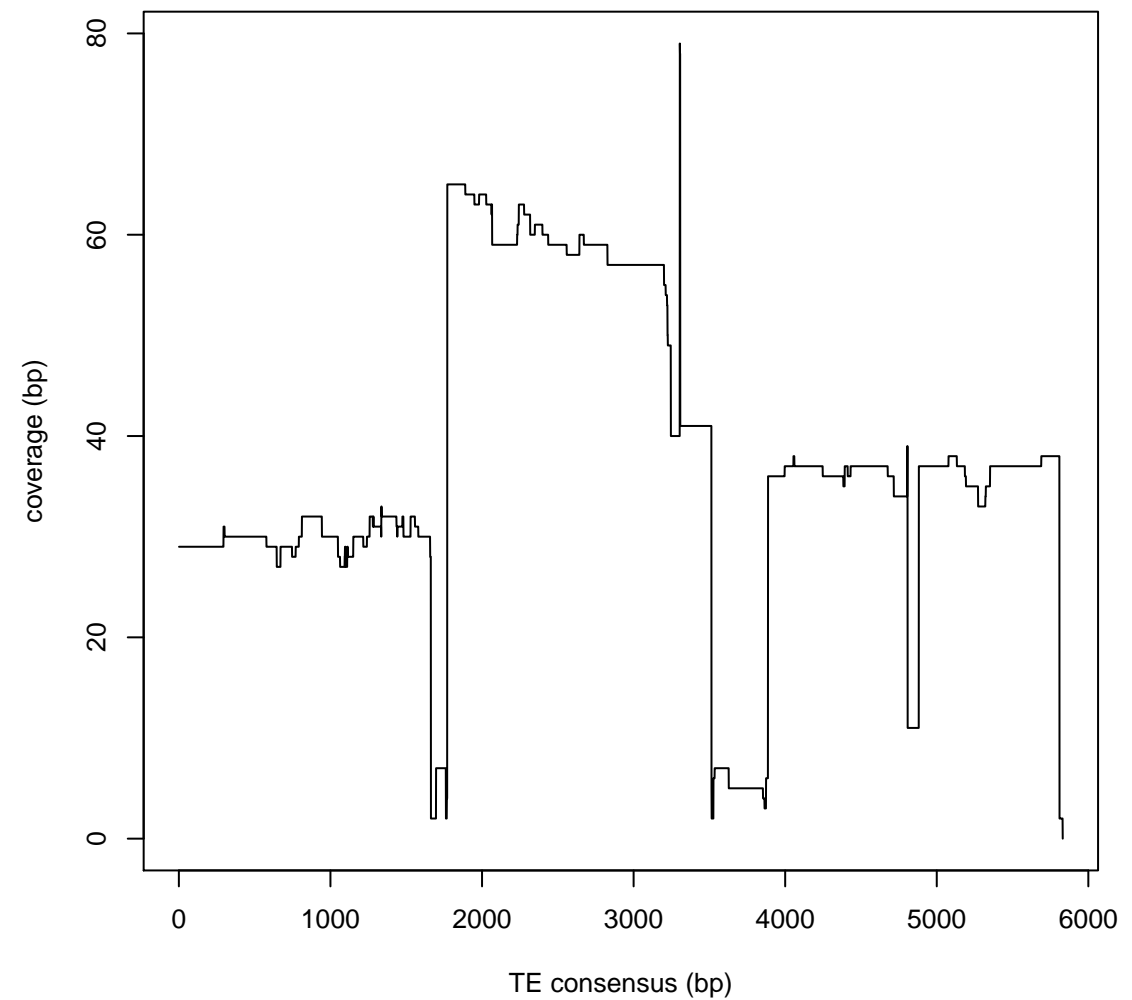


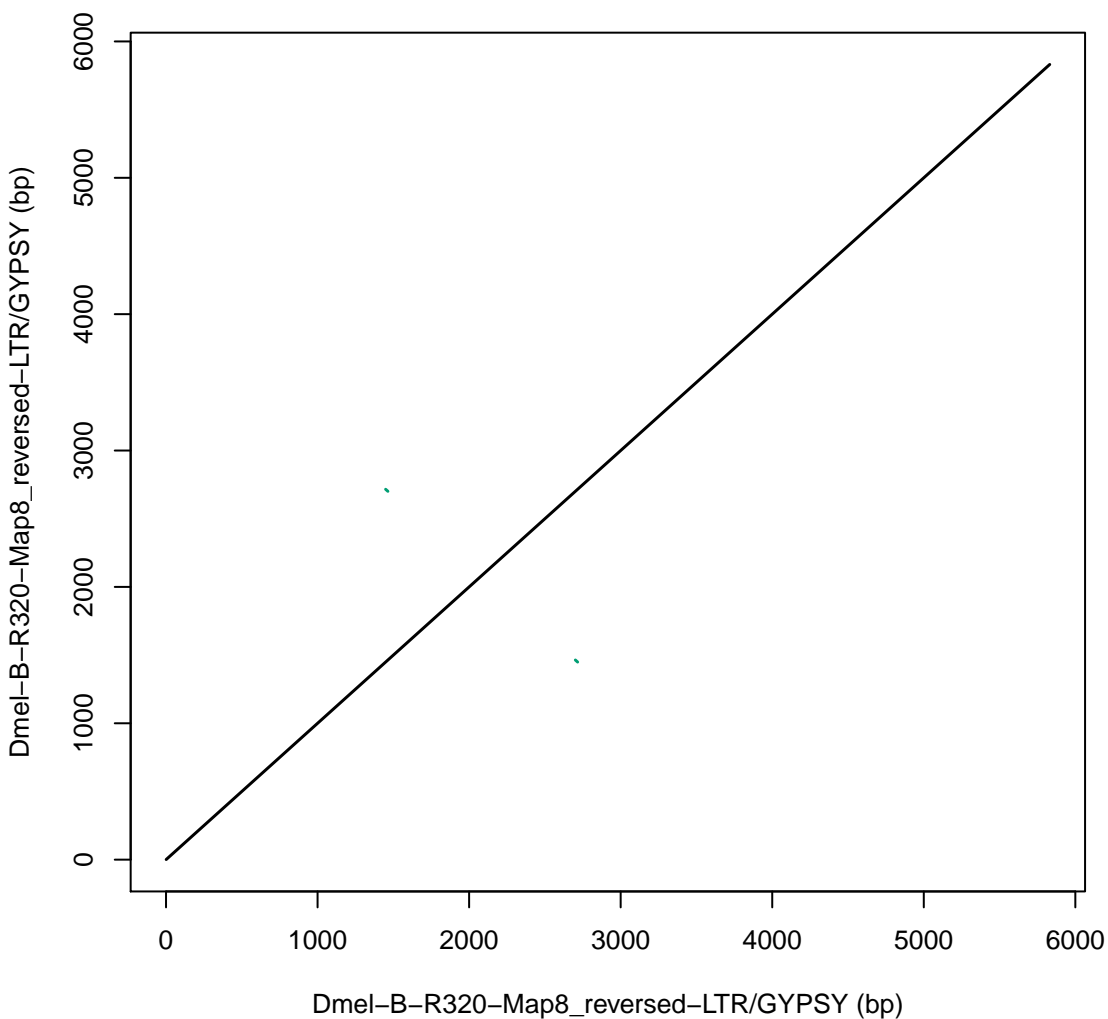
TE: Dmel-B-R320-Map8\_reversed-LTR/GYPSY  
consensus size: 5831bp; fragments: 257; full length: 2 (>=5247.9bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

