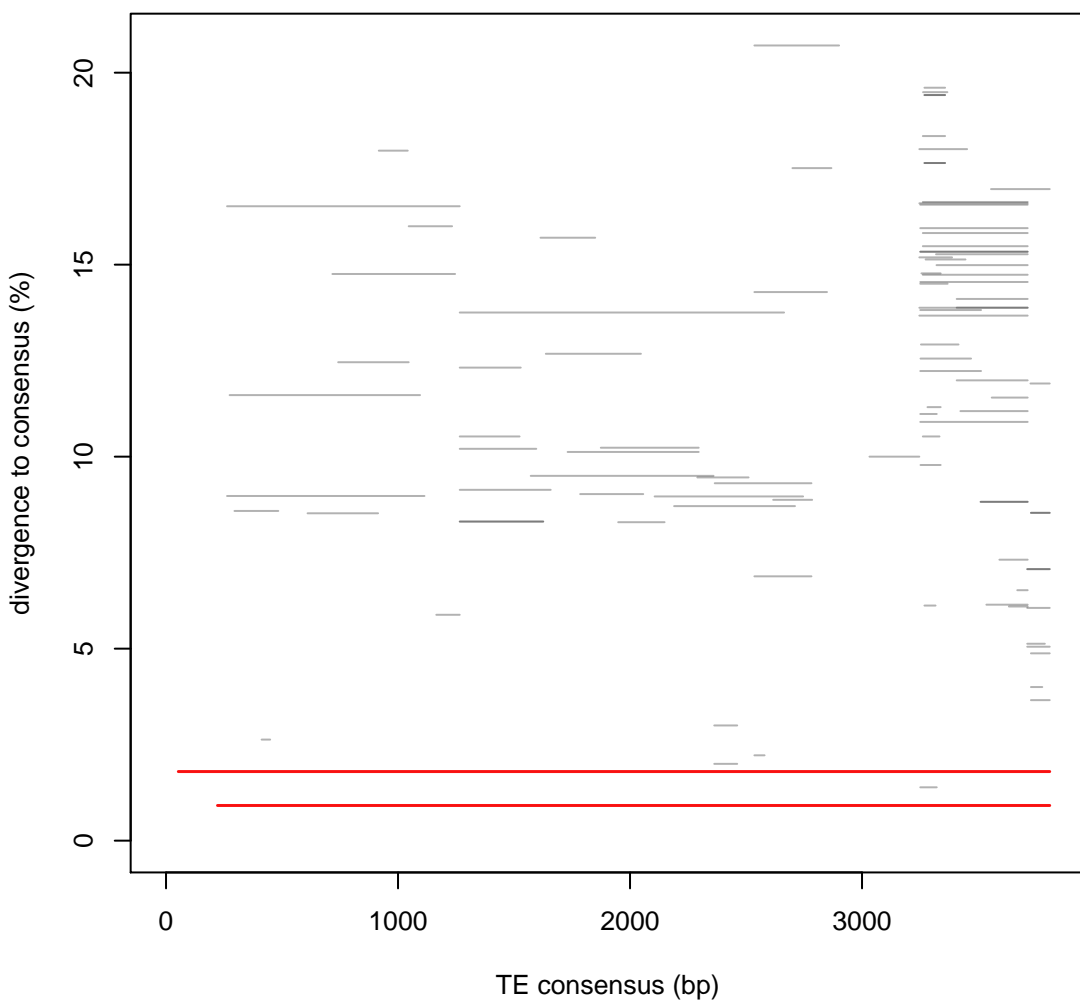
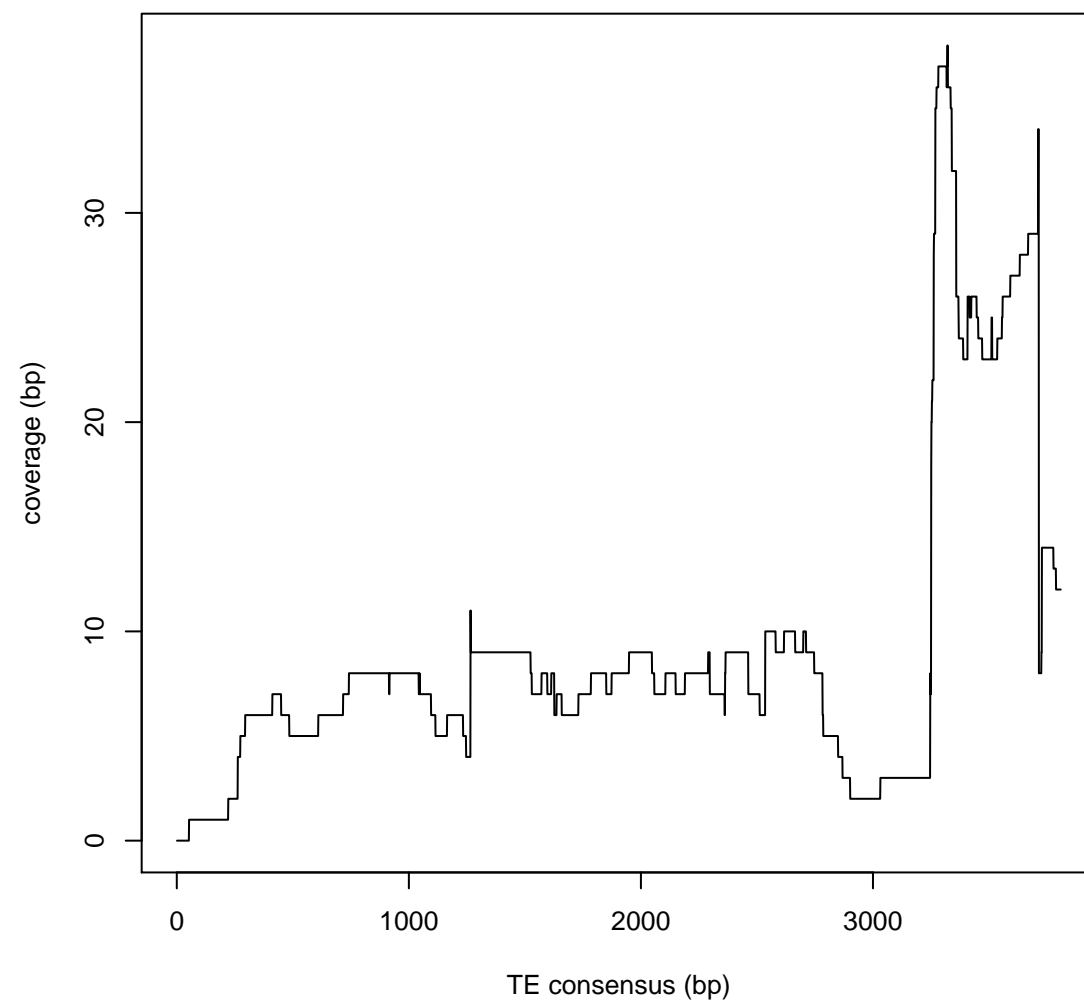


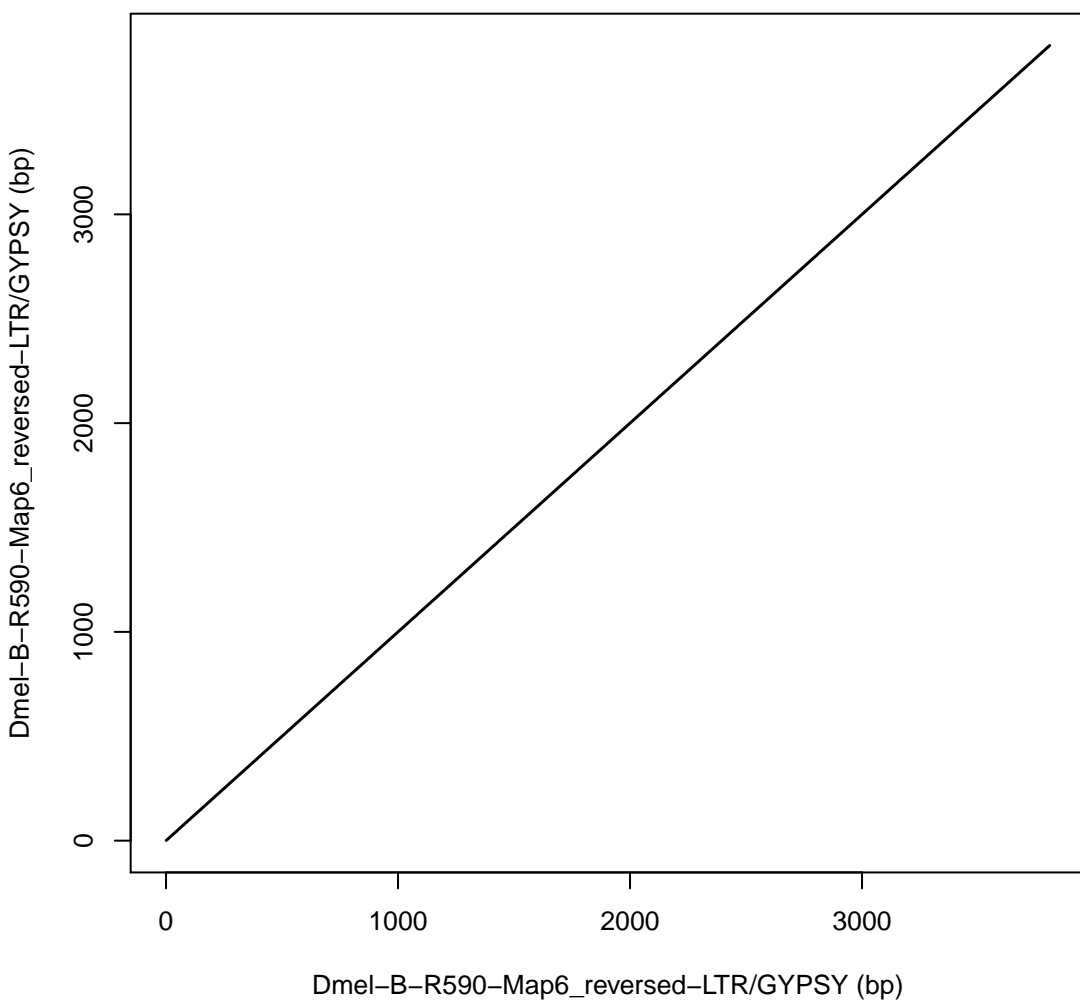
TE: Dmel-B-R590-Map6_reversed-LTR/GYPSY
consensus size: 3809bp; fragments: 100; full length: 2 (>=3428.1bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

