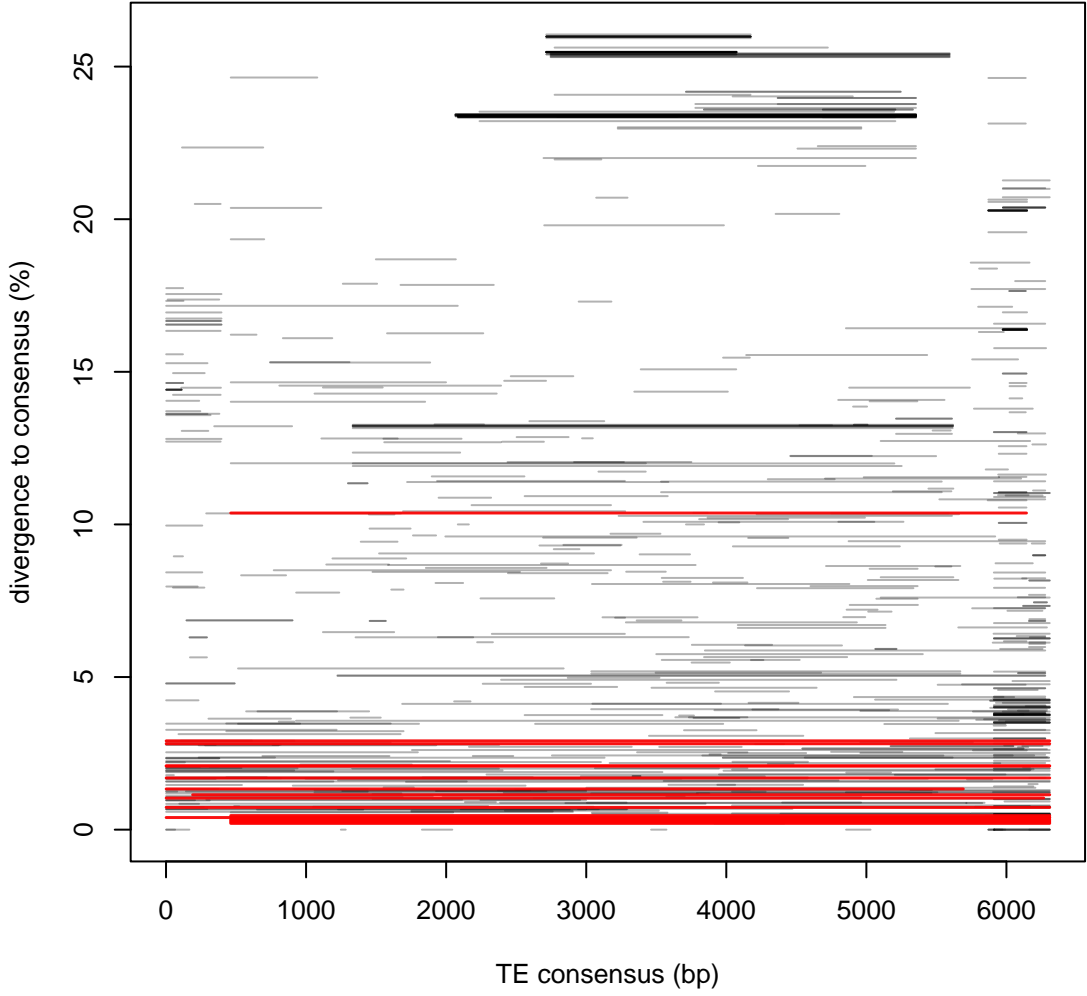
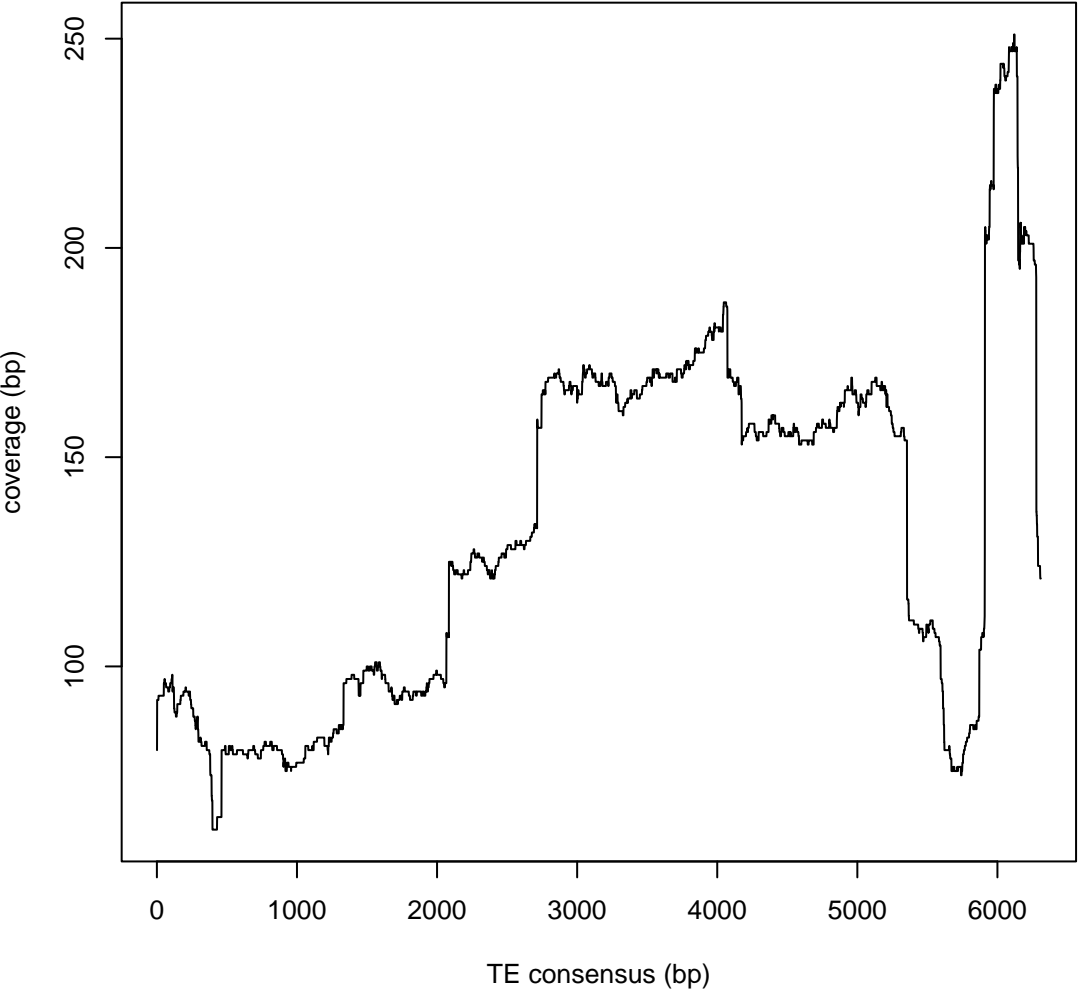


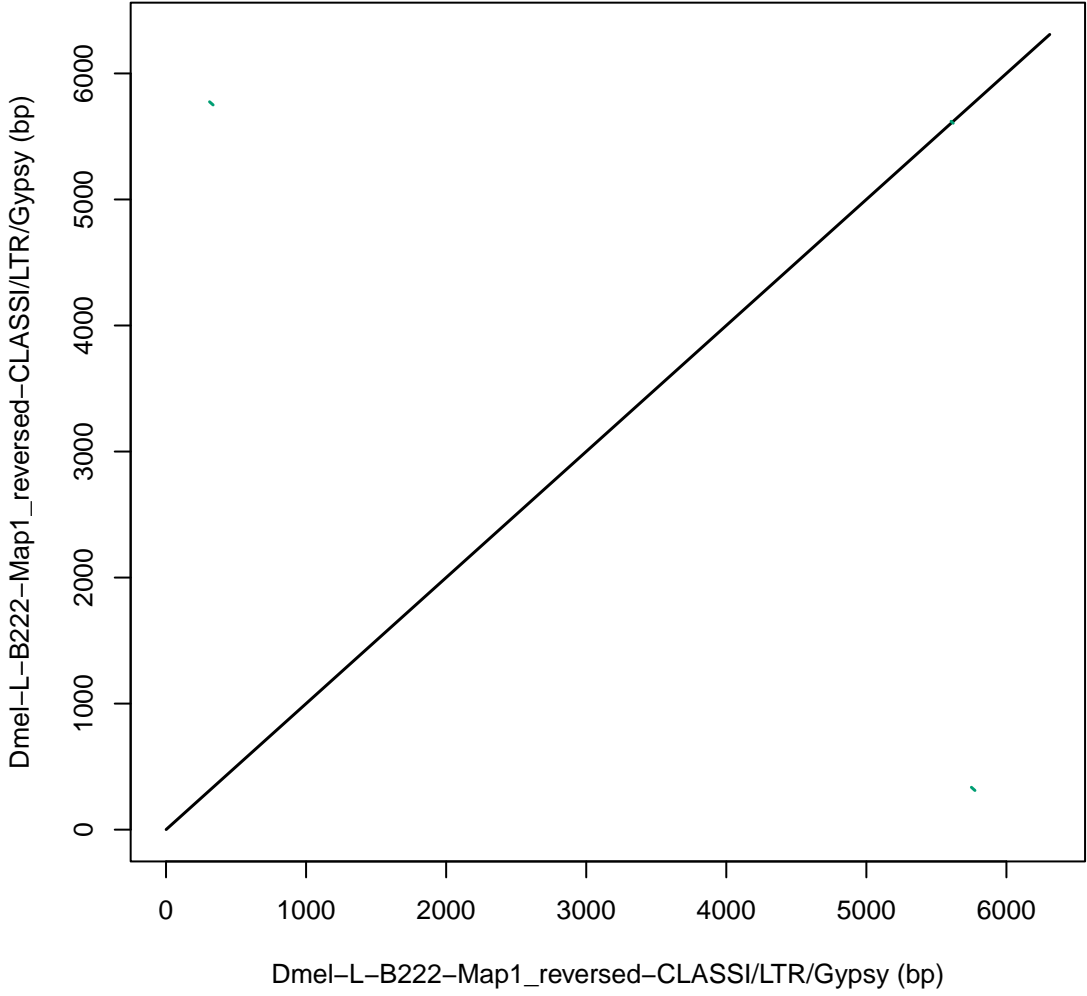
TE: Dmel-L-B222-Map1_reversed-CLASSI/LTR/Gypsy
consensus size: 6309bp; fragments: 753; full length: 18 (>=5678.1bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

