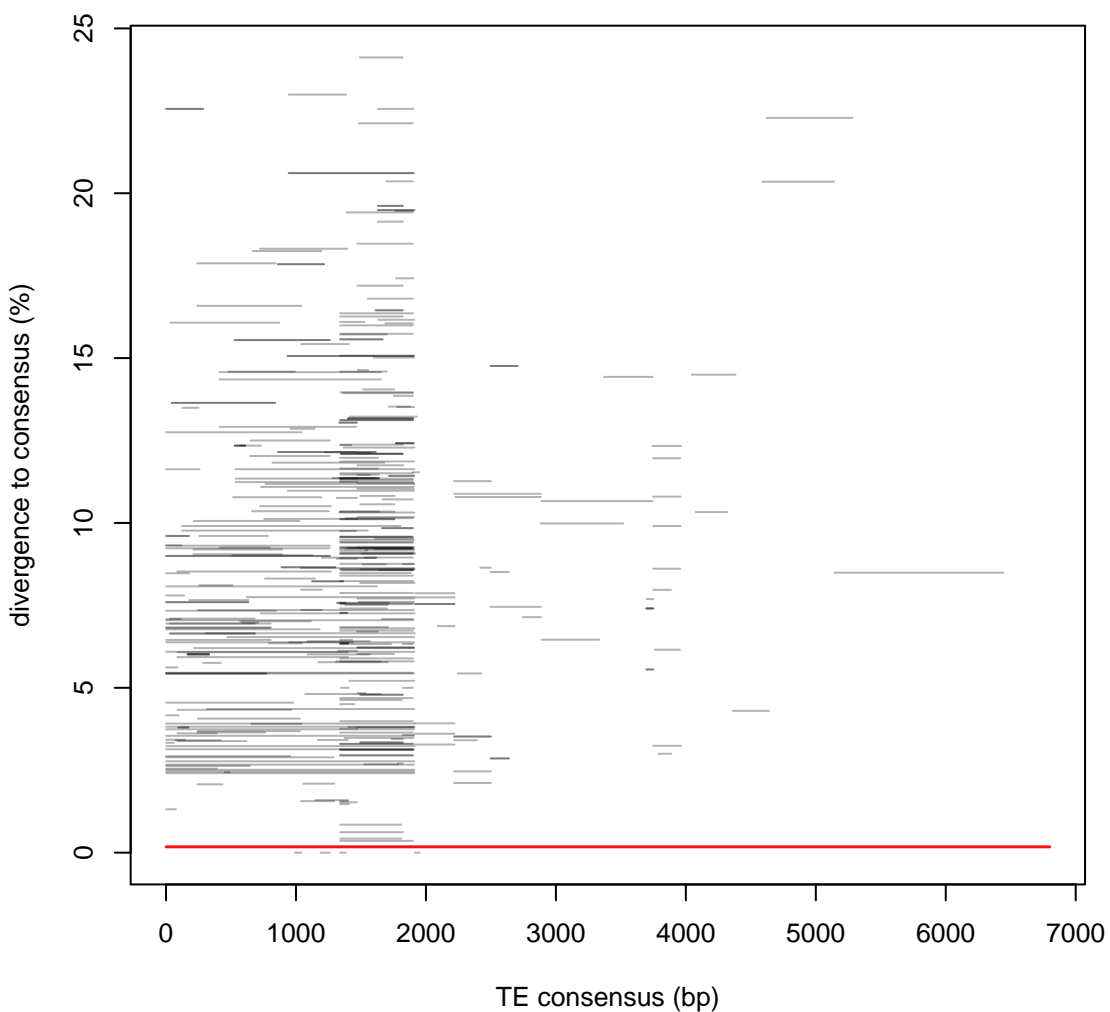
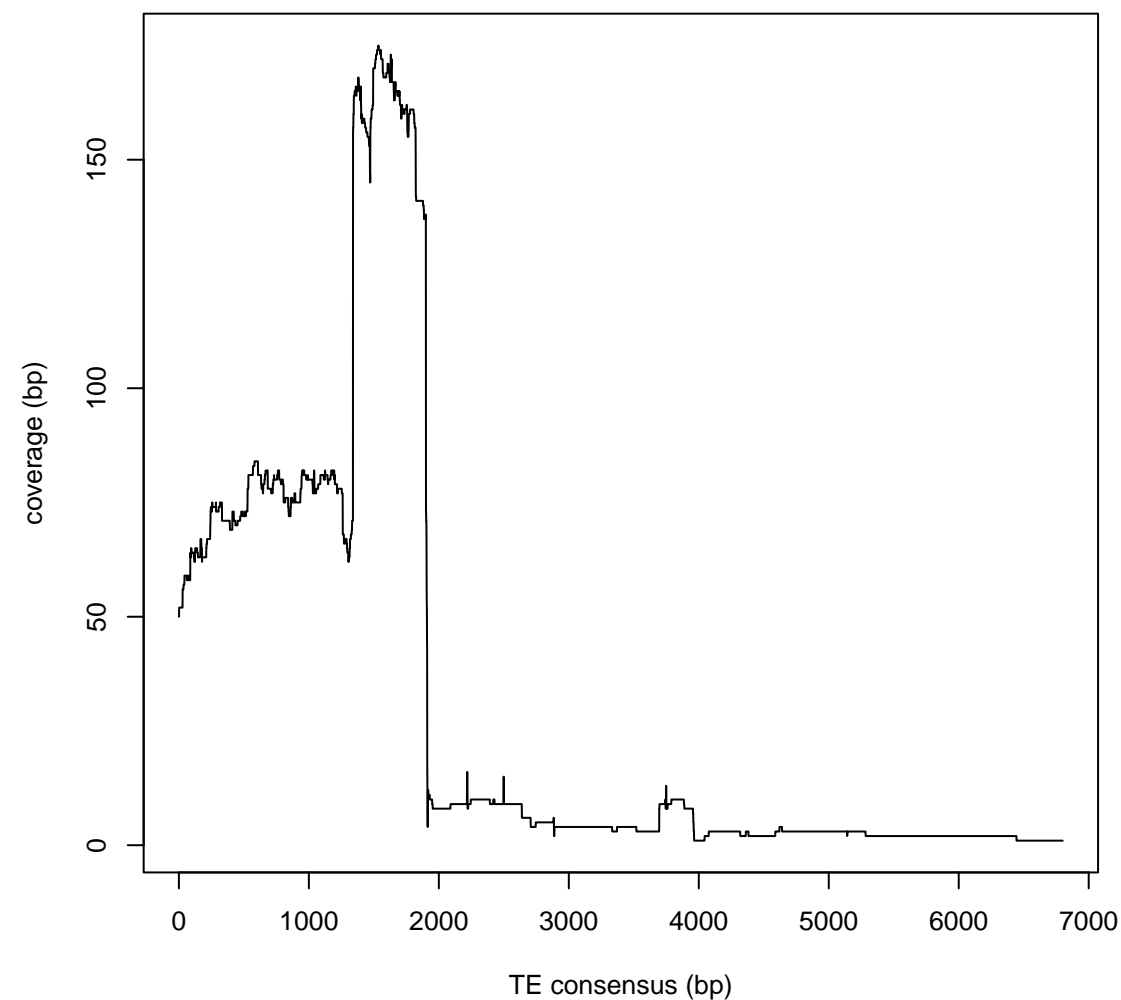


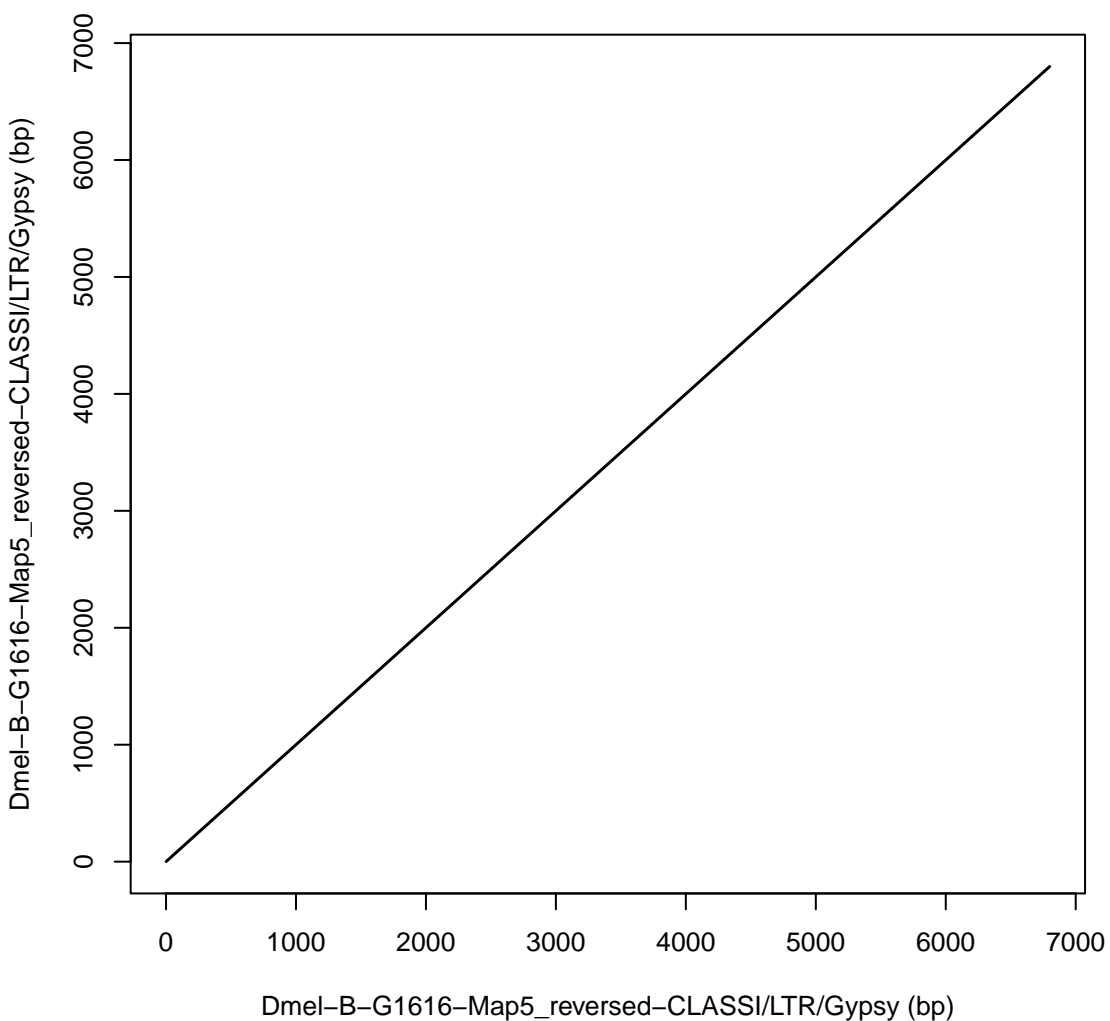
TE: Dmel-B-G1616-Map5_reversed-CLASSI/LTR/Gypsy
consensus size: 6800bp; fragments: 399; full length: 1 (>=6120bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

