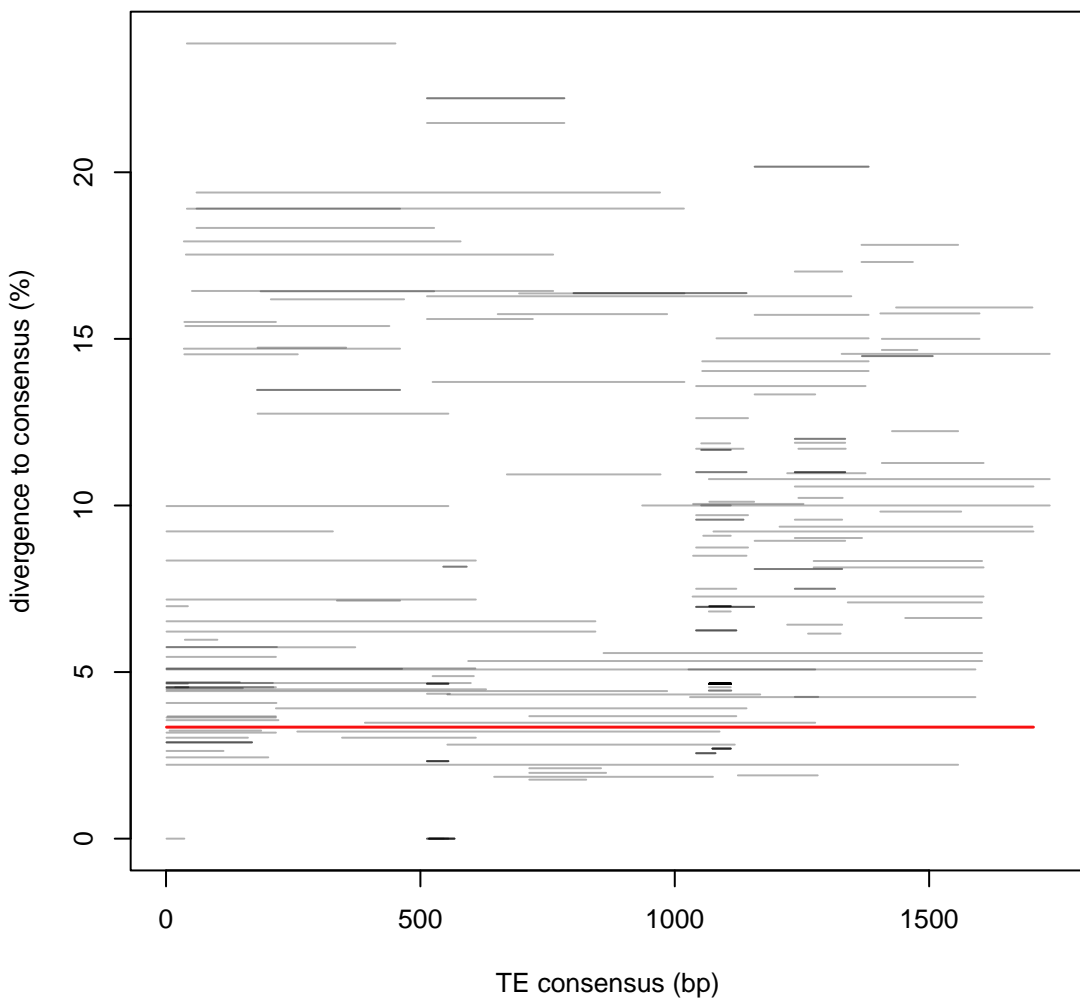
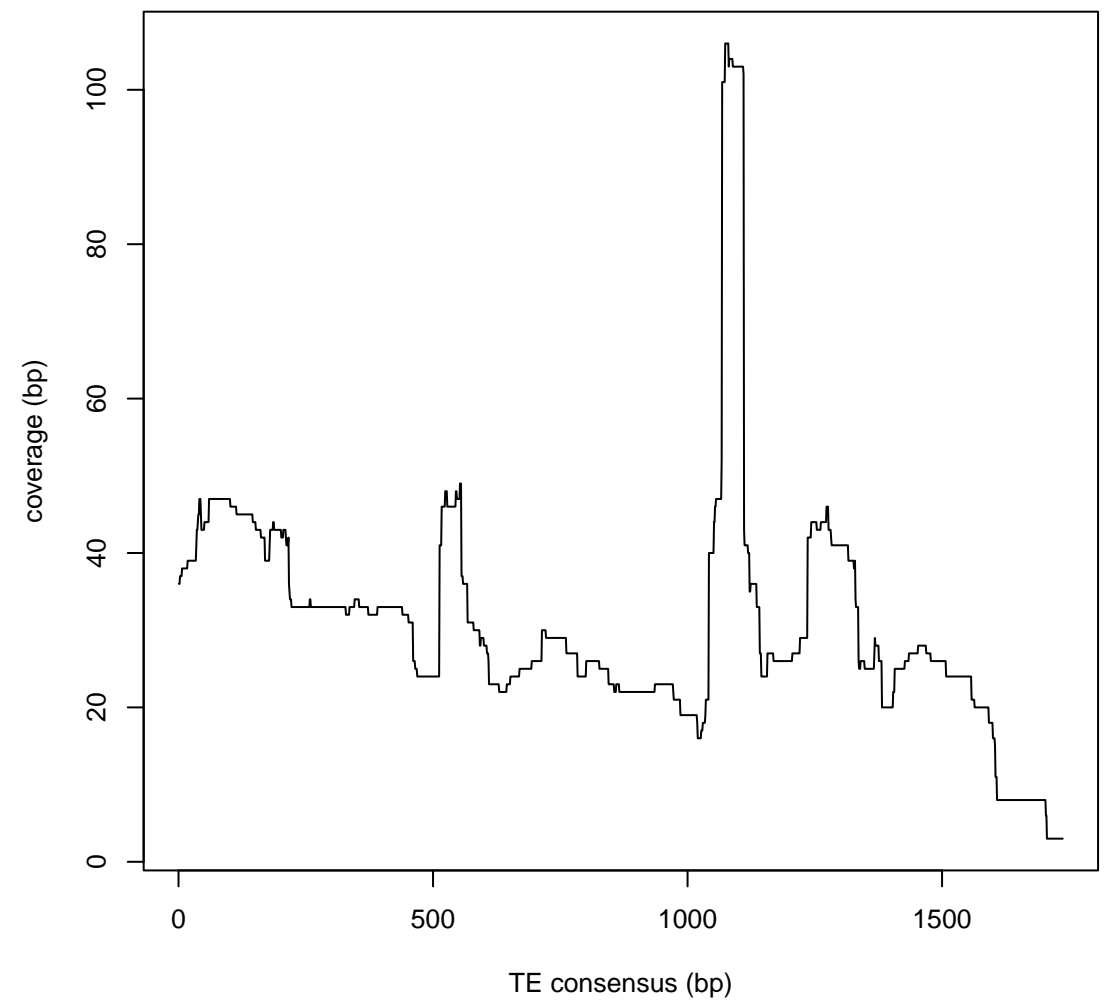


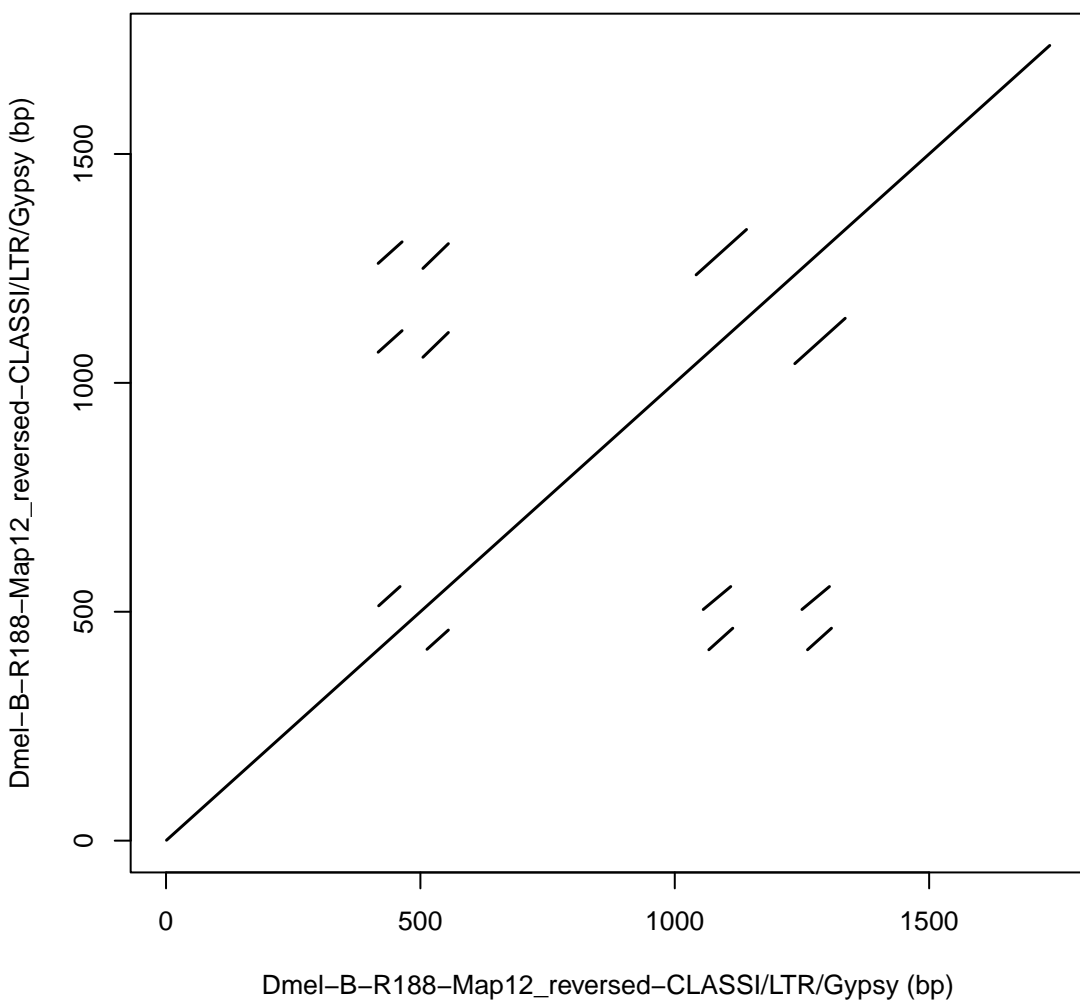
TE: Dmel-B-R188-Map12\_reversed-CLASSI/LTR/Gypsy  
consensus size: 1737bp; fragments: 239; full length: 1 (>=1563.3bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

