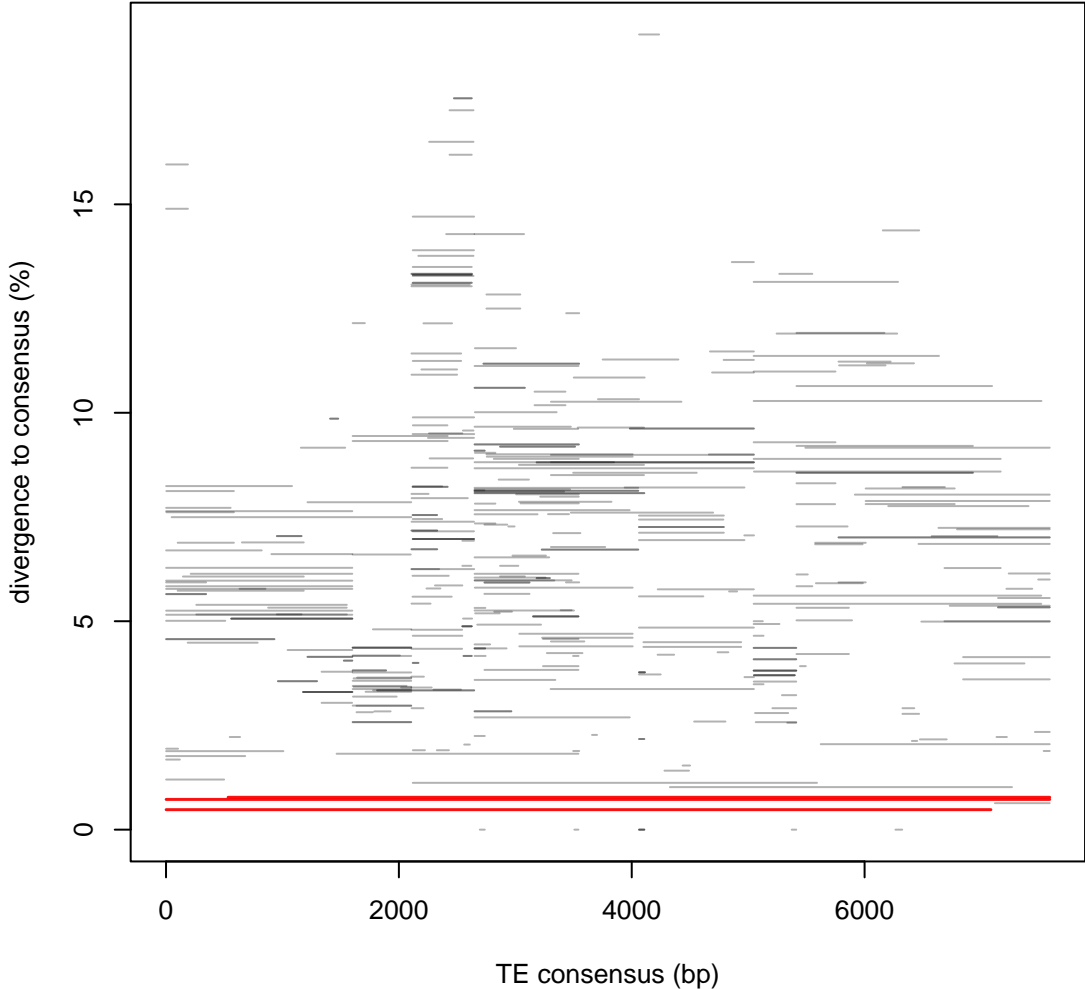
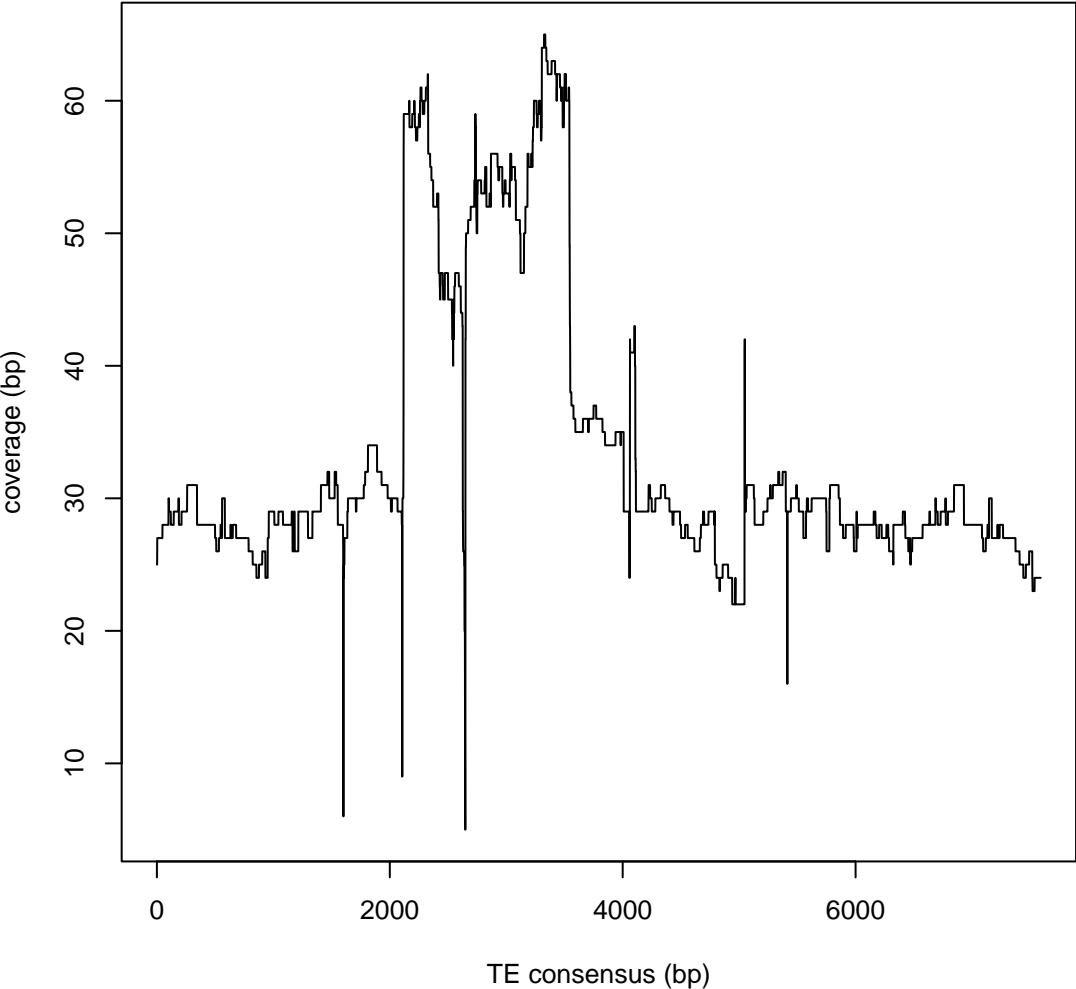


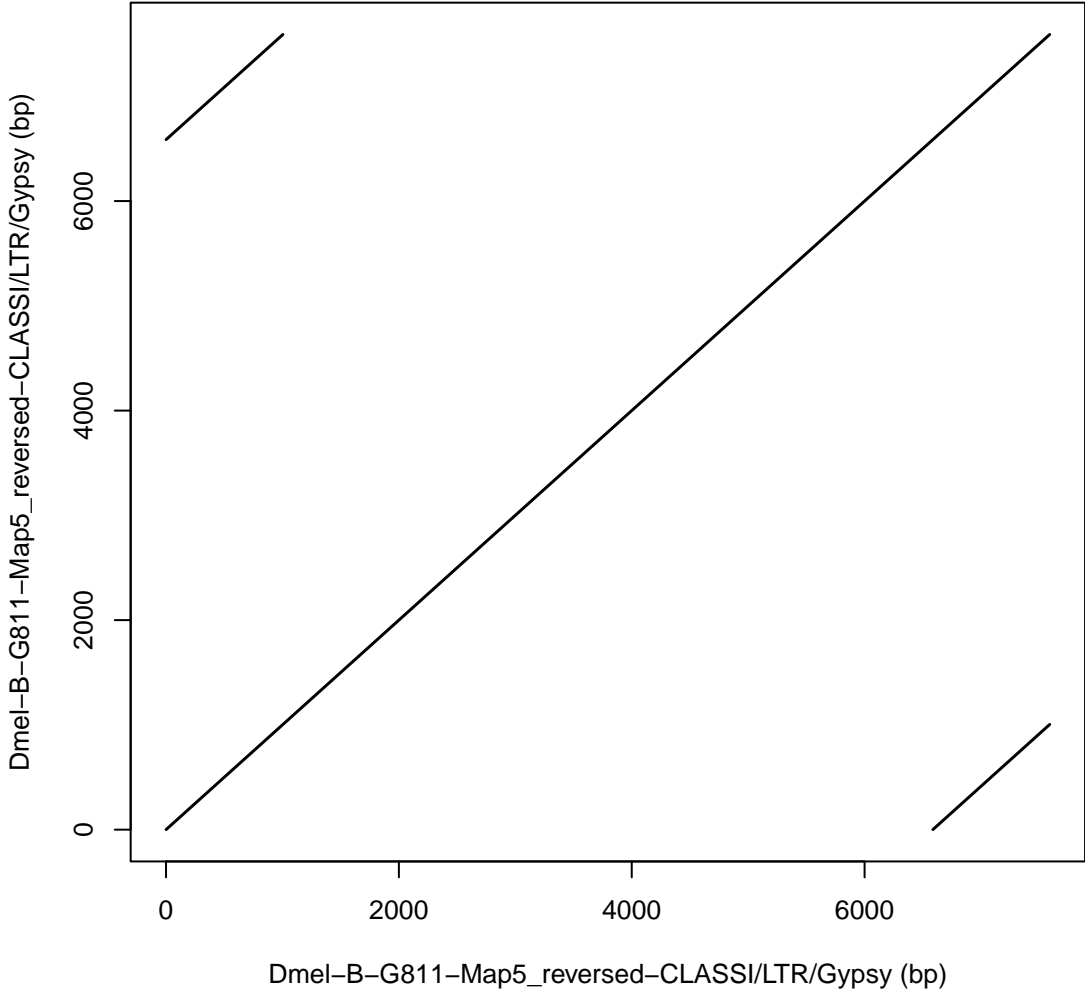
TE: Dmel-B-G811-Map5\_reversed-CLASSI/LTR/Gypsy  
consensus size: 7590bp; fragments: 412; full length: 3 (>=6831bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

