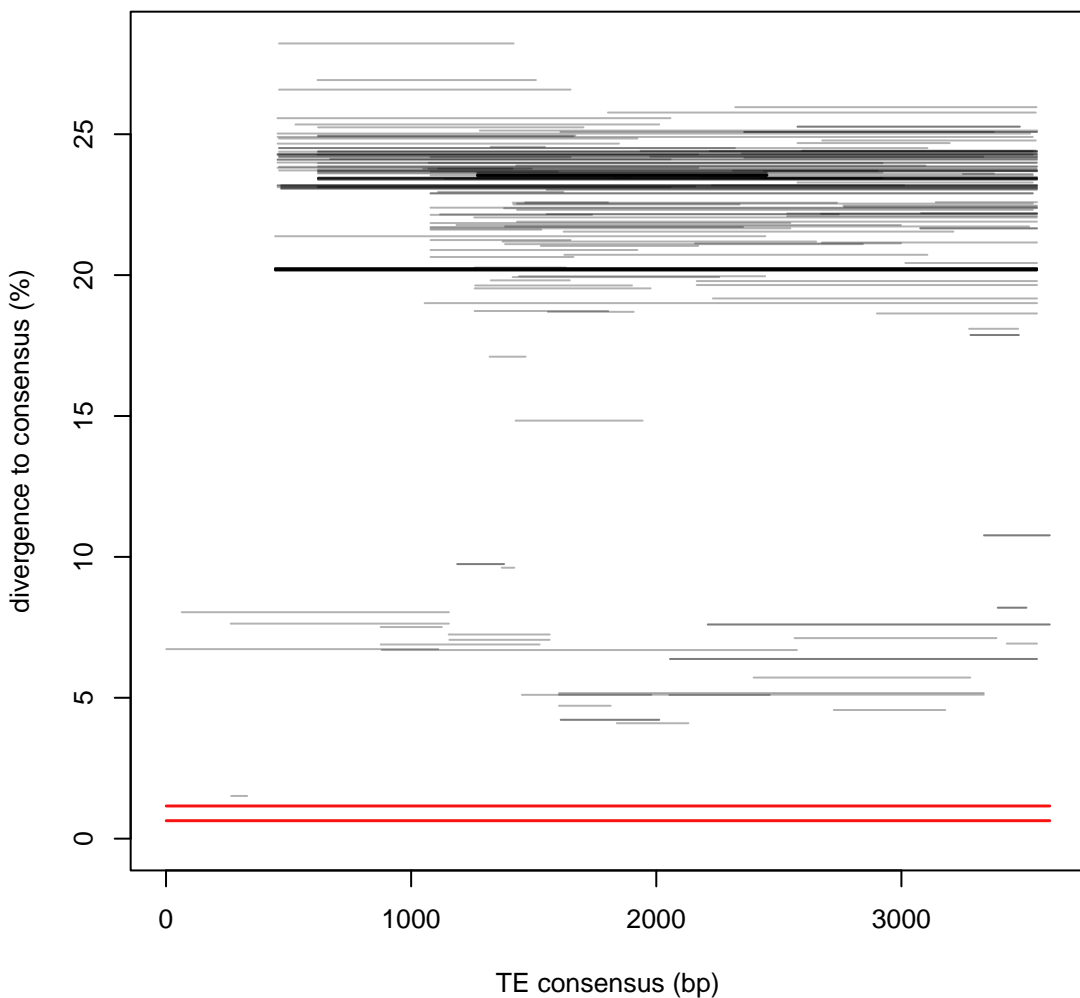
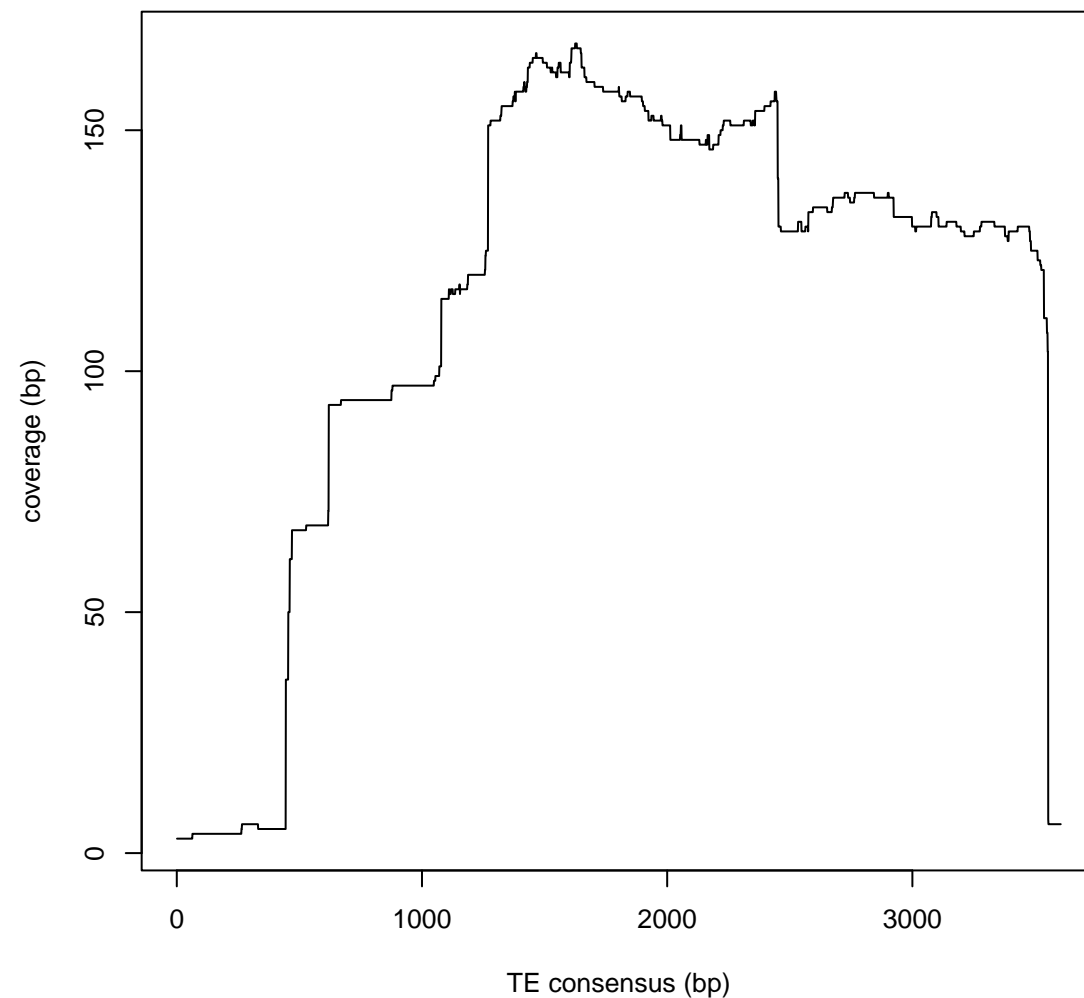


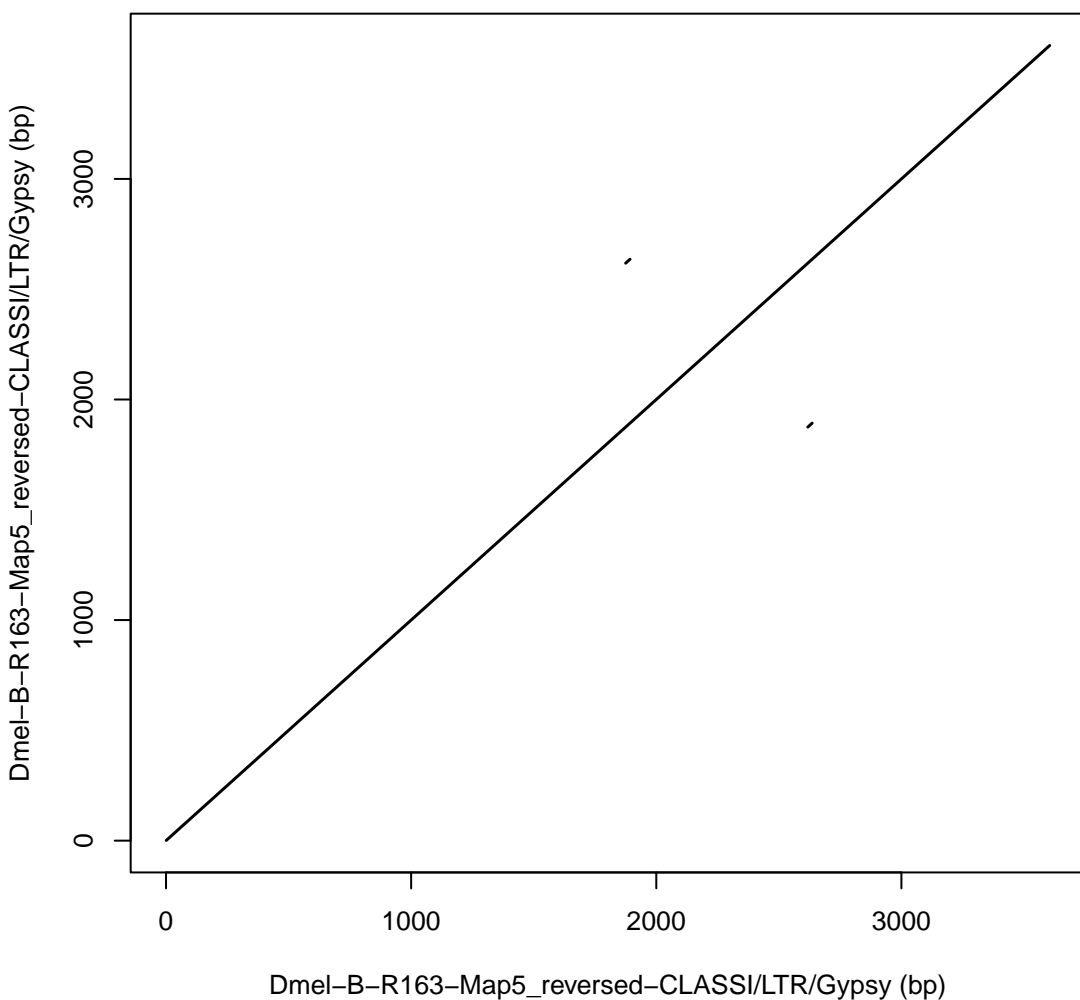
TE: Dmel-B-R163-Map5\_reversed-CLASSI/LTR/Gypsy  
consensus size: 3605bp; fragments: 244; full length: 2 (>=3244.5bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

