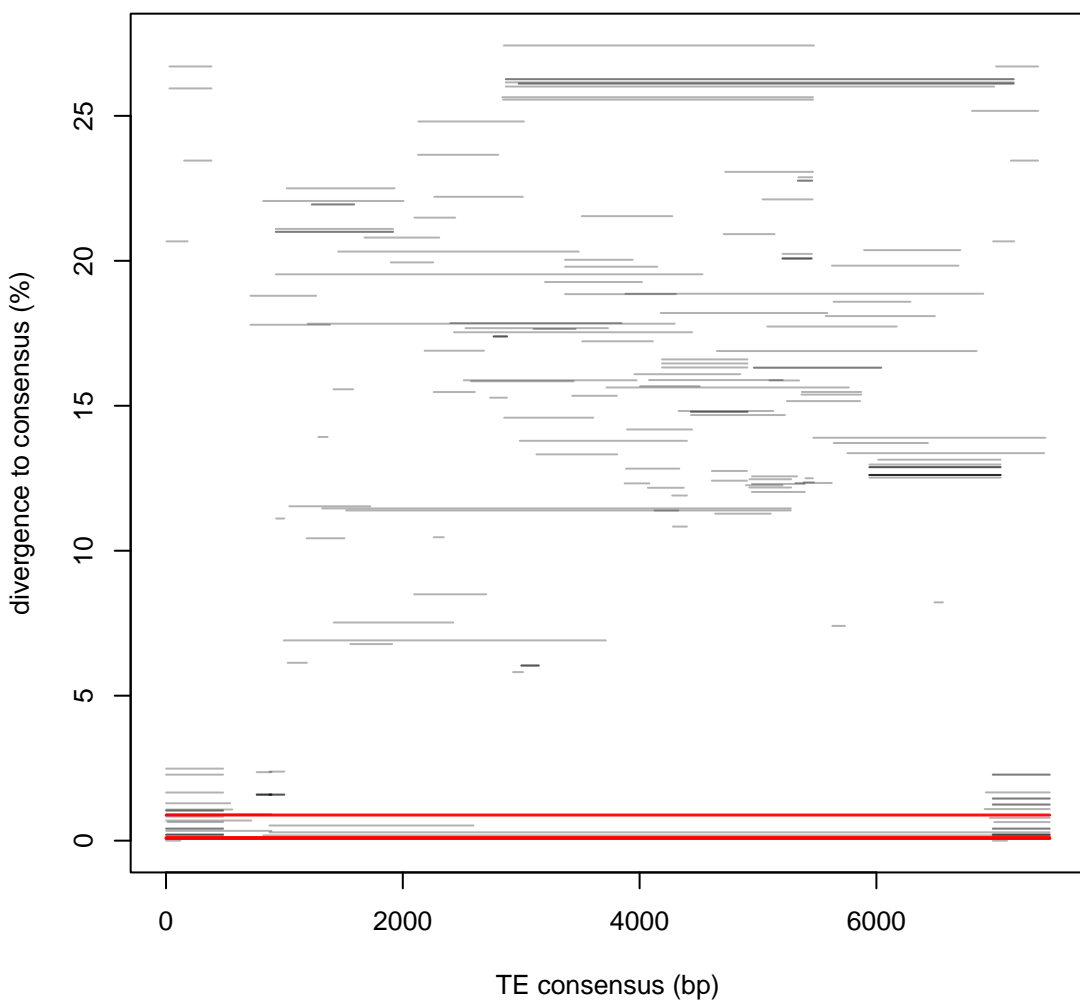
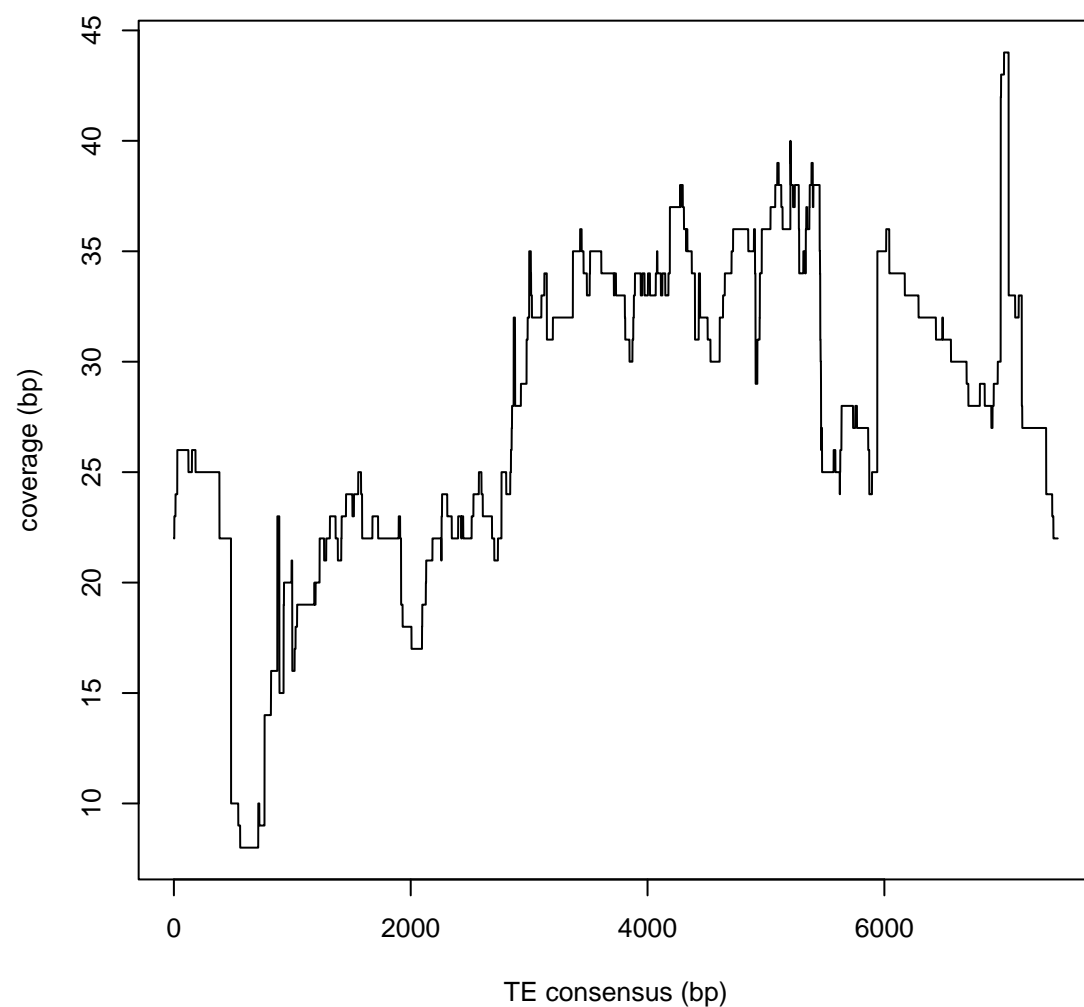


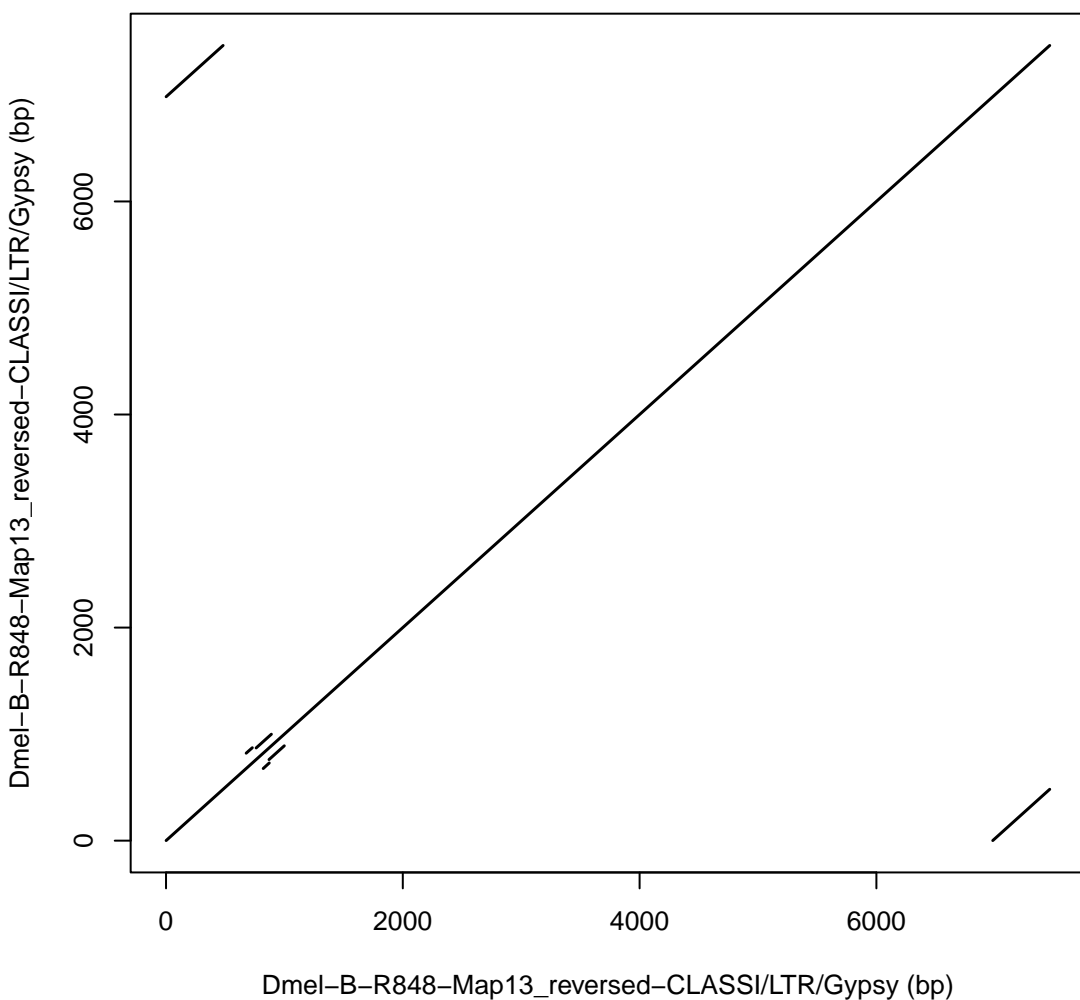
TE: Dmel-B-R848-Map13\_reversed-CLASSI/LTR/Gypsy  
consensus size: 7464bp; fragments: 196; full length: 4 (>=6717.6bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

