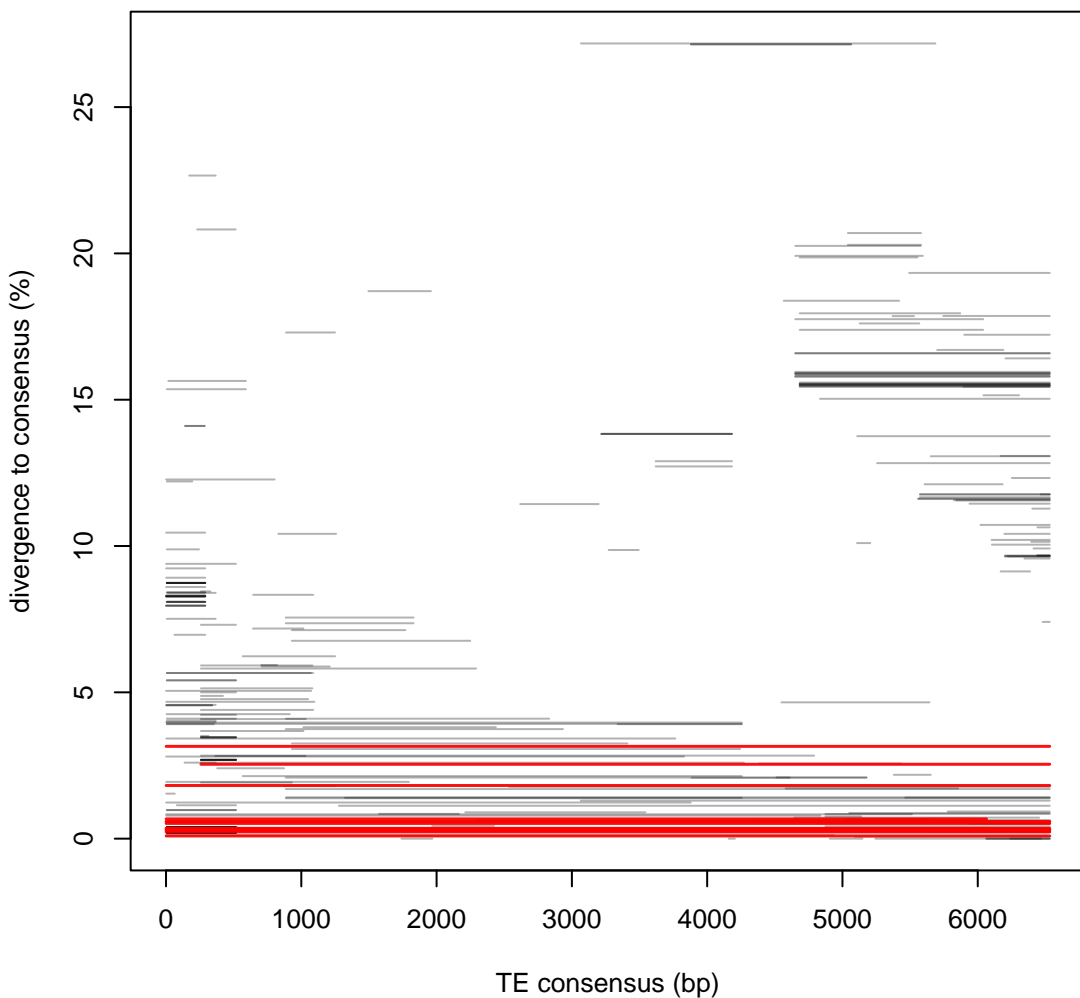
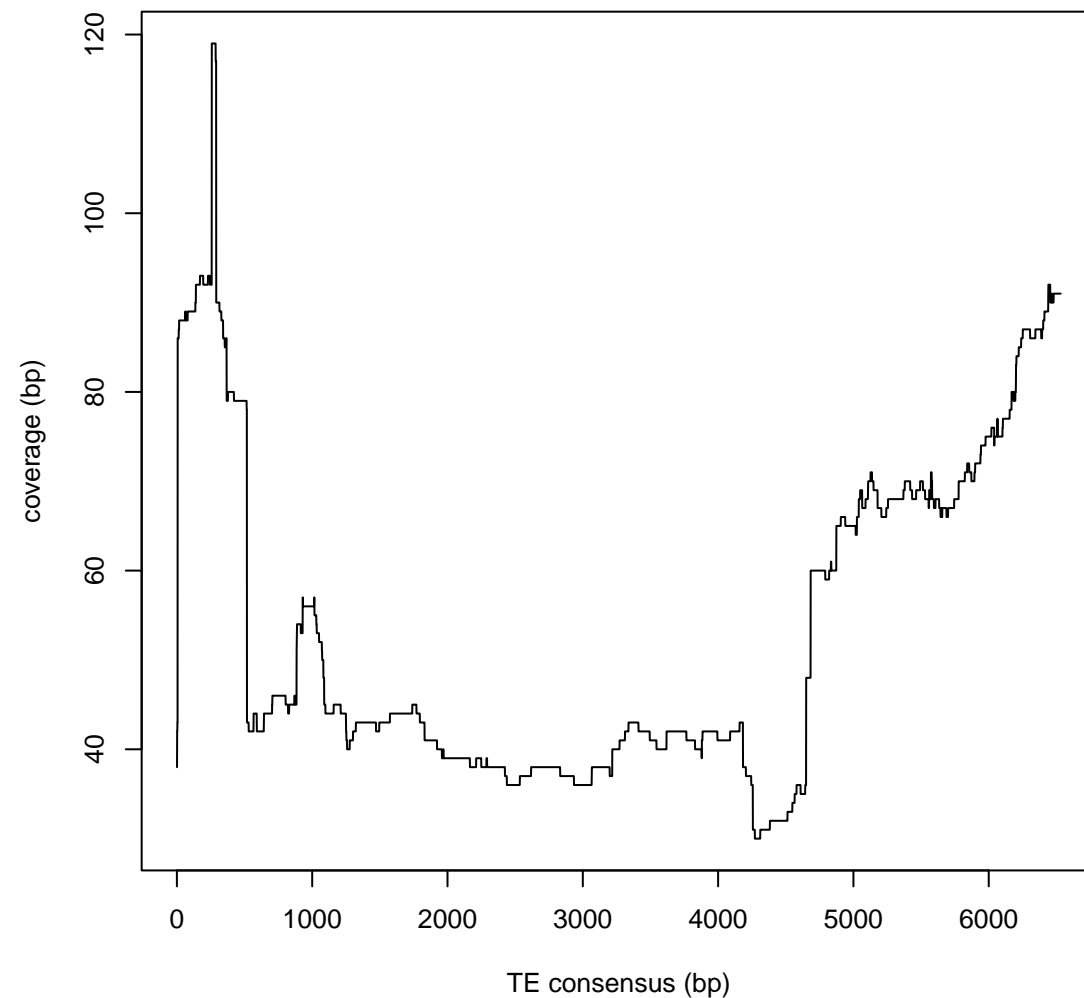


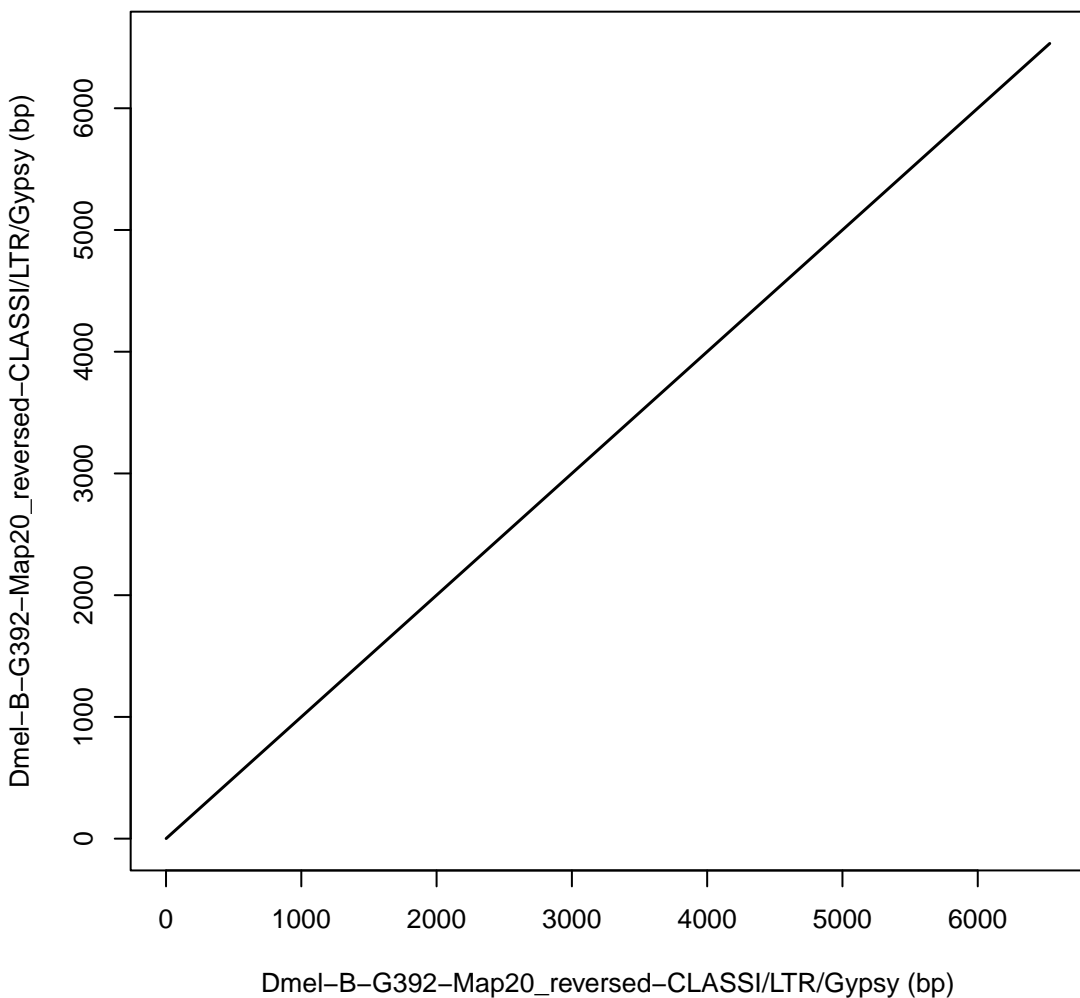
TE: Dmel-B-G392-Map20\_reversed-CLASSI/LTR/Gypsy  
consensus size: 6532bp; fragments: 273; full length: 13 (>=5878.8bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

