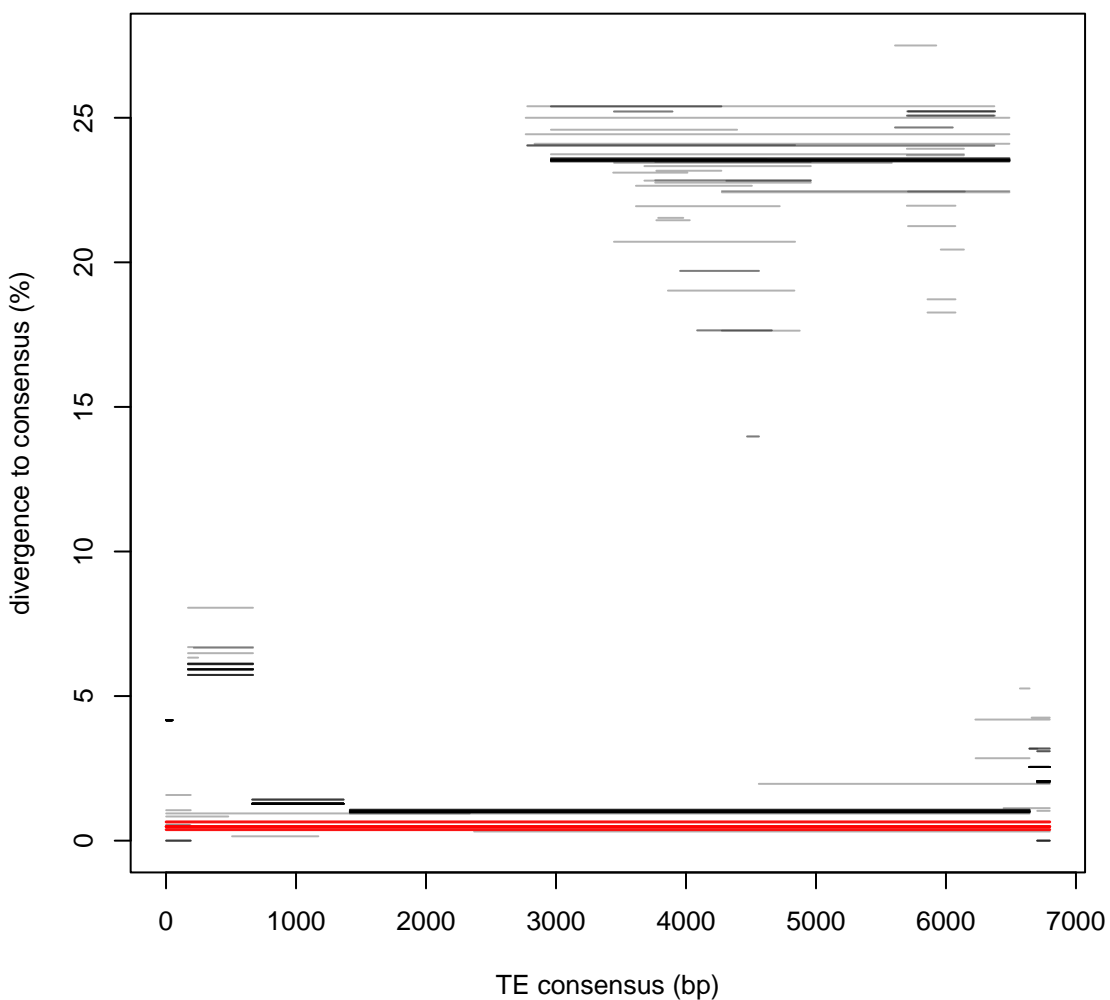
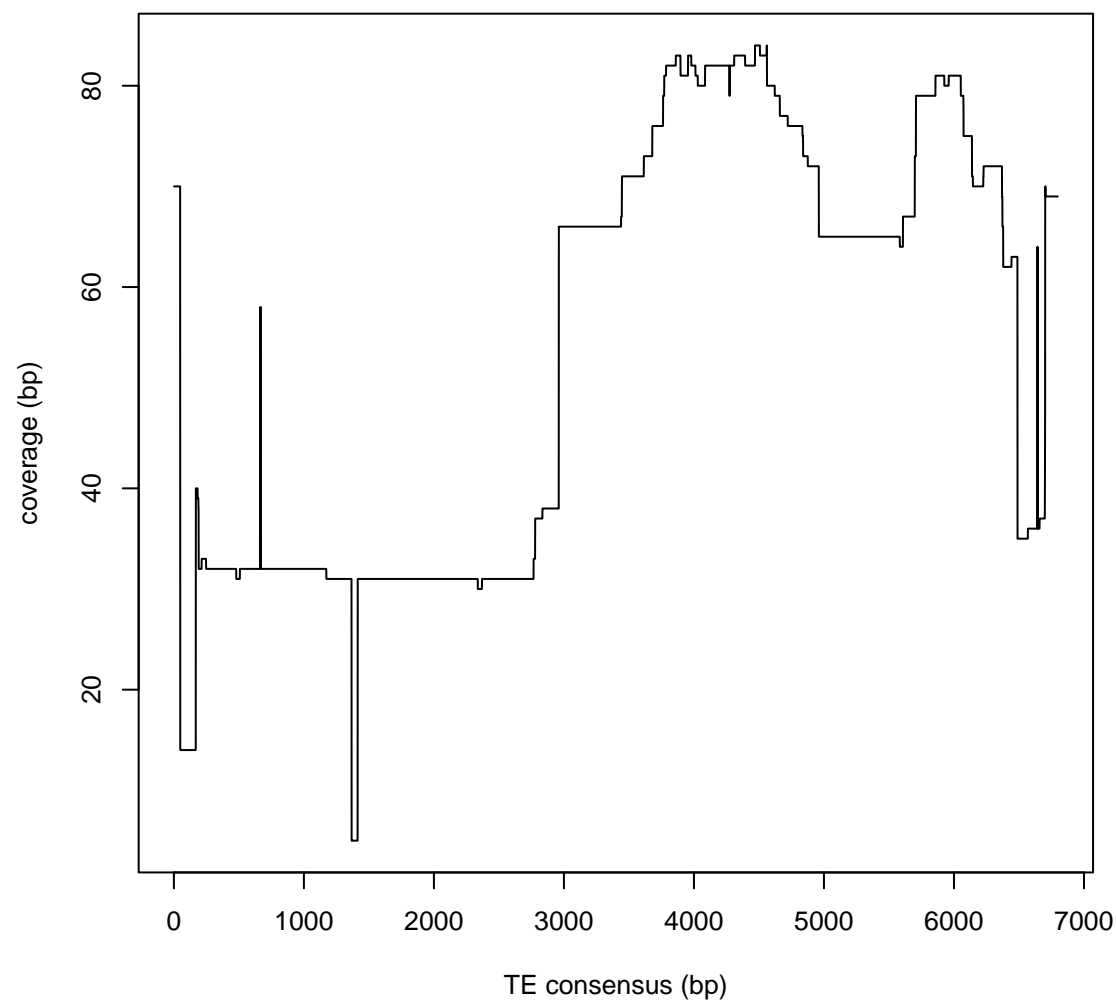


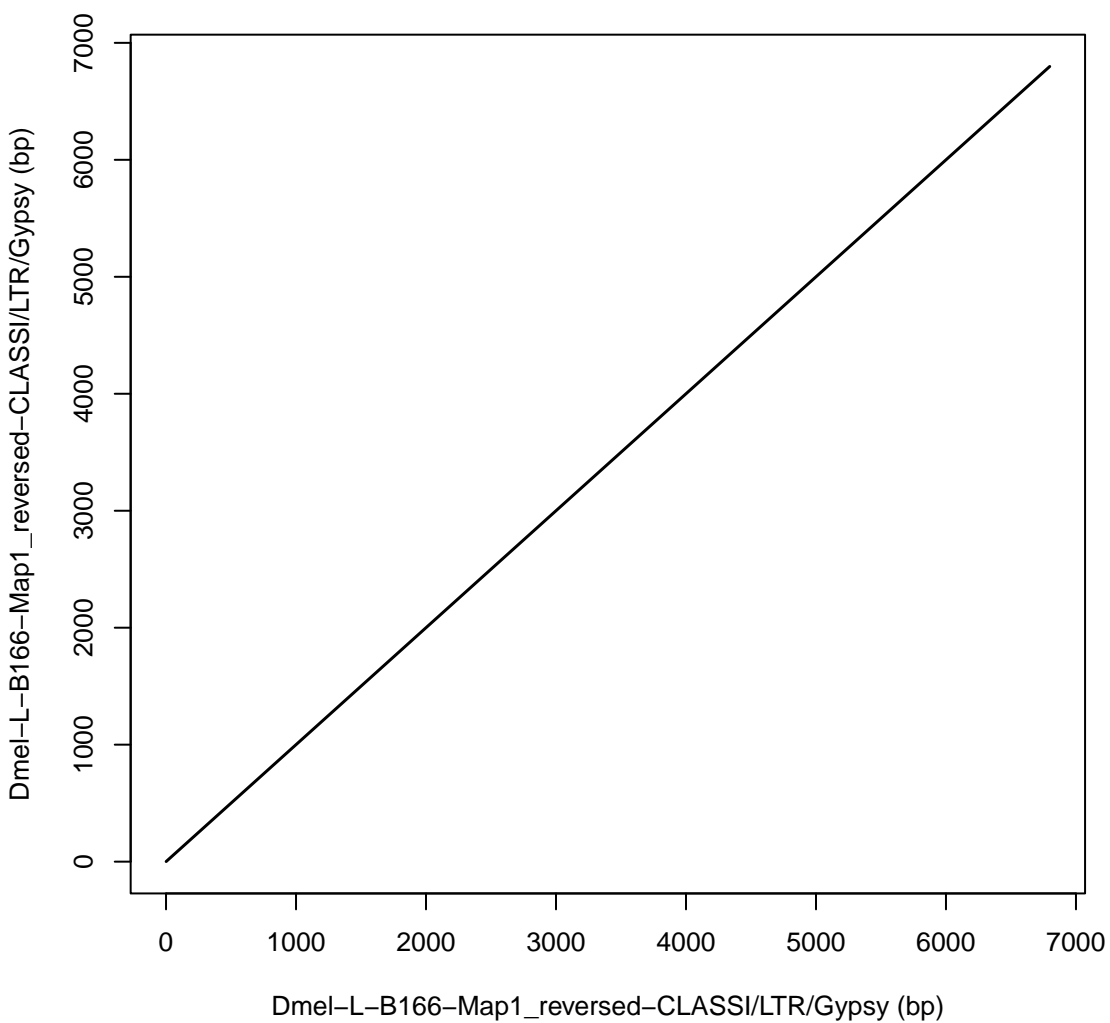
TE: Dmel-L-B166-Map1\_reversed-CLASSI/LTR/Gypsy  
consensus size: 6798bp; fragments: 298; full length: 4 (>=6118.2bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

