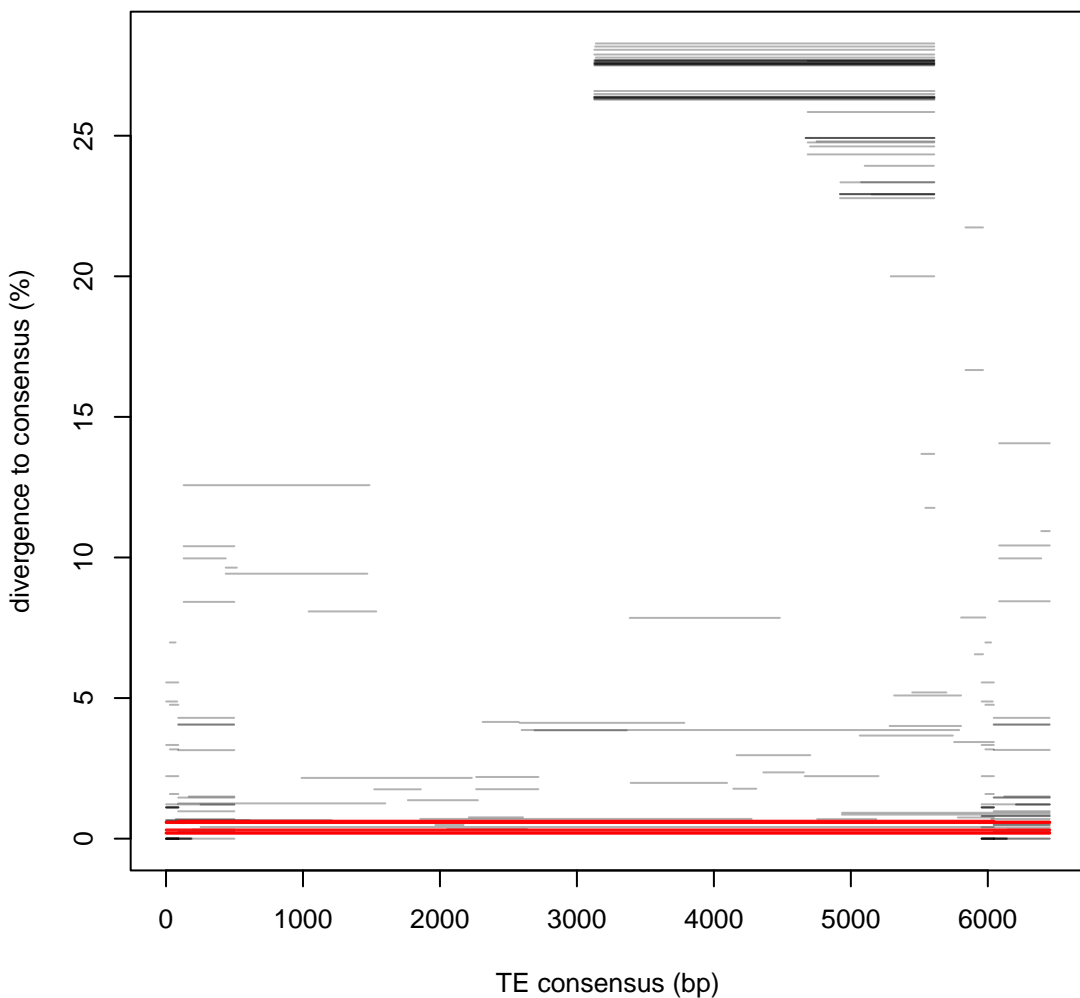
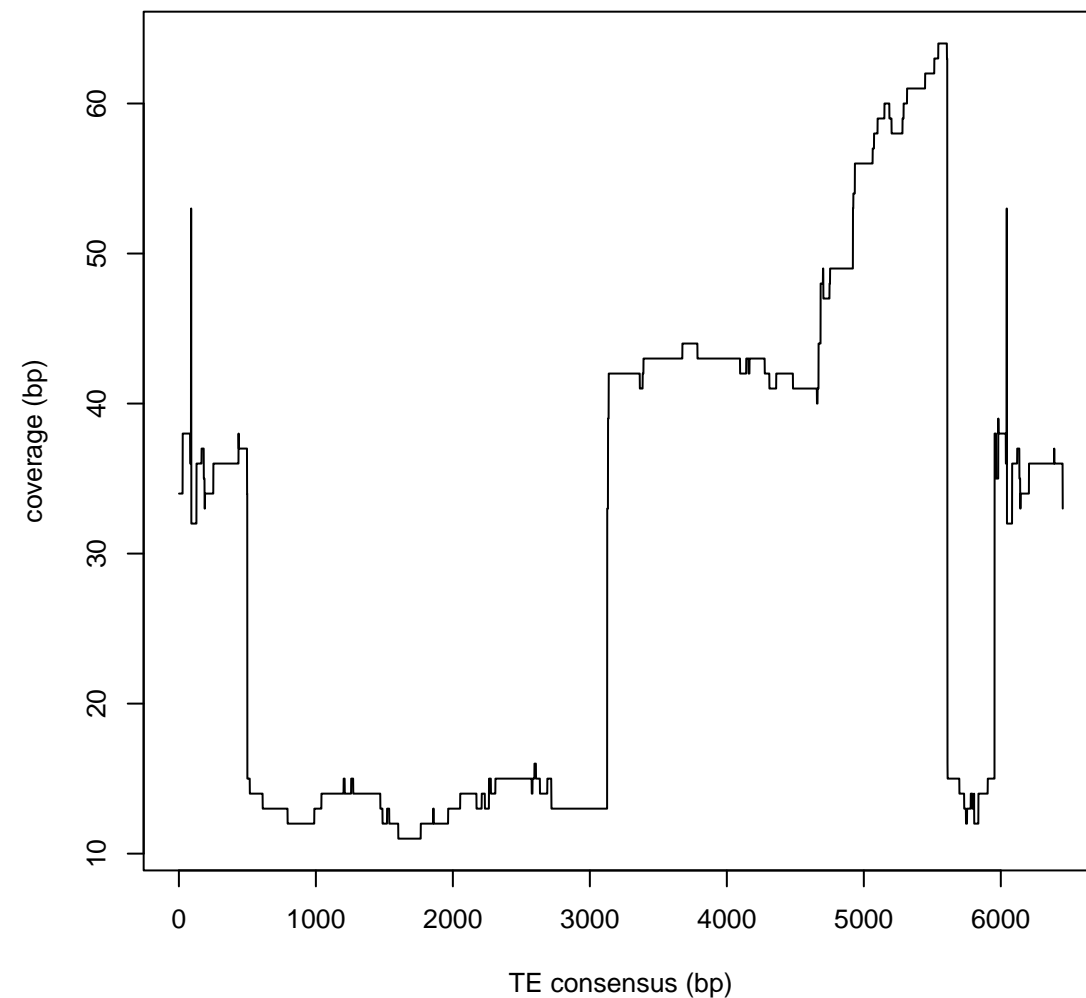


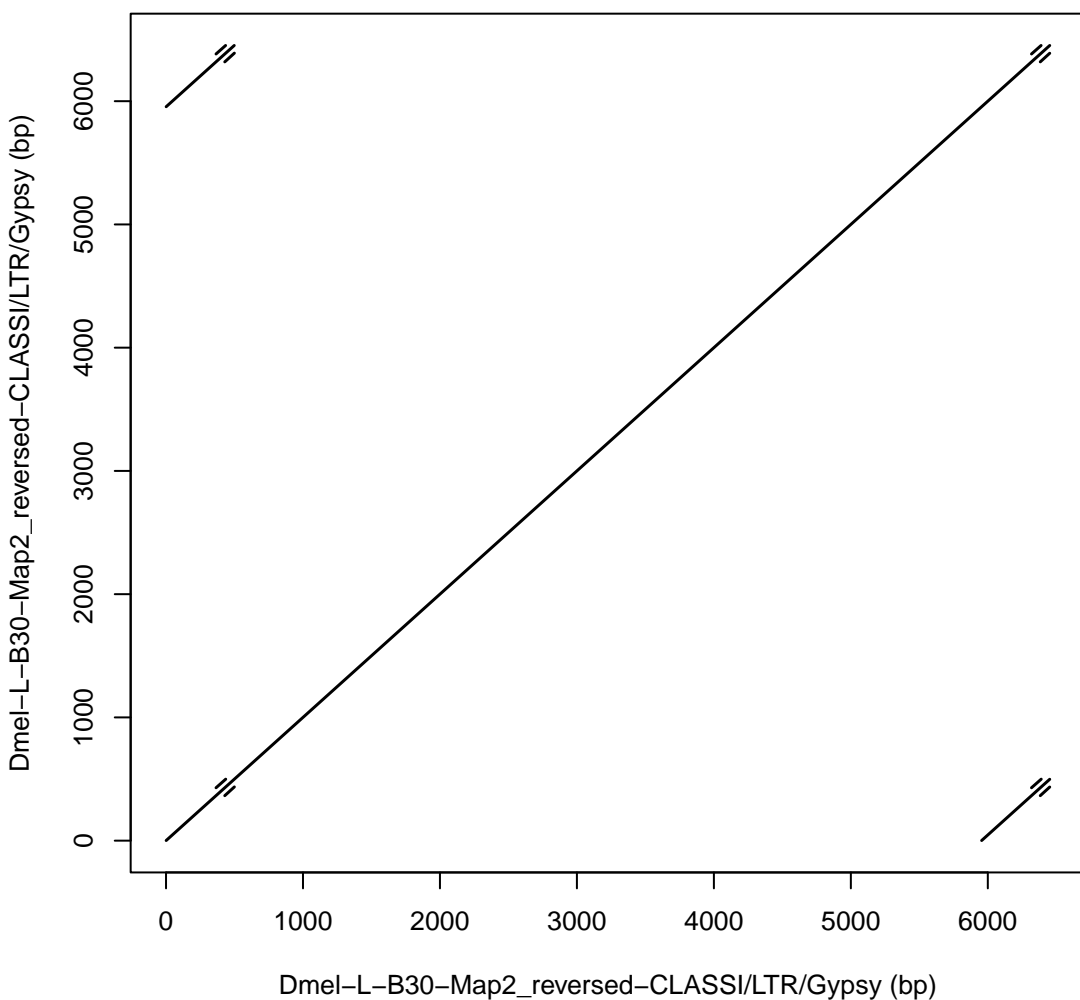
TE: Dmel-L-B30-Map2_reversed-CLASSI/LTR/Gypsy
consensus size: 6452bp; fragments: 205; full length: 6 (>=5806.8bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

