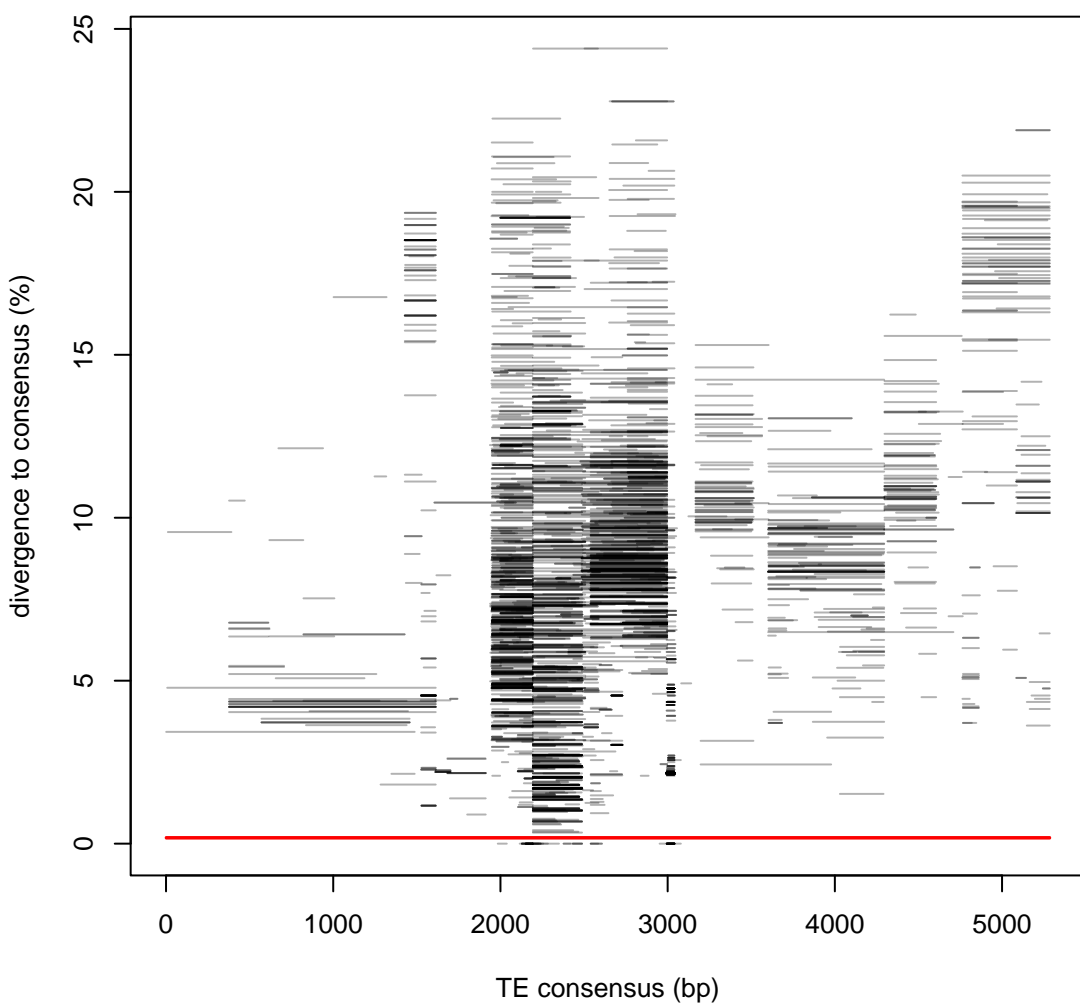
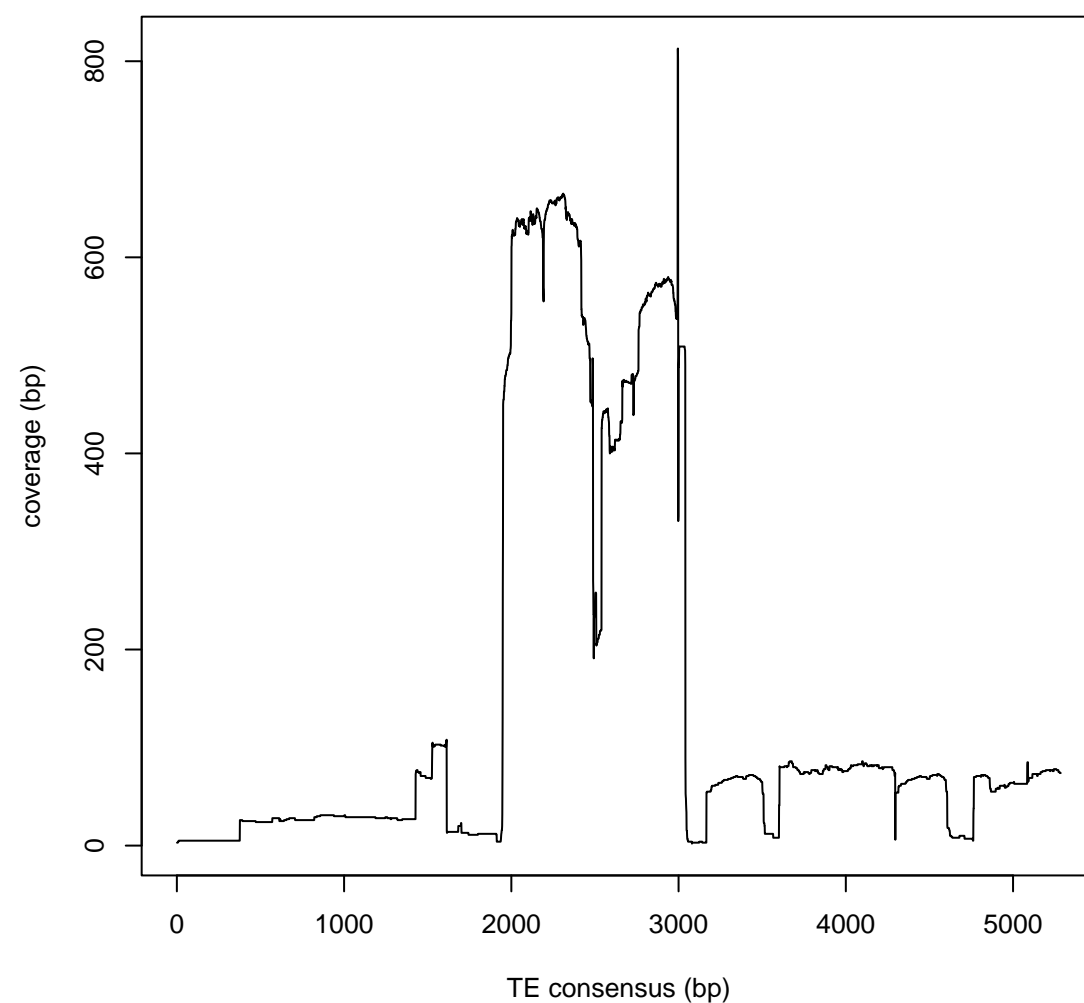


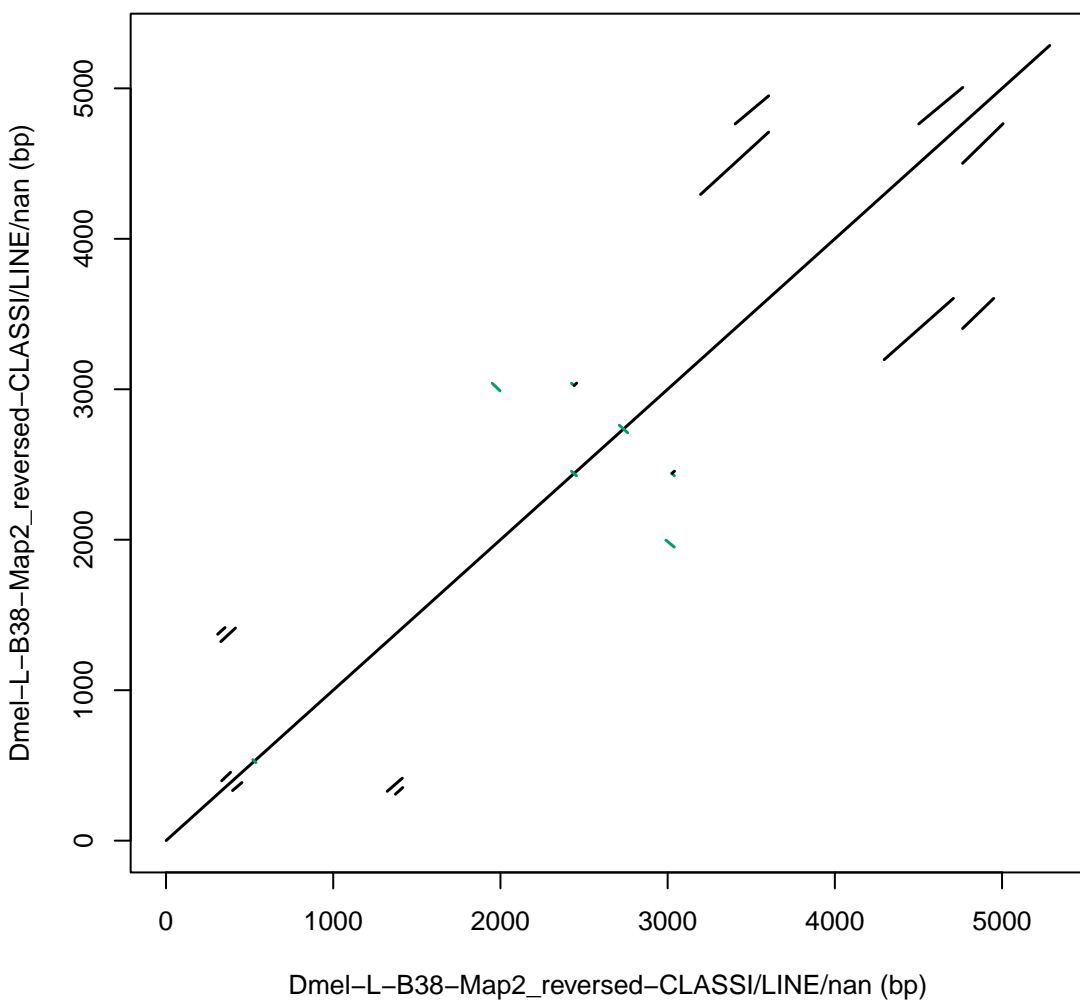
TE: Dmel-L-B38-Map2_reversed-CLASSI/LINE/nan
consensus size: 5285bp; fragments: 3179; full length: 2 (>=4756.5bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

