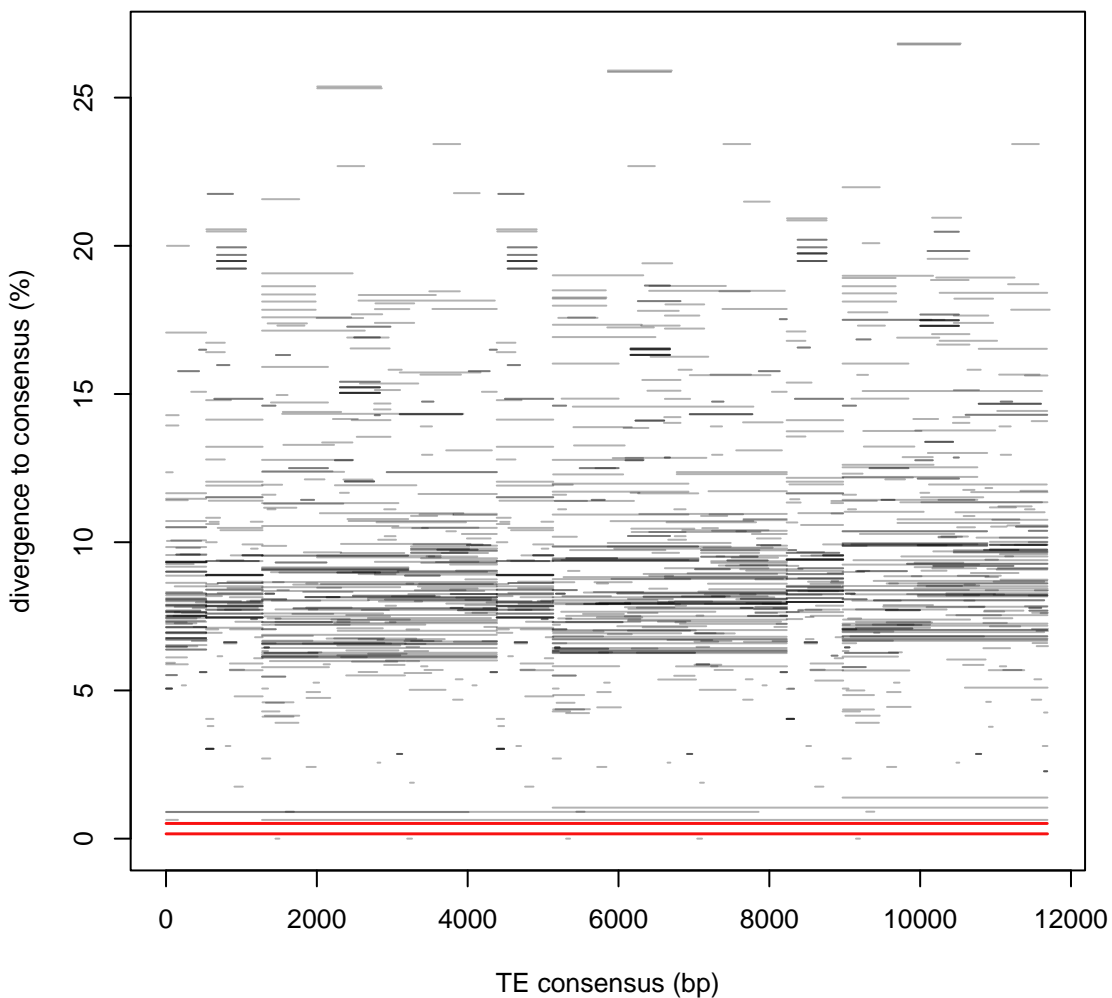
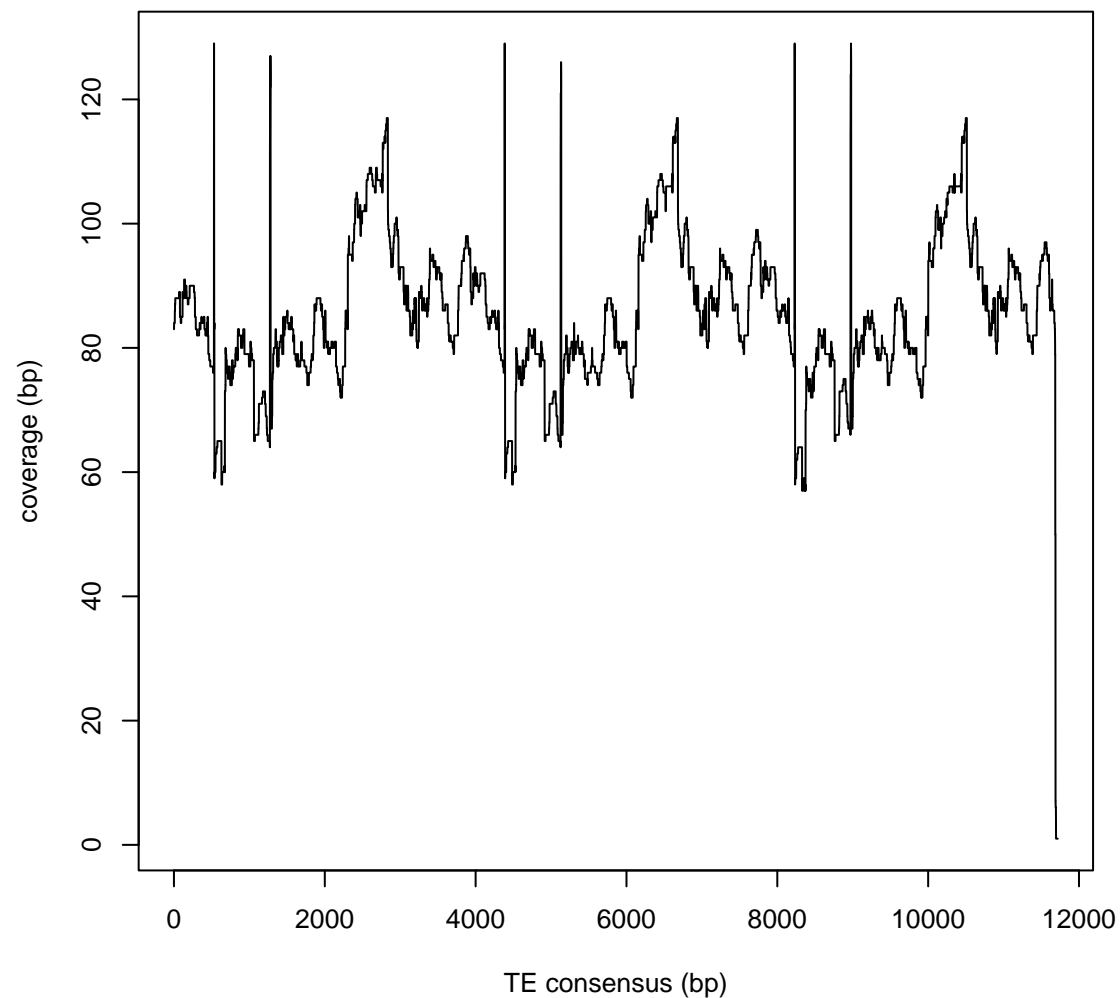


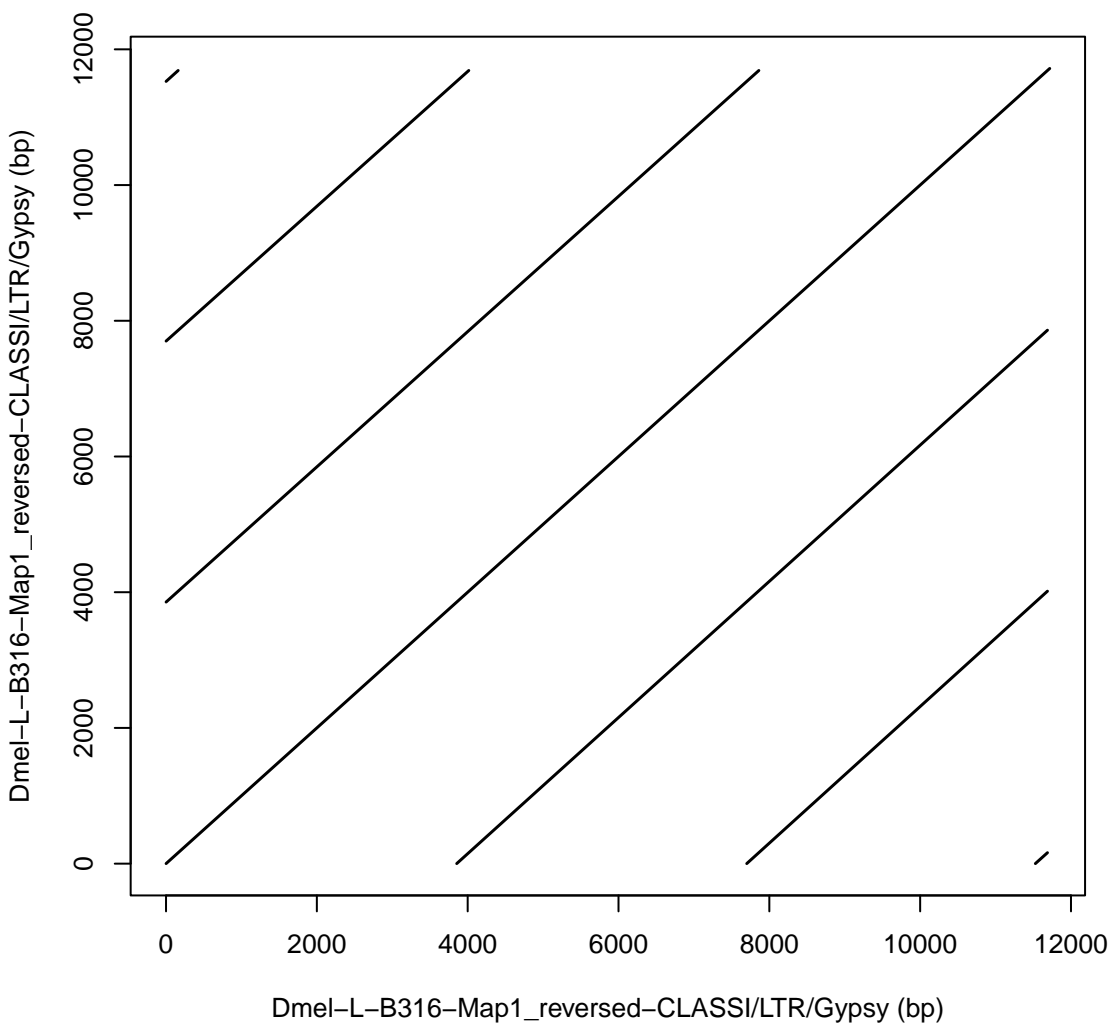
TE: Dmel-L-B316-Map1_reversed-CLASSI/LTR/Gypsy
consensus size: 11718bp; fragments: 1448; full length: 2 (>=10546.2bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

