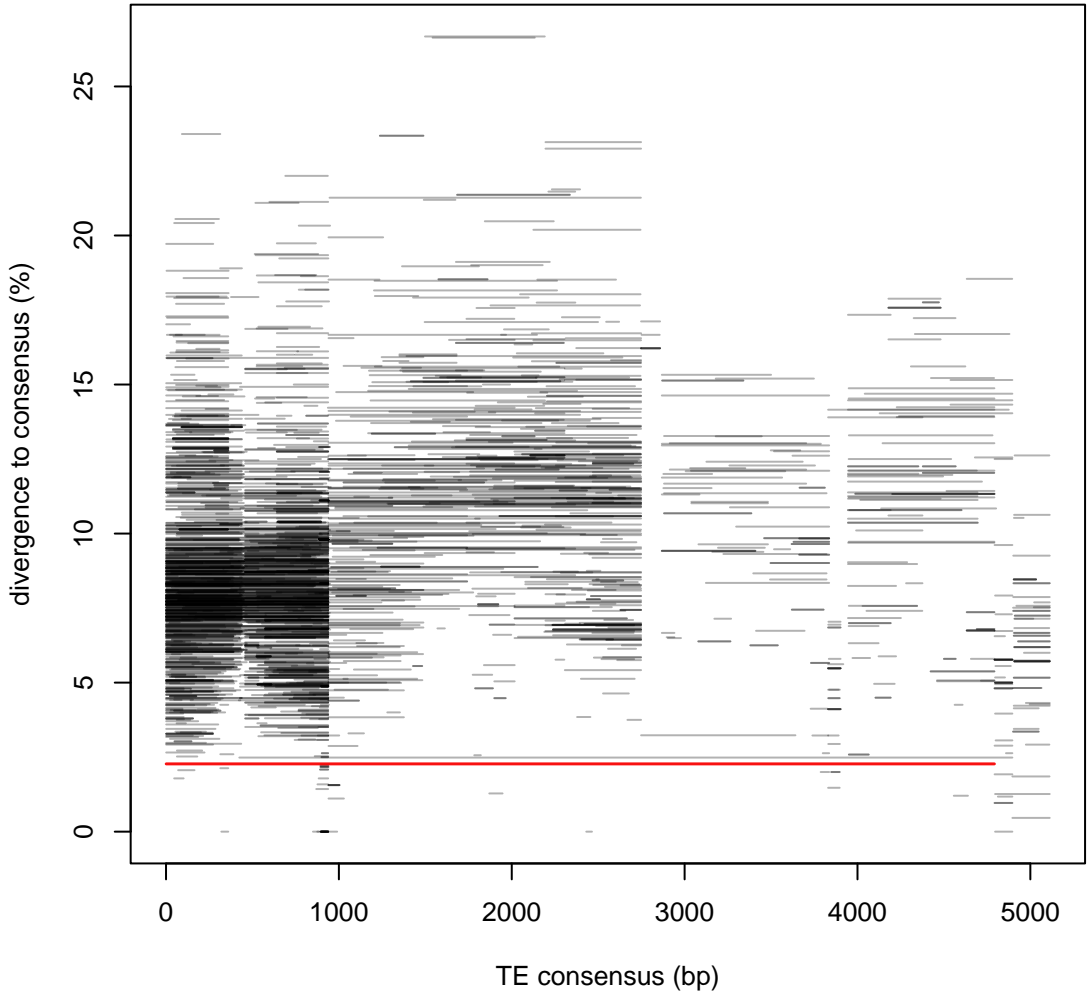
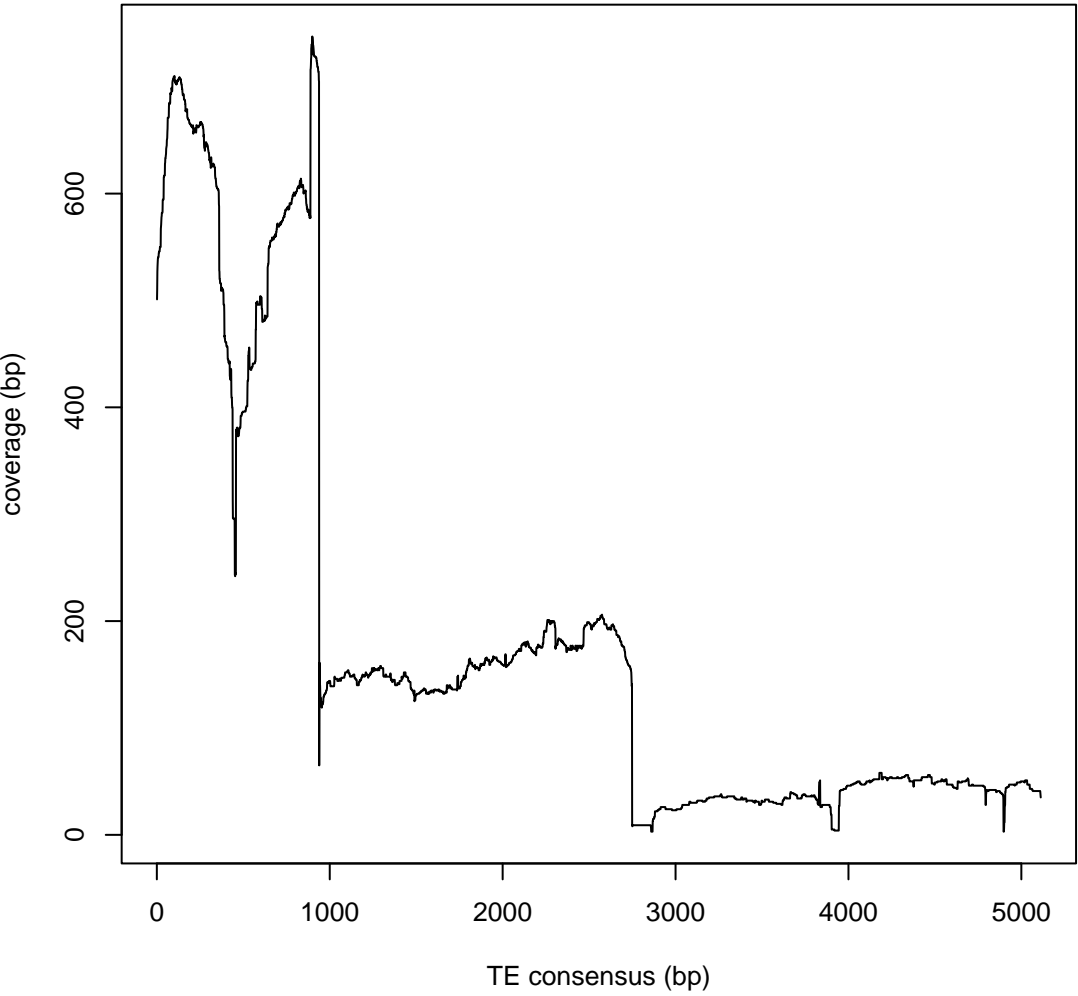


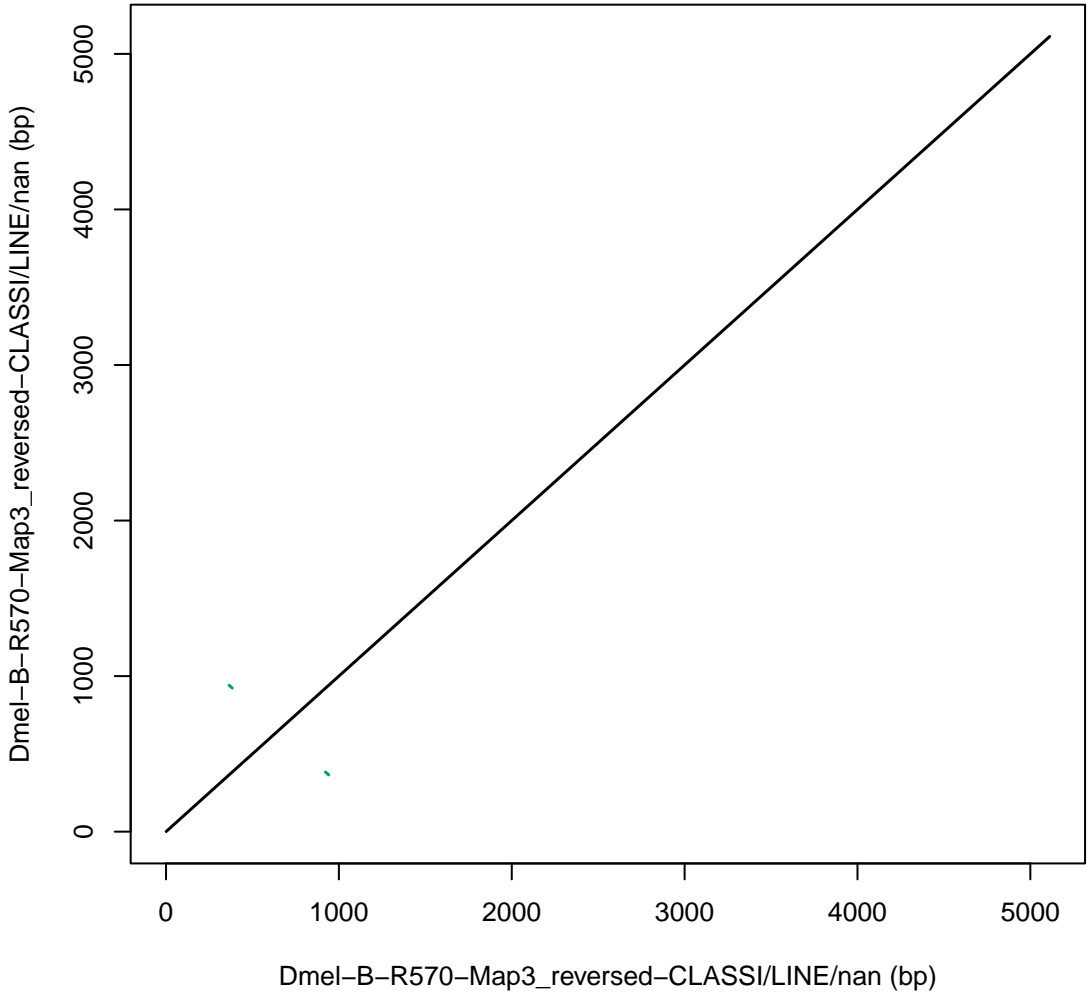
TE: Dmel-B-R570-Map3_reversed-CLASSI/LINE/nan
consensus size: 5112bp; fragments: 2400; full length: 1 (>=4600.8bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

