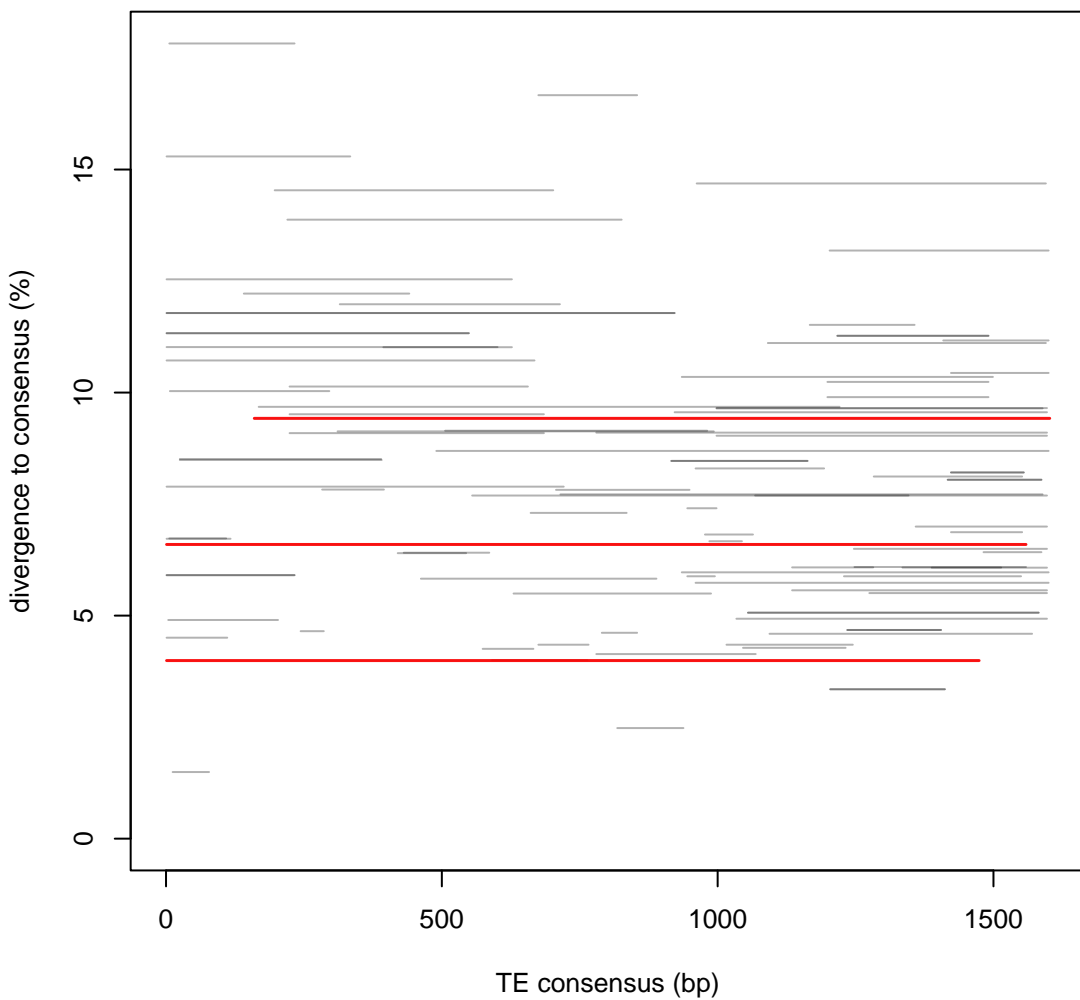
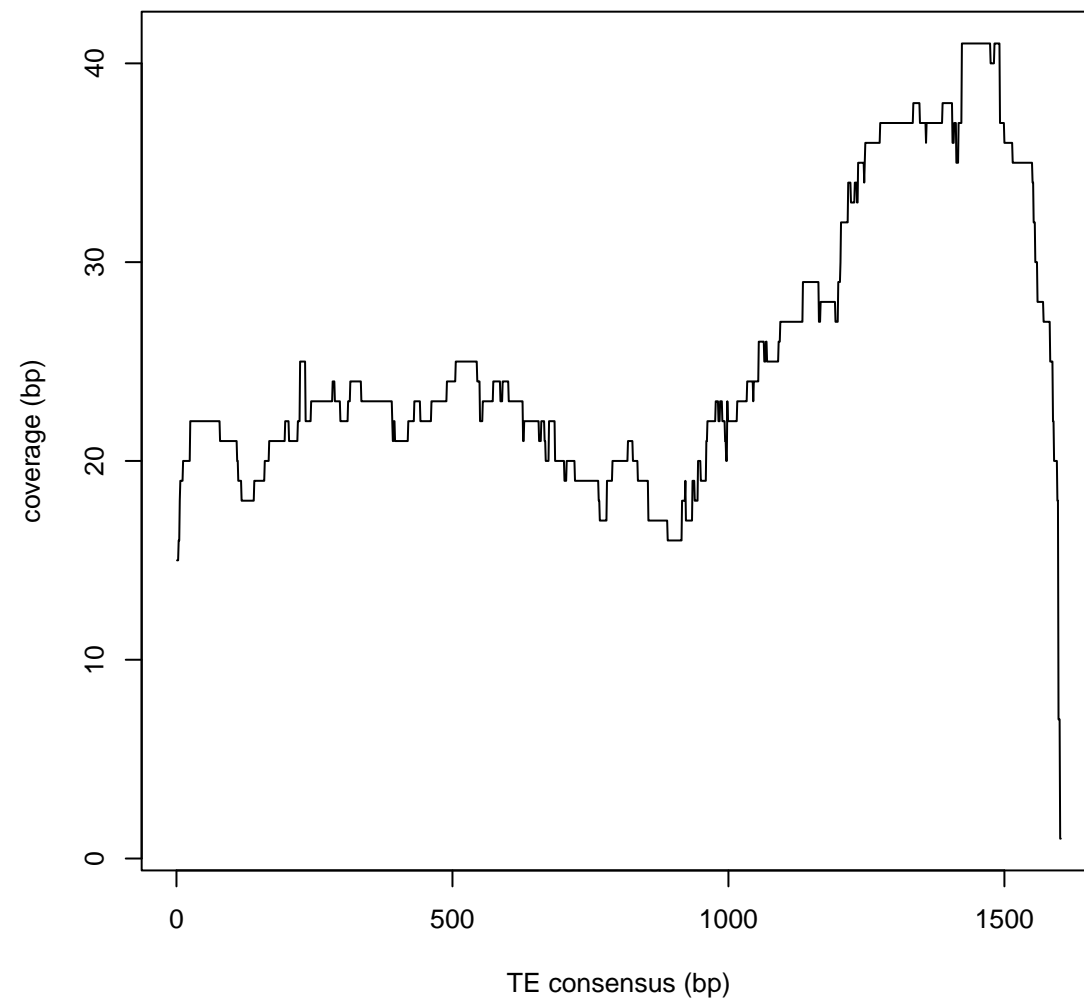


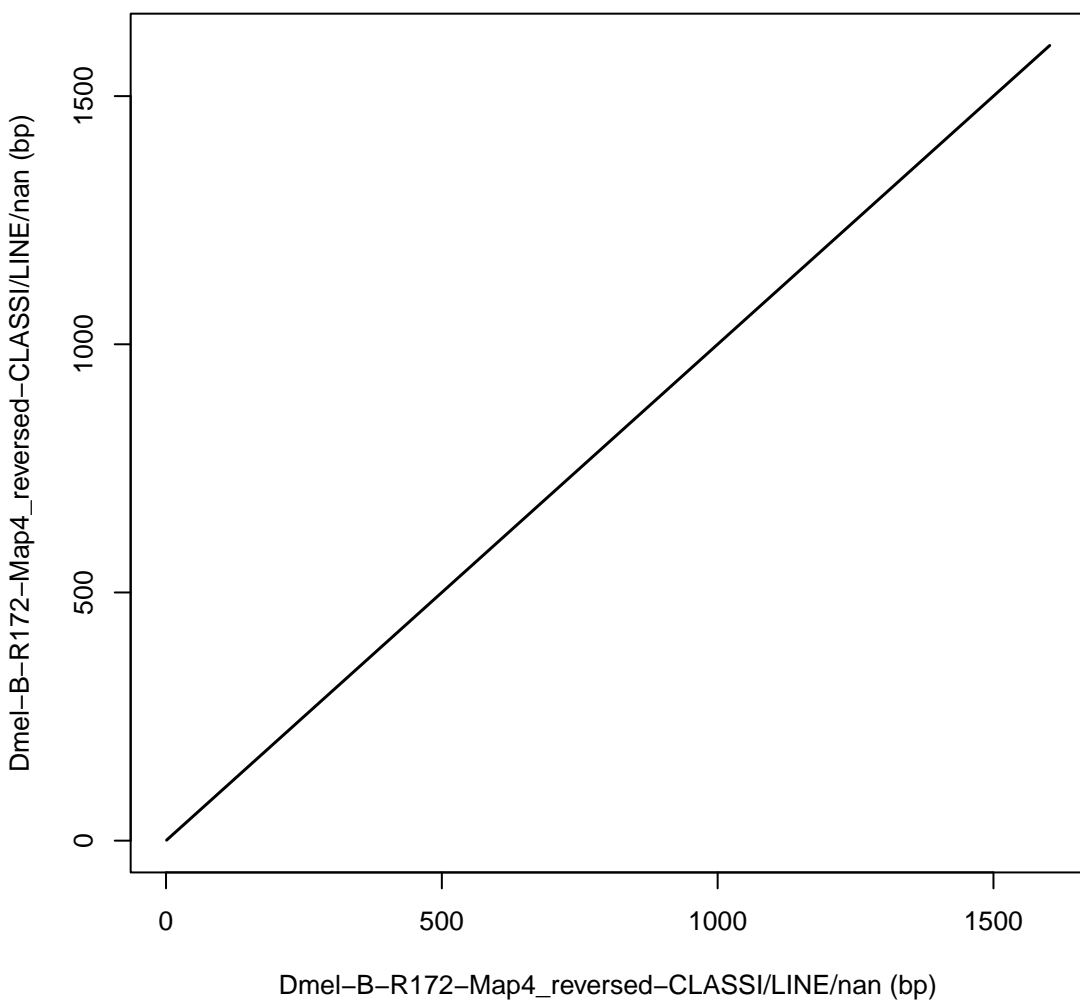
TE: Dmel-B-R172-Map4_reversed-CLASSI/LINE/nan
consensus size: 1602bp; fragments: 104; full length: 3 (>=1441.8bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

