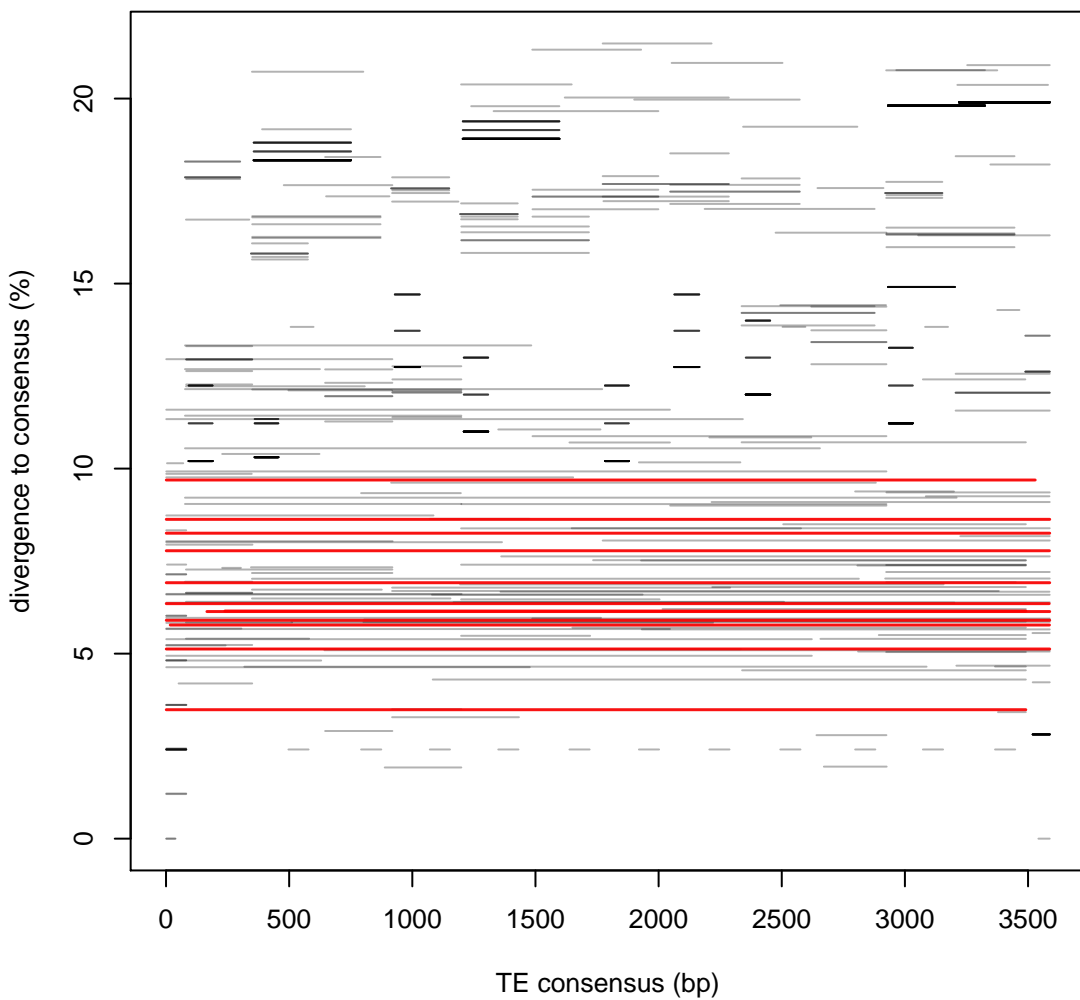
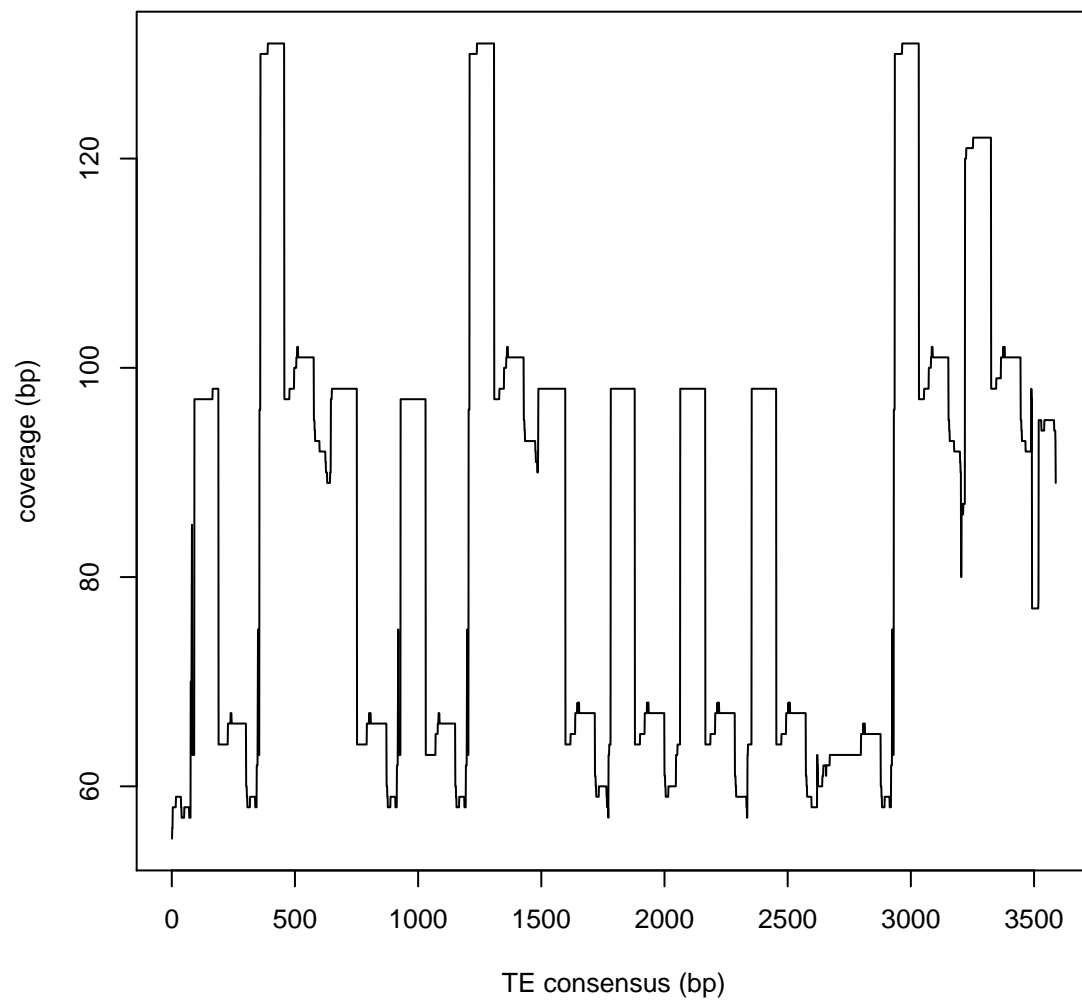


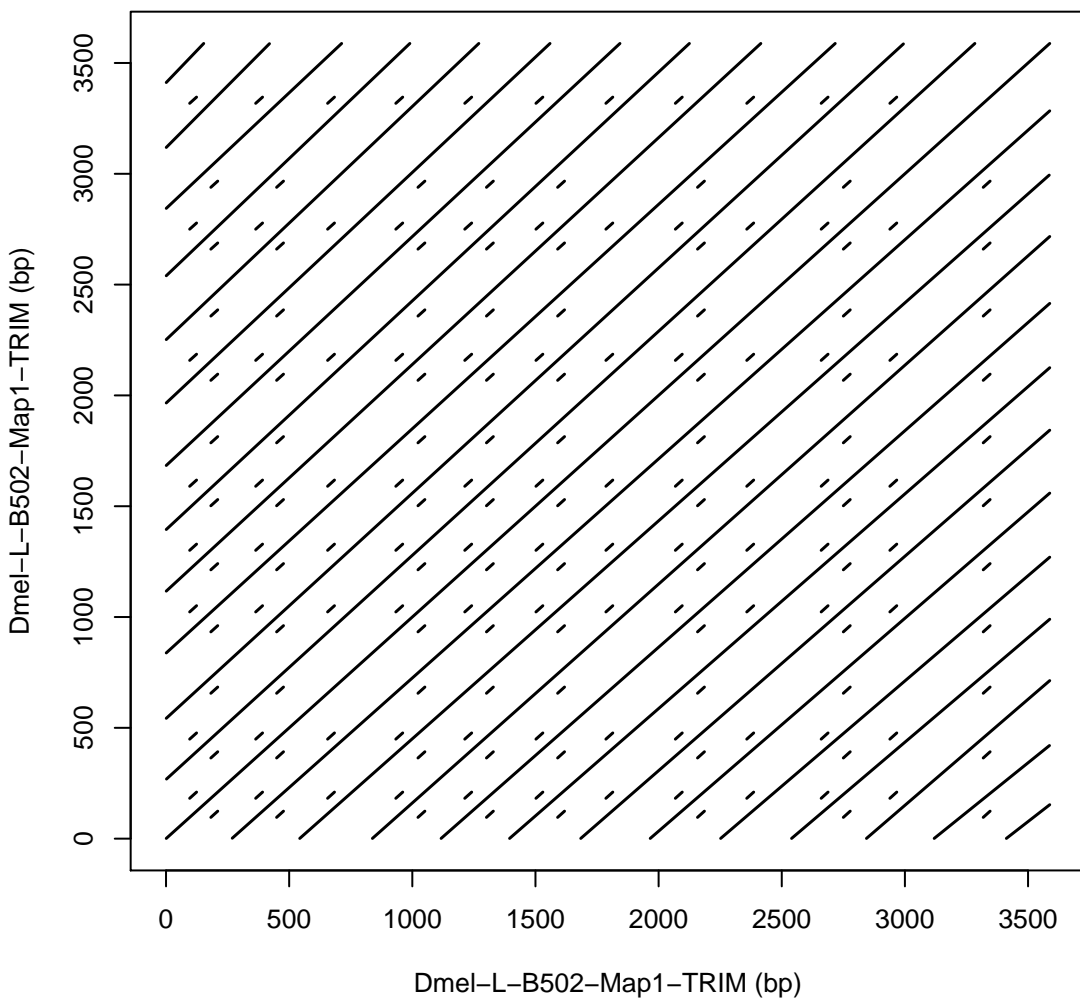
TE: Dmel-L-B502-Map1-TRIM
consensus size: 3588bp; fragments: 712; full length: 12 (≥ 3229.2 bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

