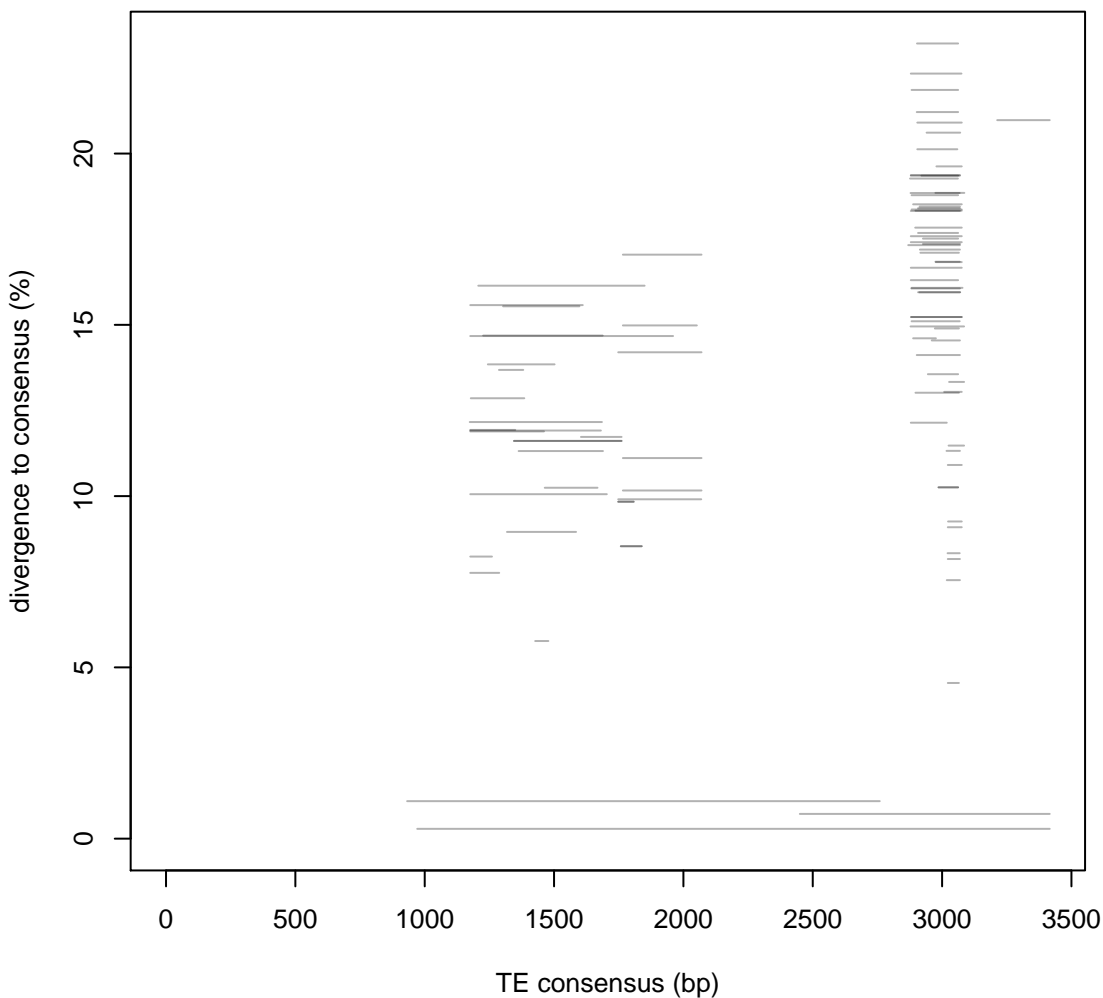
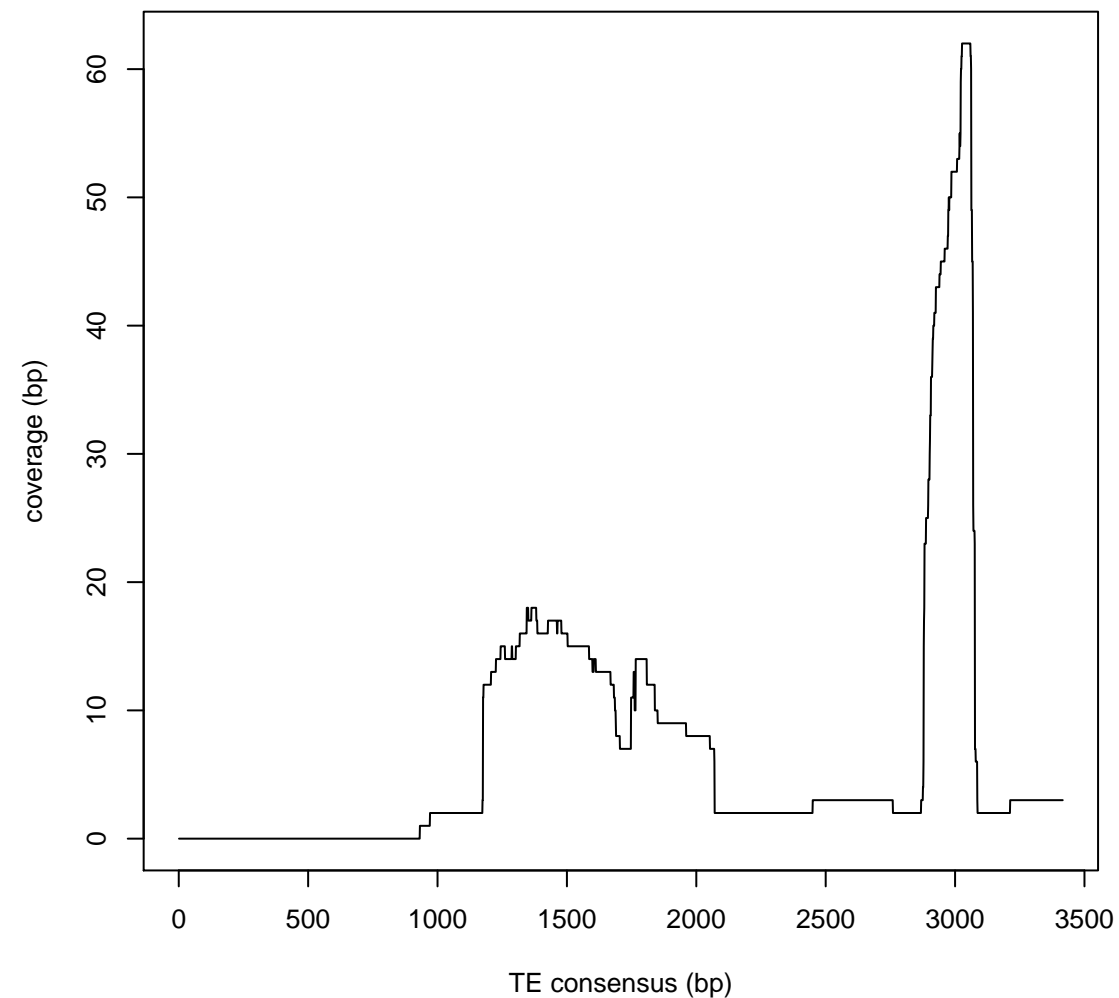


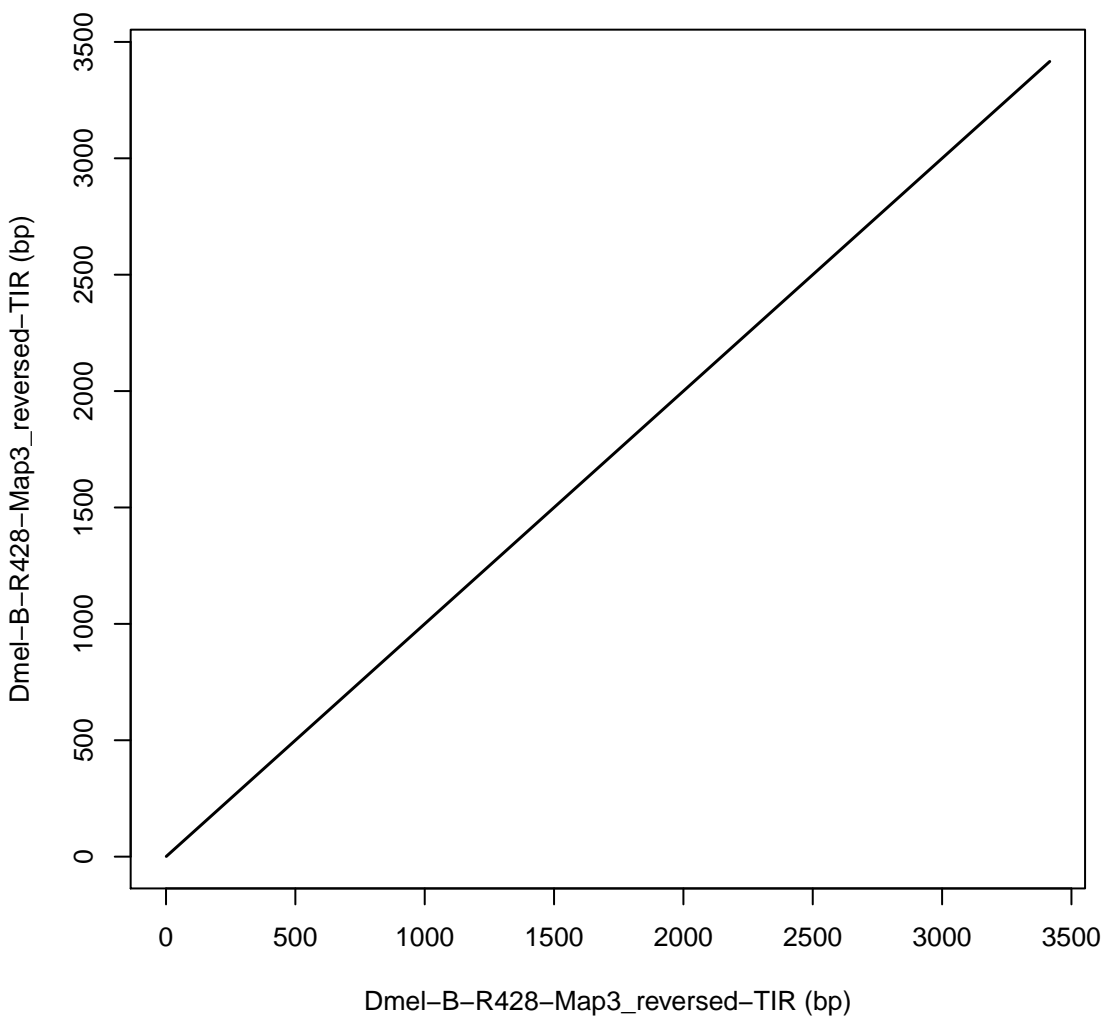
TE: Dmel-B-R428-Map3_reversed-TIR
consensus size: 3416bp; fragments: 98; full length: 0 (>=3074.4bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

