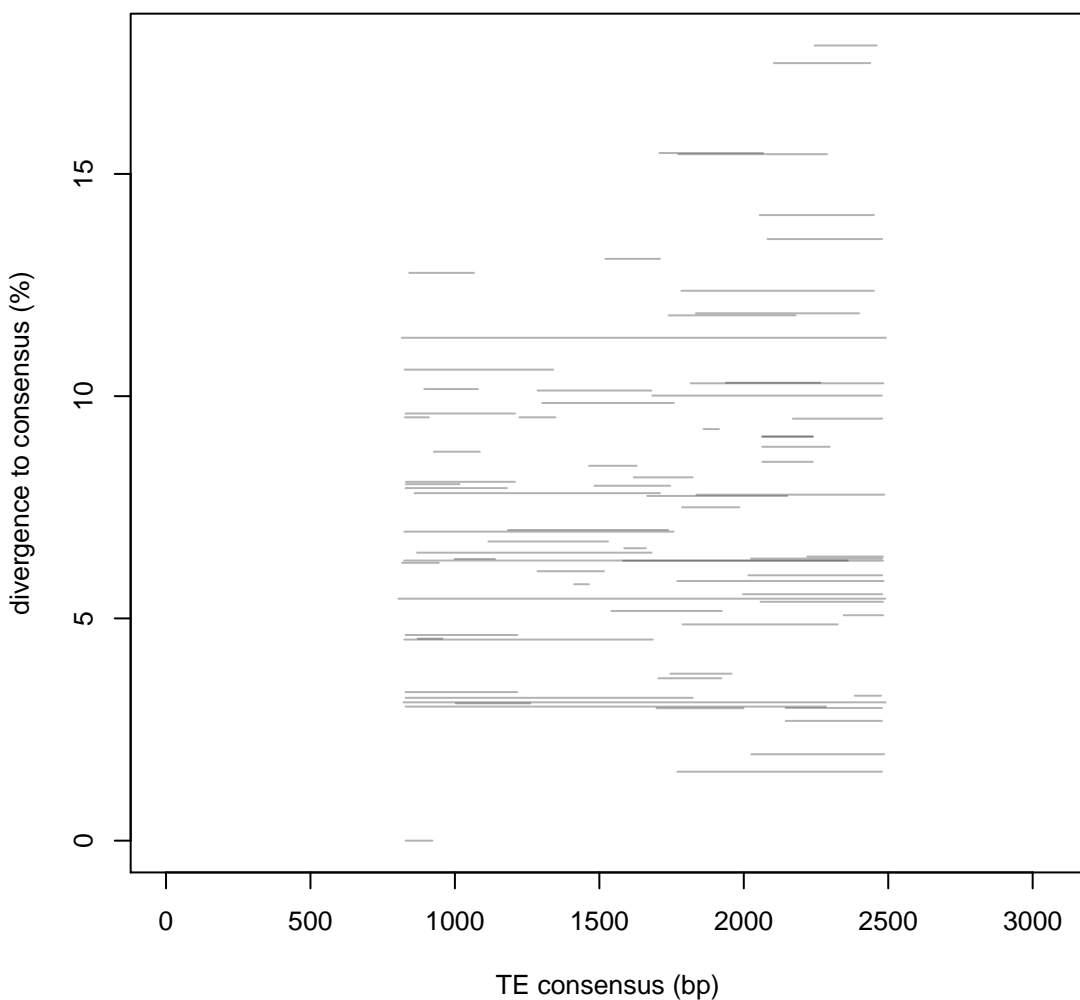
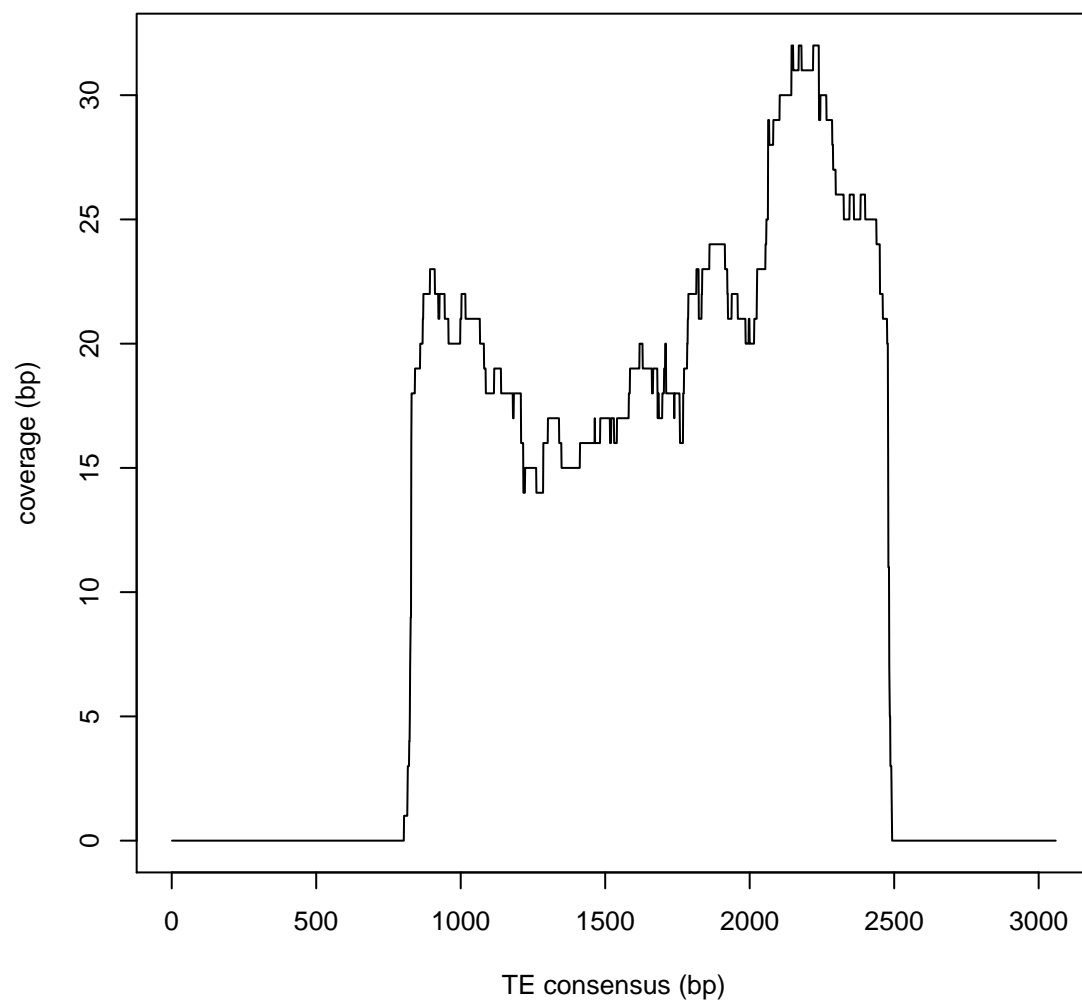


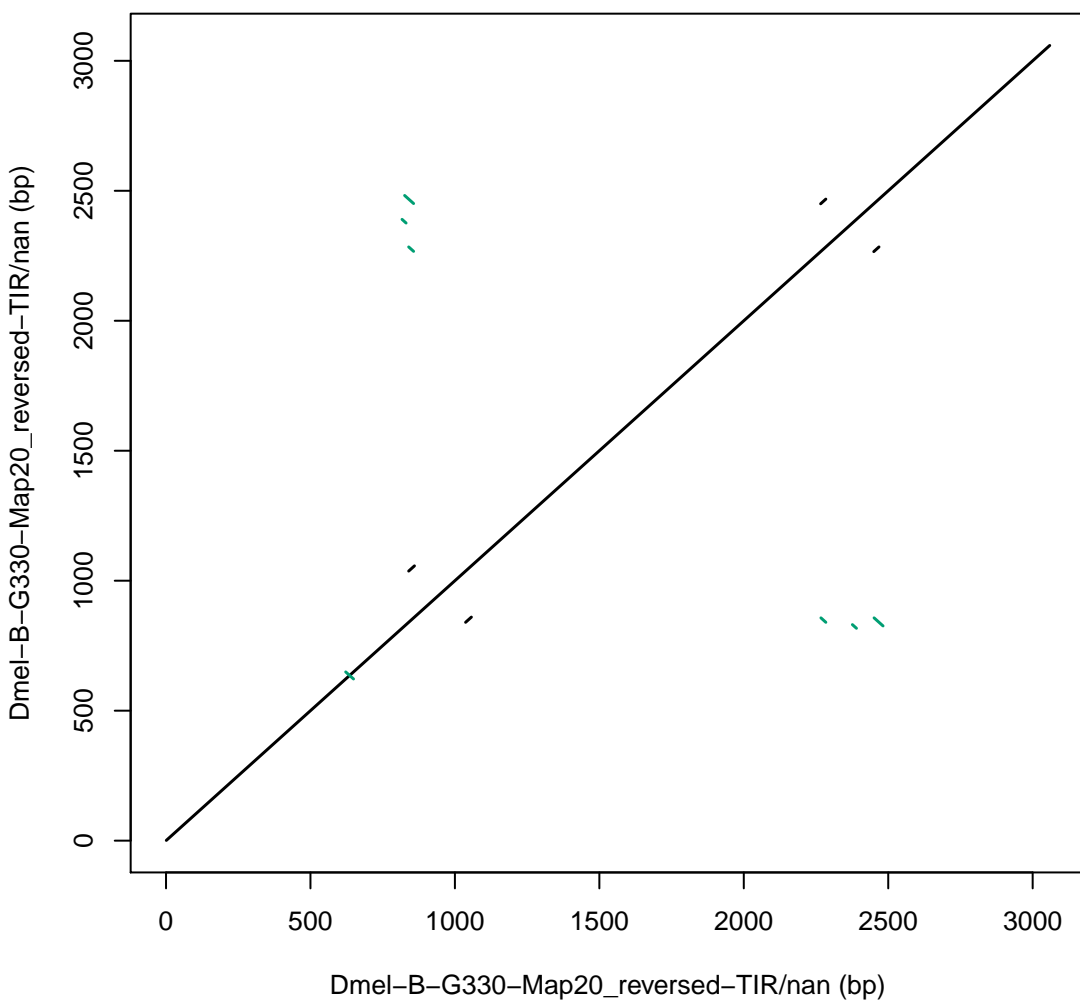
TE: Dmel-B-G330-Map20_reversed-TIR/nan
consensus size: 3059bp; fragments: 77; full length: 0 (>=2753.1bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

