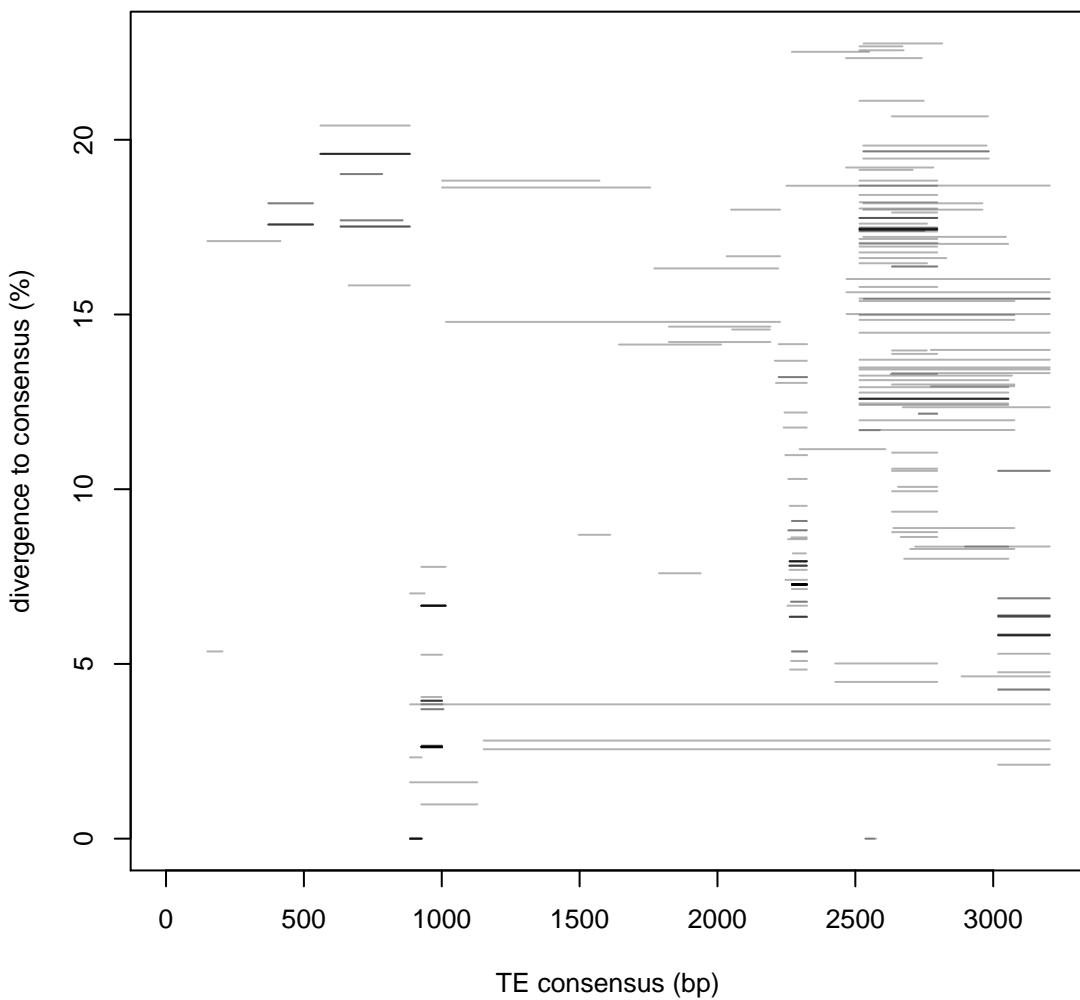
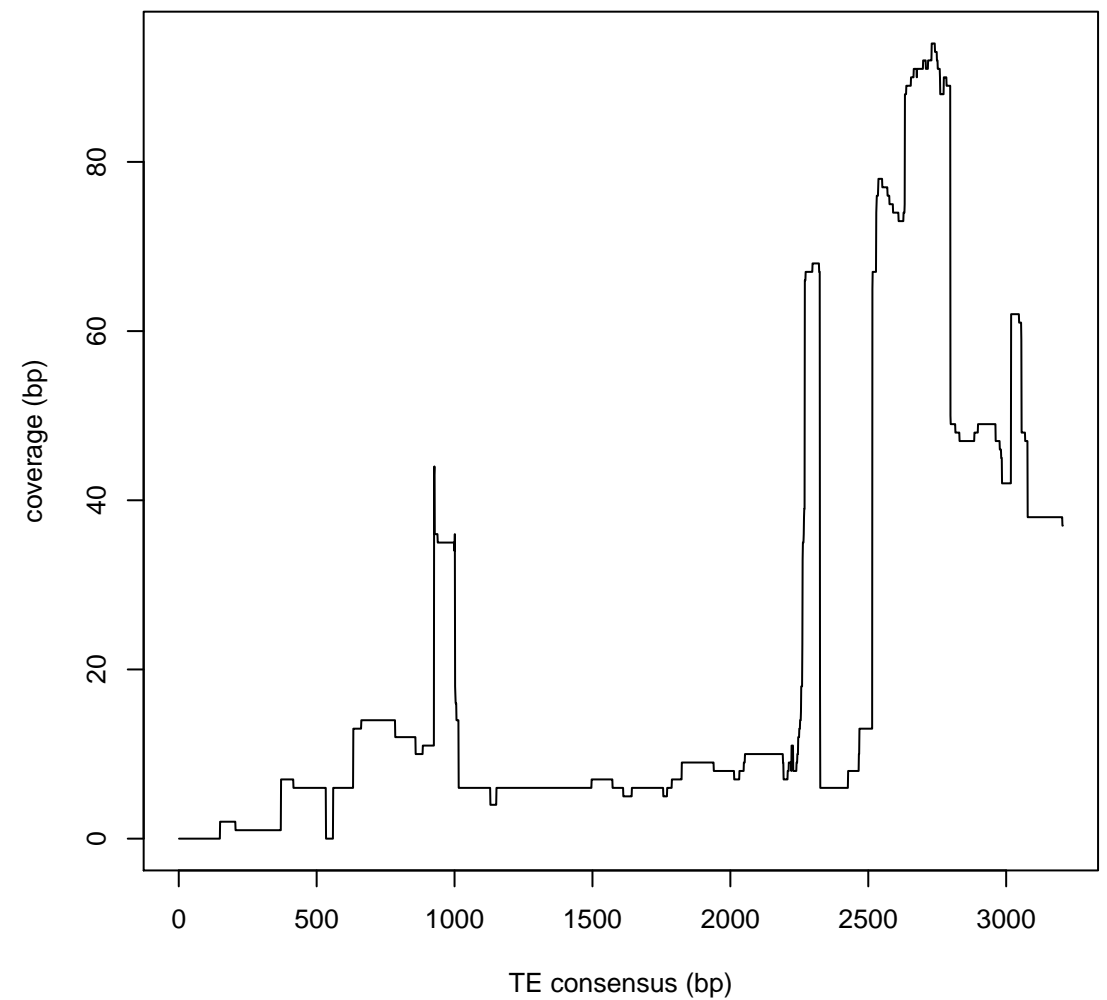


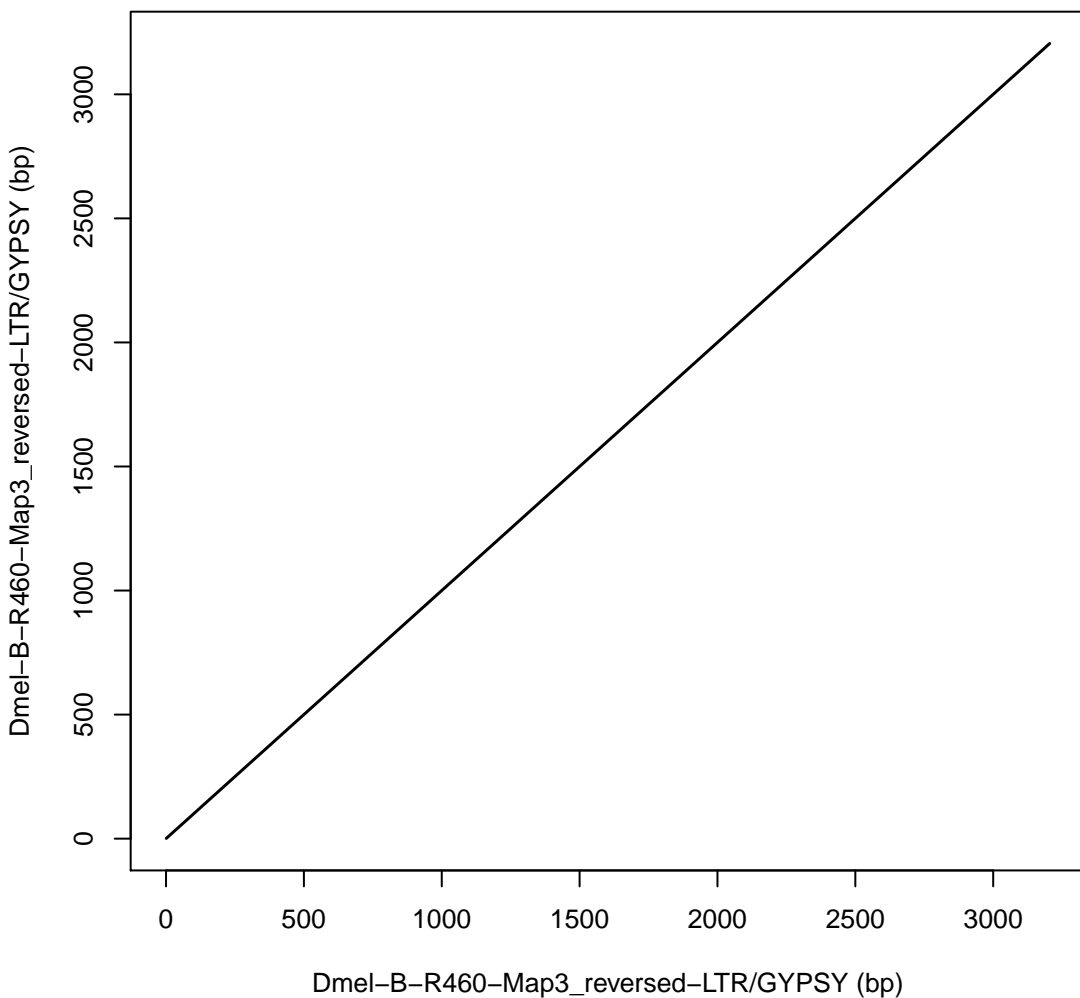
TE: Dmel-B-R460-Map3_reversed-LTR/GYPY
consensus size: 3205bp; fragments: 265; full length: 0 (>=2884.5bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

