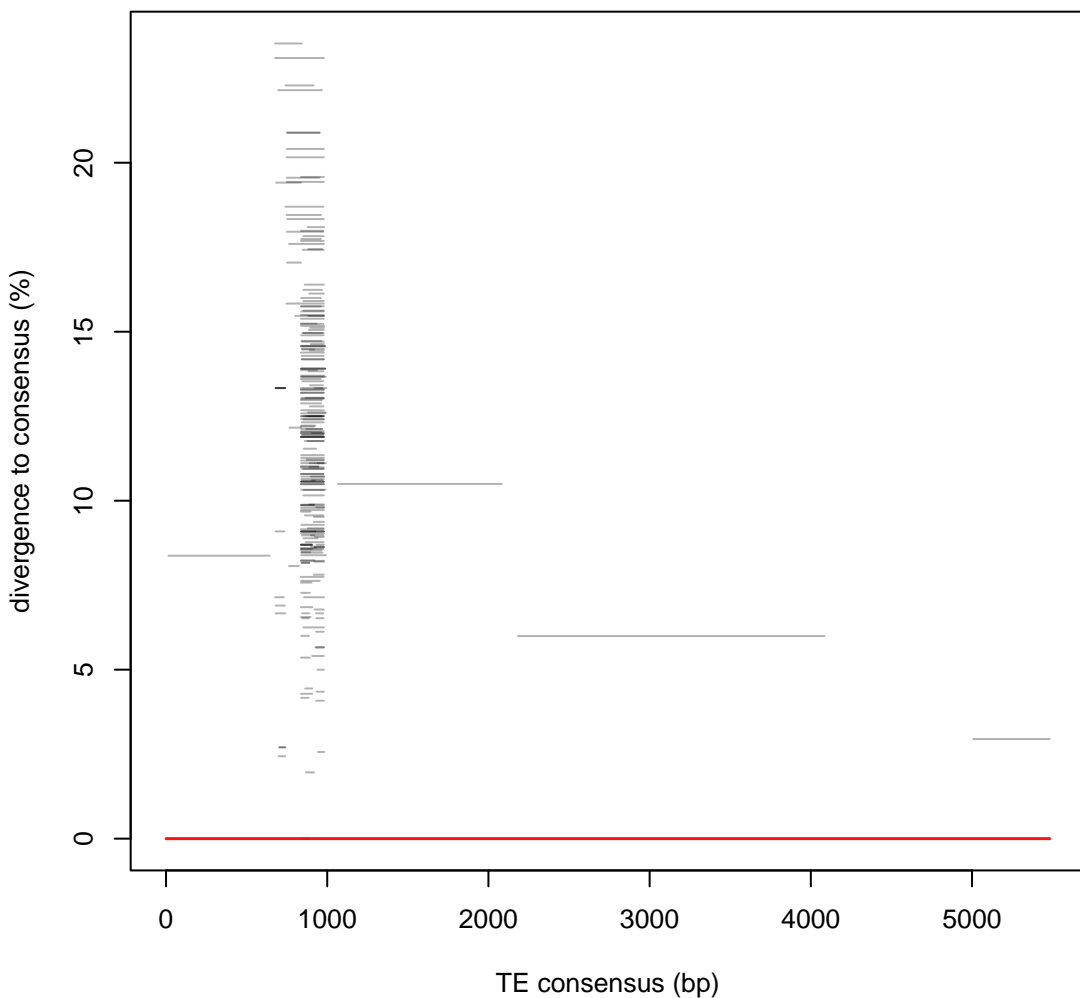
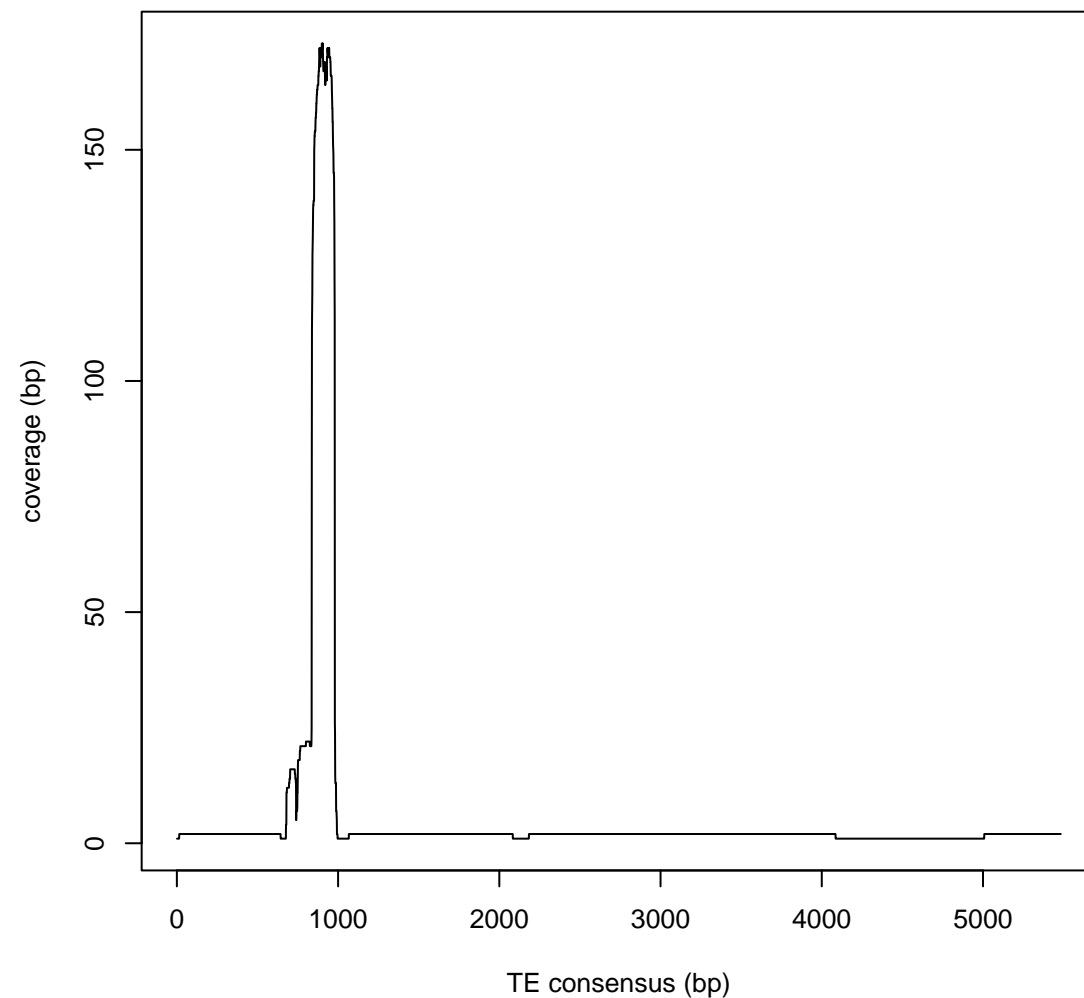


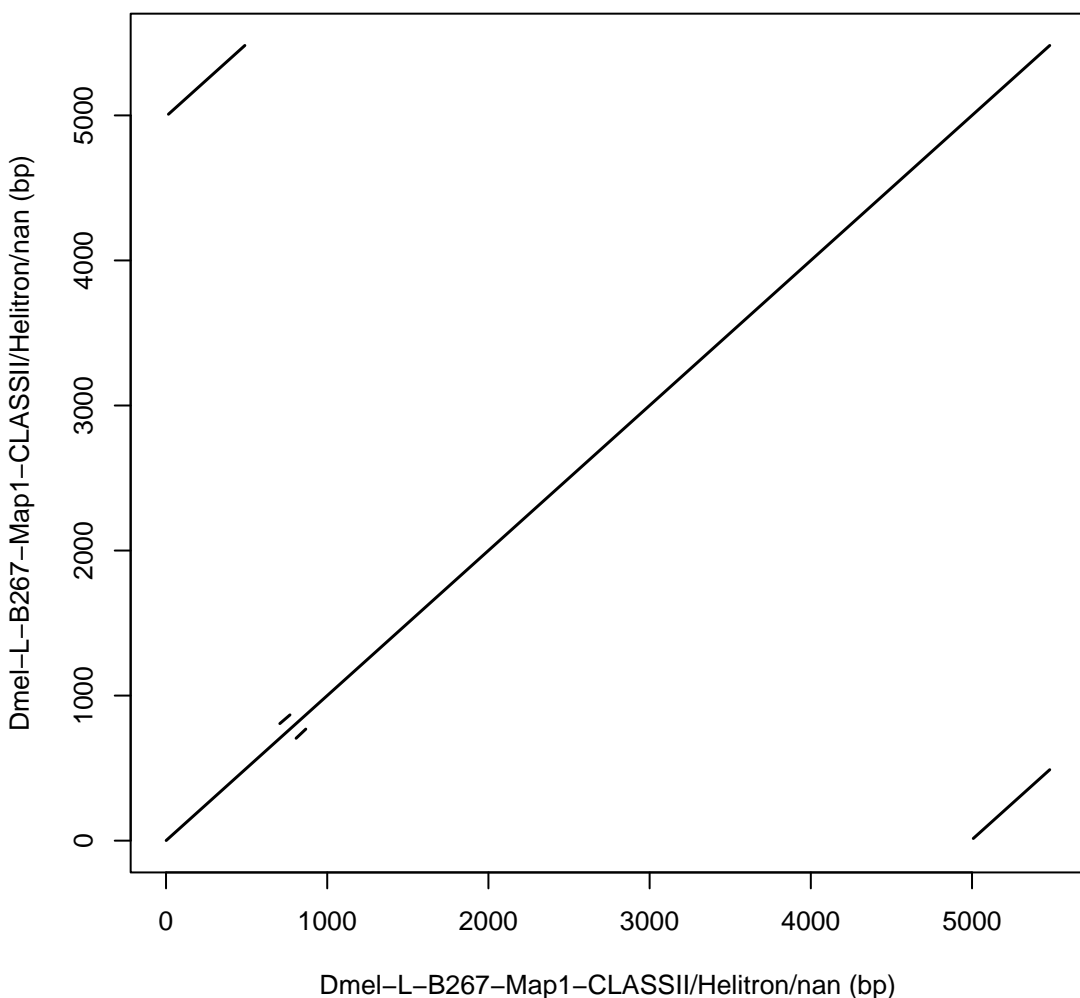
TE: Dmel-L-B267-Map1-CLASSII/Helitron/nan
consensus size: 5482bp; fragments: 231; full length: 1 (>=4933.8bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

