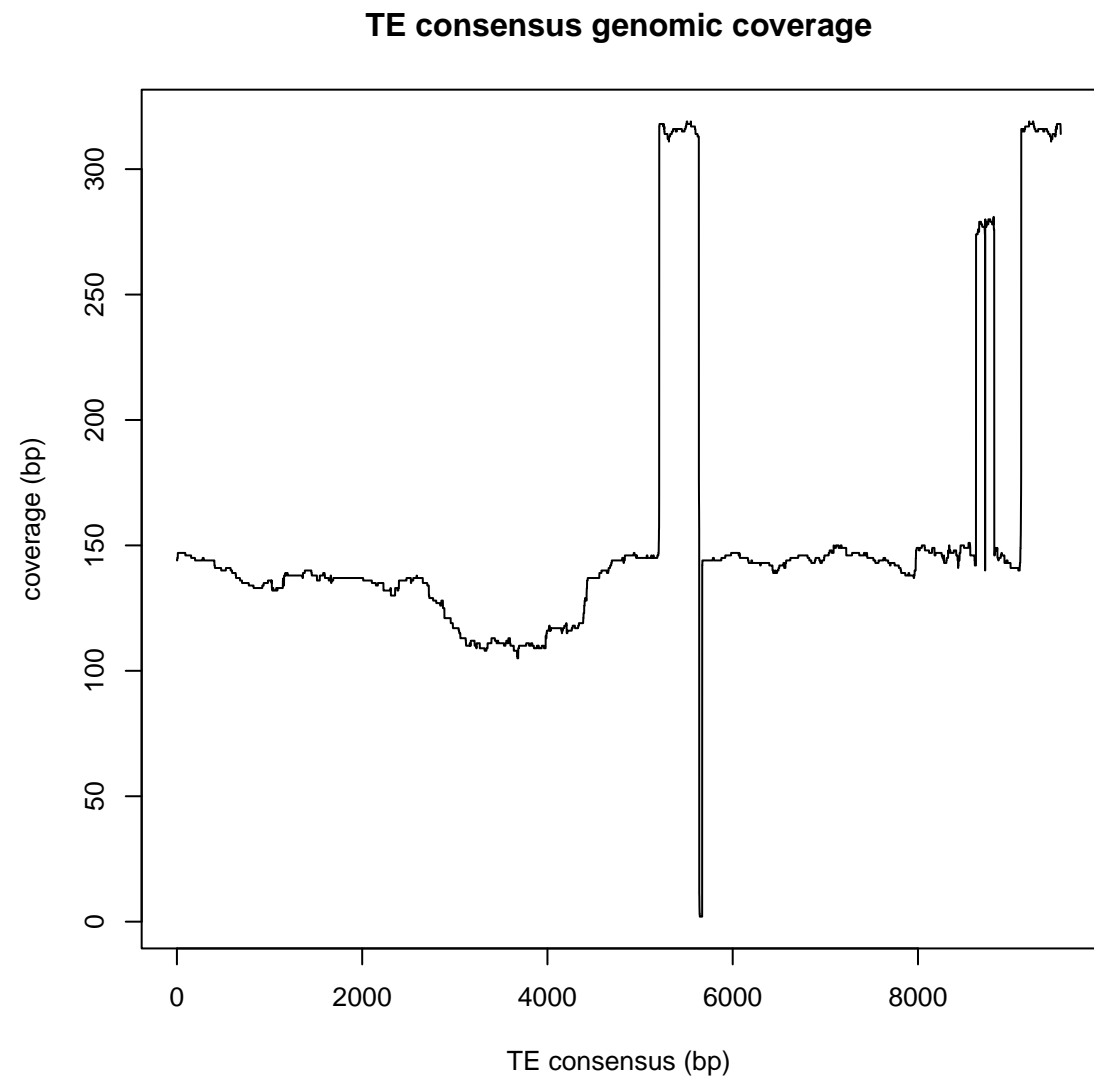
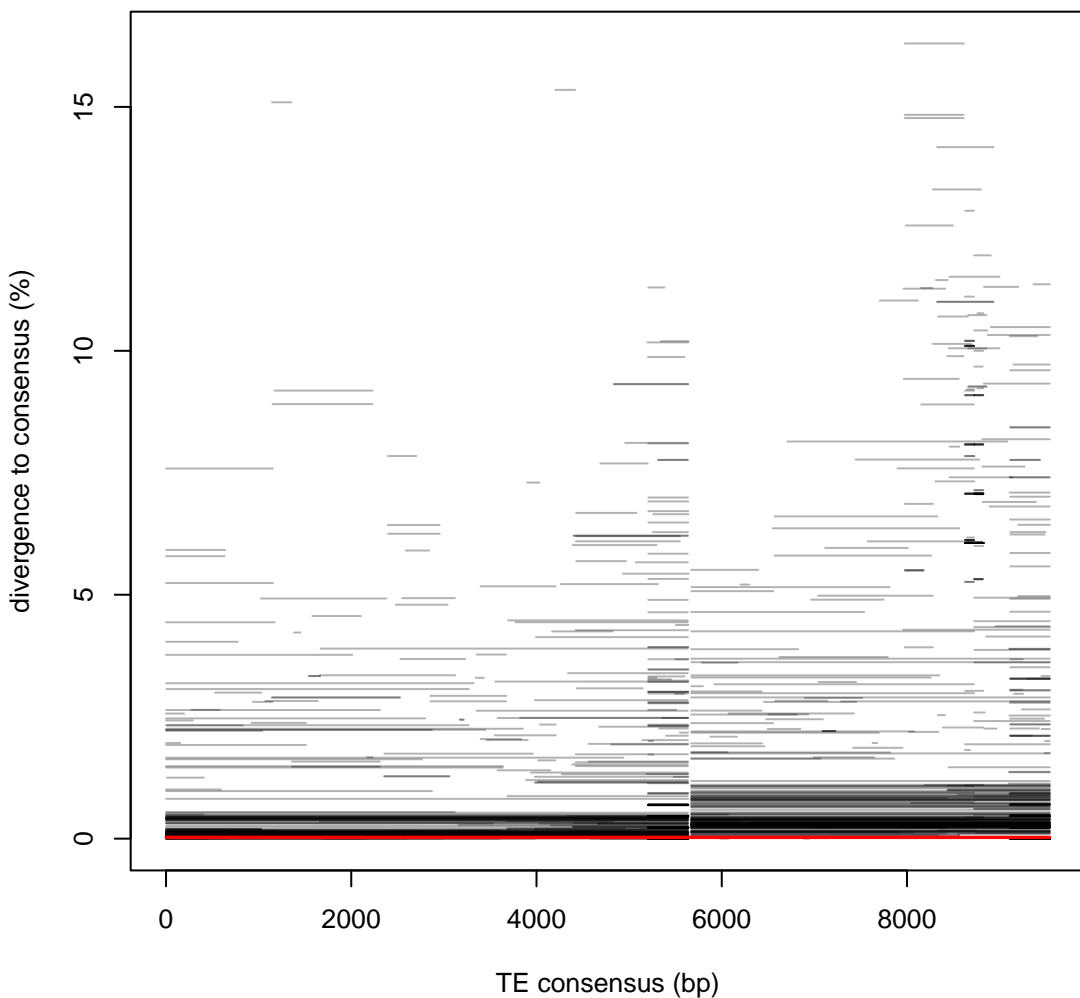
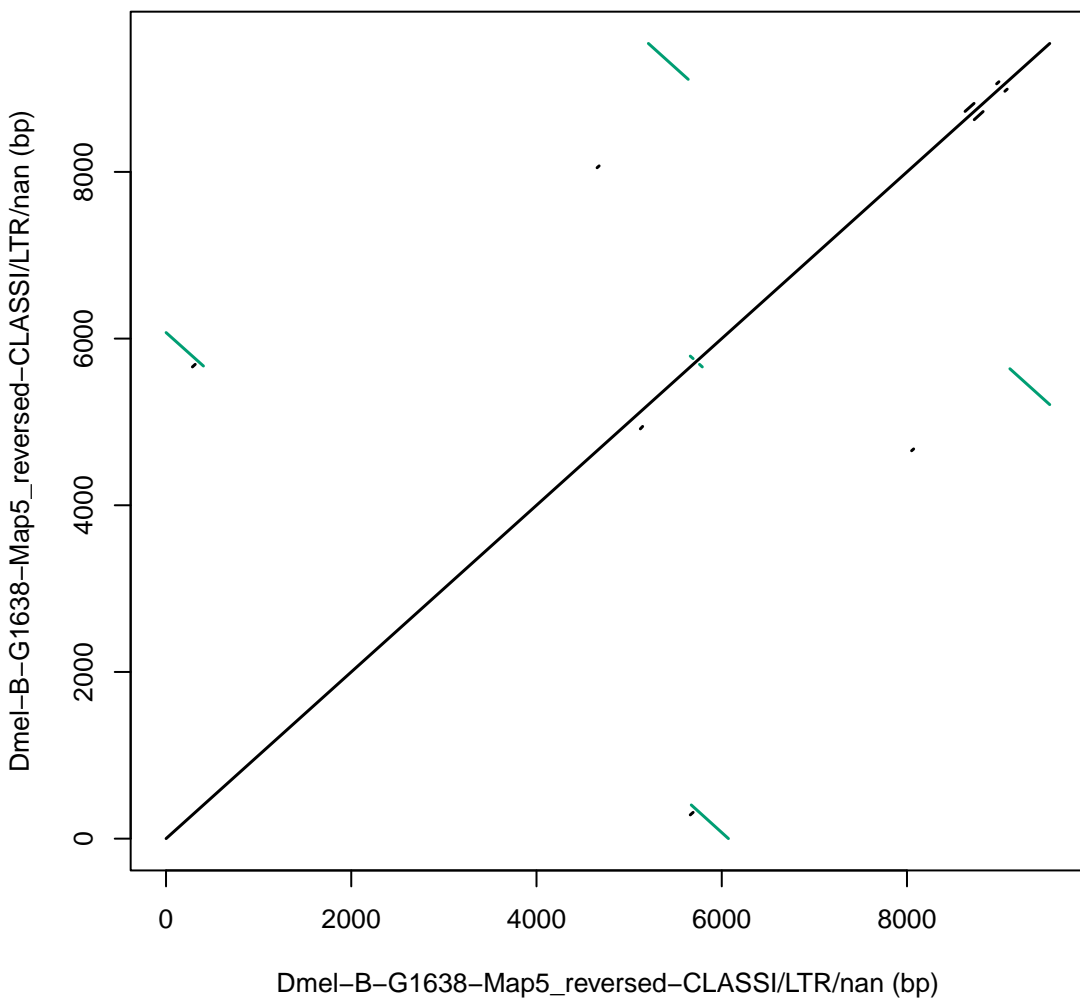


TE: Dmel-B-G1638-Map5_reversed-CLASSI/LTR/nan
consensus size: 9541bp; fragments: 1165; full length: 2 (>=8586.9bp)



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

