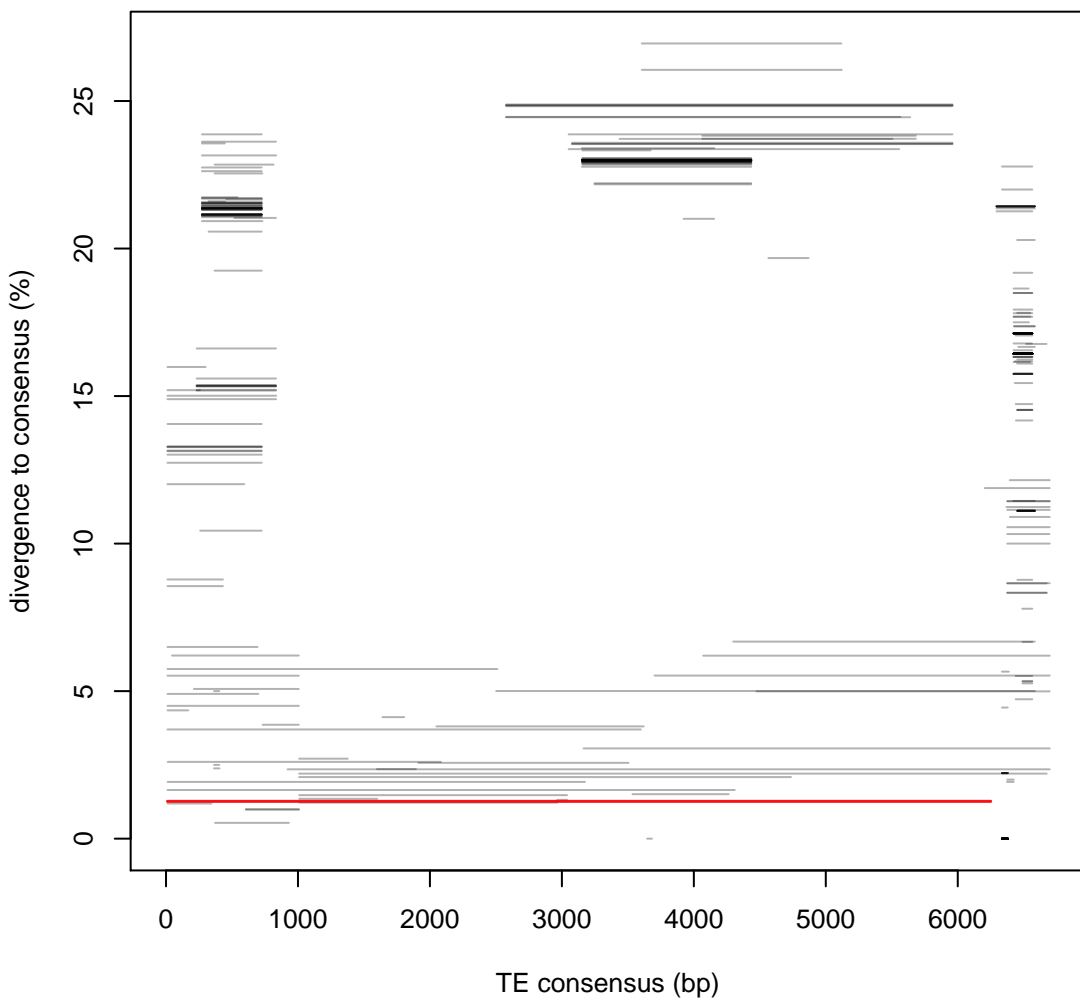
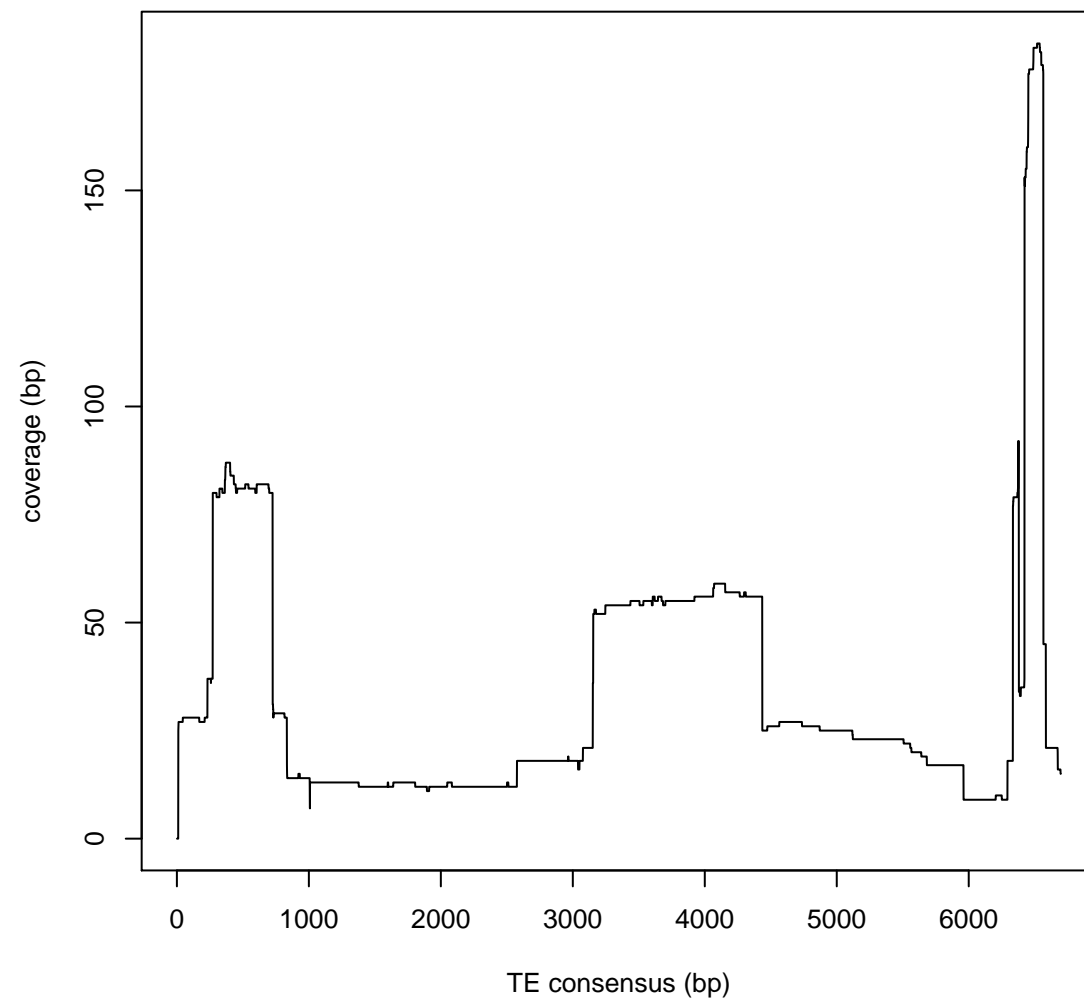


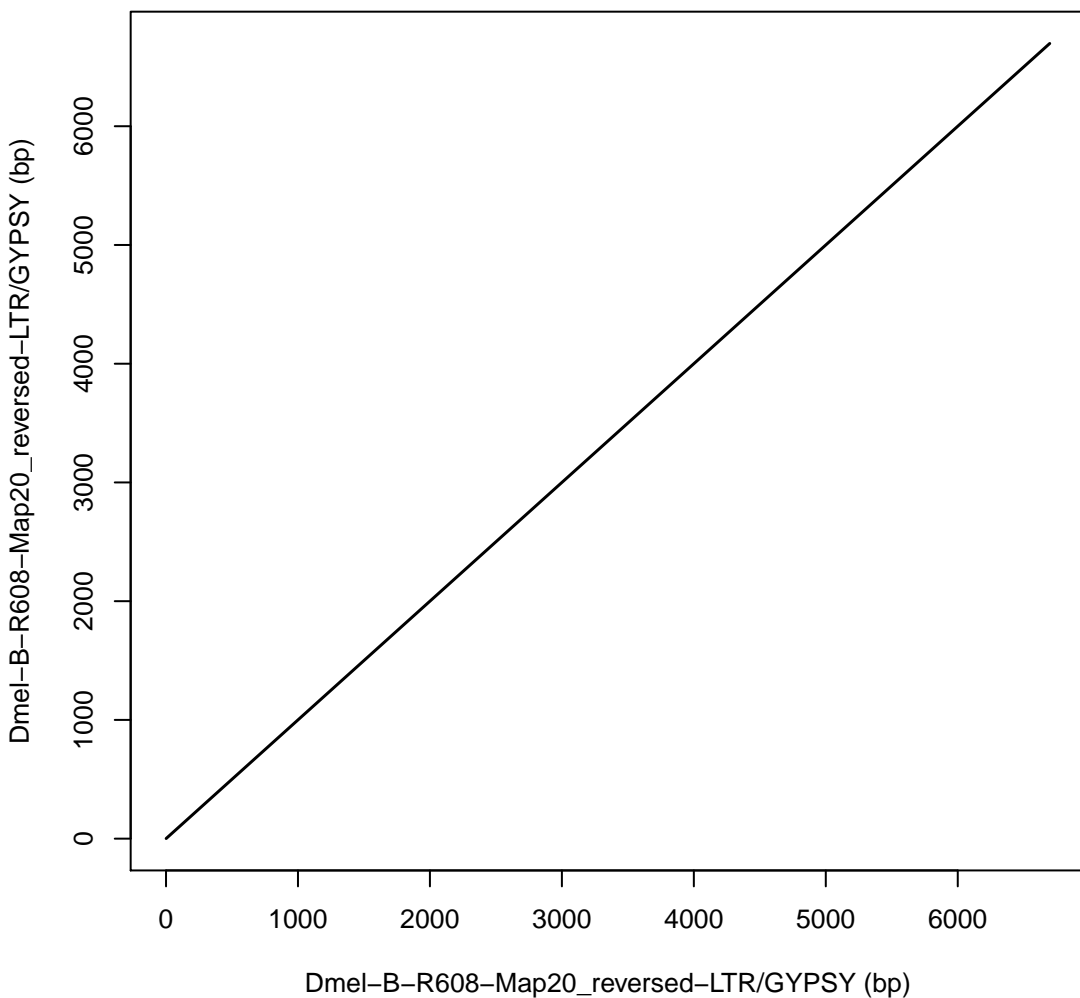
TE: Dmel-B-R608-Map20\_reversed-LTR/GYPSY  
consensus size: 6697bp; fragments: 404; full length: 1 (>=6027.3bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

