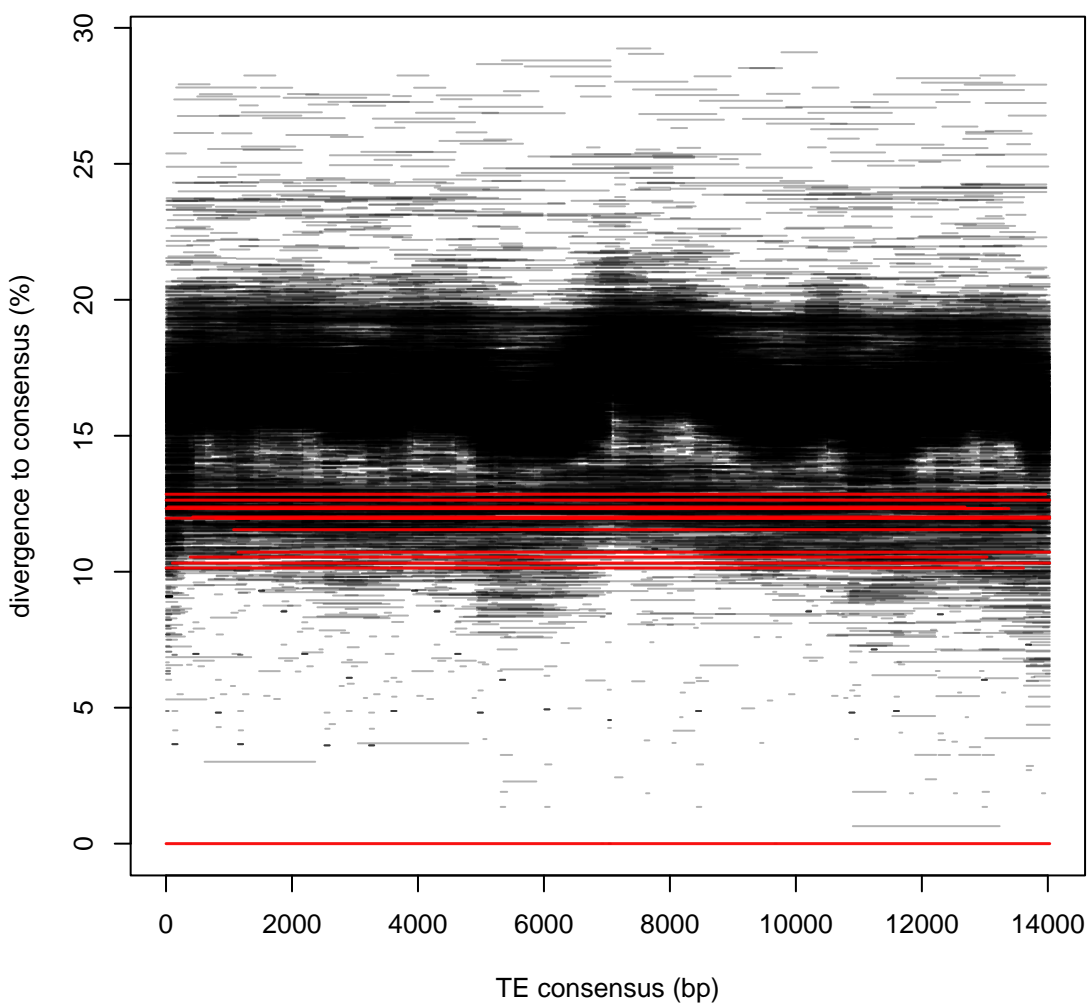
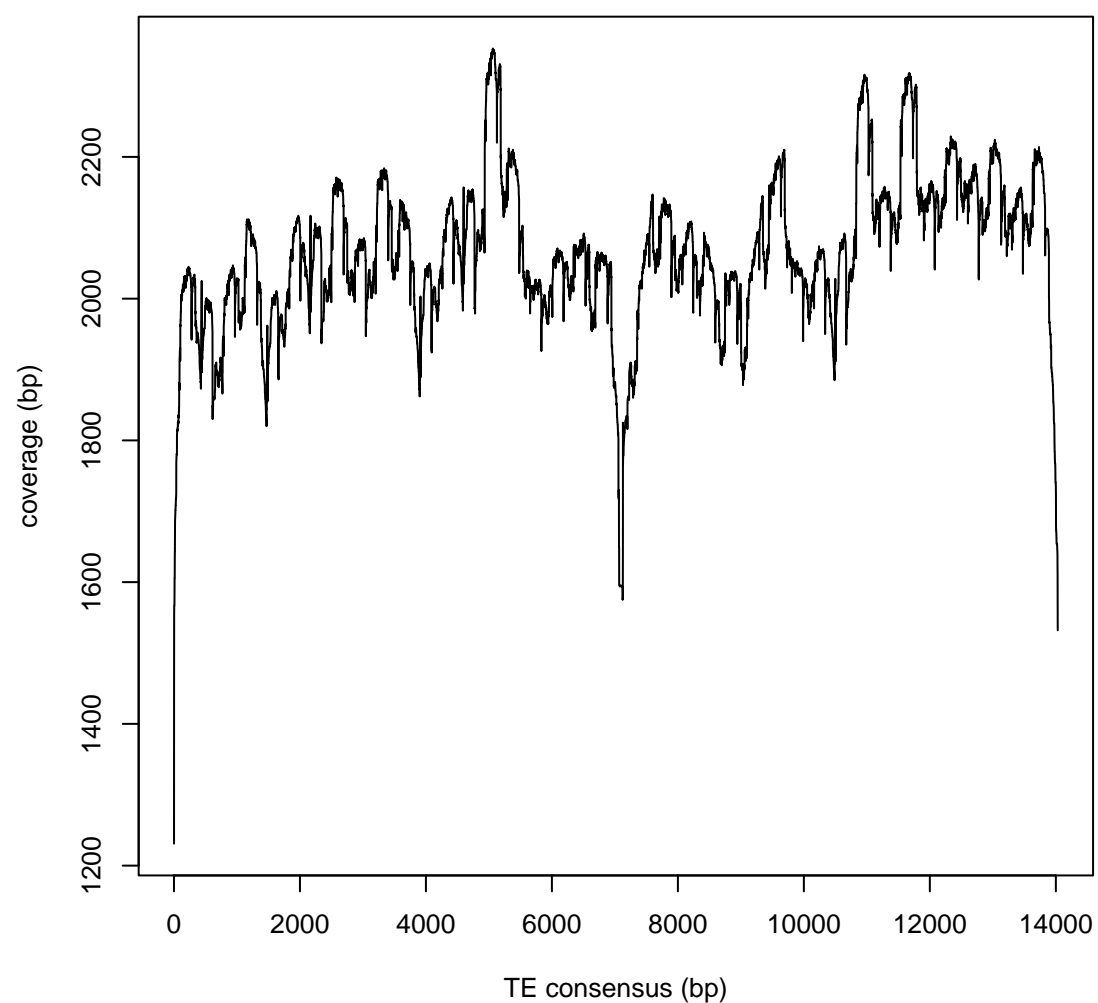


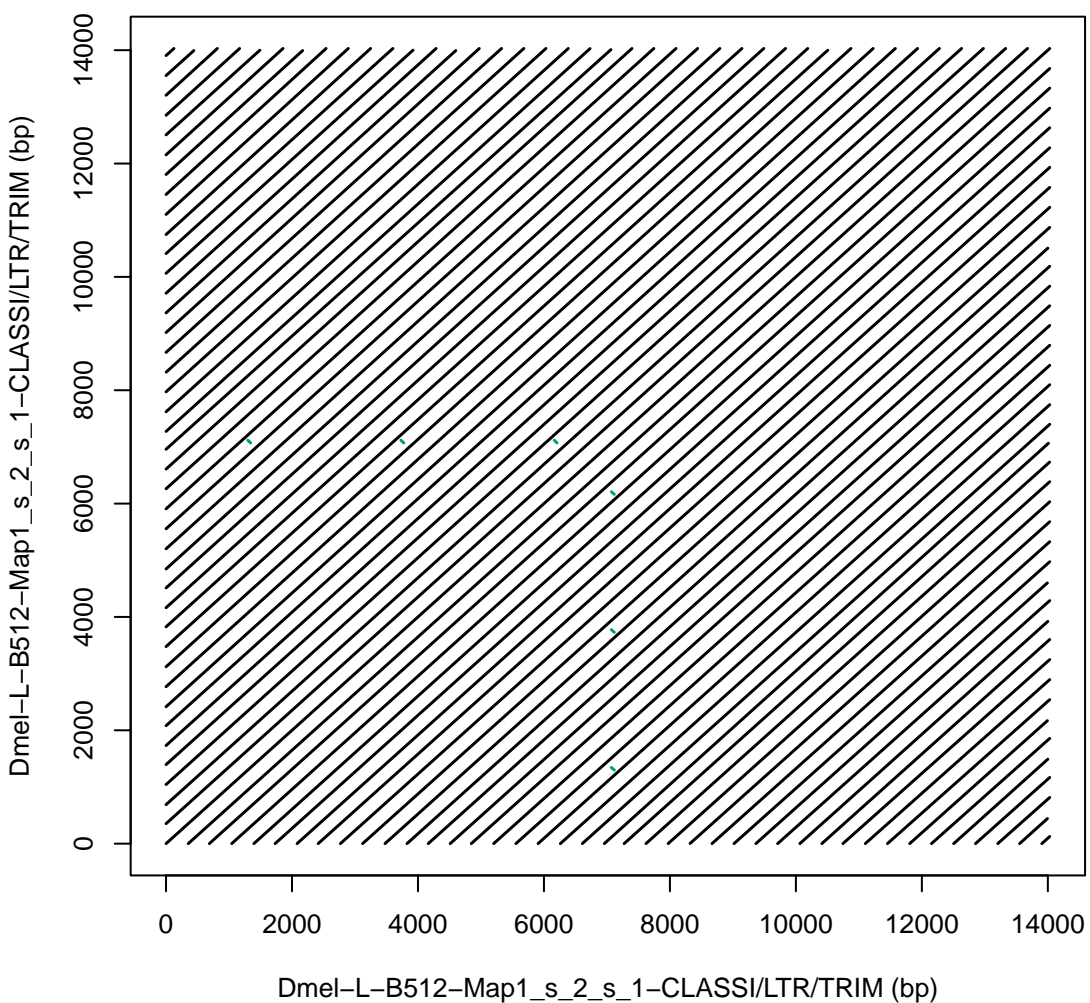
TE: Dmel-L-B512-Map1\_s\_2\_s\_1-CLASSI/LTR/TRIM  
consensus size: 14030bp; fragments: 26437; full length: 14 (>=12627bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

