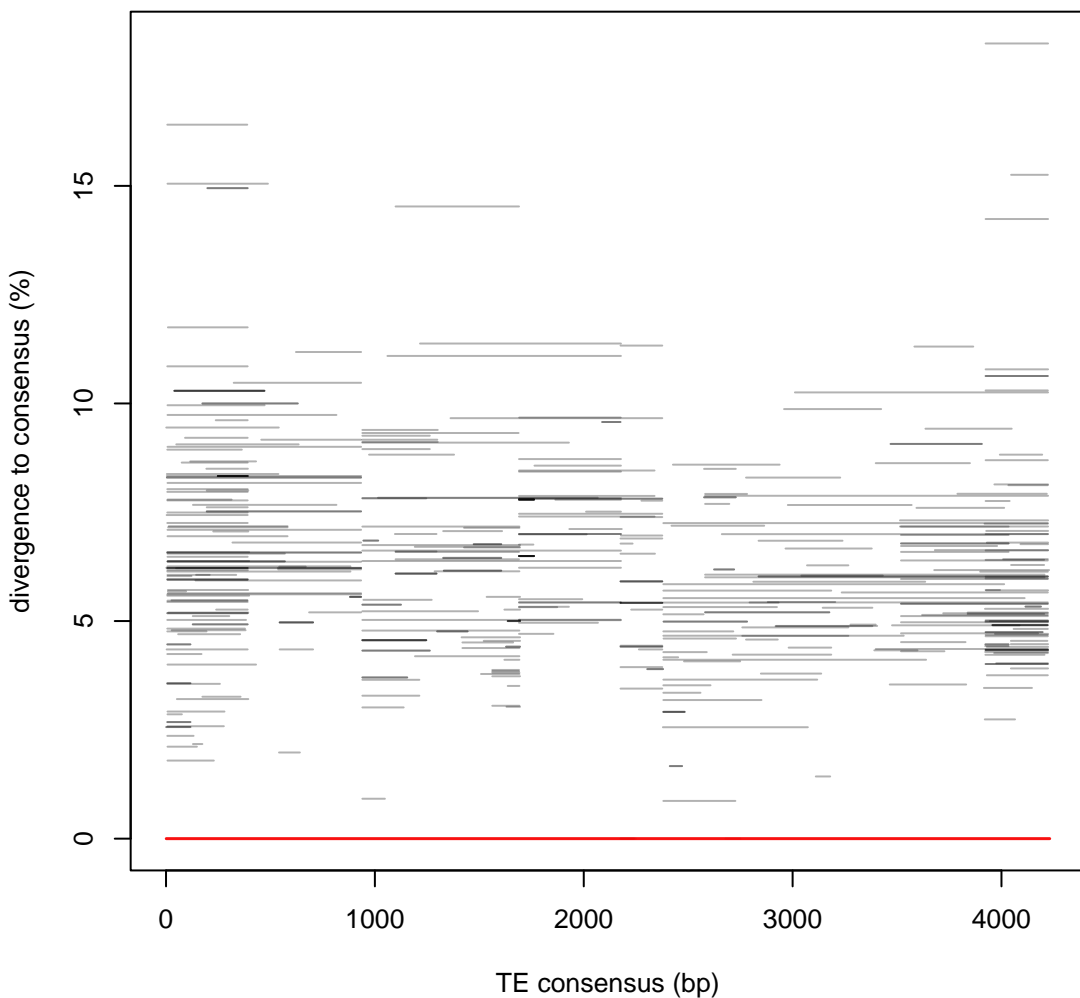
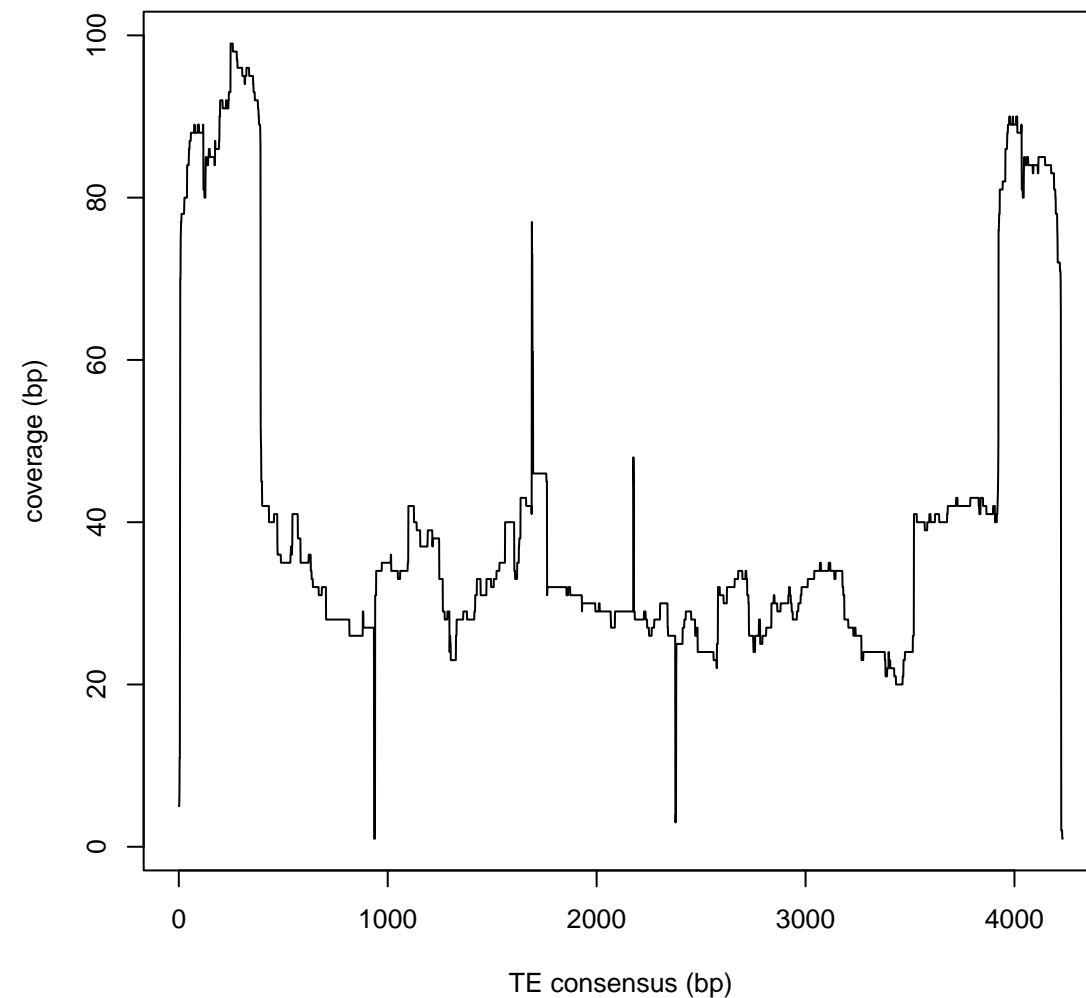


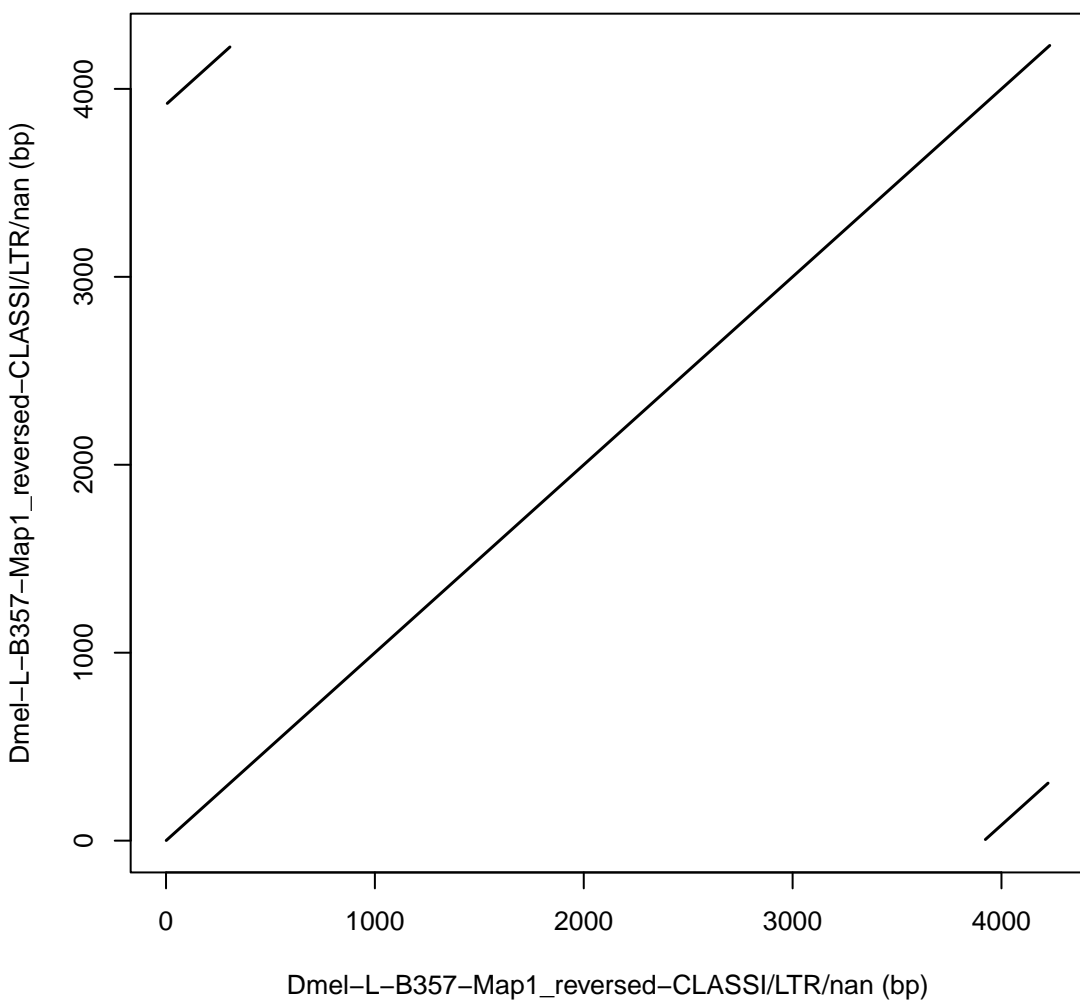
TE: Dmel-L-B357-Map1\_reversed-CLASSI/LTR/nan  
consensus size: 4231bp; fragments: 447; full length: 1 (>=3807.9bp)



### TE consensus genomic coverage



### TE consensus self dotplot (blastn)



### TE consensus structure and protein hits

