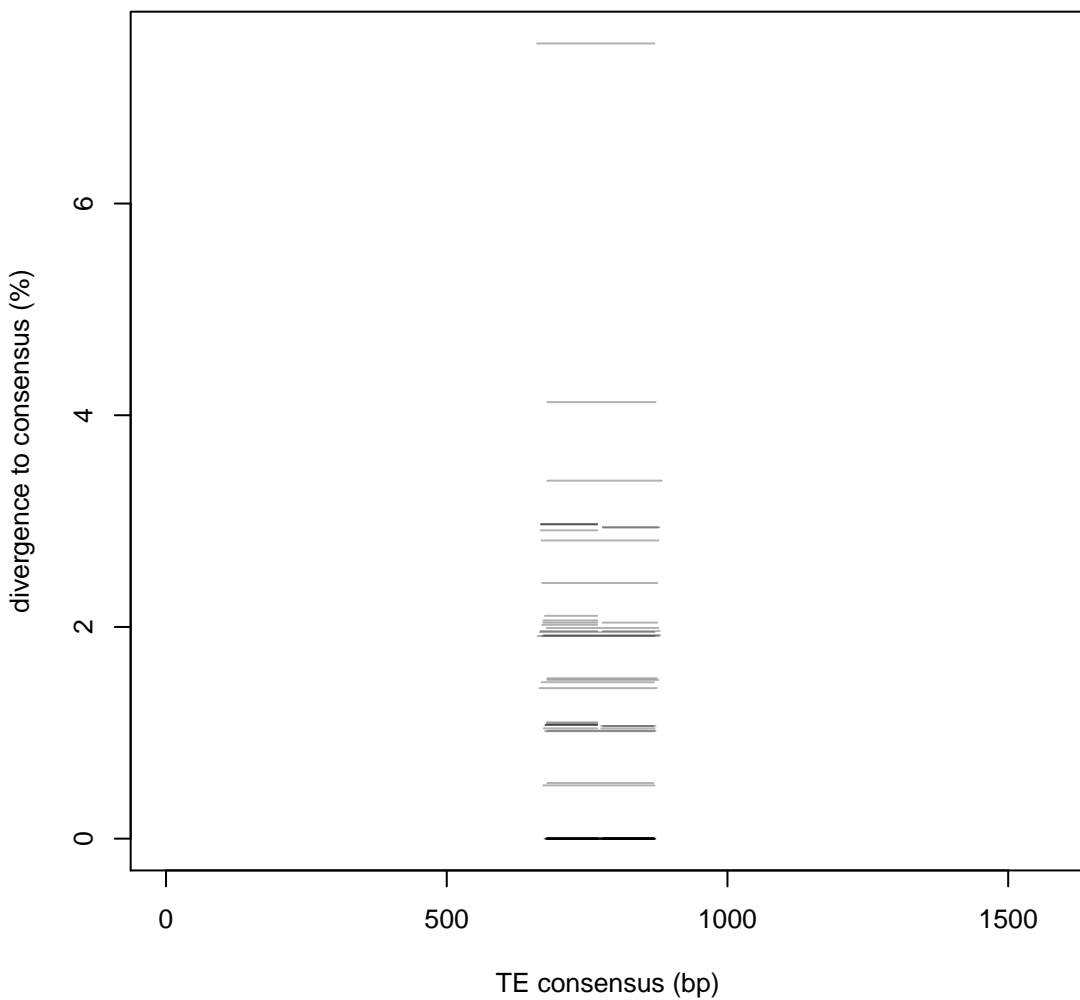
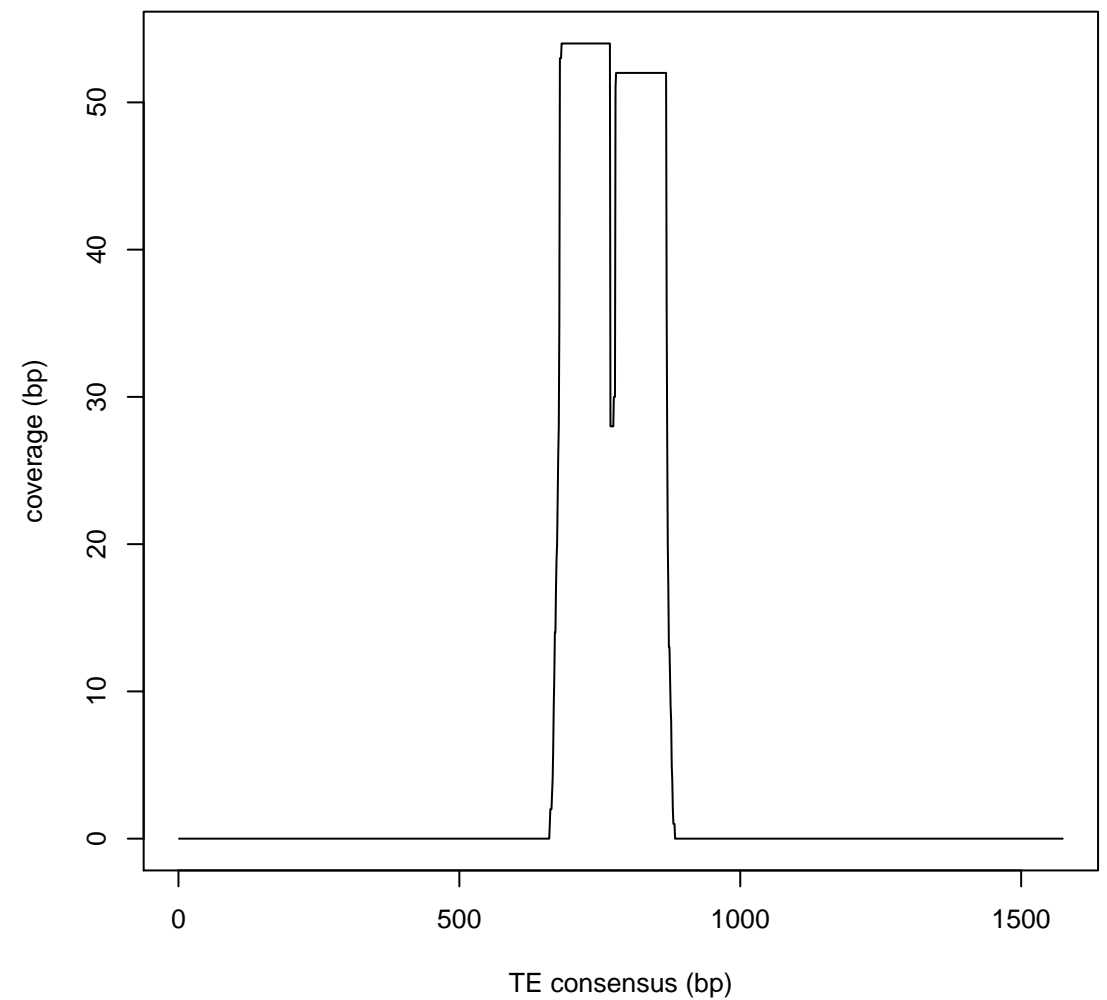


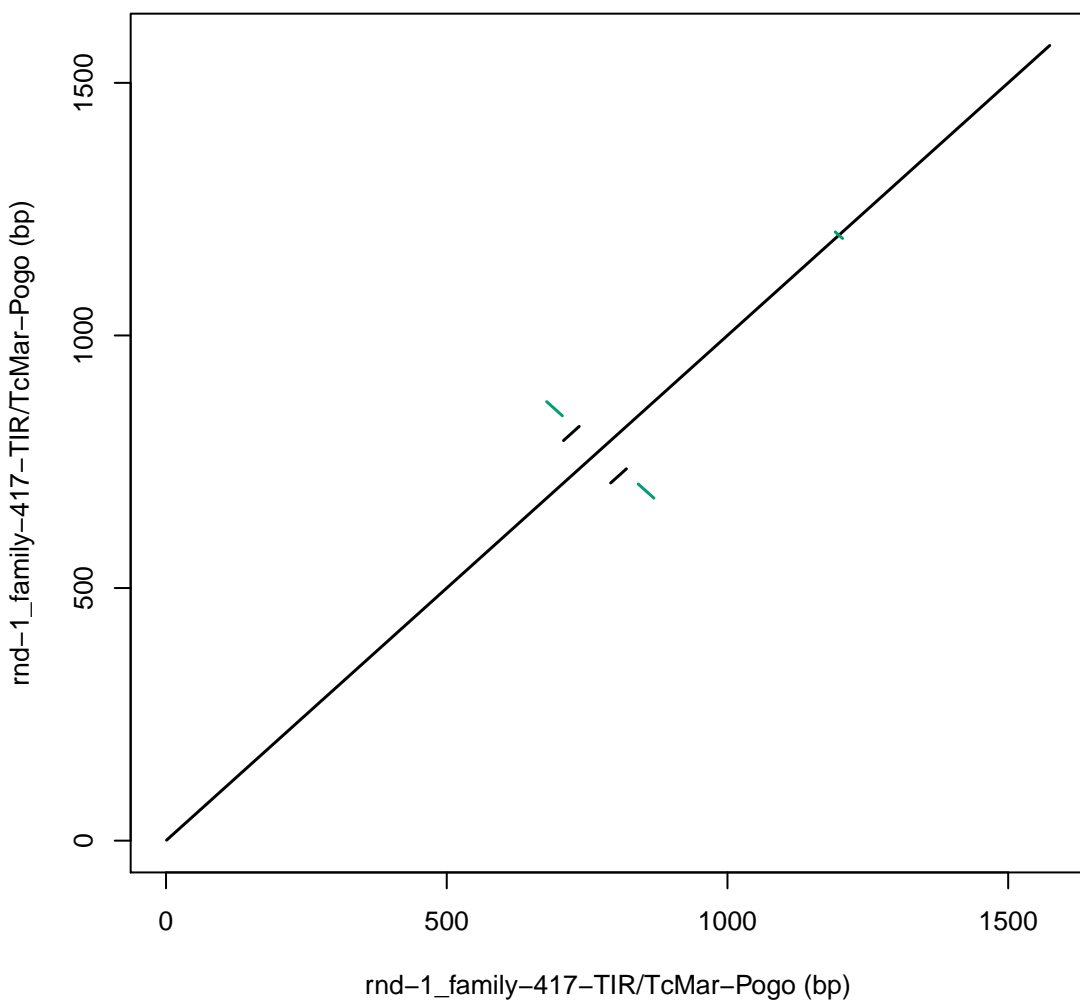
TE: rnd-1_family-417-TIR/TcMar-Pogo
consensus size: 1574bp; fragments: 78; full length: 0 (≥ 1416.6 bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

