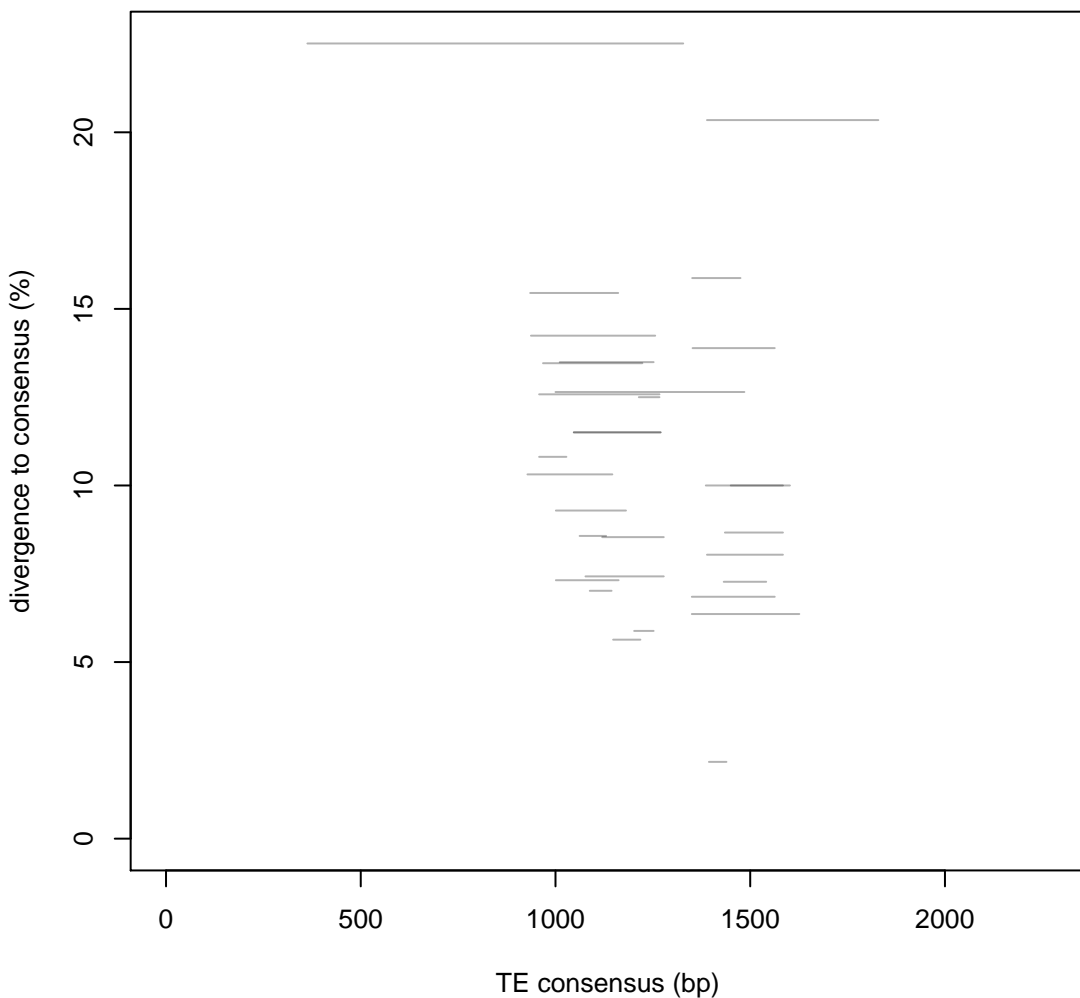
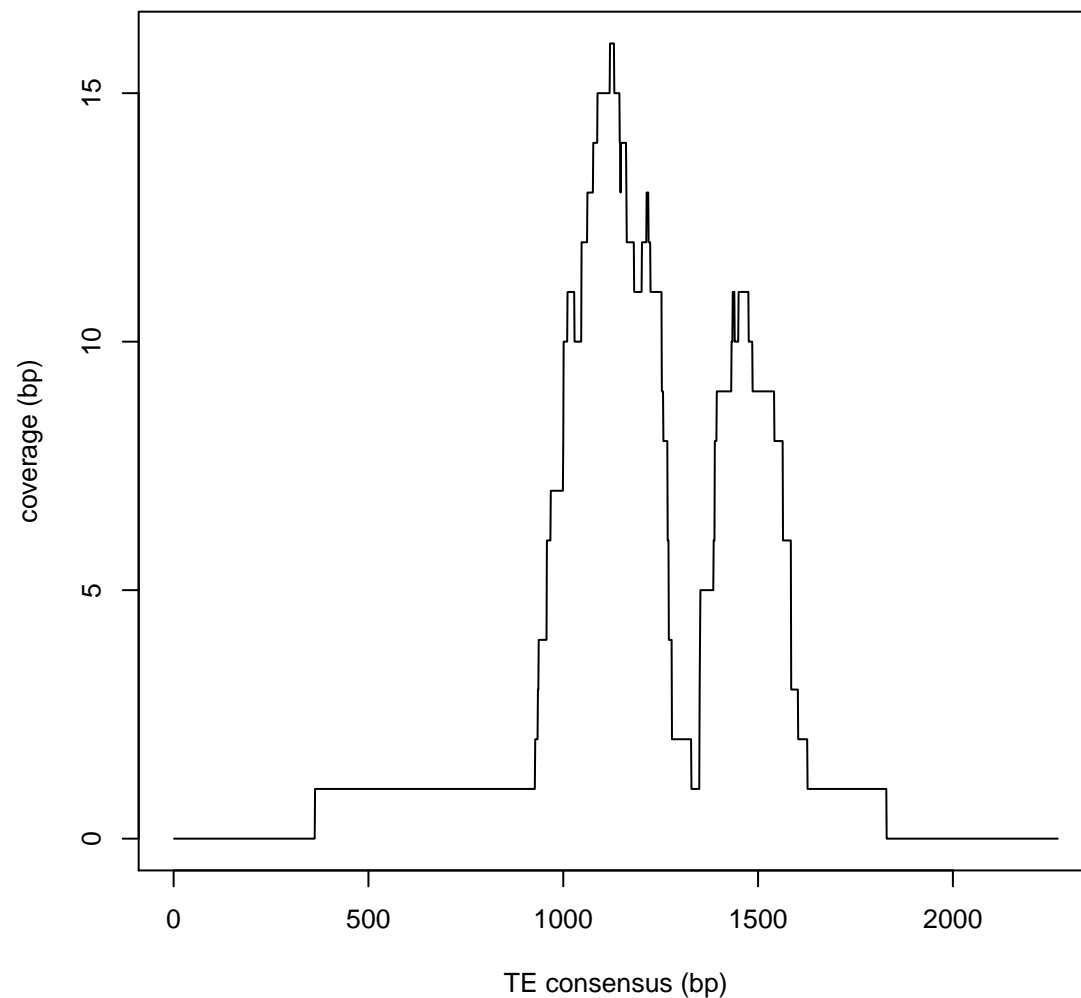


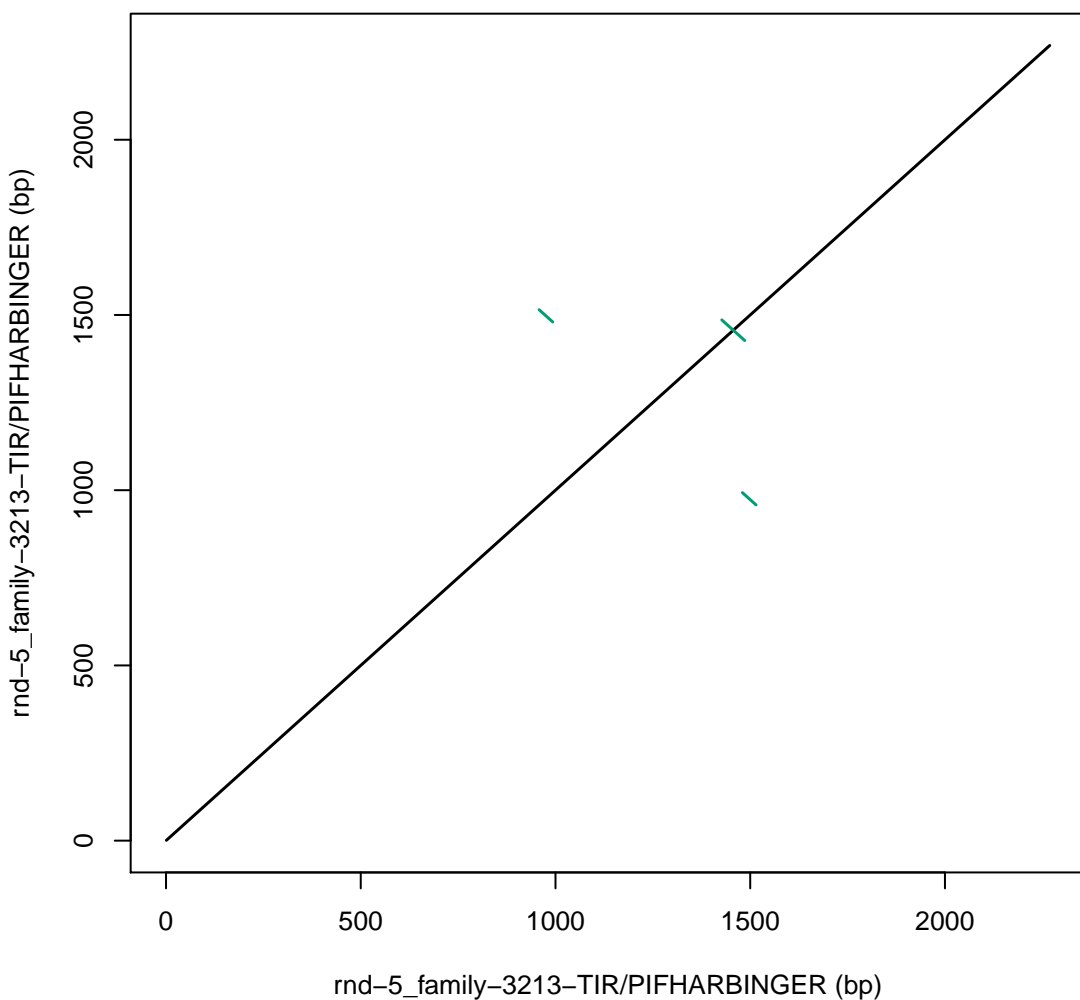
TE: rnd-5_family-3213-TIR/PIFHARBINGER
consensus size: 2269bp; fragments: 31; full length: 0 (≥ 2042.1 bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

