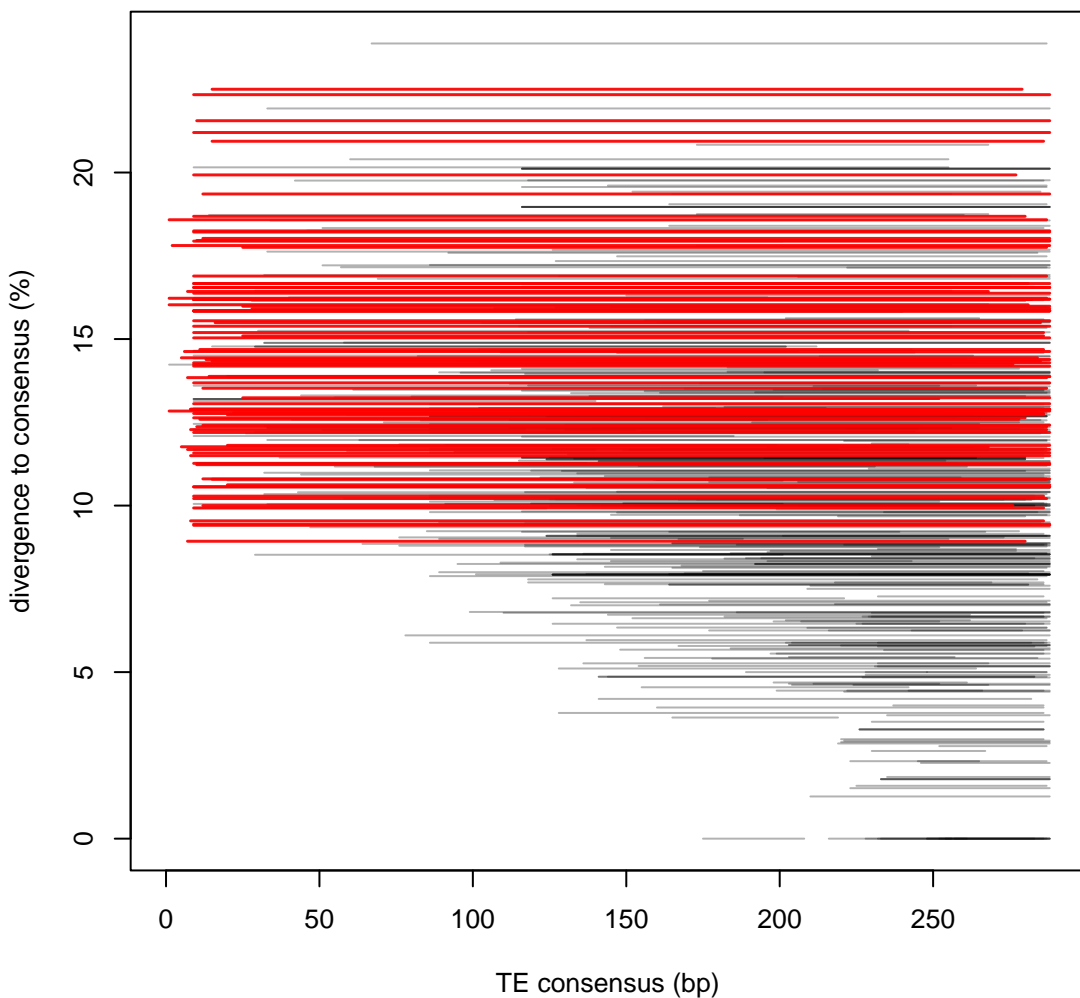
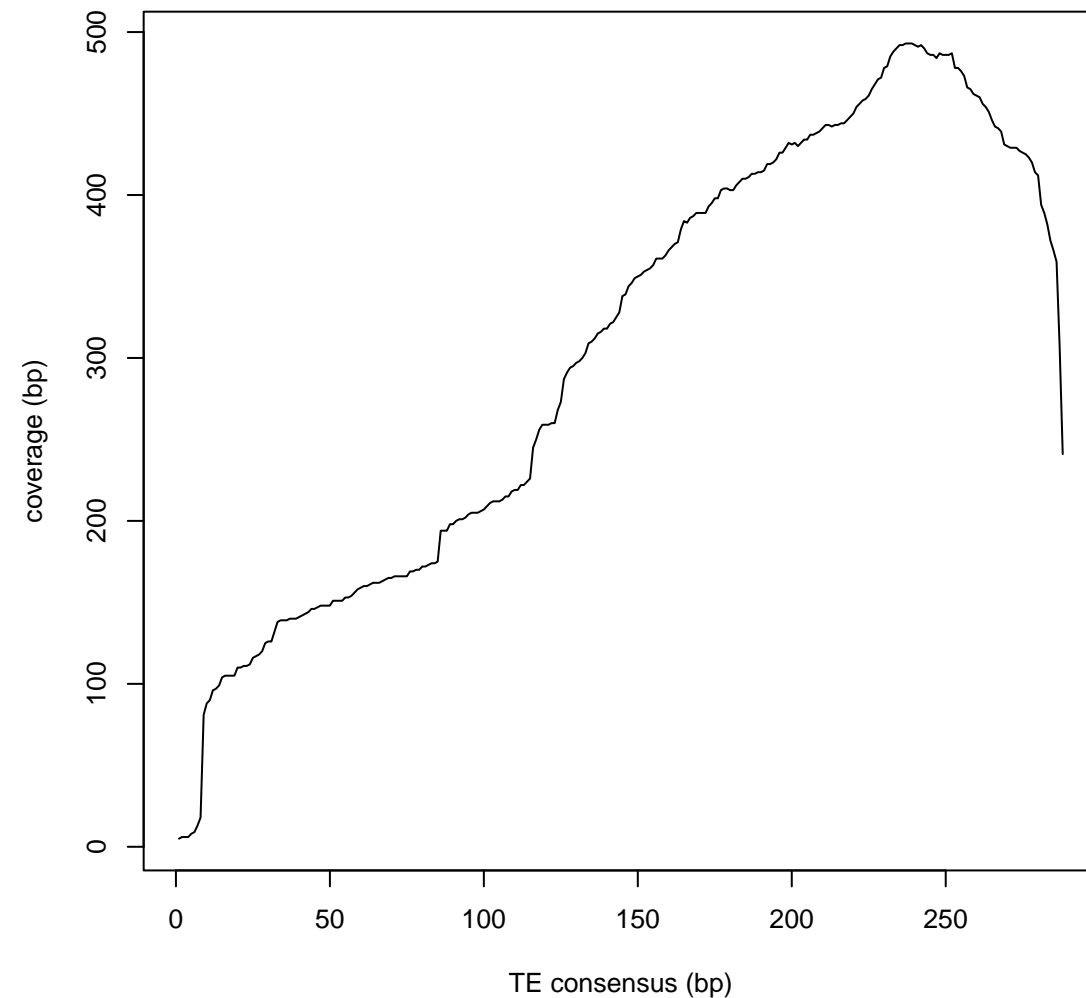


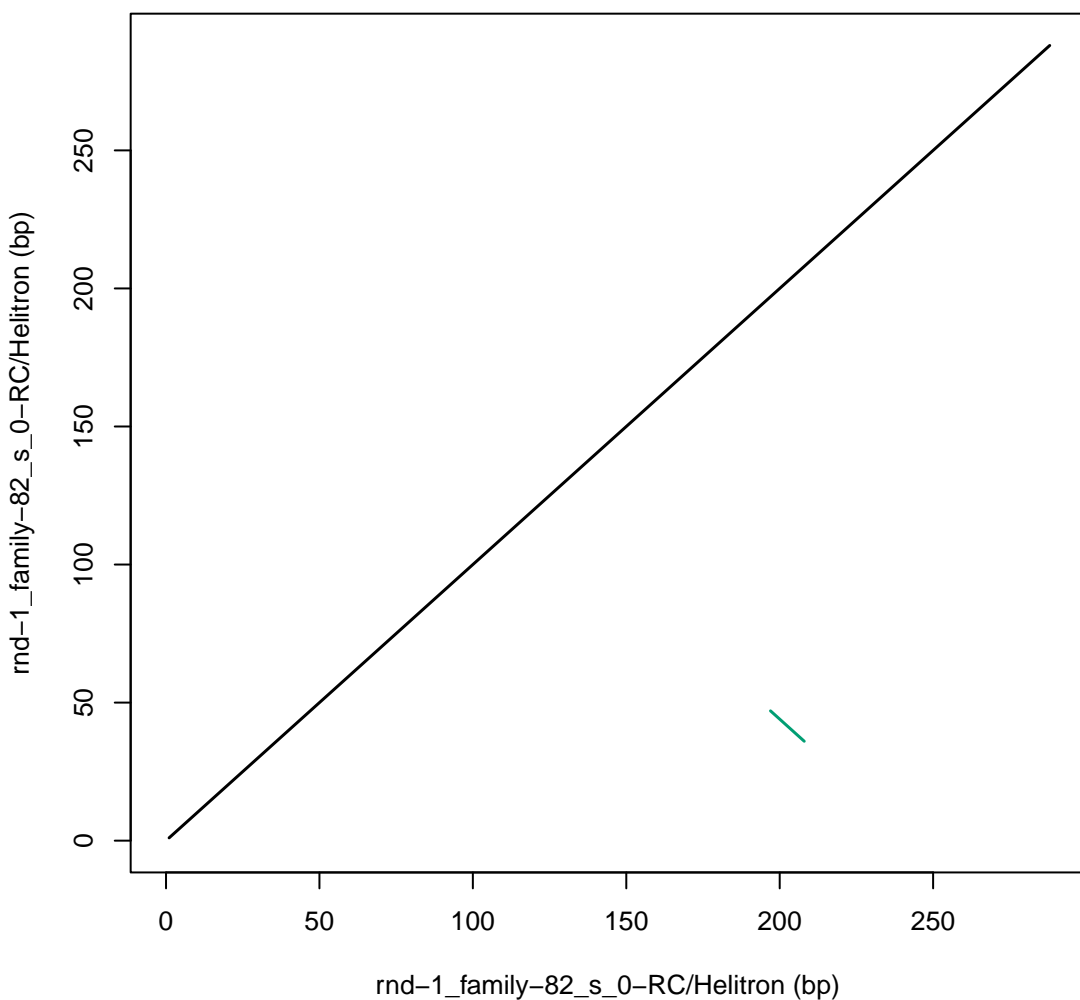
TE: rnd-1_family-82_s_0-RC/Helitron
consensus size: 288bp; fragments: 537; full length: 89 (≥ 259.2 bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

