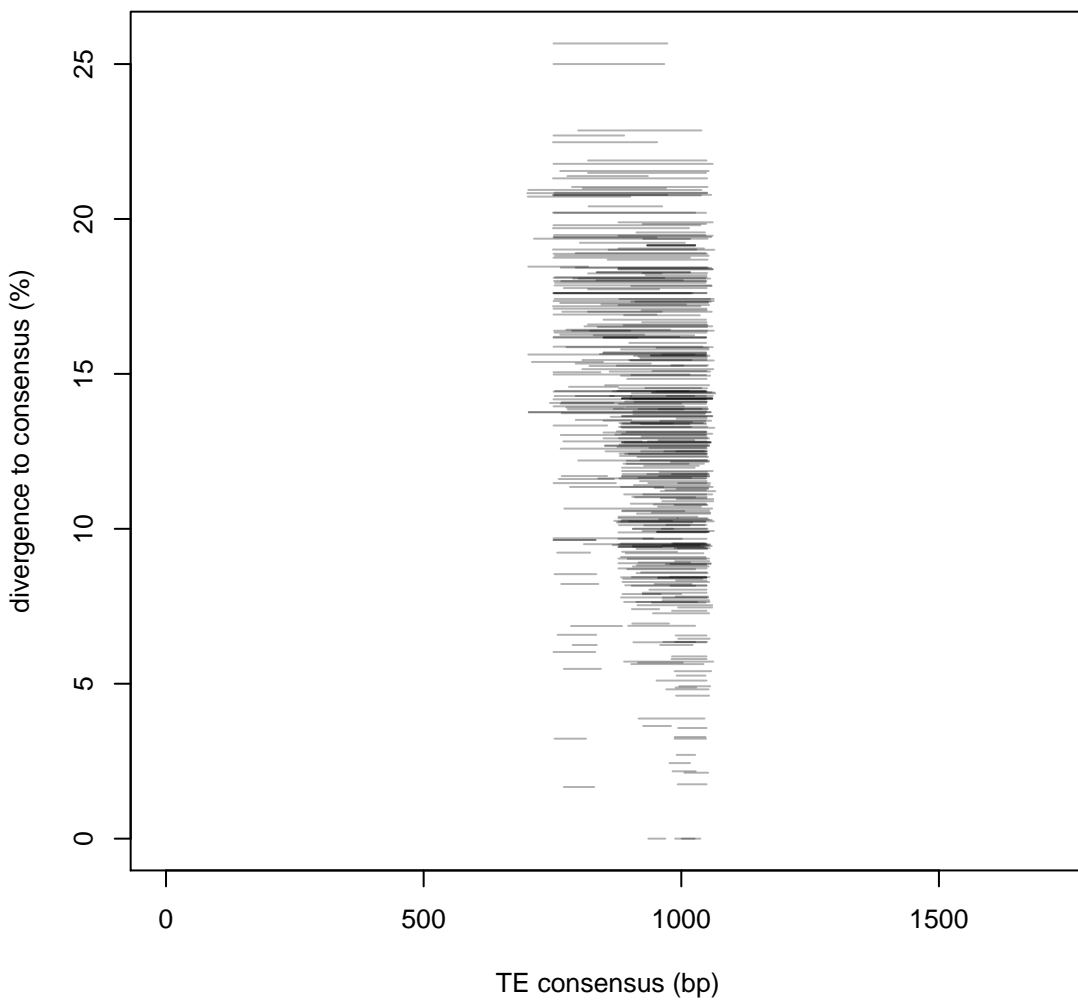
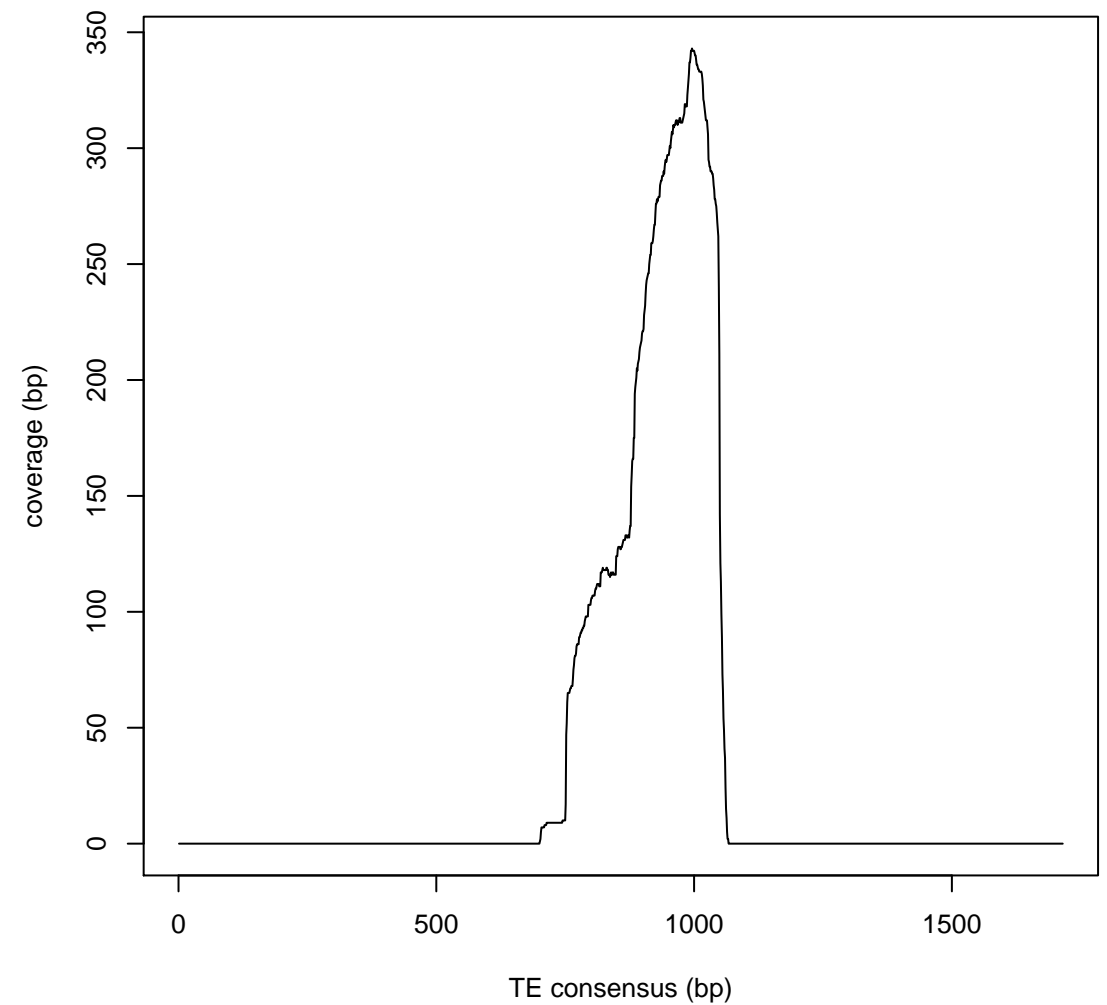


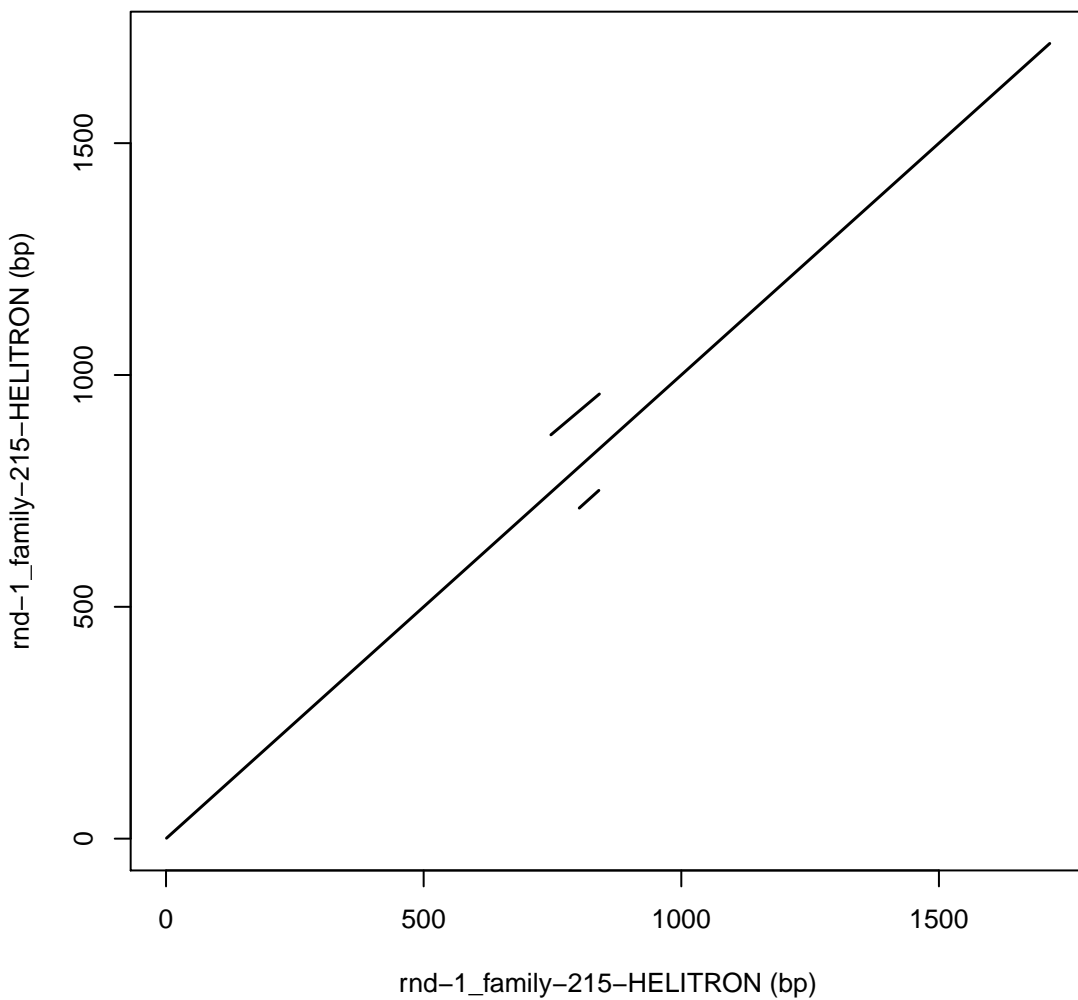
TE: rnd-1\_family-215-HELITRON  
consensus size: 1715bp; fragments: 405; full length: 0 ( $\geq 1543.5$ bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

