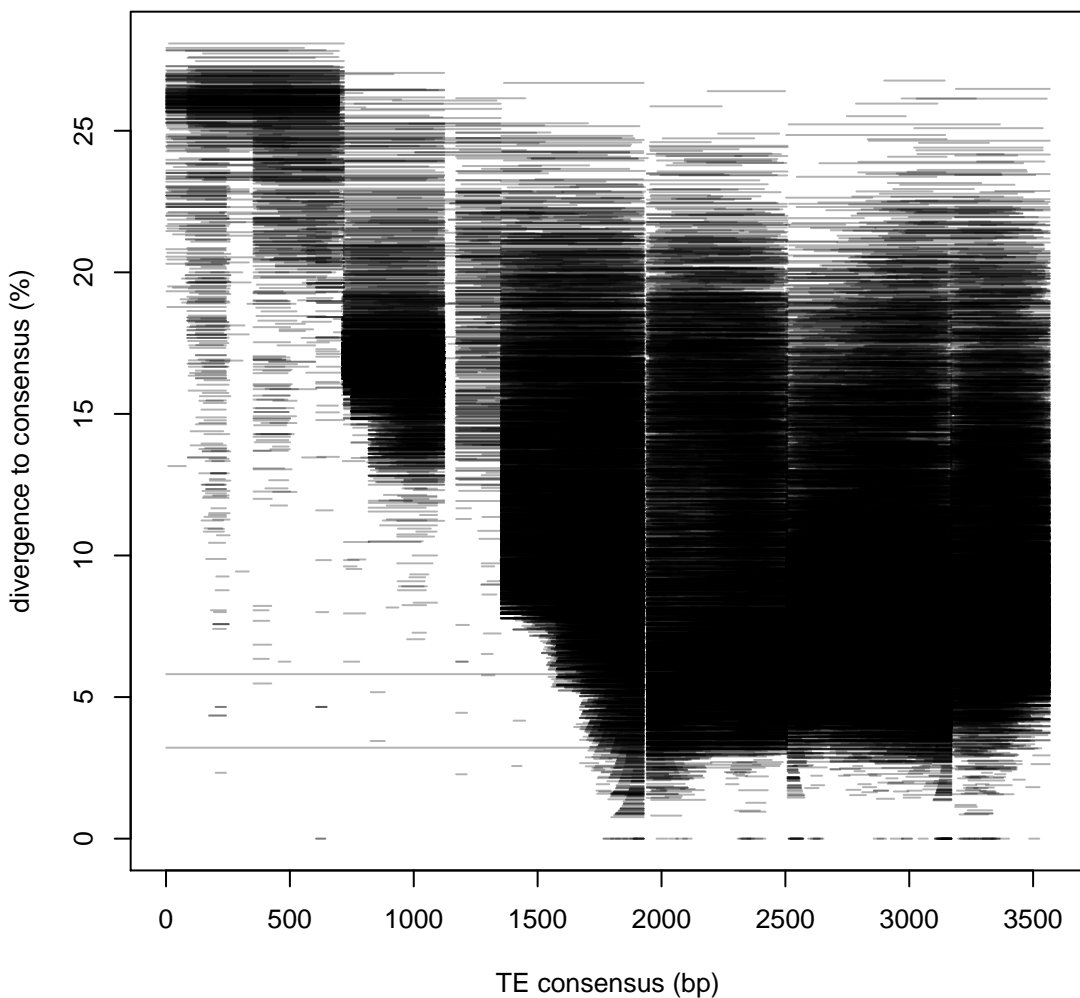
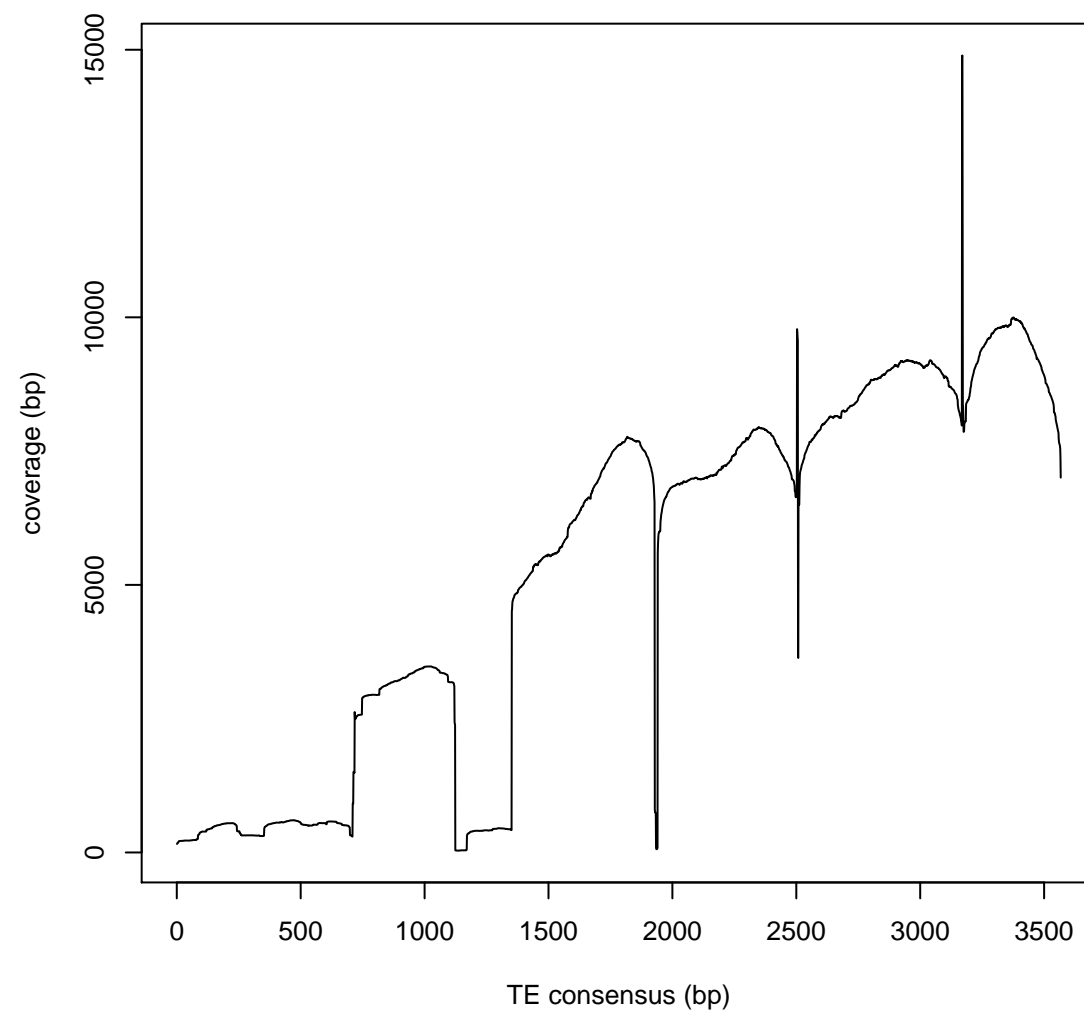


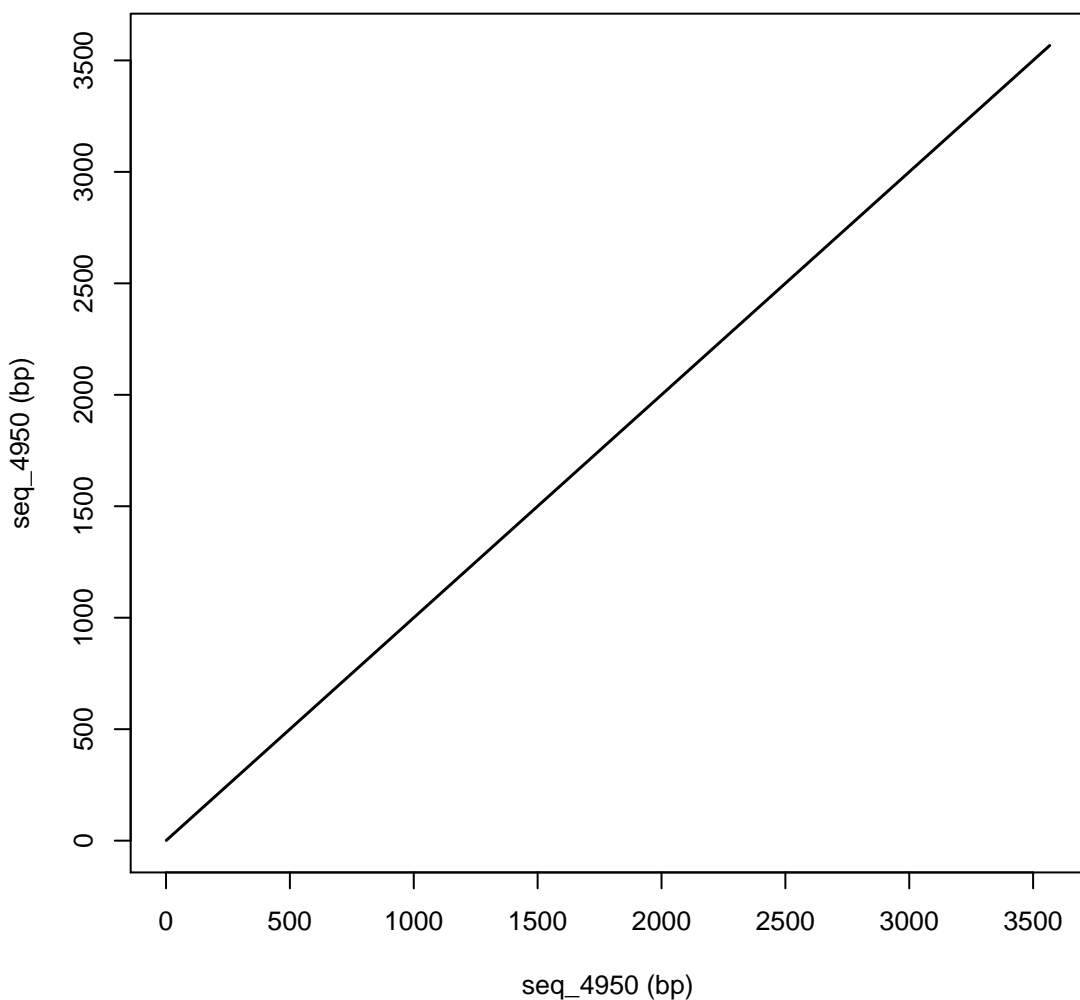
TE: seq_4950
consensus size: 3567bp; fragments: 46452; full length: 0 (>=3210.3bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

