TE: Dmel-B-R301-Map9_reversed-CLASSI/LINE/nan
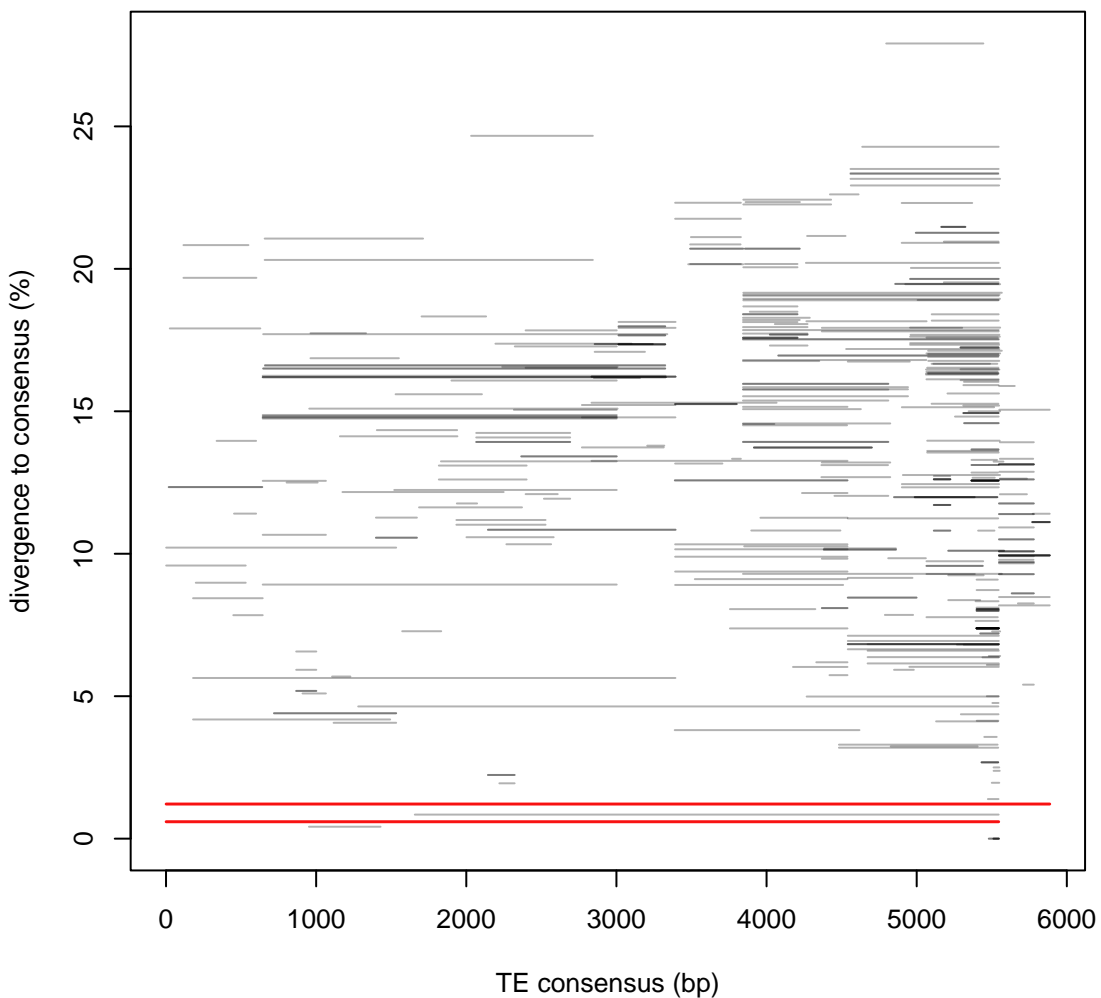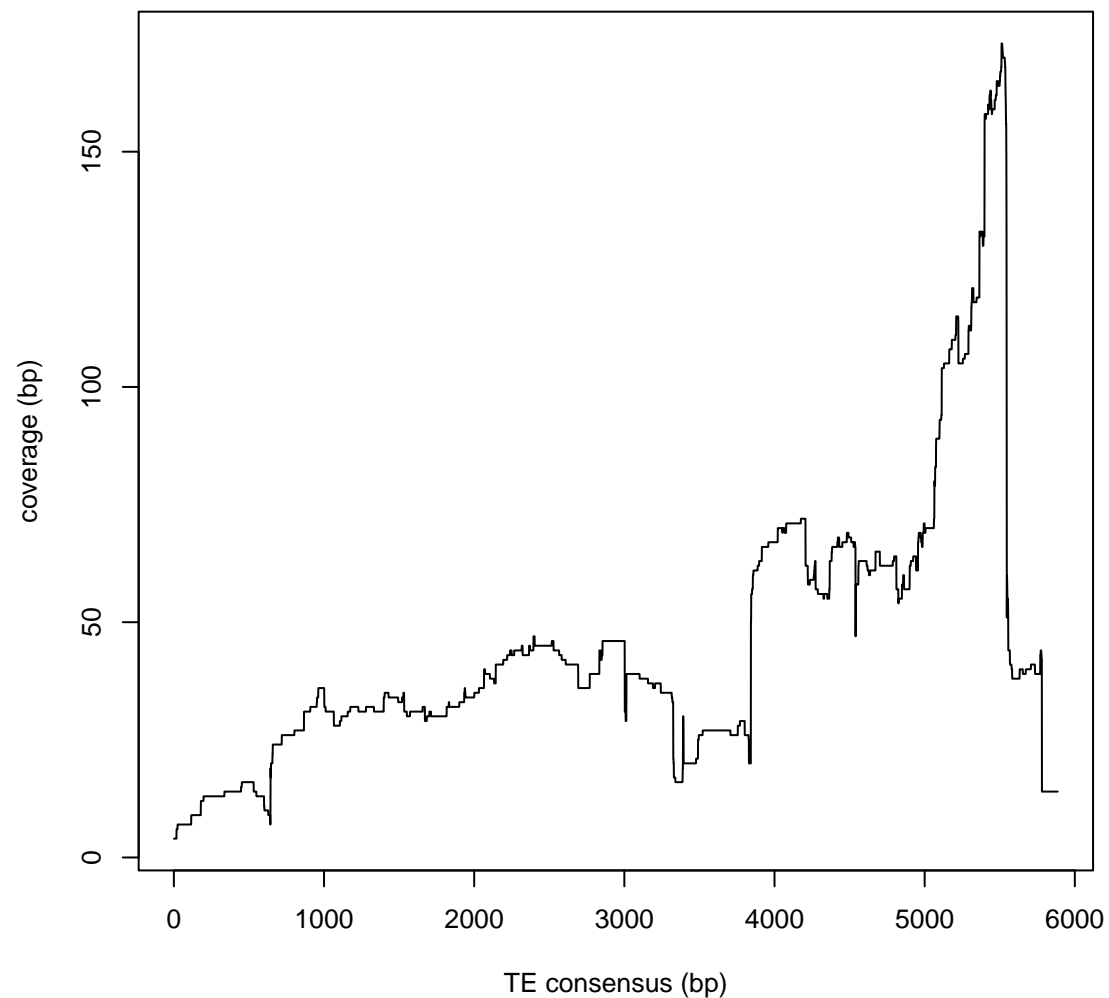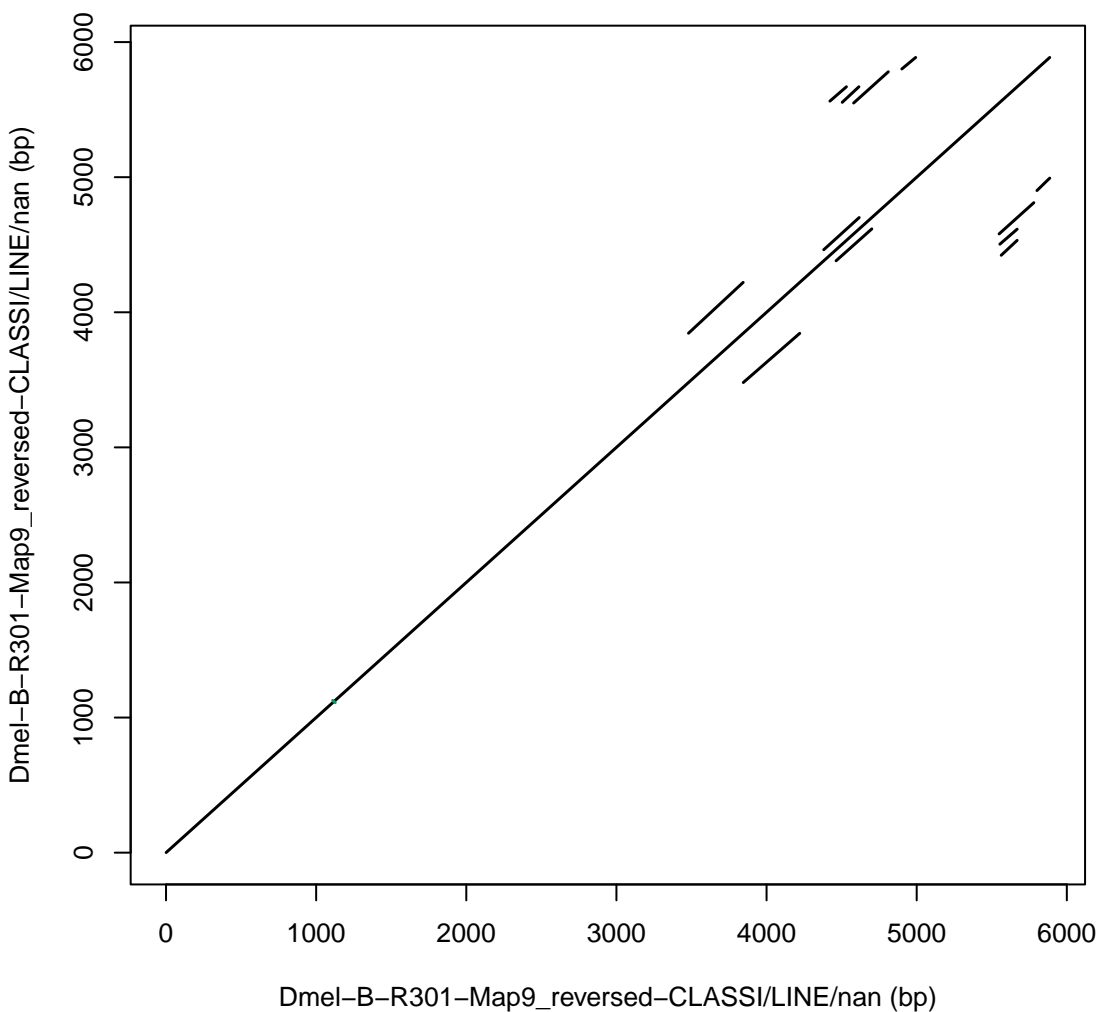**consensus size: 5886bp; fragments: 448; full length: 2 (>=5297.4bp)**

divergence to consensus (%)

TE consensus (bp)

TE consensus genomic coverage

coverage (bp)

TE consensus (bp)

TE consensus self dotplot (blastn)

Dmel-B-R301-Map9_reversed-CLASSI/LINE/nan (bp)

Dmel-B-R301-Map9_reversed-CLASSI/LINE/nan (bp)

TE consensus structure and protein hits

UN-LINE-4_OS_pol LINE/L1
HETA_gag LINE/I-Jockey

Dmel-B-R301-Map9_reversed-CLASSI/LINE/nan (bp)