TE: Dmel–L–B83–Map1–CLASSI/LTR/LARD
consensus size: 9037bp; fragments: 2; full length: 2 (>=8133.3bp)

divergence to consensus (%)
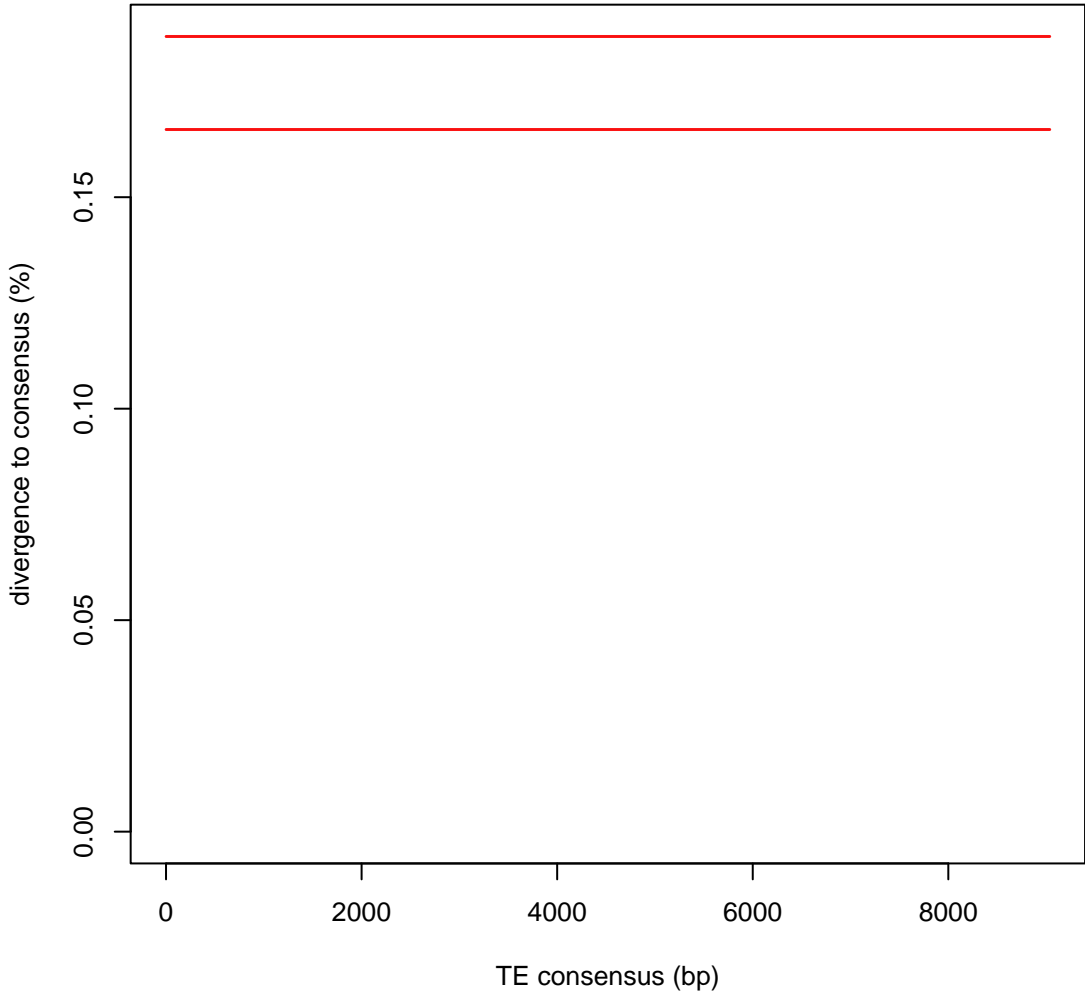
TE consensus (bp)

TE consensus genomic coverage

coverage (bp)
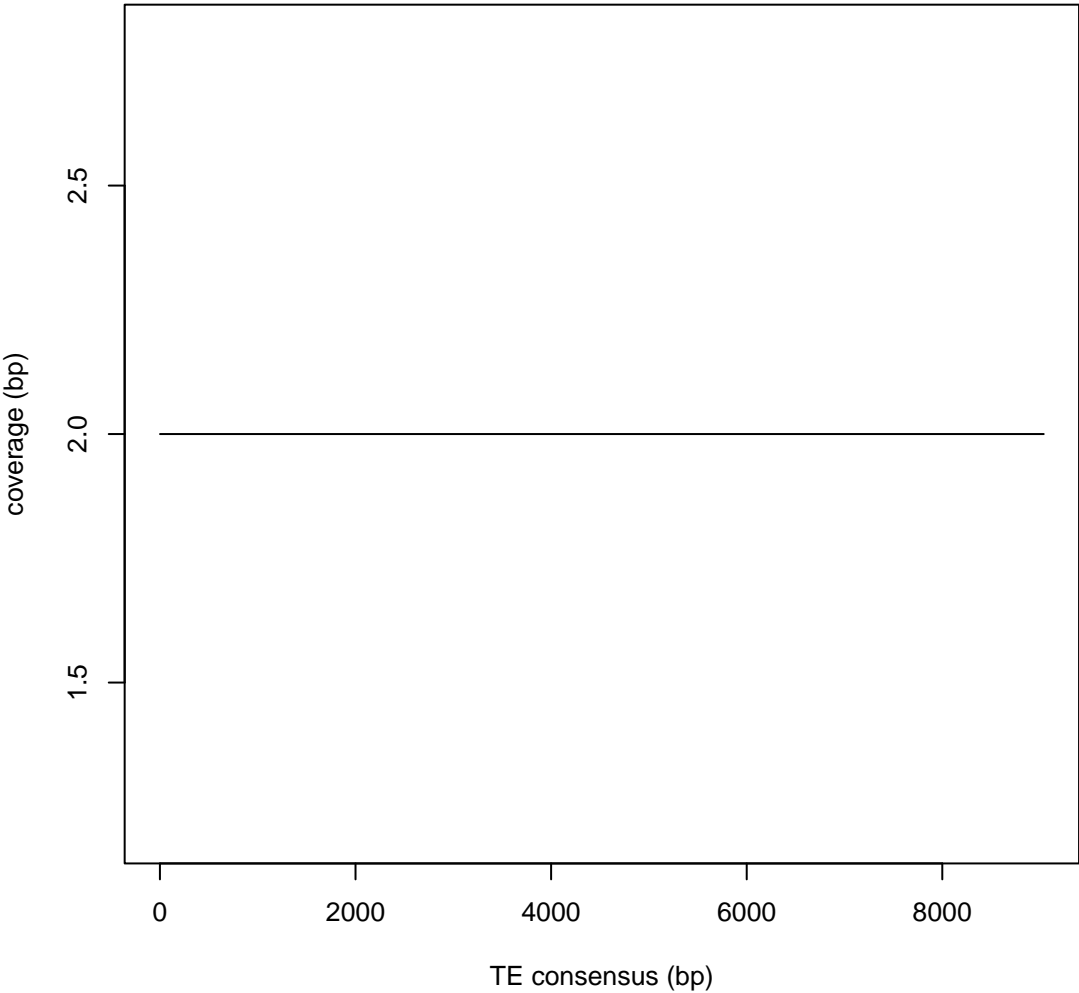
TE consensus (bp)

TE consensus self dotplot (blastn)

Dmel–L–B83–Map1–CLASSI/LTR/LARD (bp)

Dmel–L–B83–Map1–CLASSI/LTR/LARD (bp)
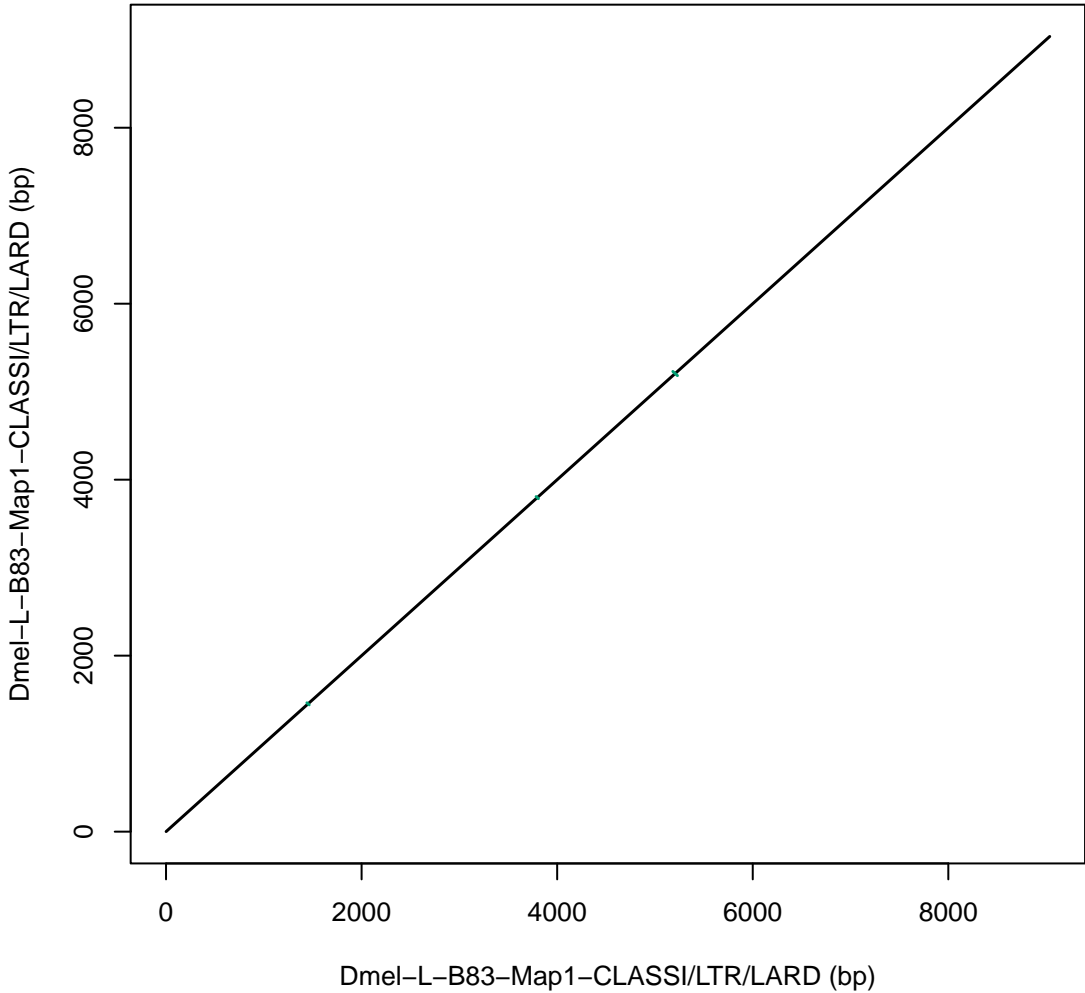
TE consensus structure and protein hits

Crack–1_CP_pol LINE/L2

UN–3176712_Ath_gagpol LINE/L1

UN–4538901_Ath_pol LINE/

L1–39_XT_pol LINE/

Dmel–L–B83–Map1–CLASSI/LTR/LARD (bp)