TE: DmeI−L−B526−Map1−TRIM/nan
consensus size: 1389bp; fragments: 7; full length: 2 (>=1250.1bp)

divergence to consensus (%) — TE consensus (bp)
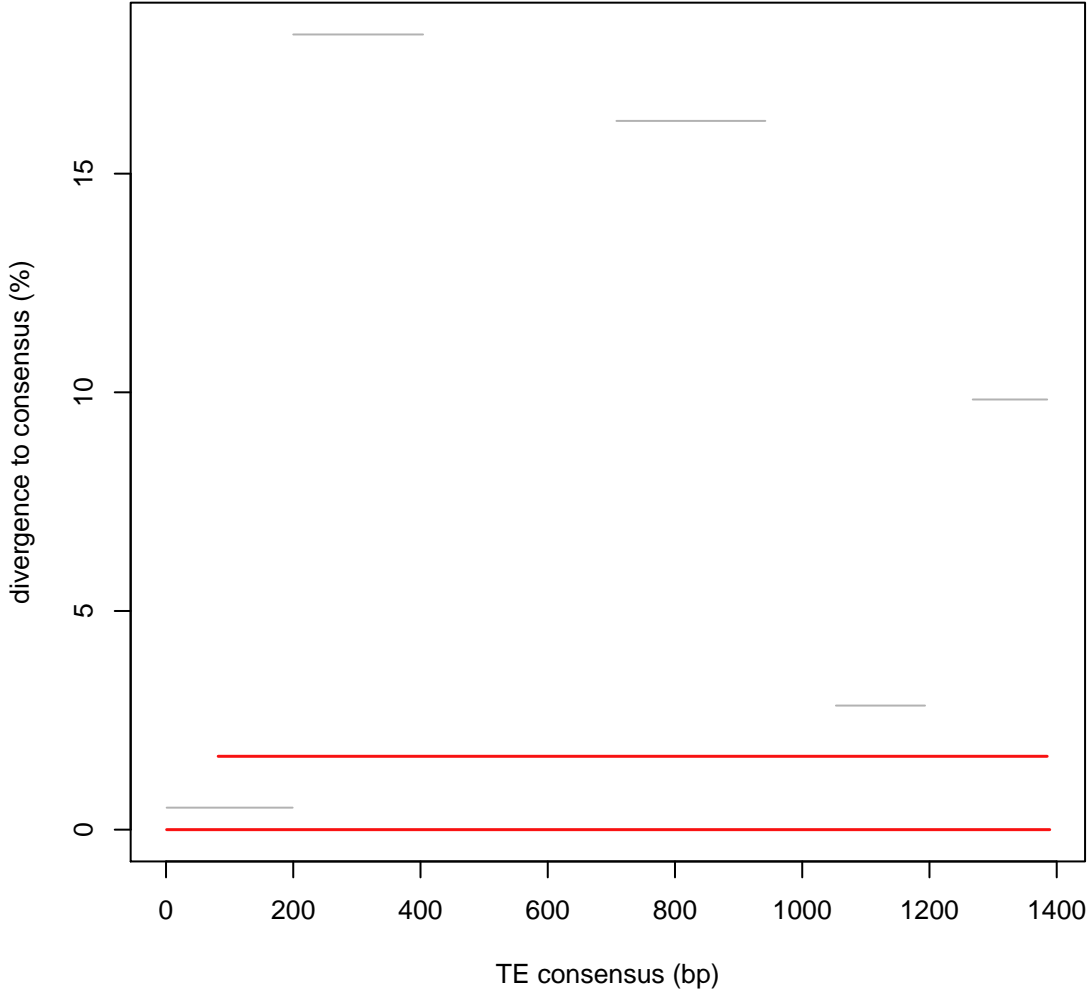
TE consensus genomic coverage
coverage (bp) — TE consensus (bp)
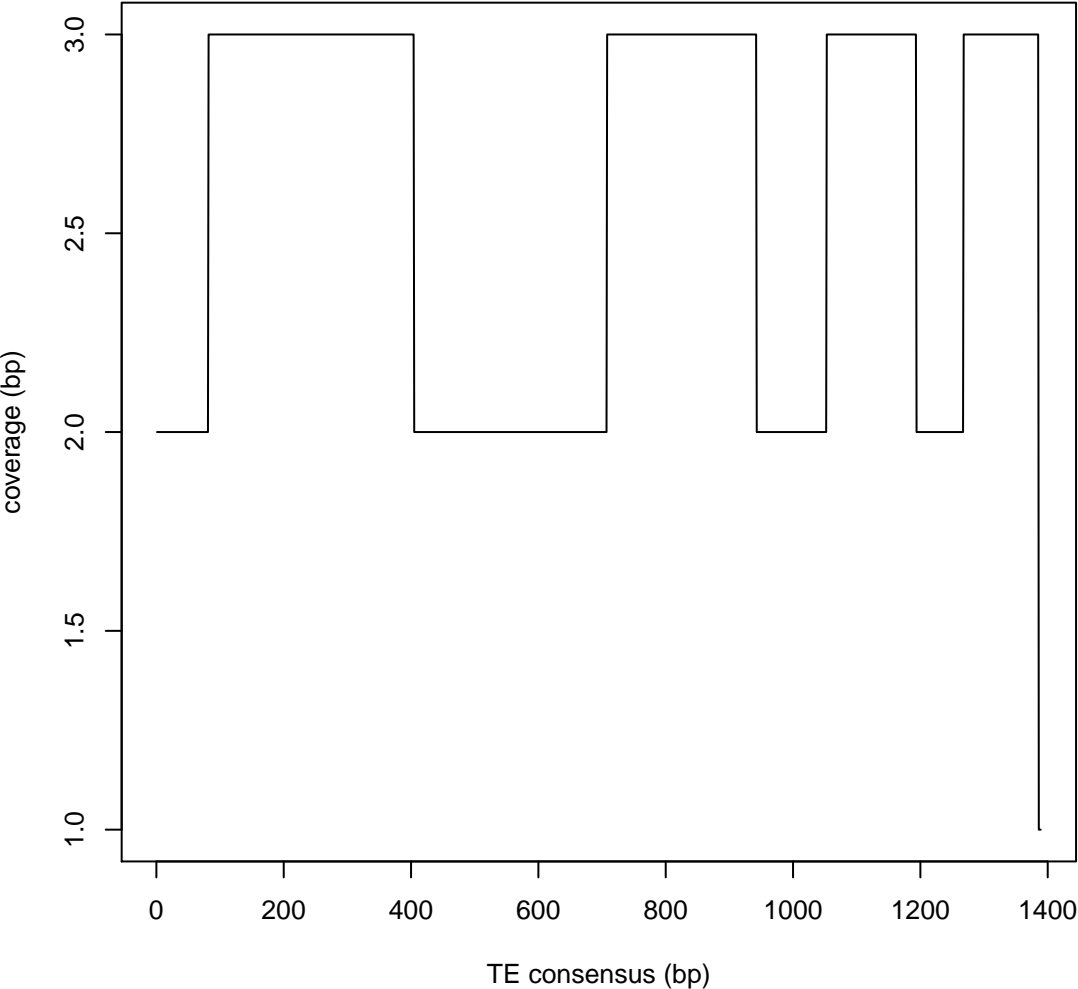
TE consensus self dotplot (blastn)
DmeI−L−B526−Map1−TRIM/nan (bp) — DmeI−L−B526−Map1−TRIM/nan (bp)
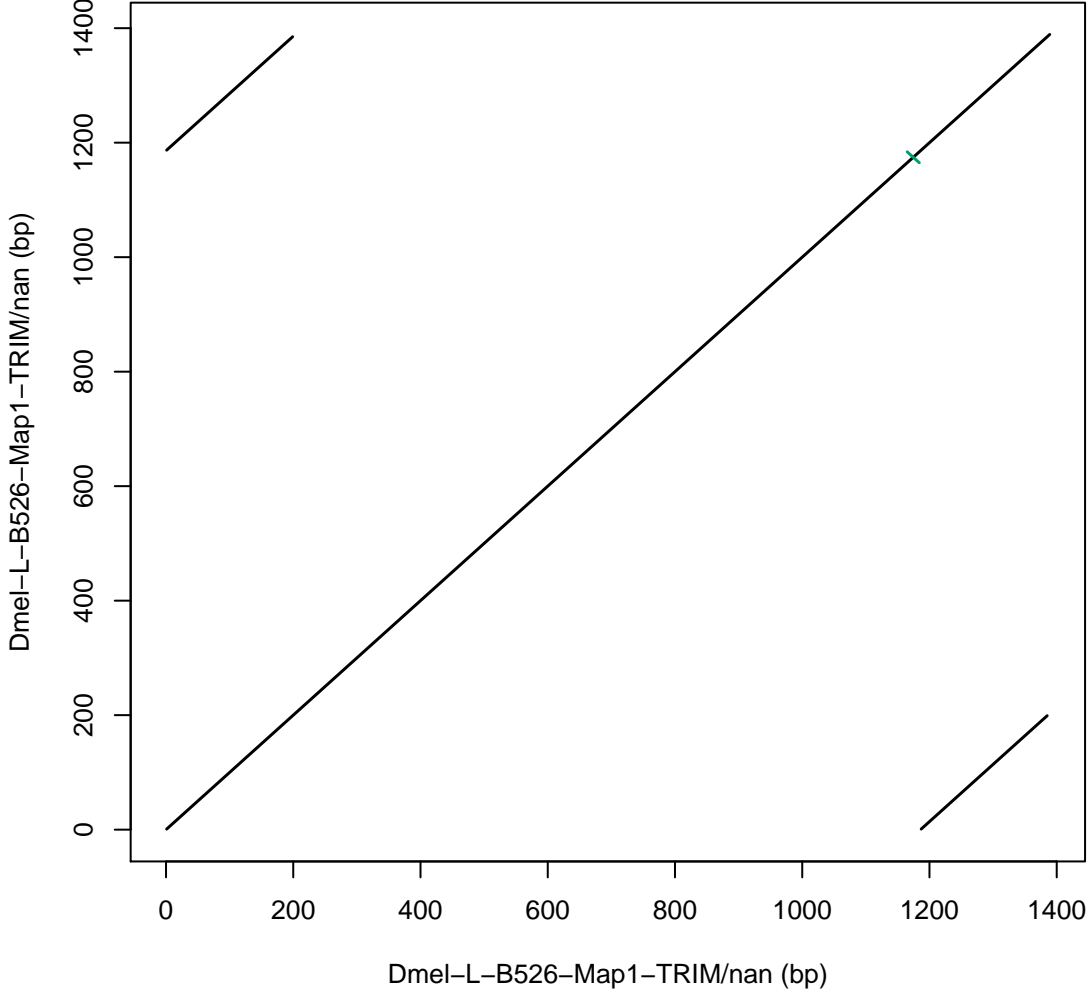
TE consensus structure and protein hits
Copia−68_SB LTR/Copia
Gypsy−24_SI_1p LTR/Gypsy
DmeI−L−B526−Map1−TRIM/nan (bp)