**TE: seq_7002**
**consensus size: 3029bp; fragments: 29013; full length: 1 (>=2726.1bp)**

TE consensus (bp)

divergence to consensus (%)
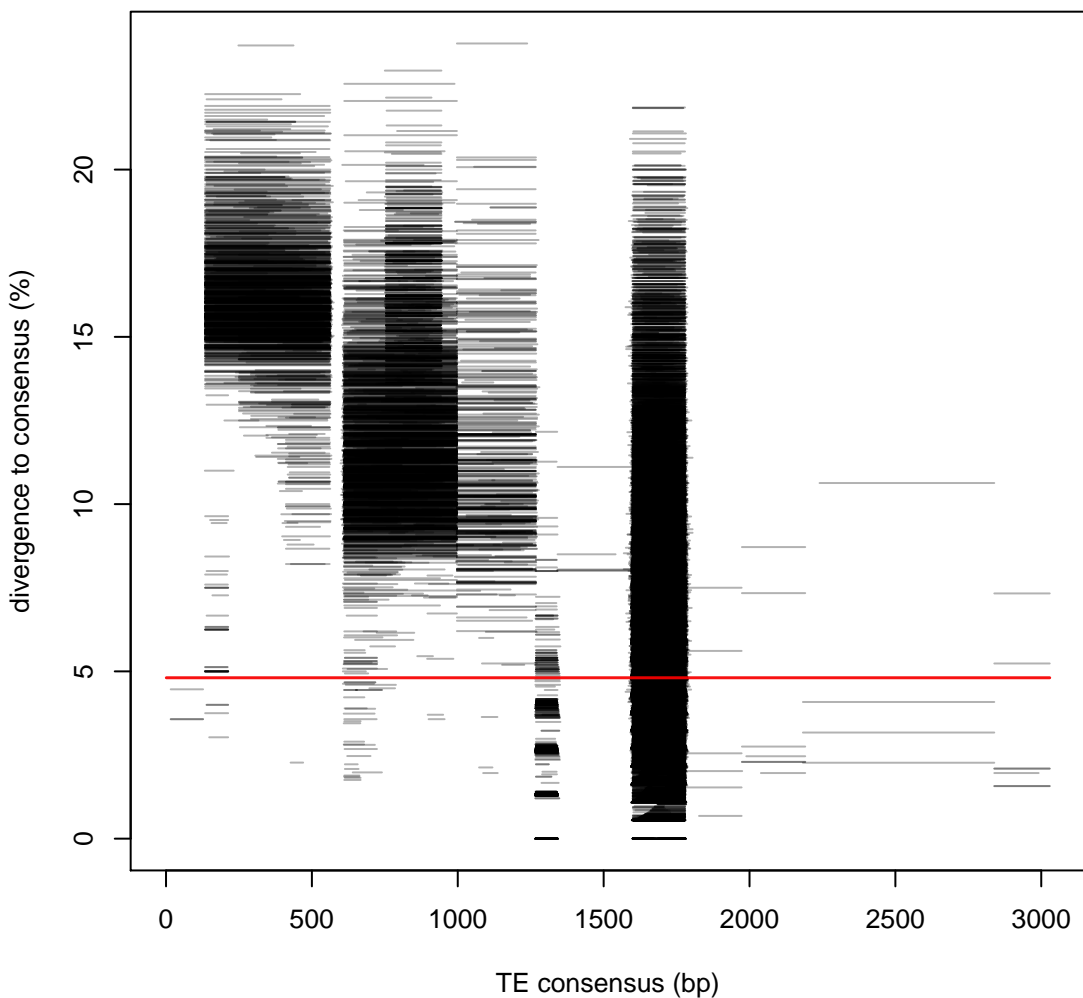
**TE consensus genomic coverage**

coverage (bp)
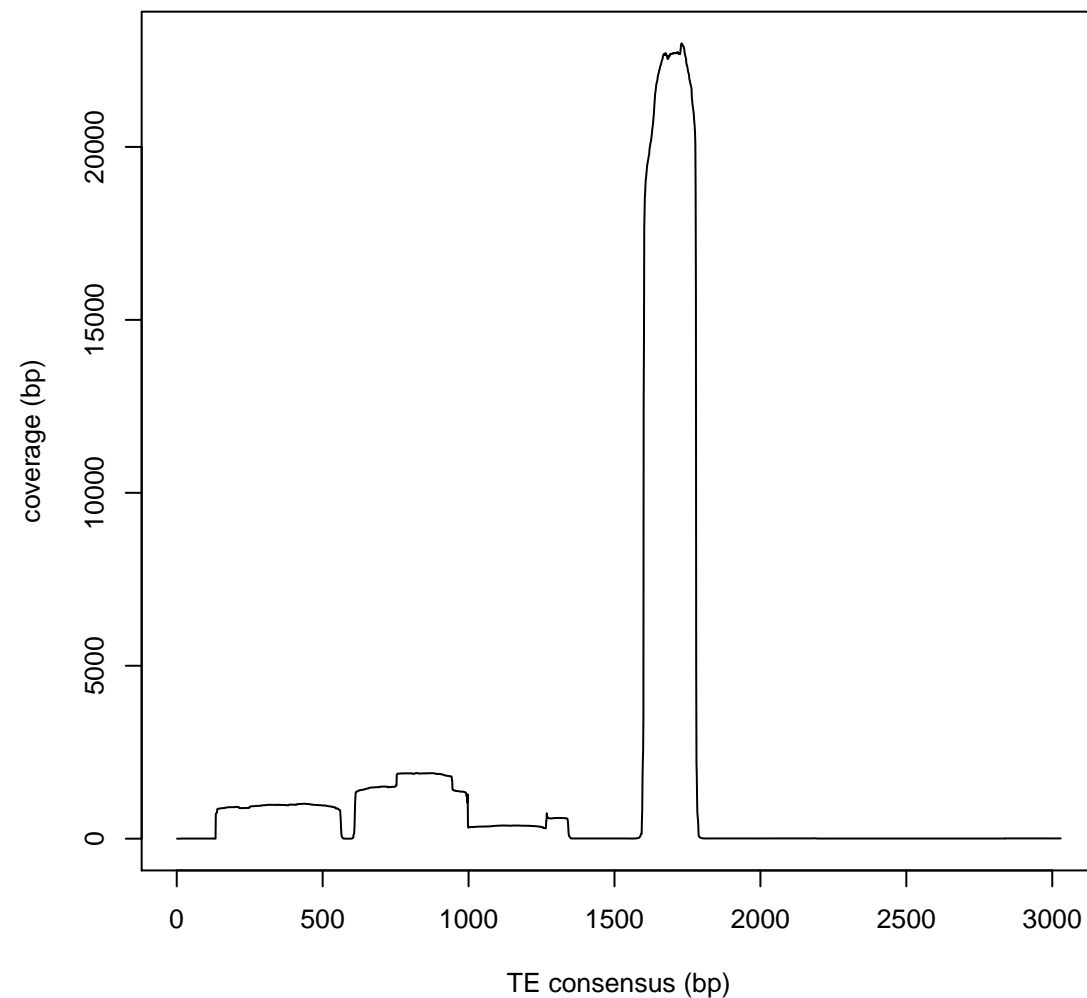
TE consensus (bp)

**TE consensus self dotplot (blastn)**

seq_7002 (bp)

seq_7002 (bp)
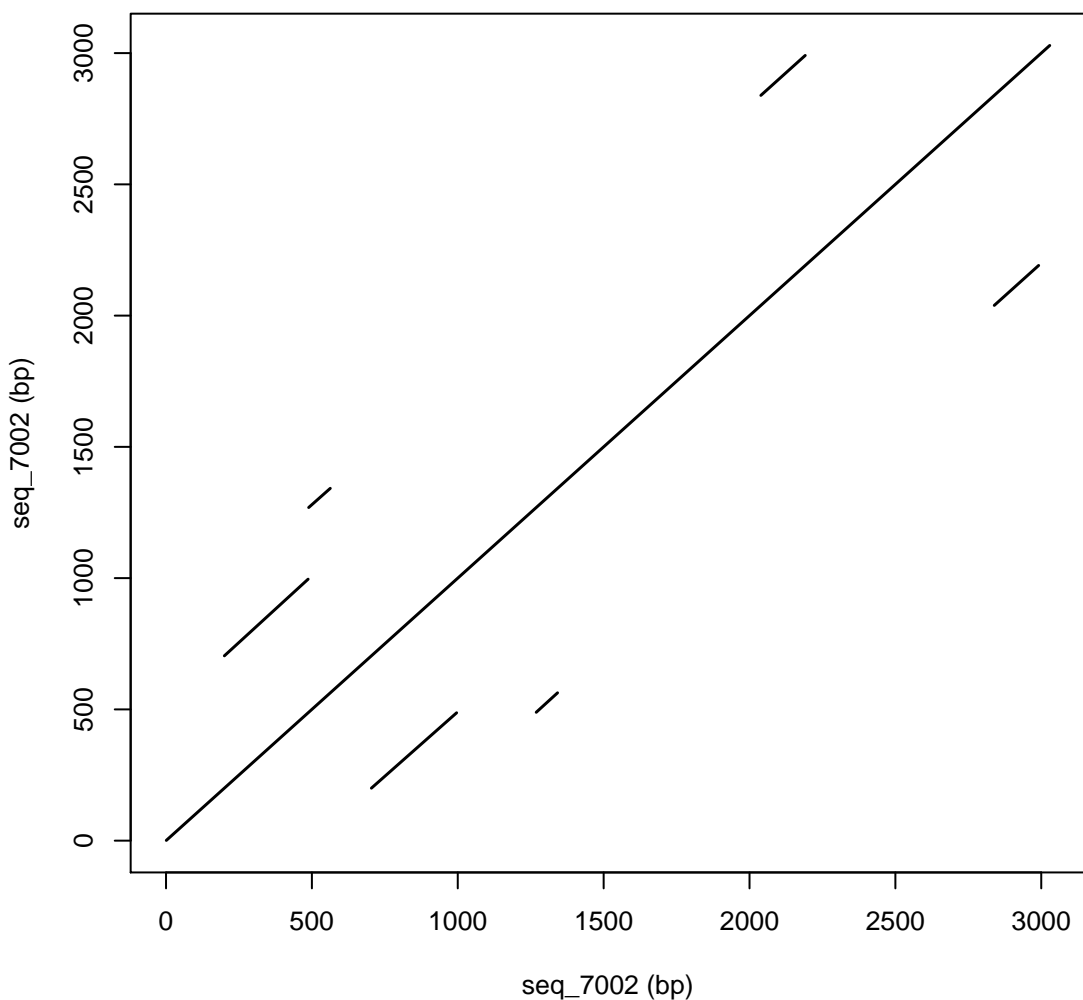
**TE consensus structure and protein hits**

Gypsy−146_AA LTR/Gypsy
Gypsy−8_CQ_1p LTR/Gyps

seq_7002 (bp)