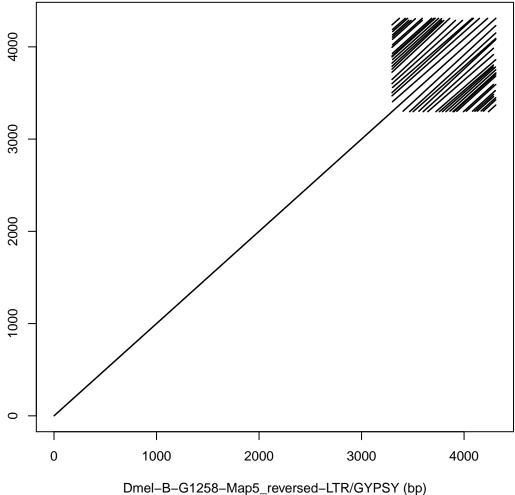
TE: Dmel-B-G1258-Map5_reversed-LTR/GYPSY consensus size: 4310bp; fragments: 12241; full length: 0 (>=3879bp) divergence to consensus (%) coverage (bp) TE consensus (bp) TE consensus self dotplot (blastn)

TE consensus genomic coverage



Dmel-B-G1258-Map5_reversed-LTR/GYPSY (bp)

TE consensus structure and protein hits

TE consensus (bp)

