

siteID: chr11_35425496

Yellow : matches to reference hg19 based on blat

Light blue: indel rs371417146, A → GAGGAAACAGCTCAAAGGCAAAGG

Purple: AluSx

Red: Additional sequence

Bold Green: Region of similarity

Bold Underline: Candidate Target Site Duplication

!
<hg19_dna_range=chr11:35425003-35425797

CTGGTAAGAGGATTTTCATGCAAGCCTGCACATGTGTGGCTGCCCTGTAGGACTGGCTACATAATGT
GTGGGTCTGCACGTAATTTGGGCAAAATGAAATCTTGAGACCCCTTGTTCAAATTAACATTTCAA
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TCT

>contig

CTGGTAAGAGGATTTTCATGCAAGCCTGCACATGTGTGGCTGCCCTGTAGGACTGGCTACATAATGT
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Alignment (89.5% identity)

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