PQS in B19V ITRs: Hairpin configuration, Left End

+strand Flip

```
CGCCGCTTG-TCTTAGTGTCAAGGCAACCCCAAGCAAGCTGGCCCAGAGCCAACCCTAATTCCGGAAGTCCCGCCCACCGGAAGTGACGTCACAGGAAATGACGTCACAGGAAATGACGTAATTGTCCGCCATCTTGTACCGGAAGTCCCGCCTACCGGCGGCGACCGGCGGCATCTGATTTGGTGTCTTCTTTTAAATTTT -  3'
||||||||| |||||||| || | ||||||||||  |||||||||||
```

PQS in B19V ITRs: Hairpin configuration, Right End

+strand Flip

```
PQS068                                                                                                >>>>
```

LEGEND

Inverted Terminal Regions (ITR) in B19V genome. The left and right ends are shown in the hairpin configuration for positive and negative sense strands, in the ‘flip’ or flop’ configuration.

In yellow, the regions of imperfect base pairing giving rise to the ‘flip’ and flop’ configurations. Underlined, the PG4S regions predicted by QGRS mapper, in bold the G residues involved.

Gallons indicate the position of the three oligonucleotides used for CD analysis (PQS140, PQS113, PQS068). The PG4S and corresponding oligonucleotides match only one of the strands in the hairpin stem.