

Alignment of Sequence\_1: [LOC101927501 Target.xdna] with Sequence\_2: [Clone 7].  
 Similarity : 167/343 (48.69 %)

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Seq_1  1      CTCTCCCTTGCTCCCTCTCTTGCCATGTGACATGCTTGCTCCAGCTGCACCTTTTGCCAC  60
          |||
Seq_2  1      CTCTCCCTTGCTCCCTCTCTTGCCATGTGACATGCTTGCTCCAGCTGCACCTTTTGCCAC  60

Seq_1  61      AATTGTAAGCTTTGTGAGTCCCTCAACAGAAGCTGAGCAAATGCTGGCACCATGCTTCTT  120
          |||
Seq_2  61      AATTGTAAGCTTTGTGAGTCCCTCAACAGAAGCTGAGCAAATGCTGGCACCATGCTTCTT  120

Seq_1  121     GTACAGCCTaca-gaactgtgaaccaaata-----  149
          |||
Seq_2  121     GTACAGCCTACATGTA-GGGGATCCACCGACCAGAATCATGCAAGTGCGTAAGATAGTCG  179

Seq_1  150     -----AACTTTTATTTTATAAATTATCTAGCCTCAGGTATTCCTTTATAGCAAT  200
          |||
Seq_2  180     CGGGCCGGGAAACTTTTATTTTAT-----  204

Seq_1  201     GCAAAACAAACTAACACACCCTTAAACCCTATATTTAAGGCTGAGATCTTGGACCCTCCT  260
          |||
Seq_2  205     -----GG--ATCCG-TAAGTAAGG-----  220

Seq_1  261     CCTAAAATTTACCTTAAAAGGTGAAGCAAGCACTAGTCTTGGAGACTATAAATTGGAAAA  320
Seq_2  221     -----  220
  
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**Figure 8 – figure supplement 1.** Sequence alignment of gDNA from *PINCR* (Seq\_1) and *PINCR*-S1 (Seq\_2) clones. Yellow is the 44 nucleotide S1-tag inserted in *PINCR*-S1.