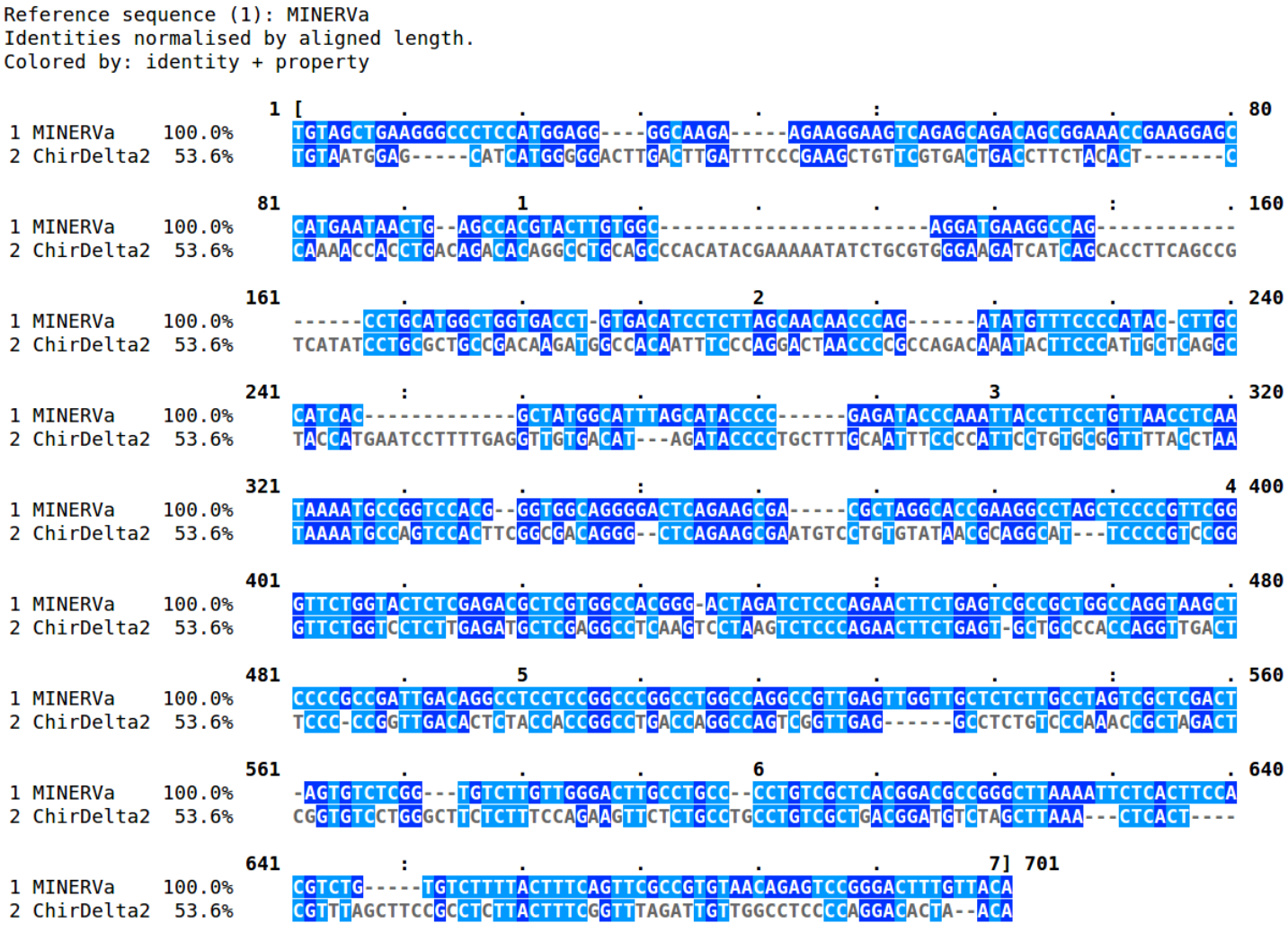

Figure S2: DNA sequence alignment of ChirDelta2 and MINERVa LTR.
DNA sequence alignment was generated using Muscle algorithm. Calculation of percent identity and visualization was performed by MView tool (www.ebi.ac.uk). MINERVa - consensual sequence of MINERVa orthologs [3]; ChirDelta2 - sequence from *R. sinicus* genome assembly (GenBank accession no. LVEH00000000).