

Rhinolophus sinicus genomic scaffold LVEH01002092.1:218-893
(Accession number:start-end)

target site
duplication proviral LTR sequence

TTTATCTGTAATGGAGCATCATGGGGACTTGACTTGATTCCGAAGCTGTCGTGACTGACCTTACACT

CAAAAACCACCTGACAGACACAGGCCTGCAGCCCACATACGAAAAATATCTGCGTGGAAAGATCATCAGCACC

TTCAGCCGTCATATCCTGCGCTGCCGACAAGATGCCACAATTCCAGGACTAACCCGCCAGACAAATACT

TCCCATTGCTCAGGCTACCATGAATCCTTTGAGGTTGTGACATAGATACCCCTGCTTGCAATTCCCCATT

polyadenylation signal site

CCTGTGCGGTTTACCTAATAAAATGCCAGTCCACTCGGCGACAGGGCTCAGAAGCGAATGTCTGTGTATA

ACGCAGGCATTCCCCGTCCGGTTCTGGTCCTCTTGAGATGCTCGAGGCCTCAAGTCCTAAGTCTCCCAGAAC

splice donor site

TTCTGAGTGCTGCCACCAGGTTGACTCCCCCGGTTGACACTCTACCAACCGGCCTGACCAGGCCAGTCGGTT

GAGGCCTCTGTCCAAACCGCTAGACTCGGTGTCCTGGCTTCTTTCCAGAAGTTCTGCCTGCCTGTCG

CTGACGGATGTCTAGCTAAACTCACTCGTTAGCTTCCGCCTCTTACTTCGGTTAGATTGTTGGCCTCCC

target site
duplication

CAGGACACTAACATTATC

Figure S1: Annotation of ChirDelta2 sequence present in R. sinicus genome assembly.
The donor splice site was predicted using the NNSPLICE 0.9 algorithm
(www.fruitfly.org/seq_tools/splice.html).