SUPPORTING INFORMATION

Figure S1: Gene Ontology (GO) analyses performed using the Gene Ontology Consortium algorithm (http://www.geneontology.org) recapitulating the enriched functions found in the pool of escaping mRNAs per condition. The color scale represents the p-value of each GO term as assessed by the algorithm.

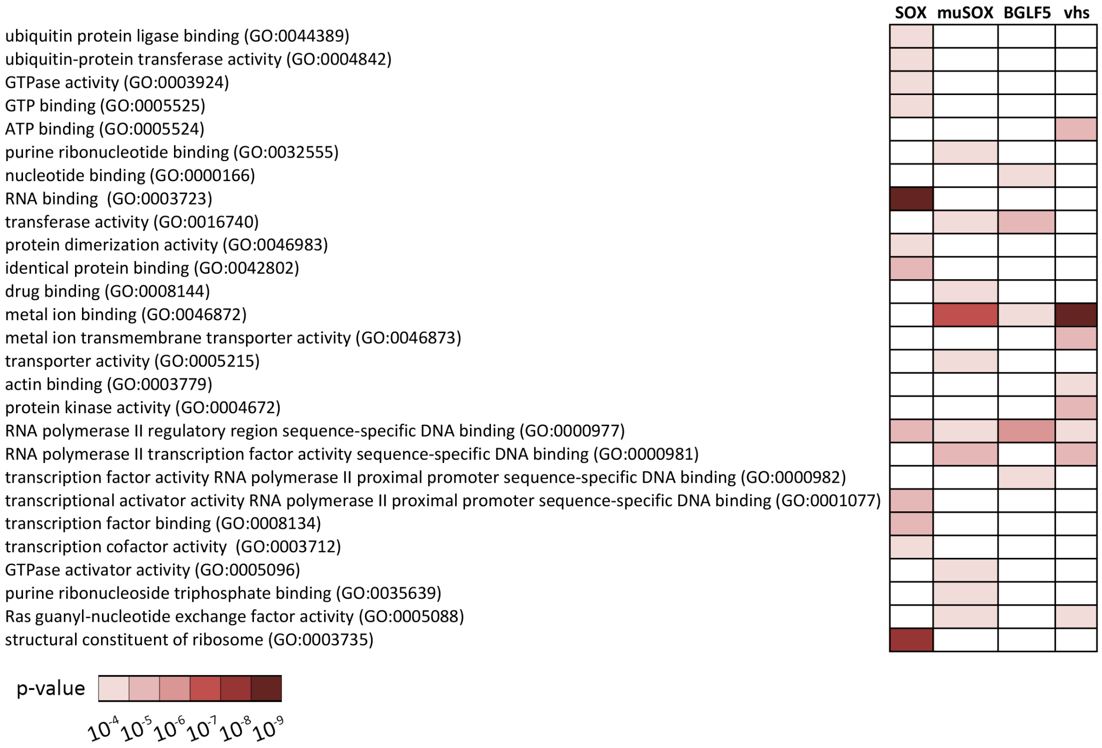

Figure S2: Sequence alignment and comparison of structure predictions obtained with RNAfold for C19ORF66 3’UTR with other known SRE transcripts: IL-6 and GADD45B.

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CLUSTAL O(1.2.4) multiple sequence alignment


GADD45          GGCCCTTCCCAGCAGCAGAA---------------TCTGTT--GAGTTGCTGCCACAAA-      42
C19ORF66        --CCCCTGCCAGGTGCAGATACAAACCAGACACGGTCTGTGGCTACTTTGTGTTATTATA      58
IL6             ------------------------------------------------------------      0


GADD45          ---CAAAAAATACAATAAATATTTGAACCCCCTCCC-------CCCCAGCACAACC----      88
C19ORF66        AGATATGAGCTCAAACCGAGATATGAATGACCTTGGGGAGCCATCTGAGGCCAAGATATT      118
IL6             ------------------------------------------------------------      0


GADD45          -------------C-----CCCCAAA---ACAACCCAACCCACGAGGACCATCGGGGGCA      127
C19ORF66        GACGGGGGGGATTCCTGGGTCCCATTTTCAGCGCCCAGGGTCACAGATCCACAGTGGGAA      178
IL6             ------------------------------------------------------------      0


GADD45          GAGTCGTTGGAG--------ACTGAAGA-GGAAGAGGAGG-----AGGAGAAGGGGA---      170
C19ORF66        GTTCTGTGGGACACATTGGCACTGAGCCACAAAGAAGGTGTGGCCAGAACAACTTGGGCT      238
IL6             ------------------------------------------------------------      0


GADD45          ----GTGAGCGGCCGCCCCCAGGGCGGA------------------------GATCCAG      201
C19ORF66        CCTGCTGACCAATGTCCTCTAGGGCCTAGGGGACAGAGGAACACAGAGTCACAGCTTCAG      298
IL6             ------------------------------------------------------------      0


GADD45          GAGC----------TGGCGGCCGCCGATCAGATGGAGAAGG--------GGGGACCCAGG      243
C19ORF66        GGGCCGAATGAGCATGGCGGCCT---TCCTGAGAGAATATGCCCCACCACGAAACTCAGC      355
IL6             ------------------------------------------------------------      0


GADD45          CCAGCAGGAGACAGGACCCCCGAAGCTGAGGCCTTGGGATGGAGCAGAAGCCGGAGTGGC      303
C19ORF66        CC---AGTAGACACCATCCTGGTAGCGG---C-TTCG------GTAGTGGCCGCCGTGGT      402
IL6             -----------------------------------------------------catgggc      7
                                                         **

GADD45          GGGGCACGCTGCCGCCTTC-----------CCCATCACGGAGGGTCCAGACTGTCCACTC      352
C19ORF66        GCCACACACCGTTGAGGTTGGAGTGGGCACAG--GCATGGTACCACCAGCCTCCCCGCTG      460
IL6             acctcagattgttgttgtt--aatgggcattccttcttctggtcagaaacctgtccact-      64
                    **    *  *   *                 *           *  **  ** **

GADD45          G-------------------GGGGTGGAGTGAGACTGA----------------CTGCAA      377
C19ORF66        GTACAGGGCACAGTTACCTGAGGGGAGAGAGAGAGTCCATGTCCTCTCACCAGAATAAAA      520
IL6             -----gggcaca------------------------------------------------      71


GADD45          GCCCCACCCTCCTT--GAGACTGGAGCTGGCGTCTGCA-----TACGA----------GA      420
C19ORF66        GCCTCTACCTGCACCTCACAGTGC--AAGGCTTTTGCCAGGCATCCCCTGGCCCCTCCCA      578
IL6             ------------------------------------------------------------      71


GADD45          GACTTGGTTGAACTTGGTTGGTCCTTGTCTGCACCCTCGACAAGACCACACTTTGGGACT      480
C19ORF66        TTCT-TATTGAATA---CAAGCCCTGATCTTCCATCTCCTCAGCAAAAAAATAGGAGCCC      634
IL6             -----------------gaacttatgttgttctctatggagaac-taaaagtatgagcgt      113
                                        *  * * *    *    *     * * *  * *

GADD45          TGGGAGCT-----------------GGGG-CTGAAGTTG---CTCTGTACCCATGAACTC      519
C19ORF66        TGGCCCCCCAACTTTCTTCAGAGTAATAGCCTTAATTCCTTC-------CCTATCTCCTT      687
IL6             taggacactattttaatt---------atttttaatttattaatatttaaatatgtg--a      162
                * *                            * ** *               **

GADD45          -CC--AGTTTGCGAATTATAGAGACAATCTATTTTGTTACTTGCACTTGTTATTCGAACC      576
C19ORF66        ACCAAA-----------GTACA----AGTCACATCTTT---CCCACCTTTTCTGCAAACT      729
IL6             agctgagtt---aatttatgta----agtcatatttat---a-----t-ttttaagaagt      206
                  *  *            *  *    *   *  *   *         * ** *   **

GADD45          ACT---------------------GAGAGCGAGATGGGAAGCATAGATATCTATATTTTT      615
C19ORF66        AGGAGTCTA--CCGT----TCATTCCTT------TATCAAAGAAAGTATCTACT---TC      774
IL6             accacttgaaacattttatgtattagttttgaaataataatggaaagtggctatg---ca      263
                *                                 *   **    *  *  ***

GADD45          ATTTCTACTATGAGGGCCTTGTAATAAATTTCTAAAGCCTCTG-----------------      658
C19ORF66        CTTTCTAGAATAAGAGTAC-----TAGCTCT---CACCCTCTGCCCTTTACTTGAACAG-      825
IL6             gttt---gaat----atcc-----tttgttt---cagagccagatcatttcttggaaagt      308
                 ***     **              *   * *    *    * *

GADD45          ------------------------------------------------------------      658
C19ORF66        -GAGTCTTGATTCTTTTTTTGCCTCATCAGAGAAGGAATCTGGACTCCCCATCCCCCCAC      884
IL6             gtaggc------------ttacctca---aataa---a--tggctaacttatac--atat      346


GADD45          ------------------------------------------------------------      658
C19ORF66        CAGGATAAAAGTCCTGACCTTTGTTCTCTTGACGGAATAAAAGCTTGCTTATCCTTATA-      943
IL6             ttttaaagaaatatttatattgtatttatataatgtataaatggtt-tttataccaataa      405


GADD45          --------------------      658
C19ORF66        --------------------      943
IL6             atggcattttaaaaaattca      425
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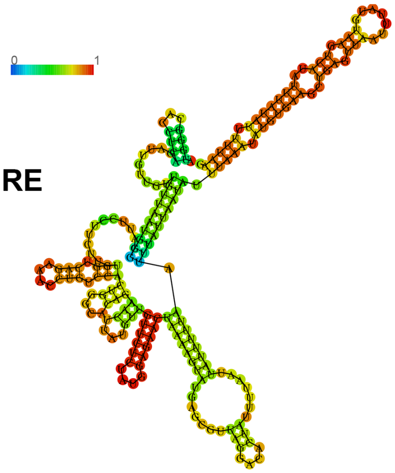
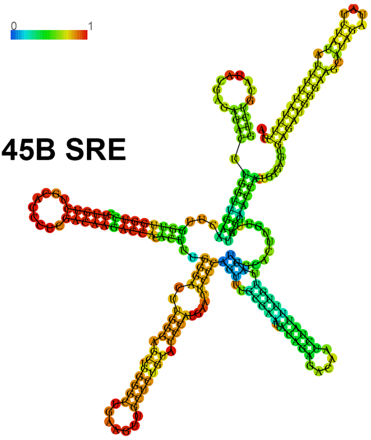
IL-6 SRE



GADD45B SRE



C19ORF66 putative SRE

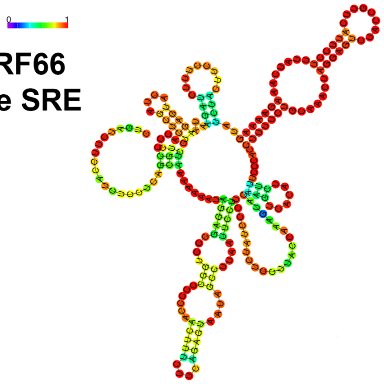


Table S1: RNA-seq dataset. Summary table combining transcript ID and FPKM scores per condition (Mock sample, SOX, muSOX, BGLF5 and vhs).

Table S2: List of mRNA escaping all endonucleases tested by comparative RNA-seq as identified by hierarchical clustering. Each tab in this table represent the fold change over mock sample for each herpesviral endonuclease. Highlighted in yellow are the transcripts selected as top 10% for further investigation.