

SUPPLEMENTARY TABLES AND FIGURES

Cell compartment-specific folding of Ty1 retrotransposon RNA genome

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Table S1 . Reverse transcription primers.

PRIMER	SEQUENCE (5'-3')
Ty1 PR_1	TCAGGTGATGGAGTGCTCAG
Ty1 PR_2	TCGTTTGCCTCTTGGGTATC
Ty1 PR_3	CATCACTCGGATTTCTCCTG
Ty1 PR_4	TTGGTGTTCCTGGAAGTGA
Ty1 PR_5	TCGAATTGTCTGTGCATTGG
Ty1 PR_6	AGACACTGGCCTGAAACTGG
Ty1 PR_7	GCCACGAGGATGTATTTTGG
Ty1 PR_8	GGAGGTGTGGAATCGGTTGG
Ty1 PR_9	GGTACGTTTGTATGATTAGTCTCA
Ty1 PR_10	GTCTCGTGATACCTTAATTTTCAG
Ty1 PR_11	TGCTGAATATCACCTCTTGC
Ty1 PR_12	CAAATTGTCACCTGACTG
Ty1 PR_13	TGCATTTTCATGTACCTTCTC
Ty1 PR_14	GCTTCCGTAGTTGAAGTACAT
Ty1 PR_15	TCTATTCCAACATACCACCC
Ty1 PR_16	CTCCTCAAGGATTTAGGAATCC
Ty1 PR_17	CATTGTTGATAAAGGCTATA
U1 PR	TAAGATCCACCCGTTCTAC

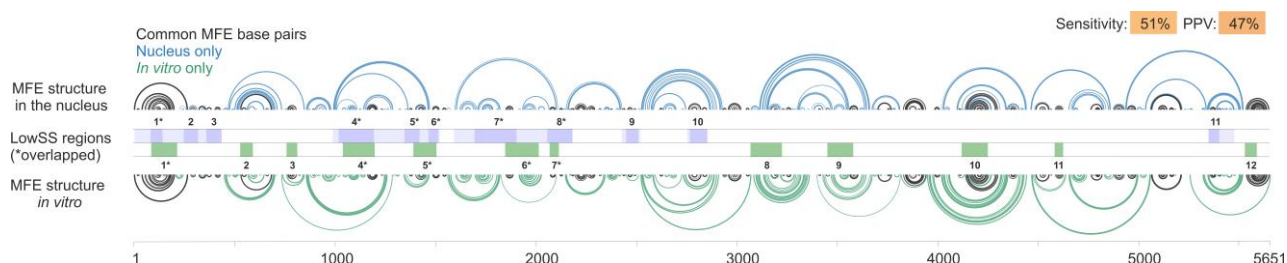


Figure S1. Comparison of SHAPE-directed MFE model predicted for nuclear and Ty1 gRNA *in vitro*. Location of lowSS regions identified for nuclear and in vitro Ty1 gRNA are presented. Overlapped regions are marked by asterix *.