Supplementary Information

a

[Mg^{2+}], mM	3.5			4.0			5.0			6.0			7.0			8.0		
Putrescine, 8 mM	+		+	+		+	+		+	+		+	+		+	+		+
Spermidine, 0.5 mM		+	+		+	+		+	+		+	+		+	+		+	+

rt→
byp→

stop→

b

	Spermine				Putrescine				Spermidine		
−	0.1	0.2	0.3	0.5	2	4	6	8	0.2	0.5	1.0

rt→
byp→
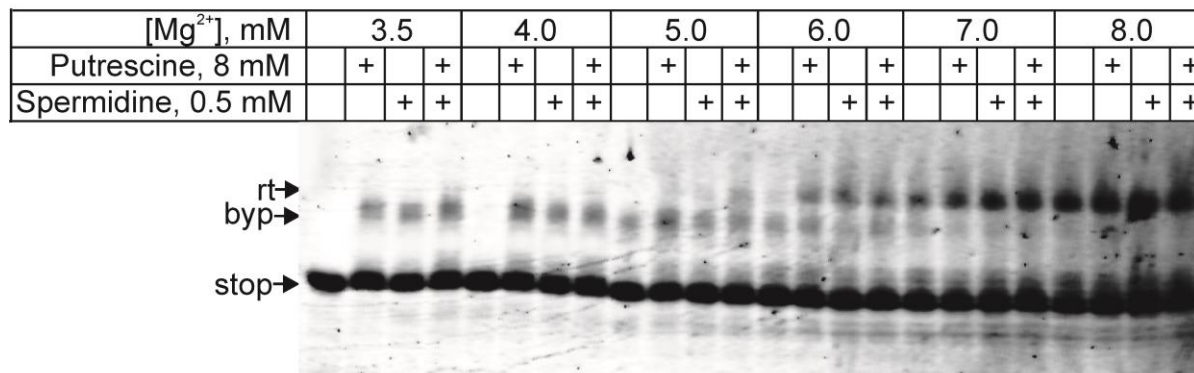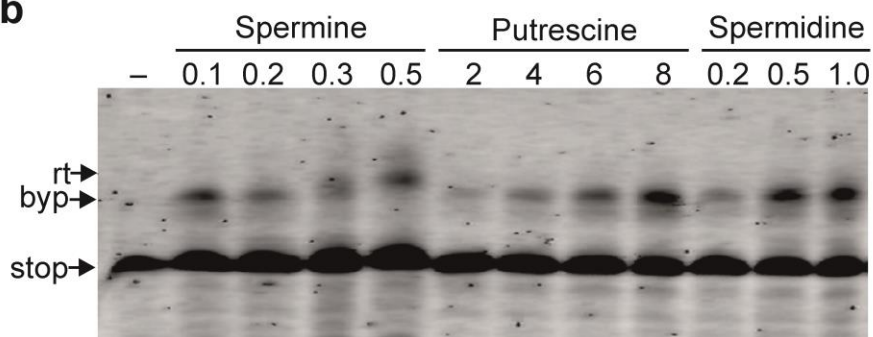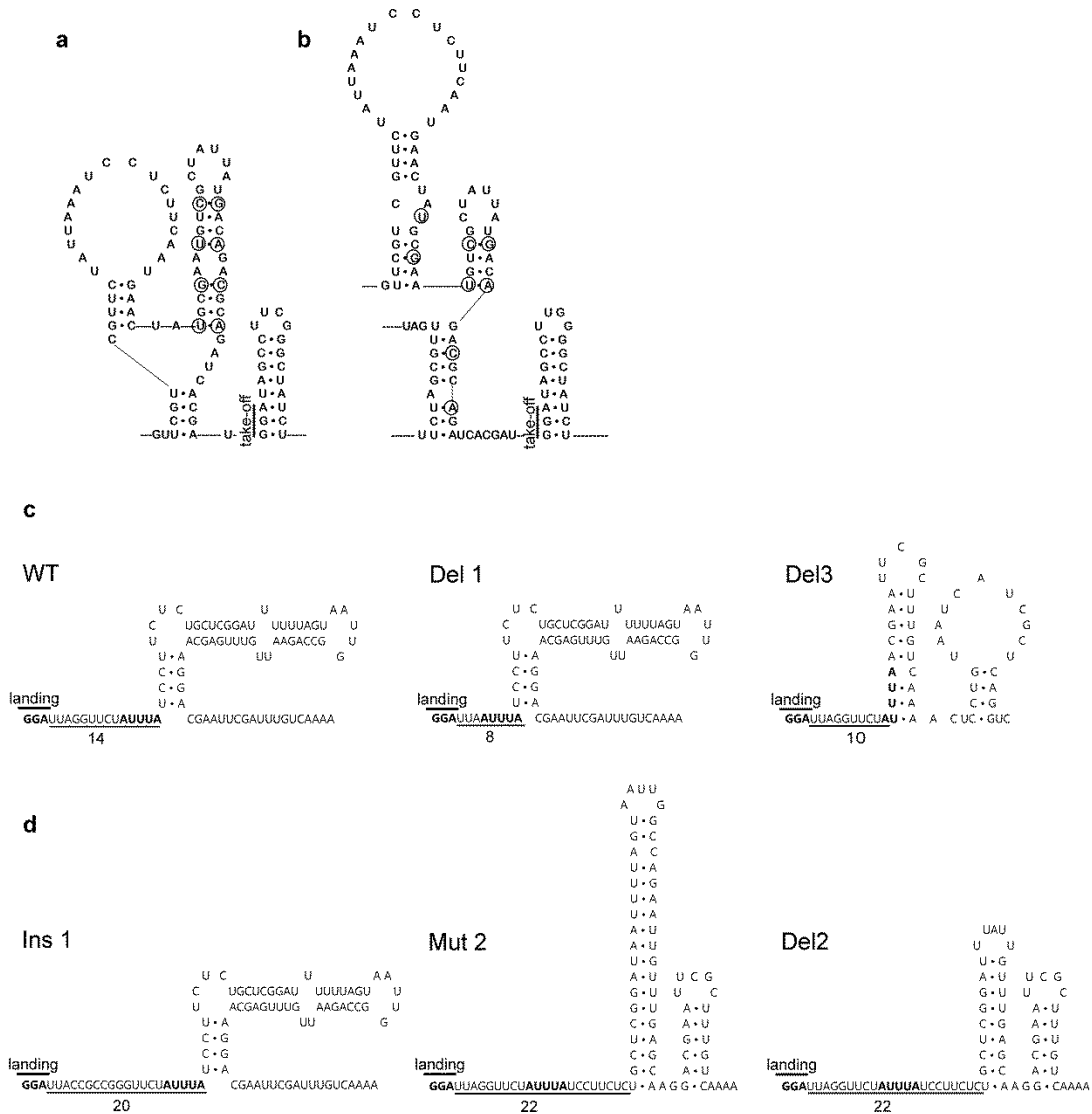
stop→

Supplementary Figure 1: Effect of polyamines on the efficiency and fidelity of bypassing.
(**a**) Addition of putrescine and spermidine at different concentrations of added Mg^{2+}. Due to the presence of GTP (1 mM) and phosphoenolpyruvate (1 mM), the estimated concentration of free Mg^{2+} is lower than indicated by 1.5 mM[16]. (**b**) Different concentrations of polyamines at constant Mg^{2+} concentration (3.5 mM added, 2.0 mM free).

a   **b**

c

WT   Del 1   Del3

d

Ins 1   Mut 2   Del2

Supplementary Figure 2. Putative mRNA secondary structures of the 5´SL and 3´SL regions upstream and downstream the gap.

(**a**) 5´SL forms a long hairpin loop as predicted by mfold and chemical probing[10]. (**b**) Alternative structure of the 5´SL suggested for the Δgap mRNA[10]. (**c**) mfold predictions for the 3´SL of the wt and various mRNA constructs that support efficient bypassing. (d) mfold predictions for the 3´SL of the mutants that abolish bypassing. Numbers indicate the distance between the landing site and the base of the putative hairpin. The AUUUA motif is shown bold for better comparison between the constructs.

Supplementary Table 1. List of primers used to introduce mutations in mRNA.

	mRNA	Reverse primer	Forward primer
1.	Mut1	GACAAAGCGAATTCGTGCTTGCTCAAACAATTCTGGCC	GGCCAGAATTGTTTGAGCAAGCACGAATTCGCTTTGTC
2.	Del1	TAATCCAATAATCTCTTAATTATGAGG	ATTTATCCTTCTCTGCTCGGATTTTTTAGTAATTGGCC
3.	Ins1	GGCCTAATCCAATAATCTCTTAATTATGAGG	GCCGTTCTATTTATCCTTCTCTGCTCGGATTTTTTAG
4.	Del2	AAATCCGAGCAGAGAAGGATAAATAGAACC	ATTGTTTGAGCAAGGACGAATTCGC
5.	Mut2	CTGGCCAATTACTAAAATTATCCGAGCAGAGAAGGATAAATAGAACC	GGTTCTATTTATCCTTCTCTGCTCGGATAATTTTAGTAATTGGCCAG
6.	Rev1	CATTAACCGGTCTTAACAAACTCGTTCCTTAAATAGAACCTAATCCAATAATCTC	ATTTTTTAGGCTCGTCTCTTCCTCGAATTCGCTTTGTCAAAACTCCTGTAATCATCGC
7.	Del3	GACAAAGCGAATTCGATAAATAGAACCTAATCC	GGATTAGGTTCTATTTATCGAATTCGCTTTGTC
8.	(UUC)$_{17}$	GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAATCCAATAATCTCTTAATTATGAGG	TTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCCCTGTAATCATCGCTCAGGTC
9.	2M	CCATCGTGATCCGCATCCGTTATAATAGCGACATTCGC	GCGAATGTCGCTATTATAACGGATGCGGATCACGATGG
10.	2MC	GCCCGAAGGCTATCCATCGTGATCCGCATCCGTTATAATAGCAACGTTTGCGTAGTTCATTGAAGAGG	CCTCTTCAATGAACTACGCAAACGTTGCTATTATAACGGATGCGGATCACGATGGATAGCCTTCGGGC
11.	4M	GCCCGAAGGCTATCCATCGTGATCCGCATCCGTTATAATAGCGACATTCGCATAGTTCATTG	CAATGAACTATGCGAATGTCGCTATTATAACGGATGCGGATCACGATGGATAGCCTTCGGGC
12.	4MC	CGTGATCCGCATCCGTTATAATAGCAACGTTTGCGTAGTTCATTGAAGAGGATTTAATAGAACG	CGTTCTATTAAATCCTCTTCAATGAACTACGCAAACGTTGCTATTATAACGGATGCGGATCACG
13.	K14E	GCAATTTATATTTTTCCATATCAACGCTAGAAGAATC	GATTCTTCTAGCGTTGATATGGAAAAATATAAATTGC
14.	K15E	GTTCTGCAATTTATATTCTTTCATATCAACGC	GCGTTGATATGAAAGAATATAAATTGCAGAAC
15.	Y16H	CATTGTTCTGCAATTTATGTTTTTTTCATATCAACGC	GCGTTGATATGAAAAAACATAAATTGCAGAACAATG
16.	K17E	CGAACATTGTTCTGCAATTCATATTTTTTCATATC	GATATGAAAAAATATGAATTGCAGAACAATGTTCG
17.	L18S	GAACGACGAACATTGTTCTGCGATTTATATTTTTTC	GAAAAAATATAAATCGCAGAACAATGTTCGTCGTTC
18.	Q19E	GAACGACGAACATTGTTCTCCAATTTATATTTTTTC	GAAAAAATATAAATTGGAGAACAATGTTCGTCGTTC
19.	N20K	GAACGACGAACATTCTTCTGCAATTTATATTTTTTC	GAAAAAATATAAATTGCAGAAGAATGTTCGTCGTTC
20.	N21K	GAACGACGAACCTTGTTCTGCAATTTATATTTTTTC	GAAAAAATATAAATTGCAGAACAAGGTTCGTCGTTC
21.	V22D	GAACGACGATCATTGTTCTGCAATTTATATTTTTTC	GAAAAAATATAAATTGCAGAACAATGATCGTCGTTC
22.	R23L	GAAGAGGATTTAATAGAACGAAGAACATTGTTCTGC	GCAGAACAATGTTCTTCGTTCTATTAAATCCTCTTC
23.	R24L	GAAGAGGATTTAATAGAAAGACGAACATTGTTCTGC	GCAGAACAATGTTCGTCTTTCTATTAAATCCTCTTC
24.	S25F	GAAGAGGATTTAATAAAACGACGAACATTGTTCTGC	GCAGAACAATGTTCGTCGTTTTATTAAATCCTCTTC
25.	I26F	GTTCATTGAAGAGGATTTAAAAGAACGACGAACATTG	CAATGTTCGTCGTTCTTTTAAATCCTCTTCAATGAAC
26.	K27I	CGCATAGTTCATTGAAGAGGATATAATAGAACGACG	CGTCGTTCTATTATATCCTCTTCAATGAACTATGCG
27.	S28F	CATTCGCATAGTTCATTGAAGAGAATTTAATAGAACG	CGTTCTATTAAATTCTCTTCAATGAACTATGCGAATG
28.	S29F	CATTCGCATAGTTCATTGAAAAGGATTTAATAGAAC	GTTCTATTAAATCCTTTTCAATGAACTATGCGAATG
29.	S30L	CGACATTCGCATAGTTCATTAAAGAGGATTTAATAG	CTATTAAATCCTCTTTAATGAACTATGCGAATGTCG
30.	NP4	GAAGAGGATTTAATAGAACGACGAACATCGTTCTTCAATTCATATTCTTTCATATCAACGCTAGAAGAATC	GATTCTTCTAGCGTTGATATGAAAGAATATGAATTGAAGAACGATGTTCGTCGTTCTATTAAATCCTCTTC
31.	NP5	GCGACATTCGCATAGTTCATTGAAGTGGATTCAATAGTACGACTAACATTGTTCTGCAATTTATATTTTTTC	GAAAAAATATAAATTGCAGAACAATGTTAGTCGTACTATTGAATCCACTTCAATGAACTATGCGAATGTCGC
32.	NP6	GAAGAGGATTTAATAGAACGACGAACGTTATTTTGTAACTTGTACTTCTTCATATCAACGCTAGAAGAATC	GATTCTTCTAGCGTTGATATGAAGAAGTACAAGTTACAAAATAACGTTCGTCGTTCTATTAAATCCTCTTC

#	Name	Sequence 1	Sequence 2
33.	NP7	GCGACATTCGCATAGTTCATAGAGGAAGACTTGATGGAGCGGCGGACATTGTTCTGCAATTTATATTTTTTC	GAAAAAATATAAATTGCAGAACAATGTCCGCCGCTCCATCAAGTCTTCCTCTATGAACTATGCGAATGTCGC
34.	gap -6	GTATTTCTATAGATAGCCCGAAGGCTATCC	ATTAAGAGATTATTGGATTAGGTTCTATTTATCCTTCTC
35.	gap -12	TTTCTATAGATAGCCCGAAGGCTATCC	AAGAGATTATTGGATTAGGTTCTATTTATCCTTCTCTGCTCGG
36.	gap +6 or (+6nt Ins1)or(+6nt unstr)	GGATAAATAGAACCTAATCCAATAATCTCTTAATTATGAGTATGAGGTATTTCTATAGATAGCC	GGCTATCTATAGAAATACCTCATACTCATAATTAAGAGATTATTGGATTAGGTTCTATTTATCC
37.	gap +12 or (+12nt Ins1)or(+12nt unstr)	TATGAGTATGAGGTATTTCTATAGATAGCCCGAAGGCTATCC	CTCATAATTAAGAGATTATTGGATTAGGTTCTATTTATCC
38.	gap +18 or (+18nt unstr)	GAGTATGAGTATGAGGTATTTCTATAGATAGCCCGAAGGCTATCC	ATACTCATAATTAAGAGATTATTGGATTAGGTTCTATTTATCC
39.	gap +24	TATGAGTATGAGTATGAGGTATTTCTATAGATAGCCCGAAGGCTATCC	CTCATACTCATAATTAAGAGATTATTGGATTAGGTTCTATTTATCC
40.	gap +30	GAGTATGAGTATGAGTATGAGGTATTTCTATAGATAGCCCGAAGGCTATCC	ATACTCATACTCATAATTAAGAGATTATTGGATTAGGTTCTATTTATCC
41.	gap +36	TATGAGTATGAGTATGAGTATGAGGTATTTCTATAGATAGCCCGAAGGCTATCC	CTCATACTCATACTCATAATTAAGAGATTATTGGATTAGGTTCTATTTATCC
42.	gap +42	GAGTATGAGTATGAGTATGAGTATGAGGTATTTCTATAGATAGCCCGAAGGCTATCC	ATACTCATACTCATACTCATAATTAAGAGATTATTGGATTAGGTTCTATTTATCC
43.	gap +6SL	CGAACGCTGTATTTCTATAGATAGCCCGAAGGCTATCC	CGCTATTAAGAGATTATTGGATTAGGTTCTATTTATCC
44.	gap +18SL	CGAACGCTTATGAGTATGAGGTATTTCTATAGATAGCCCGAAG	CGCTATTAAGAGATTATTGGATTAGGTTCTATTTATCCTTCTC
45.	gap +12SL	CGAACGCTTATGAGGTATTTCTATAGATAGCCCGAAGGCTATC	CGCTATTAAGAGATTATTGGATTAGGTTCTATTTATCCTTCTC
46.	Del12nt + 12nt Ins2	GAGAAGGATAAATAGAACCTAATCCAATAATAATAATAATAATCTCTTTTTCTATAGATAGC	GCTATCTATAGAAAAGAGATTATTATTATTATTGGATTAGGTTCTATTTATCCTTCTC
47.	+6nt Ins2	GCAGAGAAGGATAAATAGAACCTAATCCAATAATAATAATCTCTTAATTATGAGGTATTTCTATAG	CTATAGAAATACCTCATAATTAAGAGATTATTATTATTGGATTAGGTTCTATTTATCCTTCTCTGC
48.	+12nt Ins2	GCAGAGAAGGATAAATAGAACCTAATCCAATAATAATAATAATAATCTCTTAATTATGAGGTATTTCTATAG	CTATAGAAATACCTCATAATTAAGAGATTATTATTATTATTGGATTAGGTTCTATTTATCCTTCTCTGC
49.	mut GAG to AUU	GGATAAATAGAACCTAATCCAATAATAATTTAATTATGAGGTATTTCTATAG	CTATAGAAATACCTCATAATTAAATTATTATTGGATTAGGTTCTATTTATCC
50.	mut GAG to CAC	GGATAAATAGAACCTAATCCAATAATGTGTTAATTATGAGGTATTTCTATAG	CTATAGAAATACCTCATAATTAACACATTATTGGATTAGGTTCTATTTATCC
51.	mut GAG to GGAGG	GGATAAATAGAACCTAATCCAATAACCTCCTAATTATGAGGTATTTCTATAG	CTATAGAAATACCTCATAATTAGGAGGTTATTGGATTAGGTTCTATTTATCC
52.	NP1	CATTATACACCTCATAGAACTTTTCATCAGGAATCCAACCGCG	AAAAAATATAAATTGCAGAACAATGTTCGTCGTTCTATTAAATCC
53.	NP2	GGATTTAATAGAACGACGAACATCGTTCTTCAATTCATATTCTTTCATTATACACCTCATAGAAC	GTTCTATGAGGTGTATAATGAAAGAATATGAATTGAAGAACGATGTTCGTCGTTCTATTAAATCC
54.	NP3	CTGCAATTTATATTTTTTCATATGAACGCAAGAAGCATCAACTTTTAGAAATTTCATTATACACC	GGTGTATAATGAAATTTCTAAAAGTTGATGCTTCTTGCGTTCATATGAAAAAATATAAATTGCAG
55.	T0	CTAAAAAATCCGAGCAGAGATCCTTAAATAGAACCTAATCC	GGATTAGGTTCTATTTAAGGATCTCTGCTCGGATTTTTTAG

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