

Supplementary Table 4. 3' UTR sequences of *lac-Z* reporter constructs.

pMV9: Site 1 and Site 2, wild type linker.

TAATAGGCCTACTAGACCCGCGGAACTCAAGTATACCTT***TTATACAACCGTTCTACTCA***ACGCGATGTAAATATCGC
AATCCCTTT***TTATACAACCATTTCTGCCTC***TGAACCATTTGAAACCTTCTCCCGTACTCCCACCAACCATGGCCGCTGTC
ATCAGATCGCCATCTCGCGCCCGTGCCTCTGACTTCTAAGTCCAATTACTCTTCAACATCCCTACATGCTCTTTCTCC
CTGTGCTCCCACCCCTATTTTTGTTATTATCAAAAAACTTCTCTTAATTTCTTTGTTTTTTAGCTTCTTTTAAGTCA
CCTCTAACAATGAAATTGTGTAGATTCAAAAAATAGAATTAATTCGTAATAAA

pMV19: Site 1 and Site 2, mutant linker.

TAATAGGCCTACTAGACCCGCGGAACTCAAGTATACCTT***TTATACAACCGTTCTACTCA***AAGTGATGTAAATATAGG
AATGTATTT***TTATACAACCATTTCTGCCTC***TGAACCATTTGAAACCTTCTCCCGTACTCCCACCAACCATGGCCGCTGTC
ATCAGATCGCCATCTCGCGCCCGTGCCTCTGACTTCTAAGTCCAATTACTCTTCAACATCCCTACATGCTCTTTCTCC
CTGTGCTCCCACCCCTATTTTTGTTATTATCAAAAAACTTCTCTTAATTTCTTTGTTTTTTAGCTTCTTTTAAGTCA
CCTCTAACAATGAAATTGTGTAGATTCAAAAAATAGAATTAATTCGTAATAAA

pVT701: Sites 1 and 2; mutant linker designed to maintain accessibility.

TAATAGGCCTACTAGACCCGCGGAACTCAAGTATACCTT***TTATACAACCGTTCTACTCA***ACGGGATGTCCCTATCCC
AATCCCTTT***TTATACAACCATTTCTGCCTC***TGAACCATTTGAAACCTTCTCCCGTACTCCCACCAACCATGGCCGCTGTC
ATCAGATCGCCATCTCGCGCCCGTGCCTCTGACTTCTAAGTCCAATTACTCTTCAACATCCCTACATGCTCTTTCTCC
CTGTGCTCCCACCCCTATTTTTGTTATTATCAAAAAACTTCTCTTAATTTCTTTGTTTTTTAGCTTCTTTTAAGTCA
CCTCTAACAATGAAATTGTGTAGATTCAAAAAATAGAATTAATTCGTAATAAA

pVT702: Sites 1 and 2, mutant linker designed to maintain accessibility.

TAATAGGCCTACTAGACCCGCGGAACTCAAGTATACCTT***TTATACAACCGTTCTACTCA***ACCGTAGCTTATTAGCG
AATTTTCCC***TTATACAACCATTTCTGCCTC***TGAACCATTTGAAACCTTCTCCCGTACTCCCACCAACCATGGCCGCTGTC
ATCAGATCGCCATCTCGCGCCCGTGCCTCTGACTTCTAAGTCCAATTACTCTTCAACATCCCTACATGCTCTTTCTCC
CTGTGCTCCCACCCCTATTTTTGTTATTATCAAAAAACTTCTCTTAATTTCTTTGTTTTTTAGCTTCTTTTAAGTCA
CCTCTAACAATGAAATTGTGTAGATTCAAAAAATAGAATTAATTCGTAATAAA

pVT704: Sites 1 and 2, mutant linker designed to impair accessibility.

TAATAGGCCTACTAGACCCGCGGAACTCAAGTATACCTT***TTATACAACCGTTCTACTCA***ACATGCGGCAGTGATACG
CTATTTCCC***TTATACAACCATTTCTGCCTC***TGAACCATTTGAAACCTTCTCCCGTACTCCCACCAACCATGGCCGCTGTC
ATCAGATCGCCATCTCGCGCCCGTGCCTCTGACTTCTAAGTCCAATTACTCTTCAACATCCCTACATGCTCTTTCTCC
CTGTGCTCCCACCCCTATTTTTGTTATTATCAAAAAACTTCTCTTAATTTCTTTGTTTTTTAGCTTCTTTTAAGTCA
CCTCTAACAATGAAATTGTGTAGATTCAAAAAATAGAATTAATTCGTAATAAA

pVT705: Sites 1 and 2; mutant linker aimed impair accessibility.

TAATAGGCCTACTAGACCCGCGGAACTCAAGTATACCTT***TTATACAACCGTTCTACTCA***AAAGGGATGTAAATATAGG
AAACAATTT***TTATACAACCATTTCTGCCTC***TGAACCATTTGAAACCTTCTCCCGTACTCCCACCAACCATGGCCGCTGTC
ATCAGATCGCCATCTCGCGCCCGTGCCTCTGACTTCTAAGTCCAATTACTCTTCAACATCCCTACATGCTCTTTCTCC
CTGTGCTCCCACCCCTATTTTTGTTATTATCAAAAAACTTCTCTTAATTTCTTTGTTTTTTAGCTTCTTTTAAGTCA
CCTCTAACAATGAAATTGTGTAGATTCAAAAAATAGAATTAATTCGTAATAAA

pVT712: Site1- 27 nt Spacer-Site 1- 27 nt Spacer-Site1, designed for accessibility.

TAATAGGCCTACTAGACCCGCGGAACTCAAGTATACCTT***TTATACAACCGTTCTACTCA***ACGCGATGTAAATATCGCAA
TCCCTTT***TTATACAACCGTTCTACTCA***ACGCGATGTAAATATCGCAATCCCTTT***TTATACAACCGTTCTACTCA***T
GAACCATTTGAAACCTTCTCCCGTACTCCCACCAACCATGGCCGCTGTCATCAGATCGCCATCTCGCGCCCGTGCCTCTG
ACTTCTAAGTCCAATTACTCTTCAACATCCCTACATGCTCTTTCTCCCTGTGCTCCCACCCCTATTTTTGTTATTATC
AAAAAACTTCTCTTAATTTCTTTGTTTTTTAGCTTCTTTTAAGTCACCTCTAACAATGAAATTGTGTAGATTCAAAAAAT
AGAATTAATTCGTAATAAA

pVT713: Site 2- 27 nt Spacer-Site 2- 27 nt Spacer-Site 2, designed for accessibility.

TAATAGGCCTACTAGACCCGCGGAACTCAAGTATACCTT***TTATACAACCATTTCTGCCTC***ACGCGATGTAAATATCGCAATC
CCTTT***TTATACAACCATTTCTGCCTC***ACGCGATGTAAATATCGCAATCCCTTT***TTATACAACCATTTCTGCCTC***TGAACCA
TTGAAACCTTCTCCCGTACTCCCACCAACCATGGCCGCTGTCATCAGATCGCCATCTCGCGCCCGTGCCTCTGACTTCT
AAGTCCAATTACTCTTCAACATCCCTACATGCTCTTTCTCCCTGTGCTCCCACCCCTATTTTTGTTATTATCAAAAAA
CTTCTCTTAATTTCTTTGTTTTTTAGCTTCTTTTAAGTCACCTCTAACAATGAAATTGTGTAGATTCAAAAAATAGAAT
AATTCGTAATAAA

3' UTR sequences from the TAA stop codon through AATAAA polyadenylation signal. Modified *lin-41* 3' UTR were inserted between the *sacII* (CCGCGG, underlined) and *ncol* (CCATGG, underlined) sites. (The *ncol* site in pVT712 and pVT713 was modified in the course of plasmid construction). Sequences flanking the *sacII/ncol* insert are from the *unc-54* 3' UTR. *let-7* complementary site 1 and site 2 are indicated in bold italics; the 27 nt spacer sequence between site 1 and site 2 is underlined. Alignments of wild type (pMV9) and mutant (pMV19, pVT701-705) spacer sequences are shown in Supplementary Table 5.