

## Claims

We claim:

1. A polynucleotide sequence comprising a 5' UTR of *hist1h1c* or *rpl15*, wherein the 5' UTR comprises one or more point mutations that reduce formation of secondary structures in the 5' UTR.
2. The polynucleotide sequence of claim 1, wherein the 5' UTR is the 5' UTR of *hist1h1c*, and wherein the 5' UTR of *hist1h1c* lacks a start codon and comprises a kozak consensus sequence at the 3' terminus of the 5' UTR of *hist1h1c*.
3. The polynucleotide sequence of claim 2, wherein the 5' UTR of *hist1h1c* comprises substitution mutations at positions 6, 8, 26, 28, and 36 from the 5' terminus of the 5' UTR of *hist1h1c*.
4. The polynucleotide sequence of claim 3, wherein the 5' UTR of *hist1h1c* further comprises substitution mutations at positions 4, 5, 25, 27, 32, 33, 34, 41, and 42 from the 5' terminus of the 5' UTR of *hist1h1c*.
5. The polynucleotide sequence of claim 3, wherein the 5' UTR of *hist1h1c* further comprises a substitution mutation at position 13 from the 5' terminus of the 5' UTR of *hist1h1c*.
6. The polynucleotide sequence of claim 5, further comprising an insertion mutation at the 5' terminus of the 5' UTR of *hist1h1c*.
7. The polynucleotide sequence of claim 6, wherein the insertion mutation is immediately upstream of position 1 from the 5' terminus of the 5' UTR of *hist1h1c*.

8. The polynucleotide sequence of claim 9, wherein the insertion mutation is insertion of a single nucleotide.
9. The polynucleotide sequence of claim 1, wherein the 5' UTR is the 5' UTR of *rpl15*, and wherein the 5' UTR of *rpl15* lacks a start codon and comprises a kozak consensus sequence at the 3' terminus of the 5' UTR of *hist1h1c*.
10. The polynucleotide sequence of claim 9, wherein the 5' UTR of *rpl15* comprises substitution mutations at positions 11, 13, 14, 15, 24, and 26 from the 5' terminus of the 5' UTR of *rpl15*.
11. The polynucleotide sequence of claim 10, wherein the 5' UTR of *rpl15* further comprises substitution mutations at positions 25 and 27 from the 5' terminus of the 5' UTR of *rpl15*.
12. The polynucleotide sequence of claim 10, wherein the 5' UTR of *rpl15* further comprises substitution mutations at positions 12, 16, and 23 from the 5' terminus of the 5' UTR of *rpl15*.
13. The polynucleotide sequence of claim 11, further comprising an insertion mutation at the 5' terminus of the 5' UTR of *rpl15*.
14. The polynucleotide sequence of claim 13, wherein the insertion mutation is immediately upstream of position 1 from the 5' terminus of the 5' UTR of *rpl15*.
15. The polynucleotide sequence of claim 14, wherein the insertion mutation is insertion of a single nucleotide.
16. The polynucleotide sequence of any one of claims 1 to 15, further comprising a coding region located downstream of the 5' UTR of *hist1h1c* or *rpl15*.

17. The polynucleotide sequence of any one of claims 1 to 16, wherein the 5' UTR comprises SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 22, or SEQ ID NO: 23.
18. A method of increasing translation of target mRNA, the method comprising promoting translation with a modified 5' UTR comprising SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 22, or SEQ ID NO: 23, wherein the modified 5' UTR is upstream of the target mRNA in a polynucleotide sequence.
19. A method of increasing translation of target mRNA, the method comprising promoting translation with a modified 5' UTR of *hist1h1c* or *rpl15*, wherein the 5' UTR comprises one or more point mutations that reduce formation of secondary structures in the 5' UTR, wherein the modified 5' UTR is upstream of the target mRNA in a nucleotide sequence.
20. The method of claim 19, wherein the 5' UTR is the 5' UTR of *hist1h1c*, and wherein the 5' UTR of *hist1h1c* lacks a start codon and comprises a kozak consensus sequence at the 3' terminus of the 5' UTR of *hist1h1c*.
21. The method of claim 20, wherein the 5' UTR of *hist1h1c* comprises substitution mutations at positions 6, 8, 26, 28, and 36 from the 5' terminus of the 5' UTR of *hist1h1c*.
22. The method of claim 21, wherein the 5' UTR of *hist1h1c* further comprises substitution mutations at positions 4, 5, 25, 27, 32, 33, 34, 41, and 42 from the 5' terminus of the 5' UTR of *hist1h1c*.
23. The method of claim 21, wherein the 5' UTR of *hist1h1c* further comprises a substitution mutation at position 13 from the 5' terminus of the 5' UTR of *hist1h1c*.
24. The method of claim 23, further comprising an insertion mutation at the 5' terminus of the 5' UTR of *hist1h1c*.

25. The method of claim 24, wherein the insertion mutation is immediately upstream of position 1 from the 5' terminus of the 5' UTR of *hist1h1c*.
26. The method of claim 25, wherein the insertion mutation is insertion of a single nucleotide.
27. The method of claim 19, wherein the 5' UTR is the 5' UTR of *rpl15*, and wherein the 5' UTR of *rpl15* lacks a start codon and comprises a kozak consensus sequence at the 3' terminus of the 5' UTR of *hist1h1c*.
28. The method of claim 27, wherein the 5' UTR of *rpl15* comprises substitution mutations at positions 11, 13, 14, 15, 24, and 26 from the 5' terminus of the 5' UTR of *rpl15*.
29. The method of claim 28, wherein the 5' UTR of *rpl15* further comprises substitution mutations at positions 25 and 27 from the 5' terminus of the 5' UTR of *rpl15*.
30. The method of claim 28, wherein the 5' UTR of *rpl15* further comprises substitution mutations at positions 12, 16, and 23 from the 5' terminus of the 5' UTR of *rpl15*.
31. The method of claim 29, further comprising an insertion mutation at the 5' terminus of the 5' UTR of *rpl15*.
32. The method of claim 31, wherein the insertion mutation is immediately upstream of position 1 from the 5' terminus of the 5' UTR of *rpl15*.
33. The method of claim 32, wherein the insertion mutation is insertion of a single nucleotide.