**pBT346.6-H3.3-K4M-bGHpolyA plasmid sequence**

* Cloning enzymes sites: XhoI (CTCGAG), HpaI (GTTAAC), AcsI (GGCGCGCC) (page No. 1 and 2)
* Start codon: ATG (page No. 1, 2 and 5)
* Coding region (underlined) (page No. 1 and 2)
* K4M: ATG (page No. 1, 2, 3 and 5)
* Flag tag: GACTACAAGGACGACGATGACAAG (page No. 1, 2 and 5)
* HA tag: TACCCCTACGACGTGCCCGACTACGCC (page No. 1, 2 and 5)
* Stop codon: TAG (page No. 1, 2 and 6)
* bGH polyA region from pcDNA3 (page No. 1, 2, 4 and 6)

**1. Sequence result of pBT346.6-H3.3K4M-bGHpolyA by pBT346.6 forward Seq primer**

>LW01-pBT346F\_A03.ab1
NNNNNNNNNNNNNNCGGANCTTATATAACTTCGTATAATGTATGCTATACGAAGTTATTAGGTCCCTCGACCTGCTGCAGCTCGAGGCATGCGTCGACGTTTCTAGTCTAGA**CTCGAG**TGAACCATGGCCCGAACCATGCAGACTGCTCGTAAGTCCACCGGTGGGAAAGCCCCCCGCAAACAGCTGGCCACGAAAGCCGCCAGGAAAAGCGCTCCCTCTACCGGCGGGGTGAAGAAGCCTCATCGCTACAGGCCCGGGACCGTGGCGCTTCGAGAGATTCGTCGTTATCAGAAGTCGACCGAGCTGCTCATCCGGAAGCTGCCCTTCCAGAGGTTGGTGAGGGAGATCGCGCAGGATTTCAAAACCGACCTGAGGTTTCAGAGCGCAGCCATCGGTGCGCTGCAGGAGGCTAGCGAAGCGTACCTGGTGGGTCTGTTCGAAGATACCAACCTGTGTGCCATCCACGCTAAGAGAGTCACCATCATGCCCAAAGACATCCAGTTGGCTCGCCGGATACGGGGAGAGAGAGCTGCGGCCGCTGGAGGAGACTACAAGGACGACGATGACAAGTCGGCCGCTGGAGGATACCCCTACGACGTGCCCGACTACGCCTAGGAATTC**GTTAAC**GAAATCCATCACACTGGCGGCCGCTCGAGCATGCATCTAGAGGGCCCTATTCTATAGTGTCACCTAAATGCTAGAGCTCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAANNTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTNNTGTCATTCTATCTGGGGGGNNGGGGNNGGGGCAGGACAGCAAGGGGGGAGGATTGGGAANACATANCAGCATGCTGGGGATGCGTGNCTCTAT**GGCGCGCC**CAACTAGTTCTAGAGCGCNCACAGTTTGTACAAAAAGCTGACGANAANGTAAATGATATNAATATCANNNNNTAATNANATTTTGNNNNNN

**2. Reverse complement of sequence result of pBT346.6-H3.3K4M-bGHpolyA by pBT346.6 reverse Seq primer**

>LW02-pBT346R\_B03.ab1
NNNNTNNTACGANNTANTAGNTCCCTNGNNNGNTGCAGCNNNNNCATGCNTCGNNNTTTNTAGTCTAGA**CTCGAG**TNNNNANNNCGNNCATGCAGACTGCTCGTAAGTCCACCGGTGGGAAAGCCCCCCGCAAACAGCTGGCCACGAAAGCCGCCAGGAAAAGCGCTCCCTCTACCGGCGGGGTGAAGAAGCCTCATCGCTACAGGCCCGGGACCGTGGCGCTTCGAGAGATTCGTCGTTATCAGAAGTCGACCGAGCTGCTCATCCGGAAGCTGCCCTTCCAGAGGTTGGTGAGGGAGATCGCGCAGGATTTCAAAACCGACNTGAGGTTTCAGAGCGCAGCCATCGGTGCGCTGCAGGAGGCTAGCGAAGCGTACCTGGTGGGTCTGTTCGAAGATACCAACCTGTGTGCCATCCACGCTAAGAGAGTCACCATCATGCCCAAAGACATCCAGTTGGCTCGCCGGATACGGGGAGAGAGAGCTGCGGCCGCTGGAGGAGACTACAAGGACGACGATGACAAGTCGGCCGCTGGAGGATACCCCTACGACGTGCCCGACTACGCCTAGGAATTC**GTTAAC**GAAATCCATCACACTGGCGGCCGCTCGAGCATGCATCTAGAGGGCCCTATTCTATAGTGTCACCTAAATGCTAGAGCTCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTAT**GGCGCGCC**CAACTAGTTCTAGAGCGGCCGCACAAGTTTGTACAAAAAAGCTGAACGAGAAACGTAAAATGATATAAATATCAATATATTAAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAACACAACATATCCAGTCACTATGGAGCTCCAGCTTTNNNNNNNNNNNNN

**QUERY: 1. Sequence result of pBT346.6-H3.3K4M-bGHpolyA by pBT346.6 forward Seq primer**

**SBJCT: Homo sapiens H3 histone, family 3B (H3.3B) (H3F3B), NM\_005324.3**

Query 125 ATGGCCCGAACCATGCAGACTGCTCGTAAGTCCACCGGTGGGAAAGCCCCCCGCAAACAG 184

 ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 134 ATGGCCCGAACCAAGCAGACTGCTCGTAAGTCCACCGGTGGGAAAGCCCCCCGCAAACAG 193

Query 185 CTGGCCACGAAAGCCGCCAGGAAAAGCGCTCCCTCTACCGGCGGGGTGAAGAAGCCTCAT 244

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 194 CTGGCCACGAAAGCCGCCAGGAAAAGCGCTCCCTCTACCGGCGGGGTGAAGAAGCCTCAT 253

Query 245 CGCTACAGGCCCGGGACCGTGGCGCTTCGAGAGATTCGTCGTTATCAGAAGTCGACCGAG 304

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 254 CGCTACAGGCCCGGGACCGTGGCGCTTCGAGAGATTCGTCGTTATCAGAAGTCGACCGAG 313

Query 305 CTGCTCATCCGGAAGCTGCCCTTCCAGAGGTTGGTGAGGGAGATCGCGCAGGATTTCAAA 364

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 314 CTGCTCATCCGGAAGCTGCCCTTCCAGAGGTTGGTGAGGGAGATCGCGCAGGATTTCAAA 373

Query 365 ACCGACCTGAGGTTTCAGAGCGCAGCCATCGGTGCGCTGCAGGAGGCTAGCGAAGCGTAC 424

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 374 ACCGACCTGAGGTTTCAGAGCGCAGCCATCGGTGCGCTGCAGGAGGCTAGCGAAGCGTAC 433

Query 425 CTGGTGGGTCTGTTCGAAGATACCAACCTGTGTGCCATCCACGCTAAGAGAGTCACCATC 484

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 434 CTGGTGGGTCTGTTCGAAGATACCAACCTGTGTGCCATCCACGCTAAGAGAGTCACCATC 493

Query 485 ATGCCCAAAGACATCCAGTTGGCTCGCCGGATACGGGGAGAGAGAGCT 532

 ||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 494 ATGCCCAAAGACATCCAGTTGGCTCGCCGGATACGGGGAGAGAGAGCT 541

**QUERY: 2. Reverse complement of sequence result of pBT346.6-H3.3K4M-bGHpolyA by pBT346.6 reverse Seq primer**

**SBJCT: Homo sapiens H3 histone, family 3B (H3.3B) (H3F3B), NM\_005324.3**

Query 89 CATGCAGACTGCTCGTAAGTCCACCGGTGGGAAAGCCCCCCGCAAACAGCTGGCCACGAA 148

 || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 145 CAAGCAGACTGCTCGTAAGTCCACCGGTGGGAAAGCCCCCCGCAAACAGCTGGCCACGAA 204

Query 149 AGCCGCCAGGAAAAGCGCTCCCTCTACCGGCGGGGTGAAGAAGCCTCATCGCTACAGGCC 208

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 205 AGCCGCCAGGAAAAGCGCTCCCTCTACCGGCGGGGTGAAGAAGCCTCATCGCTACAGGCC 264

Query 209 CGGGACCGTGGCGCTTCGAGAGATTCGTCGTTATCAGAAGTCGACCGAGCTGCTCATCCG 268

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 265 CGGGACCGTGGCGCTTCGAGAGATTCGTCGTTATCAGAAGTCGACCGAGCTGCTCATCCG 324

Query 269 GAAGCTGCCCTTCCAGAGGTTGGTGAGGGAGATCGCGCAGGATTTCAAAACCGACNTGAG 328

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||

Sbjct 325 GAAGCTGCCCTTCCAGAGGTTGGTGAGGGAGATCGCGCAGGATTTCAAAACCGACCTGAG 384

Query 329 GTTTCAGAGCGCAGCCATCGGTGCGCTGCAGGAGGCTAGCGAAGCGTACCTGGTGGGTCT 388

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 385 GTTTCAGAGCGCAGCCATCGGTGCGCTGCAGGAGGCTAGCGAAGCGTACCTGGTGGGTCT 444

Query 389 GTTCGAAGATACCAACCTGTGTGCCATCCACGCTAAGAGAGTCACCATCATGCCCAAAGA 448

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 445 GTTCGAAGATACCAACCTGTGTGCCATCCACGCTAAGAGAGTCACCATCATGCCCAAAGA 504

Query 449 CATCCAGTTGGCTCGCCGGATACGGGGAGAGAGAGCT 485

 |||||||||||||||||||||||||||||||||||||

Sbjct 505 CATCCAGTTGGCTCGCCGGATACGGGGAGAGAGAGCT 541

**QUERY: 2. Reverse complement of sequence result of pBT346.6-H3.3K4M-bGHpolyA by pBT346.6 reverse Seq primer**

**SBJCT: pcDNA3 sequence from Addgene (bGHpolyA: 1018-1249)**

Query 1 ATCCATCACACTGGCGGCCGCTCGAGCATGCATCTAGAGGGCCCTATTCTATAGTGTCAC 60

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 951 ATCCATCACACTGGCGGCCGCTCGAGCATGCATCTAGAGGGCCCTATTCTATAGTGTCAC 1010

Query 61 CTAAATGCTAGAGCTCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTT 120

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1011 CTAAATGCTAGAGCTCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTT 1070

Query 121 GTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCC 180

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1071 GTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCC 1130

Query 181 TAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTggggggt 240

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1131 TAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGT 1190

Query 241 ggggtggggCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGAT 300

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1191 GGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGAT 1250

Query 301 GCGGTGGGCTCTAT 314

 ||||||||||||||

Sbjct 1251 GCGGTGGGCTCTAT 1264

**QUERY: Sequence result of pBT346.6-H3.3K4M-bGHpolyA**

**SBJCT: Sequence result of pBT346.6-H3.3K36M-bGHpolyA from Lenan**

* K36M: ATG

Query 1 ATGGCCCGAACCATGCAGACTGCTCGTAAGTCCACCGGTGGGAAAGCCCCCCGCAAACAG 60

 ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1 ATGGCCCGAACCAAGCAGACTGCTCGTAAGTCCACCGGTGGGAAAGCCCCCCGCAAACAG 60

Query 61 CTGGCCACGAAAGCCGCCAGGAAAAGCGCTCCCTCTACCGGCGGGGTGAAGAAGCCTCAT 120

 ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||

Sbjct 61 CTGGCCACGAAAGCCGCCAGGAAAAGCGCTCCCTCTACCGGCGGGGTGATGAAGCCTCAT 120

Query 121 CGCTACAGGCCCGGGACCGTGGCGCTTCGAGAGATTCGTCGTTATCAGAAGTCGACCGAG 180

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 121 CGCTACAGGCCCGGGACCGTGGCGCTTCGAGAGATTCGTCGTTATCAGAAGTCGACCGAG 180

Query 181 CTGCTCATCCGGAAGCTGCCCTTCCAGAGGTTGGTGAGGGAGATCGCGCAGGATTTCAAA 240

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 181 CTGCTCATCCGGAAGCTGCCCTTCCAGAGGTTGGTGAGGGAGATCGCGCAGGATTTCAAA 240

Query 241 ACCGACCTGAGGTTTCAGAGCGCAGCCATCGGTGCGCTGCAGGAGGCTAGCGAAGCGTAC 300

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 241 ACCGACCTGAGGTTTCAGAGCGCAGCCATCGGTGCGCTGCAGGAGGCTAGCGAAGCGTAC 300

Query 301 CTGGTGGGTCTGTTCGAAGATACCAACCTGTGTGCCATCCACGCTAAGAGAGTCACCATC 360

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 301 CTGGTGGGTCTGTTCGAAGATACCAACCTGTGTGCCATCCACGCTAAGAGAGTCACCATC 360

Query 361 ATGCCCAAAGACATCCAGTTGGCTCGCCGGATACGGGGAGAGAGAGCTGCGGCCGCTGGA 420

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 361 ATGCCCAAAGACATCCAGTTGGCTCGCCGGATACGGGGAGAGAGAGCTGCGGCCGCTGGA 420

Query 421 GGAGACTACAAGGACGACGATGACAAGTCGGCCGCTGGAGGATACCCCTACGACGTGCCC 480

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 421 GGAGACTACAAGGACGACGATGACAAGTCGGCCGCTGGAGGATACCCCTACGACGTGCCC 480

Query 481 GACTACGCCTAGGAATTCGTTAACGAAATCCATCACACTGGCGGCCGCTCGAGCATGCAT 540

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 481 GACTACGCCTAGGAATTCGTTAACGAAATCCATCACACTGGCGGCCGCTCGAGCATGCAT 540

Query 541 CTAGAGGGCCCTATTCTATAGTGTCACCTAAATGCTAGAGCTCGCTGATCAGCCTCGACT 600

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 541 CTAGAGGGCCCTATTCTATAGTGTCACCTAAATGCTAGAGCTCGCTGATCAGCCTCGACT 600

Query 601 GTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTG 660

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 601 GTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTG 660

Query 661 GAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTG 720

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 661 GAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTG 720

Query 721 AGTAGGTGTCATTCTATTCTggggggtggggtggggCAGGACAGCAAGGGGGAGGATTGG 780

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 721 AGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGG 780

Query 781 GAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGCGCGCC 829

 |||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 781 GAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGCGCGCC 829