**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