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<Serial Cloner V2.5> -- <11 Sep 2019   10:27>
Restriction map of sLP-mCherry_all plasmid_2
Showing restriction enzymes cutting maximum 1 time [using RELibrary as a Restriction Enzyme Library]
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   >BamHI                              >SP                                >HindIII            >TATk
   |                                   |                                  |                   |
GGATCCATGTGGTGGCGCCTGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGTGGCCCATGGTGTGGGCCaagcttTACGCCCGCAAGGCCGCCCGCCAGG  < 100
G  S  M  W  W  R  L  W  W  L  L  L  L  L  L  L  L  W  P  M  V  W  A  K  L  Y  A  R  K  A  A  R  Q  A
CCTAGGTACACCACCGCGGACACCACCGACGACGACGACGACGACGACGACACCGGGTACCACACCCGGttcgaaATGCGGGCGTTCCGGCGGGCGGTCC
         10        20        30        40        50        60        70        80        90

CCCGCGCCGATCCACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGGATAACATGGCCATCATCAAGGAGTTCATGCGCTTCAAGGTGCACATGGAGGG  < 200
  R  A  D  P  P  V  A  T  M  V  S  K  G  E  E  D  N  M  A  I  I  K  E  F  M  R  F  K  V  H  M  E  G
GGGCGCGGCTAGGTGGCCAGCGGTGGTACCACTCGTTCCCGCTCCTCCTATTGTACCGGTAGTAGTTCCTCAAGTACGCGAAGTTCCACGTGTACCTCCC
         110       120       130       140       150       160       170       180       190

CTCCGTGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCCTACGAGGGCACCCAGACCGCCAAGCTGAAGGTGACCAAGGGTGGCCCC  < 300
 S  V  N  G  H  E  F  E  I  E  G  E  G  E  G  R  P  Y  E  G  T  Q  T  A  K  L  K  V  T  K  G  G  P
GAGGCACTTGCCGGTGCTCAAGCTCTAGCTCCCGCTCCCGCTCCCGGCGGGGATGCTCCCGTGGGTCTGGCGGTTCGACTTCCACTGGTTCCCACCGGGG
         210       220       230       240       250       260       270       280       290

CTGCCCTTCGCCTGGGACATCCTGTCCCCTCAGTTCATGTACGGCTCCAAGGCCTACGTGAAGCACCCCGCCGACATCCCCGACTACTTGAAGCTGTCCT  < 400
L  P  F  A  W  D  I  L  S  P  Q  F  M  Y  G  S  K  A  Y  V  K  H  P  A  D  I  P  D  Y  L  K  L  S  F
GACGGGAAGCGGACCCTGTAGGACAGGGGAGTCAAGTACATGCCGAGGTTCCGGATGCACTTCGTGGGGCGGCTGTAGGGGCTGATGAACTTCGACAGGA
         310       320       330       340       350       360       370       380       390

                                                                                >mCherry
                                                                                |
TCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGTGGTGACCGTGACCCAGGACTCCTCCCTGCAGGACGGCGAGTTCATCTA  < 500
  P  E  G  F  K  W  E  R  V  M  N  F  E  D  G  G  V  V  T  V  T  Q  D  S  S  L  Q  D  G  E  F  I  Y
AGGGGCTCCCGAAGTTCACCCTCGCGCACTACTTGAAGCTCCTGCCGCCGCACCACTGGCACTGGGTCCTGAGGAGGGACGTCCTGCCGCTCAAGTAGAT
         410       420       430       440       450       460       470       480       490

CAAGGTGAAGCTGCGCGGCACCAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAAGACCATGGGCTGGGAGGCCTCCTCCGAGCGGATGTACCCCGAG  < 600
 K  V  K  L  R  G  T  N  F  P  S  D  G  P  V  M  Q  K  K  T  M  G  W  E  A  S  S  E  R  M  Y  P  E
GTTCCACTTCGACGCGCCGTGGTTGAAGGGGAGGCTGCCGGGGCATTACGTCTTCTTCTGGTACCCGACCCTCCGGAGGAGGCTCGCCTACATGGGGCTC
         510       520       530       540       550       560       570       580       590

GACGGCGCCCTGAAGGGCGAGATCAAGCAGAGGCTGAAGCTGAAGGACGGCGGCCACTACGACGCTGAGGTCAAGACCACCTACAAGGCCAAGAAGCCCG  < 700
D  G  A  L  K  G  E  I  K  Q  R  L  K  L  K  D  G  G  H  Y  D  A  E  V  K  T  T  Y  K  A  K  K  P  V
CTGCCGCGGGACTTCCCGCTCTAGTTCGTCTCCGACTTCGACTTCCTGCCGCCGGTGATGCTGCGACTCCAGTTCTGGTGGATGTTCCGGTTCTTCGGGC
         610       620       630       640       650       660       670       680       690

TGCAGCTGCCCGGCGCCTACAACGTCAACATCAAGTTGGACATCACCTCCCACAACGAGGACTACACCATCGTGGAACAGTACGAACGCGCCGAGGGCCG  < 800
  Q  L  P  G  A  Y  N  V  N  I  K  L  D  I  T  S  H  N  E  D  Y  T  I  V  E  Q  Y  E  R  A  E  G  R
ACGTCGACGGGCCGCGGATGTTGCAGTTGTAGTTCAACCTGTAGTGGAGGGTGTTGCTCCTGATGTGGTAGCACCTTGTCATGCTTGCGCGGCTCCCGGC
         710       720       730       740       750       760       770       780       790

                                                                                >NLS
                                                                                |
CCACTCCACCGGCGGCATGGACGAGCTGTACAAGTCCGGACTCAGATCTCGACCGGGCACCATGGCCCCTAAGAAGAAGAGGAAGGTGGAGGCGTTGCTT  < 900
 H  S  T  G  G  M  D  E  L  Y  K  S  G  L  R  S  R  P  G  T  M  A  P  K  K  K  R  K  V  E  A  L  L
GGTGAGGTGGCCGCCGTACCTGCTCGACATGTTCAGGCCTGAGTCTAGAGCTGGCCCGTGGTACCGGGGATTCTTCTTCTCCTTCCACCTCCGCAACGAA
         810       820       830       840       850       860       870       880       890

                                                  >c-Myc tag
                                                  |
CGAATTCTGCAGTCGACGCAAGCTGGGGATCTCGAGCAGAAGCTGATCAGCGAGGAGGACCTGTAA  < 966
R  I  L  Q  S  T  Q  A  G  D  L  E  Q  K  L  I  S  E  E  D  L  *
GCTTAAGACGTCAGCTGCGTTCGACCCCTAGAGCTCGTCTTCGACTAGTCGCTCCTCCTGGACATT
         910       920       930       940       950       960


Features :
BamHI        : [1 : 6 - CW]
SP           : [7 : 69 - CW]
HindIII      : [70 : 75 - CW]
TATk         : [76 : 108 - CW]
mCherry      : [127 : 834 - CW]
NLS          : [865 : 888 - CW]
c-Myc tag    : [934 : 963 - CW]
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