pExp-His-sfGFP-TEV

```
                                          SpeI
                                          >=====
ATGAATCACCATCACCATCACCATCACCATTCTGGCACTAGTGGCAGCAAAGGCGAAGAA
    90        100       110       120       130       140
M  N  H  H  H  H  H  H  H  H  S  G  T  S  G  S  K  G  E  E

CTGTTTACCGGTGTTGTTCCGATTCTGGTTGAACTGGATGGTGATGTTAATGGCCATAAA
    150       160       170       180       190       200
L  F  T  G  V  V  P  I  L  V  E  L  D  G  D  V  N  G  H  K

TTTTCAGTTCGCGGTGAAGGTGAAGGTGATGCAACCAATGGTAAACTGACCCTGAAATTT
    210       220       230       240       250       260
F  S  V  R  G  E  G  E  G  D  A  T  N  G  K  L  T  L  K  F

ATTTGCACCACCGGTAAACTGCCGGTTCCGTGGCCGACCCTGGTTACCACCCTGACCTAT
    270       280       290       300       310       320
I  C  T  T  G  K  L  P  V  P  W  P  T  L  V  T  T  L  T  Y

GGTGTTCAGTGTTTTAGCCGTTATCCGGATCATATGAAACGCCATGATTTTTTTAAAAGC
    330       340       350       360       370       380
G  V  Q  C  F  S  R  Y  P  D  H  M  K  R  H  D  F  F  K  S

GCAATGCCGGAAGGTTATGTTCAAGAACGTACCATTAGCTTTAAAGATGATGGCACCTAT
    390       400       410       420       430       440
A  M  P  E  G  Y  V  Q  E  R  T  I  S  F  K  D  D  G  T  Y

AAAACCCGTGCCGAAGTTAAATTTGAAGGTGATACCCTGGTGAATCGCATTGAACTGAAA
    450       460       470       480       490       500
K  T  R  A  E  V  K  F  E  G  D  T  L  V  N  R  I  E  L  K

GGCATTGATTTTAAAGAAGATGGTAATATTCTGGGCCATAAACTGGAATATAATTTTAAT
    510       520       530       540       550       560
G  I  D  F  K  E  D  G  N  I  L  G  H  K  L  E  Y  N  F  N

AGCCATAATGTGTATATTACCGCAGATAAACAGAAAAATGGCATTAAAGCCAATTTTAAA
    570       580       590       600       610       620
S  H  N  V  Y  I  T  A  D  K  Q  K  N  G  I  K  A  N  F  K

ATTCGCCATAATGTGGAAGATGGTAGCGTTCAGCTGGCAGATCATTATCAGCAGAATACC
    630       640       650       660       670       680
I  R  H  N  V  E  D  G  S  V  Q  L  A  D  H  Y  Q  Q  N  T

CCGATTGGTGATGGTCCGGTTCTGCTGCCGGATAATCATTATCTGAGCACCCAGAGCGTT
    690       700       710       720       730       740
P  I  G  D  G  P  V  L  L  P  D  N  H  Y  L  S  T  Q  S  V

CTGAGCAAAGATCCGAATGAAAAACGTGACCATATGGTGCTGCTGGAATTTGTTACCGCA
    750       760       770       780       790       800
L  S  K  D  P  N  E  K  R  D  H  M  V  L  L  E  F  V  T  A

          NcoI
          >=====
GCAGGTATTACCCATGGTATGGATGAACTGTATAAAGGTAGCGGTACCGAAAACCTGTAC
    810       820       830       840       850       860
A  G  I  T  H  G  M  D  E  L  Y  K  G  S  G  T  E  N  L  Y

           BsaI     XhoI                                HindIII
 >.........======   >=====                              >===
TTCCAGTGAGACCTTAATTAACTCGAGCGCATGGAGCCACCCGCAGTTCGAAAAATAAGC
    870       880       890       900       910       920
F  Q  *  -  -  -  *  -  -  -  -  -  -  -  -  -  -  -  -  -

HindIII
==
TTG

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-
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# Enzymes that cut	Frequency	Isoschizomers
BsaI	1	BsaI
HindIII	1	
NcoI	1	
SpeI	1	

XhoI	1