

PB513B-1_TRE-hHNF1fΔ-hHNF4fζ-hHNF6-EF1fζ-Bla.ape

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

CTGGAAGAGAACCCGGACCTATGAATGCCAGCTGACCATGGAAGCCATCGGAGAGCTGCACGGTGTCTCTCACGAACCTGTTCAGCTCCAGCCGAT 5000
V E E N P G P M N A Q L T M E A I G E L H G V S H E P V P A P A D
15 1
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T2A hHNF6

5010 5020 5030 5040 5050 5060 5070 5080 5090 5100
* * * * *

CTGCTCGGAGGACTCTCCTCACGCTAGAAGCAGCGTGCCCCACAGAGGATCTCATCTGCCTCCAGCTCACCCCAGATCCATGGGCATGGCTTCTCTGCTGG 5100
L L G G S P H A R S S V A H R G S H L P P A H P R S M G M A S L L D
27
>>>
hHNF6

5110 5120 5130 5140 5150 5160 5170 5180 5190 5200
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ATGGCGGACTCTGGCGCGGAGATTATCAACCACCATCACAGAGCCCCTGAGCACTCTCTGGCTGGACCTCTGCACCCCTACCATGACCATGGCCTGTGAAAC 5200
G G S G G G D Y H H H H R A P E H S L A G P L H P T M T M A C E T
61
>>>
hHNF6

5210 5220 5230 5240 5250 5260 5270 5280 5290 5300
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CCCTCCAGGCATGAGCATGCCCCACCCTACACCACACTGACCCCTCTGCAACCCCTGCCTCCTATCAGCACCGGTGTCCGACAAGTTCCACACACCATCAC 5300
P P G M S M P T T Y T T L T P L Q P L P P I S T V S D K F P H H H
94
>>>
hHNF6

5310 5320 5330 5340 5350 5360 5370 5380 5390 5400
* * * * *

CATCATCAACCACCACCATCAACCATCCACATCATCAACAGAGACTGGCCGGCAATGTGTCCGGCAGCTTTACCCTGATGAGGGACGAACGCGGACTGGCCA 5400
H H H H H H H H P H H H Q R L A G N V S G S F T L M R D E R G L A S
127
>>>
hHNF6

5410 5420 5430 5440 5450 5460 5470 5480 5490 5500
* * * * *

GCATGAACAACCTGTACACCCCTTACCACAAGGACGTGGCCGGCATGGGACAGTCTCTGTCTCCACTGTCTAGCAGCGGCTGGGCAGCATCCACAATTC 5500
M N N L Y T P Y H K D V A G M G Q S L S P L S S S G L G S I H N S
161
>>>
hHNF6

5510 5520 5530 5540 5550 5560 5570 5580 5590 5600
* * * * *

TCAGCAGGGCCTGCCTCACTACGCTCATCTGCTGCTGCCATGCCTACCGACAAGATGCTGACCCCTTAATGGCTTCGAGGCCCACCATCTGCTATGCTG 5600
Q Q G L P H Y A H P G A A M P T D K M L T P N G F E A H H P A M L
194
>>>
hHNF6

5610 5620 5630 5640 5650 5660 5670 5680 5690 5700
* * * * *

G GTAGACACGGCGAGCAGCACCTGACACCTACATCTGCTGGCATGGTGCCCATCAACGGCCTGCCACCTCATCACCTTCACGCTCATCTGAACGCCAACG 5700
G R H G E Q H L T P T S A G M V P I N G L P P H H P H A H L N A Q G
227
>>>
hHNF6

5710 5720 5730 5740 5750 5760 5770 5780 5790 5800
* * * * *

GACATGGACAGCTGCTGGGAACCGCCAGAGAACCATACTCTGTGTGACAGGCGCCAGGTGTCCAACGGCTCTAATAGCGGACAGATGGAAGAGATCAA 5800
H G Q L L G T A R E P N P S V T G A Q V S N G S N S G Q M E E I N
261
>>>
hHNF6

5810 5820 5830 5840 5850 5860 5870 5880 5890 5900
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[illegible]

Genomic map of the E1A gene region (6801-7900 bp). The map shows the E1A promoter, E1A gene (exons 1-8), E1A introns, E1A 3' UTR, SV40 polyA, and core Insulator. The E1A gene is shown in blue, introns in green, and the SV40 polyA in red. The core Insulator is shown in yellow. The map also includes a scale bar and a legend for the different regions.

Scale: 6801 6900 7000 7100 7200 7300 7400 7500 7600 7700 7800 7900

Regions: E1A promoter, E1A gene (exons 1-8), E1A introns, E1A 3' UTR, SV40 polyA, core Insulator

Key features: E1A promoter, E1A gene (exons 1-8), E1A introns, E1A 3' UTR, SV40 polyA, core Insulator

[illegible]

ColE1 origin

9310 9320 9330 9340 9350 9360 9370 9380 9390 9400

9301 CAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC 9400

ColE1 origin

9410 9420 9430 9440 9450 9460 9470 9480 9490 9500

9401 TTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCCGACCGCTGCCG 9500

ColE1 origin

9510 9520 9530 9540 9550 9560 9570 9580 9590 9600

9501 CTTATCCGGTAACATATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTA 9600

ColE1 origin

9610 9620 9630 9640 9650 9660 9670 9680 9690 9700

9601 GGCGGTGTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA 9700

ColE1 origin

9710 9720 9730 9740 9750 9760 9770 9780 9790 9800

9701 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAACACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCA 9800

ColE1 origin

9810 9820 9830 9840 9850 9860 9870 9880 9890 9900

9801 AGAAGATCCTTTTGATCTTTTCTACGGGCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACC 9900

ColE1 origin

9910 9920 9930 9940 9950 9960 9970 9980 9990 10000

9901 TAGATCCTTTTAAATTAAAAATGAAGTTTAAATCAATCTAAAGTATATATAGTAAACTTGGTCTGACAGTTA CCAATGCTTAATCAGTGAGGCACCTA 10000

W H K I L S A G I

286

Amp

10010 10020 10030 10040 10050 10060 10070 10080 10090 10100

10001 TCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCCTGACTCCCGCTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGC 10100

E A I Q R N R E D M T A Q S G T T Y I V V I R S P K G D P G L A A

277

Amp

10110 10120 10130 10140 10150 10160 10170 10180 10190 10200

10101 AATGATACCGGAGACCCACGCTACCGGCTCCAGATTATCAGCAATAAACGACGCGGGAAGGCGGAGCGCAGAAGTGGTCTGCAACTTTATCC 10200

I I G R S G R E G A G S K D A I F W G A P L A S R L L P G A V K D A

244

Amp

10210 10220 10230 10240 10250 10260 10270 10280 10290 10300

10201 GCCTCCATCCAGTCTATTAATTGTTGCGGGGAAGCTAGAGTAAGTAGTTGCGCAGTTAATAGTTTGGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGG 10300

E M W D I L Q Q R S A L T L L E G T L L K R L T T A M A V P M T T

210

Amp

10310 10320 10330 10340 10350 10360 10370 10380 10390 10400

[illegible]