

Mouse Uroplakin II Promoter

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A. General information:

We have isolated and characterized a 3.6 kb 5'-upstream sequence of mouse uroplakin II gene, and we showed that this sequence can serve as a highly bladder urothelium-specific promoter in transgenic mouse studies. This sequence has been used to drive the mouse bladder-specific expression of human growth factor, SV40-large T antigen, Ha-Ras, EGF receptor. It has also been used to achieve the urothelium-specific ablation (conventional or inducible) of various genes including Rb and p53. These studies have enabled Dr. Xue-Ru Wu to dissect the roles of various oncogenes and tumore-suppressor genes in bladder tumorigenesis.

This page contains the sequence and restriction map of this mouse UPII promoter (updated from the original paper by Lin et al PNAS 1995). Blasting this sequence against the mouse genome (NCBI) showed 99% identity. While these minor differences may not affect the utility of this promoter in your transgenic experiments, you should keep such differences in mind if you see an unexpected restriction enzyme cut pattern.

This promoter is in a pBluescript SK(+) vector, which contains the Amp-resistant gene. To amplify, transform this into JM109 or DH5 alpha and select on Amp plates and broth.

We recommend the use of KpnI as a 5' restriction enzyme to cut out the promoter. The XhoI and ApaI enzymes do not cut due to a disruption during the subcloning process. Use the map to figure out what enzyme you prefer for the 3' cut. Visit [Stratagen](#) for additional information about the vector sequence and restriction map.

If you like to use this promoter for your research or have any questions, please contact Dr. Tung-Tien Sun at sunt01@nyumc.org or Dr. Xue-Ru Wu at Xue-Ru.Wu@nyumc.org

B. References:

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C. Sequence:

> NAME = up2 : TYPE = DNA

```
CTCGAGGATCTCGGCCCTCTTCTGCATCCTTGTCTCTAAATCATTTTCATATCTTGCTAGACCTCAGTTTGAGAGA
AACGAACCTTCTCATTTTCAAGTTGAAAAAAGAGGTTCAAAGTGGCTCACTCAAAGTTACAAGCCAACACTC
ACCACTACGAGTACAATGGCCACCATTAGTGTCTGGCATGCCCCAGGAGACAGGCATGCATATTATCTAGATGAC
TGGGAGGCAGAGGGTGGCCCTAGTGAGGTCAGACTGTGGACAGATCAGGCAGATGTGGGTTCTGATCCCAATTCCT
CAGGCCGCAGAACTACTGTGGTTCAAGAAGGGGACAAAAGGACTGCAGTCCCGAACAGGAGGTCCACTTTGAGAG
CTGACTGAGCAGAAGAGGAAAGTGAAGAACTTCAGGGGCAAGAGCTTACCCTACTTTTACAGCTTTGTGTCTTCT
TTACTCCAGGGCGTCCCTGGTACTCAGTAAATGTCTGTTGGCTTGAGGAACATATGTGTAAGGAGGAAGGAGAGG
GAACTTGAGGGAGTTAAGACTCAAGAATCAATCAAGGAGAGGACAGCAGAGAAGACAGGGTTTGGGAGAGAGACTC
CAGACATTGGCCCTGGTTCCTTCTTGCCACTGTGAAACCTCCAGAGGAACTGAGTGTCTGGCTTTAAATGAT
CTCAGCACTGTCTAGTGAAGCCGCTCTGCTCAAAGAGTTATCTCTGTCTCTGTGCCGGGCTCCCTCTCTCTC
AGCTCCCAACCCCTTCTCAGCCACTGTGATGGGATAATTAGATGCGAGAGCTCAGCACAGATGATGCTCCAGTTG
CTTAGCAACTAATGGTTTCCATGGAGACCCGAAAGCACAGCCTCTAGAGCAGCCAGTGAGCAGCTCGGCAGGGCAG
GGAGAAGACGCAACTCTGCTCCTCCAGAAACCTGGGGAGGGTTAGGGTGGGGAAGGTGAGGGGGGATTGGAGGGAG
ATGGGAAGGCTTAAAGGCACAGGACCCTCATATCCCTTTAAAAATGTGACCAGAGATCTGCTCTTTTATCCACA
CTGTCTCACTTCAATTTCAAATGGGGCTTAGGAGTGACCTATATGTTCTGCTCTGCAGTAAACCAATCCTCTTC
CTGATTCCTCTAAATCCTCAGTAAACACTGTGCTATGTGGAGGTTTGGAGACTTGGCAGGAAGATCTCCTGACCC
TGACACCTACCGTGTAGCCCTCTCCGCACCCGAGTTCTCCCTCGTGTGTGATCTTCTGTGTGTAAGTGAGG
AGGAGATCTCATCTAAAGGGGACAAAAGCCAAAGGAGCTGGAAAAACAGAAATCATTCAGTTCTCCACCCAAAGGCA
GCCTGAGAAAAACCTCTGTCCCACTTTGCATTTGCATGTGTGTGTGTATGAGTGTGTGTGTATGAGTGTGTG
TGTGTATGAGTGTGTGTGTATGAGTGTGTGTGTATGAGTGTGTGTGTGTGGATGAGTGTGTGTGTGCACATG
TATGAGTGTGTCTGTGTATGATGATTATATGTGTGTCTGTGTGTGTATGAGTATGTGTGTCTGTGTGTGTG
TATGAGTATGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TGAATATGTGAATGTGAGAGTGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TGTGTGTGTGTATGAGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TGAGTCTGTGTCTCTGCGTTACCTGTAAAGCGTCATAGGAAGTTTACGAAACCATGAGATGGCTCAACAGGTA
GCTCTTGGCCACATGCCTGACATTTTGGTCCCAAGCCACATTATGAAAGGAGAGGCAATGCCACAACCTTG
CCCTCTGACCTCCACATAGACACTGTGGCACACATATGGGCACACATATAAAATAATAAATGCAACTTTAAATTTT
TGAAGAATAAAGTTTCCGGTTTACCTCAGACCCACTGTATCAGAAGCTACATCTGAACCAGTTTCTGATCGT
CCATTGCACAGTAAATTTGGAGATCGTCTGGTGTGAGAGTTCTCTCTGCTCCAGCCGAGCCCCAGGTTCTGTTGT
CTTCTACCCCTACACACTCGCAGACTTTAAGTCCACCCAGCATGGGGGAAAGGACAGAACCCATCAGCCCTTC
AGTGGCCCACTTTTCCACTAGGACCTTTCTCTGGGGTTGGGAAAATGGGTGGTTCTGGAGCAGACCTGACG
GTCTGAGCTCAGGTCTATCGAGTTCACTAGCTGAGACACCCACACCCCTGCAGCCACTTTGCAAGTACAACCTG
AGTCTCAGGTTCTGCATCTATAAAAAGCAGTGCCTTTTCAAGGAGGCATGCAGAGCCCTGGCCAGCGTCTAGAGG
AGAGGTGACTGAGTGGGGCCATGCTACTCGTCCATGGCTGGAGAACCTCCATCAGTTTCTCCAGTTAGCCTGGGG
CAGGAGAGAACCAGAGGAGCTGTGGTGTGTATGGTGTCTTCCCAACTGTTGTCCAGGCATCGAACCCAGA
CGGACCTGCACACAGTCCACCGCTGAGCCACACCCAGCCCTCCACCTCTGCTCCTGGTTACAGGATTGTTTT
GTCTTGAAGGGTTTTGTGTGTGTACTTTTTGCTTTGTTTTTCTTTTTTCTTTTTTAAACATAAGGTTTCTCTGTG
TAGCCCTAGCTGTCTGGAACCTCACTCTGTAGACCAGGCTGGCCTCAAACCTCAGAAATCCACCTTCTCCCAAGTG
CTGGGATTAAGGCATTGCGCCACCATCGCCAGCCCGGCTTGTTCCTAAGGTTTTCTGCTTTACTCGCTAC
CCGTTGCACAACCGCTTGTCTCAAGTCTGTTGTATCTACTCCACCCCACTAGCCTTGTGGACTGGACCTA
CGTTTACTGGAAACCTTCACTAACTTCCCTTGTCTCCACCTTCTGGAGAAATCTGAAGGCTCACACTGATACCT
CCGCTTCTCCAGAGTCGAGTTTCTTAGGCCTCAGTTAAATACCAGAATGGATCTCAGGCTCTGCTATCCCCAC
```

CCTACCTAACCAACCCCTCCTCTCCATCCTTACTAGCCAAAGCCCTTCAACCCTTGGGGCTTTTCCTACACCT
ACACACCAGGGCAATTTAGAACTCATGGCTCTCCTAGGAAAACGCCTACCTCCTTGGAGACAGCACCCCTCTACAG
TCCAGGAGGCAGACACTCAGACAGAGGAACTCTGTCTTCAGTCGCGGGAGTTCAGAAAAGAGCCATACTCCCCTG
CAGCTAACTAAGCTGCCAGGACCCAGCCAGAGCATCCCCCTTTAGGCCGAGGGCCAGCTCCCCAGCCTGAAAAAC
CTGTCTGGGGCCCTCCCTGAGGCTACAGTGCCCAAGGGGCAAGTTGGACTGGATTCCCAGCAGCCCTCCCCTC
CGAGACAAAATCAGCTACCCTGGGGCAGGGCCTCATTGGCCCCAGGAAAACCCAGCCTGTCAGCACCTGTTCCAGG

D. Restriction enzymes that do not cut the promoter sequence (Promega):

AatII
Acc65I
AccIII
AgeI
BamHI
BanI
BclI
BsaOI
BsrBRI
BssHII
Bst98I
BstEII
BstZI
CfoI
ClaI
Csp45I
CspI
Eco47III
Eco52I
EcoRI
EcoRV
HaeII
HhaI
HincII
HindIII
HpaI
I-PpoI
KpnI
MluI
NaeI
NarI
NgoMIV
NheI
NotI
NruI
PvuI
PvuII
SacII
Sall
ScaI
SgfI
SmaI
SnaBI
SpeI
SspI
Tth111I
VspI
XmaI

E. Restriction maps:

Sequence Range: 1 to 3648

```
>XhoII
|
>Sau3AI
|
>MboI
|
>NdeII >HaeIII
| |
>TaqI | >Sau96I
| | ||
>AvaI | >FokI
|| | |||
>XhoI >DpnI |||
|| || |||
|| |||10 ||| 20 30 40 50
CTCGAGGATCTCGGCCCTTTCTGCATCCTTGCCTAAATCATTTTCAT
GAGCTCCTAGAGCCGGGAGAAAGACGTAGGAACAGGATTTAGTAAAAGTA
```

```
>DdeI
|
60 | 70 80 90 100
ATCTTGCTAGACCTCAGTTTGAGAGAAACGAACCTTCTCATTTTCAAGTT
TAGAACGATCTGGAGTCAAACCTCTTTGCTTGGAAAGAGTAAAAGTTCAA
110 120 130 140 150
GAAAAAAAAAAGAGGTTCAAAGTGGCTCACTCAAAGTTACAAGCCAACAC
CTTTTTTTTTTCTCCAAGTTTCACCGAGTGAGTTTCAATGTTGCGTTGTG
```

```
>BstOI
|
>Alw26I
| |
>Hsp92II
|| |
>BclI >BbuI |
| | || |
>RsaI >HaeIII >SphI |
| | || |
160 | 170| 180 190 || | 200
TCACCACTACGAGTACAATGGCCACCATTAGTGTCTGGCATGCCCCAGGA
AGTGGTGATGCTCATGTTACCGGTGGTAATCACAGACCGTACGGGGTCTT
```

```
>NsiI
|
>BbuI
||
>SphI
||
>Hsp92II >XbaI >BsrSI >HaeIII
|| | | |
```

210 | 220 230 | 240 | 250
GACAGGCATGCATATTATTCTAGATGACTGGGAGGCAGAGGGGTGGCCTA
CTGTCCGTACGTATAATAAGATCTACTGACCCTCCGTCTCCCCACCGGAT

>DpnI >DpnI
| |
>MboI >NdeII
|| ||
>Sau3AI >Sau3AI
|| ||
>NdeII >MboI
|| ||

260 270 | 280 290 | 300
GTGAGGTCAGACTGTGGACAGATCAGGCAGATGTGGGTTCTGATCCCAAT
CACTCCAGTCTGACACCTGTCTAGTCCGTCTACACCCAAGACTAGGGTTA

>HaeIII
|
>DdeI |
| |
>Bsu36I |
| |
| 310 320 330 340 350
TCCTCAGGCCGAGAACTACTGTGGTTCAAGAAGGGGACAAAAGGACTGC
AGGAGTCCGGCGTCTTGATGACACCAAGTTCTTCCCCTGTTTTCTGACG

>HpaII
|
>NciI >SniI
| |
>MspI >Sau96I >DdeI
| | |
>PstI | >AvaII >AluI |
| | | | |
| | 360 | 370 380 | 390 400
AGTCCCGGAACAGGAGGTCCACTTTGAGAGCTGACTGAGCAGAAGAGGAA
TCAGGGCCTTGCTCCTCCAGGTGAAACTCTCGACTGACTCGTCTTCTCCTT

>XmnI >MboII
| |
>MboII | >MboII >AluI >AluI
| | | | ||
| 410 | 420 | 430 440 || 450
AGTGAAGAACTTCAGGGGCAAGAGCTTACCCTACTTTTACAGCTTTGTTG
TCACTTCTTGAAGTCCCGTCTCGAATGGGATGAAAATGTCGAAACAAC

>Hsp92I >RsaI
| |
>BstOI | >BstOI | >DdeI
| | | ||
460 | 470 | 480 490 500
TCTTCTTTACTCCAGGGCGTCCCTGGTACTCAGTAAATGTCTGTTGGCT
AGAAGAAATGAGGTCCCGCAGGGACCATGAGTCATTTACAGACAACCGA

>Hinfl
|
>NdeI >Tru9I |

| |
510 520 530 540 | 550
TGAGGAACATATGTGTAAGGAGGAAGGAGAGGGAAGGAACTTGAGGGAGTTAAG
ACTCCTTGTATACACATTCTCCTTCTCCTTGAACCTCCCTCAATTC

>Alw26I
|
>HinfI >MboII
| ||
|560 570 580 590 || 600
ACTCAAGAATCAATCAAGGAGAGGACAGCAGAGAAGACAGGGTTTGGGAG
TGAGTTCTTAGTTAGTTCTCCTCTCCTGTCGTCTTTCTGTCCCAAACCTC

>HaeIII
|
>Sau96I >BclI
|| |
>HinfI >AccB7I|| >BstOI >HaeIII
| | || | |
| 610 | |620| 630 | 640 650
AGAGACTCCAGACATTTGGCCCTGGTTCCTTCTTGCCACTGTGAAACCC
TCTCTGAGGTCTGTAACCGGGACCAAGGGAAGAACCGGTGACACTTTGGG

>NdeII
|
>MboI
|
>Sau3AI
|
>DraI | >DdeI
| | |
>DdeI >Tru9I >DpnI
| || ||
660| 670 ||680| || 690 700
TCCAGAGGAACTGAGTGCTGTGGCTTTAAATGATCTCAGCACTGTCAGTG
AGGTCTCCTTGACTCACGACACCGAAATTTACTAGAGTCGTGACAGTCAC

>HaeIII
|
>Sau96I
||
>NciI |
|||
>MspI | |
|||
>HpaII |
|||
710 720 730 740|| 750
AAGCCGCTCTGCTCAAAGAGTTATCCTCTTGCTCCTGTGCCGGGGCCTCC
TTCGGCGAGACGAGTTTCTCAATAGGAGAACGAGGACACGGCCCCGGAGG

>AluI
|
>DdeI | >DdeI >BstXI
| | |
760| 770 |780 790 800
CCCTCCTCTCAGCTCCCCAAACCTTCTCAGCCACTGTGATGGGATAATT

GGGAGGAGAGTCGAGGGGTTTGGGAAGAGTCGGTGACACTACCCTATTAA

>Bsp1286I
|
>BanII
|
>SacI
|
>DdeI
||
>AluI
|||
>EcoICRI >BsrSI >DdeI
||| | |
810||| 820 830 |840 850
AGATGCGAGAGCTCAGCACAGATGATGCTCCAGTTGCTTAGCAACTAATG
TCTACGCTCTCGAGTCGTGTCTACTACGAGGTCAACGAATCGTTGATTAC

>Hsp92II
|
>StyI |
| |
>NcoI | >AluI
| | |
>Alw26I | >XbaI >BsrSI >Bst71I
|| | | ||
|| 860 870 880 890 |900
GTTTCCATGGAGACCGCAAAGCACAGCCTCTAGAGCAGCCAGTGAGCAGC
CAAAGGTACCTCTGGCGTTTCGTGTCGGAGATCTCGTCCGGTCACTCGTCCG

 >BstOI
 |
>Bst71I >MboII >BstXI
| | ||
910 920 930 940 || 950
TCGGCAGGGCAGGGAGAAGACGCAACTCTGCTCCTCCAGAAACCTGGGGA
AGCCGTCCCGTCCCTCTTCTGCGTTGAGACGAGGAGGTCTTTGGACCCCT

 >Tru9I
 |
960 970 980 990 1000
GGGTTAGGGTGGGGAAGGTGAGGGGGGATTGGAGGGAGATGGGAAGGCTT
CCCAATCCCACCCCTTCCACTCCCCCTAACCTCCCTCTACCCTTCCGAA

 >DpnI
 |
 >BglII
 ||
 >NdeII
 ||
>Sau96I >Sau3AI
| ||
>SmaI >DraI >MboI
| | ||
>AvaII >Tru9I >XhoII
| || ||
1010 1020 |1030 1040 || 1050

AAAGGCACAGGACCCTCATATCCCTTTAAAAATGTGACCAGAGATCTGCT
TTTCGTGTCTGGGAGTATAGGGAAATTTTACACTGGTCTCTAGACGA

>Alw26I >DdeI

1060 1070 | 1080 1090 | 1100
CTTTTTATCCCACTGTCTCACTTCTAATTTCAAATGGGGCTTAGGAGT
GAAAAATAGGGTGTGACAGAGTGAAGATTAAAGTTTACCCGAATCCTCA

>Sau96I

>SinI >MboII
>AvaII >PstI | >HinfI
1110 1120 | 1130 1140 | 1150
GGACCTATATGGTCTGCTCTGCAGTAAACCAATCCTCTTCCTGATTCCTC
CCTGGATATACCAGACGAGACGTCATTTGGTTAGGAGAAGGACTAAGGAG

>Alw26I >BstOI

1160 1170 1180 | 1190 1200
CTAAATCCTCACGTAAACACTGTGCTATGTGGAGGTTTGAGACTTGCCAG
GATTTAGGAGTGCATTTGTGACACGATACACCTCCAAACTCTGAACGGTC

>DpnI

>BglII
>MboI
>Sau3AI
>XhoII
>NdeII >MboII >MboII >BsrSI
1210 | 1220 1230 1240 1250
GAAGATCTCCTGACCCTGACACCTACCGTGTAGCCCTTCCGCACCGC
CTTCTAGAGGACTGGGACTGTGGGATGGCACATCGGGAGAAGCCGTGGCG

>DpnI

>XhoII

>DpnI >Sau3AI

>Sau3AI >BglII

>NdeII >NdeII

>MboI >MboI

1260 1270 1280 1290 |1300

CAGTTCTCCCTCGTGTGATCTTTCTGTGTGATAAAGTGAGGAGGAGATC
GTCAAGAGGGAGCACACACTAGAAAGACACACATTTCACTCCTCCTCTAG

>AluI
|
>StyI >BstXI >XmnI
| | |
1310 1320| 1330 1340 | 1350
TCATCTAAAGGGGACAAAAGCCAAGGAGCTGGAAAAACAGAAATCATTCA
AGTAGATTTCCCTGTTTTCCGGTTCCTCGACCTTTTTGTCTTTAGTAAGT

>DdeI >Bst71I
| |
1360 1370| 1380 1390 1400
GTTCTCCACCCAAAGGCAGCCTGAGAAAAACCTCTGTCCCACTTTGCATT
CAAGAGGTGGGTTTTCCGTCGGACTCTTTTTGGAGACAGGGTGAAACGTAA

>Hsp92II
|
|1410 1420 1430 1440 1450
TGCATGTGTGTGTGTATGAGTGTGTGTGTATGAGTGTGTGTGTGTA
ACGTACACACACACATACTCACACACACATACTCACACACACACAT

1460 1470 1480 1490 1500
TGAGTGTGTGTGTATGAGTGTGTGTGTATGAGTGTGTGTGTGGA
ACTCACACACACATACTCACACACACATACTCACACACACACCT

>Bsp1286I
|
>Alw44I
| |
>FokI >Hsp92II
|| | |
1510|| |1520 1530 1540 1550
TGAGTGTGTGTGCACATGTATGAGTGTGTCTGTGTATGTATGATTATA
ACTCACACACACGTGTACATACTCACACAGACACATACTACTAATAT

1560 1570 1580 1590 1600
TGTGTGTGTCTGTGTGTGTATGAGTATGTGTGTCTGTGTGTGTATG
ACACACACAGACACACACATACTCATAACACACAGACACACACATAC

>FokI
|
1610 1620 | 1630 |1640 1650
AGTATGTGTGTCTGTGTGTGGATGAGTATGTGTGTCTGTGTGTGGA
TCATACACACAGACACACACCTACTCATAACACACAGACACACACCT

>FokI >FokI >Hsp92II
| | |
1660| 1670 1680 1690 1700
TGAGTGTGTGTGGATGTGTATGAATATGTGAATGTGAGAGTGCATGTG
ACTCACACACACCTACACATACTTATACACTTACACTCTCACGTACAC

>AccI >Hsp92II
| |
1710 |1720 1730 |1740 1750
TGTGTGTCTGTGTATACGAGTATGTGTGTGCATGTGGATAAGTGTGTG
ACACACAGACACACATATGCTCATAACACACACGTACACCTATTCACACAC

1760 1770 1780 1790 1800

TGTGTGTGTATGAGTATGTGTGTGTCTGTGTATGAGTGTTTACACCAA
ACACACACATACTCATAACACACACAGACACATACTCACAAATGTGGTT

>HinfI >Alw26I

| |
1810 1820 |1830 1840 1850
TACAGCATCTGCCTAACTCCAAATGTGAGTCTGTGTCTCTGCGTTACCTGT
ATGTCGTAGACGATTGAGGTTTACACTCAGACACAGAGACGCAATGGACA

>AccB7I

|
>Hsp92II
||

1860 1870 1880 | 1890 1900
AAGCGTCATAGGAAGTTTTACGAAACCATGAGATGGCTCAACAGGTA
TTCCGAGTATCCTTCAAATGCTTTGGTACTCTACCGAGTTGTCCATTTT

>AvaII

|
>SmaI
|

>AluI >Hsp92II >Sau96I
| | |
| 1910 |1920 1930 1940 1950
GCTTTGGCCACCATGCCTGACATTTTGGTCCCAGAAGCCACATTATGAA
CGAGAACGGTGGTACGGACTGTAAAACAGGGGTCTTCGGTGAATACTT

1960 1970 1980 1990 2000
AGGAGAGAGCCAATGCCACAACCTTGCCCTCTGACCTCCACATAGACACT
TCCTCTCTCGGTTACGGGTGTTGAACGGGAGACTGGAGGTGTATCTGTGA

>DraI

>NdeI >Bsp1286I >Tru9I
| | |
2010 2020 2030 2040 || 2050

GTGGCACACATATGGGCACACATATAAAATAATAAATGCAACTTTAAATT
CACCGTGTGTATACCGTGTGTATATTTTATTATTTACGTTGAAATTTAA

>Tru9I >DdeI

| |
2060 | 2070 2080 2090 2100
TTTAAAAGAAATTAAGTTTCGGGTTTTACCTCAGACCCACTGTATCAGAA
AAACTTTCTTTAATTCAAAGCCCCAAAATGGAGTCTGGGTGACATAGTCTT

>DpnI

|
>MboI >Sau3AI
|| |

>Sau3AI >MboI
|| |

>AluI >BsrSI >NdeII >NdeII
| | || |
| 2110 | 2120 || 2130 2140 2150
GCTACATCTGAACCAGTTTCCTGATCGTCCATTGCACAGTAAATTTGGAG
CGATGTAGACTTGGTCAAAGGACTAGCAGGTAACGTGTCATTTAAACCTC

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                >MboII
                |
                >BstOI|
                ||
            >HpaII >BanII |
                | |||
>DpnI          >MspI >Bsp1286I|
|             | |||
| 2160 2170 2180 | 2190 | |2200
ATCGTCTGGTGAGAGTTCTCTGCTCCCAGCCGAGCCCCAGGTTCTG
TAGCAGACCACTCTCAAGGAGGACGAGGGTCGGCCTCGGGGGTCCAAGAC

```

```

                >EclHKI
                |
                >Tru9I  >Hsp92II
                ||      |
            2210 2220 2230 || 2240 2250
TTGTCTTCTACCCCTACACACATCGCAGACTTTAAGTCCACCCAGCATG
AACAGAAGATGGGGATGTGTGTAGCGTCTGAAATTCAGGTGGGTCGTAC

```

```

                >HaeIII
                |
                >Sau96I
                ||
            2260 2270 2280 || 2290 2300
GGGAAAGGACAGAACCCCATCAGCCCTTCAGTGGCCCCACTTTTCCAC
CCCTTTCTCTTGGGGTAGTCGGGAAGTCACCGGGGTGAAAAGGTG

```

```

>Sau96I
|
>AvaII
|
>SmaI          >BstOI
|             |
| 2310 2320 2330 2340 2350
TAGGACCTTTCTCTGGGGTTGGGGAAAATGGGTGGTTCTGGAGCAGACC
ATCTGGAAAGAGACCCCAACCCCTTTTACCCACCAAGGACCTCGTCTGG

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```

    >Sau96I
    |
    >AvaII
    |
    >SmaI
    |
    >BanII
    ||
>Bsp1286I
    ||
    >DdeI |
    || |
>EcoICRI|      >DdeI
    ||| |      |
    >AluI |      >AluI
    ||| |      ||
>DdeI |>SmaI >TaqI >Alw26I|
| ||| | | | ||
2360 ||| 2370 | 2380 | 2390 2400

```

CTGACGGTCTGAGCTCAGGTCCTATCGAGTTCACCTAGCTGAGACACCCA
GACTGCCAGACTCGAGTCCAGGATAGCTCAAGTGGATCGACTCTGTGGGT

>Hinfl >Alw26I
| |
>PstI >Bst71I >DdeI | >DdeI
| | | | |
2410 2420 2430 | 2440 2450
CACCCCTGCAGCCACTTTGCAGTGACAACCTGAGTCTCAGGTTCTGCATC
GTGGGGACGTCGGTCAAACGTCACGTGTTGGACTCAGAGTCCAAGACGTAG

>BamI
|
>HaeIII
|
>SphI >BstOI
| | |
>BbuI >Bsp1286I
| | | |
>Hsp92II >BanII |
| | | |
2460 2470 2480 | 2490 | 2500
TATAAAAAGCAGTGCCTTTCAGGAGGGCATGCAGAGCCCCCTGGCCAGCG
ATATTTTTTCGTACCGAAAGTCTCCCGTACGTCTCGGGGGACCGGTCCG

>Hsp92II >Hsp92II
| |
>HaeIII | >StyI |
| | | |
>XbaI >DdeI >Sau96I | >NcoI |
| | | | |
| 2510 2520 ||2530| 2540 | 2550
TCTAGAGGAGAGGTGACTGAGTGGGGCCATGTCACTCGTCCATGGCTGGA
AGATCTCTCTCCACTGACTCACCCCGGTACAGTGAGCAGGTACCGACCT

>BsrSI >BstOI >Bst71I
| | |
2560 2570 2580 2590 |2600
GAACCTCCATCAGTTTCTCCCAGTTAGCCTGGGGCAGGAGAGAACCAGAG
CTTGAGGTAGTCAAAGAGGGTCAATCGGACCCCGTCTCTCTTGGTCTC

>TaqI
|
>AluI >MboII >BstOI |
| | | | |
| 2610 |2620 2630 2640 | 2650
GAGCTGTGGCTGCTGATGGTGTCTTCCCCAACTGTTGTCCCAGGCATC
CTCGACACCGACGACTACCACAAAAGAGGGTTGACAACAGGGTCCGTAG

>DdeI
|
>MspA1I
||
2660 2670 2680 || 2690 2700
GAACCCAGAGCGACCTGCACACAGTCCACCGCTGAGCCACACCCAGCC
CTTGGGGTCTCGTGGACGTGTGTCAGGTGGCGACTCGGTGTGGGGTCCG

>BstOI
|
2710 2720 2730 2740 2750
CTCCACCTCCTCTGCTCCTGGTTACAGGATGTTTTGTCTTGAAGGGTTT
GAGGTGGAGGAGACGAGGACCAATGTCTAACAAAACAGAACTTCCAAA

>Tru9I
|
2760 2770 2780 2790 | 2800
TGTTGTTGCTACTTTTTGCTTTGTTTTTCTTTTTTCTTTTTTAACATAA
ACAACAACGATGAAAAACGAAACAAAAAAGAAAAAAGAAAAAATTGTATT

>BstOI
|
>AluI >BstOI >AccI |
| | | |
2810 2820 | 2830 2840 | 2850
GGTTTCTCTGTGTAGCCCTAGCTGTCTGGAACCTACTCTGTAGACCAGG
CCAAAGAGACACATCGGGATCGACAGGACCTTGAGTGAGACATCTGGTCC

>HaeIII >DdeI >AccB7I >Tru9I
| | | |
| 2860 | 2870 2880 2890 | 2900
CTGGCCTCAAACCTCAGAAATCCACCTTCTCCCAAGTGCTGGGATTAAG
GACCGGAGTTTGAGTCTTTAGGTGGAAGGAGGGTTCACGACCCTAATTC

>NciI
|
>HpaII >Bsu36I
| |
>BsaMI >MspI >DdeI
| | |
| 2910 2920 | 2930 2940 2950
GCATTGCGCCACCATCGCCCAGCCCCGGTCTTGTTCCTAAGGTTTTCTT
CGTAAGCGGTGGTAGCGGGTGGGGGCCAGAACAAAGGATTCCAAAAGGA

2960 2970 2980 2990 3000
GCTTACTCGCTACCCGTTGCACAACCGCTTGCTGTCCAAGTCTGTTTGT
CGAAATGAGCGATGGGCAACGTGTTGGCGAACGACAGGTTTCAGACAAAACA

>BsrSI
|
>Sau96I
||
>SinI
||
>AvaII >BstOI
|| |
3010 3020 3030 || 3040 3050
ATCTACTCCACCGCCCACTAGCCTTGCTGGACTGGACCTACGTTTACCTG
TAGATGAGGTGGCGGGTGATCGGAACGACCTGACCTGGATGCAAATGGAC

>AccB7I
|
>Alw26I |
| |
3060 3070 3080 | 3090 3100

GAAGCCTTCACTAACTTCCCTTGTCTCCACCTTCTGGAGAAATCTGAAGG
CTTCGGAAGTGATTGAAGGGAACAGAGGTGGAAGACCTCTTTAGACTTCC

 >HaeIII
 |
 >StuI
 |
 >Hinfl >Ddel >Ddel
 | | ||
3110 3120 3130 3140| 3150
CTCACACTGATACCCTCCGCTTCTCCCAGAGTCGCAGTTTCTTAGGCCTC
GAGTGTGACTATGGGAGGCGAAGAGGGTCTCAGCGTCAAAGAATCCGGAG

 >Ddel
 |
 >DpnI
 ||
 >MboI |
 |||
 >Sau3AI|
 |||
 >NdeII|
 |||
>Tru9I >XhoII|
| |||
| 3160 3170| 3180 3190 3200
AGTTAAATACCAGAATTGGATCTCAGGCTCTGCTATCCCCACCCTACCTA
TCAATTTATGGTCTTAACTAGAGTCGAGACGATAGGGGTGGGATGGAT

 >FokI >StyI
 | |
 | 3210 3220 3230 3240 3250
ACCAACCCCTCTCTCCCATCCTTACTAGCCAAAGCCCTTTCAACCCTT
TGGTTGGGGGAGGAGAGGGTAGGAATGATCGGTTTCGGGAAAGTTGGGAA

 >BstOI >Hsp92II
 | |
3260 3270 | 3280 3290 | 3300
GGGGCTTTTCTACACCTACACACCAGGGCAATTTTAGAACTCATGGCTC
CCCCGAAAAGGATGTGGATGTGTGGTCCCGTAAAAATCTTGAGTACCGAG

 >StyI
 |
>StyI >Alw26I >BstOI
| || |
| 3310 3320| 3330 3340 3350
TCCTAGGAAAACGCCTACCTCCTTGGAGACAGCACCTCTACAGTCCAGG
AGGATCCTTTTGGCGATGGAGGAACCTCTGTCTGGGAGATGTCAGGTCC

 >Ddel
 |
3360 3370 3380 3390 3400
AGGCAGACACTCAGACAGGAACCTCTGTCTTTCAGTCGCGGGAGTTCCA
TCCGTCTGTGAGTCTGTCTCTTGGAGACAGGAAGTCAGCGCCCTCAAGGT

 >SniI
 |

```

                >Sau96I
                |
        >AluI  >AluI  >AvaII
        |    |    |
        >PstI >Bst71I >FokI
        ||   |   |
        >Bst71I| >DdeI | >BstOI
        | ||  | |  ||
3410  3420 || 3430| 3440  3450
GAAAGAGCCATACTCCCCTGCAGCTAACTAAGCTGCCAGGACCCAGCCAG
CTTTCTCGGTATGAGGGGACGTCGATTGATTTCGACGGTCCTGGGTGCGTC

```

```

        >AvaI  >AluI
        |    |
        >HaeIII >HaeIII|
        ||   |   |
        >Sau96I| >Sau96I |
        |||  ||  |
3460  ||3470 || 3480  3490  3500
AGCATCCCCCTTTAGGCCCGAGGGCCAGCTCCCCAGCCTGAAAAACCTGT
TCGTAGGGGGAAATCCGGGCTCCCGGTTCGAGGGGTCGGACTTTTTGGACA

```

```

>Bsp1286I
|
>BanII
|
>ApaI
|
>HaeIII          >BglI
||              |
>Sau96I| >Bsu36I  >Bsp1286I      >BsrSI
|||  |  |  |  |
>Sau96I| >DdeI  >StyI |      >HinfI
|||  |  |  |  |  ||
|||3510 | 3520  3530 | 3540  3550
CTGGGGCCCTCCCTGAGGCTACAGTGCCCAAGGGGCAAGTTGGACTGGA
GACCCGGGGAGGGACTCCGATGTCACGGGTTCGCCGTTCAACCTGACCT

```

```

        >Bst71I          >Sau96I
        |              |
        >Alw26I      >AluI  >BstOI |
        ||         |  |  |
3560  3570  3580 |3590| 3600
TTCCAGCAGCCCCTCCCACTCCGAGACAAAATCAGCTACCCTGGGGCAG
AAGGGTCGTCGGGGAGGGTGAGGCTCTGTTTTAGTCGATGGGACCCCGTC

```

```

        >HaeIII
        |
        >Sau96I
        ||
        >BglI|| >BstOI
        |||  |
>HaeIII >SfiI |      >BstOI
|  |||  |  |
| 3610| |3620  3630  3640 |
GGCTCATTGGCCCCAGGAAACCCAGCCTGTCAGCACCTGTTCCAGG
CCGGAGTAACCGGGTCTTTGGGGTCGGACAGTCGTGGACAAGGTCC

```


F. Blast Result (mouse UPII with genome)

>[ref|NT_039473.1|MM9_39513_30](#) Mus musculus chromosome 9 genomic contig, strain C57BL/6J

Length = 13248754

Score = 6837 bits (3556), Expect = 0.0
Identities = 3631/3663 (99%), Gaps = 21/3663 (0%)
Strand = Plus / Minus

Query: 6 ggatctcgccctctttctgcatcctgtcctaataatctttcatatcttgtagacctc 65
|||||
Sbjct: 3917756 ggatctcgccctctttctgcatcctgtcctaataatctttcatatcttgtagacctc 3917697

Query: 66 agtttgagagaaacgaaccttctcatttcaagttg--aaaaaaaaagaggttcaag 122
|||||
Sbjct: 3917696 agtttgagagaaacgaaccttctcatttcaagttgaaaaaaaaagaggttcaag 3917637

Query: 123 tggctcactcaaagttacaagccaactcaccactacgagtacaatggccaccattagt 182
|||||
Sbjct: 3917636 tggctcactcaaagttacaagccaactcaccactacgagtacaatggccaccattagt 3917577

Query: 183 gtctggcatgccccaggagacaggcatgatatttctagatgactgggaggcagaggg 242
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Sbjct: 3917576 gtctggcatgccccaggagacaggcatgatatttctagatgactgggaggcagaggg 3917517

Query: 243 gtggcctagttaggtcagactgtggacagatcaggcagatgtgggttctgatccaattc 302
|||||
Sbjct: 3917516 gtggcctagttaggtcagactgtggacagatcaggcagatgtgggttctgatccaattc 3917457

Query: 303 ctgagcccgagaactactgtggttcaagaaggggacaaaaggactgcagtcccgaaca 362
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Sbjct: 3917456 ctgagcccgagaactactgtggttcaagaaggggacaaaaggactgcagtcccgaaca 3917397

Query: 363 ggaggtccactttgagagctgactgagcagaagaggaaagtgaagaactcaggggcaag 422
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Query: 423 agcttacctacttttacagcttgtgtcttcttactccagggcgtccctgttactc 482
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Sbjct: 3917336 agcttacctacttttacagcttgtgtcttcttactccagggcgtccctgttactc 3917277

Query: 483 agtaaatgtctgttggttgaggaacatatgtgtaaggaggaaggagagggacttgagg 542
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Sbjct: 3917276 agtaaatgtctgttggttgaggaacatatgtgtaaggaggaaggagagggacttgagg 3917217

Query: 543 gaggtaagactcaagaatcaatcaaggagaggacagcagagaagacagggttgggagag 602
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Sbjct: 3917216 gaggtaagactcaagaatcaatcaaggagaggacagcagagaagacagggttgggagag 3917157

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Sbjct: 3917156 agactccagacattggcccttggtccctcttgccactgtgaaacctccagaggaact 3917097

Query: 663 gactgctgtggctttaatgatctcagcactgtcagtggaagccgctctgctcaagagtt 722

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Query: 723 atcctctgtcctgtgcccggg-cctccccctctcagctcccaaaccttctcag 781

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Sbjct: 3917036 atcctctgtcctgtgcccgggectccccctctcagctcccaaaccttctcag 3916977

Query: 782 cactgtgatgggataattagatgagagctcagcacagatgatgctccagttgcttag 841

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Sbjct: 3916916 caactaatggtttccatggagaccgcaaagcacagcctctagagcagccagtgcagcct 3916857

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Sbjct: 3916856 cggcagggcagggagaagacgcaactctgctctccagaaacctggggagggttagggtg 3916797

Query: 962 gggaaagtgagggggattggagggagatgggaaggcttaaggcacaggacctcatat 1021

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Query: 1022 cccttataaaatgtgaccagagatctgctcttttatcccactgtctcacttctaatt 1081

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Sbjct: 3916736 cccttataaaatgtgaccagagatctgctcttttatcccactgtctcacttctaatt 3916677

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Sbjct: 3916376 acctctgccactttgcatttgcagtggtgtgtgtatgagtggtgtgtatgagt 3916317

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Sbjct: 3916316 gttgtgtgtatgagtggtgtgtatgagtggtgtgtatgagtggtgtgtgg 3916257

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Query: 1800 atacagcatctgtaactcacaatgtgagtggtctgtctctgcgttacctgaagcgtcat 1859
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Query: 1920 acatttgggtcccagaagccacattatgaaaggagagccaatgccacaactgccc 1979
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Sbjct: 3915356 acaccctgcagccactttgcagtgacaacctgagttcaggttctgcatataaaaag 3915297

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Sbjct: 3914337 agccatactcccctcagctaactaagctgccaggaccagcagacatcccccttag 3914278

Query: 3466 gcccgaggccagctccccagcctgaaaaacctgtctggggccctccctgaggctacag 3525
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Sbjct: 3914217 tgcccaaggggcaagttggactggattccagcagccctcccactccgagacaaaatca 3914158

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Query: 3646 agg 3648
|||
Sbjct: 3914097 agg 3914095

G. Vector map

<http://www.stratagene.com/vectors/selection/plasmid1.htm>