

## Mouse Uroplakin II Promoter

Tung-Tien Sun and Xue-Ru Wu, NYU School of Medicine  
(Updated July 2010)

### 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](mailto:sunt01@nyumc.org) or Dr. Xue-Ru Wu at [Xue-Ru.Wu@nyumc.org](mailto:Xue-Ru.Wu@nyumc.org)

### B. References:

Lin, J. H., Zhao, H., and Sun, T.-T. (1995). A tissue-specific promoter that can drive a foreign gene to express in the suprabasal urothelial cells of transgenic mice. *Proc Natl Acad Sci (USA)* 92, 679-683.

Kerr, D. E., Liang, F., Bondioli, K. R., Zhao, H., Kreibich, G., Wall, R. J., and Sun, T.-T. (1998). The bladder as a bioreactor: urothelium production and secretion of growth hormone into urine. *Nature Biotechnol* 16, 75-79.

- Zhang, Z. T., Pak, J., Shapiro, E., Sun, T.-T., and Wu, X. R. (1999). Urothelium-specific expression of an oncogene in transgenic mice induced the formation of carcinoma in situ and invasive transitional cell carcinoma. *Cancer Res* 59, 3512-3517.
- Zhang, Z. T., Pak, J., Huang, H. Y., Shapiro, E., Sun, T. T., Pellicer, A., and Wu, X. R. (2001). Role of Ha-ras activation in superficial papillary pathway of urothelial tumor formation. *Oncogene* 20, 1973-1980.
- Cheng, J., Huang, H., Zhang, Z. T., Shapiro, E., Pellicer, A., Sun, T. T., and Wu, X. R. (2002). Overexpression of epidermal growth factor receptor in urothelium elicits urothelial hyperplasia and promotes bladder tumor growth. *Cancer Res* 62, 4157-4163.
- Cheng, J., Huang, H., Pak, J., Shapiro, E., Sun, T. T., Cordon-Cardo, C., Waldman, F. M., and Wu, X.-R. (2003). Allelic loss of p53 gene is associated with maintenance, but not progression, of mouse carcinoma in situ of the bladder. *Cancer Res* 63, 179-185.
- Gao, J., Huang, H.Y., Pak, J., Cheng, J., Zhang, Z.T., Shapiro, E., Pellicer, A., Sun, T.T., and Wu, X.R. (2004). p53 deficiency provokes urothelial proliferation and synergizes with activated Ha-ras in promoting urothelial tumorigenesis. *Oncogene* 23, 687-696.
- Mo, L., Cheng, J., Lee, E.Y., Sun, T.T., and Wu, X.R. (2005). Gene deletion in urothelium by specific expression of Cre recombinase. *Am J Physiol Renal Physiol* 289, F562-568.
- Salz, W., Eisenberg, D., Plescia, J., Garlick, D.S., Weiss, R.M., Wu, X.R., Sun, T.T., and Altieri, D.C. (2005). A survivin gene signature predicts aggressive tumor behavior. *Cancer Res* 65, 3531-3534.
- Wu, Xue-Ru. "Urothelial tumorigenesis: a tale of divergent pathways". *Nature reviews. Cancer*. 2005; 5: 713
- Johnson, A.M., Conover, D.L., Huang, J., Messing, E.M., Ning, R., O'Connell, M.J., Rossi, M.A., Sun, T.T., Wood, R.W., Wu, X.R., *et al.* (2006). Early detection and measurement of urothelial tumors in mice. *Urology* 67, 1309-1314.
- Liu, W., Evanoff, D.P., Chen, X., and Luo, Y. (2007). Urinary bladder epithelium antigen induces CD8+ T cell tolerance, activation, and autoimmune response. *J Immunol* 178, 539-546.
- Liu, W., Deyoung, B.R., Chen, X., Evanoff, D.P., and Luo, Y. (2008). RDP58 inhibits T cell-mediated bladder inflammation in an autoimmune cystitis model. *J Autoimmun* 30, 257-265.

Wu, Xue-Ru. "Biology of urothelial tumorigenesis: insights from genetically engineered mice". *Cancer Metastasis Reviews*. 2009; 28: 281

Schnegelsberg, B., Sun, T.T., Cain, G., Bhattacharya, A., Nunn, P.A., Ford, A.P., Vizzard, M.A., and Cockayne, D.A. (2010). Overexpression of NGF in mouse urothelium leads to neuronal hyperinnervation, pelvic sensitivity, and changes in urinary bladder function. *Am J Physiol Regul Integr Comp Physiol* 298, R534-547.

Zhou, H., Liu, Y., He, F., Mo, L., Sun, T.T., and Wu, X.R. (2010). Temporally and Spatially Controllable Gene Expression and Knockout in Mouse Urothelium. *Am J Physiol Renal Physiol*.

### C. Sequence:

> NAME = up2 : TYPE = DNA

```
CTCGAGGATCTCGGCCCTCTTCTGCATCCTTGTCTCTAAATCATTTTCATATCTTGCTAGACCTCAGTTTGAGAGA
AACGAACCTTCTCATTTTCAAGTTGAAAAAAGAGGTTCAAAGTGGCTCACTCAAAGTTACAAGCCAACACTC
ACCACTACGAGTACAATGGCCACCATTAGTGTCTGGCATGCCCCAGGAGACAGGCATGCATATTATCTAGATGAC
TGGGAGGCAGAGGGTGGCCCTAGTGAGGTCAGACTGTGGACAGATCAGGCAGATGTGGGTTCTGATCCCAATTCCT
CAGGCCGCAGAACTACTGTGGTTCAAGAAGGGGACAAAAGGACTGCAGTCCCGAACAGGAGGTCCACTTTGAGAG
CTGACTGAGCAGAAGAGGAAAGTGAAGAACTTCAGGGGCAAGAGCTTACCCTACTTTTACAGCTTTGTGTCTTCT
TTACTCCAGGGCGTCCCTGGTACTCAGTAAATGTCTGTTGGCTTGAGGAACATATGTGTAAGGAGGAAGGAGAGG
GAACTTGAGGGAGTTAAGACTCAAGAATCAATCAAGGAGAGGACAGCAGAGAAGACAGGGTTTGGGAGAGAGACTC
CAGACATTTGGCCCTGGTTCCTTCTTGCCACTGTGAAACCTCCAGAGGAACTGAGTGTCTGGCTTTAAATGAT
CTCAGCACTGTCTGAGTGAAGCCGCTCTGCTCAAAGAGTTATCTCTGTCTCTGTGCCGGGCTCCCTCTCTCTC
AGCTCCCAACCCCTTCTCAGCCACTGTGATGGGATAAATAGATGCGAGAGCTCAGCACAGATGATGCTCCAGTTG
CTTAGCAACTAATGGTTTCCATGGAGACCCGAAAGCACAGCCTCTAGAGCAGCCAGTGAGCAGCTCGGCAGGGCAG
GGAGAAGACGCAACTCTGCTCCTCCAGAAACCTGGGGAGGGTTAGGGTGGGGAAGGTGAGGGGGGATTGGAGGGAG
ATGGGAAGGCTTAAAGGCACAGGACCCTCATATCCCTTTAAAAATGTGACCAGAGATCTGCTCTTTTATCCACA
CTGTCTCACTTCAATTTCAAATGGGGCTTAGGAGTGACCTATATGTTCTGCTCTGCAGTAAACCAATCCTCTTC
CTGATTCCTCTAAATCCTCAGTAAACACTGTGCTATGTGGAGGTTTGGAGACTTGGCAGGAAGATCTCCTGACCC
TGACACCTACCGTGTAGCCCTCTCCGCACCCGAGTTCTCCCTCGTGTGTGATCTTCTGTGTGTAAGTGAGG
AGGAGATCTCATCTAAAGGGGACAAAAGCCAAAGGAGCTGGAAAAACAGAAATCATTCAGTTCTCCACCCAAAGGCA
GCCTGAGAAAAACCTCTGTCCACTTTGCATTTGCATGTGTGTGTGTATGAGTGTGTGTGTATGAGTGTGTG
TGTGTATGAGTGTGTGTGTATGAGTGTGTGTGTATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TATGAGTGTGTGTGTATGATTATATGTGTGTGTCTGTGTGTGTGTATGAGTATGTGTGTCTGTGTGTGTG
TATGAGTATGTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TGAATATGTGAATGTGAGAGTGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TGTGTGTGTGTATGAGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TGAGTCTGTGTCTCTGCGTTACCTGTAAAGCGTCATAGGAAGTTTACGAAACCATGAGATGGCTCAACAGGTA
GCTCTTGGCCACATGCCTGACATTTTGGTCCCAAGCCACATTATGAAAGGAGAGCCAATGCCACAACCTTG
CCCTCTGACCTCCACATAGACACTGTGGCACACATATGGGCACACATATAAAATAATAAATGCAACTTTAAATTTT
TGAAGAATAAAGTTTCCGGTTTACCTCAGACCCACTGTATCAGAAGCTACATCTGAACCAGTTTCTGATCGT
CCATTGCACAGTAAATTTGGAGATCGTCTGGTGTGAGAGTTCTCTCTGCTCCAGCCGAGCCCCAGGTTCTGTTGT
CTTCTACCCCTACACACTCGCAGACTTTAAGTCCACCCAGCATGGGGGAAAGGACAGAACCCATCAGCCCTTC
AGTGGCCCACTTTTCCACTAGGACCTTTCTCTGGGGTTGGGAAAATGGGTGGTTCTGGAGCAGACCTGACG
GTCTGAGCTCAGGTCTATCGAGTTCACTAGCTGAGACACCCACACCCCTGCAGCCACTTTGCAAGTACAACCTG
AGTCTCAGGTTCTGCATCTATAAAAAGCAGTGCCTTTTCAAGGAGGCATGCAGAGCCCTGGCCAGCGTCTAGAGG
AGAGGTGACTGAGTGGGGCCATGCTACTCGTCCATGGCTGGAGAACCTCCATCAGTTTCTCCAGTTAGCCTGGGG
CAGGAGAGAACCAGAGGAGCTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
CGGACCTGCACACAGTCCACCGCTGAGCCACACCCAGCCCTCCACCTCTGCTCCTGGTTACAGGATTGTTTT
GTCTTGAAGGGTTTTGTGTGTGTACTTTTTGCTTTGTTTTTTCTTTTTTTTAAACATAAGGTTTCTCTGTG
TAGCCCTAGCTGTCTGGAACCTCACTCTGTAGACCAGGCTGGCCTCAAACCTCAGAAATCCACCTTCTCCCAAGTG
CTGGGATTAAGGCATTGCGCCACCATCGCCAGCCCGGCTTGTTCCTAAGGTTTTCTGCTTTACTCGCTAC
CCGTTGCACAACCGCTTGTCTCAAGTCTGTTGTATCTACTCCACCCCACTAGCCTTGTGTGACTGGACCTA
CGTTTACTGGAAACCTTCACTAACTTCCCTTGTCTCCACCTTCTGGAGAAATCTGAAGGCTCACACTGATACCT
CCGCTTCTCCAGAGTCGAGTTTCTTAGGCCTCAGTTAAATACCAGAATGGATCTCAGGCTCTGCTATCCCCAC
```

CCTACCTAACCAACCCCTCCTCTCCATCCTTACTAGCCAAAGCCCTTCAACCCTTGGGGCTTTTCCTACACCT  
ACACACCAGGGCAATTTAGAACTCATGGCTCTCCTAGGAAAACGCCTACCTCCTTGGAGACAGCACCCCTCTACAG  
TCCAGGAGGCAGACACTCAGACAGAGGAACTCTGTCTTCAGTCGCGGGAGTTCAGAAAGAGCCATACTCCCCTG  
CAGCTAACTAAGCTGCCAGGACCCAGCCAGAGCATCCCCCTTTAGGCCGAGGGCCAGCTCCCCAGCCTGAAAAAC  
CTGTCTGGGGCCCTCCCTGAGGCTACAGTGCCCAAGGGGCAAGTTGGACTGGATTCCCAGCAGCCCTCCCCTC  
CGAGACAAAATCAGCTACCCTGGGGCAGGGCCTCATTGGCCCCAGGAAACCCAGCCTGTCAGCACCTGTTCCAGG

**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  
TCAGGGCCTTGCTCCAGGTGAAACTCTCGACTGACTCGTCTTCTCCTT

>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

TGTGTGTGTATGAGTATGTGTGTGTCTGTGTATGAGTGTTCACACCAA  
ACACACACATACTCATAACACACACAGACACATACTCACAAATGTGGTT

>HinfI >Alw26I

| |  
1810 1820 |1830 1840 1850  
TACAGCATCTGCCTAACTCCAAATGTGAGTCTGTGTCTCTGCGTTACCTGT  
ATGTCGTAGACGATTGAGGTTTACTACTCAGACACAGAGACGCAATGGACA

>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  
CACCGTGTGTATACCGTGTGTATATTTATTATTTACGTTGAAATTTAA

>Tru9I >DdeI

| |  
2060 | 2070 2080 2090 2100  
TTTGAAGAAATTAAGTTTCGGGTTTTACCTCAGACCCACTGTATCAGAA  
AAACTTTCTTTAATTCAAAGCCCCAAAATGGAGTCTGGGTGACATAGTCTT

>DpnI

|  
>MboI >Sau3AI

|| |  
>Sau3AI >MboI

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

```

                >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

```

```

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

```

CTGACGGTCTGAGCTCAGGTCCTATCGAGTTCACCTAGCTGAGACACCCA  
GACTGCCAGACTCGAGTCCAGGATAGCTCAAGTGGATCGACTCTGTGGGT

>HinfI >Alw26I  
| |  
>PstI >Bst71I >DdeI | >DdeI  
| | | | |  
2410 2420 2430 | 2440 2450  
CACCCCTGCAGCCACTTTGCAGTGACAACCTGAGTCTCAGGTTCTGCATC  
GTGGGGACGTCGGTCAAACGTCACGTGTTGACTCAGAGTCCAAGACGTAG

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

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

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

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

>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 >DdeI >DdeI  
| | |  
3110 3120 3130 3140 | 3150  
CTCACACTGATACCCTCCGCTTCTCCCAGAGTCGCAGTTTCTTAGGCCTC  
GAGTGTGACTATGGGAGGCGAAGAGGGTCTCAGCGTCAAAGAATCCGGAG

>DdeI  
|  
>DpnI  
||  
>MboI |  
|||  
>Sau3AI|  
|||  
>NdeII|  
|||  
>Tru9I >XhoII|  
| |||  
| 3160 3170 | 3180 3190 3200  
AGTTAAATACCAGAATTGGATCTCAGGCTCTGCTATCCCCACCCTACCTA  
TCAATTTATGGTCTTAACCTAGAGTCCGAGACGATAGGGGTGGGATGGAT

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

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

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

>DdeI  
|  
3360 3370 3380 3390 3400  
AGGCAGACACTCAGACAGGAACCTCTGTCTTTCAGTCGCGGGAGTTCCA  
TCCGTCTGTGAGTCTGTCTCTTGGAGACAGGAAGTCAGCGCCCTCAAGGT

>SniI  
|

```

                >Sau96I
                |
        >AluI  >AluI  >AvaII
        |    |    |
        >PstI  >Bst71I >FokI
        ||    |    |
        >Bst71I| >DdeI | >BstOI
        | || | | ||
3410  3420 || 3430 | 3440  3450
GAAAGAGCCATACTCCCTGCAGCTAACTAAGCTGCCAGGACCCAGCCAG
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
GACCCCGGGGAGGGACTCCGATGTCACGGGTTCGCCGTTCAACCTGACCT

```

```

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

```

```

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

```



## F. Blast Result (mouse UPII with genome)

>[ref|NT\\_039473.1|Jm9\\_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 ggatctcgccctctttctgcatcctgtcctaataatctttcatatcttgctagacctc 65  
|||||  
Sbjct: 3917756 ggatctcgccctctttctgcatcctgtcctaataatctttcatatcttgctagacctc 3917697

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

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

Query: 183 gtctggcatgccccaggagacaggcatgatatttctagatgactgggaggcagaggg 242  
|||||  
Sbjct: 3917576 gtctggcatgccccaggagacaggcatgatatttctagatgactgggaggcagaggg 3917517

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

Query: 303 ctgagcccgagaactactgtggttcaagaaggggacaaaaggactgcagtcccgaaca 362  
|||||  
Sbjct: 3917456 ctgagcccgagaactactgtggttcaagaaggggacaaaaggactgcagtcccgaaca 3917397

Query: 363 ggaggtccactttgagagctgactgagcagaagaggaaagtgaagaactcaggggcaag 422  
|||||  
Sbjct: 3917396 ggaggtccactttgagagctgactgagcagaagaggaaagtgaagaactcaggggcaag 3917337

Query: 423 agcttacctacttttacagcttgtgtcttcttactccagggcgtccctgttactc 482  
|||||  
Sbjct: 3917336 agcttacctacttttacagcttgtgtcttcttactccagggcgtccctgttactc 3917277

Query: 483 agtaaatgtctgttgcttgaggaaacatgtgtaaggaggaaggagaggggaacttgagg 542  
|||||  
Sbjct: 3917276 agtaaatgtctgttgcttgaggaaacatgtgtaaggaggaaggagaggggaacttgagg 3917217

Query: 543 gaggtaagactcaagaatcaatcaaggagaggacagcagagaagacagggttgggagag 602  
|||||  
Sbjct: 3917216 gaggtaagactcaagaatcaatcaaggagaggacagcagagaagacagggttgggagag 3917157

Query: 603 agactccagacattggcctgttccttcttgccactgtgaaacctccagaggaact 662  
|||||

Sbjct: 3917156 agactccagacattggcccttggtccctcttgccactgtgaaacctccagaggaact 3917097

Query: 663 gactgctgtggctttaatgatctcagcactgtcagtggaagccgctctgctcaagagtt 722

|||||  
Sbjct: 3917096 gagtgctgtggctttaatgatctcagcactgtcagtggaagccgctctgctcaagagtt 3917037

Query: 723 atcctctgtcctgtgcccggg-cctccccctctcagctcccaaaccttctcag 781

|||||  
Sbjct: 3917036 atcctctgtcctgtgcccggggcctccccctctcagctcccaaaccttctcag 3916977

Query: 782 cactgtgatgggataattagatgcgagagctcagcacagatgatgctccagttgcttag 841

|||||  
Sbjct: 3916976 cactgtgatgggataattagatgcgagagctcagcacagatgatgctccagttgcttag 3916917

Query: 842 caactaatggtttccatggagaccgcaaagcacagcctctagagcagccagtgcagcagct 901

|||||  
Sbjct: 3916916 caactaatggtttccatggagaccgcaaagcacagcctctagagcagccagtgcagcagct 3916857

Query: 902 cggcagggcagggagaagacgcaactctgctctccagaaacctggggagggttagggtg 961

|||||  
Sbjct: 3916856 cggcagggcagggagaagacgcaactctgctctccagaaacctggggagggttagggtg 3916797

Query: 962 gggaaagtgagggggattggagggagatgggaaggcttaaggcacaggacctcatat 1021

|||||  
Sbjct: 3916796 gggaaagtgagggggattggagggagatgggaaggcttaaggcacaggacctcatat 3916737

Query: 1022 cccttataaaatgtgaccagagatctgctcttttatcccactgtctcacttctaatt 1081

|||||  
Sbjct: 3916736 cccttataaaatgtgaccagagatctgctcttttatcccactgtctcacttctaatt 3916677

Query: 1082 tcaaatggggcttaggagtgacctatattggtctgctctgcagtaaaccaatcctctcc 1141

|||||  
Sbjct: 3916676 tcaaatggggcttaggagtgacctatattggtctgctctgcagtaaaccaatcctctcc 3916617

Query: 1142 tgattcctcctaaatcctcagtaaacactgtgctatgtggaggttgagactgccagg 1201

|||||  
Sbjct: 3916616 tgattcctcctaaatcctcagtaaacactgtgctatgtggaggttgagactgccagg 3916557

Query: 1202 aagatctcctgaccctgacaccctaccgtgtagccctcttcgaccgccagttctcct 1261

|||||  
Sbjct: 3916556 aagatctcctgaccctgacaccctaccgtgtagccctcttcgaccgccagttctcct 3916497

Query: 1262 cgtgtgtgatctttctgtgtgtaaagtgaggaggagatctcatctaaagggacaaaagc 1321

|||||  
Sbjct: 3916496 cgtgtgtgatctttctgtgtgtaaagtgaggaggagatctcatctaaagggacaaaagc 3916437

Query: 1322 caaggagctggaaaaacagaaatca-ttc-agtctccaccaaaaggcagcctgagaaaa 1379

|||||  
Sbjct: 3916436 caaggagctggaaaaacagaaatcagttccagttctccaccaaaaggcagcctgagaaaa 3916377

Query: 1380 acctctgtcccatttgcatgtgtgtgtgtatgagtggtgtgtgtatgagt 1439

|||||  
Sbjct: 3916376 acctctgccactttgcatttgcattgtgtgtgtatgagtggtgtgtatgagt 3916317

Query: 1440 gtgtgtgtatgagtggtgtgtatgagtggtgtgtatgagtggtgtgtgg 1499  
|||||  
Sbjct: 3916316 gtgtgtgtatgagtggtgtgtatgagtggtgtgtatgagtggtgtgtgg 3916257

Query: 1500 atgagtggtgtgcacatgtatgagtggtctgtgtatgattatgtgtgt 1559  
|||||  
Sbjct: 3916256 atgagtggtgtgcacatgtatgagtggtctgtgtatgattatgtgtgt 3916197

Query: 1560 ctgtgtgtgtatgagtggtgtctgtgtgtatgagtggtgtctgtgt 1619  
|||||  
Sbjct: 3916196 ctgtgtgtgtatgagtggtgtctgtgtgtatgagtggtgtctgtgt 3916137

Query: 1620 gtggatgagtggtgtctgtgtgtggatgagtggtgtggatgtatgaat 1679  
|||||  
Sbjct: 3916136 gtggatgagtggtgtctgtgtgtggatgagtggtgtggatgtatgaat 3916077

Query: 1680 gtgaatgtgagtgcatgtgtgtctgtgtatatacagtggtgtcatgtgg 1739  
|||||  
Sbjct: 3916076 gtgaatgtgagtgcatgtgtgtctgtgtatatacagtggtgtcatgtgg 3916017

Query: 1740 ataagtgtgtgtgtgtatgagtggtgtgtctgtgtatgagtggttacca 1799  
|||||  
Sbjct: 3916016 ataagtgtgtgtgtgtatgagtggtgtgtctgtgtatgagtggttacca 3915957

Query: 1800 atacagcatctgtaactcacaatgtgagtggtctgtctctgcgttacctgaagcgtcat 1859  
|||||  
Sbjct: 3915956 atacagcatctgtaactcacaatgtgagtggtctgtctctgcgttacctgaagcgtcat 3915897

Query: 1860 aggaagtttacgaaacatgagatggctcaacaggtaaaagctctgccaccatgcctg 1919  
|||||  
Sbjct: 3915896 aggaagtttacgaaacatgagatggctcaacaggtaaaagctctgccaccatgcctg 3915837

Query: 1920 acatttgggtcccagaagccacattatgaaaggagagccaatgccacaactgccc 1979  
|||||  
Sbjct: 3915836 acatttgggtcccagaagccacattatgaaaggagagccaatgccacaactgccc 3915777

Query: 1980 tctgacctccatagacactgtggcacacatatgggcacacataaaataataatgc 2039  
|||||  
Sbjct: 3915776 tctgacctccatagacactgtggcacacatatgggcacacataaaataataatgc 3915717

Query: 2040 aactttaaattttgaaagaattaagtttcgggtttacctcagaccctgtatcaga 2099  
|||||  
Sbjct: 3915716 aactttaaattttgaaagaattaagtttcgggtttacctcagaccctgtatcaga 3915657

Query: 2100 agctacatctgaaccagtttctgatcgtccattgcacagtaatttgagatcgtctgg 2159  
|||||  
Sbjct: 3915656 agctacatctgaaccagtttctgatcgtccattgcacagtaatttgagatcgtctgg 3915597

Query: 2160 tgagagttcctcctgccagccggagccccaggttctgttcttctaccctaca 2219  
|||||  
Sbjct: 3915596 tgagagttcctcctgccagccggagccccaggttctgttcttctaccctaca 3915537

Query: 2220 cacatcgacagcttaagtccaccagcatgggggaaaggacagaacccatcagccctt 2279  
|||||  
Sbjct: 3915536 cacattcgacagcttaagtccaccagcatgggggaaaggacagaacccatcagccctt 3915477

Query: 2280 cagtggccccacttttccactaggaccttctctggggtggggaaaatgggtgttcc 2339  
|||||  
Sbjct: 3915476 cagtggccccacttttccactaggaccttctctggggtggggaaaatgggtgttcc 3915417

Query: 2340 tggagcagacctgacggtctgagctcaggtcctatcgagttcacctagctgagacacc 2399  
|||||  
Sbjct: 3915416 tggagcagacctgacggtctgagctcaggtcctatcgagttcacctagctgagacacc 3915357

Query: 2400 acaccctgcagccactttgcagtgacaacctgagttcaggttctgcatataaaaag 2459  
|||||  
Sbjct: 3915356 acaccctgcagccactttgcagtgacaacctgagttcaggttctgcatataaaaag 3915297

Query: 2460 cagtgccttcaggaggcatgcagagccccctggccagcgtctagaggagaggtgactg 2519  
|||||  
Sbjct: 3915296 cagtgccttcaggaggcatgcagagccccctggccagcgtctagaggagaggtgactg 3915237

Query: 2520 agtggggccatgtcactcgtccatggctggagaacctccatcagtttctccagttagcc 2579  
|||||  
Sbjct: 3915236 agtggggccatgtcactcgtccatggctggagaacctccatcagtt-ctccagttagcc 3915178

Query: 2580 tggggcaggagagaaccagaggagctgtggctgctgatggttttctcccaactgttg 2639  
|||||  
Sbjct: 3915177 tggggcaggagagaaccagaggagctgtggctgctgatggttttctcccaactgttg 3915118

Query: 2640 tccaggcatgaacccagagcgcacctgcacacagtcaccctgagccacccccagc 2699  
|||||  
Sbjct: 3915117 tccaggcatgaacccagagcgcacctgcacacagtcaccctgagccacccccagc 3915058

Query: 2700 cctccacctctgctcctggttacaggattgttt-gtcttgaagggtttgtgttg 2758  
|||||  
Sbjct: 3915057 cctccacctctgctcctggttacaggattgtttgtcttgaagggtttgtgttg 3914998

Query: 2759 ctacttttgcttgtttt-t----cttttctttt-----aacataaggtt 2805  
|||||  
Sbjct: 3914997 ctacttttgcttgttttgttttcttttttttttttaacataaggtt 3914938

Query: 2806 ctctgttagcctagctgctcctggaactcactctgtagaccaggctggcctcaaactca 2865  
|||||  
Sbjct: 3914937 ctctgttagcctagctgctcctggaactcactctgtagaccaggctggcctcaaactca 3914878

Query: 2866 gaaatccacctctcccaagtctgggattaaggcattgccaccatgccagcccc 2925  
|||||  
Sbjct: 3914877 gaaatccacctctcccaagtctgggattaaggcattgccaccatgccagcccc 3914818

Query: 2926 cggtctgtttcctaaggttttctgctttactcgtaccggtgcacaaccgcttgctg 2985  
|||||  
Sbjct: 3914817 tggctgtttcctaaggttttctgctttactcgtaccggtgcacaaccgcttgctg 3914758

Query: 2986 tccaagctgtttgtatctactccaccgccactagccttgctggactggacactgctt 3045  
|||||  
Sbjct: 3914757 tccaagctgtttgtatctactccactgccactagccttgctggactggacactgctt 3914698

Query: 3046 acctggaagccttactaactccctgtctccaccttggagaaatctgaaggctcac 3105  
|||||  
Sbjct: 3914697 acctggaagccttactaactccctgtctccaccttggagaaatctgaaggctcac 3914638

Query: 3106 actgataccctcgccttctccagagtcgcagtttcttaggcctcagttaaataccagaa 3165  
|||||  
Sbjct: 3914637 actgataccctcgccttctccagagtcgcagtttcttaggcctcagttaaataccagaa 3914578

Query: 3166 ttggatctcaggctctgctatccccaccctactaaccaaccctcctctccatcctt 3225  
|||||  
Sbjct: 3914577 ttggatctcaggctctgctatccccaccctactaaccaaccctcctctccatcctt 3914518

Query: 3226 actagccaaagcccttcaaccctggggctttctcacctacacaccagggaattt 3285  
|||||  
Sbjct: 3914517 actagccaaagcccttcaaccctggggctttctcacctacacaccagggaattt 3914458

Query: 3286 tagaactcatggctctcctaggaaaacgctactccttggagacagcacctctacagt 3345  
|||||  
Sbjct: 3914457 tagaactcatggctctcctaggaaaacgctactccttggagacagcacctctacagt 3914398

Query: 3346 ccaggaggcagacactcagacagaggaactctgtcctcagtcgaggagttccagaaag 3405  
|||||  
Sbjct: 3914397 ccaggaggcagacactcagacagaggaactctgtcctcagtcgaggagttccagaaag 3914338

Query: 3406 agccatactcccctcagctactaactagctgccaggaccagccagagcatcccccttag 3465  
|||||  
Sbjct: 3914337 agccatactcccctcagctactaactagctgccaggaccagccagagcatcccccttag 3914278

Query: 3466 gcccgaggccagctccccagcctgaaaaacctgtctggggccctccctgaggctacag 3525  
|||||  
Sbjct: 3914277 gcccgaggccagctccccagcctgaaaaacctgtctggggccctccctgaggctacag 3914218

Query: 3526 tgcccaaggggcaagttggactggattccagcagcccctcccactccgagacaaaatca 3585  
|||||  
Sbjct: 3914217 tgcccaaggggcaagttggactggattccagcagcccctcccactccgagacaaaatca 3914158

Query: 3586 gctaccctggggcaggcctcattggccccaggaaacccagcctgtcagcacctgttc 3645  
|||||  
Sbjct: 3914157 gctaccctggggcaggcctcattggccccaggaaacccagcctgtcagcacctgttc 3914098

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

## **G. Vector map**

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