

## Human *LMP7-TAP2* sequence:

LMP7 exon 5 -->

1 CATGGGACTCGGCTCTCAGGAAATATGTTCTCCACGGGTAGTGGGAACACTTATGCCTAC 112800

61 GGGGTCATGGACAGTGGCTATCGGCCAATCTTAGCCCTGAAGAGGCCTATGACCTTGGC 112860

121 CGCAGGGCTATTGCTTATGCCACTCACAGAGACAGCTATTCTGGAGGCGTTGTCAATAGT 112920  
-----T0.1F----->

start of region screened for polymorphism  
----->

181 AAGAGACCAATGCTCCCACCACCATGCCTGGGAGGAGTCGGCGGGTGGTGGGGGGGTGA 112980  
-----T0.2F----->  
-----T0.2F2----->

5' truncated Alu element -->

241 TTTAAGATTGAGAAACCAGCCTGGCCAACATGGCGAAACCCCGTCTCTACTAAACTACA 113040  
T  
T

301 AAAATTAGCCGGACGTGGTGACGGGTGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCA 113100

361 GGAGAATCACTTGAACCTGGGAGGTGGAGCTTGCAGTGAGCCAAGATGGCGCCACTGCAT 113160  
T2C/T  
T

421 TCCAGTCTGGGCCACAGAGTGAGACTCCTTCTCAAAGAAAAAAAAAGAAAAATGATTGAGA 113220

481 GACTCAAAGGAGGGAGAGTAGTAGGGAGGAAATTTTCAGAGTCAGAAGAAGGGCATTAAA 113280

541 GGCCCAGTCATATGGTTTTTAAGCTTGCGCATGTGTCTTGTGTGCTGCCTTCAACATAACAT 113340

601 CAGTGACAGGAACTTGCTGAGGTGAAAGGTGACTCCATGTTCTTTTCTCATTTGTCCACA 113400

LMP7 exon 6 -->

661 GTGTACCACATGAAGGAAGATGGTTGGGTGAAAGTAGAAAGTACAGATGTCAGTGACCTG 113460

ter

721 CTGCACCAGTACCGGGAAGCCAATCAATAATGGTGGTGGTGGCAGCTGGGCAGGTCTCCT 113520

781 CTGGGAGGTCTTGGCCGACTCAGGGACCTAAGCCACGTTAAGTCCAAGGAGAAGAAGAGG 113580

841 CCTAGCCTGAGCCAAAGAGAGAGTACGGGCTCAGCAGCCAGAGGAGGCCGGTGAAGTGCA 113640

901 TCTTCTGCGTGTCTCTATTTGAACAAGCATTTCCTCCAGGAAGTTTCTGGGTGCCCA 113700

polyA signal

961 CTAAGTAGAATAAAGAAAAACGGTTATAAATACCTCTGTCTTGTGGCTGAATGGGGTTGG 113760  
<-----T1.0R----->

1021 GCCTGTGGTTGTTGGGTGGGGCAGAAAGTAAAGAGACGCTTTTTCTGGAGAAGGGGCTCA 113820

1081 GACCCCTATCTAAGAAATGTGGCCTCACCACATAGTTCTTCTGGGGTTTCTTCCACAC 113880

1141 TCATCTCTCAAGACCTCAGGAAGGCTGCTCATTGCTGTCCATGGACACTTGTTTGCAAT 113940

1201 TTCACATAGGTTAGGGTCCTTTCCATAGAGAGGCACCTGGGGACTCCTGTGTGTCCATT 114000  
T3T/C  
C

1261 GTTAATGGTTTGGAGAACAGGGAGTAGGGCACCTAGGATAACTGTTTTTACTTTATAGA 114060

1321 GTAGGATGAAAAAGCTTCCACTTCACTTTAATATGGTAATCATATAAACACCATAACCATT 114120

1381 TATCCCAAATAACACTTTGGAGATATTGGATATTGAATATAAAGACAGACATTAAGGGTC 114180

1441 TAATTTTCATGATGTGTCATGCTGAATTGCAAGATGGCAGGACTATAATTTTAGAGGAAGA 114240  
----- T1.4F --- >

1501 AGAGATCAGGAGGACTCCCCTAAGTGAGGAGTGTGGGGAAAATGTAAAAGATCCAGGTTA 114300  
<-----T1.5R----->

1561 GAAGAAAAGAGACACACATCATGAGATTTTCGGAATCATGCTGGAACATGGACCATGTCA 114360

1621 CTTTCCAGAAAATAAAGGAAACAAATGCTTAAAAGTAGGAGCATGAGCTTGAGCATGGAG 114420

1681 CTTTTTTTCATTAGAGAGAGATTCTTAAAAATGCCAGAATGAATAGAGTTGTAAAACCTTTAG 114480

1741 CGAGCCCCTACTTAAAAATCCCTCCTCCCCACCACCCTATTTTAAACTTTAAGTACTCC 114540  
-----

1801 TTGGTAGTCACACAGGTAACATTTCAAATGGTGATCTGGAATCCAAGCGACCCCTCCTT 114600  
--T1.8F---->

1861 TGGGGAATTTGTTTGTGTTGTTGTTTGTAGTTTGGGAGGTGGTTTCAATCTGAAGAGTCC 114660

1921 TTTCTGGAATAAACGAATCTTTCTGTTGCATAGGAAGGCTCTGGGTCTCAGGAAGGATATTT 114720  
T4T/A  
A  
----- T4FT/A ----->

1981 AAAAAACCTAATTACTGTTCTAAACAGTGTTAAAATAGAACAAGAACCAAAGCTCAGTACG 114780  
T5G/A T6T/C T7G/C  
A C C  
---T7FG/C-----Y----->  
-----T6FT/C----->

2041 GGGCATTTCCTCATAGGCTGAAGGTGCGCCCAACATAATTTGGAGTACAGACTCAGAGG 114840  
----- T2.0F ----->

2101 CACCTGAACACGCGCCAGCTCAAGGTGCTCCGGCTGAGAAGGACGGATGAAGATGAACGC 114900

2161 TCAGGGCCTACTAAATTCAAAGTCTGTACGTGAAAATCCCCTTTGGCCTGGTGAGATTGG 114960

2221 TTGGAACCTTCTATTTAGGAGAGCCCGGCTCGCTCGCTAAAACCTGGAGCTTGCATGGAA 115020

2281 GAGGGCACTTTTTTTTTTTTTAGACGAAGTCTCACTCTTGTCGCCAGGCTGGAGTGCAAT 115080

2341 GACCCGATCTCGGCTCACTGAAACCTCTGCCTCCTGAGTTCAAGCGATTCCCCTGCCTCA 115140

2401 GCCTCCCGAGTAGCTGGGATTACAGGCGTCCGCCACCACGCCCTGGCTAATTTTTGTATT 115200

2461 TTTAGTAGAGACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACCCCTGACCTCAGG 115260  
--

2521 CGATCCGCCCCGCTCGCCTCCCAAAGTGCTGTGATTACAGGCGTGAGCCACCGCGCCGG 115320  
T8G/A <--- full length Alu element  
A  
---T8FG/A----->

2581 ACCAGAAAGAAGGCACCTTCTTAATAGTAGGCTCAGAGCTTGAAGTAGTAACTTTGAGAAA 115380

2641 ATTCAGTGATTCTCCAATTACAAAGCATTCTCCAATTACAAAGCAAGGACAACAGATAAA 115440  
T9A/C  
C

2701 GTTGCCCTTGAGACAACGTATTTTACTTAATGATAAAGAAACATTTTTGCAGTTTTATA 115500  
-----T2.7F----->

2761 TCCCAGAGTAACCGCCACTAAAGGCGAGTGAGACTCATTGCAGGCCCTGTACAGTGCGAAC 115560  
<-----T2.8R----->

2821 CAGAGTTCGGGCTCCAGTTCCGCTGTCTGCGGGTCTCGCGCGCCCCCTCCCGCGGCCCA 115620

2881 GCCCAGAATGAAGGCTTGGCTGGGGAAGCGAAAGCGAAAGCTGCCCGAGCCCTGACGCC 115680  
T10C/T T11G/A  
T A  
---T10/11FCG/TA--->

2941 CGCCCTGGCCGAGCGTAGCTGGCGGACCAGAGCCGGTAGCGAGGTTGGGAGAGACGGAGC 115740  
----- T2.9F ----->



4381 TCTTATTATAGGAACAAGTTATGAGTGAAGGTAGTACAAAAGGAATTTAAGTCTCAGATG 117180  
T17G/A  
G  
-----T17FA/G----->  
<--

4441 GAATGTCTCTCAGTTGTCTCTCAACATTCCTAGGTCCATGAAATTCATTTCTTTCTGCC 117240  
----T17RA/G-----

4501 TCCTACCTCCTACCCCTAAGTCTGTCTCCAAAGTATCTCTCCAGGGTCACTCTCTCAGGA 117300  
T18T/C  
C

4561 TGGGTATGCTTCTCCCTCTCACTCTTCTTTCCAGCTCATCTTGCTAATCCCTGAAGATC 117360  
T19C/T T20TAA/CAG  
T C G

4621 TTACTCTGAGGCTTATCACCTTTCTTTCCAGAATCATTACTCTTTTCCCTTCACTTGCTT 117420  
-----T21FC/T-

4681 TCCTTTCTCTTTCTAGACATACTCAAACAAACAACTGTTTGATAAGGCTGGGACTGGGA 117480  
T21C/T  
T  
----->  
<-----T21RC/T-----

4741 TGAGGTGAGCGAGGCACCTGGGGTGCAAAGTTTAAGGAGGTGTGCACTCACCTTACCCAA 117540  
T22A/G  
G

4801 ATCCCAGCCGGCCTGATTGTCTCTATTTTTATGGTCATACTTAATTTAGAGTACCCTCGA 117600  
Approximate centre of male recombination hotspot

4861 AAACCATTTTATTGTGCCTTCATTCATCCTGGCTGCTTTCTGCTGAAACTACAGTCTGTG 117660  
T23C/T  
T  
----C---  
-----T23FC/T----->  
<----

4921 CACTGCATAACGATGTTTAGGTCAATGATGGGCCACATATAAGATGGTGGACCCACAAGA 117720  
T24T/A  
--T5.0F2----> A -----T5.0F----->  
----T23RC/T--W---

4981 TTATAATACCATATTTTTACTGTACCTTTTTCTATGTTTAGATACACAAATACTTACTTCT 117780

5041 GTGTTACAGTCGCCACAGTGTAGGTGCAGTCTATGTTGTACAGATTTGTAGCCTAGG 117840  
T25C/T  
T  
<-----T5.1R----->  
-----T25FC/T----->  
<-----T25RC/T----->

5101 AGCAATAGGCTAAACTACATGGCCTAGGTGTGCAGTAGGCTATGACATCTAGGTTTGTGT 117900  
T26T/A  
A

5161 AAGTACACTCTATGATGTTTCATACAACGATGAAACCATCTAACGACACATTTCTCAGAAC 117960  
T27G/A T28C/T  
A T

5221 ACATCCCTGTCATTAAGTACAAACCCTCATTATATCATGTCTGACTATTCCAAACGCCT 118020  
T29ATT/CTC  
C C  
|ancestral state ambiguous

5281 CTTCAATATGGTAACTAAATTTGTATTAGAAACATATATTTTGTAAAATACATGCTTTTA 118080

5341 TGCTTTATATTTTTTCTCTAAGTGTACTGTAGCATGTAGTTGGTCTAAGAGGGATTTT 118140

Approximate 3' limit of male recombination hotspot

5401 CCAACTCGAAGGATGACAGATGGGAATCACATGACTCTGGGGCTCCAGAGAATTGTGGGG 118200  
T30C/A  
A

5461 GCAGGGAATTTATTATTGCAGTTC~~C~~CATGATGAAGTATCTATGATGACAGAGAAGGGCTT 118260  
-----T5.5F----->

5521 TGGGTATGGGGCAGGAAGGAGACCAAGGCGGAGGAGACGCACAGAGGGACAAGCCTGAGG 118320  
<-----T5.6R-----

5581 GACGCTGGGACAGAAGCAAGCACTGGGATACTTGT~~T~~TTTCACAATATCTTTTCCCTTCTAT 118380  
-----T31FT/C-----

5641 TGTAGT~~T~~TTCTATTTGTGTCTAGTACAGAGTGCCTCCATAAATACTTGTAAATTTGTACA 118440  
T31T/C  
C <-----T5.7R-----  
----->  
<-----T31RT/C-----

5701 TGTATGATTTTGTCTCACATCTAGCTCACCATGTCTCCTCTTTCTTCTTCTCCTCTGTGT 118500

5761 ATTCCTTACCTCTTCTCTCTCTGTGTGTCTGTCTCTCATTCTTTCTCTTTTGCCCCTCC 118560

5821 TGGCATGCTTTCCCTGACTTTGCGCTTCTCTGCACTCCTGGCTTGCTCCTCTGTTTCAC 118620

5881 CCGCTGGCTTGCTCCTTCTCTGCATCTCCCTCCCTCTTATTCTCCTACCCACAGCTCA 118680  
TAP2 exon 3 -->

5941 CTGTCTGCAGGCTGCCGAGGAGGCTGCTTCACCTACACCATGTCTCGAATCAACTTGCGG 118740  
-----T6.0F-----

6001 ATCCGGGAGCAGCTTTTCTCCTCCCTGCTGCGCCAGGACCTCGGTTTCTTCCAGGAGACT 118800  
---->

6061 AAGACAGGTGGGGCCTGG~~A~~GTCCAGGTCTGAGATTCCCATGGACATCCCTTGCCCCTCAG 118860  
T32A/T  
T

6121 TGACCTTCCACCCACAGCCTCTCCTCCTGCCTTACCCGTATGCCAGGACCTGGGGATGC 118920

6181 TTTTCTCTTGT~~T~~TGGGACAGGGTGGAGAAGCAGCCTCCACTGTCCCTCTGCAAGTGAAGG 118980

6241 AGGATGTTTACAGAGGAGGGGGCTGTGTCTAGAGGGAACGGTCAGGAGGGAGTTTCTGGGGC 119040

6301 CCTGCAGTACACATGGTTTCCCTTTTCCCTCACCTGCTCTGTCCCTCTTAGGGGAGCTGAA 119100  
TAP2 exon 4 -->

6361 CTCACGGCTGAGCTCGGATACCACCCTGATGAGTAACTGGCTTCCCTTTAAATGCCAATGT 119160

6421 GCTCTTGCGAAGCCTGGTGAAAGTGGTGGGGCTGTATGGCTTCATGCTCAGCATATCGCC 119220

6481 TCGACTCACCTCCTTTCTCTGCTGCACATGCCCTTACAATAGCAGCGGAGAAGGTGTA 119280  
-----T6.5F----->

6541 CAACACCCGCCATCAGGTGAGCGTGCATGTAAGGGAACCCCAAGGGAGAATAAACTGA 119340  
<-----T6.6R-----

6601 CAGGTGAGGAGGCTTCCACATTTGTGGCTAGAGGATCCCTTAGAGAGAGATGTTCTCTTC 119400

6661 TCAGCCATTAGGGGAGAAGGTATATTGTAGTATATACTACATTTTGT~~T~~TGTCCAGCCATC 119460  
T33A/G T34G/A  
G A

6721 CAACAATGGATATTTGACTTTCAGAAGATTCATGATTCTCCAGAACGTAA~~A~~CAAAATGT 119520  
T35+/-  
---

6781 AAAGTGTATGTGAAGGTATGGGGAGGGAATAGGAAGGGGAGATGATAGGCGATGATAAC 119580

6841 TTTTCATTAGCTTCTCAAAGGAGTCTGTACATCCCCGCCCCACTGCGAAGATTA~~A~~AAA 119640

6901 TGGTTTCTTAGAGGCTTTTAGGCAGGGAGATTTTCCCTTTAAATCAGCAGAAGAAGTCT 119700

6961 GGATGCAGCATAGGGAAAGGAGGCGTCATCAGGAAGTCCTAAGTCTGAATGTCAGCTCCA 119760  
<----- T6.9R -----

7021 CCTTCTCTTTTCTCTTATATTGTGGTAAAACATACATAACATAAAATTTACCATTTCAA 119820

7081 CCATTTGAAGTGTACAGTTCAGTGACATTTAGGAAACCCACATTGTTATTGGGTAGCCAT 119880  
T36aG/T T36bG/A  
T A  
<---

7141 CATCACCATCCATCTCCAGAACTTTTTTCATCTTCCTAAAATGAAACTCTGTACCCACTA 119940  
 ---T36bRG/A-----

7201 AATAGTAACTGCCTACTACCCCAACCCCTGGCCGCTGGCAACCTCCATTGTACCTTCTG 120000  
<----- T7.2R -----  
<----- T7.2R2 -----

7261 TCTCCATGAATTGTGATGACTCCCGGTGCGGTACGTAAGTGGAAACCATAACAGTATTTGTC 120060  
T37C/A  
A <----- T7.3R -----  
<-----T37RC/A -----

7321 TTTTTGTGACTGGCATAATTTTACTTAGCGTAATGTCTTCAGGCCTCATCCATATTGTAGC 120120  
-----T7.4F----->

7381 ATGTGTTAGAATTTCCCTCCCTTTTAAGGCTGAATAATATTCTGTTGTGTGCATATATCAC 120180

7441 ATTTTGATTATCCATTCATCTGTCAATGGACATTTGCGTTGTTTCCACCTTTTGGCTGTT 120240  
<-----T7.5R-----
T38G/A  
A

7501 GTGAATTATGCTGCTGTGGACATGAGTGTACACCTGTTTGAACCCCTGCTTTTGGTTCTT 120300  
<-----T7.5R2-----

7561 TTGGGTATATACTTAGAAGTGGAGCTGCTGGATCATATGGCAATTCTATTTAACAATTTT 120360

7621 TGAGGAACCATGTATTAGTCCATTTTTACGCTGCTGATAAAGACATACCCAAGATTGGGC 120420

7681 AATTTACAAAAGAAAAGAGGTTTATTGGACTTACAGTTCCATGTGGCTGGGAAGACCTCAA 120480  
T39-/+  
|+C  
<-

7741 ATCATGGCGGAAGGTGAAAAGACACATTTCCACATGGCAGCAGACAAGAGAAAAGACAGCTT 120540  
--- T39R-/+ -----

7801 GTGCAGGGGAATTCCCTTTTTTAAAACCATTATATCTCGTGAGACTTATTCAATATCACA 120600

7861 AGAACAGCATGGGAAAGACTTGCCCTCATGATTCAATTACCTCCTACCCAGTCCCTCCCA 120660  
-----T7.9F----->

7921 CAACACATGGGAATTCAGATCAGATATGGGTAGGGACACAGCCAGATCGTATCAAACCA 120720

7981 CCATACAGTTTTCCATAGCGGCAGCACCATTTTAAATTCACCAGCAGTGCATAAGGTT 120780

8041 TCCAATTTCTCCACATCCTCATCAACACCACTTTCTGTTGTCTTTTTTTTTTAATAGCCAT 120840  
<-----T8.1R-----

8101 TCTAATGGTGATTAGGTGATTAGGATTATCTCATTGTGGTTTTGATTTGCATTTCCCTAA 120900

8161 TGATTAGTAAATATTGAGCATCTTTTCGTGTGATTTTGGCCACTTATGTTTCTTTCTTGA 120960

8221 AAGAAATGCTGCAAGTTCTTTGCCATTTTCTGATTTTTTTTTTAAGTTGTGGGAGTTCAC 121020

8281 TATATGTTTTGCCTATTAATTTCCATCAGATATATGATTCACAAATATTTTCTTGTATT 121080

8341 TCATGGTTGCTTTTTCACTCTGTTGCTAGAGTTCTTTGATGCACAAACGTTTTAAATTCT 121140

8401 GATGAAGTCTGATTTATCTATTTTTTGTGCTGTGCGTTTGGTGTATATCCAAGAAAT 121200

8461 CACTGCCAAATCTAGTGGCATGAGGCTTTTCTTCTACATTTTCTAGGAGTTTATAGTG 121260

8521 TTAGCTCTTATGTTTAGGCCTCTGATCCATTTGGAATTACATCTCCACCTTTCTTAACTA 121320  
-----

8581 TCTGTGGCTCCTTGGGAAAACCTACCCCTTCTTTCCTGATTCAGACACTGGGGATGGGAAA 121380  
---T8.6F----->
T40G/A  
A

8641 TTACCTCAAATGAAGGTTAAAAAATTGCATGTATCTCCTATACTACCTAACACTGAGAG 121440  
 <-----T8.7R----->

8701 CTCAATAATATTTTGTTCCTTGCTCCTTCACTCTTATTCCTTCTGGAAAGAAGAGTAAG 121500

8761 GAAGAGGGGAGAGAAAACAGTTTGGTATTTTTAGGTAGACTAGGGAGCATCTCACTGGCTGG 121560

8821 AGTAAGATGTGGGGCCTGCTGTCTTTGCACATCAGCCCTGGTGTTTGCTGGCCCTCTTT 121620

TAP2 exon 5 -->

8881 TCCAGGAAGTGCTTCGGGAGATCCAGGATGCAGTGGCCAGGGCGGGCAGGTGGTGCGGG 121680

8941 AAGCCGTTGGAGGGCTGCAGACCGTTCGCAGTTTTGGGGCCGAGGAGCATGAAGTCTGTC 121740

9001 GCTATAAAGAGGCCCTTGAACAATGTCGGCAGCTGTATTGGCGGAGAGACCTGGAACGCG 121800

T41G/A, replacement val/ile

9061 CCTTGTACCTGCTCGTAAGGAGGGTAAGATACCAGAGTGGTTGTGAAAGGAGCCCAGGAA 121860  
 A -----T9.1F----->

9121 AGGGGGAGGGCAAGGGAAGAGGAAACTACAGCTGGTTCTAGAGGCCTTTGCAGCTCAGTC 121920

9181 TCATAGAGGCAGAGAGGGGGAAAGAATGGGAAGATTCCCAGCCTCATCTCTTTCTTCTCC 121980

TAP2 exon 6-->T42G/T, silent

9241 TCTTCCAGGTGCTGCACCTTGGGGGTGCAGATGCTGATGCTGAGCTGTGGGCTGCAGCAGA 122040  
 T

9301 TGCAGGATGGGGAGCTCACCCAGGGCAGCCTGCTTTCCTTTTATGATCTACCAGGAGAGCG 122100

9361 TGGGGAGCTATGTGCAGGTGAGCGAGAAGCCAAGCCTGCTCTCCTTTTTTCCCTCTCTTT 122160

9421 TTCTTTGTGACTCCTGGGCCTTGGGCTTTATTTGTTCTTTTTAACAATACAATAACAAA 122220

9481 CCAAAACCCGCAAGTAATTTTGTCTATGGAGAATTTTAAACATATGCCAAAAATGAGACAA 122280

T43A/G

9541 AATAATATTACAAACTCACATGTATACATCCTGTGCTTTAACAATGATCAACTCATGCC 122340  
 G

T44A/C

9601 AATCTTGTGGATCTGTATCCCCAGCCACTTCCCCCACCCTATATTATTCTGAAGCAAAT 122400  
 C

9661 CCAAGATATTGTATACTTTCATCTGTAAATATTTTCAGTATGTTTCTTAAAAATACAAACA 122460

9721 TCTTTAAAAGTGTATAACAACAAAGCCATTATCACACCAAAAAATTAACAGTAGTTCTTA 122520

T45C/T

9781 AAATTTATCAAATAGTCAATTGTCAAATTTCCACTTGTGGTATCCATGTAGTATATGTGT 122580  
 T <-----T9.8R----->

end of region screened for polymorphism  
 ----->

9841 ATGAGTGTGTTTATTATACTTTGCTTAAATCAGGATCCAGAAATGGTCCACATATTGTGA 122640  
 ---

<-----T9.9R----->

9901 CTGGTTGATACATCTTTAAGTCTGTCTGTCTATCTATCCATCCATCTATCCATCC 122700

9961 ATCCACCCATCAATCCATGTATCTGTCTAAAAGTTTCCCTTGCACAGTTTATTTGTTGAA 122760

## TAP2 allele-specific oligonucleotides.

TA1G	5' CCAGCCTGGCCAACATGG 3'	located in an Alu element, also shows a perfect match to positions 2482-2499 in a second Alu element
TA1T	5' CCAGCCTTGCCAACATGG 3'	
TA2C	5' AAGATGGCGCCACTGCAT 3'	
TA2T	5' AAGATGGTGCCACTGCAT 3'	
TA3T	5' CTGTGTGTTCCATTGTTA 3'	
TA3C	5' CTGTGTGCTCCATTGTTA 3'	
TA4T	5' CTCTGGGT CAGGAAGGAT 3'	
TA4A	5' CTCTGGGACAGGAAGGAT 3'	
TA5G	5' AATTACTGTTCTAAACAG 3'	
TA5A	5' AATTACTATTCTAAACAG 3'	
TA6T	5' AGAACCAAAGCTCAGTAC 3'	
TA6C	5' AGAACCAAAGCCAGTAC 3'	
TA7G	5' CAGTACGGGCATTTCCC 3'	
TA7C	5' CAGTACCGGGCATTTCCC 3'	
TA8G	5' CCGCCTCGCCTCCCAA 3'	
TA8A	5' CCGCCTCAGCCTCCCAA 3'	
TA9A	5' ACAGATAAAGTTGCCCTT 3'	
TA9C	5' ACAGATACAGTTGCCCTT 3'	
TA10C	5' AAGGCCTTGGCTGGGGAA 3'	
TA10T	5' AAGGCCTTGGTTGGGGAA 3'	
TA11G	5' TGGGGAAACGAAAAGCGAA 3'	
TA11A	5' TGGGGAAACGAAAAGCGAA 3'	
TA12T	5' GCAGAAGTCCCCGGAGCT 3'	
TA12C	5' GCAGAAGCCCCGGAGCT 3'	
TA13G	5' CAACAGGACGCAGCCCA 3'	
TA13A	5' CAACAGGAACGCAGCCCA 3'	
TA14A	5' ATAGGATAAAATGAGAAG 3'	
TA14G	5' ATAGGATGAAAATGAGAAG 3'	
TA15G	5' GGGCCTGGCACCAGCAC 3'	
TA15C	5' GGGCCTGCGCACCAGCAC 3'	
TA16G	5' GGTAGGTGGTGGGCAGCT 3'	
TA16A	5' GGTAGGTAGTGGGCAGCT 3'	
TA17A	5' GTCTCAGATGGAATGTCT 3'	
TA17G	5' GTCTCAGGTGGAATGTCT 3'	

TA18T 5' GTCACTCTCTCAGGATGG 3'  
TA18C 5' GTCACTCCCTCAGGATGG 3'  
TA19C 5' TCTCCCTCTCACTCTTCT 3'  
TA19T 5' TCTCCCTTTCACCTTCT 3'  
TA20TAA 5' ATCTTGCTAATCCCTGAA 3'  
TA20TAG 5' ATCTTGCTAGTCCCTGAA 3'  
TA20CAA 5' ATCTTGCCAATCCCTGAA 3'  
TA20CAG 5' ATCTTGCCAGTCCCTGAA 3'  
TA21C 5' CCTTTCTCTTTCTAGACA 3'  
TA21T 5' CCTTTCTTTTTCTAGACA 3'  
TA22A 5' TTACCCAATCCCAGCCG 3'  
TA22G 5' TTACCCAGATCCCAGCCG 3'  
TA23C 5' CTACAGTCGTGCACTGCA 3'  
TA23T 5' CTACAGTTGTGCACTGCA 3'  
TA24T 5' ATAACGATGTTTAGGTCA 3'  
TA24A 5' ATAACGAAGTTTAGGTCA 3'  
TA25C 5' GTGCAGTCATATGTTGTA 3'  
TA25T 5' GTGCAGTTATATGTTGTA 3'  
TA26T 5' GGAGCAATAGGCTAAACT 3'  
TA26A 5' GGAGCAAAGGCTAAACT 3'  
TA27G 5' ATACAACGATGAAACCAT 3'  
TA27A 5' ATACAACAATGAAACCAT 3'  
TA28C 5' CATCTAACGACACATTTT 3'  
TA28T 5' CATCTAATGACACATTTT 3'  
TA29ATT 5' TCTGACTATTCCAAACGC 3'  
TA29ATC 5' TCTGACTATCCCAAACGC 3'  
TA29CTT 5' TCTGACTCTTCCAAACGC 3'  
TA29CTC 5' TCTGACTCTCCCAAACGC 3'  
TA30C 5' AGGATGACAGATGGGAAT 3'  
TA30A 5' AGGATGAAAGATGGGAAT 3'  
TA31T 5' TTGTAGTTTTCTATTGTG 3'  
TA31C 5' TTGTAGTCTTCTATTGTG 3'  
TA32A 5' GGCCTGGAGTCCAGGTCT 3'  
TA32T 5' GGCCTGGTGTCCAGGTCT 3'  
TA33A 5' CTCAGCCATTAGGGGAGA 3'  
TA33G 5' CTCAGCCGTTAGGGGAGA 3'

TA34G 5' GGAGAAGGTATATTGTAG 3'  
TA34A 5' GGAGAAGATATATTGTAG 3'  
TA35+ 5' CTGTAAACAAAAATGTAA 3'  
TA35- 5' AACTGTAAAAAATGTAAA 3'  
TA36GG 5' TTGGGTAGCCATCATCAC 3'  
TA36GA 5' TTGGGTAAACCATCATCAC 3'  
TA36TG 5' TTGGTTAGCCATCATCAC 3'  
TA36TA 5' TTGGTTAAACCATCATCAC 3'  
TA37C 5' TGACTCCCGGTGCGGTAC 3'  
TA37A 5' TGACTCCAGGTGCGGTAC 3'  
TA38G 5' CATTTGCGTTGTTTCCAC 3'  
TA38A 5' CATTTGCAATTGTTTCCAC 3'  
TA39- 5' AGACCTCAAATCATGGCG 3'  
TA39+ 5' GACCTCACAAATCATGGCG 3'  
TA40G 5' CTTTCCTGATTCAGACAC 3'  
TA40A 5' CTTTCCTAATTCAGACAC 3'  
TA41G 5' CCTGCTCGTAAGGAGGGT 3'  
TA41A 5' CCTGCTCATAAGGAGGGT 3'  
TA42G 5' ACTTGGGGGTGCAGATGC 3'  
TA42T 5' ACTTGGGTGTGCAGATGC 3'  
TA43A 5' CACATGTATACATCCTGT 3'  
TA43G 5' CACATGTGTACATCCTGT 3'  
TA44A 5' CCCACCCATATTATTCTG 3'  
TA44C 5' CCCACCCCTATTATTCTG 3'  
TA45C 5' ATTTCCAATTGTGGTATC 3'  
TA45T 5' ATTTCCATTTGTGGTATC 3'