

Figure S2. Results of singleplex PCRs, cloning and sequencing of ambiguous positions.

Eight indels and two C->T substitutions in the BVA2 sequence generated by multiplex PCRs and pyrosequencing were checked by novel singleplex PCRs with subsequent cloning and Sanger sequencing of the amplification products. Positions are numbered according to BRS. Nucleotides identical to the reference sequence are indicated by dots.

123-250 (221+2C)

```
ref      TGTAGCTGGACTTAACTGCATCTTGAGCACCAGCATAATGATAAGCATGGACATTACAGT
CLO1     .....
CLO2     .....
CLO3     .....A.....
CLO4     .....
CLO5     .....A.
*****
```

2
2
1

```
ref      CAATGGTCACAGGACATAAATTATATTATATATCCCCC-TTCATAAAAATTTCCCCCTT
CLO1     .....
CLO2     .....T.....C.....
CLO3     .....
CLO4     .....T.....
CLO5     .....
*****
```

```
ref      AAATATCTA
CLO1     .....
CLO2     .....
CLO3     .....
CLO4     .....
CLO5     ...A....
*** *****
```

237-399 (362-363del)

```
ref      CCCTTAAATATCTACCACCACCTTTTAACAGACTTTTCCCTAGATACTTATTTAAATTTTT
CLO1     .....T.....
CLO2     .....
CLO3     .....
CLO4     .....
CLO5     .....
CLO6     .....A.....
*****
```

```
ref      CACGCTTTCAATACTCAATTTAGCACTCCAAACAAAGTCAATATATAAACGCAGGCCCCC
CLO1     ...A.....G....
CLO2     .....T.....G....
CLO3     .....T.....
CLO4     .....
CLO5     .....
CLO6     .....
*** *****
```

3
6
3

```
ref      CCCCCCGTTGATGTAGCTTAACCCAAAGCAAGGCACTGAAAA
CLO1     .....
CLO2     .....
CLO3     .....
CLO4     .....
CLO5     .....G.....
CLO6     .....GG.....
*****
```

561-721 (587+C)

5
8
7
ref TCACGACGCCTTGCTTAACCACACCCC-ACGGGAAACAGCAGTGACAAAAATTAAGCCAT
CLO1 .T.....C.....
CLO2C.....
CLO3C.....
CLO4C...A.....
CLO5C.....
* *****

ref AAACGAAAGTTTGACTAAGTTATATTAATTAGGGTTGGTAAATCTCGTGCCAGCCACCGC
CLO1
CLO2
CLO3
CLO4
CLO5T.....
* *****

ref GGTCATACGATTAACCCAAGCTAACAGGAGTACGGCGTAAAA
CLO1
CLO2
CLO3
CLO4A.....
CLO5
* *****

1981-2161 (2048 C->T)

ref AATTAAGAAAGCGTTAAAGCTCAACAACAAAAATTAATAGATTCCAACAACAAATGAT
CLO1
CLO2A..
CLO3
CLO4A..
CLO5
* *****

2
0
4
8

ref TAACTCCTAGCCCCAATACTGGACTAATCTATTATAGAATAGAAGCAATAATGTTAATA
CLO1T.....
CLO2
CLO3
CLO4
CLO5T.....
* *****

ref TGAGTAACAAGAAAAATTTCTCCTTGCATAAGTCTAAGTCAGTGCCTGATAATACTCT
CLO1
CLO2
CLO3
CLO4
CLO5T.....
* *****

ref G
CLO1 .
CLO2 .
CLO3 .
CLO4 .
CLO5 .
*

3269-3441 (3341 C->T)

```
ref      ATTAAAGAACCACCTACGACCCGCTACATCTTCAGCCTCAATATTTATCCTAGCACCTAT
CLO1     .....
CLO2     .....
CLO3     .....
CLO4     .....A.....
CLO5     .....
*****
```

3
3
4
1

```
ref      CATAGCTTTAGGCCTAGCCTTAACCATGTGAATTCCCCTACCAATACCCTATCCTCTTA
CLO1     .....
CLO2     .....
CLO3     .....
CLO4     .....
CLO5     .....T.....
*****
```

```
ref      TCAACATAAACCTAGGAGTCCTATTTATACTAGCCATATCAAGCCTAGCCGTATA
CLO1     .....T.....
CLO2     .....T.....
CLO3     .....
CLO4     .....
CLO5     .....
*****
```

8144-8308 (8258+A)

```
ref      ACGTCAACATGACTGACAATGATCTTATCAATATTCTTGACCCTTTTTATCATCTTTCA
CLO1     .....
CLO2     .....
CLO3     .....
CLO4     .....T.....
CLO5     .....
*****
```

8
2
5
8

```
ref      ACTAAAAGTTTCAAAACACAACCTTTTATCACAATCCAGAACTGACACCAACAAAAATAT
CLO1     .....A.....
CLO2     .....
CLO3     .....
CLO4     .....
CLO5     .....A.....
*****
```

```
ref      TAAAACAAAACACCCCTTGAGAAACAAAATGAACGAAAATTTATTTA
CLO1     .....A.....
CLO2     .....
CLO3     .....T.....
CLO4     .....
CLO5     .....
*****
```

12624-12750 (12676+C)

1
2
6
7
6

```
ref      CTTATATAACCGCATCGGCGACATTGGTTTCATTTTAGCAATAGCATGGTTCCTAACAA
CLO1     .....G.....
```

CLO2
CLO3
CLO4T.....
CLO5T.....

ref ATCTCAATACCTGAGACCTCCAACAGATCTTCATACTAAACCCAAGCGACTCAAACATA
CLO1A.....
CLO2
CLO3
CLO4
CLO5

ref CCCTTGATT
CLO1
CLO2
CLO3
CLO4A...
CLO5

13684-13870 (13801+A)

ref TTATACATCGCCTAGCTCCATACATAAATTTATCAATAAGCCAAAAATCAGCATCCTCC
CLO1T.....
CLO2
CLO3
CLO4
CLO5

1
3
8
0
1

ref CTTCTAGACCTAATCTGACTAGAAAGCCATCCTACCAAAAACCATCTCACTCGCCCAAAT
CLO1
CLO2TT.....
CLO3
CLO4
CLO5

ref AAAAGCATCTACCCTGGTCACAAACCAAAAAGGCCTGATCAAACCTATATT
CLO1
CLO2
CLO3
CLO4
CLO5A.....
