

Supplement 1. PQS sequences in the N gene of Wuhan-Hu-1: A) Overlap not included; B) overlap included; C) the sequence view of PQSs in the gene.

A QGRS sequences found (overlaps not included)

| Position | Length | QGRS | G-Score |
|----------|--------|--|---------|
| 508 | 29 | GGCTTCTACGCAGAAAGGAGCAGAGGCGG | 9 |
| 630 | 15 | GGCTGGCAATGGCGG | 18 |
| 850 | 19 | GGAAATTTGGGGACCAGG | 14 |
| 961 | 30 | GGCATGGAAGTCACACCTTCGGGAACGTGG | 11 |

B QGRS sequences found (overlaps included)

| Position | Length | QGRS | G-Score |
|----------|--------|--|---------|
| 508 | 29 | GGCTTCTACGCAGAAAGGAGCAGAGGCGG | 9 |
| 508 | 29 | GGCTTCTACGCAGAAAGGAGCAGAGGCGG | 8 |
| 608 | 28 | GGGAACTTCTCCTGCTAGAATGGCTGG | 3 |
| 630 | 15 | GGCTGGCAATGGCGG | 18 |
| 850 | 19 | GGAAATTTGGGGACCAGG | 14 |
| 859 | 26 | GGGGACCAAGAACTAATCAGACAAAGG | 7 |
| 961 | 30 | GGCATGGAAGTCACACCTTCGGGAACGTGG | 11 |
| 961 | 30 | GGCATGGAAGTCACACCTTCGGGAACGTGG | 10 |

C

Search Parameters: QGRS Max Length: 30 | Min G-Group Size: 2 | Loop size: from 0 to 36 | Loop search string:

| Gene Information | |
|---------------------|------------------------------------|
| Gene ID: | Number of Products: 1 |
| Gene Symbol: | Number of poly A Signals: |
| Gene Size: 1260 nt. | QGRS found: 4 |
| | QGRS found (including overlaps): 8 |

```

000001 ATGTCTGATA ATGGACCCCA AATCAGCGA AATGCACCCG GCATTACGTT TGGTGGACCC TCAGATTCAA CTGGCAGTAA CCAGAATGGA GAACGCAGTG
000101 GGGCGCGATC AAAACACCGT CGGCCCCCAAG GTTTACCCAA TAATACTGCG TCTTGGTCA CCGTCTCAC TCAACATGGC AAGGAAGACC TTRAAATCCC
000201 TCGAGGACAA GCGCTTCCAA TTAACACCAA TAGCAGTCCA GATGACCAA TTGGCTACTA CCGAAGAGCT ACCAGACGAA TTCGTGGTGG TGRCGGTRAA
000301 ATGAARAGTC TCAGTCCAAG ATGGTATTTT TACTACCTAG GAACCTGGCC AGAAGCTGGA CTTCCTCATG GTGCTAACAA AGACGGCCTC ATATGGGTTG
000401 CAACGTAGGG AGCCTTGAAT ACACCAAAG ATCACATTGG CACCCGCAAT CCGTCTAACA ATGCTGCAAT CGTGTACAA CTTCCTCAAG GAACCAACAT
000501 GCCAAAAGGC TTCTACGCAG AAGGGAGCAG AGGCGG CAGT CAAGCCTCTT CTCGTTCCTC ATCACGTAGT CGCAACAGTT CAAGAAATTC AACTCCAGGC
000601 AGCAGTAGGG GAACTTCTCC TGCTAGAATG GCTGGCAATG GCGGTGATGC TGCTCTGCT TTGCTGCTGC TTGACAGATT GAACCAAGCTT GAGAGCAAAA
000701 TGTCTGGTAA AGGCCAACAA CAACAGGCC AACTGTCTAC TAAGAATCT GCTGCTGAGG CTTCTAAGAA GCCTCGGCAA AAACGTACTG CCRCCTAARGC
000801 ATACAAATGA ACACAGCTT TCGGCAGAGC TGGTCCAGAA CAACCCAA GGAATTTTGG GGACCAGGAA CTAATCAGAC AAGGAAGTGA TTACAAACAT
000901 TGGCCGCAAA TTGCACAATT TGCCTCCAGC GCTTCAGCGT TCTTCGGAAT GTCGCGCATT GGCAATGGAG TCACACCTTC GGGAAACGTGG TTGACCTACA
001001 CAGGTGCCAT CAAATTGGAT GACAAAGATC CAATTTCAA AGATCAAGTC ATTTTGTCTGA ATAAGCATAT TGACGCATAC AAAACATTC CACCAACAGA
001101 GCCTAAAAGG GACAAAAGAA AGAAGGCTGA TGAACCTCAA GCCTTACCGC AGAGACAGAA GAAACAGCAA ACTGTGACTC TTCTTCTCTG TCAGATTTT
001201 GATGATTCTT CCAACAAAT GCAACAAATC ATGAGCAGTG CTGACTCAAC TCAGGCCTAA
    
```

Supplement 2. PQS sequences in the N gene of the Alpha variant: A) Overlap not included; B) overlap included; C) the sequence view of PQSs in the gene.

A Search Parameters: QGRS Max Length: 30 | Min G-Group Size: 2 | Loop size: from 0 to 36 | Loop search string:

QGRS sequences found (overlaps not included)

| Position | Length | QGRS | G-Score |
|----------|--------|--|---------|
| 508 | 29 | GGCTTCTACGCAGAAGGGAGCAGAGGCGG | 9 |
| 630 | 15 | GGCTGGCAATGGCGG | 18 |
| 850 | 19 | GGAAATTTTGGGGACCAGG | 14 |
| 961 | 30 | GGCATGGAAGTCACACCTTCGGGAACGTGG | 11 |



B QGRS sequences found (overlaps included)

| Position | Length | QGRS | G-Score |
|----------|--------|--|---------|
| 508 | 29 | GGCTTCTACGCAGAAGGGAGCAGAGGCGG | 9 |
| 508 | 29 | GGCTTCTACGCAGAAGGGAGCAGAGGCGG | 8 |
| 630 | 15 | GGCTGGCAATGGCGG | 18 |
| 850 | 19 | GGAAATTTTGGGGACCAGG | 14 |
| 859 | 26 | GGGGACCAGGAACCTAATCAGACAAAGG | 7 |
| 961 | 30 | GGCATGGAAGTCACACCTTCGGGAACGTGG | 11 |
| 961 | 30 | GGCATGGAAGTCACACCTTCGGGAACGTGG | 10 |

C Search Parameters: QGRS Max Length: 30 | Min G-Group Size: 2 | Loop size: from 0 to 36 | Loop search string:

| Gene Information | |
|---------------------|------------------------------------|
| Gene ID: | Number of Products: 1 |
| Gene Symbol: | Number of poly A Signals: |
| Gene Size: 1260 nt. | QGRS found: 4 |
| | QGRS found (including overlaps): 7 |

```

000001 ATGTCTCTAA ATGSAACCCA AATCAGCGA AATGCACCCC GCATTACGTT TGGTGGACCC TCAGATTCAA CTGGCAGTAA CCAGAAATGGA GAACGCAGTG
000101 GGGCGCGATC AAAACAAAGT CGGCCCCRAG GTTTRACCCAA TAATACTGCG TCTTGGTTCA CCGCTCTCRG TCRACATGGC AAGGAAGACC TTAARTTCCC
000201 TCGAGGACAA GGCCTTCCAA TTAACACCAA TAGCAGTCCA GATGACAAA TTGGCTACTA CCGAAGAGCT ACCAGACGAA TTCGTGGTGG TGACGGTAAA
000301 ATGAAAGATC TCAGTCCAAAG ATGGTATTTT TACTACCTAG GAATCGGGCC AGAAGCTGGA CTTCCTATG GTGCTAACAA AGACGGCCTC ATATGGGTTG
000401 CAACTGAGGG AGCCTTGAAT ACACCAAAAG ATCACATTGG CACCCGCAAT CCTGCTAACA ATGCTGCAAT CGTGTACAA CTTCCTCAAG GAACACATT
000501 GCCAAAAGC TTCTACGCAG AAGGGAGCAG AGGCGGAGT CAAGCCTCTT CTCGTTCCCTC ATCACGTAGT CGCAACAGTT CAAGAAATTC AACTCCAGGC
000601 AGCAGTAAAC GAACTTCTCC TGCTGAAATG GCTGGCAATG GCGGTGATGC TGCTCTGCT TTGCTGCTGC TTGACAGATT GAACCACTT GAGAGCAAAA
000701 TGTTTTGTAA AGGCCAACAA CAACAAGGCC AACTGTCTAC TAAGAAATCT GCTGCTGAGG CTTTAAAGAA GCCTCGGCAA AAACGTAAGT CCACTAAAGC
000801 ATACAATGTA ACACAAGCTT TCGGCAGAGC TGGTCCAGAA CAACCCAAAG GAAATTTTGG GGACCCAGGAA CTAATCAGAC AAGGAAGTGA TTACAAACAT
000901 TGGCCGCAAA TTGCACAATT TGCCCCAGC GOTTACAGCT TCTTCGGAAT GTCCGCGATT GGCATGGGAG TCACACCTTC GGGAACTGG TTGACCTACA
001001 CAGGTGCCAT CAATTTGGAT GACAAGATC CAAATTTCAA AGATCAAGTC ATTTTGTGTA ATAAACATAT TGACGCATAC AAACACATTC CACCACAGA
001101 GCCTAAAGG GACAAAAGA AGAAGGCTGA TGAACCTCAA GCCTTACCGC AGAGACAGAA GAAACAGCAA ACTGTGACTC TTCTTCTGTC TGACAGTTTG
001201 GATGATTTCT CCAACAATT GCAACAATCC ATGAGCAGTG CTGACTCAAC TCAGGCCTAA
    
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Supplement 3. PQS sequences in the N gene of the Bata variant: A) Overlap not included; B) overlap included; C) the sequence view of PQSs in the gene.

A Search Parameters: QGRS Max Length: 30 | Min G-Group Size: 2 | Loop size: from 0 to 36 | Loop search string:

QGRS sequences found (overlaps not included)

| Position | Length | QGRS | G-Score |
|----------|--------|--|---------|
| 508 | 29 | GGCTTCTACGCAGAAGGGAGCAGAGGCCGG | 9 |
| 630 | 15 | GGCTGGCAATGGCGG | 18 |
| 850 | 19 | GGAAATTTTGGGGACCAGG | 14 |
| 961 | 30 | GGCATGGAAGTCACACCTTCGGGAACGTGG | 11 |

B QGRS sequences found (overlaps included)

| Position | Length | QGRS | G-Score |
|----------|--------|---|---------|
| 508 | 29 | GGCTTCTACGCAGAAGGGAGCAGAGGCCGG | 9 |
| 508 | 29 | GGCTTCTACGCAGAAGGGAGCAGAGGCCGG | 8 |
| 608 | 28 | GGGGAATTTCTCCTGCTAGAATGGCTGG | 3 |
| 630 | 15 | GGCTGGCAATGGCGG | 18 |
| 850 | 19 | GGAAATTTTGGGGACCAGG | 14 |
| 859 | 26 | GGGGACCAAGAACTAATCAGACAAAGG | 7 |
| 961 | 30 | GGCATGGAAGTCACACCTTCGGGAACGTGG | 11 |
| 961 | 30 | GGCATGGGAAGTCACACCTTCGGGAACGTGG | 10 |

C Search Parameters: QGRS Max Length: 30 | Min G-Group Size: 2 | Loop size: from 0 to 36 | Loop search string:

| Gene Information | |
|---------------------|------------------------------------|
| Gene ID: | Number of Products: 1 |
| Gene Symbol: | Number of poly A Signals: |
| Gene Size: 1260 nt. | QGRS found: 4 |
| | QGRS found (including overlaps): 8 |

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000001 ATGTGTGATA ATGGACCCCA AAATCAGCGA AATGCACCCC GCATTACGTT TGGTGGACCC TCAGATTCAA CTGGCAGTAA CCAGAATGGA GAACGCAGTG
000101 GGGCGCGATC AAAACAACGT CGGCCCCAAAG GTTTACCCAA TAATACTGGG TCTTGGTTCA CCGCTOTCAC TCAACATGGC AAGGAAGACC TTAATTTCCC
000201 TCGAGGRCAA GGCCTTCCAA TTRACACCAA TAGCAGTCCA GATGACCAA TTGGTACTA CCGRAGAGCT ACCAGACGAA TCGTGGTGG TGACGGTAAA
000301 ATGAAAGATC TCAGTCCAAG ATGGTATTTT TACTACCTAG GAACTGGGCC AGAAGCTGGA CTTCCTATG GTGCTAACAA AGACGGCCTC ATATGGGTTG
000401 CAACTGAGGG AGCCTTGAAT ACACCAAAAAG ATCACATTGG CACCCGCAAT COTGCTAACA ATGCTGCAAT CGTGTACAAA CTTCCTCAAG GAACACATT
000501 GCCAAAAGGC TTCTACGCGAG AAGGGAGCAG AGGCGGCACT CAAGCCTCTT CTCGTTCCCT ATCAAGTAGT CGAACAGTT CAAGAAATTC AACTCCAGGC
000601 AGCAGTAGGG GAATTTCTCC TGCTAGAATG GCTGGCAATG GCGGTGATGC TGCTCTTGGT TTGCTGCTGC TTGACAGATT GAACCACTT GAGAGCAAAA
000701 TGCTGTGTA AGGCCAACAA CAACAAGGCC AAATGTGCAC TAAGAAATCT GCTGCTGAGG CTTCCTAAGAA GCCTCGGCAA AAACCTACTG CCACCTAAGC
000801 ATACAAATGA ACACRAGCTT TCGGCAGACG TGGTCCAGAA CAACCCCAAG GAAATTTTGG GGACCAGGAA CTAATCAGAC AAGGAACTGA TTACAAACAT
000901 TGGCCGCAAA TTGCRCRATT TGCCCCCAGC GOTTCCAGCT TCTTCGGRAT GTCCGCAATT GGCRTGGGAG TCACACCTTC GGGAACCTGG TTGACCTACA
001001 CAGGTGCCAT CAAATTTGAT GACAAAGATC CAAATTTCAA AGATCAAGTC ATTTTGTGTA ATAAGCATAT TGACGCATAC AAAACATTCC CACCAACAGA
001101 GCCTAAAAGG GACAAAARA AGAAGGCTGA TGAACCTCAA GCCTTACCG AGAGACAGAA GAAACAGCAA ACTGTGACTC TTCTTCCTGC TGCGAGATTTG
001201 GATGATTTCT CCAARCAATT GCARCAATCC ATGAGCAGTG CTGACTCAAC TCAGGCCTAA
    
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Supplement 4. PQS sequences in the N gene of the Gamma variant: A) Overlap not included; B) overlap included; C) the sequence view of PQSs in the gene.

A QGRS sequences found (overlaps not included)

| Position | Length | QGRS | G-Score |
|----------|--------|--|---------|
| 508 | 29 | GGCTTCTACGCAGAAGGGAGCAGAGGCCGG | 9 |
| 630 | 15 | GGCTGGCAATGGCGG | 18 |
| 850 | 19 | GGAAATTTGGGGACCAGG | 14 |
| 961 | 30 | GGCATGGAAGTCACACCTTCGGGAACGTGG | 11 |

B QGRS sequences found (overlaps included)

| Position | Length | QGRS | G-Score |
|----------|--------|--|---------|
| 508 | 29 | GGCTTCTACGCAGAAGGGAGCAGAGGCCGG | 9 |
| 508 | 29 | GGCTTCTACGCAGAAGGGAGCAGAGGCCGG | 8 |
| 630 | 15 | GGCTGGCAATGGCGG | 18 |
| 850 | 19 | GGAAATTTGGGGACCAGG | 14 |
| 859 | 26 | GGGGACCAGGAACCTAACAGACAAGG | 7 |
| 961 | 30 | GGCATGGAAGTCACACCTTCGGGAACGTGG | 11 |
| 961 | 30 | GGCATGGAAGTCACACCTTCGGGAACGTGG | 10 |

C Search Parameters: QGRS Max Length: 30 | Min G-Group Size: 2 | Loop size: from 0 to 36 | Loop search string:

| Gene Information | |
|---------------------|------------------------------------|
| Gene ID: | Number of Products: 1 |
| Gene Symbol: | Number of poly A Signals: |
| Gene Size: 1260 nt. | QGRS found: 4 |
| | QGRS found (including overlaps): 7 |

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000001 ATGTCTGATA ATGGACCCCA AATCAGCGA AATGCACCCC GCATTACGTT TGGTGGACCC TCAGATTCAA CTGGCAGTAA CCAGAATGGA GAAGCAGTG
000101 GGGCGCGATC AAAACRACGT CGGCCCCAAAG GTTTACCCAA TAATACTGCG TCTTGGTTCA CCGCTCTCAC TCAACATGGC AAGGAAGACC TTAATTTCCC
000201 TCGAGGACAA GCGCTCCCAA TTAACACCAA TAGCAGTCCA GATGACCAA TTGGCTACTA CCGAAGAGCT ACCAGACGAA TTCGTGGTGG TGACGGTAAA
000301 ATGAAAGATC TCAGTCCAAG ATGGTATTTT TACTACCTAG GAACTGGGCC AGAAGCTGGA CTTCCTATG GTGCTAACAA AGACCGCATC ATATGGGTTG
000401 CAACTGAGGG AGCCTTGAAT ACACCAAAG ATCACATTGG CACCCGCAAT COTGCTAACA ATGCTGCAAT CGTGCTACAA CTTCCTCAAG GAACAACATT
000501 GCCAAAAGGC TTCTACGCAG AAGGAGCCAG AGGCGGCAGT CRAAGCCTCTT CTCGTTCCCTC ATCACGTAGT CGCAACAGTT CAAGAAATTC AACTCCAGGC
000601 AGCAGTAAAC GAACTTCTCC TGCTAGAATG GCTGGCAATG GCGGTGATGC TGCTCTTCTT TTGCTGCTGC TTGACAGATT GAACCGACTT GAGAGCAAAA
000701 TGTCTGGTAA AGGCCAACAA CAAACAAGGC AACTGTCCAC TAAGAAATCT GCTGCTGAGG CTTCCTAAGAA GCCTCGGCAA AAACCTACTG CCCTAAAGC
000801 ATACAATGTA ACACAAGCTT TCGGCAGACG TGGTCCAGAA CAACCCAAAG GAAATTTTGG GGACCAGGAA CTRACCAGAC AAGGAATGTA TTACAACAT
000901 TGGCCGCAAA TTGCACAATT TGCCCCCAGC GCTTCAGCGT TCTTGGAAAT GTCGCGCATT GGCATGGAAG TCACACCTTC GGGAAACGTGG TTGACCTACA
001001 CAGGTGCCAT CAAATTTGGAT GACAAAGATC CAAATTTCAA AGATCAAGTC ATTTTGTCTGA ATAAGCATAT TGACGCATAC AAAACATTC CACCAACAGA
001101 GCCTAAAAG GACAAAAGA AGAAGGCTGA TGAACCTCAA GCCTTACCGC AGAGACAGAA GAAACAGCAA ACTGTGACTC TTCTTCTGTC TGCAATTTG
001201 GATGATTTCT CCAACAATTC GCRAACAATC ATGAGCAGTG CTGACTCAAC TCAGCCCTAA
    
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Supplement 5. PQS sequences in the N gene of Delta variant: A) Overlap not included; B) overlap included; C) the sequence view of PQSs in the gene.

A QGRS sequences found (overlaps not included)

| Position | Length | QGRS | G-Score |
|----------|--------|--|---------|
| 178 | 29 | GGCAAGGAAGGCCTTAAATTCCTCGAGG | 7 |
| 508 | 29 | GGCTTCTACGCAGAAGGGAGCAGAGGCCG | 9 |
| 850 | 19 | GGAAATTTGGGGACCAGG | 14 |
| 961 | 30 | GGCATGGAAGTCACACCTTCGGGAACGTGG | 11 |

B QGRS sequences found (overlaps included)

| Position | Length | QGRS | G-Score |
|----------|--------|--|---------|
| 178 | 29 | GGCAAGGAAGGCCTTAAATTCCTCGAGG | 7 |
| 183 | 30 | GGAAGGCCTTAAATTCCTCGAGGACAAGG | 7 |
| 508 | 29 | GGCTTCTACGCAGAAGGGAGCAGAGGCCG | 9 |
| 508 | 29 | GGCTTCTACGCAGAAGGGAGCAGAGGCCG | 8 |
| 850 | 19 | GGAAATTTGGGGACCAGG | 14 |
| 859 | 26 | GGGGACCAGGAACTAATCAGACAAAGG | 7 |
| 961 | 30 | GGCATGGAAGTCACACCTTCGGGAACGTGG | 11 |
| 961 | 30 | GGCATGGAAGTCACACCTTCGGGAACGTGG | 10 |

C

| Gene Information | |
|---------------------|------------------------------------|
| Gene ID: | Number of Products: 1 |
| Gene Symbol: | Number of poly A Signals: |
| Gene Size: 1260 nt. | QGRS found: 4 |
| | QGRS found (including overlaps): 8 |

```

000001 ATGTCGTGATA ATGGACCCCA AAATCAGCGA AATGCAACCC GCATTACGTT TGGTGGACCC TCAGATTCAA CTGGCAGTAA CCAGAAATGGA GAACGCAGTG
000101 GGGCGCGATC AAAACAACGT CGGCCCCAAG GTTTACCCAA TAATACTGCG TCTTGGTTCA CCGCTCTCAC TCAACATGGC AAGGAAGGCC TTAATTCCTC
000201 TCGAGGACAA GCGTTCCTCA TTAACACCAA TAGCAGTCCA GATGACCAA TTGGCTACTA CCGAAGAGCT ACCAGACGAA TTCGTGGTGG TGACGGTAAA
000301 ATGAAAGATC TCAGTCCAAG ATGGTATPFC TACTACCTAG GAACCTGGGC AGAAGCTGGA CTTCCTATG GTGCTAACAA AGACGGCATC ATATGGGTTG
000401 CAACCTGAGGG AGCCTTGAAT ACACCAAAAG ATCACATTGG CACCCGCAAT CCTGCTAACA ATGCTGCAAT CGTGCTACAA CTTCCTCAAG GAACAACATT
000501 GCCAAAAGGC TTCTACGCAG AAGGGAGCAG AGGCGGCAGT CAAGCCCTFT CTCGTTCCTC ATCACGTAGT CGCAACAGTT CAAGAAATTC AACTCCAGGC
000601 AGCAGTATGG GAACTTCCTC TGCTRGAATG GCTGGCAATG GCTGTGRTGC TGCTCTTGCT FTGCTGCTGC TTGACRATT GARCCAGCTT GAGAGCAAAA
000701 TGCTCGTAA AGGCCAACAA CAACAAGGCC AAACGTGCAC TAAGAAATCT GCTGCTGAGG CTTCTAAGAA GCCTCGGCAA AAACGTAAGT CCACTAAAGC
000801 ATACAATGTA ACACAAGCTT TCGGCAGAGC TGGTCCAGAA CAAACCCAA GGAATTTTGG GGACCCAGGAA CTAATCAGAC AAGGAAGTGA TTACAAACAT
000901 TGGCCGCAAA TTGCACAATT TGCCCCCAGC GCTTCAGCGT TCTTCGGAAT GTCCGCGATT GGCATGGGAG TCACACCTTC GGGAACTGGG TTGACCTACA
001001 CAGTGCCAT CAAATGGAT GACARAGATC CAAATTTCAA AGATCARGTC ATTTTGTGTA ATAAGCATAT TGACGCATAC AAACATTC CACCAACRGA
001101 GCCTAAAAAG GACAAAAAGA AGAAGCTTA TGAARCTCAA GCCTTACC GCAGACAGAA GAARACAGAA ACTGTGACTC TTCTTCTGCTG TGCAATTTG
001201 GATGATTTCT CCAACAATT GCAACAATCC ATGAGCAGTG CTGACTCAAC TCAGGCCTAA
    
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Supplement 6. PQS sequences in N gene of Omicron variant: A) Overlap not included; B) overlap included; C) the sequence view of PQSs in the gene.

A

| Position | Length | QGRS | G-Score |
|----------|--------|--|---------|
| 73 | 22 | GGCAGTAACCAGAATGGTGGGG | 8 |
| 499 | 29 | GGCTTCTACGCAGAAGGGAGCAGAGGC | 9 |
| 621 | 15 | GGCTGGCAATGGCGG | 18 |
| 841 | 19 | GGAAATTTGGGGACCAGG | 14 |
| 952 | 30 | GGCATGGAAGTCACACCTTCGGGAACGTGG | 11 |

B

| Position | Length | QGRS | G-Score |
|----------|--------|--|---------|
| 73 | 22 | GGCAGTAACCAGAATGGTGGGG | 8 |
| 88 | 27 | GGTGGGGCGCGATCAAAACAACGTCCG | 3 |
| 499 | 29 | GGCTTCTACGCAGAAGGGAGCAGAGGC | 9 |
| 499 | 29 | GGCTTCTACGCAGAAGGGAGCAGAGGC | 8 |
| 621 | 15 | GGCTGGCAATGGCGG | 18 |
| 841 | 19 | GGAAATTTGGGGACCAGG | 14 |
| 850 | 26 | GGGGACCAGGAACATAACAGACAAGG | 7 |
| 952 | 30 | GGCATGGAAGTCACACCTTCGGGAACGTGG | 11 |
| 952 | 30 | GGCATGGAAGTCACACCTTCGGGAACGTGG | 10 |

C

Search Parameters: QGRS Max Length: 30 | Min G-Group Size: 2 | Loop size: from 0 to 36 | Loop search string:

| Gene Information | |
|---------------------|------------------------------------|
| Gene ID: | Number of Products: 1 |
| Gene Symbol: | Number of poly A Signals: |
| Gene Size: 1251 nt. | QGRS found: 5 |
| | QGRS found (including overlaps): 9 |

```

000001 ATGCTGTGATA ATGGACCCCA AAATCAGCGA AATGCACTCC GCATTACGTT TGGTGGACCC TCAGATTCAA CTGGCAGTAA CCAGAATGGT GGGGCGCGAT
000101 CAAAACAACG TCGGCCCCAA GGTTTACCCA ATAATACTGC GTCTTGGTTC ACCGCTCTCA CTCAACATGG CAAGGAAGAC CTTAAATTCC CTCGAGGACA
000201 AGGCGTTCCA ATTAACACCA ATAGCAGTCC AGATGACCAA ATTGGCTACT ACCGAAGAGC TACCAGACGA ATTCGTGGTG GTGACGGTAA AATGAAAGAT
000301 CTCAGTCCAA GATGGTATTT CTA CTACTACCTA GGAACCTGGC CAGAAGCTGG ACTTCCCTAT GGTGCTAACA AAGACGGCAT CATATGGGTT GCAACTGAGG
000401 GAGCCTTGAA TACACCAAAA GATCACATTG GCACCCGCAA TCCTGTAAAC AATGCTGCAA TCGTGTACAA ACTTCCCTAA GGAACAACAT TGCCAAAAGG
000501 CTTCTACGCA GAAGGGAGCA GAGGCGGCAG TCAAGCCTCT TCTCGTTCCT CATCACGTAG TCGCAACAGT TCAAGAAATT CAACTCCAGG CAGCAGTAAA
000601 CGAACTTCTC CTGCTAGAAT GGCTGGCAAT GGCCTGTATG CTGCTCTTGC TTTGCTGCTG CTTGACAGAT TGAACCACTG TGAGAGCAAA ATGTCCTGGTA
000701 AAGGCCAACA ACAACRAGGC CAAACTGTCA CTAAGAAATC TGCTGTGAG GCTTCTAAGA AGCCTCGGCA AAAACGTA CTGCCACTAAG CATAACAATG
000801 AACACAAGCT TTCGGCAGAC GTGGTCCAGA ACAACCCCAA GGAAATTTTG GGGACCAGGA ACTAATCAGA CAAGGAAGT ATTACAACA TTGGCCGCAA
000901 ATTGCACAA TTGCCCCAG CGCTTCAGCG TTCTTCGGAA TGTCGCGCAT TGGCATGGAA GTCACACCTT CGGGAACGTG GPTGACCTAC ACAGGTGCCA
001001 TCAAATTTGA TGACAAAGAT CCAAATTTCA AAGATCAAGT CATTTTGTG AATAAGCATA TTGACGCATA CAAAACATTC CCACCAACAG AGCCTAAAAA
001101 GGACAAAAG AAGAAGGCTG ATGAAACTCA AGCCTTACCG CAGAGACAGA AGAAACAGCA AACTGTGACT CTTCTTCTG CTGCAGATTT GGATGATTT
001201 TCCAAACAAT TGCAACAATC CATGAGCAGT GCTGACTCAA CTCAGGCCTA A
    
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Supplement 7. The N gene and amino acid sequence in the Delta variant: A) N gene sequences (28247-29506); B) N protein amino acid sequences (1-419)

A

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                                                    atgt ctgataatgg
28261 accccaaaat cagcgaaatg caccgccat tacgtttggt ggaccctcag attcaactgg
28321 cagtaaccag aatggagaac gcagtggggc gcgatcaaaa caacgtcggc cccaaggttt
28381 acccaataat actgcgtctt ggttcaccgc tctcactcaa catggcaagg aaggccttaa
28441 attccctcga ggacaaggcg ttccaattaa caccaatagc agtccagatg accaaattgg
28501 ctactaccga agagctacca gacgaattcg tgggtggtgac ggtaaaatga aagatctcag
28561 tccaagatgg tatttctact acctaggaac tgggccagaa gctggacttc cctatggtgc
28621 taacaaagac ggcatacatat gggttgcaac tgagggagcc ttgaatacac caaaagatca
28681 cattggcacc cgcaatcctg ctaacaatgc tgcaatcgtg ctacaacttc ctcaaggaac
28741 aacattgcca aaaggcttct acgcagaagg gagcagagggc ggcagtcaag cctcttctcg
28801 ttctcatca cgtagtcgca acagttcaag aaattcaact ccaggcagca gtatgggaac
28861 ttctcctgct agaatggctg Ccaatggctg tgatgctgct cttgctttgc tgctgcttga
28921 cagattgaac cagcttgaga gcaaaatgtc tggtaaaggc caacaacaac aaggccaaac
28981 tgtcactaag aaatctgctg ctgaggcttc taagaagcct cggcaaaaac gtactgccac
29041 taaagcatac aatgtaacac aagctttcgg cagacgtggt ccagaacaaa cccaaggaaa
29101 ttttggggac caggaactaa tcagacaagg aactgattac aaacattggc cgcaaattgc
29161 acaatttgcc cccagcgtct cagcgttctt cggaatgctg cgcattggca tggaaagtac
29221 accttcggga acgtggttga cctacacagg tgccatcaaa ttggatgaca aagatccaaa
29281 tttcaaagat caagtcattt tgctgaataa gcatattgac gcatacaaaa cattcccacc
29341 aacagagcct aaaaaggaca aaaagaagaa ggcttatgaa actcaagcct taccgcagag
29401 acagaagaaa cagcaactg tgactcttct tctctgctgca gatttggatg atttctccaa
29461 acaattgcaa caatccatga gcagtgctga ctcaactcag gcctaa

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B

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1-44 MSDNGPQNQRNAPRITFGGSPDSTGNSQNGERSGARSKQRRPQG
45-102 LPNNTASWFTALTQHGKEGLKFPBQGVPIINTNSSPDDQIGYYRRATRIRIGGDGKMK
103-160 DLSPRWYFYLLGTGPEAGLPYGANKDGI IWVATEGALNTPKDHIGTRNPANNAIVLQ
161-218 LPQGTTLPGFYAEGSRGGSQASSRSSSRNSTRNTPGSSMGTSPARMAGNGCDAA
219-276 LALLLLDRLNQLESKMSGKQQQQGQTVTKKSAAEASKKPRQKRTATKAYNVTQAFGR
277-334 RGPEQTQGNFGDQELIRQGTDYKHWPIAQFAPSASAFFGMSRIGMEVTPSGTWLTYT
335-392 GAIKLDDKDPNFKDQVILLNKHIDAYKTFPPTEPKKDKKKKAYETQALPQRQKKQQTV
393-419 TLLPAADLDDFSKQLQQSMSSADSTQA

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