

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	GGGGAACCTCTCCTGCTAGAATGGCTGG	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 AATGCACCCC 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 TCAGTCCAAAG ATGGTATTTT TACTACCTAG GAACCTGGCC AGAAGCTGGA CTCCCTATG GTGCTAACAA AGACGGCCTC ATATGGGTTG
000401 CAACGTAGGG AGCCTTGAAT ACACCAAAG ATCACATTGG CACCCGCAAT CCGTCTAACA ATGCTGCAAT CGTGTACAA CTTCCTCAAG GAACACATT
000501 GCCAAAAGGC TTCTACGCAG AAGGGAGCAG AGGCGG CAGT CAAGCCTCTT CTCGTCCCTC ATCACGTAGT CGCAACAGTT CAAGAAATTC AACTCCAGGC
000601 AGCAGTAGGG GAACTTCTCC TGCTAGAATG GCTGGCAATG GCGGTGATGC TGCTCTGCTC TTGCTGCTGC TTGACAGATT GAACCAAGCTT GAGAGCAAAA
000701 TGTCTGGTAA AGGCCAACAA CAACAGGCC AACTGTCTAC TAAGAAATCT GCTGCTGAGG CTTCTAAGAA GCCTCGGCAA AAACGTACTG CCRCTAARGC
000801 ATACAAATGA ACACAGCTT TCGGCAGAGC TGGTCCAGAA CAACCCAAAG GAAATTTTGG GGACCAGGAA CTAATCAGAC AAGGAAGTGA TTACAAACAT
000901 TGGCCGCAAA TTGCACAATT TGCCTCCAGC GCTTCAGCGT TCTTCGGAAT GTCGGCGATT GGCAATGGAG TCACACCTTC GGGAAACGTGG TTGACCTACA
001001 CAGGTGCCAT CAAATTGGAT GACAAAGATC CAATTTCAA AGATCAAGTC ATTTTGTCTGA ATAAGCATAT TGACGCATAC AAAACATTC CACCAACAGA
001101 GCCTAAAAAG GACAAAAAGA AGAAGGCTGA TGAACCTCAA GCCTTACCGC AGAGACAGAA GAAACAGCAA ACTGTGACTC TTCTTCTCTG TCAGATTTTG
001201 GATGATTCTT CCAACAAATT GCAACAAATC ATGAGCAGTG CTGACTCAAC TCAGGCCTAA
    
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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	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
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 CCAGAATGGA GAACGCAGTG
000101 GGGCGCGATC AAAACAAAGT CGGCCCCRAG GTTTRACCAA TAATACTGCG TCTTGGTTCA CCGCTCTCRG TCRACATGGC AAGGAAGACC TTAARTTCCC
000201 TCGAGGACAA GGCCTTCCAA TTAACACCAA TAGCAGTCCA GATGACAAA TTGGCTACTA CCGAAGAGCT ACCAGACGAA TTCGTGGTGG TGACGGTAAA
000301 ATGAAAGATC TCACTCCAAAG ATGGTATTTT TACTACCTAG GAATCGGGCC AGAAGCTGGA CTTCCTCATG GTGCTAACAA AGACGGCCTC ATATGGGTGG
000401 CAACTGAGGG AGCCTTGAAT ACACCAAAAG ATCACATTGG CACCCGCAAT CCTGCTAACA ATGCTGCAAT CGTGTACAAA CTTCCTCAAG GAACAACTT
000501 GCCAAAAGC TTCTACGCAG AAGGGAGCAG AGGCCGCAGT CAAGCCTCTT CTCGTTCCCT ATCACGTAGT CGCAACAGTT CAAGAAATTC AACTCCAGGC
000601 AGCAGTAAAC GAACCTCTCC TGCTAGARTG GCTGGCAATG GCGGTGATGC TGCTCTGCTT TTGCTGCTGC TTGACAGATT GAACCACTT GAGAGCAAAA
000701 TGTTTTGTAA AGGCCAACAA CAACAAGGCC AACTGTCTAC TAAGAAATCT GCTGCTGAGG CTTCTAAGAA GCCTCGGCAA AAACGCTACTG CCACTAAAGC
000801 ATACAATGTA ACACAAGCTT TCGGCAGAGC TGGTCCAGAA CAACCCAAAG GAAATTTTGG GGACCCAGGAA CTAATCAGAC AAGGAACCTGA TTACAAACAT
000901 TGGCCGCAAA TTGCACAATT TGCCCCAGC GOTTACAGCT TCTTCGGAAT GTCCGCGATT GGCATGGGAG TCACACCTTC GGGAACTGGG TTGACCTACA
001001 CAGGTGCCAT CAATTTGGAT GACAAGATC CAAATTTCAA AGATCAAGTC ATTTTGTGTA ATARGCATA TACGCGCATA AAACACCTCC CACCACAGAA
001101 GCCTAAAGG GACAAAAGA AGAAGGCTGA TGAACCTCAA GCCTTACCGC AGAGACAGAA GAAACAGCAA ACTGTGACTC TTCTTCTGTC TGACAGATTG
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	GGAAATTTTGGGACCAGG	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	GGAAATTTTGGGACCAGG	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

```

000001 ATGTGTGATA ATGGACCCCA AAATCAGCGA AATGCACCCC GCATTACGTT TGGTGGACCC TCAGATTCAA CTGGCAGTAA CCAGAATGGA GAACGCAGTG
000101 GGGCGCGATC AAAACAACGT CGGCCCCAAAG GTTTACCCAA TAATACTGGG TCTTGGTTCA CCGCTOTCAC TCAACATGGC AAGGAAGACC TTAATTTCCC
000201 TCGAGGRCRA GGCCTTCCAA TTRACACCAA TAGCAGTCCA GATGACCAA TTGGTACTA CCGRAGAGCT ACCAGACGAA TTCGTGGTGG TGACGGTRAA
000301 ATGAAAGATC TCAGTCCAAG ATGATATTTT TACTACCTAG GAATCGGGCC AGAAGCTGGA CTTCCTATG GTGCTAACAA AGACGGCCTC ATATGGGTTG
000401 CAACTGAGGG AGCCTTGAAT ACACCCAAAAG ATCACATTGG CACCCGCAAT COTGCTAACA ATGCTGCAAT CGTGTACAAA CTTCCTCAAG GAACACATT
000501 GCCAAAAGGC TTCTACGCGAG AAGGGAGCAG AGGCGGCGT CAAGCCTCTT CTCGTTCCCT ATCAAGTAGT CGAACAGTT CAAGAAATTC AACTCCAGGC
000601 AGCAGTAGGG GAATTTCTCC TGCTAGAATG GCTGGCAATG GCGGTGATGC TGCTCTTGGT TTGCTGCTGC TTGACAGATT GAACCACTT GAGAGCAAAA
000701 TGTCCTGGTAA AGGCCAACAA CAACAAGGCC AAATGTGCAC TAAGAAATCT GCTGCTGAGG CTTCTAAGAA GCCTCGGCAA AAACCTACTG CCACATAAGC
000801 ATACAAATGA ACACRAGCTT TCGGCAGACG TGGTCCAGAA CAACCCCAAG GAAATTTTGG GGACCAAGAA CTAATCAGAC AAGGAACTGA TTACAAACAT
000901 TGGCCGCAA TTGCRCRATT TGCCCCACGC GCTTCAGCGT TCTTCGGRAT GTCCGCAATT GGCRTGGGAG TCACACCTTC GGGAACGTGG TTGACCTACA
001001 CAGGTGCCAT CAAATTTGGT GACAAAGATC CAAATTTCAA AGATCAAGTC ATTTTGTGTA ATAAGCATAT TGACGCATAC AAAACATTCC CACCAACAGA
001101 GCCTAAAAGG GACAAAAGA AGAAGGCTGA TGAACCTCAA GCCTTACCG AGAGACAGAA GAAACAGCAA ACTGTGACTC TTCTTCCTGC TGCAAGATTTG
001201 GATGATTTCT CCAACCAATT GCACCAATCC 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	GGCTTCTACGCAGAAGGGAGCAGAGGCGG	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	GGCTTCTACGCAGAAGGGAGCAGAGGCGG	9
508	29	GGCTTCTACGCAGAAGGGAGCAGAGGCGG	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

```

000001 ATGTCTGATA ATGGACCCCA AATCAGCGA AATGCACCCC GCATTACGTT TGGTGGACCC TCAGATTCAA CTGGCAGTAA CCAGAATGGA GAACGCAGTG
000101 GGGCGCGATC AAAACRACGT CGGCCCCAAAG GTTTACCCAA TAATACTGCG TCTTGGTTCA CCGCTCTCAC TCAACATGGC AAGGAAGACC TTAATTTCCC
000201 TCGAGGACAA GCGCTTCCAA TTAACACCAA TAGCAGTCCA GATGACCAA TTGGCTACTA CCGAAGAGCT ACCAGACGAA TTCGTGGTGG TGACGGTAAA
000301 ATGAAAGATC TCAGTCCAAAG ATGGTATTTT TACTACCTAG GAACTGGGCC AGAAGCTGGA CTTCCTATG GTGCTAACAA AGACGGCATC ATATGGGTTG
000401 CAACTGAGGG AGCCTTGAAT ACACCAAAG ATCACATTGG CACCCGCAAT COTGCTAACA ATGCTGCAAT CGTGCTACAA CTTCTCAAG GAACAACAT
000501 GCCAAAAGGC TTCTACGCAG AAGGAGCCAG AGGCGGCAGT CRAAGCCTCT CTCGTTCCCT ATCACGTAGT CGCAACAGTT CAAGAAATTC AACTCCAGGC
000601 AGCAGTAAAC GAACTTCTCC TGCTAGAATG GCTGGCAATG GCGGTGATGC TGCTCTTCTG TTGCTGCTGC TTGACAGATT GAACAGGCTT GAGAGCAAAA
000701 TGCTTGSTAA AGGCCAACAA CAAACAAGGC AACTGTCCAC TAAGAAATCT GCTGCTGAGG CTTCTAAGAA GCCTCGGCRA AAACGTAAGT CCRCTAAGC
000801 ATACAATGTA ACACAAGCTT TCGGCAGACG TGGTCCAGAA CAACCCAAAG GAAATTTTGG GGACCAGGAA CTRACCAGAC AAGGAAGTGA TTACAACAT
000901 TGGCCGCAAA TTGCACAATT TGCCCCCAGC GCTTCAGCGT TCTTGGAAAT GTCGCGCATT GGCATGGAAG TCACACCTTC GGGAAACGTGG TTGACCTACA
001001 CAGGTGCCAT CAAATTTGAT GACAAAGATC CAAATTTCAA AGATCAAGT ATTTTGTCTA ATAAGCATAT TGACGCATAC AAAACATTC CACCAACAGA
001101 GCCTAAAAAG GACAAAAAGA AGAAGGCTGA TGAACCTCAA GCCTTACCGC AGAGACAGAA GAAACAGCAA ACTGTGACTC TTCTTCTGTC TGCAATTTG
001201 GATGATTTCT CCAACAATTT 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 AATGCACCCC GCATTACGTT TGGTGGACCC TCAGATTCAA CTGGCAGTAA CCAGAAATGGA GAACGCAGTG
000101 GGGCGCGATC AAAACAACGT CGGCCCCAAAG GTTTACCCAA TAATACTGCG TCTTGGTTCA CCGCTCTCAC TCAACATGGC AAGGAAGGCC TTAATTCCTC
000201 TCGAGGACAA GCGTTCCTCA TTAACACCAA TAGCAGTCCA GATGACCAA TTGGCTACTA CCGAAGAGCT ACCAGACGAA TTCGTGGTGG TGACGGTAAA
000301 ATGAAAGATC TCAGTCCAAAG 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 TTGACRGATT GARCCAGCTT GAGAGCAAAA
000701 TGCTCGGTAA AGGCCAACAA CAACAAGGCC AAACGTGCAC TAAGAAATCT GCTGCTGAGG CTTCTAAGAA GCCTCGGCAA AAACGTAAGC CCACTAAAGC
000801 ATACAATGTA ACACAAGCTT TCGGCAGAGC TGGTCCAGAA CAAACCCAA GGAATTTTGG GGACCCAGGAA CTAATCAGAC AAGGAAGTGA TTACAAACAT
000901 TGGCCGCAAA TTGCACAATT TGCCCCCAGC GCTTCAGCGT TCTTCGGAAT GTCCGCGCATT GGCATGGGAG TCACACCTTC GGGAAAGTGG TTGACCTACA
001001 CAGGTGCCAT CAAATGGAT GACARAGATC CAAATTTCAA AGATCARGTC ATTTTGTGTGA ATAAGCATAT TGACGCATAC AAACCATTC CACCAACRGA
001101 GCCTAAAAAG GACAAAAAGA AGAAGGCTTA TGAARCTCAA GCCTTACC GC AGAGACAGAA GAARACAGAA ACTGTGACTC TTCTTCTGCT TGACGATTTG
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	GGGGACCAGGAAGTCAATCAGACAAGG	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 CTACTACCTA GGAACCTGGC CAGAAGCTGG ACTTCCCTAT GGTGCTAACA AAGACGGCAT CATATGGGTT GCAACTGAGG
000401 GAGCCTTGAA TACACCAAAA GATCACATTG GCACCCGCAA TCCTGTAAAC AATGCTGCAA TCGTGTACA ACTTCCTCAA GGAACAACAT TGCCAAAAGG
000501 CTCTACGCA GAAGGGAGCA GAGGCGGCAG TCAAGCCTCT TCTCGTCCCT CATCAGTAG TCGCAACAGT TCAAGAAATT CAACTCCAGG CAGCAGTAAA
000601 CGAACTTCTC CTGCTAGAAT GGCTGGCAAT GGCCTGTATG CTGCTCTTGC TTTGCTGCTG CTTGACAGAT TGAACAGCT TGAGAGCAAA ATGTCGTGTA
000701 AAGGCCAACA ACAACRAGGC CAAACTGTCA CTAAGAAATC TGCTGTGAG GCTTCTAAGA AGCCTCGGCA AAAACGTAAT GCCACTAAG CATACAATGT
000801 AACACAAGCT TTCGGCAGAC GTGGTCCAGA ACAACCCCAA GGAAATTTTG GGGACCAGGA ACTAATCAGA CAAGGAAGCT ATTACAACA TTGGCCGCAA
000901 ATTGCACAA TFGCCCCAG CGCTTCAGCG TTCTTCGGAA TGTCGCGCAT TGGCATGGAA GTCACACCTT CGGGAACGTG GPTGACCTAC ACAGGTGCCA
001001 TCAAATTGGA 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 tggtggtgac ggtaaaatga aagatctcag
28561 tccaagatgg tatttctact acctaggaac tgggccagaa gctggacttc cctatggtgc
28621 taacaaagac ggcatacatat gggttgcaac tgagggagcc ttgaatacac caaaagatca
28681 cattggcacc cgcaatcctg ctaacaatgc tgcaatcgtg ctacaacttc ctcaaggaac
28741 aacattgcc aagggcttct acgcagaagg gagcagaggg ggcagtcaag cctcttctcg
28801 ttctcatca cgtagtcgca acagttcaag aaattcaact ccaggcagca gtatgggaac
28861 ttctcctgct agaatggctg Tcaatggctg tgatgctgct cttgctttgc tgctgcttga
28921 cagattgaac cagcttgaga gcaaatgtc tggtaaaggc caacaacaac aaggccaac
28981 tgtcactaag aaatctgctg ctgaggcttc taagaagcct cggcaaaaac gtactgccac
29041 taaagcatac aatgtaacac aagctttcgg cagacgtggt ccagaacaaa cccaaggaaa
29101 ttttggggac caggaactaa tcagacaagg aactgattac aacattggc cgcaaattgc
29161 acaatttgcc cccagcgtt cagcgttctt cggaatgtcg 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 tctgctgca gatttgatg atttctcaa
29461 acaattgcaa caatccatga gcagtgtgta ctcaactcag gcctaa

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B

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1-44  MSDNGPQNQRNAPRITFGGSPDSTGSNQNTERSARSKQRRPQG
45-102 LPNNTASWFTALTQHGKEGLKFPRGQVPIINTNSSPDDQIGYYRRATRIRGGDGKMK
103-160 DLSPRWYFYLLGTGPEAGLPYGANKDGI IWWATEGALNTPKDHIGTRNPANNAIVLQ
161-218 LPQGTTLPKGFYAEGSRGGSQASSRSSSRNSTRNTPGSSMGTSPARMANGCDAA
219-276 LALLLLDRLNQLESKMSGKQQQQGQTVTKKSAAEASKKPRQKRTATKAYNVTQAFGR
277-334 RGPEQTQGNFGDQELIRQGTDYKHWPIAQFAPSASAFFGMSRIGMEVTPSGTWLTYT
335-392 GAIKLDDKDPNFKDQVILLNKHIDAYKTFPPTEPKKDKKKKAYETQALPQRQKKQQTV
393-419 TLLPAADLDDFSKQLQQSMSSADSTQA

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