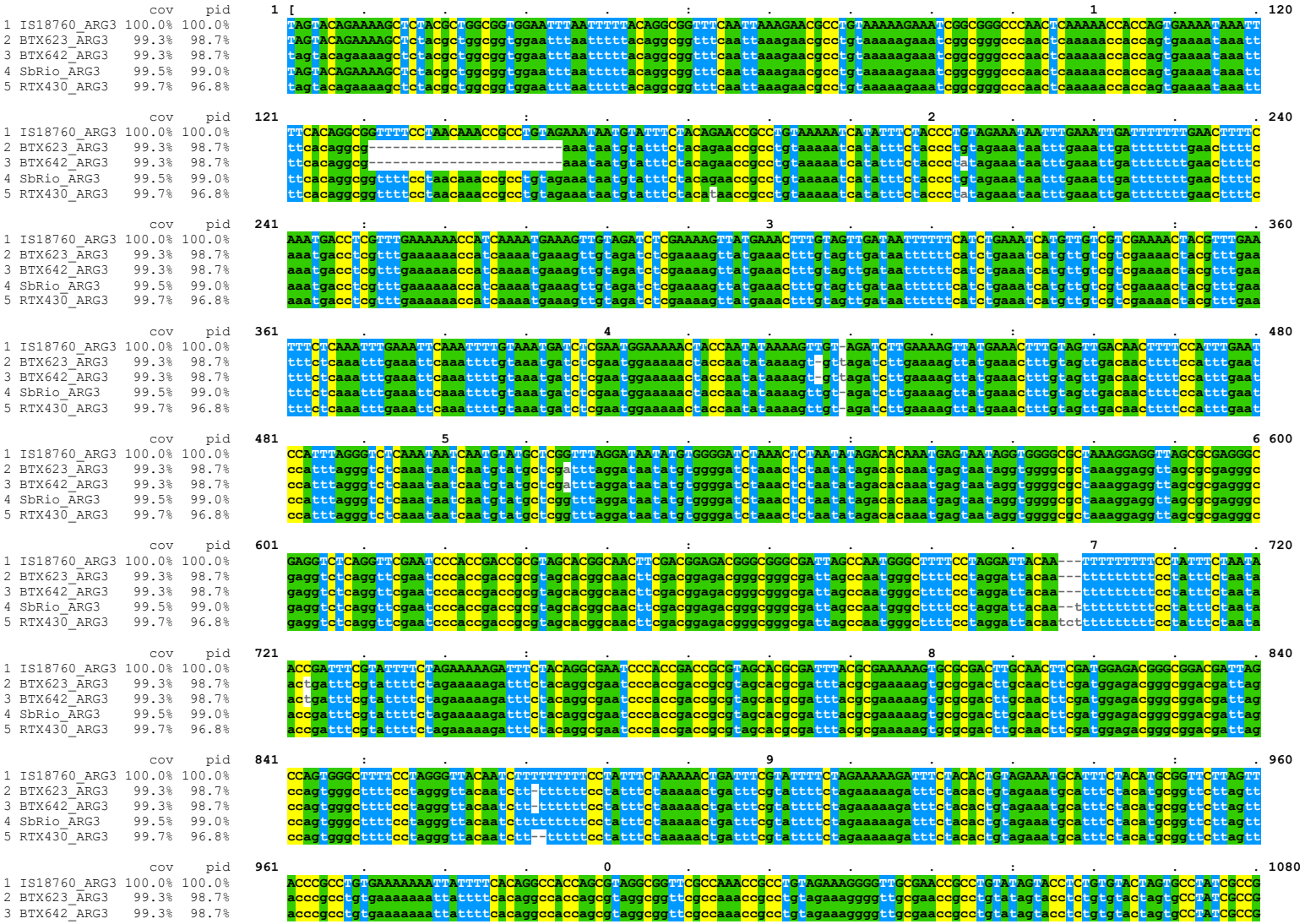
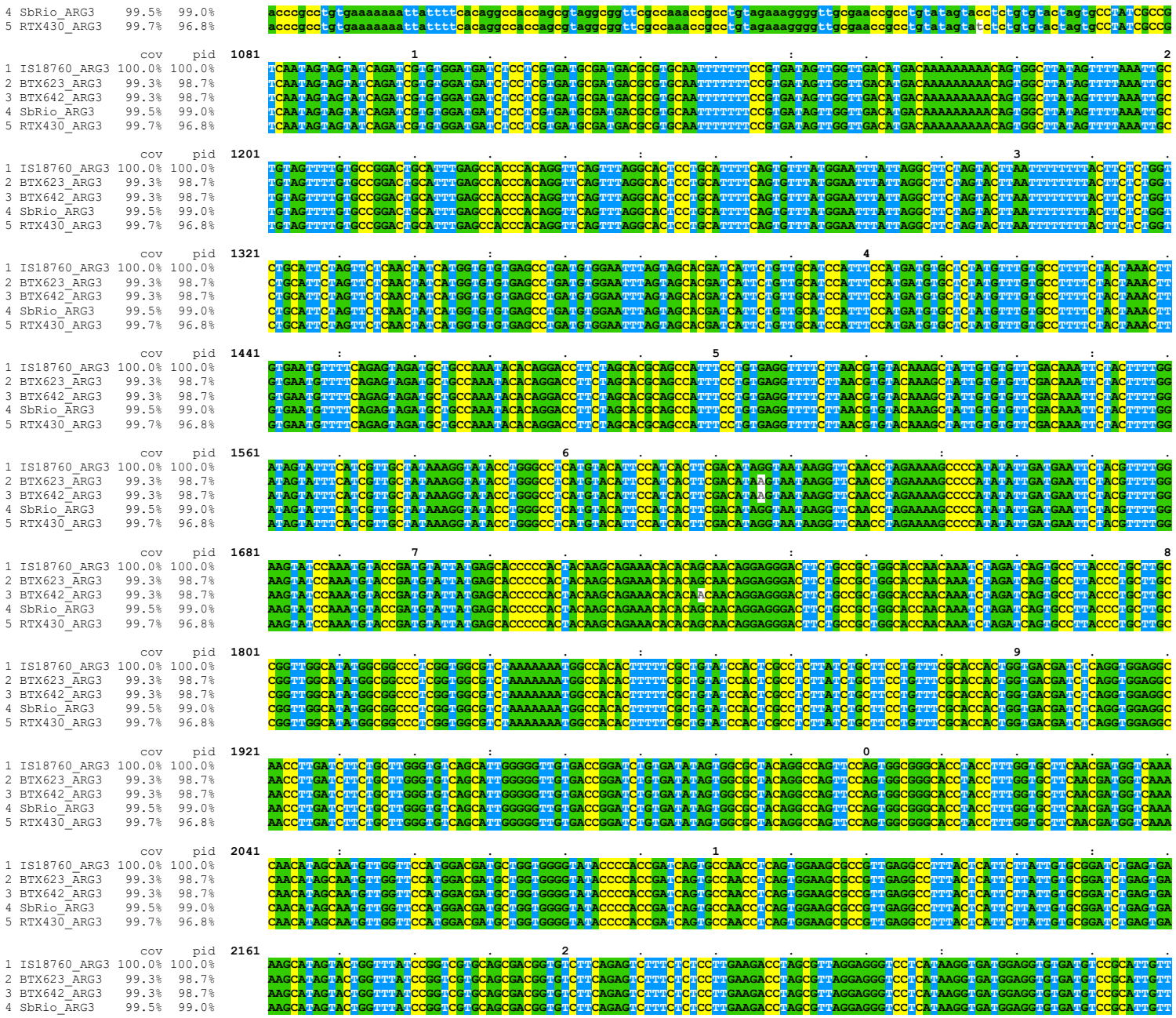
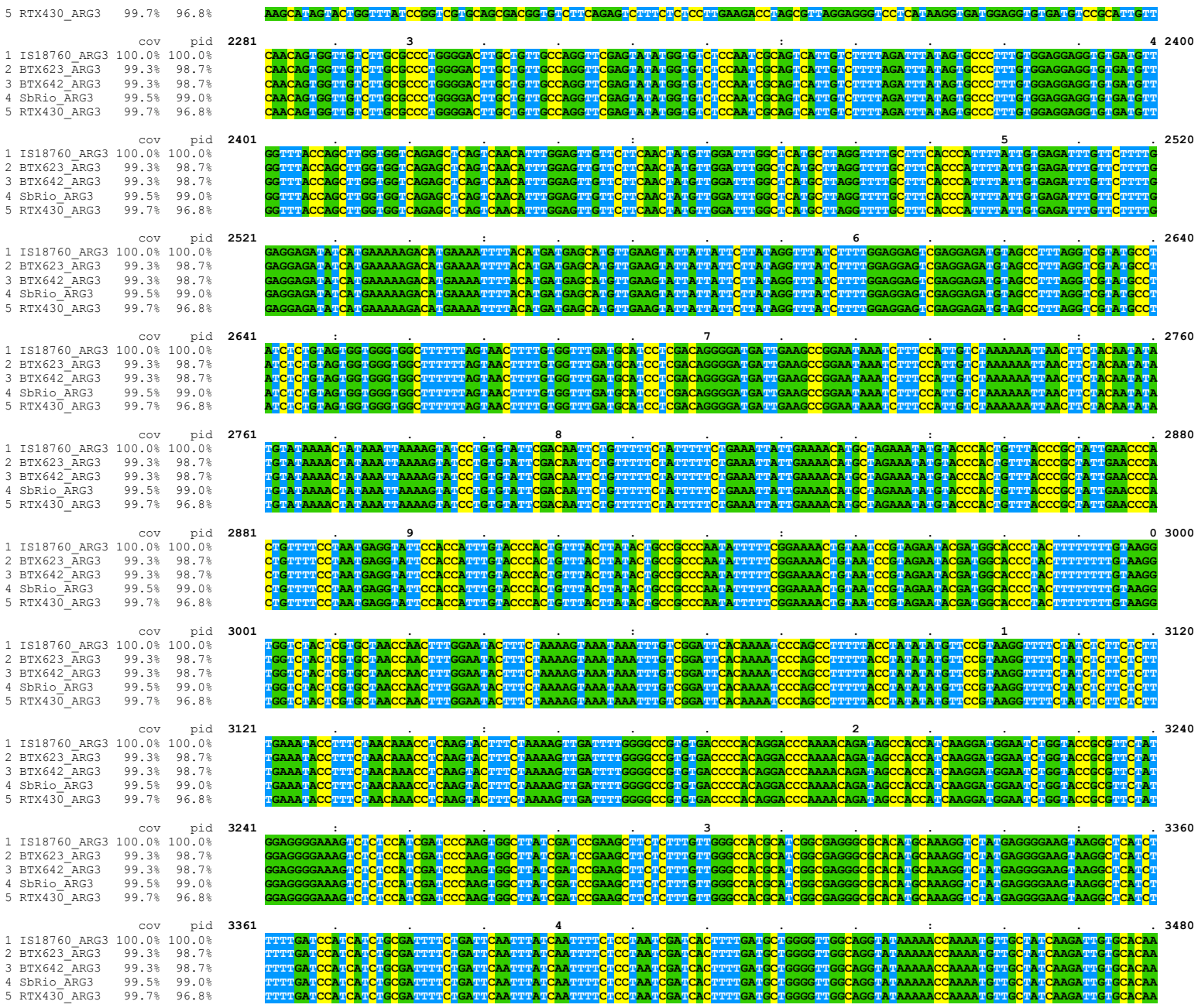
Supplemental_file_4 – corresponds to page 80-81.

Alignment of the genomic sequences of the 15.6 Kb wild-type *ARG3* locus with the four reference genomes. The susceptible parent TAM428 carries the BTx623 genomic sequence throughout *ARG3* locus.



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cov pid
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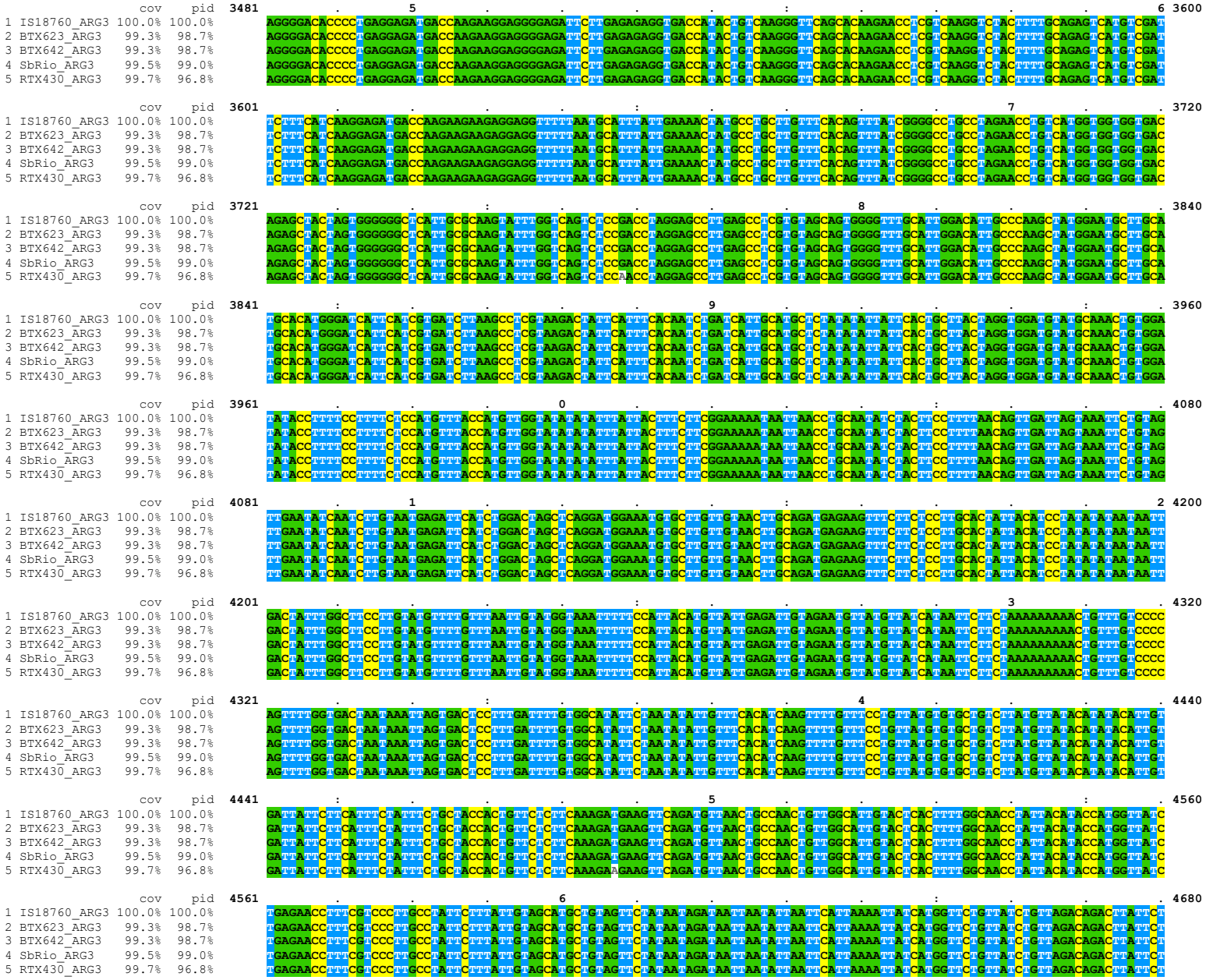
3 BTX642_ARG3 99.3% 98.7%
4 SbRio_ARG3 99.5% 99.0%
5 RTX430_ARG3 99.7% 96.8%
2281
2400
2401
2520
2521
2640
2641
2760
2761
2880
2881
3000
3001
3120
3121
3240
3241
3360
3361
3480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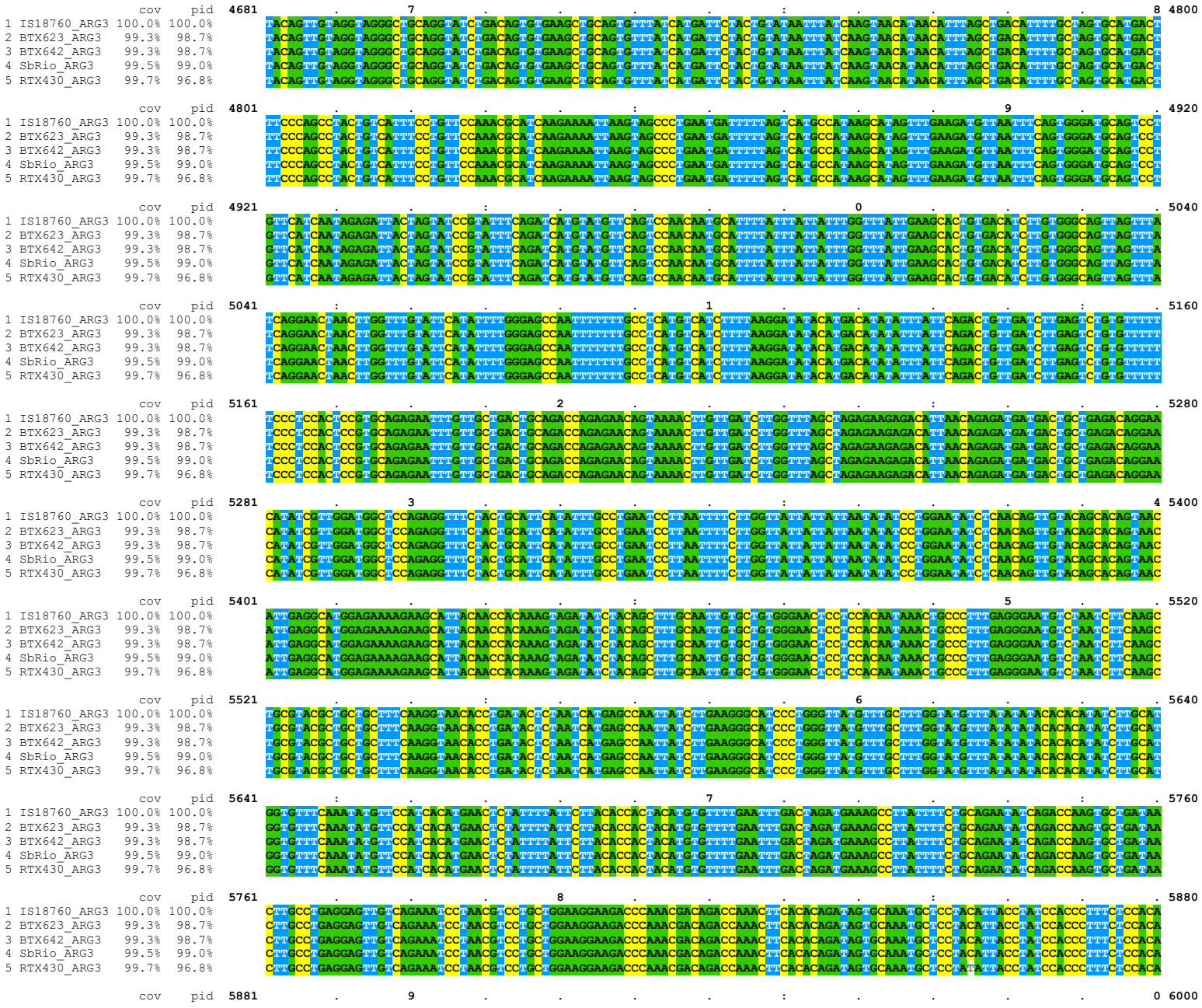
5 RTX430_ARG3 99.7% 96.8%
3481 3600
3601 3720
3721 3840
3841 3960
3961 4080
4081 4200
4201 4320
4321 4440
4441 4560
4561 4680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5 RTX430_ARG3 99.7% 96.8%
4681 4800
4801 4920
4921 5040
5041 5160
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5281 5400
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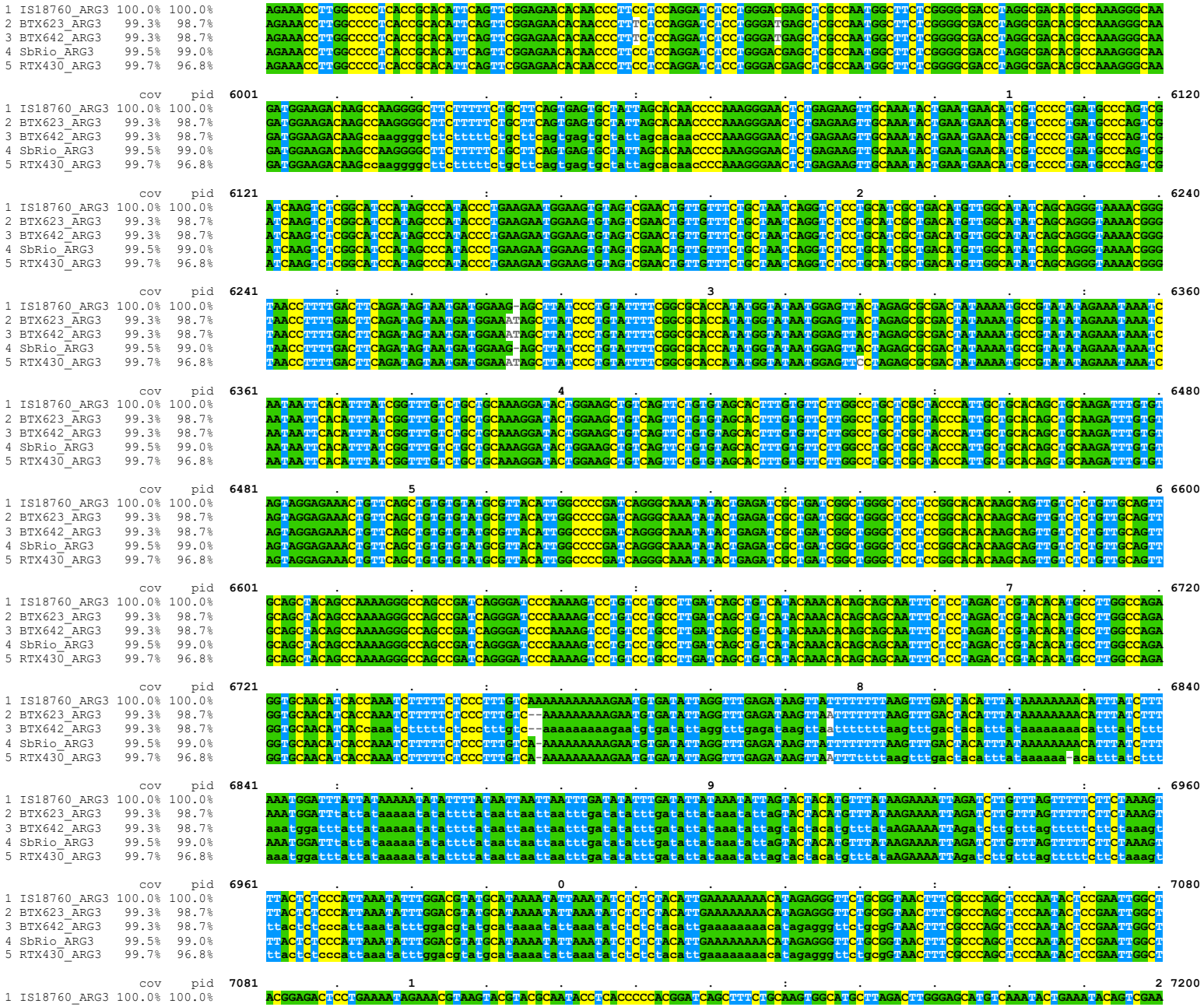
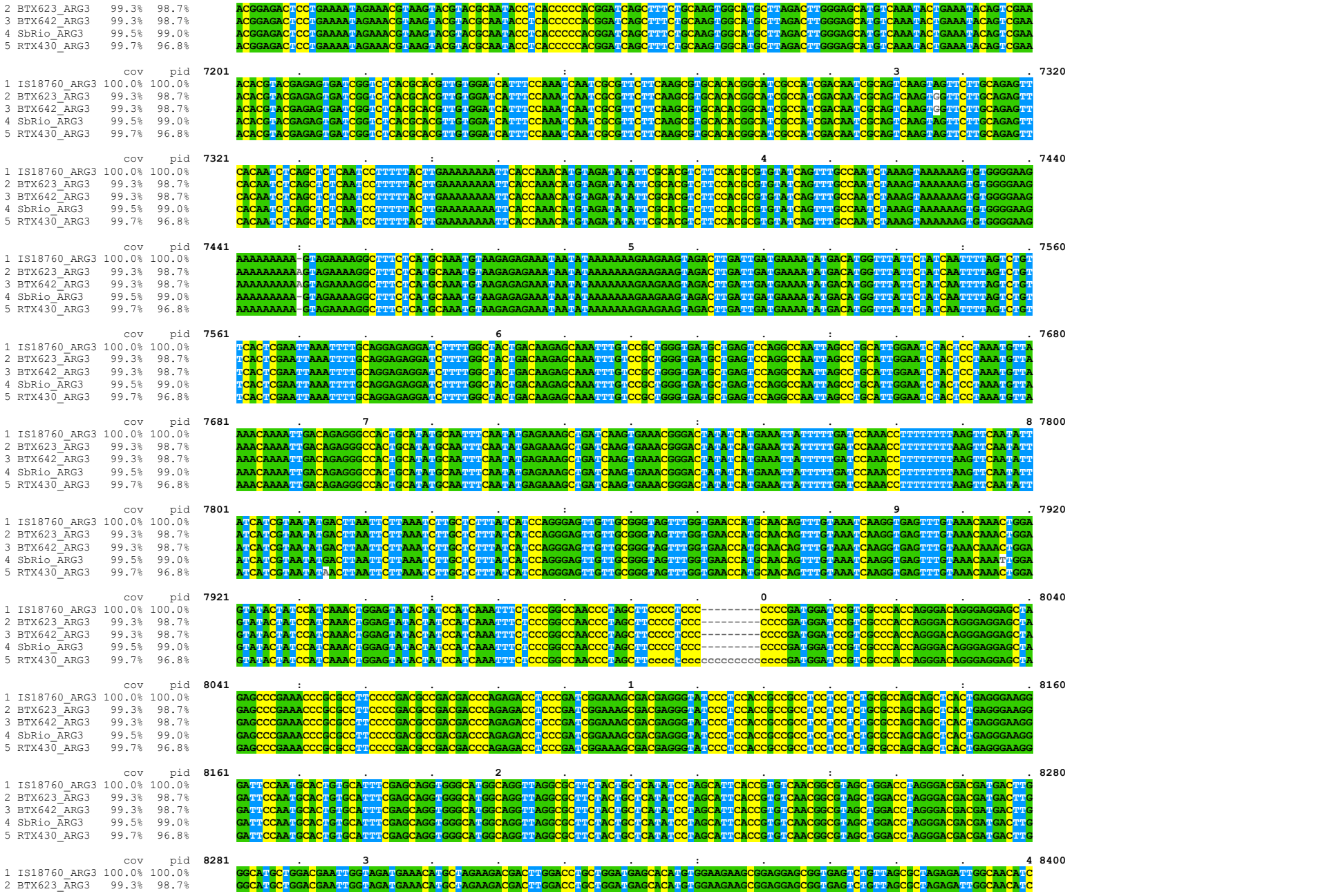
5881 6000

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5 RTX430_ARG3 99.7% 96.8%
cov pid
1 IS18760_ARG3 100.0% 100.0%
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7201
7320
7321
7440
7441
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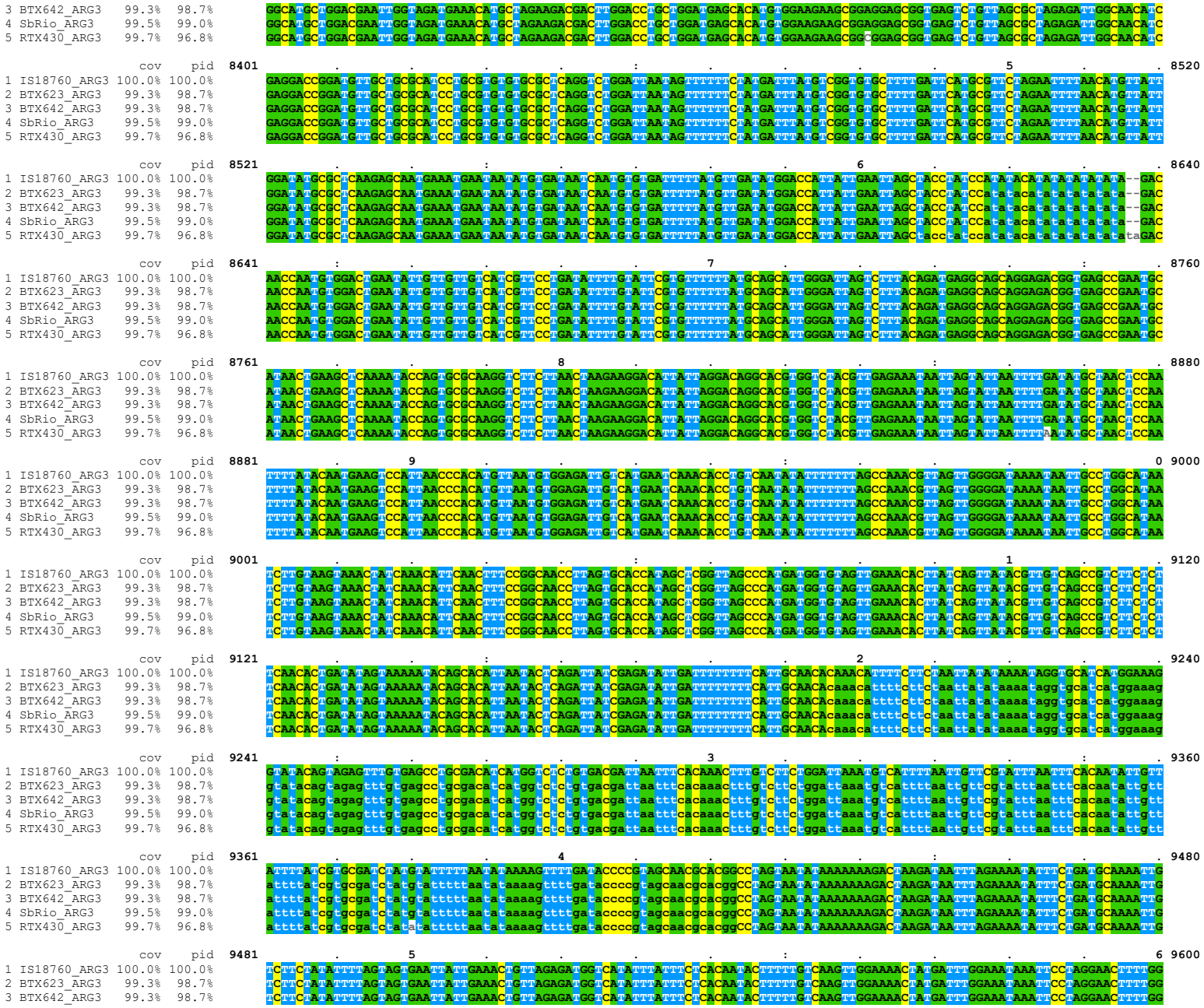
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5 RTX430_ARG3 99.7% 96.8%
cov pid 8521 8640
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cov pid 8881 9000
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5 RTX430_ARG3 99.7% 96.8%
cov pid 9121 9240
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2 BTX623_ARG3 99.3% 98.7%
3 BTX642_ARG3 99.3% 98.7%
4 SbRio_ARG3 99.5% 99.0%
5 RTX430_ARG3 99.7% 96.8%
cov pid 9241 9360
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5 RTX430_ARG3 99.7% 96.8%
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3 BTX642_ARG3 99.3% 98.7%
4 SbRio_ARG3 99.5% 99.0%
5 RTX430_ARG3 99.7% 96.8%
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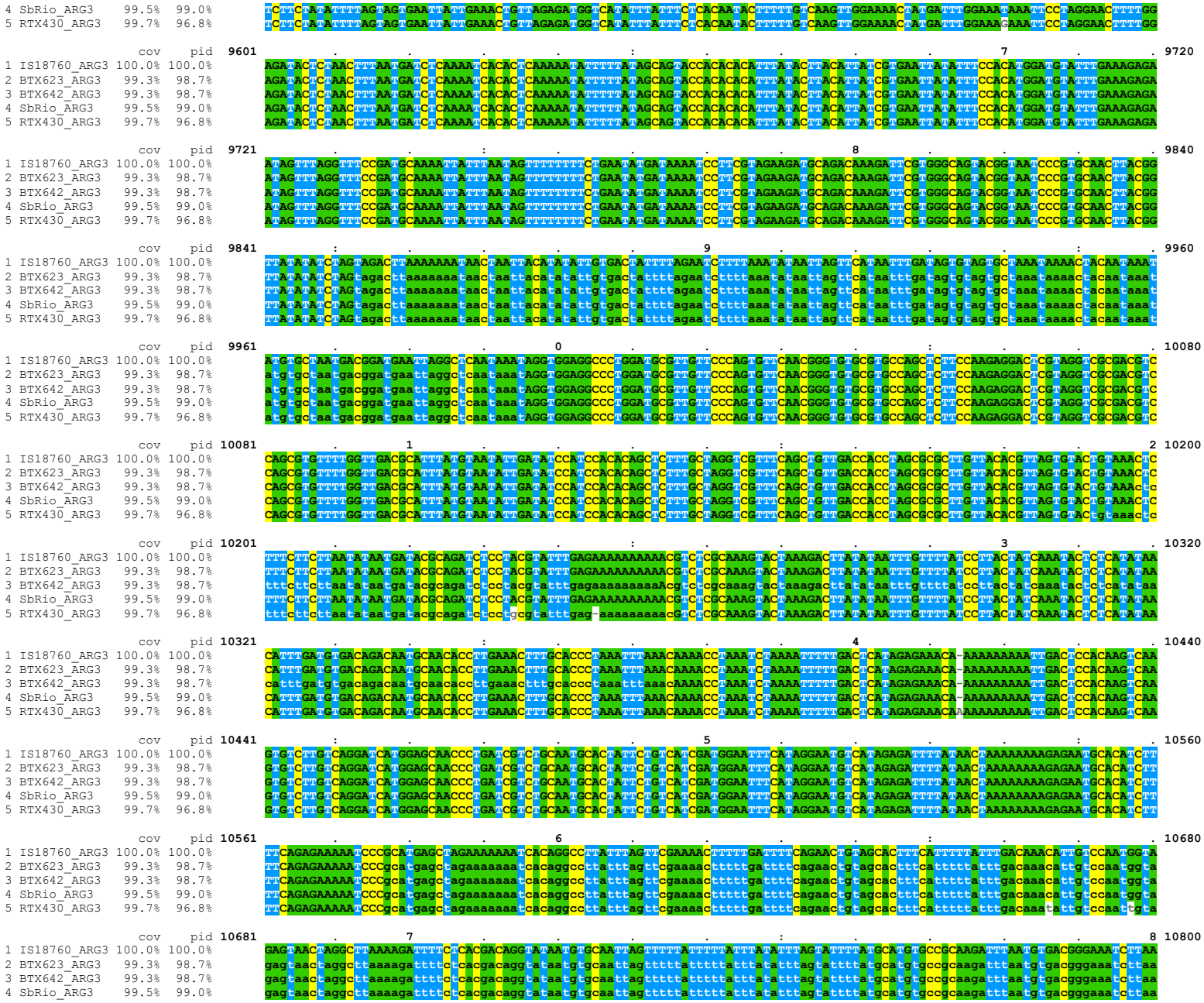

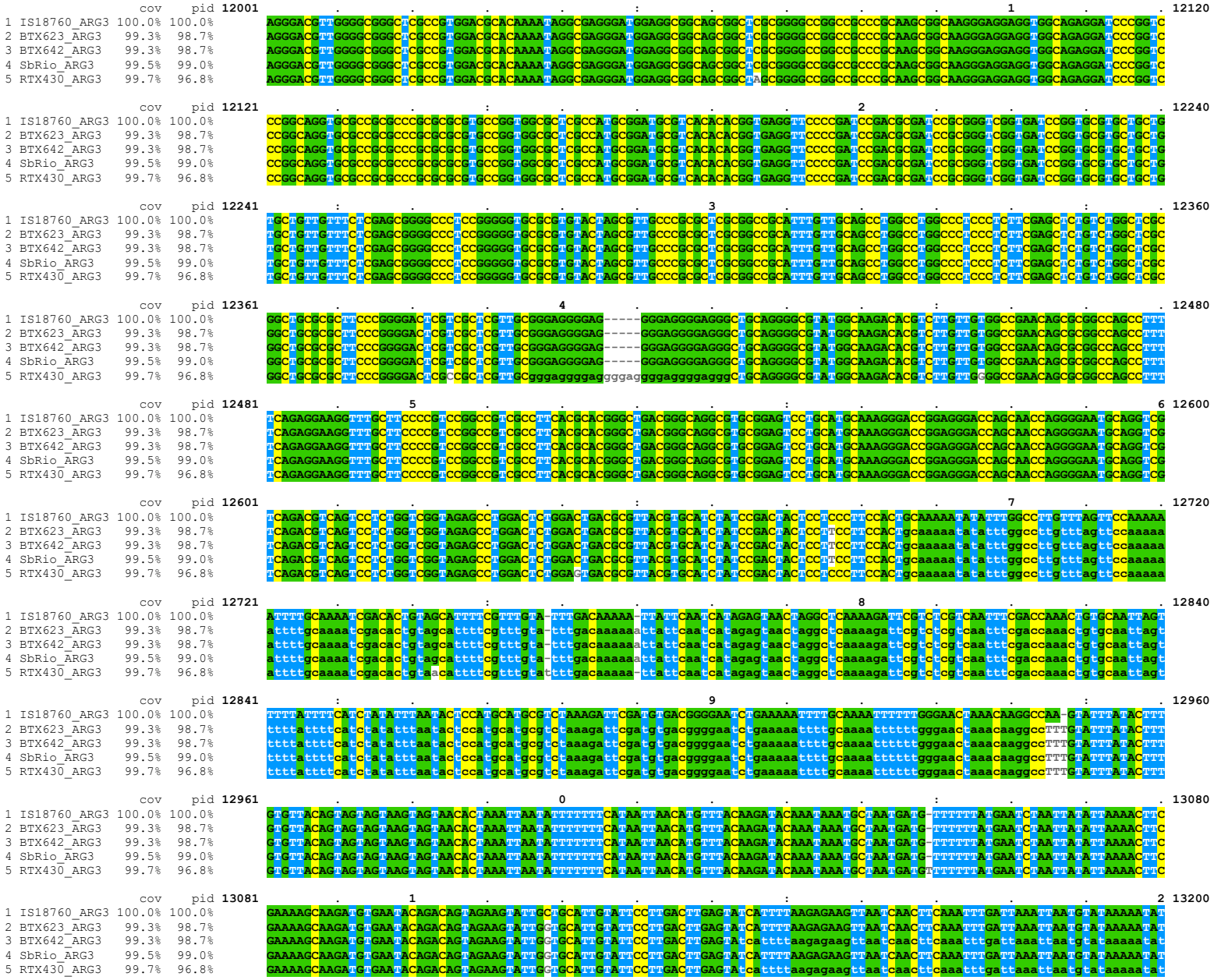
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cov pid 12121 12240
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cov pid 12241 12360
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cov pid 13081 13200
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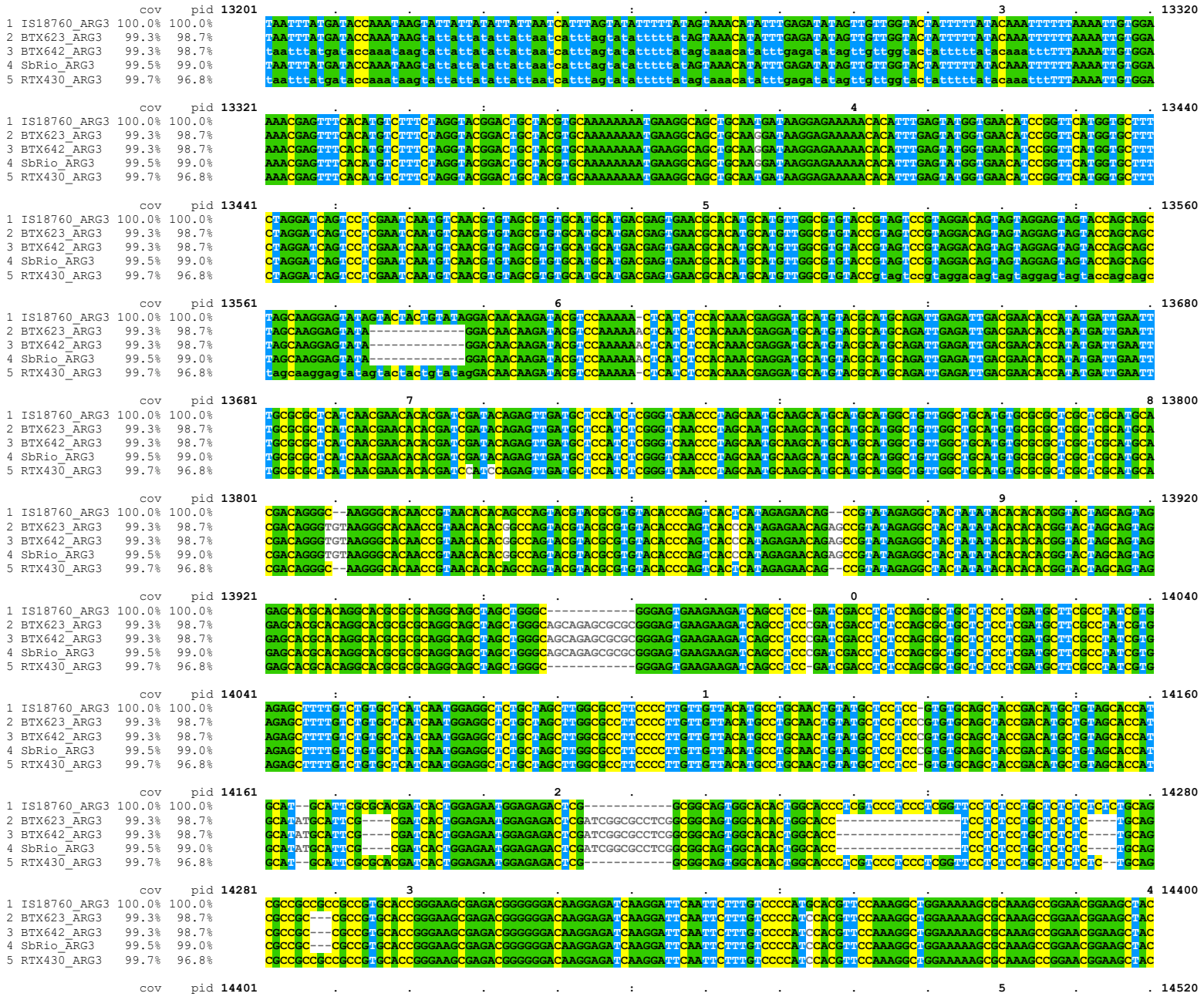
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3 BTX642_ARG3 99.3% 98.7%
4 SbRio_ARG3 99.5% 99.0%
5 RTX430_ARG3 99.7% 96.8%
cov pid 13441 13560
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2 BTX623_ARG3 99.3% 98.7%
3 BTX642_ARG3 99.3% 98.7%
4 SbRio_ARG3 99.5% 99.0%
5 RTX430_ARG3 99.7% 96.8%
cov pid 13561 13680
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3 BTX642_ARG3 99.3% 98.7%
4 SbRio_ARG3 99.5% 99.0%
5 RTX430_ARG3 99.7% 96.8%
cov pid 13681 13800
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2 BTX623_ARG3 99.3% 98.7%
3 BTX642_ARG3 99.3% 98.7%
4 SbRio_ARG3 99.5% 99.0%
5 RTX430_ARG3 99.7% 96.8%
cov pid 13801 13920
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3 BTX642_ARG3 99.3% 98.7%
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cov pid 13921 14040
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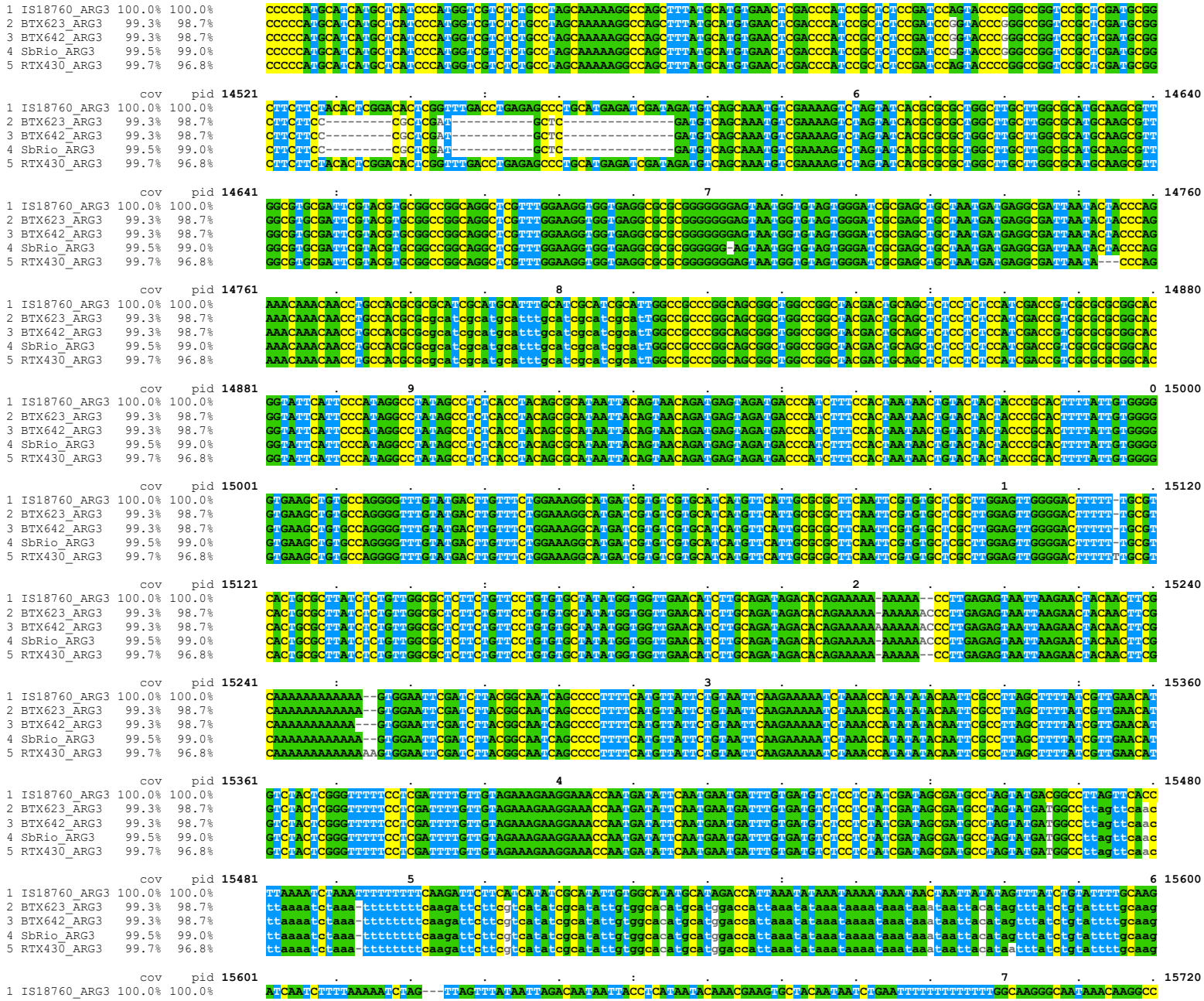

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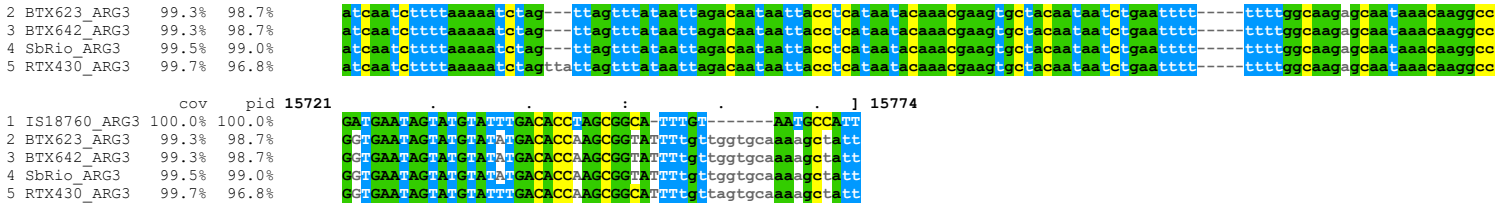
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cov pid 15721 . . : . .] 15774
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