# COVID-19 subject deWit\_RM7\_Vehicle

2020-10-02

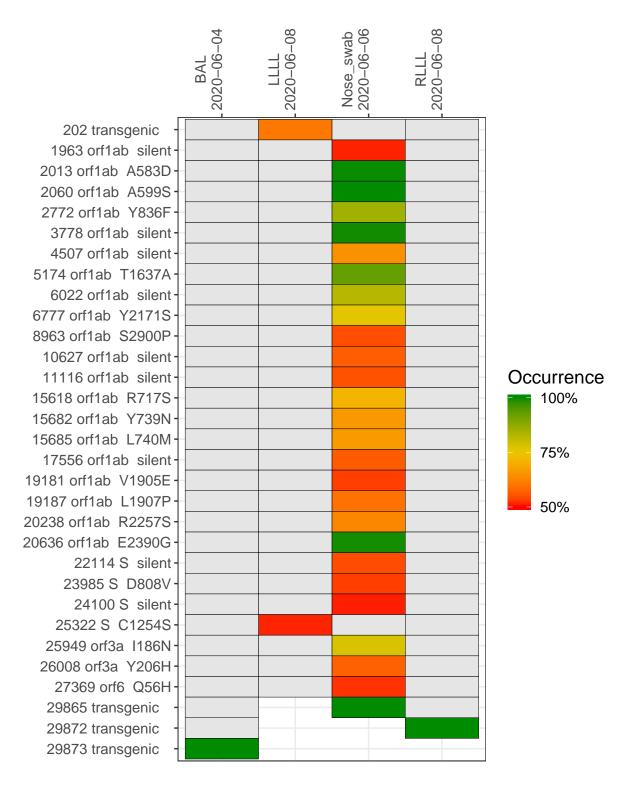
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

Table 1. Sample summary.

Experiment	Туре	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP8003-1	single experiment	NA	Nose_swab	2020-06-06	8.63	99.3%	99.0%
VSP8015-1	single experiment	NA	Rectal_swab	2020-06-03	29.98	100.0%	99.9%
VSP8017-1	single experiment	NA	LLLL	2020-06-08	11.71	99.9%	99.9%
VSP8035-1	single experiment	NA	RLLL	2020-06-08	29.84	100.0%	100.0%
VSP8036-1	single experiment	NA	$\operatorname{BAL}$	2020-06-04	29.87	100.0%	100.0%

#### Variants shared across samples

The heat map below shows how variants (reference genome USA-WA1-2020) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 for more reads, the alternative base is found in > 50% of read pairs and the variant yields a PHRED score > 20. Gray tiles denote positions where the variant was not the major variant or no variants were found. The relative base compositions of each experiment used to calculate tiles are shown in the following plot where the total number of position reads are shown atop of each plot.

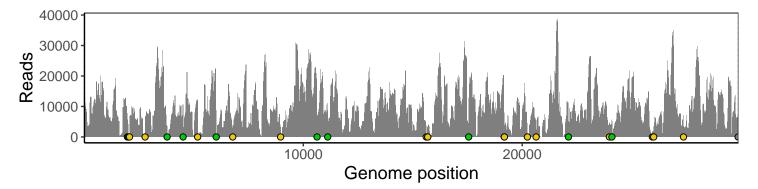


202 transgenic 10726 4417 3678 12479 1963 orf1ab silent 28273 17241 7431 27679 2013 orf1ab A583D 24135 14631 3834 20510 2060 orf1ab A599S 23840 11755 37 19933 2772 orf1ab Y836F 12246 7769 277 12146 3778 orf1ab silent 16634 8956 2000 16536 4507 orf1ab silent 17600 14702 9874 16451 5174 orf1ab T1637A 35485 12306 3876 20643 6022 orf1ab silent 15017 1677 4015 11631 6777 orf1ab Y2171S 8963 orf1ab S2900P 29243 4120 3052 13540 8963 orf1ab S2900P 29243 5181 3175 19344 10627 orf1ab silent 22177 12988 8832 12988 8932 12988 1116 orf1ab silent 22177 12988 8832 12988 8832 12988 15682 orf1ab T739N 14956 2157 3412 12766 15685 orf1ab L740M 15000 2127 3412 12766 15685 orf1ab S1ent 35411 10957 10065 24532 No 1485 1568 0rf1ab R747S 2778 1568 0rf1ab L740M 15000 2127 3412 12766 17556 orf1ab silent 35411 10957 10065 24532 No 1485 12612 2038 orf1ab R2257S 27160 17391 612 18333 1568 22114 S silent 26193 11212 11006 18356 22114 S silent 26193 11212 11006 18356 22308 S D808V 25471 22342 4698 17234 20608 orf3a Y206H 21021 8376 3625 17061 27389 orf6 C56H 27637 21387 763 3625 17061 29873 transgenic 71 7 29873 transgenic 71 7 29873 transgenic 71 29873 transg		BAL 2020-06-04	LLLL 2020-06-08	Nose_swab 2020-06-06	RLLL 2020-06-08	
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20238 orf1ab R2257S	19181 orf1ab V1905E	24845	1566	7811	13019	
20636 orf1ab E2390G       21623       5819       2365       15168         22114 S silent       26193       11212       11006       18356         23985 S D808V       25471       22342       4608       17234         24100 S silent       31520       21993       5221       23647         25322 S C1254S       23868       5673       9753       15613         25949 orf3a I186N       13158       7248       9       11294         26008 orf3a Y206H       21021       8376       3525       17051         27369 orf6 Q56H       27637       21387       7163       23361         29872 transgenic       454       667       983         29872 transgenic       71       7         29873 transgenic       61	19187 orf1ab L1907P	24325	1596	7945	12612	No data
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29865 transgenic       454       667       983         29872 transgenic       71       7         29873 transgenic       61       61	26008 orf3a Y206H	21021	8376	3525	17051	
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	29872 transgenic	71			7	
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VSP8036 VSP8003		7-	7	<u></u>	10	
%SP8		3036	3017	3003	3035	
		SP8	SP8	SP8	SPE	
		>	>	>	>	

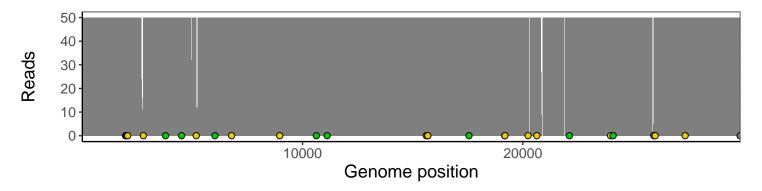
## Analyses of individual experiments and composite results.

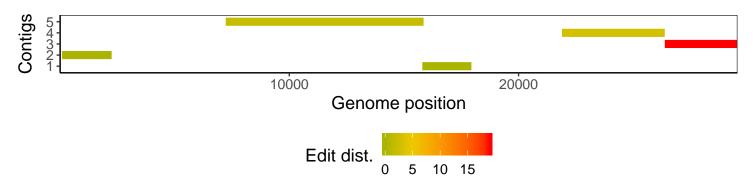
## $VSP8003-1 \mid 2020-06-06 \mid Nose\_swab \mid SRR11783603 \mid genomes \mid single \; experiment$

The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



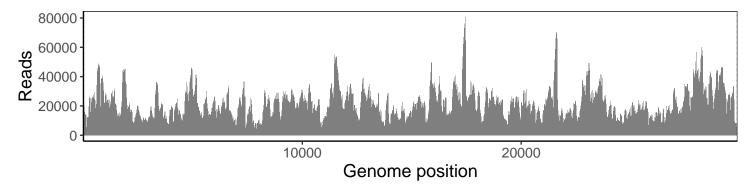
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



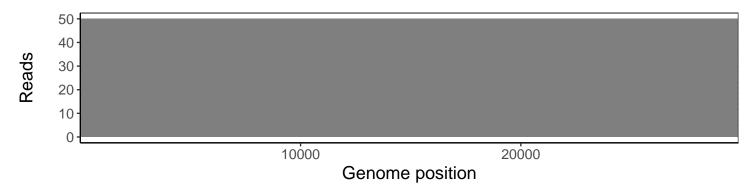


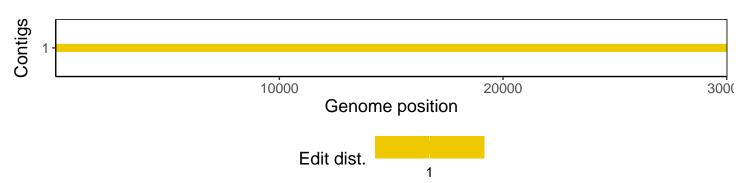
### $VSP8015\text{-}1 \mid 2020\text{-}06\text{-}03 \mid Rectal\_swab \mid SRR11783600 \mid genomes \mid single \ experiment$

The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



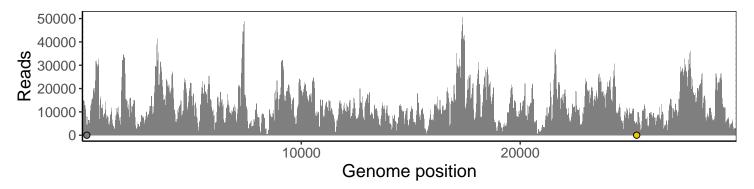
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



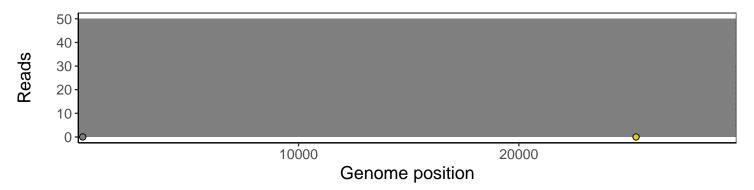


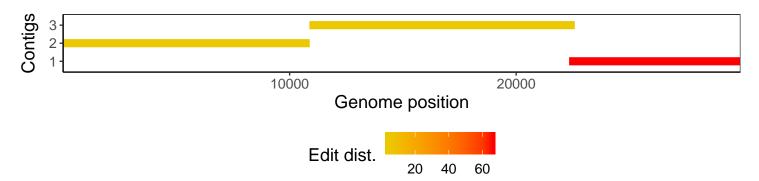
### $VSP8017\text{-}1 \mid 2020\text{-}06\text{-}08 \mid LLLL \mid SRR11783604 \mid genomes \mid single \ experiment$

The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



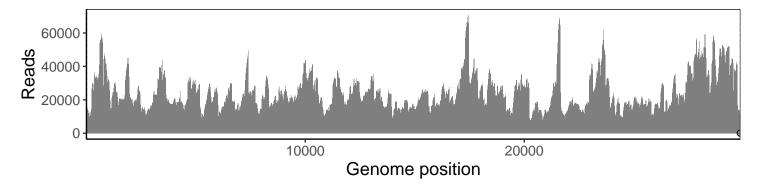
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



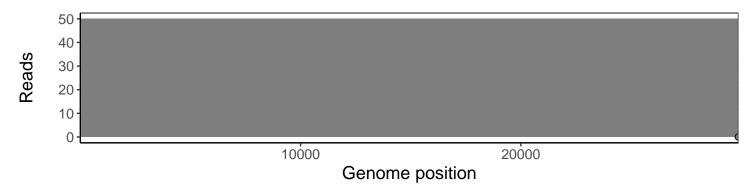


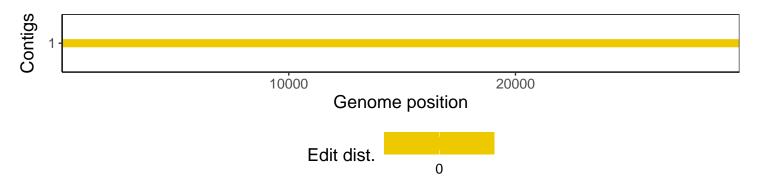
#### $VSP8035\text{-}1 \mid 2020\text{-}06\text{-}08 \mid RLLL \mid SRR11783601 \mid genomes \mid single \ experiment$

The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



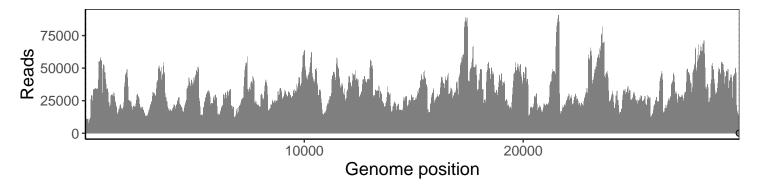
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.





## $VSP8036\text{-}1 \mid 2020\text{-}06\text{-}04 \mid BAL \mid SRR11783605 \mid genomes \mid single \ experiment$

The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



Excerpt from plot above focusing on reads coverage from 0 to 50 NT.

