X

x

Reference Genome: H1N1pdm_ref.fasta
Clade assignment: 6B.1A.5a.1

Clade assignment and HA sequence stats

Table 1: NextClade results. A. Clade assignment given to the strain using Nextclade. Highlighting the quality (qc) scores and qualitative assignment.

seqName	clade	qc.overallScore	qc.overallStatus
HUP_19_007_S3-CY266191_1_4	6B.1A.5a.1	0	good

B. Number of SNPs/indels.

totalSubstitutions	totalDeletions	totalInsertions	totalFrameShifts
65	0	0	0

C. Amino acid level effects of SNPs/indels.

totalAminoacidSubstitutions	totalAminoacidDeletions	totalAminoacidInsertions
25	0	0

Read stats

Table 2: Read quality stats using fastp and number of paired reads aligned to reference.

total___before	total___after	passed_filter__	low_quality__	too_many_N__	aligned
7576334	7233804	7233804	339394	456	1077305

Coverage and Depth

Table 3: Percent of genome covered by 1 or 5 reads and per-base read depth stats per segment.

segment_id	segment	perc_gt_1	perc_gt_5	mean_depth	median_depth	min_depth	max_depth	std_depth
CY266198_1_1	1	100	100.00	1472.42	219.0	63	8020	2379.74
CY266197_1_2	2	100	100.00	170.55	149.0	28	545	108.72
CY266196_1_3	3	100	100.00	844.55	481.0	161	3782	764.02
CY266191_1_4	4	100	99.77	5760.21	6784.0	1	8020	2124.91
CY266194_1_5	5	100	100.00	5109.54	5060.0	1142	8010	1393.41
CY266193_1_6	6	100	100.00	6298.41	6784.0	1084	8022	1492.09
CY266192_1_7	7	100	100.00	7691.38	7904.5	2820	8035	639.11
CY266195_1_8	8	100	100.00	7725.97	7923.0	2690	8040	654.46

Variants

Table 4: Counts of all variants per segment.

segment_id	segment	count_vars
CY266198_1_1	1	93
CY266197_1_2	2	115
CY266196_1_3	3	83
CY266191_1_4	4	151
CY266194_1_5	5	97
CY266193_1_6	6	125
CY266192_1_7	7	51
CY266195_1_8	8	71

Table 5: Counts of major variants per segment (>=50% of reads contain variant).

segment_id	segment	count_vars
CY266198_1_1	1	64
CY266197_1_2	2	52
CY266196_1_3	3	59
CY266191_1_4	4	66
CY266194_1_5	5	42
CY266193_1_6	6	52
CY266192_1_7	7	21
CY266195_1_8	8	27

Figure 1: Read depth and coverage map.

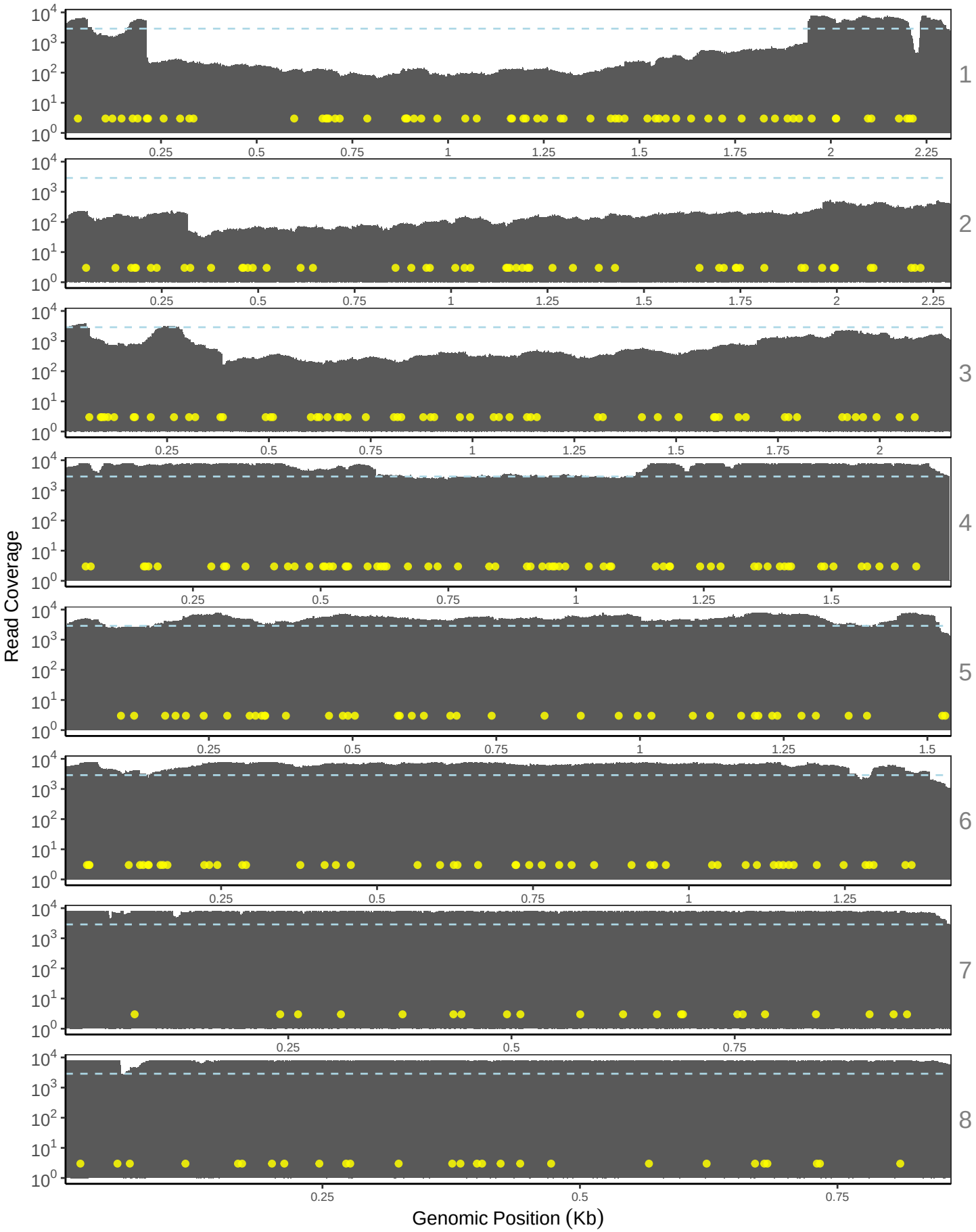
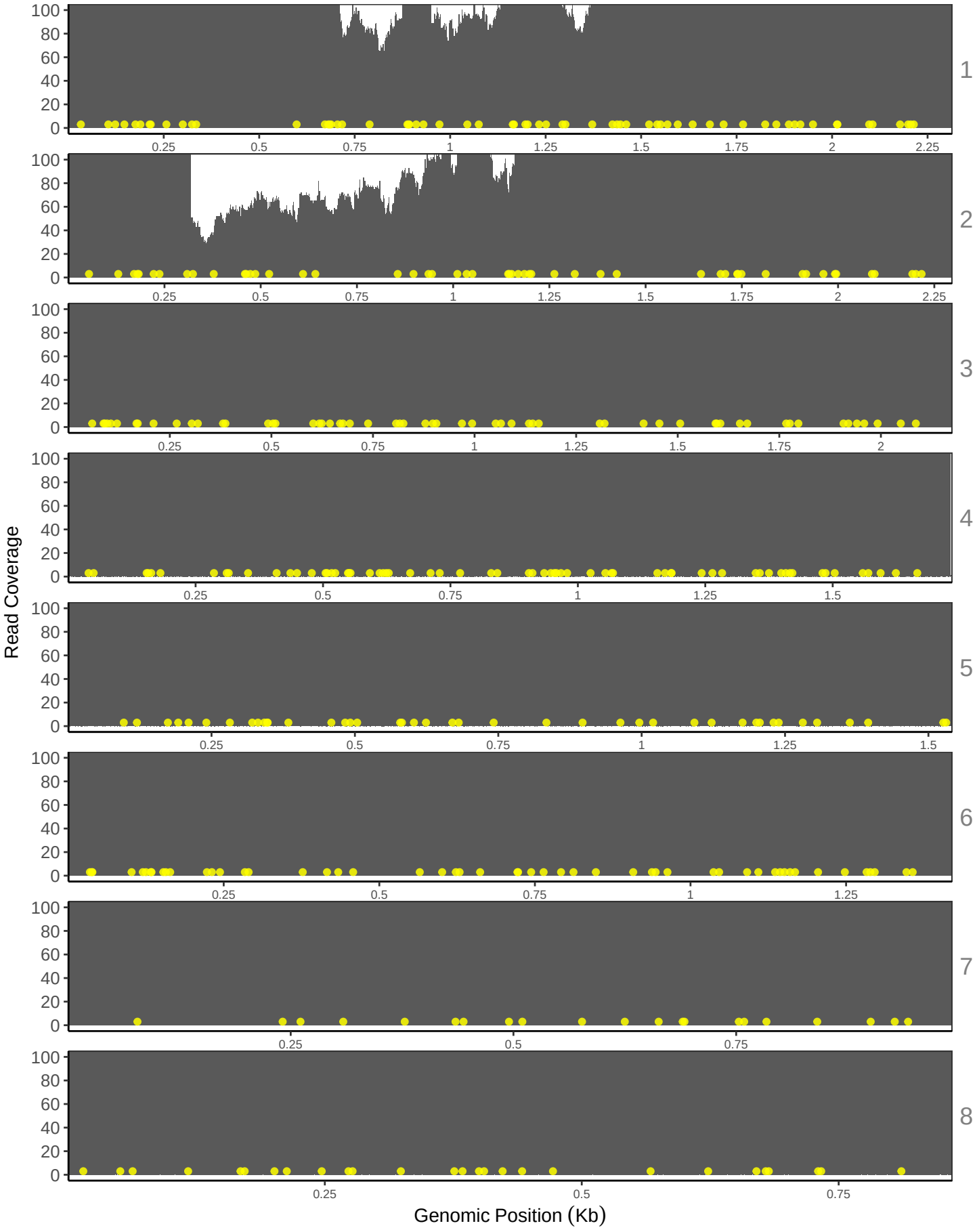


Figure 2: Read depth and coverage map zoomed at a depth of 100 reads.



Reference strain selection

Table 6: Summary of read coverage and depth for reference strain alignment using a randomized subset of reads.

reference	segment_count	segment_coverage_average	segment_average_read_depth
H1N1pdm_ref	8	0.78	18.31
H1N1_A_Brisbane_59_2007	8	0.35	5.28
H3N2_ref	7	0.37	5.48
IBV_Yamagata_ref	0	0.00	0.00
H6N2_Massachusetts	0	0.00	0.00
IBV_Victoria_ref	0	0.00	0.00

Table 7: Per-segment read coverage for reference strain alignment using a randomized subset of reads.

segment	H1N1_A_Brisbane_59_2007.fasta	H1N1pdm_ref.fasta	H3N2_ref.fasta
1	0.29	0.54	0.27
2	0.03	0.22	0.10
3	0.18	0.51	0.18
4	0.17	1.00	NA
5	0.54	0.99	0.60
6	0.27	1.00	0.03
7	0.79	1.00	0.82
8	0.51	1.00	0.60

Table 8: Per-segment read depth for reference strain alignment using a randomized subset of reads.

segment	H1N1_A_Brisbane_59_2007.fasta	H1N1pdm_ref.fasta	H3N2_ref.fasta
1	1.35	3.75	0.71
2	0.03	0.24	0.12
3	0.31	1.17	0.30
4	1.68	13.92	NA
5	1.84	7.72	2.20
6	0.60	8.80	0.03
7	18.59	38.70	16.70
8	17.80	72.18	18.26

Software environment

Software/R package	Version
R	3.4.1
bwa	0.7.15-r1140
samtools	1.7 Using htslib 1.7
bcftools	1.8 Using htslib 1.8
pangolin	3.1.16
genbankr	1.6.1
optparse	1.7.1
forcats	0.5.1
stringr	1.4.0
dplyr	1.0.7
purrr	0.3.4
readr	2.1.1
tidyr	1.1.4
tibble	3.1.6
ggplot2	3.3.5
tidyverse	1.3.1
ShortRead	1.36.1
GenomicAlignments	1.14.2
SummarizedExperiment	1.8.1
DelayedArray	0.4.1
matrixStats	0.61.0
Biobase	2.38.0
Rsamtools	1.30.0
GenomicRanges	1.30.3
GenomeInfoDb	1.14.0
Biostrings	2.46.0
XVector	0.18.0
IRanges	2.12.0
S4Vectors	0.16.0
BiocParallel	1.12.0
BiocGenerics	0.24.0