Confirmed and divergent variants between independent analysis pipelines

Genotypes predicted by CLC method

Table S2A. Shared variants of A and B versus reference genome.

Locus (base)	Type	Reference *	Allele	Reference allele	Coverage (A/B)	Allele Frequency (A/B)	Forward/reverse balance (A/B)**	Average quality (A/B)†
241	SNV	C	T	No	67/6	100.0/100.0	0.37/0.38	35.6/36.0
1059	SNV	C	T	No	144/55	100.0/92.7	0.48/0.26	35.6/35.4
3037	SNV	C	T	No	89/425	100.0/99.8	0.42/0.19	35.6/35.5
14408#	SNV	C	T	No	73/1145	100.0/99.6	0.40/0.43	35.7/35.6
23403	SNV	A	G	No	6859/10484	99.9/99.9	0.19/0.46	35.7/35.6
25563	SNV	G	T	No	421/757	100.0/99.1	0.45/0.48	35.2/35.4

Table S2B. Case A specific variants versus reference genome.

Locus (base)	Type	Reference *	Allele	Reference allele	Coverage	Allele Frequency	Forward/reverse balance**	Average quality†
539	SNV	C	T	No	141	99.3	0.45	35.6
4113	SNV	C	T	No	159	70.4	0.38	35.6
7921	SNV	A	G	No	182	98.9	0.49	35.7
16741	SNV	G	T	No	173	99.4	0.47	35.6

Table S2C. Case B specific variants versus reference genome.

Locus (base)	Type	Reference *	Allele	Reference allele	Coverage	Allele Frequency	Forward/reverse balance**	Average quality†
8140	SNV	C	T	No	1046	85.0	0.43	35.6
11102	SNV	C	T	No	1713	99.9	0.44	35.5
14407#	SNV	C	T	No	1145	99.7	0.43	35.6
15190	SNV	G	C	No	139	90.6	0.33	35.7
15981	SNV	C	T	No	224	100.0	0.38	35.5
26013	SNV	C	T	No	1415	99.2	0.38	35.5
29466	SNV	C	T	No	86	98.8	0.07	35.8

Table S2D. Insertions and deletions in Case B

Locus (base)	Type	Reference *	Allele	Reference allele	Coverage	Allele Frequency	Forward/reverse balance**	Average quality†
2084	Deletion	C	-	No	93	95.69892473	0.1170212766	34.01123596
5310	Deletion	C	-	No	590	93.05084746	0.1911504425	25.60473588
6018^6019	Insertion	-	C	No	143	98.6013986	0	34.78014184
15977	Deletion	A	-	No	212	100	0.3606557377	32.30660377

Genotypes predicted by Freebayes

Table S2E. Shared variants of A and B versus reference genome.

Locus (base)	Type	Reference *	Allele	Reference allele	Coverage (A/B)	Allele Frequency (A/B)
241	SNV	C	T		101/7	99.0/100.0
1059	SNV	C	T		183/26	99.5/92.3
3037	SNV	C	T		129/373	100.0/100.0
14408	SNV	C	T		83/476	100.0/100.0
23403	SNV	A	G		5662/6675	99.8/99.9
25563	SNV	G	T		538/294	100.0/99.7

Table S2F. Case A specific variants versus reference genome.

Locus (base)	Type	Reference *	Allele	Reference allele	Coverage	Allele Frequency
539	SNV	C	T		191	97.4
7921	SNV	A	G		238	97.9
16741	SNV	G	T		217	100.0

Table S2G. Case B specific variants versus reference genome.

Locus (base)	Type	Reference *	Allele	Reference allele	Coverage	Allele Frequency
8140	SNV	C	T		567	89.8
11102	SNV	C	T		772	99.7
14407	SNV	C	T		476	99.8
15190	SNV	G	C		102	94.1
15981	SNV	C	T		124	100.0
26013	SNV	C	T		657	98.6
29466	SNV	C	T		57	96.5

Table S2H. Insertions and deletions in Case B

Locus (base)	Type	Reference *	Allele	Reference allele	Coverage	Allele Frequency
2084	Deletion	C	-		49	81.6
6018^6019	Insertion	-	C		122	100.0

*Wuhan-Hu-1, GenBank: MN908947.3
**Ratio of forward to reverse reads covering the locus
†Phred score
#Both pipelines classified this as an MNV. The two variants are split for clarity.

Table S2l. Insertions and deletions in Case B

Locus (base)	Type	Reference *	Allele	Reference allele	Coverage	Allele Frequency
22832	Deletion	A	-		802	82.5

Forward/reverse balance (A/B)**	Average quality (A/B)†

Forward/reverse balance**	Average quality†

Forward/reverse balance**	Average quality†

Forward/reverse	Average quality†