

1 **Supplementary Data**

2 **Additional file 1 as Supplementary Tables**

3 Table S1. General sequencing information and statistics

4 Table S2. Quantification by different variant callers for NS gene segment variants mixed at
5 different proportions

6 Table S3. Relation between depth of coverage and minor variant authentication. Minor
7 variants with depth of coverage below 30 were false positives. Green
8 circles: depth >30; Yellow triangles: >20 and ≤30; Red diamonds ≤20.

9 Table S4. Validation experimental results for minor variant authentication. Four sets of
10 Influenza A H1N1 whole genome sequencing data using Ion PGM Sequencer and GS
11 Junior. Only results of gene segments HA, NA and NS are shown

12 Table S5. Differences between observed and expected mixture ratios and Standard deviation
13 of quantification within the same run

14 Table S6. Friedman test post hoc analysis for evaluation on difference in quantification
15 between different variant ratios

16 Table S7. TukeyHSD post-hoc analysis for evaluation on difference in quantification
17 between different variant callers

18 Table S8. 95% confidence intervals constructed by Agresti-Coull method for observed
19 mixture ratios and the error from the expected actual mixture ratios

20 **Additional file 2 as Supplementary Figure**

21 Figure S1. Depth of coverage by TMAP (above) and BWA (below) for segment NS from 7
22 datasets of all the ten runs

23 The complete coverage information from DiBayes is not available from manufacturer
24 software. The three vertical lines are drawn at positions 173, 435 and 575. An inset is shown
25 on the right for a magnified view of the mapping around position 435.

26

27