Supplementary information

Influence of H7N9 virus infection and associated treatment on human gut microbiota

Running title: H7N9 influence on human gut microbiota

Nan Qin^{1,2}*†, Beiwen Zheng^{1,2}*, Jian Yao^{1,2}*, Lihua Guo¹, Jian Zuo¹, Lingjiao Wu¹, Jiawei Zhou^{1,2}, Lin Liu^{1,2}, Jing Guo¹, Shujun Ni¹, Ang Li¹, Yixin Zhu^{1,2}, Weifeng Liang^{1,2}, Yonghong Xiao^{1,2}, S. Dusko Ehrlich^{3,4}, LanJuan Li^{1,2}†

¹State Key Laboratory for Diagnosis and Treatment of Infectious Diseases, the First Affiliated College of Medicine, Zhejiang University, 310003 Hangzhou, China; ²Collaborative Innovation Center for Diagnosis and Treatment of Infectious Diseases, Zhejiang University, 310003 Hangzhou, China and ³Metagenopolis, Institut National de la Recherche Agronomique, 78350, Jouy en Josas, France; ⁴King's College London, Centre for Host-Microbiome Interactions, Dental Institute Central Office, Guy's Hospital, London Bridge, London SE1 9RT, UK.

*These authors contributed equally to this work.

†Correspondence: Prof. Lanjuan Li, State Key Laboratory for Diagnosis and Treatment of Infectious Diseases, First Affiliated Hospital, College of Medicine, Zhejiang University, No. 79 Qingchun Rd., Hangzhou City 310003, China (ljli@zju.edu.cn). or Dr. Nan Qin, State Key Laboratory for Diagnosis and Treatment of Infectious Diseases, First Affiliated Hospital, College of Medicine, Zhejiang University, No. 79 Qingchun Rd., Hangzhou City 310003, China (nqin@zju.edu.cn).

SUPPLEMENTARY FIGURE AND TABLE LEGENDS

Figure S1: Clustering scores for enterotypes at the genus levelusing four different methods: Prediction strength scores, Calinski-Harabasz, average silhouette scores and WB score. Each one has three different metrics. The x-axis shows the cluster number, and the y-axis shows the score.

Figure S2: Clustering results based on the Spearman correlation co efficiency of all samples. A: At the species level. B: At the genus level.

Table S1: Patients characteristics.

Table S2: Phenotype information of 31 healthy controls.

Table S3: Data Production of 93 samples from 26 H7N9 virus infected patients.

Table S4: Reference genomes downloaded from the NCBI and HMP database (version 20120810)

Table S5: Shannon index of the samples from the selected patients.

Table S6: MGS annotation.