SDC2: Supplementary Figures for Detection of plasmid-mediated tigecycline resistance gene *tet*(X4) in a *Salmonella enterica* serovar Llandoff isolate

Yanan Wang1,2,#, Fei Liu2,#, Xuebin Xu3,#, Hua Huang4, Na Lyu2, Sufang Ma2, Luping Chen2, Mengyu Mao2,5, Yongfei Hu6, Xiaofeng Song7, Jing Li2, Yuanlong Pan2, Aiping Wang8, Gaiping Zhang1,8, Baoli Zhu2,9,10,11, George F. Gao2,9,12,\*

1College of Veterinary Medicine, Henan Agricultural University, Zhengzhou, Henan, China;

2CAS Key Laboratory of Pathogen Microbiology and Immunology, Institute of Microbiology, Chinese Academy of Sciences (CAS), Beijing, China;

3Department of Microbiology, Shanghai Municipal Center for Disease Control and Prevention, Shanghai, China;

4Beijing Products Quality Supervision and Inspection Institute, Beijing, China;

5Institutes of Physical Science and Information Technology, Anhui University, Hefei, Anhui, China;

6State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing, China;

7National Institute for Communicable Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing, China;

8School of Life Sciences, Zhengzhou University, Zhengzhou, Henan, China;

9Savaid Medical School, University of Chinese Academy of Sciences, Beijing, China;

10Beijing Key Laboratory of Antimicrobial Resistance and Pathogen Genomics, Beijing, China;

11Department of Pathogenic Biology, School of Basic Medical Sciences, Southwest Medical University, Luzhou, Sichuan, China;

12Chinese Center for Disease Control and Prevention (China CDC), Beijing, China.

#These authors contributed equally to this work.

**\*Corresponding author:** George F. Gao, CAS Key Laboratory of Pathogen Microbiology and Immunology, Institute of Microbiology, Chinese Academy of Sciences (CAS), NO.1 Beichen West Road, Chaoyang District, Beijing 100101, China. E-mail: gaof@im.ac.cn

# YW, FL and XX contributed equally to this work.



Figure S1. Source location of *Salmonella enterica* serovar Llandoff strain genomes used in this study. The blue color indicates the presence of this serovar.



Figure S2. The phylogenomic relationship among 20 *Salmonella enterica* serovar Llandoff strains. The 20 *S.* Llandoff isolates were distributed in 11 countries on four continents and grouped into different sublineages. SH16G3606 was closer to the *S.* Llandoff strains in Guatemala, the USA, and Mexico in the evolutionary tree. “100” represent bootstrap value and “0.05” represents distance scale.



Figure S3. Comparison analysis of *tet*(X4)-positive *Salmonella enterica* contigs.