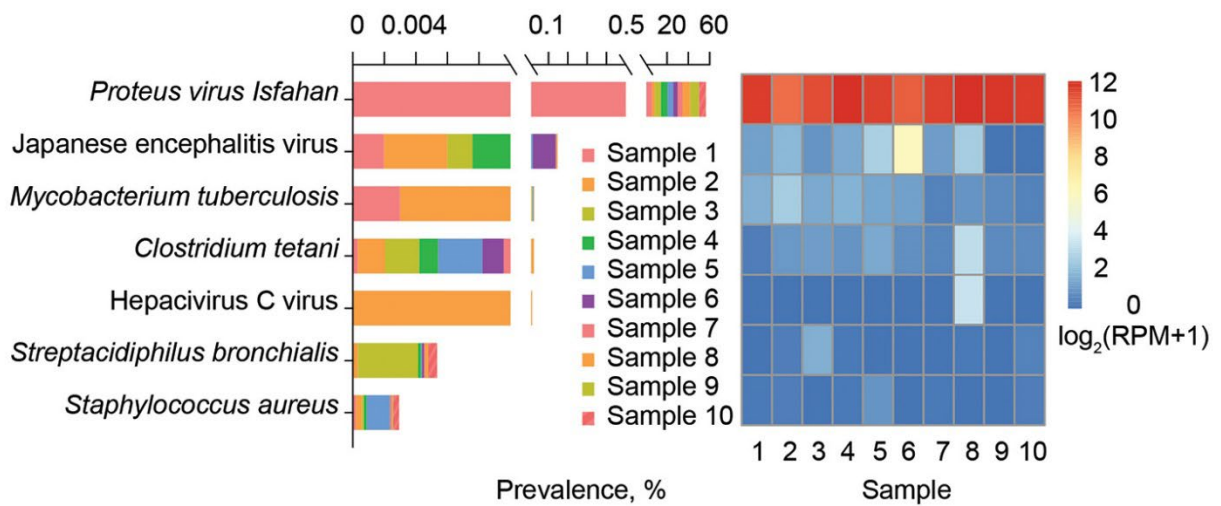
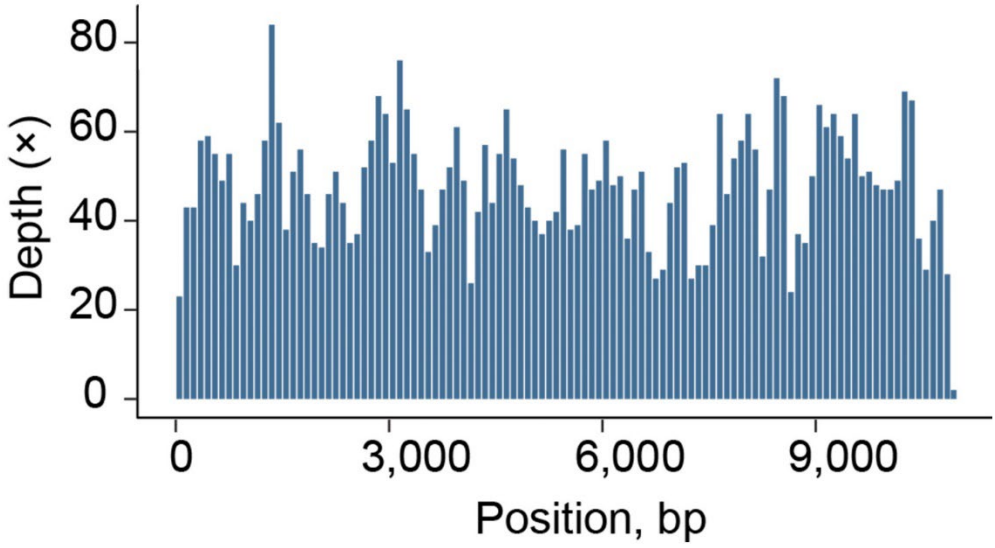


Identifying Japanese Encephalitis Virus Using Metatranscriptomic Sequencing, Xinjiang Province, China

Appendix



Appendix Figure 1. A) Prevalence and B) relative abundance of 7 potential pathogens in the study population. Prevalence indicates the proportion of each pathogenic reads/million nonhost reads. Side bar colors in panel B are keyed to abundance values. RPM: reads/million nonhost reads.



Appendix Figure 2. Genome coverage of Japanese encephalitis virus in sample 6 sequencing. The x axis represents genome position, and the y axis represents sequencing depth.