



S4 Fig. Survey Analysis on the Utilization of Genomic Data. (A) Survey participants' research experience and primary areas of research. As a result, the survey revealed that the majority of respondents have over 10 years of experience in genomic data research, with over

80% of them actively engaged in cancer-related research. (B) Methods used in genomic research and analysis. Among omics data, more than 50% of respondents generate whole-genome sequencing (WGS) and whole-exome sequencing (WES) data, along with transcriptome data. The primary method for data generation involves utilizing in-house servers owned by individual research teams (approximately 80%). (C) Network security measures implemented in genomic research. Regarding network security, approximately 70% of respondents reported the segregation of internal and external networks, facilitating data sharing and provision through internal networks. (D) Participants' experience with using genomic data. About 44.2% of respondents have experience opening genomic data for publication purposes. Data sharing primarily occurs within the same institution (40.4%), while sharing with other institutions, whether within or outside the institution, is less common. (E) Primary types of genomic data and file formats used in data sharing. The survey found that approximately 30% of data shared and provided is genomic and transcriptomic data, with FASTQ files being the preferred file format (51.9%).