Functional genomics experiments, such as RNA sequencing, reveal important information about

dynamic changes in gene expression under different conditions. There is great desire to share these databecause they are extremely valuable for biomedical and disease research. The raw reads are not shared because of privacy concerns. To enable safe sharing, aggregated formats such as read depth signal profiles and gene expression quantifications are used. Projects such as GTEx and ENCODE publicly share these data because they ostensibly do not leak much identifying information. We study the leakage from genome-wide signal profiles when signal profile is used for genotyping genomic deletions. We present information theoretic measures for genotypability of deletions and leakage therefrom. We develop practical genotyping methods and demonstrate that an individual can be identified within a large sample in the context of linking attacks. We finally present an anonymization method that removes much of the leakage from signal profiles.