

Fig.S2

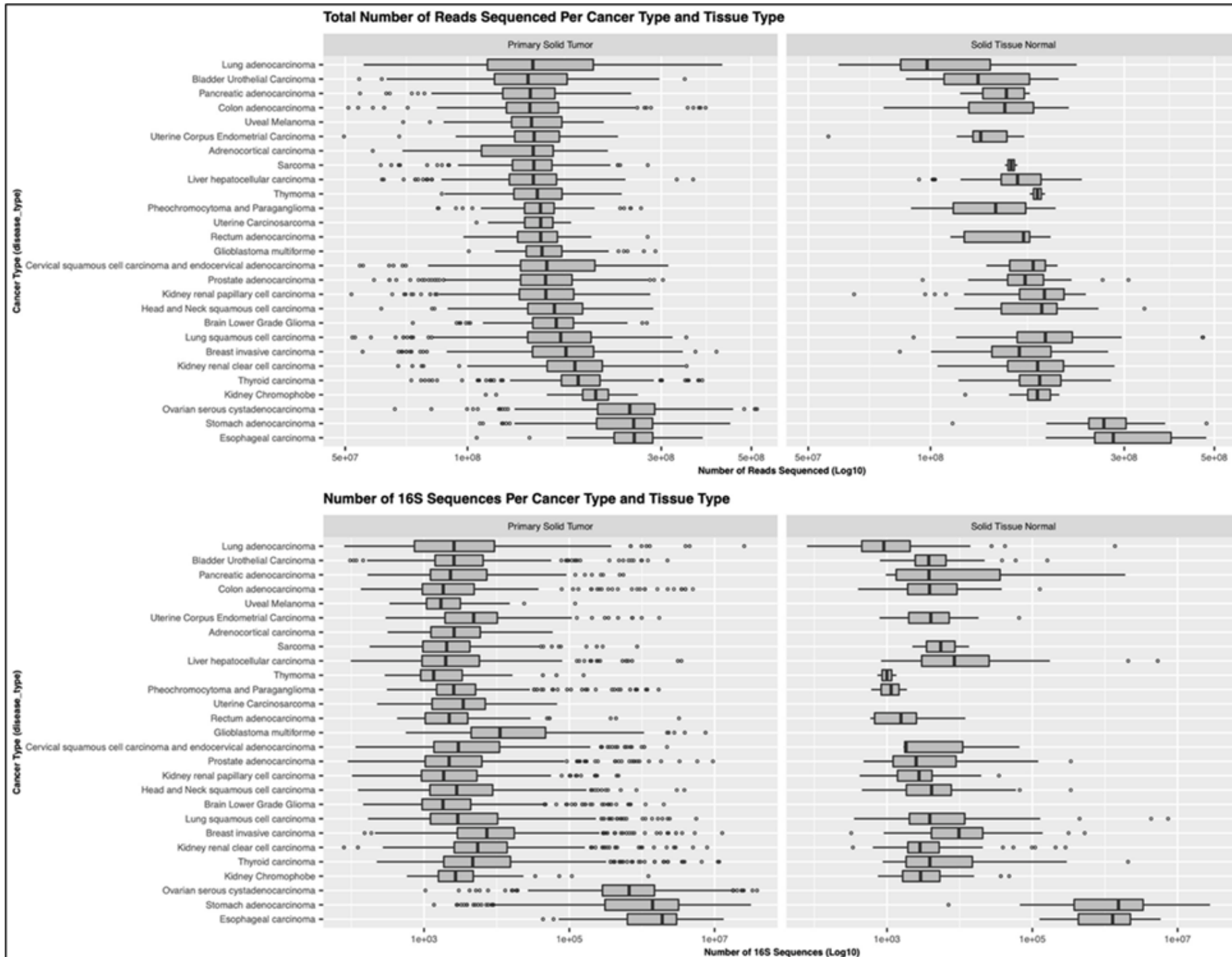


Fig.S2 Top panel - Total number of reads sequenced per cancer type and tissue type (primary solid tumor and solid tissue normal). **Bottom panel - Number of 16S sequences per cancer type and tissue type** (primary solid tumor and solid tissue normal). The total number of reads was determined in the different cancer samples belonging to the TCGA data set, as described in Materials and Methods.