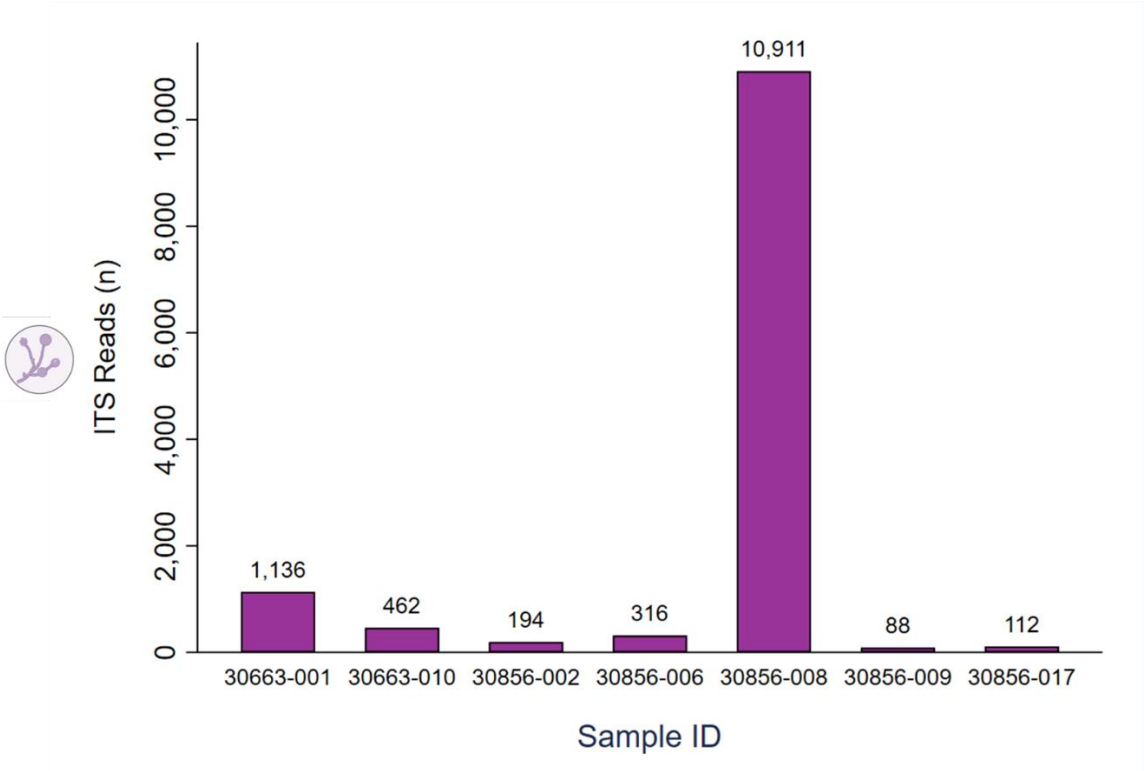


Supplementary Figure S2. Fungal taxonomic composition of cytology samples based on ITS sequencing. The bar chart shows the relative abundance of detected fungal species. *Candida albicans* was the only species identified with sufficient read depth in 7 out of 66 samples. ITS read counts, indicated on each bar, ranged from 88 to 10,911. The ITS read counts were significantly lower than those observed with 16S sequencing.