**Figure Legends**

**Figure 1. Summary of variants identified among all strains.** (A) The number of variants per gene has a long right tail. The inset panel is the same data, zoomed-in for genes with at least 50 variants for visualization purposes. (B) There was no correlation between gene length and the number of variants per base pair in each gene (p = 0.20).

**Figure 2. Phylognetic analysis of all sequenced strains.** (A) The majority of ST93 strains fall into two well-supported clades, magnified in (B) for ease of viewing. ST93A (purple background) and ST93B (yellow background). Bootstrap values >50 are indicated with the numeric boostrap value. Strains isolated from patients that died are indicated by a red diamond at the end of the terminal branch.

**Figure 3. Variants that were common to all ST93 genomes are dispersed among 2715 genes.**

A small number of clustered genes have a large number of variants. In each cluster the gene with the highest number of variants is indicated. Genes with more than 20 variants and named genes are indicated. Table S2 lists all genes with 10 or more variants.

**Figure 4: Clade specific variants.** (A) Variants that are specific to ST93A (purple) and ST93B (yellow) clades are distributed across the genome. (B) Upstream variants are the majority class found in all ST93 genomes (“allST93”) and among the variants that are specific to either clade. By contrast, ST93A variants were more likely to be nonsynonymous and less likely to be downstream compared to allST93 or ST93B varients. The distribution of ST93A and ST93 variant classes are significantly different (p = 0.009) (C) IL2 cytokine levels in the CSF and In vitro phagocyte uptake differed between ST93A and ST93B strains (t-test results: IL2, *p* = 0.022; uptake, *p* = 0.011).

**Figure 6. Comparing variant frequencies across the genome.** The relative frequency of variants per gene for significant genes (red dots) compared to all sequenced variants across all genomes (black line) and all variants that were variable within ST93 genomes (grey line). The only genes shown here are those with at least one potential significant variant, hence the grey and black lines doesn’t go down to 0.

**Figure 7. Deletion strain virulence in mice.** Groups of five 6-8 week old C57Bl/6 mice were infected intranasally with 5 X 104 cells. Progression to severe morbidity was monitored for 35 days and mice were sacrificed when endpoint criteria were reached. Strains were tested in two separate experiments indicated as E1 or E2, respectively.