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A genome-scale phenotype map of *Francisella novicida*M. Enstrom¹, K. Held¹, C. Manoil¹¹University of Washington, Genome Sciences, Seattle, United States

We constructed a genotype-phenotype “map” of *F. novicida* in which the genes required for growth under 35 different nutritional and stress conditions were identified. To do this, we developed methods for the large-scale analysis of a comprehensive, sequence-defined transposon mutant library of the organism. Mutants from 384-well source plates were robotically spotted onto test media, and subsequent growth was quantified using image analysis. Confirmed phenotypes were identified for mutations inactivating about a quarter of the organism’s nonessential genes. This analysis has provided experimental tests of genome annotation assignments, and has led to the discovery of new genes associated with nearly every phenotype examined. The map should help provide a foundation for understanding intrinsic antibiotic resistance, virulence, and other complex traits in terms of more fundamental processes of the organism.