Tularemia is a potentially fatal disease caused by the Category A bioterrorism agent *Francisella tularensis*. Aminoglycosides, fluoroquinolones, and tetracyclines can be used to treat tularemia; however, there is a high incidence of relapse and treatment failures when using these drugs. Furthermore, there is no tularemia vaccine licensed for use in the United States. Therefore, new antibiotics that target *F. tularensis* are being investigated. A novel family of resazurin-based antibiotics called resazomycins exhibit antimicrobial activity against *F. tularensis* and other Gram-negative pathogens including *Neisseria gonorrhoeae*. The mode of action of resazomycins has yet to be determined. To elucidate potential targets of resazurin (Rz), we screened for spontaneous Rz-resistant (Rzr) *F. tularensis* LVS mutants. Through the screen, 93% of all Rzr mutants sequenced contained mutations within the coding regions of FTL_0421, FTL_0895, and FTL_1504. In addition, 100% of all Rzr mutants sequenced contained a mutation approximately 50bp upstream of the gene FTL_0445. To understand the effect the mutation has on transcription of FTL_0445, RNA was isolated from wild-type LVS and an Rzr mutant (Rzr1). Quantitative reverse transcription PCR revealed FTL_0445 was upregulated in Rzr1 compared to wild-type LVS. To determine the role of FTL_0445 in Rz resistance, an FTL_0445 null deletion mutant is being generated in Rzr1 using standard molecular genetic techniques. Upon completion, the Rz sensitivity of the deletion mutant will be assessed using agar dilution assays. Understanding the role of FTL_0445 in Rz susceptibility would facilitate further development of these compounds as potential treatments for tularemia and gonorrhea.