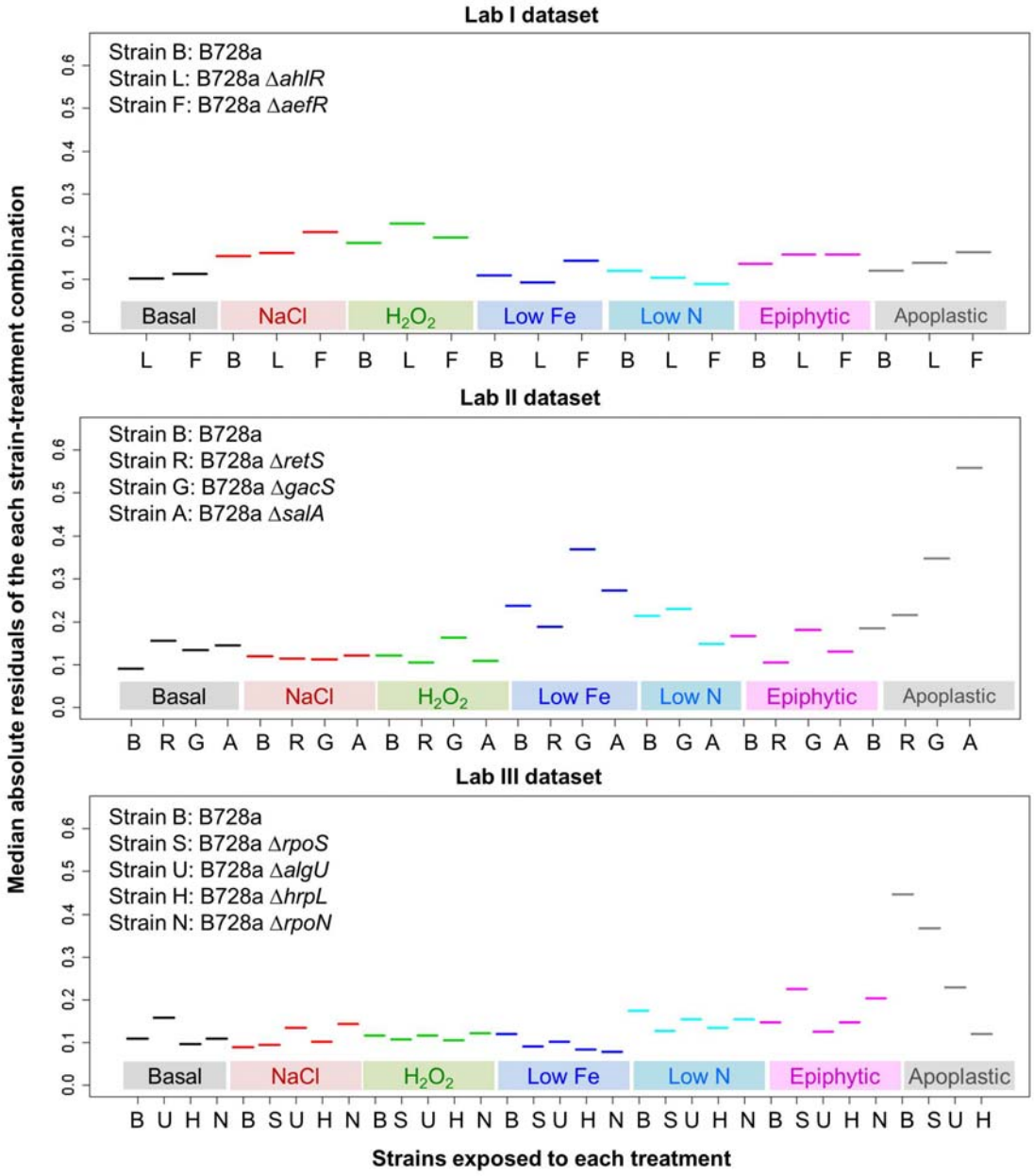

Fig S1. Relative variation in transcript levels among each of the strain-treatment combinations based on median absolute residuals computed from our linear model analyses. The datasets were generated in three independent laboratories, designated I, II and III, and each laboratory examined a distinct set of strains that were subjected to the same treatments. The treatments are as defined in Fig 1. Values are not shown for four samples: B728a in the basal medium (lab I) (this sample was repeated and was ultimately included in the analysis); Δ*retS* in the low N medium (lab II), Δ*rpoS* in the basal medium (lab III), and Δ*rpoN* in apoplastic sites (lab III) (these samples were each represented by only one replicate in the microarray analysis). The variability was particularly high among the replicates subjected to iron starvation in lab II, likely due to technical variation during amendment with the iron chelator, and among the replicates of the cells recovered from the apoplast in labs II and III. Despite efforts to employ uniform plant incubation conditions, environmental variability may have been high in these laboratories due to seasonal variation between sampling times in ambient humidity, particularly as associated with indoor heating.