



**Figure S1. Multidimensional scaling analysis of RNA-seq datasets.**

Multidimensional scaling (MDS) plot contrasting the top 500 most variable genes among all 24 individual RNA-seq datasets (four biological replicates per each group:  $+/+$  uninjured (orange),  $+/Rel^{del}$  uninjured (pink),  $Rel^{del}/Rel^{del}$  uninjured (yellow),  $+/+$  injured (green),  $+/Rel^{del}$  injured (purple), and  $Rel^{del}/Rel^{del}$  uninjured (lime green)). Each pair of points reflects the best dissimilarity (Euclidean distance) estimated between the two samples.