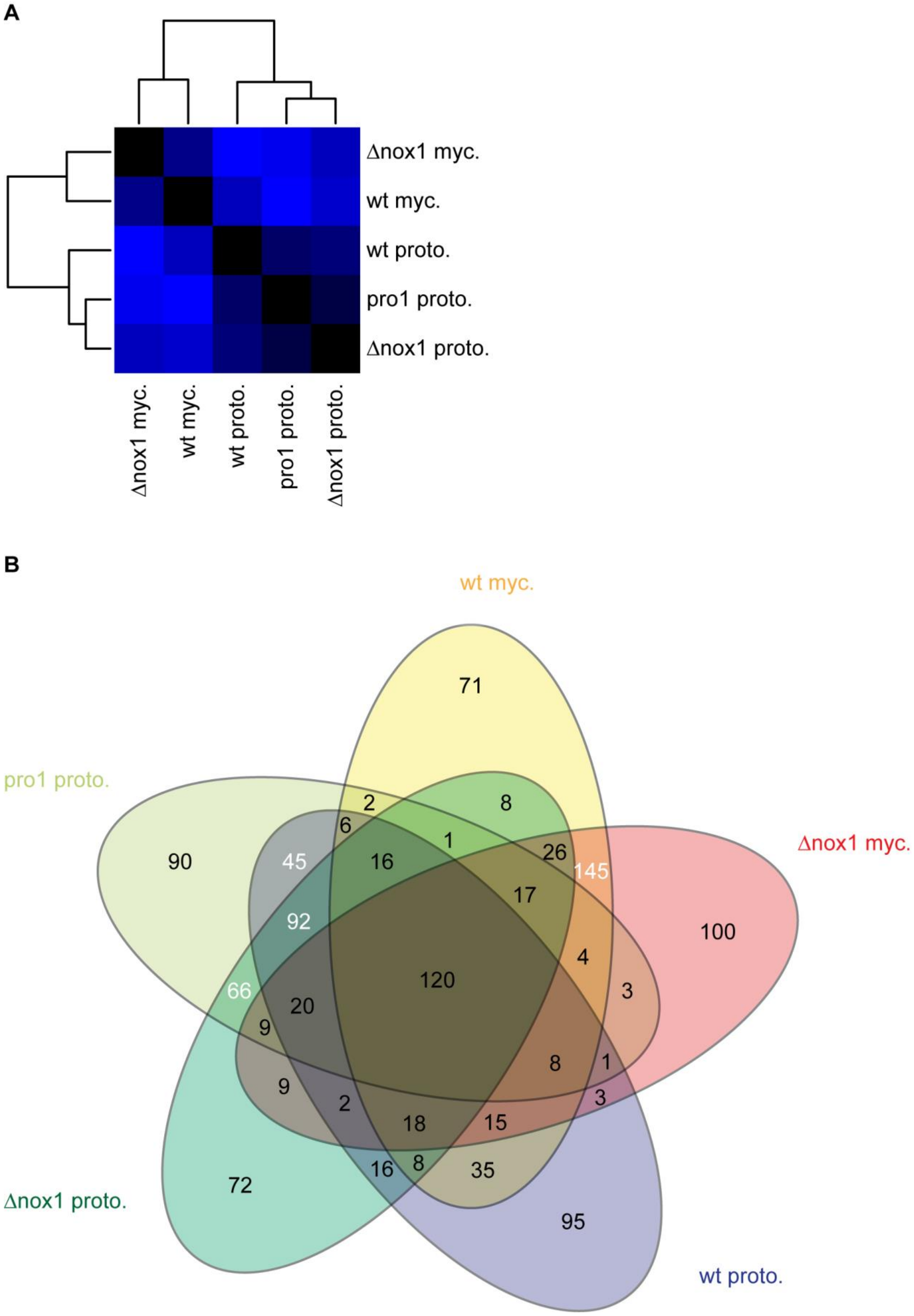

Figure S6 Expression patterns of protoperithecia are distinct from total mycelial samples. (A) Heatmap of correlation coefficients (Spearman) calculated from normalized read counts for classical analysis from protoperithecial (proto.) and mycelial (myc.) samples. Clustering and heatmap were done in R. (B) Venn diagrams of top 500 genes in different samples. Numbers of genes that are in the top 500 group for one or more or the five samples are given. In this analysis, only reads that map within 100 to 400 bases from the 3’ end of the mRNA were used to account for the 3’ bias in the microdissection samples and different mRNA lengths. Numbers for the four intersections containing the highest numbers of genes are indicated in white (not counting fields that represent genes occuring in all or only in one group). These intersections are wt mycelia and Δnox1 mycelia (145), wt protoperithecia and Δnox1 protoperithecia and pro1 protoperithecia (92), Δnox1 protoperithecia and pro1 protoperithecia (66), and wt protoperithecia and pro1 protoperithecia (45).