



Figure 7- figure supplement 3. UMAP groupings vary significantly for Absence across *V. dahliae* strain. (A) Scatter plot showing each 11,429 genes as a point following the UMAP results. Each gene is colored according to its absence count across 42 *V. dahliae* strains. (B) Box plot showing the distribution of gene absence counts for each of the three UMAP groups. (C) Similar plot as shown in A, but only genes that have an absence count greater than zero are plotted. (D) Similar to B, but only genes that have an absence count greater than zero are plotted. Pairwise comparisons were performed using Conover's test, with Holm multiple testing correction. There were 2130, 8140 and 1159 genes in UMAP Group1, 2 and 3 respectively for A and B. There were 666, 3156 and 441 genes in UMAP Group1, 2 and 3 respectively for C and D. ns, non-significant $\alpha = 0.05$; ****, p-value < 0.0001.