



Supplemental Fig. S10. Clustering analysis of selected metabolic markers that discriminate against NAD treatment (top) and inducible NAD-overproduction in *nadC* (bottom) The normalized intensities of 32 important discriminators (selected in Fig. S9 and detailed in Table S3) are presented as heatmaps for the comparisons between Control (Ctrl) and NAD⁺ (NAD, 1 mM) treatments in **A**, and WT and *nadC* with or without quinolinate (Q) in **B**. Above each panel, the scale indicates the relative concentrations of the corresponding metabolic markers (green = low, red = high). Clustering analysis (Pearson correlation, Single linkage) was performed using MeV (v 4.9). Colored circles indicate putative identifications of metabolic pathways.