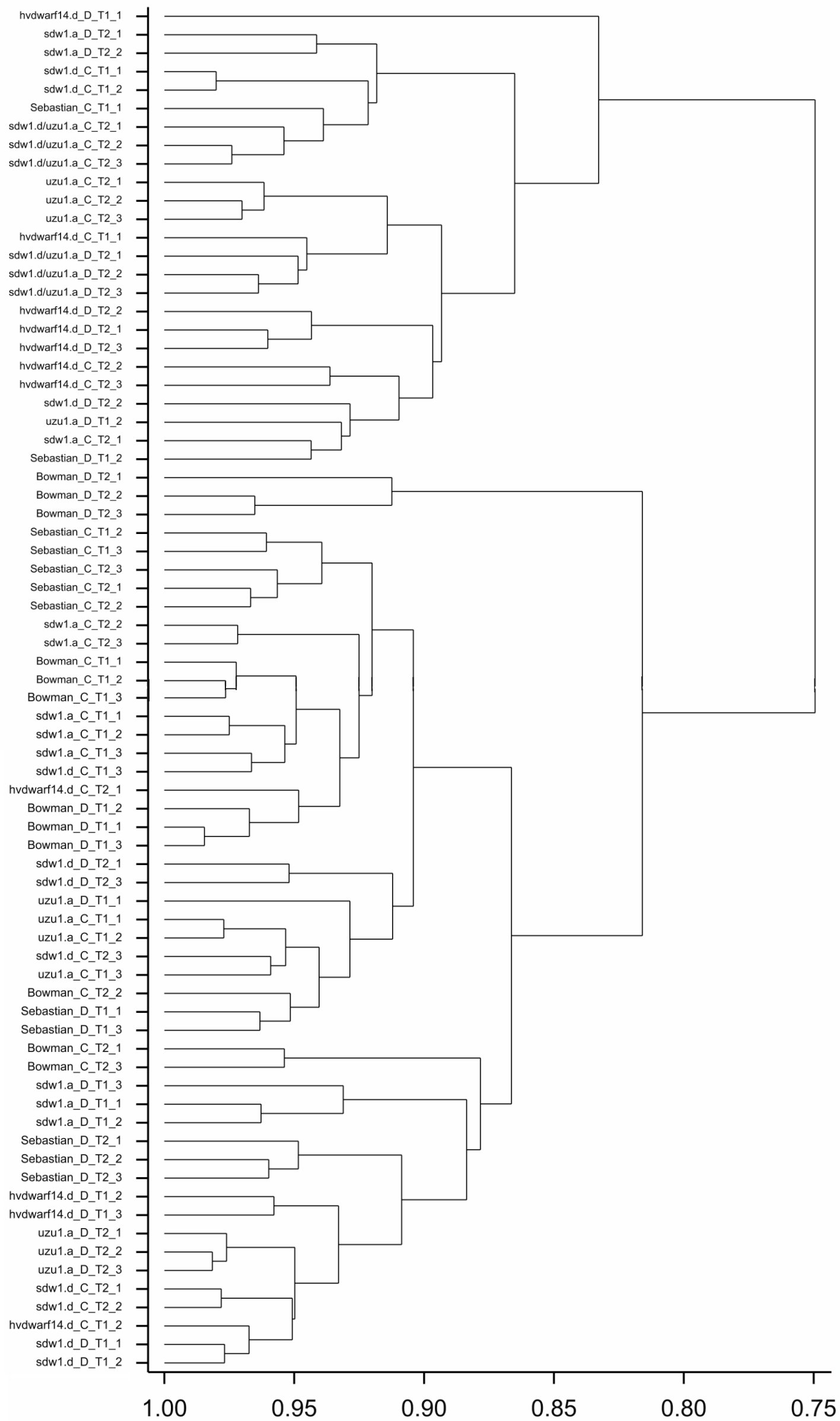


**Figure S2A.** Hierarchical clustering of 109 samples in mRNA-seq assay based on count data for 8,957 genes in the top quartile of between-samples variance; sample name from left to right as follows: genotype\_treatment\_time point\_replication



**Figure S2B.** Hierarchical clustering of 74 samples based on data for 4,970 proteins; sample name from left to right as follows: genotype\_treatment\_time point\_replication