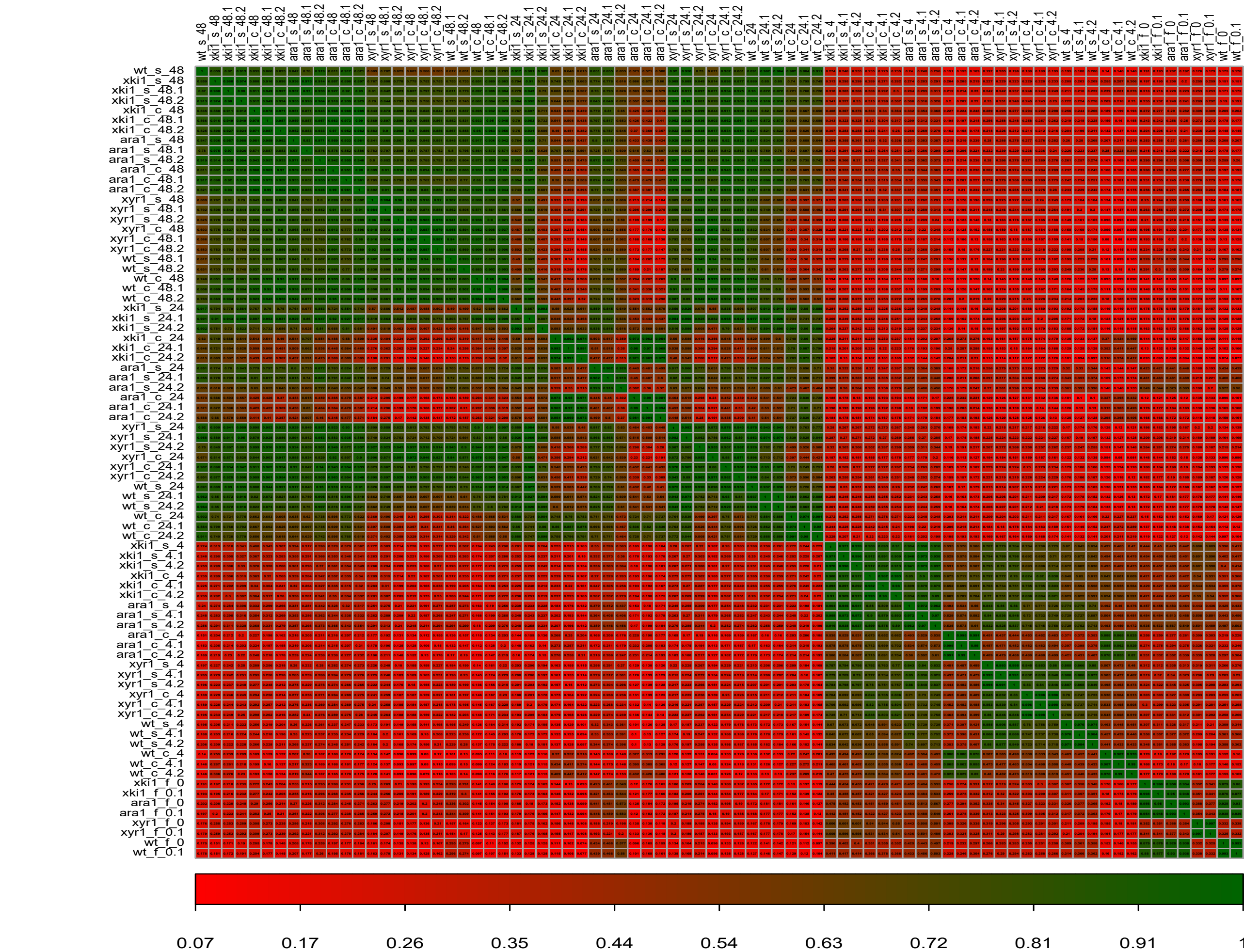




Additional file 5. Pearson correlation matrix of *T. reesei* transcriptomes.

Raw gene counts were used to evaluate the level of correlation between biological replicates using Pearson's correlation. Pearson correlation matrix were performed in R (v3.4.0) statistical language and environment, the cor function from the stats base package and the corplot (v 0.77) package were used for the analysis. One sample (wt on SBH at 48h) was removed from the dataset because it correlated poorly with its replicates.