

Description of Additional Supplementary Files

Supplementary Data 1: Nop7-TAP qMS data of two replicates. Nop7-TAP particles were purified from untreated and 2 minutes usnic acid treated cells. Intensities normalized to the bait protein are shown for each replicate. Proteins were sorted according to their normalized intensities in the sample of the untreated wildtype. Peptide (P), Unique Peptides (U.P) and Confidence score (C. sc.; > 500 in yellow) are listed for each replicate. The mean and the standard deviation (> 10% in red) of the two replicates were calculated. Factors with an abundance below the threshold (mean untreated < 0.001) were not included in the analysis. Top 10% abundant proteins are highlighted in green. Selected assembly factors for bar chart highlighted in blue.

Supplementary Data 2: Nsa1-TAP qMS data of two replicates. Nsa1-TAP particles were purified from untreated and 2 minutes usnic acid treated cells. Intensities normalized to the bait protein are shown for each replicate. Proteins were sorted according to their normalized intensities in the sample of the untreated wildtype. Peptide (P), Unique Peptides (U.P) and Confidence score (C. sc.; > 500 in yellow) are listed for each replicate. The mean and the standard deviation (> 10% in red) of the two replicates were calculated. Factors with an abundance below the threshold (mean untreated < 0.001) were not included in the analysis, except pre-60S assembly factors. Top 10% abundant proteins are highlighted in green. Selected assembly factors for bar chart highlighted in blue.