



**Supplemental Figure 5. Correlation between the 985 mitochondrion related genes were estimated using Pearson correlation without centralization (Non-Centralized data) and Pearson correlation with CSE preprocessing (CSE preprocessed data).** For each approach 484,620 correlations were estimated and the 0.5 % (2423) gene correlations with the highest absolute value were used to predict edges in the corresponding gene co-expression network. **(A)** Estimated density functions over all estimated correlations for non-centralized data (green) and CSE preprocessed data (red). The black line shows the density for correlations estimated on simulated noise. **(B)** The estimated correlations for the two approaches plotted against each other. Edges shared by both approaches are marked blue (620 (25.6 %) of the edges were shared), unique edges for the CSE preprocessing network are marked red, and unique edges for the Non-centralized network are marked green.