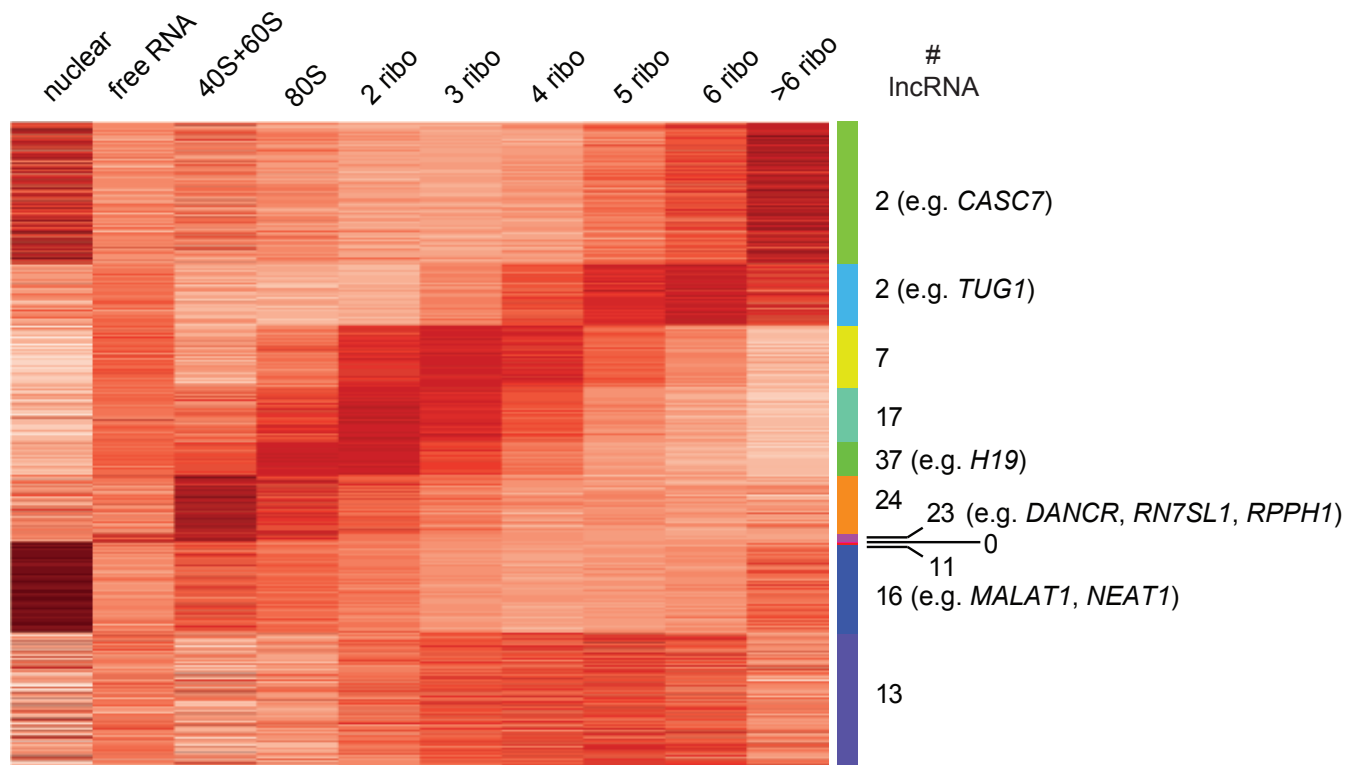




**Additional file 7) Clustering of the data without sncRNAs does not affect the finding of IncRNAs in cytosolic and ribosomal fractions.** Read counts of only the protein-coding transcripts and IncRNAs were normalized across the samples and k-means clustering was applied generating 11 clusters. The number of IncRNAs present in each of the clusters is indicated on the right.