

Figure S1. Functional analysis of differentially expressed protein-coding RNAs using Panther 17.0. ATP – adenosine triphosphate; GO – gene ontology term.

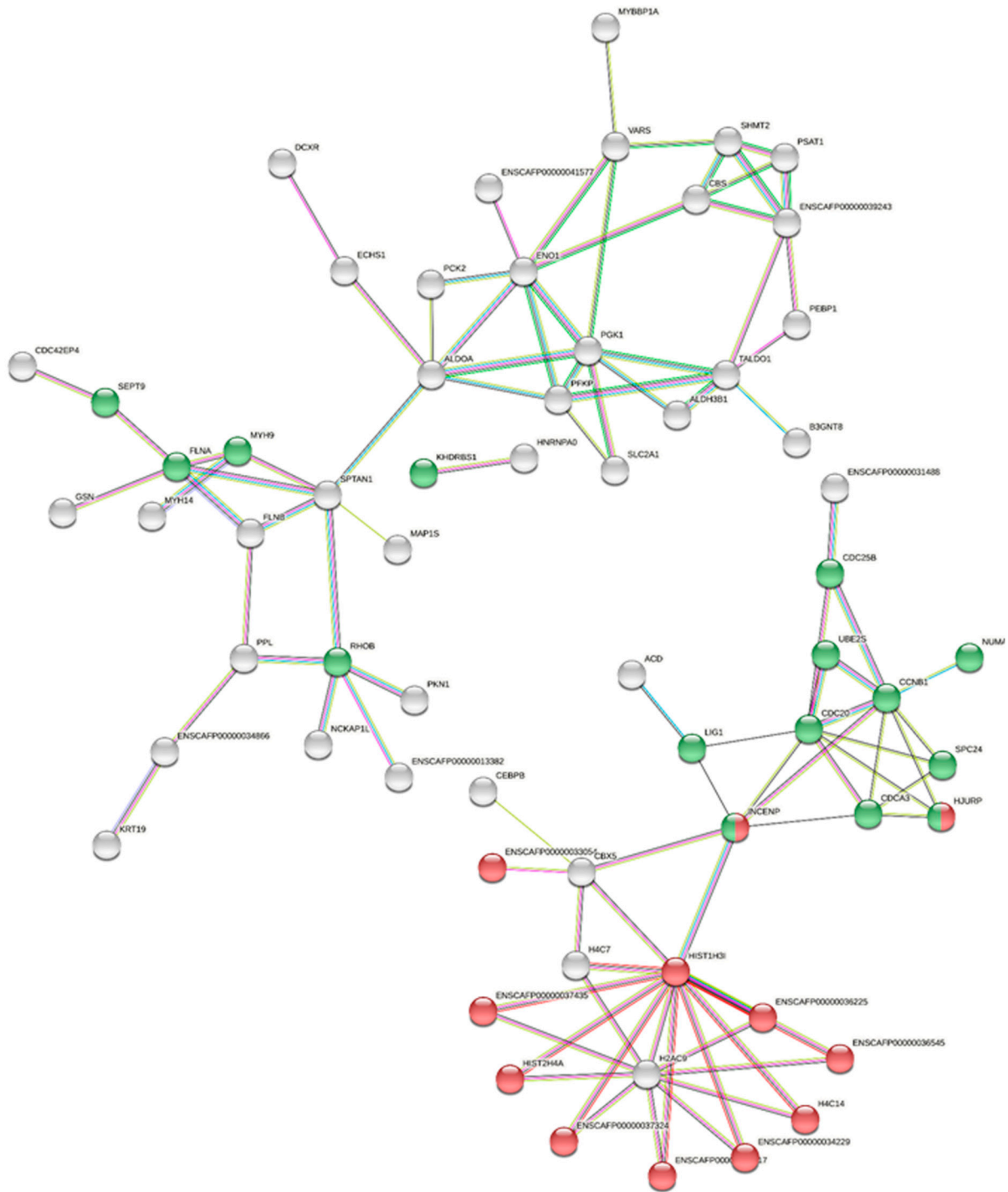


Figure S2. The interaction network of proteins encoded by transcripts underexpressed in exosomes isolated from IAV-infected MDCK cells, shown after STRING pathway analysis. Colors indicate GO annotations: green – GO:0007049 “Biological process – Cell cycle”; red – GO:0006323 “Biological process – DNA packaging”.

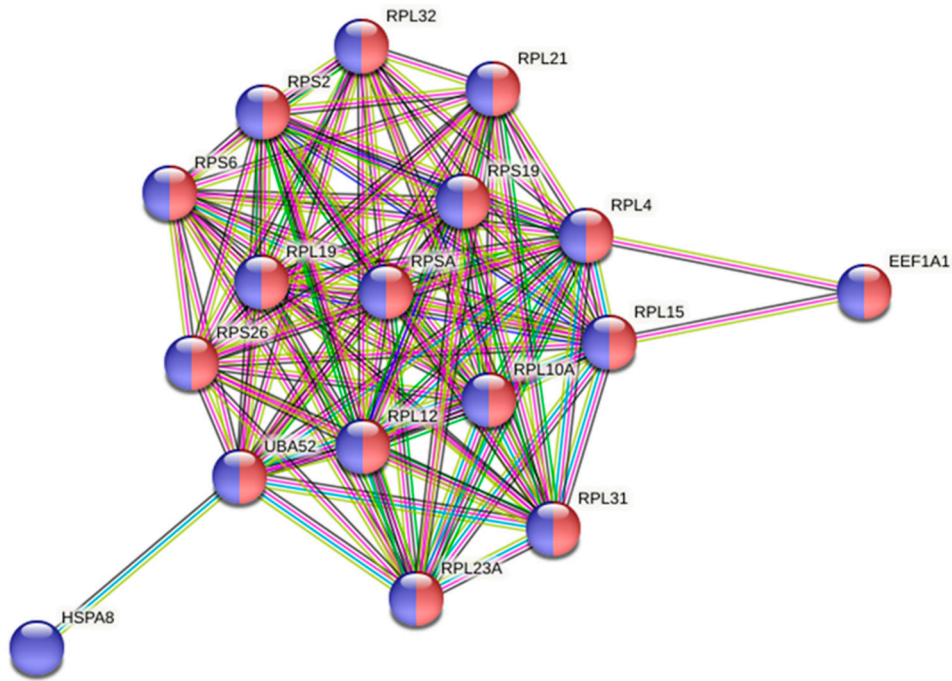


Figure S3. The interaction network of parental proteins of pseudogenes differentially expressed in exosomes isolated from IAV-infected MDCK cells, shown by STRING pathway analysis. Colors indicate GO annotations: red – GO:0006412 “Biological process – Translation”; blue – GO:0010467 “Biological process – Gene expression”.

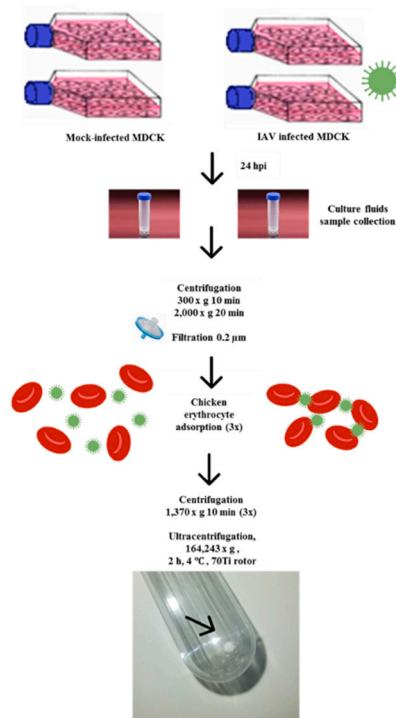


Figure S4. Overview of exosome isolation procedure, hpi – hours post inoculation.

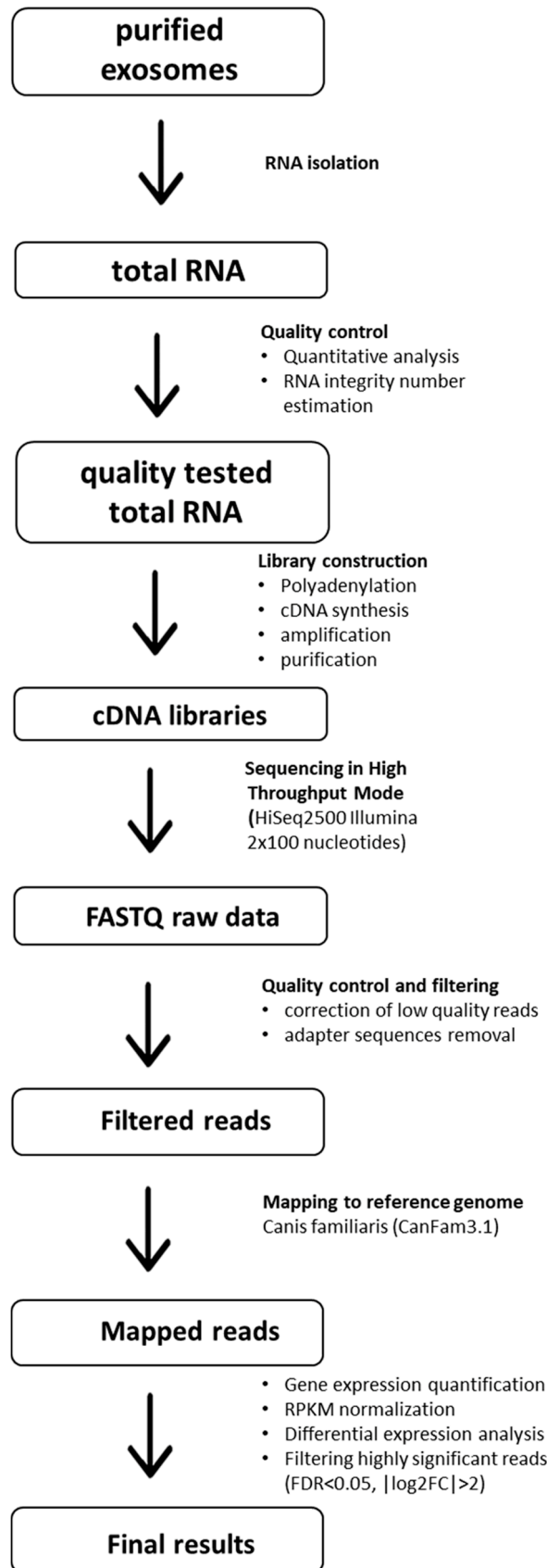


Figure S5. Overview of the analysis procedure of differentially expressed RNA in exosomes isolated from influenza-infected and mock-infected MDCK cells.

cDNA – complimentary DNA; RPKM – reads per kilobase of transcript per million reads mapped

Table S1. List of differently expressed RNAs in exosomes secreted by influenza infected cells

Table S2. Number of reads mapped to protein coding regions of influenza virus A/equi/Kentucky/81 reference genome (CY028828.1 - CY028835.1)