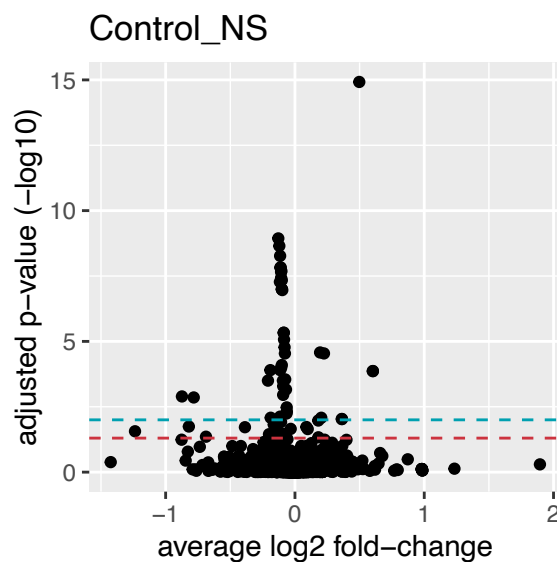


Pathway analysis



Volcano plot summarising the GSEA analysis. Contains all the pathways mapped to the Reactome database each point represents one pathway with its position on the x-axis determined by its average log2 fold change within the pathway. The y-axis position is determined by the pathways' p-value (FDR adjusted) with lower p-values positioned higher on the plot due to the inverse log ($-\log_{10}$); The red line indicates the position on the y-axis where the adjusted p-value = 0.05, the blue line 0.01.

Top-regulated pathways

Cholesterol biosynthesis (R-HSA-191273)

| | Control_NS |
|------------|-------------------|
| Regulation | Up |
| FDR | < 0.001 |
| Av. FC | 0.497 |
| N Genes | 26 |

Regulation of cholesterol biosynthesis by SREBP (SREBF) (R-HSA-1655829)

| | Control_NS |
|------------|-------------------|
| Regulation | Up |
| FDR | < 0.001 |
| Av. FC | 0.195 |
| N Genes | 56 |

Activation of gene expression by SREBF (SREBP) (R-HSA-2426168)

| | Control_NS |
|------------|-------------------|
| Regulation | Up |
| FDR | < 0.001 |
| Av. FC | 0.224 |
| N Genes | 43 |

Cholesterol biosynthesis via desmosterol (R-HSA-6807047)

| | Control_NS |
|------------|-------------------|
| Regulation | Up |
| FDR | < 0.001 |
| Av. FC | 0.603 |
| N Genes | 4 |

Cholesterol biosynthesis via lathosterol (R-HSA-6807062)

| | Control_NS |
|------------|-------------------|
| Regulation | Up |
| FDR | < 0.001 |
| Av. FC | 0.603 |
| N Genes | 4 |

tRNA processing in the mitochondrion (R-HSA-6785470)

| | Control_NS |
|------------|--------------|
| Regulation | Up |
| FDR | 0.008 |
| Av. FC | 0.204 |
| N Genes | 42 |

Virus Assembly and Release (R-HSA-168268)

| | Control_NS |
|------------|--------------|
| Regulation | Up |
| FDR | 0.009 |
| Av. FC | 0.363 |
| N Genes | 2 |

Assembly of Viral Components at the Budding Site (R-HSA-168316)

| | Control_NS |
|------------|--------------|
| Regulation | Up |
| FDR | 0.009 |
| Av. FC | 0.363 |
| N Genes | 2 |

FASTK family proteins regulate processing and stability of mitochondrial RNAs (R-HSA-9837092)

| | Control_NS |
|------------|--------------|
| Regulation | Up |
| FDR | 0.011 |
| Av. FC | 0.181 |
| N Genes | 19 |

COPI-independent Golgi-to-ER retrograde traffic (R-HSA-6811436)

| | Control_NS |
|------------|--------------|
| Regulation | Up |
| FDR | 0.019 |
| Av. FC | 0.088 |
| N Genes | 46 |

Metabolism of steroids (R-HSA-8957322)

| | Control_NS |
|------------|--------------|
| Regulation | Up |
| FDR | 0.023 |
| Av. FC | 0.099 |
| N Genes | 123 |

rRNA processing in the mitochondrion (R-HSA-8868766)

| | Control_NS |
|------------|--------------|
| Regulation | Up |
| FDR | 0.047 |
| Av. FC | 0.181 |
| N Genes | 38 |

Response of EIF2AK4 (GCN2) to amino acid deficiency (R-HSA-9633012)

| | Control_NS |
|------------|-------------------|
| Regulation | Down |
| FDR | < 0.001 |
| Av. FC | -0.129 |
| N Genes | 91 |

Eukaryotic Translation Elongation (R-HSA-156842)

| | Control_NS |
|------------|-------------------|
| Regulation | Down |
| FDR | < 0.001 |
| Av. FC | -0.121 |
| N Genes | 83 |

Peptide chain elongation (R-HSA-156902)

| | Control_NS |
|------------|-------------------|
| Regulation | Down |
| FDR | < 0.001 |
| Av. FC | -0.115 |
| N Genes | 79 |

Eukaryotic Translation Termination (R-HSA-72764)

| | Control_NS |
|------------|-------------------|
| Regulation | Down |
| FDR | < 0.001 |
| Av. FC | -0.11 |
| N Genes | 83 |

Selenocysteine synthesis (R-HSA-2408557)

| | Control_NS |
|------------|-------------------|
| Regulation | Down |
| FDR | < 0.001 |
| Av. FC | -0.112 |
| N Genes | 83 |

Formation of a pool of free 40S subunits (R-HSA-72689)

| | Control_NS |
|------------|-------------------|
| Regulation | Down |
| FDR | < 0.001 |
| Av. FC | -0.105 |
| N Genes | 91 |

Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC) (R-HSA-975956)

| | Control_NS |
|------------|-------------------|
| Regulation | Down |
| FDR | < 0.001 |
| Av. FC | -0.107 |
| N Genes | 85 |

Viral mRNA Translation (R-HSA-192823)

| | Control_NS |
|------------|-------------------|
| Regulation | Down |
| FDR | < 0.001 |
| Av. FC | -0.107 |
| N Genes | 79 |

L13a-mediated translational silencing of Ceruloplasmin expression (R-HSA-156827)

| | Control_NS |
|------------|-------------------|
| Regulation | Down |
| FDR | < 0.001 |
| Av. FC | -0.102 |
| N Genes | 101 |

Selenoamino acid metabolism (R-HSA-2408522)

| | Control_NS |
|------------|-------------------|
| Regulation | Down |
| FDR | < 0.001 |
| Av. FC | -0.116 |
| N Genes | 105 |

Eukaryotic Translation Initiation (R-HSA-72613)

| | Control_NS |
|------------|-------------------|
| Regulation | Down |
| FDR | < 0.001 |
| Av. FC | -0.101 |
| N Genes | 109 |

Cap-dependent Translation Initiation (R-HSA-72737)

| | Control_NS |
|------------|-------------------|
| Regulation | Down |
| FDR | < 0.001 |
| Av. FC | -0.101 |
| N Genes | 109 |

GTP hydrolysis and joining of the 60S ribosomal subunit (R-HSA-72706)

| | Control_NS |
|------------|-------------------|
| Regulation | Down |
| FDR | < 0.001 |
| Av. FC | -0.098 |
| N Genes | 102 |

Nonsense-Mediated Decay (NMD) (R-HSA-927802)

| | Control_NS |
|------------|-------------------|
| Regulation | Down |
| FDR | < 0.001 |
| Av. FC | -0.087 |
| N Genes | 105 |

Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC) (R-HSA-975957)

| | Control_NS |
|------------|-------------------|
| Regulation | Down |
| FDR | < 0.001 |
| Av. FC | -0.087 |
| N Genes | 105 |

Influenza Viral RNA Transcription and Replication (R-HSA-168273)

| | Control_NS |
|------------|-------------------|
| Regulation | Down |
| FDR | < 0.001 |
| Av. FC | -0.084 |
| N Genes | 125 |

Major pathway of rRNA processing in the nucleolus and cytosol (R-HSA-6791226)

| | Control_NS |
|------------|-------------------|
| Regulation | Down |
| FDR | < 0.001 |
| Av. FC | -0.08 |
| N Genes | 171 |

rRNA processing in the nucleus and cytosol (R-HSA-8868773)

| | Control_NS |
|------------|-------------------|
| Regulation | Down |
| FDR | < 0.001 |
| Av. FC | -0.078 |
| N Genes | 181 |

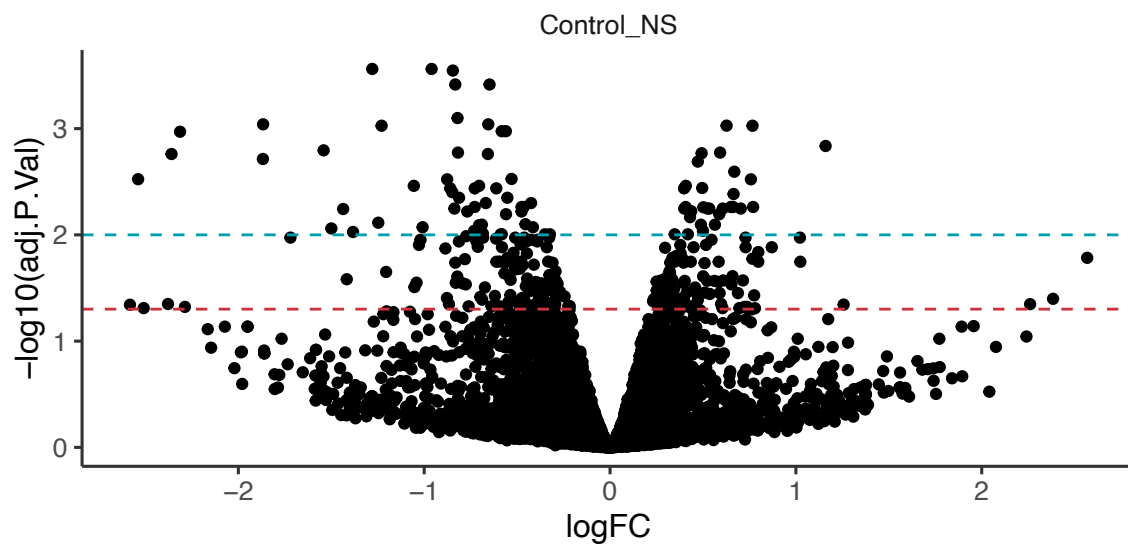
Formation of the ternary complex, and subsequently, the 43S complex (R-HSA-72695)

| | Control_NS |
|------------|-------------------|
| Regulation | Down |
| FDR | < 0.001 |
| Av. FC | -0.102 |
| N Genes | 49 |

Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S (R-HSA-72662)

| | Control_NS |
|------------|-------------------|
| Regulation | Down |
| FDR | < 0.001 |
| Av. FC | -0.107 |
| N Genes | 57 |

Protein / Gene level results



Top up-regulated protein/genes

Control_NS

| Identifier | logFC | AveExpr | t | P.Value | adj.P.Val | B |
|------------|-----------|----------|-----------|---------|-----------|----------|
| STARD4 | 0.6269767 | 5.855519 | 10.325053 | 7.0e-07 | 0.0009376 | 6.531139 |
| HSD17B7 | 0.7665604 | 4.145393 | 10.212590 | 8.0e-07 | 0.0009392 | 6.311632 |

| Identifier | logFC | AveExpr | t | P.Value | adj.P.Val | B |
|------------|-----------|----------|----------|---------|-----------|----------|
| FGF1 | 1.1599173 | 2.610482 | 9.360287 | 1.8e-06 | 0.0014571 | 5.133912 |
| OTUD1 | 0.5922230 | 6.363517 | 9.047698 | 2.5e-06 | 0.0016812 | 5.289344 |
| PPL | 0.4928045 | 6.922342 | 8.983472 | 2.6e-06 | 0.0017047 | 5.218036 |
| DPYSL2 | 0.4722407 | 7.259081 | 8.637866 | 3.8e-06 | 0.0020435 | 4.844040 |
| TM7SF2 | 0.6684746 | 6.756545 | 8.401344 | 5.0e-06 | 0.0025437 | 4.587652 |
| MAP3K7CL | 0.7579712 | 3.899901 | 8.122379 | 6.8e-06 | 0.0030015 | 4.274503 |
| TUBA1A | 0.4077416 | 9.394441 | 7.930915 | 8.5e-06 | 0.0034562 | 4.034652 |
| TGFBR1 | 0.4958749 | 6.726674 | 7.842555 | 9.4e-06 | 0.0036203 | 3.944711 |

Top down-regulated protein/genes
Control_NS

| Identifier | logFC | AveExpr | t | P.Value | adj.P.Val | B |
|------------|------------|----------|------------|---------|-----------|----------|
| PSG1 | -1.2795536 | 6.669333 | -14.429719 | 0.0e+00 | 0.0002745 | 9.671383 |
| NR2F1 | -0.9599362 | 5.967708 | -13.577149 | 0.0e+00 | 0.0002745 | 9.074079 |
| PTGIS | -0.8459189 | 9.437413 | -12.999894 | 1.0e-07 | 0.0002841 | 8.742560 |
| PVR | -0.6484618 | 7.964049 | -12.104053 | 1.0e-07 | 0.0003845 | 8.064760 |
| GPX1 | -0.8326514 | 5.761857 | -11.989130 | 2.0e-07 | 0.0003845 | 7.920132 |
| CYP24A1 | -0.8206274 | 9.721705 | -10.941612 | 4.0e-07 | 0.0007951 | 7.099960 |
| CAMK2A | -0.6550722 | 4.582633 | -10.621915 | 5.0e-07 | 0.0009116 | 6.719940 |
| ELF3 | -1.8668112 | 3.602457 | -10.479898 | 6.0e-07 | 0.0009116 | 6.348448 |
| AKAP12 | -1.2292902 | 6.630273 | -10.113167 | 8.0e-07 | 0.0009394 | 6.343191 |
| CAPN5 | -0.5606533 | 7.089405 | -9.839732 | 1.1e-06 | 0.0010583 | 6.083384 |