# Supplementary file

July 23, 2022

## Contents

# 1 Data pre-processing

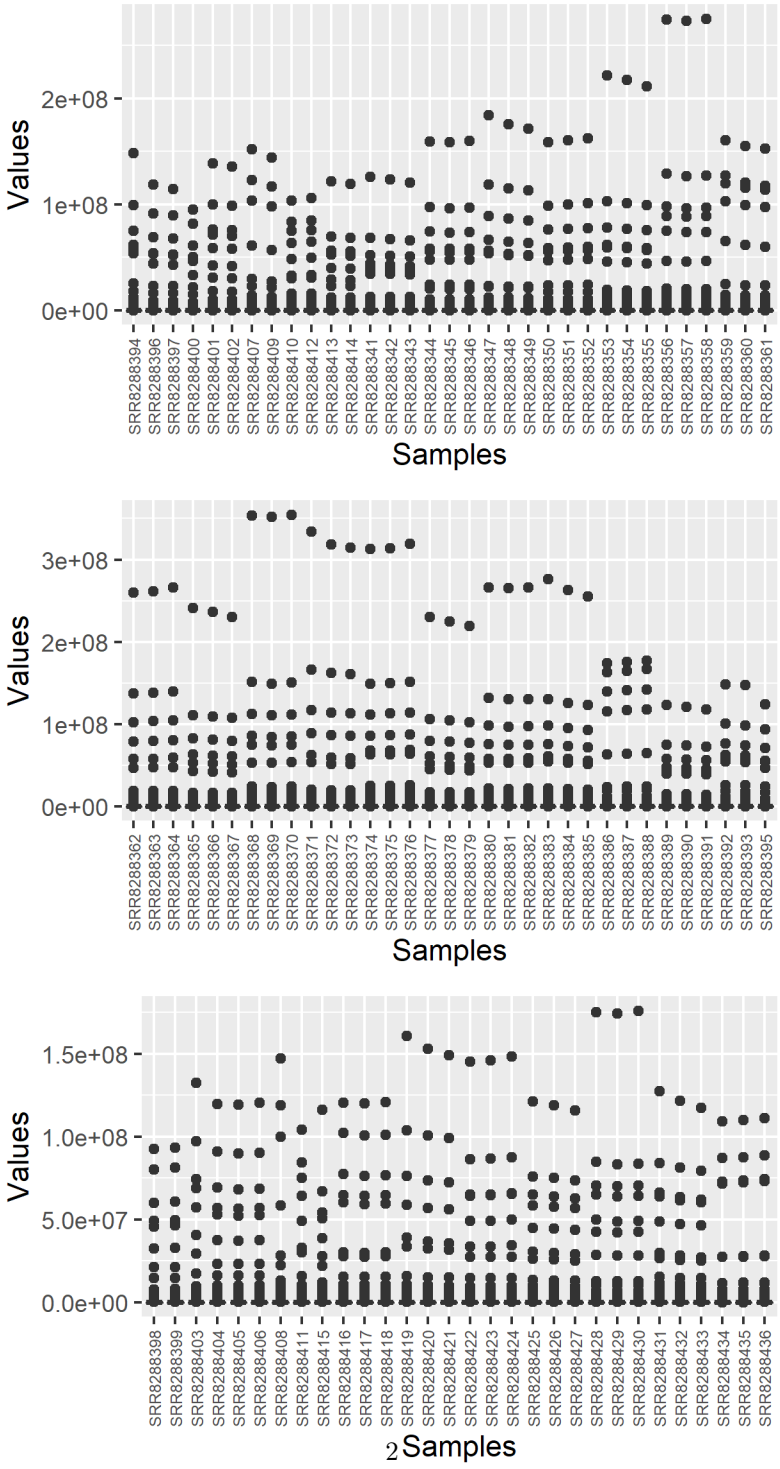



Figure 1: Raw counts

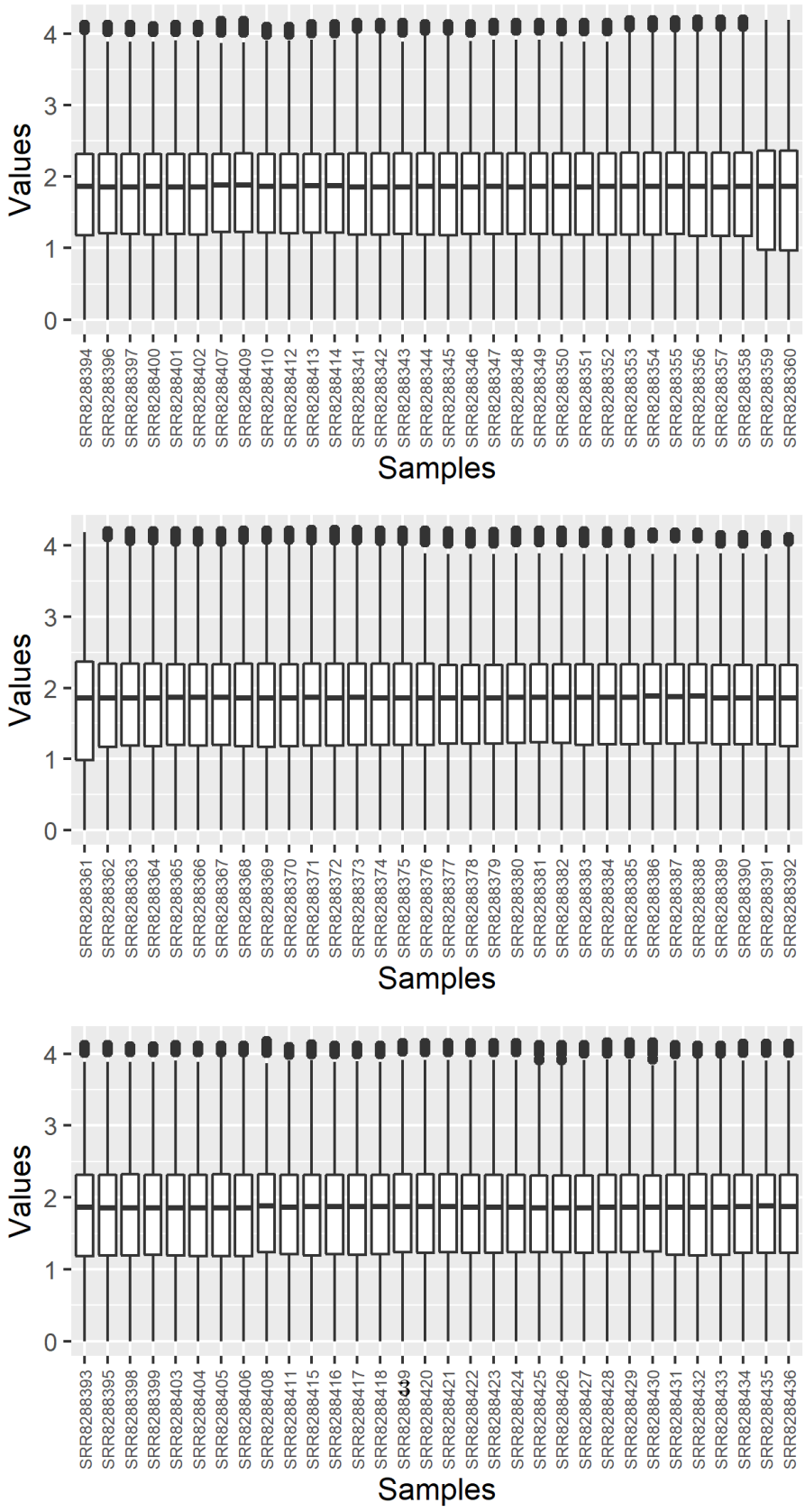



Figure 2: Processed counts

## 2 Hclustering results

Figure 3: Hclustering result, *all-ages* case

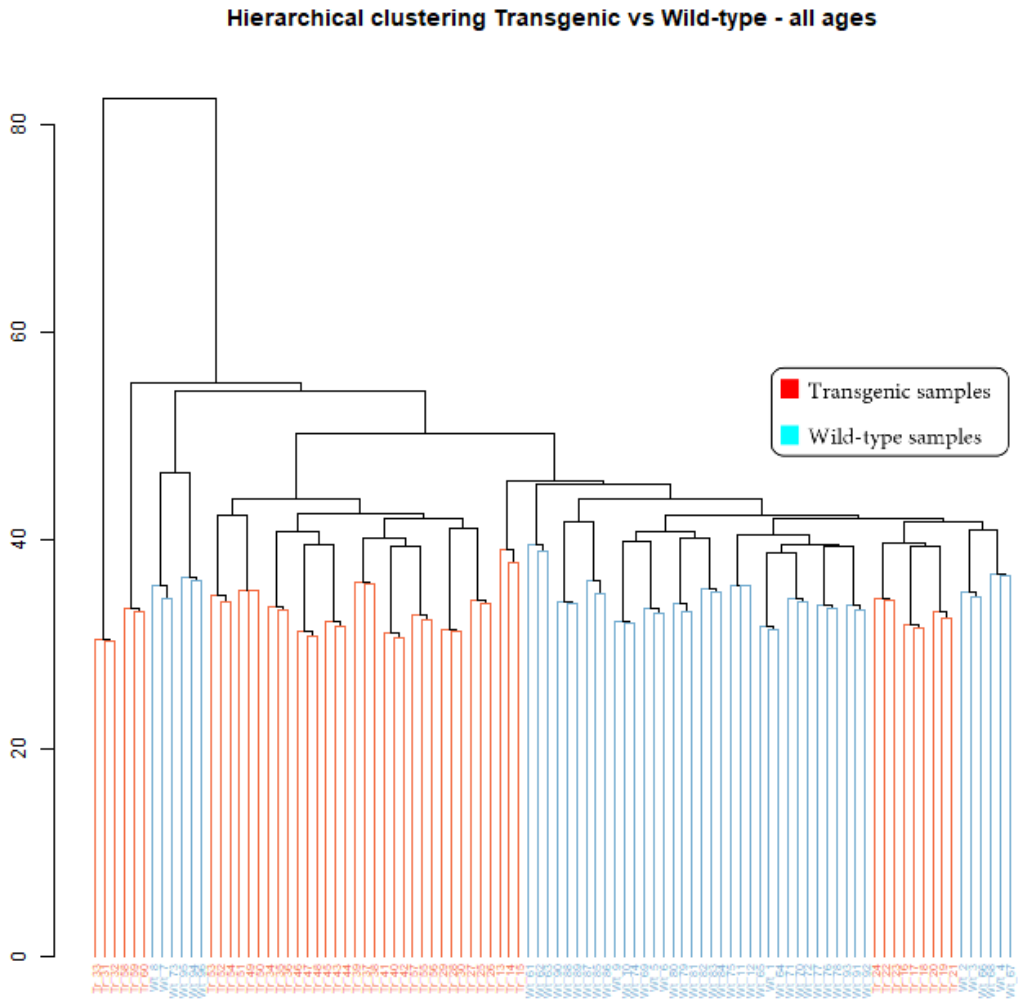
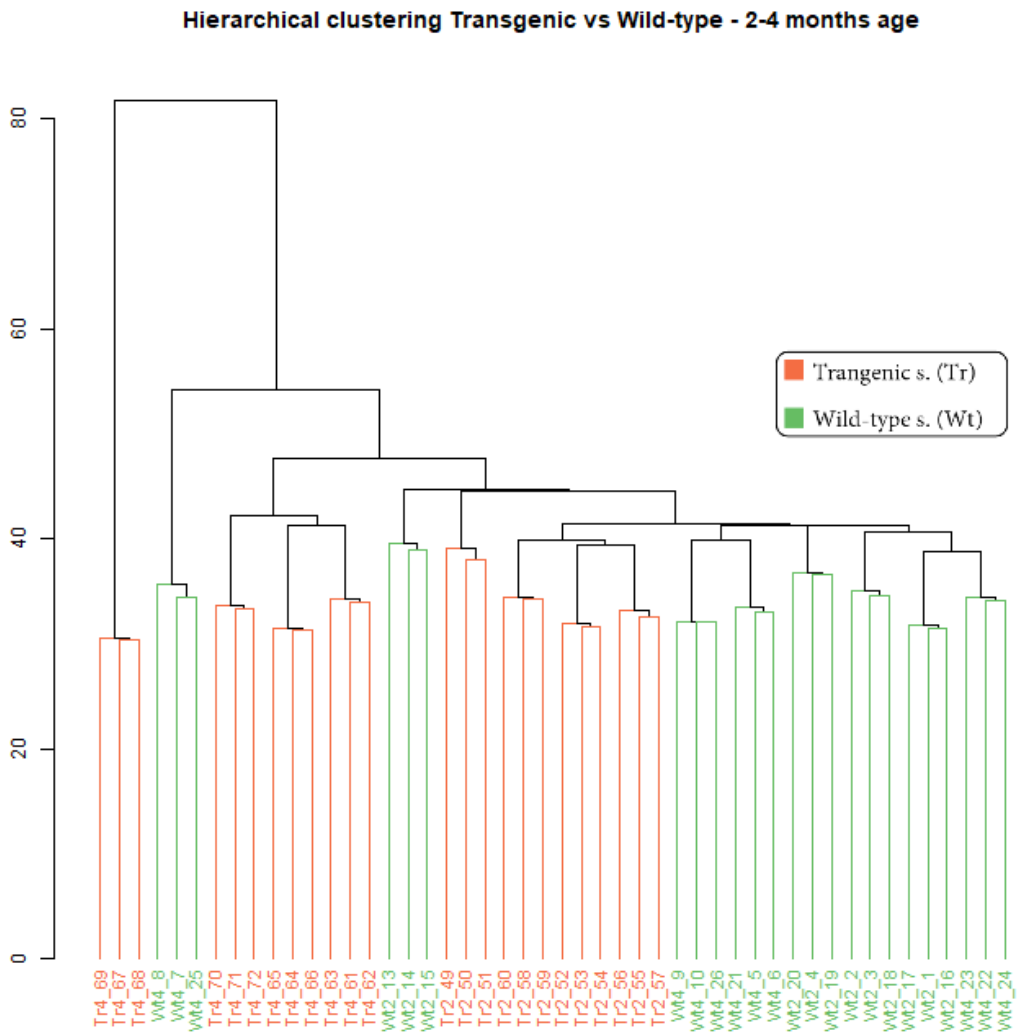


Figure 4: Hclustering result, *young samples* case



## 3 Importance values

Figure 5: Importance results, *all-ages* case

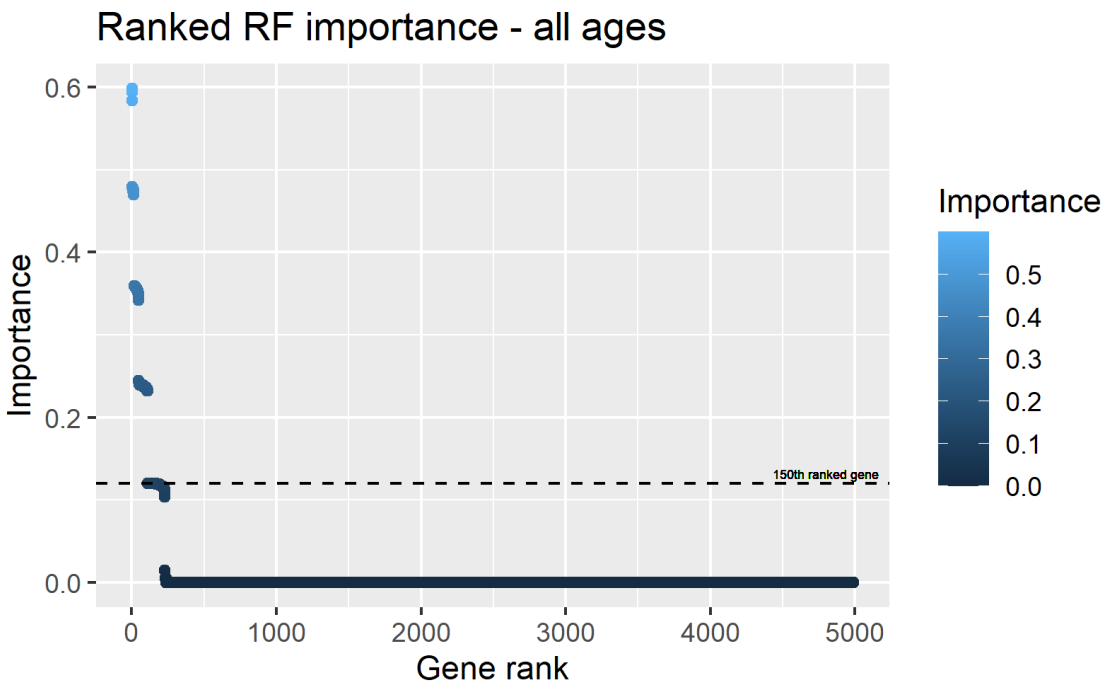
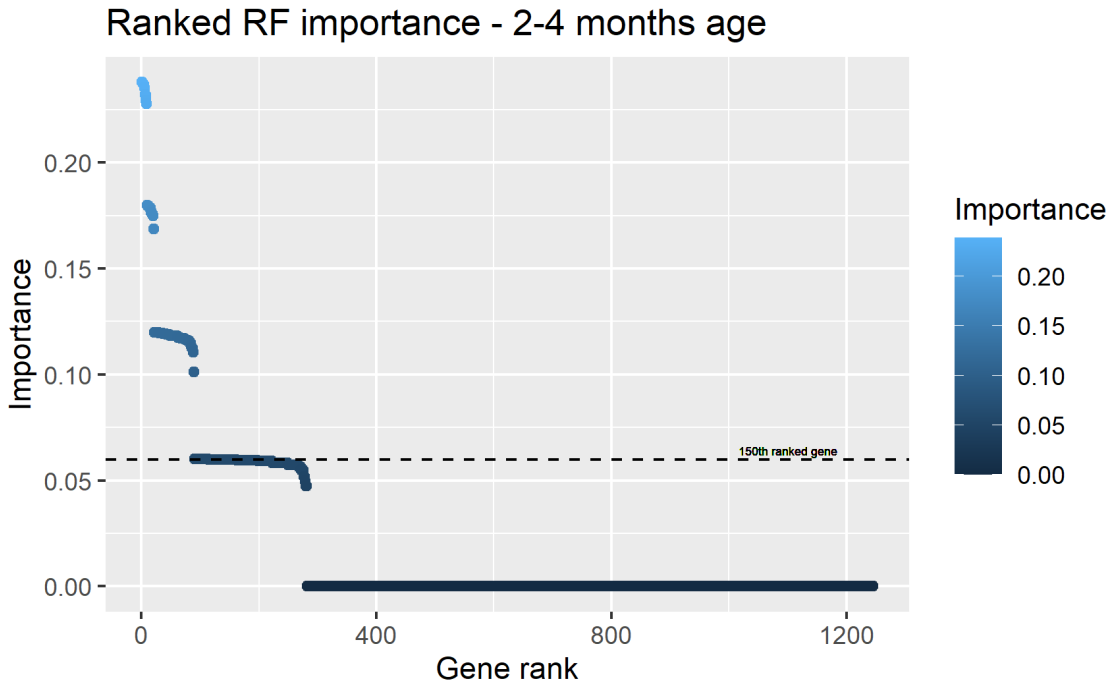
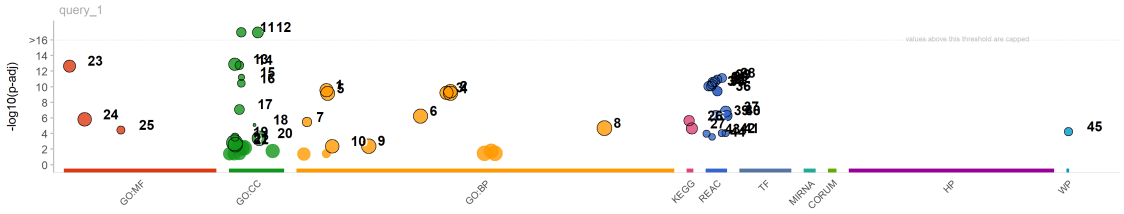


Figure 6: Importance results, *young samples* case



# 4 Enrichment results

Figure 7: Enrichment g:plot, *all-ages* case




| id | source | term_id | term_name | term_size | p_value |
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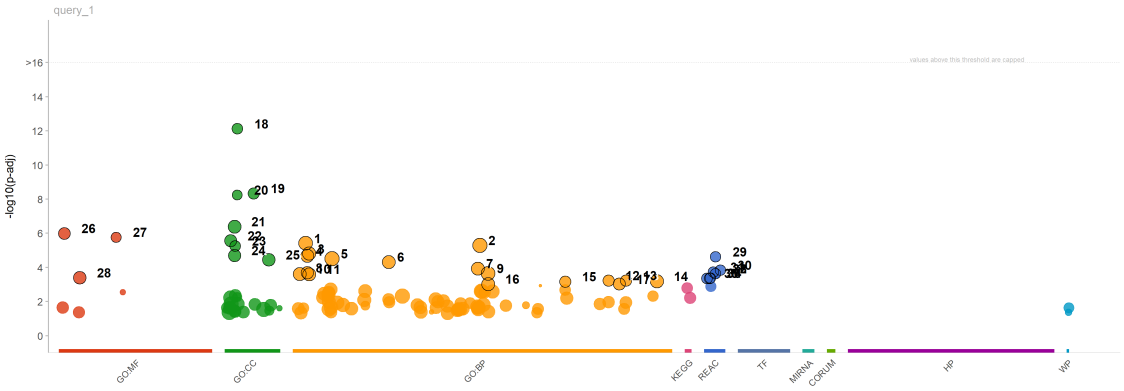
| 1 | GO:BP | GO:0006412 | translation | 716 | 2.7e-10 |
| 2 | GO:BP | GO:0043604 | amide biosynthetic process | 857 | 3.8e-10 |
| 3 | GO:BP | GO:0043043 | peptide biosynthetic process | 739 | 5.6e-10 |
| 4 | GO:BP | GO:0043603 | cellular amide metabolic process | 1170 | 7.1e-10 |
| 5 | GO:BP | GO:0006518 | peptide metabolic process | 910 | 7.2e-10 |
| 6 | GO:BP | GO:0034645 | cellular macromolecule biosynthetic process | 1174 | 6.0e-07 |
| 7 | GO:BP | GO:0002181 | cytoplasmic translation | 115 | 3.5e-06 |
| 8 | GO:BP | GO:1901566 | organonitrogen compound biosynthetic process | 1659 | 2.1e-05 |
| 9 | GO:BP | GO:0016477 | cell migration | 1505 | 4.1e-03 |
| 10 | GO:BP | GO:0006954 | inflammatory response | 745 | 4.5e-03 |
| 11 | GO:CC | GO:0022626 | cytosolic ribosome | 111 | 1.1e-21 |
| 12 | GO:CC | GO:0044391 | ribosomal subunit | 200 | 4.6e-20 |
| 13 | GO:CC | GO:0005840 | ribosome | 419 | 1.3e-13 |
| 14 | GO:CC | GO:0015935 | small ribosomal subunit | 80 | 1.7e-13 |
| 15 | GO:CC | GO:0022627 | cytosolic small ribosomal subunit | 46 | 6.2e-12 |
| 16 | GO:CC | GO:0022625 | cytosolic large ribosomal subunit | 63 | 3.8e-11 |
| 17 | GO:CC | GO:0015934 | large ribosomal subunit | 125 | 8.3e-08 |
| 18 | GO:CC | GO:0042788 | polysomal ribosome | 34 | 7.9e-06 |
| 19 | GO:CC | GO:0005844 | polysome | 72 | 2.7e-04 |
| 20 | GO:CC | GO:0045202 | synapse | 1499 | 4.1e-04 |
| 21 | GO:CC | GO:0005829 | cytosol | 4082 | 1.6e-03 |
| 22 | GO:CC | GO:0005887 | integral component of plasma membrane | 1515 | 2.7e-03 |
| 23 | GO:MF | GO:0003735 | structural constituent of ribosome | 351 | 2.1e-13 |
| 24 | GO:MF | GO:0005198 | structural molecule activity | 790 | 1.6e-06 |
| 25 | GO:MF | GO:0019843 | rRNA binding | 70 | 3.6e-05 |
| 26 | KEGG | KEGG:03010 | Ribosome | 164 | 2.3e-06 |
| 27 | KEGG | KEGG:05171 | Coronavirus disease - COVID-19 | 233 | 2.3e-05 |
| 28 | REAC | REAC:R-MMU-1799339 | SRP-dependent cotranslational protein targeting to membrane | 88 | 7.7e-12 |
| 29 | REAC | REAC:R-MMU-975956 | Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC) | 90 | 1.2e-11 |
| 30 | REAC | REAC:R-MMU-156827 | L13a-mediated translational silencing of Ceruloplasmin expression | 107 | 2.2e-11 |
| 31 | REAC | REAC:R-MMU-72706 | GTP hydrolysis and joining of the 60S ribosomal subunit | 108 | 2.6e-11 |
| 32 | REAC | REAC:R-MMU-72689 | Formation of a pool of free 40S subunits | 97 | 4.6e-11 |
| 33 | REAC | REAC:R-MMU-72613 | Eukaryotic Translation Initiation | 115 | 8.6e-11 |
| 34 | REAC | REAC:R-MMU-72737 | Cap-dependent Translation Initiation | 115 | 8.6e-11 |
| 35 | REAC | REAC:R-MMU-927802 | Nonsense-Mediated Decay (NMD) | 109 | 3.8e-10 |
| 36 | REAC | REAC:R-MMU-975957 | Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC) | 109 | 3.8e-10 |
| 37 | REAC | REAC:R-MMU-72766 | Translation | 216 | 1.5e-07 |
| 38 | REAC | REAC:R-MMU-72312 | rRNA processing | 166 | 5.0e-07 |
| 39 | REAC | REAC:R-MMU-6791226 | Major pathway of rRNA processing in the nucleolus and cytosol | 166 | 5.0e-07 |
| 40 | REAC | REAC:R-MMU-8868773 | rRNA processing in the nucleus and cytosol | 166 | 5.0e-07 |
| 41 | REAC | REAC:R-MMU-72649 | Translation initiation complex formation | 55 | 9.3e-05 |
| 42 | REAC | REAC:R-MMU-72702 | Ribosomal scanning and start codon recognition | 55 | 9.3e-05 |
| 43 | REAC | REAC:R-MMU-72662 | Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S | 56 | 1.1e-04 |
| 44 | REAC | REAC:R-MMU-72695 | Formation of the ternary complex, and subsequently, the 43S complex | 48 | 2.8e-04 |
| 45 | WP | WP:WP163 | Cytoplasmic ribosomal proteins | 78 | 5.9e-05 |

*g:Profiler (biit.cs.ut.ee/gprofiler)*

Figure 8: Enrichment g:plot, *young samples* case




| id | source | term_id | term_name | term_size | p_value |
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| 1 | GO:BP | GO:0002376 | immune system process | 2849 | 3.9e-06 |
| 2 | GO:BP | GO:0048731 | system development | 4533 | 5.1e-06 |
| 3 | GO:BP | GO:0002682 | regulation of immune system process | 1507 | 1.6e-05 |
| 4 | GO:BP | GO:0002520 | immune system development | 1080 | 2.1e-05 |
| 5 | GO:BP | GO:0007275 | multicellular organism development | 5045 | 3.1e-05 |
| 6 | GO:BP | GO:0030097 | hemopoiesis | 970 | 4.9e-05 |
| 7 | GO:BP | GO:0048534 | hematopoietic or lymphoid organ development | 1016 | 1.2e-04 |
| 8 | GO:BP | GO:0002521 | leukocyte differentiation | 605 | 2.1e-04 |
| 9 | GO:BP | GO:0051239 | regulation of multicellular organismal process | 2854 | 2.3e-04 |
| 10 | GO:BP | GO:0001775 | cell activation | 1165 | 2.4e-04 |
| 11 | GO:BP | GO:0002684 | positive regulation of immune system process | 994 | 2.5e-04 |
| 12 | GO:BP | GO:1902107 | positive regulation of leukocyte differentiation | 184 | 5.8e-04 |
| 13 | GO:BP | GO:1903708 | positive regulation of hemopoiesis | 184 | 5.8e-04 |
| 14 | GO:BP | GO:2000026 | regulation of multicellular organismal development | 1494 | 6.6e-04 |
| 15 | GO:BP | GO:0097529 | myeloid leukocyte migration | 221 | 6.8e-04 |
| 16 | GO:BP | GO:0051241 | negative regulation of multicellular organismal process | 1078 | 9.5e-04 |
| 17 | GO:BP | GO:1903131 | mononuclear cell differentiation | 468 | 9.6e-04 |
| 18 | GO:CC | GO:0022626 | cytosolic ribosome | 111 | 7.5e-13 |
| 19 | GO:CC | GO:0044391 | ribosomal subunit | 200 | 4.7e-09 |
| 20 | GO:CC | GO:0022625 | cytosolic large ribosomal subunit | 63 | 5.7e-09 |
| 21 | GO:CC | GO:0009986 | cell surface | 1117 | 4.1e-07 |
| 22 | GO:CC | GO:0005840 | ribosome | 419 | 2.7e-06 |
| 23 | GO:CC | GO:0015934 | large ribosomal subunit | 125 | 5.5e-06 |
| 24 | GO:CC | GO:0009897 | external side of plasma membrane | 594 | 2.0e-05 |
| 25 | GO:CC | GO:0098552 | side of membrane | 792 | 3.6e-05 |
| 26 | GO:MF | GO:0003735 | structural constituent of ribosome | 351 | 1.0e-06 |
| 27 | GO:MF | GO:0019843 | rRNA binding | 70 | 1.7e-06 |
| 28 | GO:MF | GO:0005198 | structural molecule activity | 790 | 4.1e-04 |
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| 31 | REAC | REAC:R-MMU-156827 | L13a-mediated translational silencing of Ceruloplasmin expression | 107 | 1.9e-04 |
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| 33 | REAC | REAC:R-MMU-927802 | Nonsense-Mediated Decay (NMD) | 109 | 2.3e-04 |
| 34 | REAC | REAC:R-MMU-72689 | Formation of a pool of free 40S subunits | 97 | 4.2e-04 |
| 35 | REAC | REAC:R-MMU-72737 | Cap-dependent Translation Initiation | 115 | 4.4e-04 |
| 36 | REAC | REAC:R-MMU-72613 | Eukaryotic Translation Initiation | 115 | 4.4e-04 |

*g:Profiler (biit.cs.ut.ee/gprofiler)*

Figure 9: Enrichment enrichGO, *all-ages* case

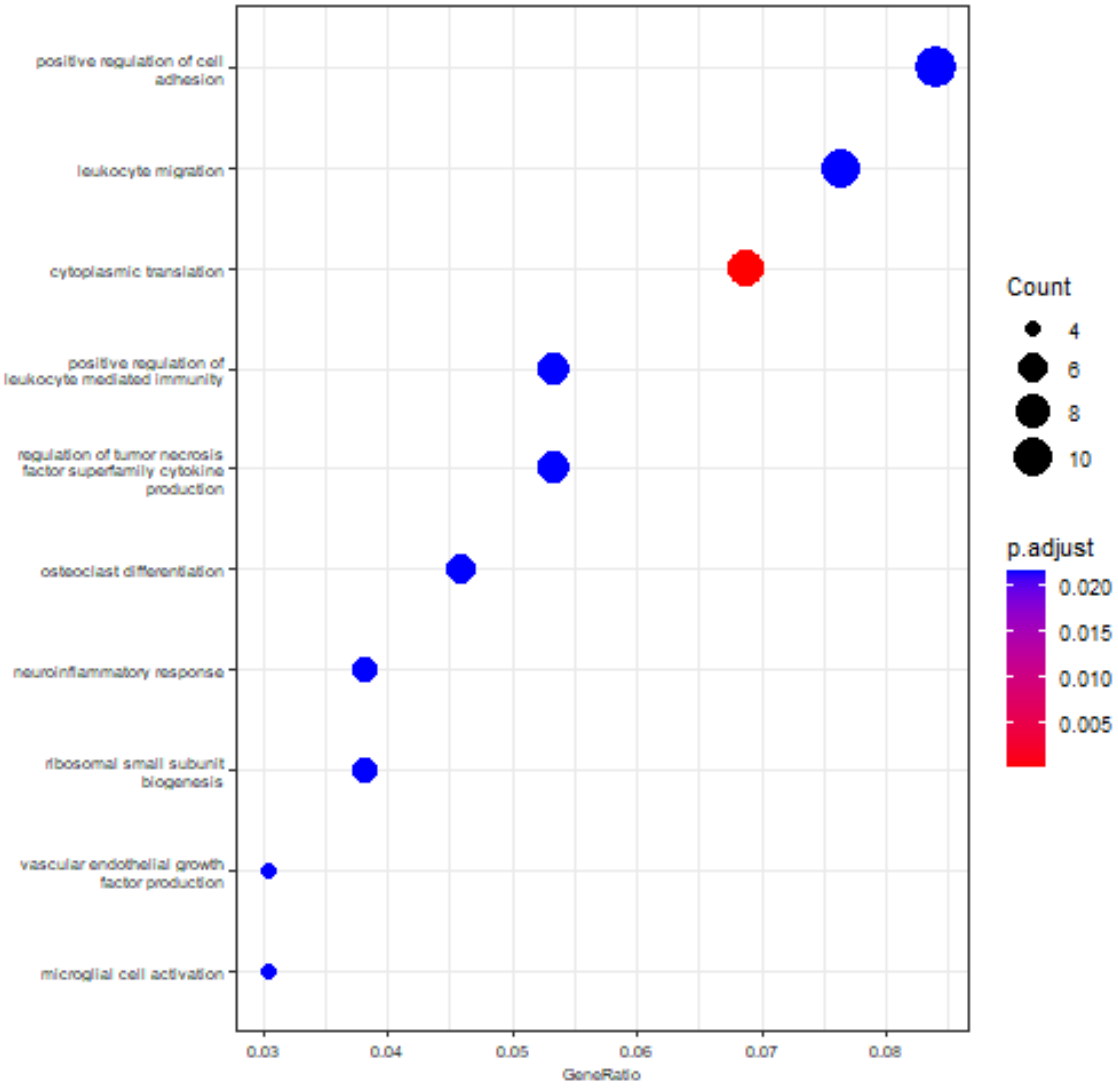

Figure 10: Enrichment enrichGO, *young samples* case