

**Supplementary Material to:**

**Plasma Proteomic Profiling of Septic Shock and Acute Pancreatitis  
Identifies Shared Signatures and Disease-specific Pathways**

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**Table S1a.** Counts of proteins meeting differential expression conditions for significant upregulation across three condition groups.

| Significance conditions   | Count                    |                          |                               |
|---------------------------|--------------------------|--------------------------|-------------------------------|
|                           | Septic shock vs. Control | Pancreatitis vs. Control | Septic shock vs. Pancreatitis |
| Log2FC > 0.5              | 227                      | 189                      | 155                           |
| Adjusted p-value < 0.05   | 231                      | 83                       | 29                            |
| Significantly upregulated | 113                      | 46                       | 7                             |

**Septic shock vs. Control:** ACY1', 'ADAMTSL2', 'ALDOA', 'ARHGAP1', 'ASL', 'B2M', 'BASP1', 'CALR', 'CAST', 'CCN2', 'CD163', 'CD177', 'CHI3L1', 'COL11A2', 'COL1A1', 'COL1A2', 'COL2A1', 'COL5A1', 'COL6A1', 'CRP', 'CST3', 'CTSB', 'CTSD', 'CTSL', 'CTS2', 'DDT', 'DPP3', 'EPHB4', 'F8', 'FAH', 'FGL2', 'FSTL1', 'GALNT2', 'GANAB', 'GOLM1', 'GOT1', 'GPI', 'GRN', 'GSTO1', 'H3-4', 'H4C1; H4C2; H4C3; H4C4; H4C5; H4C6; H4C8; H4C9; H4C11; H4C12; H4C13; H4C14; H4C15; H4-16', 'HSP90AA1', 'HSP90AB1', 'HSPA4', 'HSPA8', 'ICAM1', 'IGFBP4', 'IL18BP', 'IL1R2', 'IL1RL1', 'ITIH3', 'LAMB1', 'LAMC1', 'LBP', 'LCN2', 'LCP1', 'LGALS3BP', 'LMNB1', 'LRG1', 'LTA4H', 'LTBP2', 'MARCKS', 'MMP8', 'MMP9', 'MPO', 'MRC1', 'NID1', 'NPC2', 'NUCB1', 'ORM1', 'PDIA4', 'PGD', 'PGK1', 'PLA2G2A', 'PLIN3', 'PRKCSH', 'PSAP', 'PSMA1', 'PSMA3', 'PSMA4', 'PSMA5', 'PSMA6', 'PSMA7', 'PSMB2', 'PSMB3', 'PSMB4', 'REG1A', 'REG1B', 'RRBP1', 'S100A12', 'S100A8', 'S100A9', 'SAA1', 'SAA2', 'SEMA4B', 'SERPINA3', 'SERPINB1', 'SIRPA', 'SIRPB1', 'SOD2', 'SPP1', 'TALDO1', 'TIMP1', 'TKT', 'TNC', 'TRAP1', 'VCAM1', 'VCAN', 'VIM', 'VSIG4', 'VWF', 'YWHAE', 'YWHAG'

**Pancreatitis vs. Control:** 'APOA5', 'BPGM', 'CA1', 'CAT', 'CDHR2', 'CHI3L1', 'COL6A1', 'CPA1', 'CRP', 'CTSB', 'CTSD', 'CTS2', 'EPHB4', 'F8', 'GALNT2', 'IGFBP4', 'IL1RL1', 'LBP', 'LCP1', 'LRG1', 'LTA4H', 'MAN1A1', 'MMP8', 'MMP9', 'NID1', 'NUCB1', 'ORM1', 'ORM2', 'PRDX2', 'PRSS2', 'PSMA1', 'PSMA6', 'PSMB7', 'REG1B', 'S100A12', 'S100A8', 'S100A9', 'SAA1', 'SAA2', 'SERPINA3', 'TALDO1', 'TIMP1', 'TKT', 'VIM', 'VSIG4', 'VWF'

**Septic shock vs. Pancreatitis:** 'CD163', 'COTL1', 'GANAB', 'HSP90AA1', 'MARCKS', 'PSAP', 'SERPINB1'

**Table S1b.** Counts of proteins meeting differential expression conditions for significant downregulation across three condition groups.

| Significance conditions     | Count                    |                          |                               |
|-----------------------------|--------------------------|--------------------------|-------------------------------|
|                             | Septic shock vs. Control | Pancreatitis vs. Control | Septic shock vs. Pancreatitis |
| Log2FC < -0.5               | 222                      | 169                      | 152                           |
| Adjusted p-value < 0.05     | 231                      | 83                       | 29                            |
| Significantly downregulated | 118                      | 37                       | 22                            |

**Septic shock vs. Control:** 'A1BG', 'ACE', 'ADAMTS13', 'ADGRG6', 'ADIPOQ', 'AFM', 'AHSG', 'AOC3', 'APOA4', 'APOB', 'APOC1', 'APOC4', 'APOD', 'APOF', 'APOH', 'APOM', 'ATRN', 'AZGP1', 'B3GNT2', 'B4GAT1', 'BCHE', 'BIN2', 'BTD', 'C1QA', 'C1QB', 'C1RL', 'C3', 'C5', 'C6', 'C8A', 'C8B', 'C8G', 'CACNA2D1', 'CDH13', 'CETP', 'CFH', 'CFI', 'CHL1', 'CLEC3B', 'CLU', 'CNDP1', 'CNTN1', 'CNTN3', 'COLEC10', 'CPB2', 'CRISP3', 'CRTAC1', 'DBH', 'DPP4', 'ECM1', 'ENG', 'ENPEP', 'F10', 'F11', 'F12', 'F13A1', 'F2', 'FAP', 'FCN3', 'FETUB', 'GC', 'GPLD1', 'GPNMB', 'GSN', 'HABP2', 'HGFAC', 'HRG', 'IGFALS', 'IGFBP3', 'IGHV3-7', 'IL1RAP', 'ITGB1', 'ITGB3', 'ITIH1', 'ITIH2', 'ITIH4', 'KIT', 'KLKB1', 'KNG1', 'LAMP1', 'LCAT', 'LUM', 'MASP1', 'MCAM', 'MEGF8', 'MINPP1', 'MYH9', 'MYL12B', 'NCAM1', 'PCOLCE', 'PCYOX1', 'PGLYRP2', 'PI16', 'PLEK', 'PLG', 'PON1', 'PON3', 'PROC', 'PROS1', 'PROZ', 'PTPRJ', 'RAB10', 'RBP4', 'SELENOP', 'SELL', 'SERPINA4', 'SERPINA5', 'SERPINA6', 'SERPINA7', 'SERPINC1', 'SERPIND1', 'SERPINF2', 'SHBG', 'SPP2', 'SUN3', 'TTR', 'TUBB1', 'UMOD'

**Pancreatitis vs. Control:** 'ABI3BP', 'ACE', 'ADA2', 'AFM', 'AHSG', 'APOA4', 'APOD', 'ATRN', 'BTD', 'CDH13', 'CHL1', 'CLEC3B', 'CNDP1', 'CNTN1', 'CRISP3', 'CRTAC1', 'ECM1', 'F12', 'F13A1', 'FAP', 'FETUB', 'GPLD1', 'GPNMB', 'GSN', 'HGFAC', 'HRG', 'IGFBP3', 'ITIH1', 'ITIH2', 'KLKB1', 'NCAM1', 'PGLYRP2', 'SELENOP', 'SELL', 'SERPINA4', 'SERPINA5', 'SERPIND1']

**Septic shock vs. Pancreatitis:** 'AFM', 'APOA5', 'APOC2', 'APOC3', 'APOC4', 'APOE', 'APOF', 'APOH', 'BPGM', 'C6', 'CPA1', 'F2', 'F9', 'HABP2', 'LRG1', 'MAN1A1', 'PCYOX1', 'PLG', 'PRDX2', 'PROC', 'PTPRJ', 'SNCA'

Table S2 - Septic Shock versus Control

| GENE SYMBOL   | GENE NAME                           | NCBI<br>GENE<br>ID   | UNIPROT<br>ID          | KEGG PATHWAYS                                                                                             | LOG2FC | -LOG10<br>P-<br>VALUE | ADJUSTED<br>P-VALUE |
|---------------|-------------------------------------|----------------------|------------------------|-----------------------------------------------------------------------------------------------------------|--------|-----------------------|---------------------|
| <b>CRP</b>    | C-reactive protein                  | <a href="#">1401</a> | <a href="#">P02741</a> | -                                                                                                         | 4,40   | 13,76                 | 0,00e+00            |
| <b>MMP8</b>   | Matrix metalloproteinase 8          | <a href="#">4317</a> | <a href="#">P22894</a> | -                                                                                                         | 4,30   | 9,04                  | 6,02e-08            |
| <b>CHI3L1</b> | Chitinase-3-like protein 1 (YKL-40) | <a href="#">1116</a> | <a href="#">P36222</a> | -                                                                                                         | 4,15   | 8,22                  | 2,23e-07            |
| <b>IL1RL1</b> | Interleukin 1 receptor-like 1 (ST2) | <a href="#">9173</a> | <a href="#">Q01638</a> | Cytokine-cytokine receptor interaction (hsa04060)                                                         | 4,02   | 9,80                  | 1,54e-08            |
| <b>COL1A1</b> | Collagen type I alpha 1 chain       | <a href="#">1277</a> | <a href="#">P02452</a> | PI3K-Akt signaling pathway (hsa04151)<br>L interaction (hsa04512)<br>Focal adhesion (hsa04510)            | 3,75   | 3,45                  | 1,92e-03            |
| <b>COL1A2</b> | Collagen type I alpha 2 chain       | <a href="#">1278</a> | <a href="#">P08123</a> | PI3K-Akt signaling pathway (hsa04151)<br>ECM-receptor interaction (hsa04512)<br>Focal adhesion (hsa04510) | 3,37   | 3,72                  | 1,12e-03            |

|                                                                                                 |                                             |                      |                                                         |                                                                                                                        |      |      |          |
|-------------------------------------------------------------------------------------------------|---------------------------------------------|----------------------|---------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------|------|------|----------|
| <b>COL2A1</b>                                                                                   | Collagen type II alpha 1 chain              | <a href="#">1280</a> | <a href="#">P02458</a>                                  | PI3K-Akt signaling pathway (hsa04151)<br>ECM-receptor interaction (hsa04512)<br>Focal adhesion (hsa04510)              | 3,11 | 2,60 | 9,94e-03 |
| <b>SAA2</b>                                                                                     | Serum amyloid A2                            | <a href="#">6289</a> | <a href="#">P0DJ19</a>                                  | -                                                                                                                      | 3,03 | 4,06 | 5,72e-04 |
| <b>SAA1</b>                                                                                     | Serum amyloid A1                            | <a href="#">6288</a> | <a href="#">P0DJ18</a>                                  | -                                                                                                                      | 2,90 | 4,83 | 1,31e-04 |
| <b>REG1B</b>                                                                                    | Regenerating family member 1 beta           | <a href="#">5968</a> | <a href="#">P48304</a>                                  | -                                                                                                                      | 2,86 | 5,73 | 2,55e-05 |
| <b>REG1A</b>                                                                                    | Regenerating family member 1 alpha          | <a href="#">5967</a> | <a href="#">P05451</a>                                  | -                                                                                                                      | 2,71 | 3,32 | 2,39e-03 |
| <b>H4C1; H4C2; H4C3; H4C4; H4C5; H4C6; H4C8; H4C9; H4C11; H4C12; H4C13; H4C14; H4C15; H4-16</b> | Histone cluster 4, H4 variants (H4C1–H4C16) | Various              | <a href="#">Various</a> (e.g., <a href="#">P62805</a> ) | Neutrophil extracellular trap formation (hsa04613)<br>Systemic lupus erythematosus (hsa05322)<br>Alcoholism (hsa05034) | 2,67 | 2,19 | 2,23e-02 |
| <b>H3-4</b>                                                                                     | Histone H3.4 (H3 family member 4)           | <a href="#">8290</a> | <a href="#">Q16695</a>                                  | Neutrophil extracellular trap formation (hsa04613)<br>Systemic lupus erythematosus (hsa05322)<br>Alcoholism (hsa05034) | 2,66 | 2,09 | 2,61e-02 |

|                |                                                      |                       |                        |                                                                                                                          |      |      |          |
|----------------|------------------------------------------------------|-----------------------|------------------------|--------------------------------------------------------------------------------------------------------------------------|------|------|----------|
| <b>LCN2</b>    | Lipocalin 2                                          | <a href="#">3934</a>  | <a href="#">P80188</a> | IL-17 signaling pathway (hsa04657)                                                                                       | 2,66 | 5,48 | 3,92e-05 |
| <b>MPO</b>     | Myeloperoxidase                                      | <a href="#">4353</a>  | <a href="#">P05164</a> | Neutrophil extracellular trap formation (hsa04613)<br>Drug metabolism - other enzymes (hsa00983)<br>Phagosome (hsa04145) | 2,55 | 5,27 | 5,91e-05 |
| <b>COL11A2</b> | Collagen type XI alpha 2 chain                       | <a href="#">1302</a>  | <a href="#">P13942</a> | Protein digestion and absorption (hsa04974)<br>Cytoskeleton in muscle cells (hsa04820)                                   | 2,52 | 2,81 | 6,44e-03 |
| <b>VSIG4</b>   | V-set and immunoglobulin domain-containing protein 4 | <a href="#">11326</a> | <a href="#">Q9H7M9</a> | Complement and coagulation cascades (hsa04610)                                                                           | 2,48 | 5,24 | 6,20e-05 |
| <b>S100A12</b> | S100 calcium-binding protein A12                     | <a href="#">6283</a>  | <a href="#">P80511</a> | Cornified envelope formation (hsa04382)                                                                                  | 2,46 | 2,17 | 2,27e-02 |
| <b>TIMP1</b>   | TIMP metalloproteinase inhibitor 1                   | <a href="#">7076</a>  | <a href="#">P01033</a> | HIF-1 signaling pathway (hsa04066 )                                                                                      | 2,45 | 9,12 | 5,65e-08 |
| <b>CTSB</b>    | Cathepsin B                                          | <a href="#">1508</a>  | <a href="#">P07858</a> | Lysosome (hsa04142)<br>Antigen processing and presentation (hsa04612)<br>Apoptosis (hsa04210)                            | 2,40 | 8,48 | 1,45e-07 |
| <b>SPP1</b>    | Secreted phosphoprotein 1                            | <a href="#">6696</a>  | <a href="#">P10451</a> | Focal adhesion (hsa04510)                                                                                                | 2,35 | 3,87 | 8,36e-04 |

|                |                                               |                       |                        |                                                                                                                                  |      |      |          |
|----------------|-----------------------------------------------|-----------------------|------------------------|----------------------------------------------------------------------------------------------------------------------------------|------|------|----------|
|                |                                               |                       |                        | Toll-like receptor signaling pathway (hsa04620)<br>PI3K-Akt signaling pathway (hsa04151)                                         |      |      |          |
| <b>MARCKS</b>  | Myristoylated alanine-rich C-kinase substrate | <a href="#">4082</a>  | <a href="#">P29966</a> | Fc gamma R-mediated phagocytosis (hsa04666)<br>MicroRNAs in cancer (hsa05206)                                                    | 2,27 | 5,68 | 2,68e-05 |
| <b>NUCB1</b>   | Nucleobindin 1                                | <a href="#">4924</a>  | <a href="#">Q02818</a> | -                                                                                                                                | 2,25 | 3,92 | 7,66e-04 |
| <b>LBP</b>     | Lipopolysaccharide-binding protein            | <a href="#">3929</a>  | <a href="#">P18428</a> | NF-kappa B signaling pathway (hsa04064)<br>Toll-like receptor signaling pathway (hsa04620)<br>Alcoholic liver disease (hsa04936) | 2,24 | 3,89 | 8,10e-04 |
| <b>IL18BP</b>  | Interleukin 18-binding protein                | <a href="#">10068</a> | <a href="#">O95998</a> | -                                                                                                                                | 2,20 | 3,76 | 1,03e-03 |
| <b>VCAN</b>    | versican                                      | <a href="#">1462</a>  | <a href="#">P13611</a> | Cell adhesion molecules (hsa04514)<br>Cytoskeleton in muscle cells (hsa04820)                                                    | 2,17 | 5,24 | 6,20e-05 |
| <b>PLA2G2A</b> | Phospholipase A2 group IIA                    | <a href="#">5320</a>  | <a href="#">P14555</a> | Arachidonic acid metabolism (hsa00590)<br>Glycerophospholipid                                                                    | 2,14 | 2,52 | 1,15e-02 |

|               |                                                    |                       |                        |                                                                                                                                    |      |      |          |
|---------------|----------------------------------------------------|-----------------------|------------------------|------------------------------------------------------------------------------------------------------------------------------------|------|------|----------|
|               |                                                    |                       |                        | metabolism (hsa00564)<br>Linoleic acid metabolism<br>(hsa00591)                                                                    |      |      |          |
| <b>TRAP1</b>  | TNF receptor-associated protein 1                  | <a href="#">10131</a> | <a href="#">Q12931</a> | Parkinson disease (hsa05012)<br>Pathways of neurodegeneration -<br>multiple diseases (hsa05022)                                    | 2,13 | 2,23 | 2,08e-02 |
| <b>MMP9</b>   | Matrix metalloproteinase 9                         | <a href="#">4318</a>  | <a href="#">P14780</a> | IL-17 signaling pathway<br>(hsa04657)<br>TNF signaling pathway<br>(hsa04668)<br>Leukocyte transendothelial<br>migration (hsa04670) | 2,12 | 4,23 | 4,13e-04 |
| <b>VWF</b>    | von Willebrand factor                              | <a href="#">7450</a>  | <a href="#">P04275</a> | PI3K-Akt signaling pathway<br>(hsa04151)<br>Complement and coagulation<br>cascades (hsa04610)<br>Platelet activation (hsa04611)    | 2,09 | 7,28 | 1,24e-06 |
| <b>S100A8</b> | S100 calcium-binding protein A8<br>(Calgranulin A) | <a href="#">6279</a>  | <a href="#">P05109</a> | IL-17 signaling pathway<br>(hsa04657)<br>Cornified envelope formation<br>(hsa04382)                                                | 2,09 | 2,55 | 1,09e-02 |
| <b>SOD2</b>   | Superoxide dismutase 2                             | <a href="#">6648</a>  | <a href="#">P04179</a> | FoxO signaling pathway<br>(hsa04068)                                                                                               | 2,02 | 1,95 | 3,43e-02 |



|               |                                |                      |                        |                                                              |      |      |          |
|---------------|--------------------------------|----------------------|------------------------|--------------------------------------------------------------|------|------|----------|
|               |                                |                      |                        | Peroxisome (hsa04146)                                        |      |      |          |
|               |                                |                      |                        | Longevity regulating pathway (hsa04211)                      |      |      |          |
| <b>COL5A1</b> | Collagen type V alpha 1 chain  | <a href="#">1291</a> | <a href="#">P20908</a> | Cytoskeleton in muscle cells (hsa04820)                      | 1,95 | 2,62 | 9,50e-03 |
|               |                                |                      |                        | Protein digestion and absorption (hsa04974)                  |      |      |          |
| <b>DDT</b>    | D-dopachrome tautomerase       | <a href="#">1652</a> | <a href="#">P30046</a> | -                                                            | 1,94 | 3,16 | 3,25e-03 |
| <b>VIM</b>    | Vimentin                       | <a href="#">7431</a> | <a href="#">P08670</a> | Cytoskeleton in muscle cells (hsa04820)                      | 1,90 | 4,08 | 5,54e-04 |
|               |                                |                      |                        | Epstein-Barr virus infection (hsa05169)                      |      |      |          |
|               |                                |                      |                        | MicroRNAs in cancer (hsa05206)                               |      |      |          |
| <b>PSMA1</b>  | Proteasome 20s subunit alpha 1 | <a href="#">5682</a> | <a href="#">P25786</a> | Proteasome (hsa03050)                                        | 1,88 | 4,12 | 5,18e-04 |
|               |                                |                      |                        | Prion disease (hsa05020)                                     |      |      |          |
|               |                                |                      |                        | Pathways of neurodegeneration - multiple diseases (hsa05022) |      |      |          |
| <b>ACY1</b>   | Aminoacylase 1                 | <a href="#">95</a>   | <a href="#">Q03154</a> | Arginine biosynthesis (hsa00220)                             | 1,88 | 2,15 | 2,37e-02 |
|               |                                |                      |                        | Metabolic pathways (hsa01100)                                |      |      |          |
|               |                                |                      |                        | Biosynthesis of amino acids (hsa01230)                       |      |      |          |

|                 |                                                     |                       |                        |                                                                                                                                                   |      |       |          |
|-----------------|-----------------------------------------------------|-----------------------|------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------|------|-------|----------|
| <b>COL6A1</b>   | Collagen type VI alpha 1                            | <a href="#">1291</a>  | <a href="#">P12109</a> | PI3K-Akt signaling pathway (hsa04151)<br>ECM-receptor interaction (hsa04512)<br>Focal adhesion (hsa04510)                                         | 1,86 | 7,40  | 9,86e-07 |
| <b>NID1</b>     | Nidogen 1 (Entactin)                                | <a href="#">4811</a>  | <a href="#">P14543</a> | Cytoskeleton in muscle cells (hsa04820)                                                                                                           | 1,84 | 11,14 | 1,20e-09 |
| <b>HSP90AA1</b> | heat shock protein 90 alpha family class A member 1 | <a href="#">3320</a>  | <a href="#">P07900</a> | Protein processing in endoplasmic reticulum (hsa04141)<br>PI3K-Akt signaling pathway (hsa04217)<br>Antigen processing and presentation (hsa04612) | 1,83 | 3,72  | 1,12e-03 |
| <b>DPP3</b>     | Dipeptidyl peptidase 3                              | <a href="#">10072</a> | <a href="#">Q9NY33</a> | -                                                                                                                                                 | 1,82 | 5,02  | 8,92e-05 |
| <b>GPI</b>      | Glucose-6-phosphate isomerase                       | <a href="#">2821</a>  | <a href="#">P06744</a> | Glycolysis/Gluconeogenesis (hsa00010)<br>Pentose phosphate pathway (hsa00030)<br>Starch and sucrose metabolism (hsa00500)                         | 1,82 | 3,74  | 1,08e-03 |
| <b>S100A9</b>   | S100 calcium-binding protein A9                     | <a href="#">6280</a>  | <a href="#">P06702</a> | IL-17 signaling pathway (hsa04657)                                                                                                                | 1,81 | 2,23  | 2,08e-02 |

|              |                                        |                       |                        |                                                                                                                                                                   |      |      |          |
|--------------|----------------------------------------|-----------------------|------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|------|----------|
|              |                                        |                       |                        | Cornified envelope formation<br>(hsa04382)                                                                                                                        |      |      |          |
| <b>ASL</b>   | Argininosuccinate lyase                | <a href="#">435</a>   | <a href="#">P04424</a> | Arginine biosynthesis<br>(hsa00220)<br>Biosynthesis of amino acids<br>(hsa01230)<br>Metabolic pathways (hsa01100)                                                 | 1,78 | 2,18 | 2,27e-02 |
| <b>TKT</b>   | Transketolase                          | <a href="#">7086</a>  | <a href="#">P29401</a> | Pentose phosphate pathway<br>(hsa00030)<br>Carbon metabolism (hsa01200)<br>Biosynthesis of amino acids<br>(hsa01230)                                              | 1,75 | 5,33 | 5,20e-05 |
| <b>GOT1</b>  | Glutamic-oxaloacetic<br>transaminase 1 | <a href="#">2805</a>  | <a href="#">P17174</a> | Alanine, aspartate and glutamate<br>metabolism (hsa00250)<br>Phenylalanine, tyrosine and<br>tryptophan biosynthesis<br>(hsa00400)<br>Carbon metabolism (hsa01200) | 1,73 | 2,65 | 9,03e-03 |
| <b>CTSD</b>  | Cathepsin D                            | <a href="#">1509</a>  | <a href="#">P07339</a> | Sphingolipid signaling pathway<br>(hsa04071)<br>Lysosome (hsa04142)<br>Apoptosis (hsa04210)                                                                       | 1,72 | 7,67 | 5,90e-07 |
| <b>GOLM1</b> | Golgi membrane protein 1               | <a href="#">51280</a> | <a href="#">Q8NBJ4</a> | -                                                                                                                                                                 | 1,67 | 5,70 | 2,62e-05 |

|                 |                                                     |                      |                        |                                                                                                                                                   |      |      |          |
|-----------------|-----------------------------------------------------|----------------------|------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------|------|------|----------|
| <b>TALDO1</b>   | Transaldolase 1                                     | <a href="#">6888</a> | <a href="#">P37837</a> | Pentose phosphate pathway (hsa00030)<br>Carbon metabolism (hsa01200)<br>Biosynthesis of amino acids (hsa01230)                                    | 1,66 | 4,99 | 9,36e-05 |
| <b>LTBP2</b>    | Latent TGF-beta binding protein 2                   | <a href="#">4053</a> | <a href="#">Q14767</a> | -                                                                                                                                                 | 1,66 | 5,56 | 3,42e-05 |
| <b>ORM1</b>     | Orosomucoid 1                                       | <a href="#">5004</a> | <a href="#">P02763</a> | -                                                                                                                                                 | 1,65 | 2,66 | 8,88e-03 |
| <b>CCN2</b>     | Cellular communication network factor 2             | <a href="#">1490</a> | <a href="#">P29279</a> | Apelin signaling pathway (hsa04371)<br>Hippo signaling pathway (hsa04390)                                                                         | 1,63 | 2,74 | 7,54e-03 |
| <b>HSP90AB1</b> | Heat shock protein 90 alpha family class B member 1 | <a href="#">3326</a> | <a href="#">P08238</a> | Protein processing in endoplasmic reticulum (hsa04141)<br>PI3K-Akt signaling pathway (hsa04151)<br>Antigen processing and presentation (hsa04612) | 1,58 | 3,20 | 3,08e-03 |
| <b>PSMA4</b>    | Proteasome 20S subunit alpha 4                      | <a href="#">5685</a> | <a href="#">P25789</a> | Proteasome (hsa03050)<br>Prion disease (hsa05020)<br>Pathways of neurodegeneration - multiple diseases (hsa05022)                                 | 1,58 | 2,54 | 1,11e-02 |

|              |                                |                       |                        |                                                                                                                   |      |      |          |
|--------------|--------------------------------|-----------------------|------------------------|-------------------------------------------------------------------------------------------------------------------|------|------|----------|
| <b>PSAP</b>  | Prosaposin                     | <a href="#">5660</a>  | <a href="#">P07602</a> | Lysosome (hsa04142)<br>Sphingolipid metabolism (hsa00600)                                                         | 1,57 | 4,50 | 2,41e-04 |
| <b>CTSZ</b>  | Cathepsin Z                    | <a href="#">1522</a>  | <a href="#">Q9UBR2</a> | Lysosome (hsa04142)<br>Apoptosis (hsa04210)                                                                       | 1,56 | 5,84 | 2,09e-05 |
| <b>MRC1</b>  | Mannose receptor C-type 1      | <a href="#">4360</a>  | <a href="#">P22897</a> | Phagosome (hsa04145)<br>Tuberculosis (hsa05152)                                                                   | 1,56 | 4,76 | 1,51e-04 |
| <b>LMNB1</b> | Lamin B1                       | <a href="#">4001</a>  | <a href="#">P20700</a> | Apoptosis (hsa04210)<br>Cytoskeleton in muscle cells (hsa04820)                                                   | 1,55 | 2,45 | 1,31e-02 |
| <b>PSMB2</b> | Proteasome 20S subunit beta 2  | <a href="#">5690</a>  | <a href="#">P49721</a> | Proteasome (hsa03050)<br>Prion disease (hsa05020)<br>Pathways of neurodegeneration - multiple diseases (hsa05022) | 1,54 | 2,09 | 2,61e-02 |
| <b>PLIN3</b> | Perilipin 3                    | <a href="#">10226</a> | <a href="#">O60664</a> | -                                                                                                                 | 1,54 | 2,80 | 6,60e-03 |
| <b>PGD</b>   | Phosphogluconate dehydrogenase | <a href="#">5226</a>  | <a href="#">P52209</a> | Pentose phosphate pathway (hsa00030)<br>Glutathione metabolism (hsa00480)<br>Carbon metabolism (hsa01200)         | 1,53 | 3,34 | 2,36e-03 |
| <b>PSMA6</b> | Proteasome 20S subunit alpha 6 | <a href="#">5687</a>  | <a href="#">P60900</a> | Proteasome (hsa03050)<br>Prion disease (hsa05020)                                                                 | 1,51 | 2,72 | 7,79e-03 |

|              |                                      |                      |                        |                                                              |      |      |          |
|--------------|--------------------------------------|----------------------|------------------------|--------------------------------------------------------------|------|------|----------|
|              |                                      |                      |                        | Pathways of neurodegeneration - multiple diseases (hsa05022) |      |      |          |
| <b>PSMA7</b> | Proteasome 20S subunit alpha 7       | <a href="#">5688</a> | <a href="#">O14818</a> | Proteasome (hsa03050)                                        | 1,50 | 2,20 | 2,20e-02 |
|              |                                      |                      |                        | Prion disease (hsa05020)                                     |      |      |          |
|              |                                      |                      |                        | Pathways of neurodegeneration - multiple diseases (hsa05022) |      |      |          |
| <b>IL1R2</b> | Interleukin 1 receptor type 2        | <a href="#">7850</a> | <a href="#">P27930</a> | Cytokine-cytokine receptor interaction (hsa04060)            | 1,50 | 3,33 | 2,39e-03 |
|              |                                      |                      |                        | Hematopoietic cell lineage (hsa04640)                        |      |      |          |
|              |                                      |                      |                        | Human T-cell leukemia virus 1 infection (hsa05166)           |      |      |          |
| <b>B2M</b>   | Beta-2-microglobulin                 | <a href="#">567</a>  | <a href="#">P61769</a> | Antigen processing and presentation (hsa04612)               | 1,50 | 3,01 | 4,42e-03 |
|              |                                      |                      |                        | Human cytomegalovirus infection (hsa05163)                   |      |      |          |
|              |                                      |                      |                        | Human T-cell leukemia virus 1 infection (hsa05166)           |      |      |          |
| <b>HSPA4</b> | Heat shock protein family A member 4 | <a href="#">3308</a> | <a href="#">P34932</a> | Tight junction (hsa04530)                                    | 1,49 | 4,26 | 3,84e-04 |
|              |                                      |                      |                        | Antigen processing and presentation (hsa04612)               |      |      |          |
|              |                                      |                      |                        | Lipid and atherosclerosis (hsa05417)                         |      |      |          |

|               |                                                                              |                       |                        |                                                                                                                                  |      |      |          |
|---------------|------------------------------------------------------------------------------|-----------------------|------------------------|----------------------------------------------------------------------------------------------------------------------------------|------|------|----------|
| <b>YWHAG</b>  | Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein gamma | <a href="#">7532</a>  | <a href="#">P61981</a> | Cell cycle (hsa04110)<br>PI3K-Akt signaling pathway (hsa04151)<br>Hippo signaling pathway (hsa04390)                             | 1,46 | 4,28 | 3,78e-04 |
| <b>PSMB4</b>  | Proteasome 20S subunit beta 4                                                | <a href="#">5692</a>  | <a href="#">P28070</a> | Proteasome (hsa03050)<br>Prion disease (hsa05020)<br>Pathways of neurodegeneration - multiple diseases (hsa05022)                | 1,43 | 2,21 | 2,16e-02 |
| <b>CD177</b>  | CD177 molecule                                                               | <a href="#">57126</a> | <a href="#">Q8N6Q3</a> | -                                                                                                                                | 1,42 | 3,16 | 3,25e-03 |
| <b>CD163</b>  | CD163 molecule                                                               | <a href="#">9332</a>  | <a href="#">Q86VB7</a> | -                                                                                                                                | 1,40 | 4,61 | 2,03e-04 |
| <b>GSTO1</b>  | Glutathione S-transferase omega 1                                            | <a href="#">9446</a>  | <a href="#">P78417</a> | Glutathione metabolism (hsa00480)<br>Drug metabolism by cytochrome P450 (hsa00982)<br>Drug metabolism - other enzymes (hsa00983) | 1,40 | 3,45 | 1,90e-03 |
| <b>PRKCSH</b> | PRKCSH beta subunit glucosidase II                                           | <a href="#">5589</a>  | <a href="#">P14314</a> | Protein processing in endoplasmic reticulum (hsa04141)                                                                           | 1,39 | 4,17 | 4,68e-04 |
| <b>PSMA3</b>  | Proteasome 20S subunit alpha 3                                               | <a href="#">5684</a>  | <a href="#">P25788</a> | Proteasome (hsa03050)<br>Prion disease (hsa05020)                                                                                | 1,39 | 2,13 | 2,46e-02 |

|              |                                                                                |                       |                        |                                                              |      |      |          |
|--------------|--------------------------------------------------------------------------------|-----------------------|------------------------|--------------------------------------------------------------|------|------|----------|
|              |                                                                                |                       |                        | Pathways of neurodegeneration - multiple diseases (hsa05022) |      |      |          |
| <b>CTSL</b>  | Cathepsin L                                                                    | <a href="#">1514</a>  | <a href="#">P07711</a> | Lysosome (hsa04142)                                          | 1,37 | 3,28 | 2,60e-03 |
|              |                                                                                |                       |                        | Antigen processing and presentation (hsa04612)               |      |      |          |
|              |                                                                                |                       |                        | Apoptosis (hsa04210)                                         |      |      |          |
| <b>FSTL1</b> | Follistatin like 1                                                             | <a href="#">11167</a> | <a href="#">Q12841</a> | -                                                            | 1,37 | 3,50 | 1,75e-03 |
| <b>PDIA4</b> | Protein disulfide isomerase family A member 4                                  | <a href="#">9601</a>  | <a href="#">P13667</a> | Protein processing in endoplasmic reticulum (hsa04141)       | 1,37 | 2,52 | 1,15e-02 |
|              |                                                                                |                       |                        | Thyroid hormone synthesis (hsa04918)                         |      |      |          |
|              |                                                                                |                       |                        | Vibrio cholerae infection (hsa05110)                         |      |      |          |
| <b>YWHAE</b> | Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon | <a href="#">7531</a>  | <a href="#">P62258</a> | PI3K-Akt signaling pathway (hsa04151)                        | 1,36 | 3,16 | 3,25e-03 |
|              |                                                                                |                       |                        | Cell cycle (hsa04110)                                        |      |      |          |
|              |                                                                                |                       |                        | Hippo signaling pathway (hsa04390)                           |      |      |          |
| <b>RRBP1</b> | Ribosome binding protein 1                                                     | <a href="#">6238</a>  | <a href="#">Q9P2E9</a> | Protein processing in endoplasmic reticulum (hsa04141)       | 1,35 | 2,10 | 2,59e-02 |



|              |                                |                      |                        |                                                                                                                                  |      |      |          |
|--------------|--------------------------------|----------------------|------------------------|----------------------------------------------------------------------------------------------------------------------------------|------|------|----------|
| <b>FAH</b>   | Fumarylacetoacetate hydrolase  | <a href="#">2184</a> | <a href="#">P16930</a> | Tyrosine metabolism (hsa00350)<br>Metabolic pathways (hsa01100)                                                                  | 1,31 | 2,32 | 1,73e-02 |
| <b>LTA4H</b> | Leukotriene A4 hydrolase       | <a href="#">4048</a> | <a href="#">P09960</a> | Arachidonic acid metabolism (hsa00590)<br>Metabolic pathways (hsa01100)                                                          | 1,31 | 5,18 | 7,01e-05 |
| <b>PSMB3</b> | Proteasome 20S subunit beta 3  | <a href="#">5691</a> | <a href="#">P49720</a> | Proteasome (hsa03050)<br>Prion disease (hsa05020)<br>Pathways of neurodegeneration - multiple diseases (hsa05022)                | 1,29 | 1,82 | 4,40e-02 |
| <b>LCPI</b>  | Lymphocyte cytosolic protein 1 | <a href="#">3936</a> | <a href="#">P13796</a> | -                                                                                                                                | 1,29 | 4,32 | 3,50e-04 |
| <b>CALR</b>  | Calreticulin                   | <a href="#">811</a>  | <a href="#">P27797</a> | Protein processing in endoplasmic reticulum (hsa04141)<br>Antigen processing and presentation (hsa04612)<br>Phagosome (hsa04145) | 1,29 | 2,89 | 5,53e-03 |
| <b>TNC</b>   | Tenascin C                     | <a href="#">3371</a> | <a href="#">P24821</a> | PI3K-Akt signaling pathway (hsa04151)<br>Focal adhesion (hsa04510)<br>ECM-receptor interaction (hsa04512)                        | 1,26 | 4,05 | 5,88e-04 |
| <b>PSMA5</b> | Proteasome 20S subunit alpha 5 | <a href="#">5686</a> | <a href="#">P28066</a> | Proteasome (hsa03050)<br>Prion disease (hsa05020)                                                                                | 1,23 | 1,97 | 3,32e-02 |

|               |                                                   |                       |                        |                                                                                                                                  |      |      |          |
|---------------|---------------------------------------------------|-----------------------|------------------------|----------------------------------------------------------------------------------------------------------------------------------|------|------|----------|
|               |                                                   |                       |                        | Pathways of neurodegeneration - multiple diseases (hsa05022)                                                                     |      |      |          |
| <b>FGL2</b>   | Fibrinogen like 2                                 | <a href="#">10875</a> | <a href="#">Q14314</a> | -                                                                                                                                | 1,21 | 3,19 | 3,08e-03 |
| <b>CAST</b>   | Calpastatin                                       | <a href="#">831</a>   | <a href="#">P20810</a> | Shigellosis (hsa05131)                                                                                                           | 1,21 | 2,52 | 1,15e-02 |
| <b>ICAM1</b>  | Intercellular adhesion molecule 1                 | <a href="#">3383</a>  | <a href="#">P05362</a> | NF-kappa B signaling pathway (hsa04064)<br>Leukocyte transendothelial migration (hsa04670)<br>Cell adhesion molecules (hsa04514) | 1,20 | 1,99 | 3,16e-02 |
| <b>BASP1</b>  | Brain abundant membrane attached signal protein 1 | <a href="#">10409</a> | <a href="#">P80723</a> | -                                                                                                                                | 1,20 | 3,37 | 2,23e-03 |
| <b>GALNT2</b> | Polypeptide N-acetylgalactosaminyltransferase 2   | <a href="#">2590</a>  | <a href="#">Q10471</a> | Mucin type O-glycan biosynthesis (hsa00512)<br>Other types of O-glycan biosynthesis (hsa00514)<br>Metabolic pathways (hsa01100)  | 1,19 | 4,27 | 3,84e-04 |
| <b>SIRPB1</b> | Signal regulatory protein beta 1                  | <a href="#">10326</a> | <a href="#">O00241</a> | Efferocytosis (hsa04148)<br>Osteoclast differentiation (hsa04380I)                                                               | 1,17 | 3,37 | 2,23e-03 |
| <b>GANAB</b>  | Glucosidase II alpha subunit                      | <a href="#">23193</a> | <a href="#">Q14697</a> | Protein processing in endoplasmic reticulum (hsa04141)                                                                           | 1,16 | 3,44 | 1,95e-03 |

|                 |                                              |                       |                        |                                                |      |      |          |
|-----------------|----------------------------------------------|-----------------------|------------------------|------------------------------------------------|------|------|----------|
|                 |                                              |                       |                        | N-Glycan biosynthesis<br>(hsa00510)            |      |      |          |
|                 |                                              |                       |                        | Metabolic pathways (hsa01100)                  |      |      |          |
| <b>EPHB4</b>    | EPH receptor B4                              | <a href="#">2050</a>  | <a href="#">P54760</a> | Axon guidance (hsa04360)                       | 1,16 | 4,97 | 9,59e-05 |
| <b>IGFBP4</b>   | Insulin like growth factor binding protein 4 | <a href="#">3487</a>  | <a href="#">P22692</a> | -                                              | 1,13 | 4,58 | 2,11e-04 |
| <b>ALDOA</b>    | Aldolase, fructose-bisphosphate A            | <a href="#">226</a>   | <a href="#">P04075</a> | Glycolysis/Gluconeogenesis (hsa00010)          | 1,12 | 2,07 | 2,70e-02 |
|                 |                                              |                       |                        | Fructose and mannose metabolism (hsa00051)     |      |      |          |
|                 |                                              |                       |                        | Carbon metabolism (hsa01200)                   |      |      |          |
| <b>SERPINA3</b> | Serpin family A member 3                     | <a href="#">12</a>    | <a href="#">P01011</a> | -                                              | 1,11 | 4,13 | 5,12e-04 |
| <b>ARHGAP1</b>  | Rho GTPase activating protein 1              | <a href="#">392</a>   | <a href="#">Q07960</a> | -                                              | 1,11 | 2,09 | 2,61e-02 |
| <b>F8</b>       | Coagulation factor VIII                      | <a href="#">2157</a>  | <a href="#">P00451</a> | Complement and coagulation cascades (hsa04610) | 1,07 | 3,90 | 7,90e-04 |
| <b>SERPINB1</b> | Serpin family B member 1                     | <a href="#">1992</a>  | <a href="#">P30740</a> | -                                              | 1,00 | 4,72 | 1,63e-04 |
| <b>NPC2</b>     | NPC intracellular cholesterol transporter 2  | <a href="#">10577</a> | <a href="#">P61916</a> | Lysosome (hsa04142)                            | 1,00 | 2,44 | 1,36e-02 |
|                 |                                              |                       |                        | Cholesterol metabolism (hsa04979)              |      |      |          |
| <b>LAMC1</b>    | Laminin subunit gamma 1                      | <a href="#">3915</a>  | <a href="#">P11047</a> | PI3K-Akt signaling pathway (hsa04151)          | 0,97 | 4,41 | 2,87e-04 |

|                 |                                                 |                        |                        |                                                                                                                            |      |      |          |
|-----------------|-------------------------------------------------|------------------------|------------------------|----------------------------------------------------------------------------------------------------------------------------|------|------|----------|
|                 |                                                 |                        |                        | Focal adhesion (hsa04510)<br>ECM-receptor interaction<br>(hsa04512)                                                        |      |      |          |
| <b>VCAM1</b>    | Vascular cell adhesion molecule 1               | <a href="#">7412</a>   | <a href="#">P19320</a> | NF-kappa B signaling pathway<br>(hsa04064)<br>Cell adhesion molecules<br>(hsa04514)<br>TNF signaling pathway<br>(hsa04668) | 0,96 | 3,12 | 3,50e-03 |
| <b>LGALS3BP</b> | Galectin 3 binding protein                      | <a href="#">3959</a>   | <a href="#">Q08380</a> | -                                                                                                                          | 0,93 | 2,33 | 1,71e-02 |
| <b>PGK1</b>     | Phosphoglycerate kinase 1                       | <a href="#">5230</a>   | <a href="#">P00558</a> | Glycolysis/Gluconeogenesis<br>(hsa00010)<br>Carbon metabolism (hsa01200)<br>Biosynthesis of amino acids<br>(hsa01230)      | 0,91 | 1,90 | 3,76e-02 |
| <b>SIRPA</b>    | Signal regulatory protein alpha                 | <a href="#">140885</a> | <a href="#">P78324</a> | Efferocytosis (hsa04148)<br>Osteoclast differentiation<br>(hsa04380I)                                                      | 0,90 | 2,54 | 1,11e-02 |
| <b>CST3</b>     | Cystatin C                                      | <a href="#">1471</a>   | <a href="#">P01034</a> | Salivary secretion (hsa04970)                                                                                              | 0,90 | 2,59 | 1,01e-02 |
| <b>GRN</b>      | Granulin precursor                              | <a href="#">2896</a>   | <a href="#">P28799</a> | -                                                                                                                          | 0,89 | 1,92 | 3,62e-02 |
| <b>HSPA8</b>    | Heat shock protein family A<br>(Hsp70) member 8 | <a href="#">3312</a>   | <a href="#">P11142</a> | Spliceosome (hsa03040)<br>MAPK signaling pathway<br>(hsa04010)                                                             | 0,87 | 1,94 | 3,52e-02 |

|                 |                                                  |                        |                        |                                                                                                                          |       |      |          |
|-----------------|--------------------------------------------------|------------------------|------------------------|--------------------------------------------------------------------------------------------------------------------------|-------|------|----------|
|                 |                                                  |                        |                        | Protein processing in<br>endoplasmic reticulum<br>(hsa04141)                                                             |       |      |          |
| <b>LRG1</b>     | Leucine rich alpha-2-glycoprotein<br>1           | <a href="#">116844</a> | <a href="#">P02750</a> | -                                                                                                                        | 0,85  | 2,99 | 4,53e-03 |
| <b>ADAMTSL2</b> | ADAMTS like 2                                    | <a href="#">9719</a>   | <a href="#">Q86TH1</a> | -                                                                                                                        | 0,82  | 1,92 | 3,60e-02 |
| <b>SEMA4B</b>   | Semaphorin 4B                                    | <a href="#">10509</a>  | <a href="#">Q9NPR2</a> | Axon guidance (hsa04360)                                                                                                 | 0,74  | 2,26 | 1,97e-02 |
| <b>LAMB1</b>    | Laminin subunit beta 1                           | <a href="#">3912</a>   | <a href="#">P07942</a> | PI3K-Akt signaling pathway<br>(hsa04151)<br>Focal adhesion (hsa04510)<br>ECM-receptor interaction<br>(hsa04512)          | 0,72  | 1,93 | 3,54e-02 |
| <b>ITIH3</b>    | Inter-alpha-trypsin inhibitor heavy<br>chain 3   | <a href="#">3699</a>   | <a href="#">Q06033</a> | -                                                                                                                        | 0,50  | 1,79 | 4,72e-02 |
| <b>MINPP1</b>   | Multiple inositol-polyphosphate<br>phosphatase 1 | <a href="#">9562</a>   | <a href="#">Q9UNW1</a> | Glycolysis/Gluconeogenesis<br>(hsa00010)<br>Inositol phosphate metabolism<br>(hsa00562)<br>Metabolic pathways (hsa01100) | -0,55 | 2,64 | 9,24e-03 |
| <b>C1RL</b>     | Complement C1r subcomponent<br>like              | <a href="#">51279</a>  | <a href="#">Q9NZP8</a> | -                                                                                                                        | -0,59 | 2,13 | 2,46e-02 |
| <b>BIN2</b>     | Bridging integrator 2                            | <a href="#">51411</a>  | <a href="#">Q9UBW5</a> | -                                                                                                                        | -0,61 | 1,92 | 3,60e-02 |
| <b>MCAM</b>     | Melanoma cell adhesion molecule                  | <a href="#">4162</a>   | <a href="#">P43121</a> | -                                                                                                                        | -0,64 | 2,01 | 3,07e-02 |

|              |                                             |                       |                        |                                                                                                           |       |      |          |
|--------------|---------------------------------------------|-----------------------|------------------------|-----------------------------------------------------------------------------------------------------------|-------|------|----------|
| <b>MEGF8</b> | Multiple EGF like domains 8                 | <a href="#">1954</a>  | <a href="#">Q7Z7M0</a> | Hedgehog signalling pathway (hsa04340)                                                                    | -0,65 | 3,37 | 2,23e-03 |
| <b>ITIH4</b> | Inter-alpha-trypsin inhibitor heavy chain 4 | <a href="#">3700</a>  | <a href="#">Q14624</a> | -                                                                                                         | -0,67 | 2,18 | 2,26e-02 |
| <b>LAMP1</b> | Lysosomal associated membrane protein 1     | <a href="#">3916</a>  | <a href="#">P11279</a> | Lysosome (hsa04142)<br>Phagosome (hsa04145)<br>Autophagy (hsa04140)                                       | -0,69 | 3,46 | 1,90e-03 |
| <b>F10</b>   | Coagulation factor X                        | <a href="#">2159</a>  | <a href="#">P00742</a> | Complement and coagulation cascades (hsa04610)                                                            | -0,74 | 1,77 | 4,87e-02 |
| <b>RAB10</b> | RAB10, member RAS oncogene family           | <a href="#">10890</a> | <a href="#">P61026</a> | Endocytosis (hsa04144)<br>AMPK signalling pathway (hsa04152)                                              | -0,76 | 2,29 | 1,82e-02 |
| <b>CFI</b>   | Complement factor I                         | <a href="#">3426</a>  | <a href="#">P05156</a> | Complement and coagulation cascades (hsa04610)<br>Staphylococcus aureus infection (hsa05150)              | -0,81 | 2,72 | 7,79e-03 |
| <b>GPNMB</b> | Glycoprotein nmb                            | <a href="#">10457</a> | <a href="#">Q14956</a> | -                                                                                                         | -0,81 | 2,13 | 2,48e-02 |
| <b>FCN3</b>  | Ficolin 3                                   | <a href="#">8547</a>  | <a href="#">O75636</a> | -                                                                                                         | -0,81 | 1,80 | 4,63e-02 |
| <b>ITGB1</b> | Integrin subunit beta 1                     | <a href="#">3688</a>  | <a href="#">P05556</a> | PI3K-Akt signaling pathway (hsa04151)<br>Focal adhesion (hsa04510)<br>ECM-receptor interaction (hsa04512) | -0,81 | 3,07 | 3,87e-03 |

|                 |                                        |                       |                        |                                                                                                                                                     |       |      |          |
|-----------------|----------------------------------------|-----------------------|------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------|-------|------|----------|
| <b>ACE</b>      | Angiotensin I converting enzyme        | <a href="#">1636</a>  | <a href="#">P12821</a> | Renin-angiotensin system (hsa04614)<br>Renin secretion (hsa04924)<br>Coronavirus disease - COVID-19 (hsa05171)                                      | -0,83 | 3,66 | 1,25e-03 |
| <b>LUM</b>      | Lumican                                | <a href="#">4060</a>  | <a href="#">P51884</a> | Proteoglycans in cancer (hsa05205)                                                                                                                  | -0,84 | 2,41 | 1,42e-02 |
| <b>ADGRG6</b>   | Adhesion G protein-coupled receptor G6 | <a href="#">57211</a> | <a href="#">Q86SQ4</a> | -                                                                                                                                                   | -0,86 | 2,35 | 1,63e-02 |
| <b>PROS1</b>    | Protein S                              | <a href="#">5627</a>  | <a href="#">P07225</a> | Complement and coagulation cascades (hsa04610)<br>Efferocytosis (hsa04148)                                                                          | -0,87 | 2,97 | 4,74e-03 |
| <b>C5</b>       | Complement C5                          | <a href="#">727</a>   | <a href="#">P01031</a> | Complement and coagulation cascades (hsa04610)<br>Neutrophil extracellular trap formation (hsa04613)<br>Regulation of actin cytoskeleton (hsa04810) | -0,88 | 2,91 | 5,37e-03 |
| <b>SELL</b>     | Selectin L                             | <a href="#">6402</a>  | <a href="#">P14151</a> | Cell adhesion molecules (hsa04514)                                                                                                                  | -0,89 | 2,29 | 1,85e-02 |
| <b>SERPINF2</b> | Serpin family F member 2               | <a href="#">5345</a>  | <a href="#">P08697</a> | Complement and coagulation cascades (hsa04610)                                                                                                      | -0,90 | 3,69 | 1,19e-03 |

|              |                                              |                      |                        |                                                                                                                                            |       |      |          |
|--------------|----------------------------------------------|----------------------|------------------------|--------------------------------------------------------------------------------------------------------------------------------------------|-------|------|----------|
| <b>PTPRJ</b> | Protein tyrosine phosphatase receptor type J | <a href="#">5795</a> | <a href="#">Q12913</a> | Adherens junction (hsa04520)<br>Chemical carcinogenesis - reactive oxygen species (hsa05208)                                               | -0,90 | 6,08 | 1,32e-05 |
| <b>AOC3</b>  | Amine oxidase copper containing 3            | <a href="#">8639</a> | <a href="#">Q16853</a> | Glycine, serine and threonine metabolism (hsa00260)<br>Tyrosine metabolism (hsa00350)<br>Phenylalanine metabolism (hsa00360)               | -0,90 | 2,49 | 1,21e-02 |
| <b>AZGP1</b> | Alpha-2-glycoprotein 1, zinc-binding         | <a href="#">563</a>  | <a href="#">P25311</a> | -                                                                                                                                          | -0,93 | 3,12 | 3,53e-03 |
| <b>C8B</b>   | Complement C8 beta chain                     | <a href="#">732</a>  | <a href="#">P07358</a> | Complement and coagulation cascades (hsa04610)<br>Regulation of actin cytoskeleton (hsa04810)<br>Coronavirus disease – COVID-19 (hsa05171) | -0,93 | 1,95 | 3,43e-02 |
| <b>MASP1</b> | MBL associated serine protease 1             | <a href="#">5648</a> | <a href="#">P48740</a> | Complement and coagulation cascades (hsa04610)<br>Staphylococcus aureus infection (hsa05150)<br>Coronavirus disease – COVID-19 (hsa05171)  | -0,93 | 3,02 | 4,30e-03 |



|                 |                                  |                       |                        |                                                                                                                                                      |       |      |          |
|-----------------|----------------------------------|-----------------------|------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------|-------|------|----------|
| <b>ENPEP</b>    | Glutamyl aminopeptidase          | <a href="#">2028</a>  | <a href="#">Q07075</a> | Renin-angiotensin system<br>(hsa04614)                                                                                                               | -0,94 | 1,76 | 4,94e-02 |
| <b>CNTN3</b>    | Contactin 3                      | <a href="#">5067</a>  | <a href="#">Q9P232</a> | -                                                                                                                                                    | -0,95 | 3,07 | 3,87e-03 |
| <b>C8G</b>      | Complement C8 gamma chain        | <a href="#">733</a>   | <a href="#">P07360</a> | Complement and coagulation<br>cascades (hsa04610)<br>Regulation of actin cytoskeleton<br>(hsa04810)<br>Coronavirus disease – COVID-<br>19 (hsa05171) | -0,96 | 3,33 | 2,38e-03 |
| <b>COLEC10</b>  | Collectin subfamily member 10    | <a href="#">10584</a> | <a href="#">Q9Y6Z7</a> | -                                                                                                                                                    | -0,97 | 1,87 | 3,97e-02 |
| <b>SERPINA7</b> | Serpin family A member 7         | <a href="#">6906</a>  | <a href="#">P05543</a> | Thyroid hormone synthesis<br>(hsa04918)                                                                                                              | -0,98 | 4,65 | 1,87e-04 |
| <b>B4GAT1</b>   | Beta-1,4-glucuronyltransferase 1 | <a href="#">11041</a> | <a href="#">O43505</a> | Mannose type O-glycan<br>biosynthesis (hsa00515)<br>Metabolic pathways (hsa01100)                                                                    | -0,99 | 5,16 | 7,10e-05 |
| <b>F13A1</b>    | Coagulation factor XIII A chain  | <a href="#">2162</a>  | <a href="#">P00488</a> | Complement and coagulation<br>cascades (hsa04610)<br>Coronavirus disease – COVID-<br>19 (hsa05171)                                                   | -0,99 | 2,88 | 5,57e-03 |
| <b>F11</b>      | Coagulation factor XI            | <a href="#">2160</a>  | <a href="#">P03951</a> | Complement and coagulation<br>cascades (hsa04610)                                                                                                    | -1,00 | 2,12 | 2,49e-02 |
| <b>C8A</b>      | Complement C8 alpha chain        | <a href="#">731</a>   | <a href="#">P07357</a> | Complement and coagulation<br>cascades (hsa04610)                                                                                                    | -1,02 | 3,51 | 1,69e-03 |

|               |                                                                |                        |                        |                                                                       |       |      |          |
|---------------|----------------------------------------------------------------|------------------------|------------------------|-----------------------------------------------------------------------|-------|------|----------|
|               |                                                                |                        |                        | Regulation of actin cytoskeleton (hsa04810)                           |       |      |          |
|               |                                                                |                        |                        | Coronavirus disease – COVID-19 (hsa05171)                             |       |      |          |
| <b>DPP4</b>   | Dipeptidyl peptidase 4                                         | <a href="#">1803</a>   | <a href="#">P27487</a> | Virion – Hepatitis viruses (hsa03272)                                 | –1,03 | 5,77 | 2,41e-05 |
|               |                                                                |                        |                        | Protein digestion and absorption (hsa04974)                           |       |      |          |
| <b>MYL12B</b> | Myosin light chain 12B                                         | <a href="#">103910</a> | <a href="#">O14950</a> | Focal adhesion (hsa04510)                                             | –1,05 | 2,02 | 3,00e-02 |
|               |                                                                |                        |                        | Platelet activation (hsa04611)                                        |       |      |          |
|               |                                                                |                        |                        | Leukocyte transendothelial migration (hsa04670)                       |       |      |          |
| <b>B3GNT2</b> | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyl-transferase 2 | <a href="#">10678</a>  | <a href="#">Q9N9Y7</a> | Glycosaminoglycan biosynthesis – keratan sulfate (hsa00533)           | –1,06 | 3,84 | 8,93e-04 |
|               |                                                                |                        |                        | Glycosaminoglycan biosynthesis – lacto and neolacto series (hsa00601) |       |      |          |
|               |                                                                |                        |                        | Metabolic pathways (hsa01100)                                         |       |      |          |
| <b>MYH9</b>   | Myosin heavy chain 9                                           | <a href="#">4627</a>   | <a href="#">P35579</a> | Regulation of actin cytoskeleton (hsa04810)                           | –1,07 | 2,10 | 2,60e-02 |
|               |                                                                |                        |                        | Tight junction (hsa04530)                                             |       |      |          |
|               |                                                                |                        |                        | Motor proteins (hsa04814)                                             |       |      |          |
| <b>ENG</b>    | Endoglin                                                       | <a href="#">2022</a>   | <a href="#">P17813</a> | -                                                                     | –1,09 | 3,19 | 3,08e-03 |

|                 |                                                            |                       |                        |                                                                                                                               |       |      |          |
|-----------------|------------------------------------------------------------|-----------------------|------------------------|-------------------------------------------------------------------------------------------------------------------------------|-------|------|----------|
| <b>PCOLCE</b>   | Procollagen C-endopeptidase enhancer                       | <a href="#">5118</a>  | <a href="#">Q15113</a> | -                                                                                                                             | -1,10 | 4,01 | 6,33e-04 |
| <b>C3</b>       | Complement C3                                              | <a href="#">718</a>   | <a href="#">P01024</a> | Phagosome (hsa04145)<br>Complement and coagulation cascades (hsa04610)<br>Neutrophil extracellular trap formation (hsa04613)  | -1,11 | 4,55 | 2,25e-04 |
| <b>C1QB</b>     | Complement C1q B chain                                     | <a href="#">713</a>   | <a href="#">P02746</a> | Complement and coagulation cascades (hsa04610)<br>Staphylococcus aureus infection (hsa05150)<br>Effocytosis (hsa04148)        | -1,11 | 2,68 | 8,49e-03 |
| <b>ITGB3</b>    | Integrin subunit beta 3                                    | <a href="#">3690</a>  | <a href="#">P05106</a> | PI3K-Akt signaling pathway (hsa04151)<br>Platelet activation (hsa04611)<br>Neutrophil extracellular trap formation (hsa04613) | -1,14 | 1,83 | 4,38e-02 |
| <b>ADAMTS13</b> | ADAM metalloproteinase with thrombospondin type 1 motif 13 | <a href="#">11093</a> | <a href="#">Q76LX8</a> | Platelet activation (hsa04611)                                                                                                | -1,14 | 3,63 | 1,32e-03 |
| <b>CFH</b>      | Complement factor H                                        | <a href="#">3075</a>  | <a href="#">P08603</a> | Complement and coagulation cascades (hsa04610)<br>Staphylococcus aureus infection (hsa05150)                                  | -1,16 | 2,51 | 1,15e-02 |

|               |                                                 |                        |                        |                                                                                                                                  |       |      |          |
|---------------|-------------------------------------------------|------------------------|------------------------|----------------------------------------------------------------------------------------------------------------------------------|-------|------|----------|
| <b>CHL1</b>   | Cell adhesion molecule L1 like                  | <a href="#">10752</a>  | <a href="#">O00533</a> | -                                                                                                                                | -1,20 | 5,05 | 8,49e-05 |
| <b>ADIPOQ</b> | Adiponectin, C1Q and collagen domain containing | <a href="#">9370</a>   | <a href="#">Q15848</a> | Adipocytokine signaling pathway (hsa04920)<br>PPAR signaling pathway (hsa03320)<br>AMPK signaling pathway (hsa04152)             | -1,20 | 1,81 | 4,52e-02 |
| <b>CDH13</b>  | Cadherin 13                                     | <a href="#">1012</a>   | <a href="#">P55290</a> | -                                                                                                                                | -1,21 | 8,46 | 1,45e-07 |
| <b>CRISP3</b> | Cysteine rich secretory protein 3               | <a href="#">10321</a>  | <a href="#">P54108</a> | -                                                                                                                                | -1,21 | 2,94 | 5,05e-03 |
| <b>ECM1</b>   | Extracellular matrix protein 1                  | <a href="#">1893</a>   | <a href="#">Q16610</a> | -                                                                                                                                | -1,21 | 6,12 | 1,22e-05 |
| <b>SUN3</b>   | Sad1 and UNC84 domain containing 3              | <a href="#">256979</a> | <a href="#">Q8TAQ9</a> | -                                                                                                                                | -1,25 | 4,41 | 2,87e-04 |
| <b>PI16</b>   | Peptidase inhibitor 16                          | <a href="#">221476</a> | <a href="#">Q6UXB8</a> | -                                                                                                                                | -1,25 | 3,24 | 2,84e-03 |
| <b>GC</b>     | GC vitamin D binding protein                    | <a href="#">2638</a>   | <a href="#">P02774</a> | -                                                                                                                                | -1,26 | 3,97 | 6,90e-04 |
| <b>CPB2</b>   | Carboxypeptidase B2                             | <a href="#">1361</a>   | <a href="#">Q96IY4</a> | Complement and coagulation cascades (hsa04610)<br>Pancreatic secretion (hsa04972)<br>Protein digestion and absorption (hsa04974) | -1,27 | 5,03 | 8,76e-05 |
| <b>SHBG</b>   | Sex hormone binding globulin                    | <a href="#">6462</a>   | <a href="#">P04278</a> | -                                                                                                                                | -1,27 | 2,02 | 3,00e-02 |
| <b>A1BG</b>   | Alpha-1-B glycoprotein                          | <a href="#">1</a>      | <a href="#">P04217</a> | -                                                                                                                                | -1,27 | 5,40 | 4,53e-05 |
| <b>CETP</b>   | Cholesteryl ester transfer protein              | <a href="#">1071</a>   | <a href="#">P11597</a> | Cholesterol metabolism (hsa04979)                                                                                                | -1,27 | 2,14 | 2,42e-02 |

|               |                                          |                      |                        |                                                                                                                                            |       |      |          |
|---------------|------------------------------------------|----------------------|------------------------|--------------------------------------------------------------------------------------------------------------------------------------------|-------|------|----------|
| <b>CNTN1</b>  | Contactin 1                              | <a href="#">1272</a> | <a href="#">Q12860</a> | Cell adhesion molecules (hsa04514)                                                                                                         | -1,28 | 5,44 | 4,18e-05 |
| <b>APOB</b>   | Apolipoprotein B                         | <a href="#">338</a>  | <a href="#">P04114</a> | Fat digestion and absorption (hsa04975)<br>Vitamin digestion and absorption (hsa04977)<br>Cholesterol metabolism (hsa04979)                | -1,28 | 3,82 | 9,16e-04 |
| <b>IL1RAP</b> | Interleukin 1 receptor accessory protein | <a href="#">3556</a> | <a href="#">Q9NPH3</a> | MAPK signaling pathway (hsa04010)<br>Cytokine-cytokine receptor interaction (hsa04060)<br>Th17 cell differentiation (hsa04659)             | -1,28 | 5,12 | 7,43e-05 |
| <b>C6</b>     | Complement C6                            | <a href="#">729</a>  | <a href="#">P13671</a> | Complement and coagulation cascades (hsa04610)<br>Regulation of actin cytoskeleton (hsa04810)<br>Coronavirus disease – COVID-19 (hsa05171) | -1,29 | 5,12 | 7,43e-05 |
| <b>ATRN</b>   | Attractin                                | <a href="#">8455</a> | <a href="#">O75882</a> | -                                                                                                                                          | -1,31 | 8,10 | 2,76e-07 |
| <b>LCAT</b>   | Lecithin-cholesterol acyltransferase     | <a href="#">3931</a> | <a href="#">P04180</a> | Glycerophospholipid metabolism (hsa00564)                                                                                                  | -1,32 | 5,71 | 2,61e-05 |

|                 |                                      |                       |                        |                                                                 |       |      |          |
|-----------------|--------------------------------------|-----------------------|------------------------|-----------------------------------------------------------------|-------|------|----------|
|                 |                                      |                       |                        | Cholesterol metabolism<br>(hsa04979)                            |       |      |          |
| <b>TUBB1</b>    | Tubulin beta 1 class VI              | <a href="#">81027</a> | <a href="#">Q9H4B7</a> | Phagosome (hsa04145)                                            | -1,33 | 3,26 | 2,71e-03 |
|                 |                                      |                       |                        | Motor proteins (hsa04814)                                       |       |      |          |
|                 |                                      |                       |                        | Pathways of neurodegeneration -<br>multiple diseases (hsa05022) |       |      |          |
| <b>UMOD</b>     | Uromodulin                           | <a href="#">7369</a>  | <a href="#">P07911</a> | -                                                               | -1,33 | 3,83 | 8,93e-04 |
| <b>IGHV3-7</b>  | Immunoglobulin heavy variable<br>3-7 | <a href="#">28452</a> | <a href="#">P01780</a> | -                                                               | -1,34 | 1,94 | 3,52e-02 |
| <b>FAP</b>      | Fibroblast activation protein alpha  | <a href="#">2191</a>  | <a href="#">Q12884</a> | -                                                               | -1,35 | 5,15 | 7,17e-05 |
| <b>NCAM1</b>    | Neural cell adhesion molecule 1      | <a href="#">4684</a>  | <a href="#">P13591</a> | Cell adhesion molecules<br>(hsa04514)                           | -1,36 | 7,42 | 9,78e-07 |
|                 |                                      |                       |                        | Prion disease (hsa05020)                                        |       |      |          |
|                 |                                      |                       |                        | Virion - Ebolavirus, Lyssavirus<br>and Morbillivirus (hsa03265) |       |      |          |
| <b>HABP2</b>    | Hyaluronan binding protein 2         | <a href="#">3026</a>  | <a href="#">Q14520</a> | -                                                               | -1,40 | 3,53 | 1,64e-03 |
| <b>APOH</b>     | Apolipoprotein H                     | <a href="#">350</a>   | <a href="#">P02749</a> | Cholesterol metabolism<br>(hsa04979)                            | -1,40 | 4,46 | 2,64e-04 |
| <b>APOF</b>     | Apolipoprotein F                     | <a href="#">319</a>   | <a href="#">Q13790</a> | -                                                               | -1,41 | 4,53 | 2,30e-04 |
| <b>CRTAC1</b>   | Cartilage acidic protein 1           | <a href="#">55118</a> | <a href="#">Q9NQ79</a> | -                                                               | -1,41 | 5,67 | 2,68e-05 |
| <b>SERPINA6</b> | Serpin family A member 6             | <a href="#">866</a>   | <a href="#">P08185</a> | -                                                               | -1,44 | 4,58 | 2,12e-04 |

|             |                                    |                      |                        |                                                                                                                                      |       |      |          |
|-------------|------------------------------------|----------------------|------------------------|--------------------------------------------------------------------------------------------------------------------------------------|-------|------|----------|
| <b>F2</b>   | Coagulation factor II, prothrombin | <a href="#">2147</a> | <a href="#">P00734</a> | Complement and coagulation cascades (hsa04610)<br>Platelet activation (hsa04611)<br>Phospholipase D signaling pathway (hsa04072)     | -1,44 | 8,56 | 1,31e-07 |
| <b>C1QA</b> | Complement C1q A chain             | <a href="#">712</a>  | <a href="#">P02745</a> | Complement and coagulation cascades (hsa04610)<br>Efforocytosis (hsa04148)<br>Staphylococcus aureus infection (hsa05150)             | -1,46 | 3,56 | 1,55e-03 |
| <b>CLU</b>  | Clusterin                          | <a href="#">1191</a> | <a href="#">P10909</a> | Complement and coagulation cascades (hsa04610)                                                                                       | -1,46 | 5,72 | 2,57e-05 |
| <b>KNG1</b> | Kininogen 1                        | <a href="#">3827</a> | <a href="#">P01042</a> | Complement and coagulation cascades (hsa04610)<br>cGMP-PKG signaling pathway (hsa04022)<br>Sphingolipid signaling pathway (hsa04071) | -1,47 | 6,93 | 2,61e-06 |
| <b>BTD</b>  | Biotinidase                        | <a href="#">686</a>  | <a href="#">P43251</a> | Biotin metabolism (hsa00780)<br>Vitamin digestion and absorption (hsa04977)<br>Metabolic pathways (hsa01100)                         | -1,48 | 7,97 | 3,51e-07 |
| <b>PLEK</b> | Pleckstrin                         | <a href="#">5341</a> | <a href="#">P08567</a> | -                                                                                                                                    | -1,49 | 2,84 | 6,10e-03 |

|                 |                                                               |                      |                        |                                                                                                                                   |       |      |          |
|-----------------|---------------------------------------------------------------|----------------------|------------------------|-----------------------------------------------------------------------------------------------------------------------------------|-------|------|----------|
| <b>GSN</b>      | Gelsolin                                                      | <a href="#">2934</a> | <a href="#">P06396</a> | Fc gamma R-mediated phagocytosis (hsa04666)<br>Regulation of actin cytoskeleton (hsa04810)<br>Viral carcinogenesis (hsa05203)     | -1,50 | 8,58 | 1,31e-07 |
| <b>CACNA2D1</b> | Calcium voltage-gated channel auxiliary subunit alpha2delta 1 | <a href="#">781</a>  | <a href="#">P54289</a> | MAPK signalling pathway (hsa04010)<br>Cardiac muscle contraction (hsa04260)<br>Adrenergic signalling in cardiomyocytes (hsa04261) | -1,56 | 2,02 | 3,03e-02 |
| <b>PON1</b>     | Paraoxonase 1                                                 | <a href="#">5444</a> | <a href="#">P27169</a> | -                                                                                                                                 | -1,57 | 2,89 | 5,53e-03 |
| <b>CLEC3B</b>   | C-type lectin domain family 3 member B                        | <a href="#">7123</a> | <a href="#">P05452</a> | -                                                                                                                                 | -1,58 | 7,16 | 1,59e-06 |
| <b>SERPIND1</b> | Serpin family D member 1                                      | <a href="#">3053</a> | <a href="#">P05546</a> | Complement and coagulation cascades (hsa04610)                                                                                    | -1,59 | 5,99 | 1,55e-05 |
| <b>ITIH1</b>    | Inter-alpha-trypsin inhibitor heavy chain 1                   | <a href="#">3697</a> | <a href="#">P19827</a> | -                                                                                                                                 | -1,59 | 8,93 | 7,11e-08 |
| <b>KIT</b>      | KIT proto-oncogene, receptor tyrosine kinase                  | <a href="#">3815</a> | <a href="#">P10721</a> | PI3K-Akt signaling pathway (hsa04151)<br>MAPK signaling pathway (hsa04010)                                                        | -1,64 | 2,30 | 1,79e-02 |



|                 |                                                    |                       |                        |                                                                                                                             |       |      |          |
|-----------------|----------------------------------------------------|-----------------------|------------------------|-----------------------------------------------------------------------------------------------------------------------------|-------|------|----------|
|                 |                                                    |                       |                        | Phospholipase D signaling pathway (hsa04072)                                                                                |       |      |          |
| <b>BCHE</b>     | Butyrylcholinesterase                              | <a href="#">590</a>   | <a href="#">P06276</a> | -                                                                                                                           | -1,72 | 6,02 | 1,49e-05 |
| <b>APOA4</b>    | Apolipoprotein A4                                  | <a href="#">337</a>   | <a href="#">P06727</a> | Fat digestion and absorption (hsa04975)<br>Vitamin digestion and absorption (hsa04977)<br>Cholesterol metabolism (hsa04979) | -1,73 | 5,01 | 8,92e-05 |
| <b>KLKB1</b>    | Kallikrein B1                                      | <a href="#">3818</a>  | <a href="#">P03952</a> | Complement and coagulation cascades (hsa04610)                                                                              | -1,73 | 7,93 | 3,73e-07 |
| <b>APOC4</b>    | Apolipoprotein C4                                  | <a href="#">346</a>   | <a href="#">P55056</a> | -                                                                                                                           | -1,73 | 3,18 | 3,18e-03 |
| <b>FETUB</b>    | Fetuin B                                           | <a href="#">26998</a> | <a href="#">Q9UGM5</a> | -                                                                                                                           | -1,76 | 5,51 | 3,72e-05 |
| <b>SERPINC1</b> | Serpin family C member 1                           | <a href="#">462</a>   | <a href="#">P01008</a> | Complement and coagulation cascades (hsa04610)                                                                              | -1,81 | 6,40 | 7,27e-06 |
| <b>PROZ</b>     | Protein Z, vitamin K dependent plasma glycoprotein | <a href="#">8858</a>  | <a href="#">P22891</a> | -                                                                                                                           | -1,82 | 4,51 | 2,40e-04 |
| <b>APOD</b>     | Apolipoprotein D                                   | <a href="#">347</a>   | <a href="#">P05090</a> | -                                                                                                                           | -1,84 | 7,84 | 4,21e-07 |
| <b>RBP4</b>     | Retinol binding protein 4                          | <a href="#">5950</a>  | <a href="#">P02753</a> | -                                                                                                                           | -1,86 | 5,13 | 7,43e-05 |
| <b>HGFAC</b>    | HGF activator                                      | <a href="#">3083</a>  | <a href="#">Q04756</a> | -                                                                                                                           | -1,88 | 6,42 | 7,27e-06 |
| <b>SELENOP</b>  | Selenoprotein P                                    | <a href="#">6414</a>  | <a href="#">P49908</a> | -                                                                                                                           | -1,90 | 8,41 | 1,52e-07 |
| <b>CNDP1</b>    | Carnosine dipeptidase 1                            | <a href="#">84735</a> | <a href="#">Q96KN2</a> | Histidine metabolism (hsa00340)                                                                                             | -1,90 | 4,67 | 1,81e-04 |

|                |                                                            |                        |                        |                                                             |       |       |          |
|----------------|------------------------------------------------------------|------------------------|------------------------|-------------------------------------------------------------|-------|-------|----------|
|                |                                                            |                        |                        | Beta-alanine metabolism<br>(hsa00410)                       |       |       |          |
|                |                                                            |                        |                        | Metabolic pathways (hsa01100)                               |       |       |          |
| <b>APOM</b>    | Apolipoprotein M                                           | <a href="#">55937</a>  | <a href="#">O95445</a> | -                                                           | -1,91 | 6,37  | 7,41e-06 |
| <b>AHSG</b>    | Alpha-2-HS-glycoprotein                                    | <a href="#">197</a>    | <a href="#">P02765</a> | -                                                           | -1,92 | 7,90  | 3,79e-07 |
| <b>ITIH2</b>   | Inter-alpha-trypsin inhibitor heavy chain 2                | <a href="#">3698</a>   | <a href="#">P19823</a> | -                                                           | -1,93 | 10,39 | 5,43e-09 |
| <b>DBH</b>     | Dopamine beta-hydroxylase                                  | <a href="#">1621</a>   | <a href="#">P09172</a> | Tyrosine metabolism (hsa00350)                              | -1,97 | 2,02  | 3,00e-02 |
|                |                                                            |                        |                        | Metabolic pathways (hsa01100)                               |       |       |          |
| <b>PCYOX1</b>  | Prenylcysteine oxidase 1                                   | <a href="#">51449</a>  | <a href="#">Q9UHG3</a> | Terpenoid backbone biosynthesis (hsa00900)                  | -2,01 | 7,56  | 7,31e-07 |
| <b>PGLYRP2</b> | Peptidoglycan recognition protein 2                        | <a href="#">114770</a> | <a href="#">Q96PD5</a> | -                                                           | -2,09 | 9,42  | 3,17e-08 |
| <b>PROC</b>    | Protein C, inactivator of coagulation factors Va and VIIIa | <a href="#">5624</a>   | <a href="#">P04070</a> | Complement and coagulation cascades (hsa04610)              | -2,10 | 6,85  | 2,92e-06 |
| <b>AFM</b>     | Afamin                                                     | <a href="#">173</a>    | <a href="#">P43652</a> | -                                                           | -2,13 | 9,79  | 1,54e-08 |
| <b>PON3</b>    | Paraoxonase 3                                              | <a href="#">5446</a>   | <a href="#">Q15166</a> | -                                                           | -2,14 | 6,25  | 9,25e-06 |
| <b>APOC1</b>   | Apolipoprotein C1                                          | <a href="#">341</a>    | <a href="#">P02654</a> | Cholesterol metabolism (hsa04979)                           | -2,16 | 2,95  | 4,98e-03 |
| <b>HRG</b>     | Histidine rich glycoprotein                                | <a href="#">3273</a>   | <a href="#">P04196</a> | -                                                           | -2,17 | 11,18 | 1,20e-09 |
| <b>GPLD1</b>   | Glycosylphosphatidylinositol specific phospholipase D1     | <a href="#">2822</a>   | <a href="#">P80108</a> | Glycosylphosphatidylinositol-anchor biosynthesis (hsa00563) | -2,19 | 6,87  | 2,88e-06 |
|                |                                                            |                        |                        | Metabolic pathways (hsa01100)                               |       |       |          |

|                 |                                                                |                      |                        |                                                                                                                                                    |       |       |          |
|-----------------|----------------------------------------------------------------|----------------------|------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------|-------|-------|----------|
| <b>PLG</b>      | plasminogen                                                    | <a href="#">5340</a> | <a href="#">P00747</a> | Complement and coagulation cascades (hsa04610)<br>Neuroactive ligand-receptor interaction (hsa04080)<br>Staphylococcus aureus infection (hsa05150) | -2,23 | 8,64  | 1,25e-07 |
| <b>SERPINA4</b> | Serpin family A member 4                                       | <a href="#">5267</a> | <a href="#">P29622</a> | -                                                                                                                                                  | -2,26 | 12,60 | 0,00e+00 |
| <b>IGFBP3</b>   | Insulin like growth factor binding protein 3                   | <a href="#">3486</a> | <a href="#">P17936</a> | p53 signaling pathway (hsa04115)<br>Cellular senescence (hsa04218)<br>Growth hormone synthesis, secretion and action (hsa04935)                    | -2,31 | 6,77  | 3,42e-06 |
| <b>IGFALS</b>   | insulin like growth factor binding protein acid labile subunit | <a href="#">3483</a> | <a href="#">P35858</a> | Growth hormone synthesis, secretion and action (hsa04935)                                                                                          | -2,45 | 6,39  | 7,27e-06 |
| <b>F12</b>      | Coagulation factor XII                                         | <a href="#">2161</a> | <a href="#">P00748</a> | Complement and coagulation cascades (hsa04610)                                                                                                     | -2,46 | 5,97  | 1,56e-05 |
| <b>SERPINA5</b> | Serpin family A member 5                                       | <a href="#">5104</a> | <a href="#">P05154</a> | Complement and coagulation cascades (hsa04610)                                                                                                     | -2,60 | 6,40  | 7,27e-06 |
| <b>TTR</b>      | Transthyretin                                                  | <a href="#">7276</a> | <a href="#">P02766</a> | Thyroid hormone synthesis (hsa04918)                                                                                                               | -2,91 | 6,31  | 8,39e-06 |
| <b>SPP2</b>     | Secreted Phosphoprotein 2                                      | <a href="#">6694</a> | <a href="#">Q13103</a> | -                                                                                                                                                  | -2,95 | 4,61  | 2,03e-04 |

**Table S2.** Showing significantly altered protein in the comparison of Septic shock vs. Control. Proteins classified as significantly altered if exhibiting a of log2 fold change > 0.5 or < -0.5 and an FDR adjusted p-value < 0.05. Tables showing gene symbol, gene name, NCBI gene ID, Uniprot ID, related KEGG pathways, log2 fold change, -log10 P-value and adjusted p-value. If more than 3 KEGG pathways associated to the protein the three most relevant were selected for the table.

Table S3 – Acute Pancreatitis versus Control

| GENE<br>SYMBOL | GENE NAME                             | NCBI<br>GENE<br>ID   | UNIPROT<br>ID          | KEGG PATHWAY                                                                      | LOG2FC | -LOG10<br>P-<br>VALUE | ADJUSTED<br>P-VALUE |
|----------------|---------------------------------------|----------------------|------------------------|-----------------------------------------------------------------------------------|--------|-----------------------|---------------------|
| <b>CRP</b>     | C-reactive protein                    | <a href="#">1401</a> | <a href="#">P02741</a> | -                                                                                 | 5,09   | 14,09                 | 0,00e+00            |
| <b>SAA1</b>    | Serum amyloid A1                      | <a href="#">6288</a> | <a href="#">P0DJ18</a> | -                                                                                 | 4,00   | 6,77                  | 1,86e-05            |
| <b>S100A8</b>  | S100 calcium binding protein<br>A8    | <a href="#">6279</a> | <a href="#">P05109</a> | IL-17 signaling pathway (hsa04657)<br>Cornified envelope formation<br>(hsa04382)  | 3,78   | 6,04                  | 6,70e-05            |
| <b>S100A12</b> | S100 calcium binding protein<br>A12   | <a href="#">6283</a> | <a href="#">P80511</a> | Cornified envelope formation<br>(hsa04382)                                        | 3,64   | 3,77                  | 3,13e-03            |
| <b>CHI3L1</b>  | Chitinase 3 like 1                    | <a href="#">1116</a> | <a href="#">P36222</a> | -                                                                                 | 3,61   | 5,69                  | 1,35e-04            |
| <b>MMP8</b>    | Matrix metalloproteinase 8            | <a href="#">4317</a> | <a href="#">P22894</a> | -                                                                                 | 3,31   | 5,24                  | 2,52e-04            |
| <b>S100A9</b>  | S100 calcium binding protein<br>A9    | <a href="#">6280</a> | <a href="#">P06702</a> | IL-17 signaling pathway (hsa04657)<br>Cornified envelope formation<br>(hsa04382)  | 3,20   | 5,22                  | 2,52e-04            |
| <b>SAA2</b>    | Serum amyloid A2                      | <a href="#">6289</a> | <a href="#">P0DJ19</a> | -                                                                                 | 3,02   | 3,35                  | 6,37e-03            |
| <b>CPA1</b>    | Carboxypeptidase A1                   | <a href="#">1357</a> | <a href="#">P15085</a> | Protein digestion and absorption<br>(hsa04974)<br>Pancreatic secretion (hsa04972) | 3,00   | 4,02                  | 2,42e-03            |
| <b>LBP</b>     | Lipopolysaccharide binding<br>protein | <a href="#">3929</a> | <a href="#">P18428</a> | NF-kappa B signaling pathway<br>(hsa04064)                                        | 2,94   | 5,17                  | 2,63e-04            |

|               |                                      |                      |                        |                                                                                                                                            |      |      |          |
|---------------|--------------------------------------|----------------------|------------------------|--------------------------------------------------------------------------------------------------------------------------------------------|------|------|----------|
|               |                                      |                      |                        | Toll-like receptor signaling pathway<br>(hsa04620)<br>Alcoholic liver disease (hsa04936)                                                   |      |      |          |
| <b>REG1B</b>  | Regenerating family member 1<br>beta | <a href="#">5968</a> | <a href="#">P48304</a> | -                                                                                                                                          | 2,88 | 4,87 | 4,99e-04 |
| <b>ORM1</b>   | Orosomucoid 1                        | <a href="#">5004</a> | <a href="#">P02763</a> | -                                                                                                                                          | 2,72 | 5,40 | 2,04e-04 |
| <b>PRSS2</b>  | Serine protease 2                    | <a href="#">5645</a> | <a href="#">P07478</a> | Protein digestion and absorption<br>(hsa04974)<br>Pancreatic secretion (hsa04972)<br>Neuroactive ligand-receptor<br>interaction (hsa04080) | 2,50 | 2,84 | 1,59e-02 |
| <b>IL1RL1</b> | Interleukin 1 receptor like 1        | <a href="#">9173</a> | <a href="#">Q01638</a> | Cytokine-cytokine receptor<br>interaction (hsa04060)                                                                                       | 2,44 | 3,86 | 2,85e-03 |
| <b>CAT</b>    | Catalase                             | <a href="#">847</a>  | <a href="#">P04040</a> | Glyoxylate and dicarboxylate<br>metabolism (hsa00630)<br>Carbon metabolism (hsa01200)<br>Peroxisome (hsa04146)                             | 2,32 | 5,30 | 2,35e-04 |
| <b>NUCB1</b>  | Nucleobindin 1                       | <a href="#">4924</a> | <a href="#">Q02818</a> | -                                                                                                                                          | 2,30 | 3,36 | 6,34e-03 |
| <b>MMP9</b>   | Matrix metalloproteinase 9           | <a href="#">4318</a> | <a href="#">P14780</a> | IL-17 signaling pathway (hsa04657)<br>TNF signaling pathway (hsa04668)<br>Leukocyte transendothelial migration<br>(hsa04670)               | 2,22 | 3,80 | 3,08e-03 |

|                 |                                              |                        |                        |                                                                                                                               |      |      |          |
|-----------------|----------------------------------------------|------------------------|------------------------|-------------------------------------------------------------------------------------------------------------------------------|------|------|----------|
| <b>BPGM</b>     | Bisphosphoglycerate mutase                   | <a href="#">669</a>    | <a href="#">P07738</a> | Glycolysis/Gluconeogenesis (hsa00010)<br>Glycine, serine and threonine metabolism (hsa00260)<br>Metabolic pathways (hsa01100) | 1,94 | 2,60 | 2,56e-02 |
| <b>VSIG4</b>    | V-set and immunoglobulin domain containing 4 | <a href="#">11326</a>  | <a href="#">Q9Y279</a> | Complement and coagulation cascades (hsa04610)                                                                                | 1,93 | 2,76 | 1,87e-02 |
| <b>CDHR2</b>    | Cadherin related family member 2             | <a href="#">54825</a>  | <a href="#">Q9BYE9</a> | -                                                                                                                             | 1,86 | 2,58 | 2,63e-02 |
| <b>TKT</b>      | Transketolase                                | <a href="#">7086</a>   | <a href="#">P29401</a> | Pentose phosphate pathway (hsa00030)<br>Carbon metabolism (hsa01200)<br>Biosynthesis of amino acids (hsa01230)                | 1,79 | 4,66 | 7,63e-04 |
| <b>SERPINA3</b> | Serpin family A member 3                     | <a href="#">12</a>     | <a href="#">P01011</a> | -                                                                                                                             | 1,76 | 7,26 | 9,21e-06 |
| <b>LRG1</b>     | Leucine rich alpha-2-glycoprotein 1          | <a href="#">116844</a> | <a href="#">P02750</a> | -                                                                                                                             | 1,72 | 8,10 | 2,61e-06 |
| <b>ORM2</b>     | Orosomucoid 2                                | <a href="#">5005</a>   | <a href="#">P19652</a> | -                                                                                                                             | 1,71 | 2,52 | 2,84e-02 |
| <b>CA1</b>      | Carbonic anhydrase 1                         | <a href="#">759</a>    | <a href="#">P00915</a> | Metabolic pathways (hsa01100)<br>Nitrogen metabolism (hsa00910)                                                               | 1,65 | 2,43 | 3,27e-02 |
| <b>VWF</b>      | Von Willebrand factor                        | <a href="#">7450</a>   | <a href="#">P04275</a> | PI3K-Akt signaling pathway (hsa04151) Complement and                                                                          | 1,59 | 3,91 | 2,82e-03 |

|              |                                |                        |                        |                                                              |      |      |          |
|--------------|--------------------------------|------------------------|------------------------|--------------------------------------------------------------|------|------|----------|
|              |                                |                        |                        | coagulation cascades (hsa04610)                              |      |      |          |
|              |                                |                        |                        | Platelet activation (hsa04611)                               |      |      |          |
| <b>APOA5</b> | Apolipoprotein A5              | <a href="#">116519</a> | <a href="#">Q6Q788</a> | PPAR signaling pathway (hsa03320)                            | 1,57 | 2,43 | 3,27e-02 |
| <b>VIM</b>   | Vimentin                       | <a href="#">7431</a>   | <a href="#">P08670</a> | Cytoskeleton in muscle cells (hsa04820)                      | 1,55 | 2,28 | 4,45e-02 |
|              |                                |                        |                        | Epstein-Barr virus infection (hsa05169)                      |      |      |          |
|              |                                |                        |                        | MicroRNAs in cancer (hsa05206)                               |      |      |          |
| <b>PSMA6</b> | Proteasome 20S subunit alpha 6 | <a href="#">5687</a>   | <a href="#">P60900</a> | Proteasome (hsa03050)                                        | 1,52 | 2,24 | 4,73e-02 |
|              |                                |                        |                        | Prion disease (hsa05020)                                     |      |      |          |
|              |                                |                        |                        | Pathways of neurodegeneration - multiple diseases (hsa05022) |      |      |          |
| <b>LTA4H</b> | Leukotriene A4 hydrolase       | <a href="#">4048</a>   | <a href="#">P09960</a> | Arachidonic acid metabolism (hsa00590)                       | 1,52 | 5,54 | 1,59e-04 |
|              |                                |                        |                        | Metabolic pathways (hsa01100)                                |      |      |          |
| <b>PSMB7</b> | Proteasome 20S subunit beta 7  | <a href="#">5695</a>   | <a href="#">Q99436</a> | Proteasome (hsa03050)                                        | 1,51 | 2,21 | 4,94e-02 |
|              |                                |                        |                        | Prion disease (hsa05020)                                     |      |      |          |
|              |                                |                        |                        | Pathways of neurodegeneration - multiple diseases (hsa05022) |      |      |          |
| <b>PSMA1</b> | Proteasome 20S subunit alpha 1 | <a href="#">5682</a>   | <a href="#">P25786</a> | Proteasome (hsa03050)                                        | 1,51 | 2,21 | 4,94e-02 |
|              |                                |                        |                        | Prion disease (hsa05020)                                     |      |      |          |
|              |                                |                        |                        | Pathways of neurodegeneration - multiple diseases (hsa05022) |      |      |          |

|               |                                    |                      |                        |                                                                                                                   |      |      |          |
|---------------|------------------------------------|----------------------|------------------------|-------------------------------------------------------------------------------------------------------------------|------|------|----------|
| <b>NID1</b>   | Nidogen 1                          | <a href="#">4811</a> | <a href="#">P14543</a> | Cytoskeleton in muscle cells (hsa04820)                                                                           | 1,49 | 7,30 | 9,21e-06 |
| <b>PRDX2</b>  | Peroxiredoxin 2                    | <a href="#">7001</a> | <a href="#">P32119</a> | -                                                                                                                 | 1,46 | 2,70 | 2,10e-02 |
| <b>TALDO1</b> | Transaldolase 1                    | <a href="#">6888</a> | <a href="#">P37837</a> | Pentose phosphate pathway (hsa00030)<br>Carbon metabolism (hsa01200)<br>Biosynthesis of amino acids (hsa01230)    | 1,41 | 3,10 | 1,06e-02 |
| <b>TIMP1</b>  | TIMP metalloproteinase inhibitor 1 | <a href="#">7076</a> | <a href="#">P01033</a> | HIF-1 signaling pathway (hsa04066)                                                                                | 1,41 | 3,17 | 9,19e-03 |
| <b>CTSB</b>   | Cathepsin B                        | <a href="#">1508</a> | <a href="#">P07858</a> | Lysosome (hsa04142)<br>Apoptosis (hsa04210)<br>Antigen processing and presentation (hsa04612)                     | 1,40 | 2,95 | 1,35e-02 |
| <b>F8</b>     | Coagulation factor VIII            | <a href="#">2157</a> | <a href="#">P00451</a> | Complement and coagulation cascades (hsa04610)                                                                    | 1,25 | 4,26 | 1,53e-03 |
| <b>COL6A1</b> | Collagen type VI alpha 1 chain     | <a href="#">1291</a> | <a href="#">P12109</a> | PI3K-Akt signaling pathway (hsa04151)<br>Protein digestion and absorption (hsa04974)<br>Focal adhesion (hsa04510) | 1,22 | 3,04 | 1,17e-02 |



|               |                                                  |                       |                        |                                                                                                                              |       |      |          |
|---------------|--------------------------------------------------|-----------------------|------------------------|------------------------------------------------------------------------------------------------------------------------------|-------|------|----------|
| <b>GALNT2</b> | Polypeptide N-acetylgalactosaminyl-transferase 2 | <a href="#">2590</a>  | <a href="#">Q10471</a> | Mucin type O-glycan biosynthesis (hsa00512)<br>Other O-glycan biosynthesis (hsa00514)<br>Metabolic pathways (hsa01100)       | 1,20  | 3,59 | 4,46e-03 |
| <b>EPHB4</b>  | EPH receptor B4                                  | <a href="#">2050</a>  | <a href="#">P54760</a> | Axon guidance (hsa04360)                                                                                                     | 1,12  | 3,89 | 2,85e-03 |
| <b>CTSZ</b>   | Cathepsin Z                                      | <a href="#">1522</a>  | <a href="#">Q9UBR2</a> | Lysosome (hsa04142)<br>Apoptosis (hsa04210)                                                                                  | 1,11  | 2,63 | 2,45e-02 |
| <b>MAN1A1</b> | Mannosidase alpha class 1A member 1              | <a href="#">4121</a>  | <a href="#">P33908</a> | Protein processing in ER (hsa04141)<br>N-glycan biosynthesis (hsa00510)<br>Various types of N-glycan biosynthesis (hsa00531) | 1,08  | 5,56 | 1,59e-04 |
| <b>LCPI</b>   | Lymphocyte cytosolic protein 1                   | <a href="#">3936</a>  | <a href="#">P13796</a> | -                                                                                                                            | 1,06  | 2,45 | 3,22e-02 |
| <b>IGFBP4</b> | Insulin like growth factor binding protein 4     | <a href="#">3487</a>  | <a href="#">P22692</a> | -                                                                                                                            | 0,97  | 2,84 | 1,59e-02 |
| <b>CTSD</b>   | Cathepsin D                                      | <a href="#">1509</a>  | <a href="#">P07339</a> | Sphingolipid signaling pathway (hsa04071)<br>Lysosome (hsa04142)<br>Apoptosis (hsa04210)                                     | 0,94  | 2,24 | 4,74e-02 |
| <b>ATRNL1</b> | Attractin                                        | <a href="#">8455</a>  | <a href="#">O75882</a> | -                                                                                                                            | -0,71 | 2,43 | 3,27e-02 |
| <b>ABI3BP</b> | ABI family member 3 binding protein              | <a href="#">25890</a> | <a href="#">Q7Z7G0</a> | -                                                                                                                            | -0,76 | 2,27 | 4,46e-02 |
| <b>ECM1</b>   | Extracellular matrix protein 1                   | <a href="#">1893</a>  | <a href="#">Q16610</a> | -                                                                                                                            | -0,88 | 2,92 | 1,44e-02 |

|                |                                             |                       |                        |                                                                                                                                |       |      |          |
|----------------|---------------------------------------------|-----------------------|------------------------|--------------------------------------------------------------------------------------------------------------------------------|-------|------|----------|
| <b>CDH13</b>   | Cadherin 13                                 | <a href="#">1012</a>  | <a href="#">P55290</a> | -                                                                                                                              | -0,90 | 4,59 | 8,60e-04 |
| <b>ITIH1</b>   | Inter-alpha-trypsin inhibitor heavy chain 1 | <a href="#">3697</a>  | <a href="#">P19827</a> | -                                                                                                                              | -0,98 | 3,50 | 4,84e-03 |
| <b>GPNMB</b>   | Glycoprotein nmb                            | <a href="#">10457</a> | <a href="#">Q14956</a> | -                                                                                                                              | -0,99 | 2,56 | 2,66e-02 |
| <b>BTD</b>     | Biotinidase                                 | <a href="#">686</a>   | <a href="#">P43251</a> | Biotin metabolism (hsa00780)<br>Vitamin digestion and absorption (hsa04977)<br>Metabolic pathways (hsa01100)                   | -0,99 | 3,49 | 4,86e-03 |
| <b>ACE</b>     | Angiotensin I converting enzyme             | <a href="#">1636</a>  | <a href="#">P12821</a> | Renin-angiotensin system (hsa04614)<br>Renin secretion (hsa04924)<br>Coronavirus disease - COVID-19 (hsa05171)                 | -1,04 | 4,48 | 1,05e-03 |
| <b>F13A1</b>   | Coagulation factor XIII A chain             | <a href="#">2162</a>  | <a href="#">P00488</a> | Complement and coagulation cascades (hsa04610)<br>Coronavirus disease - COVID-19 (hsa05171)                                    | -1,04 | 2,57 | 2,64e-02 |
| <b>NCAM1</b>   | Neural cell adhesion molecule 1             | <a href="#">4684</a>  | <a href="#">P13591</a> | Virion - Ebolavirus, Lyssavirus and Morbillivirus (hsa03265)<br>Cell adhesion molecules (hsa04514)<br>Prion disease (hsa05020) | -1,06 | 4,18 | 1,75e-03 |
| <b>CHL1</b>    | Cell adhesion molecule L1 like              | <a href="#">10752</a> | <a href="#">O00533</a> | -                                                                                                                              | -1,09 | 3,53 | 4,78e-03 |
| <b>SELENOP</b> | Selenoprotein P                             | <a href="#">6414</a>  | <a href="#">P49908</a> | -                                                                                                                              | -1,09 | 2,86 | 1,58e-02 |
| <b>CNTN1</b>   | Contactin 1                                 | <a href="#">1272</a>  | <a href="#">Q12860</a> | Cell adhesion molecules (hsa04514)                                                                                             | -1,10 | 3,52 | 4,80e-03 |

|                 |                                                        |                       |                        |                                                                                              |       |      |          |
|-----------------|--------------------------------------------------------|-----------------------|------------------------|----------------------------------------------------------------------------------------------|-------|------|----------|
| <b>SELL</b>     | Selectin L                                             | <a href="#">6402</a>  | <a href="#">P14151</a> | Cell adhesion molecules (hsa04514)                                                           | -1,11 | 2,89 | 1,51e-02 |
| <b>FAP</b>      | Fibroblast activation protein alpha                    | <a href="#">2191</a>  | <a href="#">Q12884</a> | -                                                                                            | -1,12 | 3,09 | 1,06e-02 |
| <b>AFM</b>      | Afamin                                                 | <a href="#">173</a>   | <a href="#">P43652</a> | -                                                                                            | -1,12 | 2,98 | 1,30e-02 |
| <b>ITIH2</b>    | Inter-alpha-trypsin inhibitor heavy chain 2            | <a href="#">3698</a>  | <a href="#">P19823</a> | -                                                                                            | -1,18 | 4,26 | 1,53e-03 |
| <b>AHSG</b>     | Alpha-2-HS-glycoprotein                                | <a href="#">197</a>   | <a href="#">P02765</a> | -                                                                                            | -1,18 | 2,97 | 1,32e-02 |
| <b>CRTAC1</b>   | Cartilage acidic protein 1                             | <a href="#">55118</a> | <a href="#">Q9NQ79</a> | -                                                                                            | -1,20 | 3,58 | 4,46e-03 |
| <b>APOD</b>     | Apolipoprotein D                                       | <a href="#">347</a>   | <a href="#">P05090</a> | -                                                                                            | -1,20 | 3,29 | 7,04e-03 |
| <b>CRISP3</b>   | Cysteine rich secretory protein 3                      | <a href="#">10321</a> | <a href="#">P54108</a> | -                                                                                            | -1,20 | 2,36 | 3,72e-02 |
| <b>KLKB1</b>    | Kallikrein B1                                          | <a href="#">3818</a>  | <a href="#">P03952</a> | Complement and coagulation cascades (hsa04610)                                               | -1,21 | 3,76 | 3,13e-03 |
| <b>CLEC3B</b>   | C-type lectin domain family 3 member B                 | <a href="#">7123</a>  | <a href="#">P05452</a> | -                                                                                            | -1,23 | 3,99 | 2,49e-03 |
| <b>SERPIND1</b> | Serpin family D member 1                               | <a href="#">3053</a>  | <a href="#">P05546</a> | Complement and coagulation cascades (hsa04610)                                               | -1,36 | 3,87 | 2,85e-03 |
| <b>GPLD1</b>    | Glycosylphosphatidylinositol specific phospholipase D1 | <a href="#">2822</a>  | <a href="#">P80108</a> | Glycosylphosphatidylinositol-anchor biosynthesis (hsa00563)<br>Metabolic pathways (hsa01100) | -1,37 | 2,52 | 2,84e-02 |
| <b>APOA4</b>    | Apolipoprotein A4                                      | <a href="#">337</a>   | <a href="#">P06727</a> | Fat digestion and absorption (hsa04975)                                                      | -1,38 | 2,77 | 1,85e-02 |

|                 |                                                 |                        |                        |                                                                                                                                     |       |      |          |
|-----------------|-------------------------------------------------|------------------------|------------------------|-------------------------------------------------------------------------------------------------------------------------------------|-------|------|----------|
|                 |                                                 |                        |                        | Vitamin digestion and absorption<br>(hsa04977)<br>Cholesterol metabolism (hsa04979)                                                 |       |      |          |
| <b>PGLYRP2</b>  | Peptidoglycan recognition<br>protein 2          | <a href="#">114770</a> | <a href="#">Q96PD5</a> | -                                                                                                                                   | -1,39 | 4,30 | 1,52e-03 |
| <b>GSN</b>      | Gelsolin                                        | <a href="#">2934</a>   | <a href="#">P06396</a> | Fc gamma R-mediated phagocytosis<br>(hsa04666)<br>Regulation of actin cytoskeleton<br>(hsa04810)<br>Viral carcinogenesis (hsa05203) | -1,43 | 6,91 | 1,63e-05 |
| <b>IGFBP3</b>   | Insulin like growth factor<br>binding protein 3 | <a href="#">3486</a>   | <a href="#">P17936</a> | p53 signaling pathway (hsa04115)<br>Cellular senescence (hsa04218)<br>Growth hormone synthesis, secretion<br>and action (hsa04935)  | -1,44 | 2,45 | 3,22e-02 |
| <b>ADA2</b>     | Adenosine deaminase 2                           | <a href="#">51816</a>  | <a href="#">Q9NZK5</a> | Purine metabolism (hsa00230)<br>Metabolic pathways (hsa01100)<br>Nucleotide metabolism (hsa01232)                                   | -1,48 | 2,56 | 2,67e-02 |
| <b>HGFAC</b>    | HGF activator                                   | <a href="#">3083</a>   | <a href="#">Q04756</a> | -                                                                                                                                   | -1,53 | 3,81 | 3,08e-03 |
| <b>SERPINA4</b> | Serpin family A member 4                        | <a href="#">5267</a>   | <a href="#">P29622</a> | -                                                                                                                                   | -1,53 | 6,57 | 2,53e-05 |
| <b>FETUB</b>    | Fetuin B                                        | <a href="#">26998</a>  | <a href="#">Q9UGM5</a> | -                                                                                                                                   | -1,57 | 3,78 | 3,13e-03 |
| <b>HRG</b>      | Histidine rich glycoprotein                     | <a href="#">3273</a>   | <a href="#">P04196</a> | -                                                                                                                                   | -1,57 | 6,18 | 5,50e-05 |

|                 |                          |                       |                        |                                                                                                        |       |      |          |
|-----------------|--------------------------|-----------------------|------------------------|--------------------------------------------------------------------------------------------------------|-------|------|----------|
| <b>CNDP1</b>    | Carnosine dipeptidase 1  | <a href="#">84735</a> | <a href="#">Q96KN2</a> | Histidine metabolism (hsa00340)<br>Beta-alanine metabolism (hsa00410)<br>Metabolic pathways (hsa01100) | -1,77 | 3,43 | 5,45e-03 |
| <b>F12</b>      | Coagulation factor XII   | <a href="#">2161</a>  | <a href="#">P00748</a> | Complement and coagulation<br>cascades (hsa04610)                                                      | -2,02 | 3,56 | 4,60e-03 |
| <b>SERPINA5</b> | Serpin family A member 5 | <a href="#">5104</a>  | <a href="#">P05154</a> | Complement and coagulation<br>cascades (hsa04610)                                                      | -2,15 | 3,91 | 2,82e-03 |

**Table S3.** Showing significantly altered protein in the comparison of Acute pancreatitis vs. Control. Proteins classified as significantly altered if exhibiting a of log2 fold change > 0.5 or < -0.5 and an FDR adjusted p-value < 0.05. Tables showing gene symbol, gene name, NCBI gene ID, Uniprot ID, related KEGG pathways, log2 fold change, -log10 P-value and adjusted p-value. If more than 3 KEGG pathways associated to the protein the three most relevant were selected for the table.

Table S4 - Septic shock versus Acute pancreatitis

| GENE<br>SYMBOL  | GENE NAME                                             | NCBI<br>GENE<br>ID    | UNIPROT<br>ID          | KEGG                                                                                                                                              | LOG2FC | -LOG10<br>P-VALUE | ADJUSTED<br>P-VALUE |
|-----------------|-------------------------------------------------------|-----------------------|------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------|--------|-------------------|---------------------|
| <b>MARCKS</b>   | Myristoylated alanine rich protein kinase C substrate | <a href="#">4082</a>  | <a href="#">P29966</a> | Fc gamma R-mediated phagocytosis (hsa04666)<br>MicroRNAs in cancer (hsa05206)                                                                     | 1,66   | 3,28              | 2,30e-02            |
| <b>HSP90AA1</b> | heat shock protein 90 alpha family class A member 1   | <a href="#">3320</a>  | <a href="#">P07900</a> | Protein processing in endoplasmic reticulum (hsa04141)<br>PI3K-Akt signaling pathway (hsa04217)<br>Antigen processing and presentation (hsa04612) | 1,57   | 2,79              | 3,82e-02            |
| <b>PSAP</b>     | Prosaposin                                            | <a href="#">5660</a>  | <a href="#">P07602</a> | Lysosome (hsa04142)<br>Sphingolipid metabolism (hsa00600)                                                                                         | 1,18   | 2,69              | 4,64e-02            |
| <b>CD163</b>    | CD163 molecule                                        | <a href="#">9332</a>  | <a href="#">Q86VB7</a> | -                                                                                                                                                 | 1,14   | 3,18              | 2,30e-02            |
| <b>GANAB</b>    | Glucosidase II alpha subunit                          | <a href="#">23193</a> | <a href="#">Q14697</a> | Protein processing in endoplasmic reticulum (hsa04141)<br>N-Glycan biosynthesis (hsa00510)<br>Metabolic pathways (hsa01100)                       | 1,09   | 3,05              | 2,59e-02            |
| <b>SERPINB1</b> | Serpin family B member 1                              | <a href="#">1992</a>  | <a href="#">P30740</a> | -                                                                                                                                                 | 0,89   | 3,85              | 1,32e-02            |

|               |                                              |                        |                        |                                                                                                                                                 |       |      |          |
|---------------|----------------------------------------------|------------------------|------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------|-------|------|----------|
| <b>COTL1</b>  | Coactosin like protein 1                     | <a href="#">23406</a>  | <a href="#">Q14019</a> | -                                                                                                                                               | 0,89  | 3,26 | 2,30e-02 |
| <b>PTPRJ</b>  | Protein tyrosine phosphatase receptor type J | <a href="#">5795</a>   | <a href="#">Q12913</a> | Adherens junction (hsa04520)<br>Chemical carcinogenesis - reactive oxygen species (hsa05208)                                                    | -0,62 | 3,19 | 2,30e-02 |
| <b>MAN1A1</b> | Mannosidase alpha class 1A member 1          | <a href="#">4121</a>   | <a href="#">P33908</a> | Protein processing in endoplasmic reticulum (hsa04141)<br>N-glycan biosynthesis (hsa00510)<br>Various types of N-glycan biosynthesis (hsa00531) | -0,66 | 2,81 | 3,77e-02 |
| <b>F2</b>     | Coagulation factor II, prothrombin           | <a href="#">2147</a>   | <a href="#">P00734</a> | Complement and coagulation cascades (hsa04610)<br>Platelet activation (hsa04611)<br>Phospholipase D signaling pathway (hsa04072)                | -0,77 | 3,10 | 2,49e-02 |
| <b>LRG1</b>   | Leucine rich alpha-2-glycoprotein 1          | <a href="#">116844</a> | <a href="#">P02750</a> | -                                                                                                                                               | -0,88 | 3,21 | 2,30e-02 |
| <b>C6</b>     | Complement C6                                | <a href="#">729</a>    | <a href="#">P13671</a> | Complement and coagulation cascades (hsa04610)<br>Regulation of actin cytoskeleton (hsa04810)<br>Coronavirus disease - COVID-19 (hsa05171)      | -0,99 | 3,25 | 2,30e-02 |
| <b>AFM</b>    | Afamin                                       | <a href="#">173</a>    | <a href="#">P43652</a> | -                                                                                                                                               | -1,01 | 2,97 | 2,81e-02 |

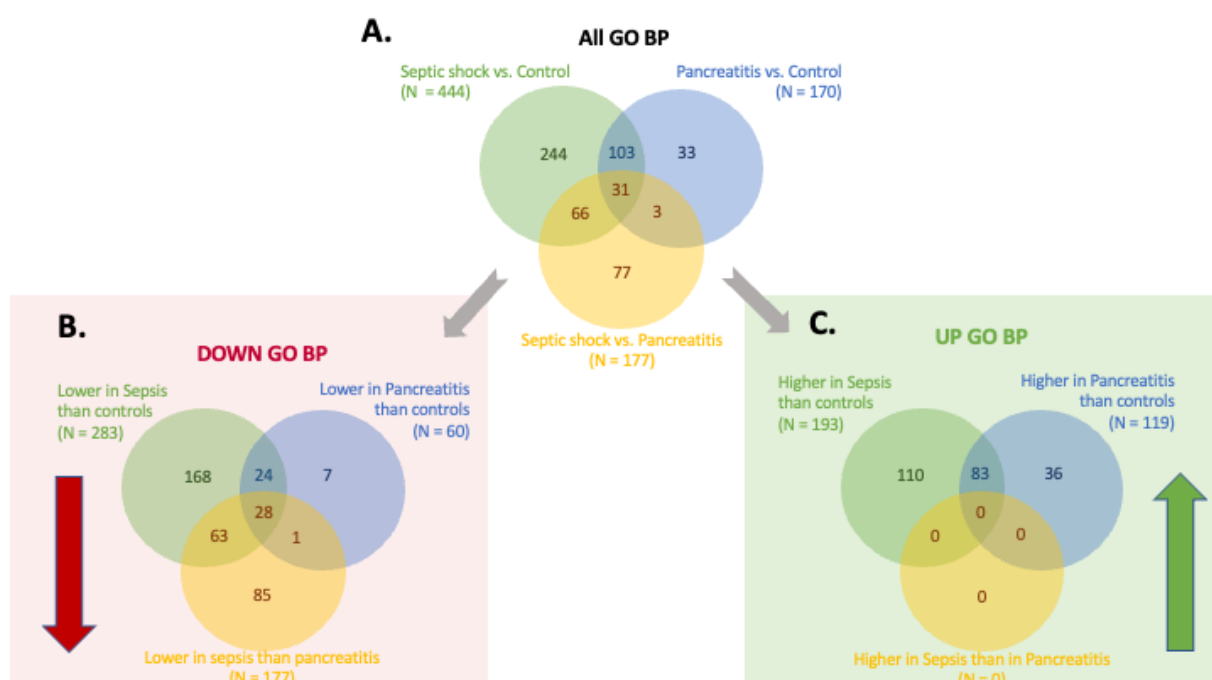
|               |                                                            |                       |                        |                                                                                                                                                    |       |      |          |
|---------------|------------------------------------------------------------|-----------------------|------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------|-------|------|----------|
| <b>APOF</b>   | Apolipoprotein F                                           | <a href="#">319</a>   | <a href="#">Q13790</a> | -                                                                                                                                                  | -1,11 | 2,92 | 3,08e-02 |
| <b>F9</b>     | Coagulation factor IX                                      | <a href="#">2158</a>  | <a href="#">P00740</a> | Complement and coagulation cascades (hsa04610)                                                                                                     | -1,11 | 4,43 | 6,51e-03 |
| <b>APOH</b>   | Apolipoprotein H                                           | <a href="#">350</a>   | <a href="#">P02749</a> | Cholesterol metabolism (hsa04979)                                                                                                                  | -1,16 | 3,17 | 2,30e-02 |
| <b>PLG</b>    | Plasminogen                                                | <a href="#">5340</a>  | <a href="#">P00747</a> | Complement and coagulation cascades (hsa04610)<br>Neuroactive ligand-receptor interaction (hsa04080)<br>Staphylococcus aureus infection (hsa05150) | -1,16 | 3,00 | 2,79e-02 |
| <b>PCYOX1</b> | Prenylcysteine oxidase 1                                   | <a href="#">51449</a> | <a href="#">Q9UHG3</a> | Terpenoid backbone biosynthesis (hsa00900)                                                                                                         | -1,22 | 3,36 | 2,30e-02 |
| <b>SNCA</b>   | Synuclein alpha                                            | <a href="#">6622</a>  | <a href="#">P37840</a> | Alzheimer disease (hsa05010)<br>Parkinson disease (hsa05012)<br>Pathways of neurodegeneration - multiple diseases (hsa05022)                       | -1,28 | 3,06 | 2,59e-02 |
| <b>APOE</b>   | Apolipoprotein E                                           | <a href="#">348</a>   | <a href="#">P02649</a> | Cholesterol metabolism (hsa04979)<br>Alzheimer's disease (hsa05010)                                                                                | -1,37 | 4,44 | 6,51e-03 |
| <b>PROC</b>   | protein C, inactivator of coagulation factors Va and VIIIa | <a href="#">5624</a>  | <a href="#">P04070</a> | Complement and coagulation cascades (hsa04610)                                                                                                     | -1,41 | 3,53 | 2,30e-02 |
| <b>PRDX2</b>  | Peroxiredoxin 2                                            | <a href="#">7001</a>  | <a href="#">P32119</a> | -                                                                                                                                                  | -1,42 | 3,16 | 2,30e-02 |
| <b>HABP2</b>  | Hyaluronan binding protein 2                               | <a href="#">3026</a>  | <a href="#">Q14520</a> | -                                                                                                                                                  | -1,48 | 3,91 | 1,32e-02 |



|              |                            |                        |                        |                                                                                                                                     |       |      |          |
|--------------|----------------------------|------------------------|------------------------|-------------------------------------------------------------------------------------------------------------------------------------|-------|------|----------|
| <b>APOA5</b> | Apolipoprotein A5          | <a href="#">116519</a> | <a href="#">Q6Q788</a> | PPAR signaling pathway<br>(hsa03320)                                                                                                | -1,67 | 3,35 | 2,30e-02 |
| <b>APOC2</b> | Apolipoprotein C2          | <a href="#">344</a>    | <a href="#">P02655</a> | Cholesterol metabolism (hsa04979)                                                                                                   | -1,94 | 3,42 | 2,30e-02 |
| <b>BPGM</b>  | Bisphosphoglycerate mutase | <a href="#">669</a>    | <a href="#">P07738</a> | Glycolysis/Gluconeogenesis<br>(hsa00010)<br>Glycine, serine and threonine<br>metabolism (hsa00260)<br>Metabolic pathways (hsa01100) | -2,00 | 3,36 | 2,30e-02 |
| <b>APOC3</b> | Apolipoprotein C3          | <a href="#">345</a>    | <a href="#">P02656</a> | PPAR signaling pathway<br>(hsa03320)<br>Cholesterol metabolism (hsa04979)                                                           | -2,20 | 4,12 | 1,01e-02 |
| <b>APOC4</b> | Apolipoprotein C4          | <a href="#">346</a>    | <a href="#">P55056</a> | -                                                                                                                                   | -2,35 | 5,41 | 2,56e-03 |
| <b>CPA1</b>  | Carboxypeptidase A1        | <a href="#">1357</a>   | <a href="#">P15085</a> | Protein digestion and absorption<br>(hsa04974)<br>Pancreatic secretion (hsa04972)                                                   | -2,85 | 4,41 | 6,51e-03 |

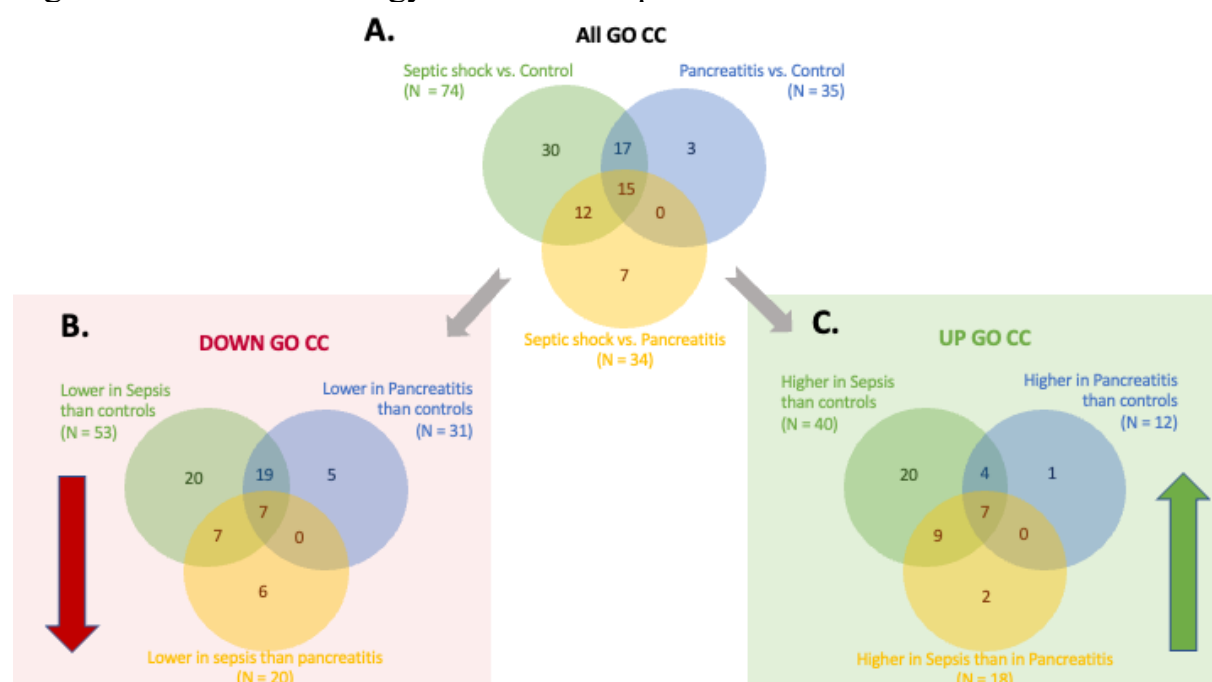
**Table S4.** Showing significantly altered protein in the comparison of Septic shock vs. Acute pancreatitis. Proteins classified as significantly altered if exhibiting a of log2 fold change > 0.5 or < -0.5 and an FDR adjusted p-value < 0.05. Tables showing gene symbol, gene name, NCBI gene ID, Uniprot ID, related KEGG pathways, log2 fold change, -log10 P-value and adjusted p-value. If more than 3 KEGG pathways associated to the protein the three most relevant were selected for the table.

Figure S1 – Gene Ontology Biological Process



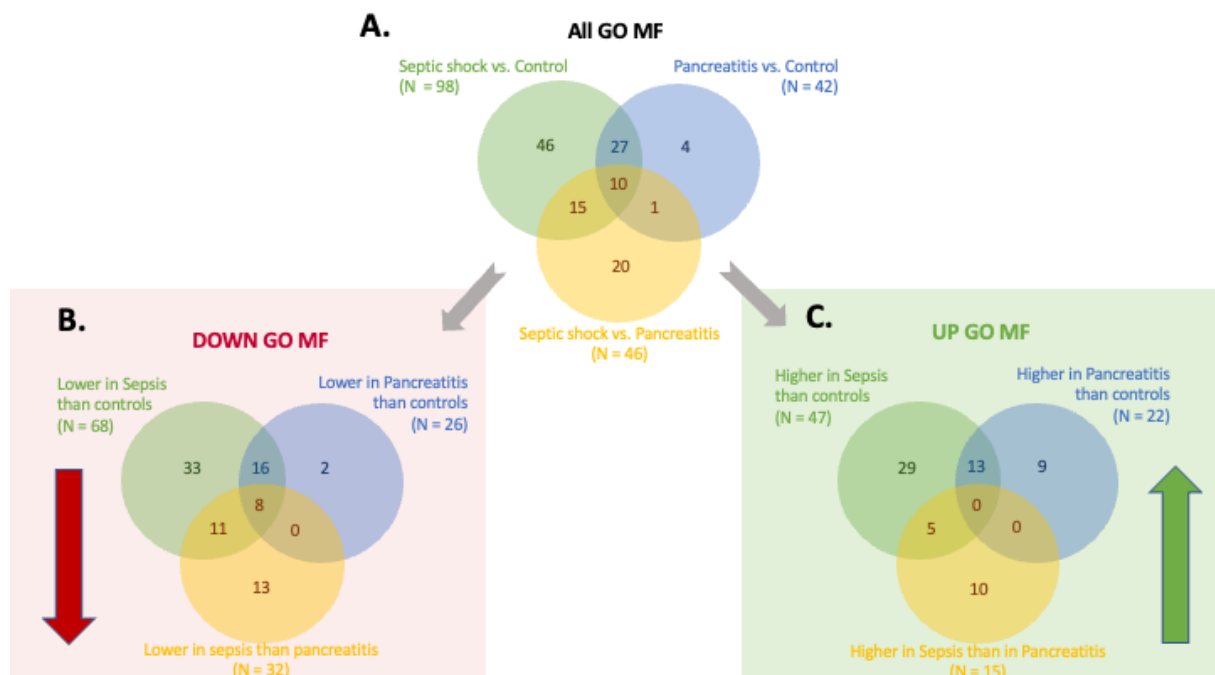
**Figure S1.** Venn diagrams showing the distribution of Gene Ontology (GO) domain Biological Process (BP) in plain numbers for the comparisons Septic shock vs. Control (green circles), Pancreatitis vs. Control (blue circles) and Septic shock vs. Pancreatitis (yellow circles). Numbers in the overlapping areas representing terms significantly altered in multiple comparisons. **A.** Terms enriched from all significantly altered proteins. **B.** Terms enriched from significantly downregulated proteins. **C.** Terms enriched from significantly upregulated proteins.

Figure S2 – Gene Ontology Cellular Component



**Figure S2.** Venn diagrams showing the distribution of Gene Ontology (GO) domain Cellular Component (CC) in plain numbers for the comparisons Septic shock vs. Control (green circles), Pancreatitis vs. Control (blue circles) and Septic shock vs. Pancreatitis (yellow circles). Numbers in the overlapping areas representing terms significantly altered in multiple comparisons. **A.** Terms enriched from all significantly altered proteins. **B.** Terms enriched from significantly downregulated proteins. **C.** Terms enriched from significantly upregulated proteins.

Figure S3 – Gene Ontology Molecular Function



**Figure S3.** Venn diagrams showing the distribution of Gene Ontology (GO) domain Molecular Function (MF) in plain numbers for the comparisons Septic shock vs. Control (green circles), Pancreatitis vs. Control (blue circles) and Septic shock vs. Pancreatitis (yellow circles). Numbers in the overlapping areas representing terms significantly altered in multiple comparisons. **A.** Terms enriched from all significantly altered proteins. **B.** Terms enriched from significantly downregulated proteins. **C.** Terms enriched from significantly upregulated proteins.

Table S5a – Gene Ontology Sepsis vs Control Up

| Description                                              | Ontology | geneID                                                                                                     | Protein Count | Adjusted P-value |
|----------------------------------------------------------|----------|------------------------------------------------------------------------------------------------------------|---------------|------------------|
| <b>acute-phase response</b>                              | BP       | CD163, CRP, F8, LBP, ORM1, SAA1, SAA2, SERPINA3                                                            | 8             | 7,57E-07         |
| <b>collagen metabolic process</b>                        | BP       | COL1A1, COL1A2, COL5A1, COL6A1, CST3, CTSB, CTSN, MMP8, MMP9, VIM                                          | 10            | 1,16E-06         |
| <b>regulation of inflammatory response</b>               | BP       | DDT, GRN, IL1RL1, LBP, MMP8, MMP9, PLA2G2A, PSMA1, PSMA6, PSMB4, S100A12, S100A8, S100A9, SAA1, SIRPA, TNC | 16            | 4,66E-06         |
| <b>extracellular matrix organization</b>                 | BP       | ADAMTSL2, COL11A2, COL1A1, COL1A2, COL2A1, COL5A1, COL6A1, CST3, LAMB1, LAMC1, LCP1, MMP8, MMP9, NID1      | 14            | 5,12E-06         |
| <b>extracellular structure organization</b>              | BP       | ADAMTSL2, COL11A2, COL1A1, COL1A2, COL2A1, COL5A1, COL6A1, CST3, LAMB1, LAMC1, LCP1, MMP8, MMP9, NID1      | 14            | 5,12E-06         |
| <b>external encapsulating structure organization</b>     | BP       | ADAMTSL2, COL11A2, COL1A1, COL1A2, COL2A1, COL5A1, COL6A1, CST3, LAMB1, LAMC1, LCP1, MMP8, MMP9, NID1      | 14            | 5,12E-06         |
| <b>regulation of integrin-mediated signaling pathway</b> | BP       | CD177, LAMB1, LAMC1, NID1, TIMP1                                                                           | 5             | 3,67E-05         |
| <b>response to lipopolysaccharide</b>                    | BP       | B2M, COL6A1, IL18BP, LBP, MMP8, MMP9, MPO, MRC1,                                                           | 13            | 4,72E-05         |

|                                                       |    |                                                                                      |    |             |
|-------------------------------------------------------|----|--------------------------------------------------------------------------------------|----|-------------|
|                                                       |    | S100A8, SIRPA, SOD2, VCAM1, VIM                                                      |    |             |
| <b>acute inflammatory response</b>                    | BP | CD163, CRP, F8, LBP, ORM1, SAA1, SAA2, SERPINA3                                      | 8  | 6,73E-05    |
| <b>response to molecule of bacterial origin</b>       | BP | B2M, COL6A1, IL18BP, LBP, MMP8, MMP9, MPO, MRC1, S100A8, SIRPA, SOD2, VCAM1, VIM     | 13 | 7,30E-05    |
| <b>positive regulation of inflammatory response</b>   | BP | DDT, GRN, IL1RL1, LBP, MMP8, PLA2G2A, S100A12, S100A8, S100A9                        | 9  | 9,74E-05    |
| <b>regulation of peptidase activity</b>               | BP | CAST, CST3, CTSD, GRN, ITIH3, MMP9, PSMA3, S100A8, S100A9, SERPINA3, SERPINB1, TIMP1 | 12 | 0,000175299 |
| <b>respiratory burst involved in defense response</b> | BP | GRN, LBP, MPO, S100A9                                                                | 4  | 0,000409484 |
| <b>collagen fibril organization</b>                   | BP | COL11A2, COL1A1, COL1A2, COL2A1, COL5A1, COL6A1                                      | 6  | 0,000629281 |
| <b>collagen catabolic process</b>                     | BP | CST3, CTSB, CTSL, MMP8, MMP9                                                         | 5  | 0,000918627 |
| <b>leukocyte cell-cell adhesion</b>                   | BP | B2M, CD177, FGL2, ICAM1, LRG1, S100A8, S100A9, SIRPA, SIRPB1, VCAM1, VSIG4, YWHAG    | 12 | 0,001169984 |
| <b>protein folding</b>                                | BP | B2M, CALR, GRN, HSP90AA1, HSP90AB1, HSPA4, HSPA8, PDIA4, TRAP1                       | 9  | 0,001169984 |
| <b>endoderm development</b>                           | BP | COL5A1, COL6A1, LAMB1, LAMC1, MMP8, MMP9                                             | 6  | 0,001414478 |
| <b>negative regulation of proteolysis</b>             | BP | CAST, CST3, CTSZ, HSP90AB1, IL1R2, ITIH3, MMP9, SERPINA3, SERPINB1, TIMP1            | 10 | 0,001414478 |
| <b>endodermal cell differentiation</b>                | BP | COL5A1, COL6A1, LAMB1, MMP8, MMP9                                                    | 5  | 0,001417831 |

|                                                                   |    |                                                                           |    |             |
|-------------------------------------------------------------------|----|---------------------------------------------------------------------------|----|-------------|
| <b>regulation of endopeptidase activity</b>                       | BP | CAST, CTSD, MMP9, PSMA3, S100A8, S100A9, SERPINA3, SERPINB1, TIMP1        | 9  | 0,001668323 |
| <b>respiratory burst involved in inflammatory response</b>        | BP | GRN, LBP, S100A9                                                          | 3  | 0,002168082 |
| <b>glucose 6-phosphate metabolic process</b>                      | BP | GPI, PGD, TALDO1, TKT                                                     | 4  | 0,002179953 |
| <b>response to reactive oxygen species</b>                        | BP | COL1A1, COL6A1, HSPA8, IL18BP, MPO, SIRPA, SOD2, TRAP1                    | 8  | 0,002179953 |
| <b>leukocyte migration</b>                                        | BP | CALR, CD177, DDT, ICAM1, LBP, S100A12, S100A8, S100A9, SAA1, SIRPA, VCAM1 | 11 | 0,002303874 |
| <b>endoderm formation</b>                                         | BP | COL5A1, COL6A1, LAMB1, MMP8, MMP9                                         | 5  | 0,002303874 |
| <b>regulation of macrophage activation</b>                        | BP | GRN, IL1RL1, LBP, MMP8, VSIG4                                             | 5  | 0,002303874 |
| <b>regulation of basement membrane organization</b>               | BP | LAMB1, LAMC1, NID1                                                        | 3  | 0,002316807 |
| <b>regulation of immune effector process</b>                      | BP | B2M, CD177, FGL2, GPI, GRN, HSPA8, ICAM1, LBP, S100A9, VSIG4, YWHAG       | 11 | 0,002316807 |
| <b>defense response to bacterium</b>                              | BP | B2M, CRP, GRN, LBP, LCN2, MPO, PLA2G2A, S100A12, S100A8, S100A9           | 10 | 0,002522087 |
| <b>extracellular matrix disassembly</b>                           | BP | CST3, LAMC1, LCP1, MMP8, MMP9                                             | 5  | 0,002684193 |
| <b>positive regulation of integrin-mediated signaling pathway</b> | BP | LAMB1, LAMC1, NID1                                                        | 3  | 0,002684193 |
| <b>neutrophil migration</b>                                       | BP | CD177, LBP, S100A12, S100A8, S100A9, SAA1                                 | 6  | 0,002684193 |
| <b>regulation of nitric oxide biosynthetic process</b>            | BP | ASL, HSP90AA1, HSP90AB1, SIRPA, SOD2                                      | 5  | 0,002684193 |
| <b>regulation of nitric oxide metabolic process</b>               | BP | ASL, HSP90AA1, HSP90AB1, SIRPA, SOD2                                      | 5  | 0,002938872 |

|                                                                 |    |                                                         |   |             |
|-----------------------------------------------------------------|----|---------------------------------------------------------|---|-------------|
| <b>integrin-mediated signaling pathway</b>                      | BP | CCN2, CD177, LAMB1, LAMC1, NID1, TIMP1                  | 6 | 0,002938872 |
| <b>respiratory system development</b>                           | BP | ADAMTSL2, BASP1, CCN2, CHI3L1, COL6A1, CTSZ, LTA4H, TNC | 8 | 0,003260604 |
| <b>antigen processing and presentation</b>                      | BP | B2M, CALR, CTSD, CTSL, FGL2, ICAM1                      | 6 | 0,003720587 |
| <b>basement membrane organization</b>                           | BP | COL6A1, LAMB1, LAMC1, NID1                              | 4 | 0,003720587 |
| <b>pyridine nucleotide metabolic process</b>                    | BP | ALDOA, COL6A1, GPI, PGD, PGK1, TALDO1, TKT              | 7 | 0,003720587 |
| <b>nicotinamide nucleotide metabolic process</b>                | BP | ALDOA, COL6A1, GPI, PGD, PGK1, TALDO1, TKT              | 7 | 0,003720587 |
| <b>regulation of extracellular matrix organization</b>          | BP | COL6A1, CST3, LAMB1, LAMC1, NID1                        | 5 | 0,003771437 |
| <b>respiratory burst</b>                                        | BP | GRN, LBP, MPO, S100A9                                   | 4 | 0,004277686 |
| <b>pyridine-containing compound metabolic process</b>           | BP | ALDOA, COL6A1, GPI, PGD, PGK1, TALDO1, TKT              | 7 | 0,00429866  |
| <b>reactive oxygen species metabolic process</b>                | BP | CCN2, CD177, COL6A1, CRP, MPO, SIRPA, SOD2, TRAP1       | 8 | 0,004456658 |
| <b>myeloid leukocyte migration</b>                              | BP | CD177, DDT, LBP, S100A12, S100A8, S100A9, SAA1, SIRPA   | 8 | 0,004486135 |
| <b>positive regulation of nitric oxide biosynthetic process</b> | BP | ASL, HSP90AA1, HSP90AB1, SOD2                           | 4 | 0,004749526 |
| <b>myeloid leukocyte activation</b>                             | BP | CD177, GRN, IL1RL1, LBP, MMP8, PLA2G2A, S100A12, VSIG4  | 8 | 0,00481307  |
| <b>nitric oxide biosynthetic process</b>                        | BP | ASL, HSP90AA1, HSP90AB1, SIRPA, SOD2                    | 5 | 0,004899976 |
| <b>positive regulation of nitric oxide metabolic process</b>    | BP | ASL, HSP90AA1, HSP90AB1, SOD2                           | 4 | 0,004899976 |
| <b>astrocyte development</b>                                    | BP | GRN, S100A8, S100A9, VIM                                | 4 | 0,005260157 |
| <b>formation of primary germ layer</b>                          | BP | COL5A1, COL6A1, GPI, LAMB1, MMP8, MMP9                  | 6 | 0,005318066 |
| <b>neutrophil chemotaxis</b>                                    | BP | LBP, S100A12, S100A8, S100A9, SAA1                      | 5 | 0,005777895 |

|                                                              |    |                                                              |   |             |
|--------------------------------------------------------------|----|--------------------------------------------------------------|---|-------------|
| <b>negative regulation of peptidase activity</b>             | BP | CAST, CST3, ITIH3, MMP9, SERPINA3, SERPINB1, TIMP1           | 7 | 0,00661418  |
| <b>lung development</b>                                      | BP | ADAMTSL2, CCN2, CHI3L1, COL6A1, CTSZ, LTA4H, TNC             | 7 | 0,00661418  |
| <b>regulation of respiratory burst</b>                       | BP | GRN, LBP, S100A9                                             | 3 | 0,00661418  |
| <b>nitric oxide metabolic process</b>                        | BP | ASL, HSP90AA1, HSP90AB1, SIRPA, SOD2                         | 5 | 0,006671354 |
| <b>respiratory tube development</b>                          | BP | ADAMTSL2, CCN2, CHI3L1, COL6A1, CTSZ, LTA4H, TNC             | 7 | 0,007112649 |
| <b>reactive nitrogen species metabolic process</b>           | BP | ASL, HSP90AA1, HSP90AB1, SIRPA, SOD2                         | 5 | 0,007112649 |
| <b>leukocyte migration involved in inflammatory response</b> | BP | LBP, S100A8, S100A9                                          | 3 | 0,007112649 |
| <b>pentose-phosphate shunt</b>                               | BP | PGD, TALDO1, TKT                                             | 3 | 0,007112649 |
| <b>chronic inflammatory response</b>                         | BP | S100A8, S100A9, VCAM1                                        | 3 | 0,007935065 |
| <b>cartilage development</b>                                 | BP | CCN2, CHI3L1, COL11A2, COL1A1, COL2A1, COL6A1, TIMP1         | 7 | 0,007935065 |
| <b>cellular response to reactive oxygen species</b>          | BP | HSPA8, IL18BP, MPO, SIRPA, SOD2, TRAP1                       | 6 | 0,007935065 |
| <b>response to zinc ion</b>                                  | BP | LTA4H, S100A8, SOD2, VCAM1                                   | 4 | 0,007935065 |
| <b>response to hydrogen peroxide</b>                         | BP | COL1A1, HSPA8, IL18BP, SIRPA, SOD2                           | 5 | 0,009471128 |
| <b>NADPH regeneration</b>                                    | BP | PGD, TALDO1, TKT                                             | 3 | 0,009930045 |
| <b>granulocyte migration</b>                                 | BP | CD177, LBP, S100A12, S100A8, S100A9, SAA1                    | 6 | 0,009961991 |
| <b>connective tissue development</b>                         | BP | CCN2, CHI3L1, COL11A2, COL1A1, COL2A1, COL5A1, COL6A1, TIMP1 | 8 | 0,009961991 |
| <b>chaperone-mediated protein complex assembly</b>           | BP | HSP90AA1, HSP90AB1, HSPA4                                    | 3 | 0,010815285 |
| <b>cellular response to lipopolysaccharide</b>               | BP | B2M, LBP, MMP8, MMP9, MRC1, SIRPA, VIM                       | 7 | 0,012135696 |



|                                                                                          |    |                                                                         |    |             |
|------------------------------------------------------------------------------------------|----|-------------------------------------------------------------------------|----|-------------|
| <b>production of molecular mediator involved in inflammatory response</b>                | BP | GRN, IL1R2, LBP, S100A9, SIRPA                                          | 5  | 0,012427428 |
| <b>proteasome-mediated ubiquitin-dependent protein catabolic process</b>                 | BP | HSP90AB1, PSMA1, PSMA3, PSMA4, PSMA5, PSMA6, PSMA7, PSMB2, PSMB3, PSMB4 | 10 | 0,013049328 |
| <b>negative regulation of endopeptidase activity</b>                                     | BP | CAST, MMP9, SERPINA3, SERPINB1, TIMP1                                   | 5  | 0,013163627 |
| <b>embryo implantation</b>                                                               | BP | CALR, MMP9, SPP1, TIMP1                                                 | 4  | 0,013537971 |
| <b>protein refolding</b>                                                                 | BP | B2M, HSP90AA1, HSPA8                                                    | 3  | 0,01421002  |
| <b>macrophage activation</b>                                                             | BP | GRN, IL1RL1, LBP, MMP8, VSIG4                                           | 5  | 0,014323321 |
| <b>leukocyte chemotaxis</b>                                                              | BP | CALR, DDT, LBP, S100A12, S100A8, S100A9, SAA1                           | 7  | 0,014993679 |
| <b>cellular response to molecule of bacterial origin</b>                                 | BP | B2M, LBP, MMP8, MMP9, MRC1, SIRPA, VIM                                  | 7  | 0,015549288 |
| <b>defense response to fungus</b>                                                        | BP | MPO, S100A12, S100A8, S100A9                                            | 4  | 0,0170454   |
| <b>negative regulation of protein processing</b>                                         | BP | CAST, CTSZ, IL1R2                                                       | 3  | 0,018044959 |
| <b>positive regulation of macrophage activation</b>                                      | BP | IL1RL1, LBP, MMP8                                                       | 3  | 0,018044959 |
| <b>cellular response to heat</b>                                                         | BP | HSP90AA1, HSP90AB1, HSPA8, YWHAE                                        | 4  | 0,018343168 |
| <b>cell chemotaxis</b>                                                                   | BP | CALR, DDT, LBP, S100A12, S100A8, S100A9, SAA1, VCAM1                    | 8  | 0,018343168 |
| <b>negative regulation of hydrolase activity</b>                                         | BP | CAST, CST3, ITIH3, MMP9, SERPINA3, SERPINB1, TIMP1                      | 7  | 0,018343168 |
| <b>positive regulation of cell adhesion</b>                                              | BP | B2M, CALR, LAMB1, LAMC1, NID1, SAA1, SIRPA, SIRPB1, VCAM1, YWHAG        | 10 | 0,018463635 |
| <b>antigen processing and presentation of exogenous peptide antigen via MHC class II</b> | BP | B2M, CTSD, CTSL                                                         | 3  | 0,01874889  |

|                                                                                |    |                                                      |   |             |
|--------------------------------------------------------------------------------|----|------------------------------------------------------|---|-------------|
| <b>antigen processing and presentation of peptide antigen</b>                  | BP | B2M, CALR, CTSD, CTSL                                | 4 | 0,019912519 |
| <b>carbohydrate derivative catabolic process</b>                               | BP | ALDOA, CHI3L1, COL6A1, CST3, CTSL, GPI, PGK1         | 7 | 0,019912519 |
| <b>negative regulation of protein maturation</b>                               | BP | CAST, CTSZ, IL1R2                                    | 3 | 0,019912519 |
| <b>positive regulation of phagocytosis</b>                                     | BP | CALR, HSPA8, SIRPA, SIRPB1                           | 4 | 0,020705241 |
| <b>monosaccharide metabolic process</b>                                        | BP | ALDOA, GOT1, GPI, GSTO1, IGFBP4, PGD, PGK1           | 7 | 0,021269851 |
| <b>positive regulation of reactive oxygen species metabolic process</b>        | BP | CD177, CRP, SIRPA, SOD2                              | 4 | 0,021320352 |
| <b>cellular extravasation</b>                                                  | BP | CD177, ICAM1, SIRPA, VCAM1                           | 4 | 0,021624455 |
| <b>response to ethanol</b>                                                     | BP | HSPA8, S100A8, SOD2, TNC, VCAM1                      | 5 | 0,021624455 |
| <b>granulocyte chemotaxis</b>                                                  | BP | LBP, S100A12, S100A8, S100A9, SAA1                   | 5 | 0,021624455 |
| <b>response to metal ion</b>                                                   | BP | B2M, CALR, GPI, HSPA8, LTA4H, S100A8, SOD2, VCAM1    | 8 | 0,021624455 |
| <b>maintenance of location</b>                                                 | BP | CALR, CRP, GSTO1, NPC2, PLIN3, S100A8, S100A9, YWHAE | 8 | 0,021624455 |
| <b>interleukin-1 production</b>                                                | BP | IL1R2, ORM1, SAA1, SERPINB1, SIRPA                   | 5 | 0,021624455 |
| <b>regulation of interleukin-1 production</b>                                  | BP | IL1R2, ORM1, SAA1, SERPINB1, SIRPA                   | 5 | 0,021624455 |
| <b>chaperone-mediated protein folding</b>                                      | BP | HSP90AB1, HSPA8, PDIA4, TRAP1                        | 4 | 0,021691265 |
| <b>cellular response to biotic stimulus</b>                                    | BP | B2M, LBP, MMP8, MMP9, MRC1, SIRPA, VIM               | 7 | 0,022333657 |
| <b>superoxide metabolic process</b>                                            | BP | CD177, CRP, MPO, SOD2                                | 4 | 0,022333657 |
| <b>antigen processing and presentation of peptide antigen via MHC class II</b> | BP | B2M, CTSD, CTSL                                      | 3 | 0,02244564  |

|                                                                                                  |    |                                                               |   |             |
|--------------------------------------------------------------------------------------------------|----|---------------------------------------------------------------|---|-------------|
| <b>negative regulation of response to external stimulus</b>                                      | BP | DDT, FGL2, GRN, PSMA1, PSMB4, SAA1, SIRPA, SPP1, VSIG4        | 9 | 0,022770751 |
| <b>response to fungus</b>                                                                        | BP | MPO, S100A12, S100A8, S100A9                                  | 4 | 0,022770751 |
| <b>gastrulation</b>                                                                              | BP | COL5A1, COL6A1, GPI, LAMB1, MMP8, MMP9                        | 6 | 0,024253817 |
| <b>glial cell development</b>                                                                    | BP | COL6A1, GRN, S100A8, S100A9, VIM                              | 5 | 0,024253817 |
| <b>antimicrobial humoral immune response mediated by antimicrobial peptide</b>                   | BP | B2M, REG1A, REG1B, S100A12, S100A9                            | 5 | 0,024253817 |
| <b>antigen processing and presentation of peptide or polysaccharide antigen via MHC class II</b> | BP | B2M, CTSD, CTSL                                               | 3 | 0,024976538 |
| <b>response to peptide hormone</b>                                                               | BP | COL1A1, COL6A1, CTSD, GOT1, LTA4H, REG1A, REG1B, TIMP1, YWHAG | 9 | 0,025006603 |
| <b>cell-substrate adhesion</b>                                                                   | BP | CALR, CCN2, COL1A1, LAMB1, LAMC1, NID1, VCAM1, VWF            | 8 | 0,025493205 |
| <b>regulation of toll-like receptor signaling pathway</b>                                        | BP | S100A8, S100A9, YWHAE                                         | 3 | 0,026267981 |
| <b>negative regulation of immune response</b>                                                    | BP | FGL2, GRN, IL1RL1, PSMA1, PSMB4, VSIG4                        | 6 | 0,026267981 |
| <b>adhesion of symbiont to host cell</b>                                                         | BP | HSP90AB1, ICAM1                                               | 2 | 0,026581499 |
| <b>positive regulation of muscle cell differentiation</b>                                        | BP | LAMB1, LAMC1, NID1, SOD2                                      | 4 | 0,027388483 |
| <b>ossification</b>                                                                              | BP | CCN2, COL1A1, COL1A2, COL2A1, COL6A1, RRBPI, SPP1, TNC, VCAN  | 9 | 0,027624868 |
| <b>endothelial cell migration</b>                                                                | BP | CALR, EPHB4, FSTL1, GPI, GRN, S100A12, S100A9                 | 7 | 0,028005217 |
| <b>positive regulation of leukocyte activation</b>                                               | BP | B2M, IL1RL1, LBP, MMP8, SIRPA, SIRPB1, VCAM1, YWHAG           | 8 | 0,028493331 |

|                                                                         |    |                                                              |   |             |
|-------------------------------------------------------------------------|----|--------------------------------------------------------------|---|-------------|
| <b>response to axon injury</b>                                          | BP | GRN, SOD2, SPP1, TNC                                         | 4 | 0,028874521 |
| <b>antigen processing and presentation of exogenous peptide antigen</b> | BP | B2M, CTSD, CTSL                                              | 3 | 0,03025745  |
| <b>regulation of neuroinflammatory response</b>                         | BP | GRN, MMP8, MMP9                                              | 3 | 0,03025745  |
| <b>cellular response to UV-A</b>                                        | BP | MMP9, TIMP1                                                  | 2 | 0,03025745  |
| <b>negative regulation of defense response</b>                          | BP | FGL2, GRN, PSMA1, PSMB4, SAA1, SIRPA, VSIG4                  | 7 | 0,032351759 |
| <b>chemotaxis</b>                                                       | BP | CALR, DDT, LBP, S100A12, S100A8, S100A9, SAA1, SEMA4B, VCAM1 | 9 | 0,03249319  |
| <b>astrocyte differentiation</b>                                        | BP | GRN, S100A8, S100A9, VIM                                     | 4 | 0,03249319  |
| <b>taxis</b>                                                            | BP | CALR, DDT, LBP, S100A12, S100A8, S100A9, SAA1, SEMA4B, VCAM1 | 9 | 0,03310743  |
| <b>response to mechanical stimulus</b>                                  | BP | CHI3L1, COL1A1, COL6A1, GPI, MPO, TNC                        | 6 | 0,033302001 |
| <b>regulation of reactive oxygen species metabolic process</b>          | BP | CD177, CRP, SIRPA, SOD2, TRAP1                               | 5 | 0,033701983 |
| <b>glyceraldehyde-3-phosphate metabolic process</b>                     | BP | TALDO1, TKT                                                  | 2 | 0,033701983 |
| <b>skin morphogenesis</b>                                               | BP | COL1A1, COL1A2                                               | 2 | 0,033701983 |
| <b>cellular response to thyroid hormone stimulus</b>                    | BP | CTSB, CTSL                                                   | 2 | 0,033701983 |
| <b>neutrophil activation</b>                                            | BP | CD177, GRN, PLA2G2A                                          | 3 | 0,034162982 |
| <b>response to vitamin</b>                                              | BP | COL1A1, SOD2, SPP1, TNC                                      | 4 | 0,034439929 |
| <b>positive regulation of cell activation</b>                           | BP | B2M, IL1RL1, LBP, MMP8, SIRPA, SIRPB1, VCAM1, YWHAG          | 8 | 0,034809022 |
| <b>response to testosterone</b>                                         | BP | CALR, GPI, SPP1                                              | 3 | 0,035125287 |
| <b>superoxide anion generation</b>                                      | BP | CD177, CRP, SOD2                                             | 3 | 0,035125287 |
| <b>lung epithelium development</b>                                      | BP | ADAMTSL2, COL6A1, LTA4H                                      | 3 | 0,035125287 |
| <b>humoral immune response</b>                                          | BP | B2M, GPI, REG1A, REG1B, S100A12, S100A9, VSIG4               | 7 | 0,035498025 |
| <b>NADP metabolic process</b>                                           | BP | PGD, TALDO1, TKT                                             | 3 | 0,035498025 |

|                                                                                                                    |    |                                                         |   |             |
|--------------------------------------------------------------------------------------------------------------------|----|---------------------------------------------------------|---|-------------|
| <b>glycolytic process</b>                                                                                          | BP | ALDOA, COL6A1, GPI, PGK1                                | 4 | 0,035498025 |
| <b>monosaccharide biosynthetic process</b>                                                                         | BP | GOT1, GPI, PGD, PGK1                                    | 4 | 0,035498025 |
| <b>mononuclear cell migration</b>                                                                                  | BP | CALR, DDT, ICAM1, S100A12, SAA1, SIRPA                  | 6 | 0,035498025 |
| <b>fructose 6-phosphate metabolic process</b>                                                                      | BP | GPI, TALDO1                                             | 2 | 0,035498025 |
| <b>adhesion of symbiont to host</b>                                                                                | BP | HSP90AB1, ICAM1                                         | 2 | 0,035498025 |
| <b>leukocyte aggregation</b>                                                                                       | BP | S100A8, S100A9                                          | 2 | 0,035498025 |
| <b>positive regulation of endocytosis</b>                                                                          | BP | B2M, CALR, HSPA8, SIRPA, SIRPB1                         | 5 | 0,035498025 |
| <b>generation of precursor metabolites and energy</b>                                                              | BP | ALDOA, COL6A1, GPI, PGD, PGK1, SOD2, TALDO1, TKT, TRAP1 | 9 | 0,035498025 |
| <b>ADP catabolic process</b>                                                                                       | BP | ALDOA, COL6A1, GPI, PGK1                                | 4 | 0,037459797 |
| <b>regulation of apoptotic signaling pathway</b>                                                                   | BP | COL2A1, CTSL, ICAM1, MMP9, S100A8, S100A9, SOD2, TRAP1  | 8 | 0,037712419 |
| <b>protein tetramerization</b>                                                                                     | BP | ALDOA, B2M, COL6A1, SOD2                                | 4 | 0,037948091 |
| <b>cellular oxidant detoxification</b>                                                                             | BP | GSTO1, MPO, S100A9, SOD2                                | 4 | 0,037948091 |
| <b>response to oxidative stress</b>                                                                                | BP | COL1A1, COL6A1, HSPA8, IL18BP, MPO, SIRPA, SOD2, TRAP1  | 8 | 0,037948091 |
| <b>pyridine nucleotide catabolic process</b>                                                                       | BP | ALDOA, COL6A1, GPI, PGK1                                | 4 | 0,037948091 |
| <b>T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell</b> | BP | FGL2, ICAM1                                             | 2 | 0,037948091 |
| <b>outer mitochondrial membrane organization</b>                                                                   | BP | HSP90AA1, HSPA4                                         | 2 | 0,037948091 |
| <b>protein insertion into mitochondrial outer membrane</b>                                                         | BP | HSP90AA1, HSPA4                                         | 2 | 0,037948091 |
| <b>positive regulation of striated muscle contraction</b>                                                          | BP | GSTO1, HSP90AA1                                         | 2 | 0,037948091 |

|                                                                 |    |                                                         |   |             |
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| <b>actin crosslink formation</b>                                | BP | LCP1, MARCKS                                            | 2 | 0,037948091 |
| <b>response to UV-A</b>                                         | BP | MMP9, TIMP1                                             | 2 | 0,037948091 |
| <b>phagocytosis</b>                                             | BP | CALR, CRP, HSPA8, LBP, SIRPA, SIRPB1                    | 6 | 0,037948091 |
| <b>purine nucleoside diphosphate catabolic process</b>          | BP | ALDOA, COL6A1, GPI, PGK1                                | 4 | 0,037948091 |
| <b>purine ribonucleoside diphosphate catabolic process</b>      | BP | ALDOA, COL6A1, GPI, PGK1                                | 4 | 0,037948091 |
| <b>muscle cell apoptotic process</b>                            | BP | COL6A1, HSP90AA1, HSPA8, SOD2                           | 4 | 0,037948091 |
| <b>regulation of phagocytosis</b>                               | BP | CALR, HSPA8, SIRPA, SIRPB1                              | 4 | 0,038995289 |
| <b>regulation of cysteine-type endopeptidase activity</b>       | BP | CAST, CTSD, MMP9, S100A8, S100A9                        | 5 | 0,038995289 |
| <b>antigen processing and presentation of exogenous antigen</b> | BP | B2M, CTSD, CTSL                                         | 3 | 0,039237856 |
| <b>response to nutrient</b>                                     | BP | COL1A1, SOD2, SPP1, TNC, VCAM1                          | 5 | 0,039517214 |
| <b>pyridine-containing compound catabolic process</b>           | BP | ALDOA, COL6A1, GPI, PGK1                                | 4 | 0,039517214 |
| <b>positive regulation of response to biotic stimulus</b>       | BP | GRN, HSP90AA1, HSPA8, LBP, S100A8, S100A9, YWHAE, YWHAG | 8 | 0,039746496 |
| <b>ribonucleoside diphosphate catabolic process</b>             | BP | ALDOA, COL6A1, GPI, PGK1                                | 4 | 0,039746496 |
| <b>ADP metabolic process</b>                                    | BP | ALDOA, COL6A1, GPI, PGK1                                | 4 | 0,039746496 |
| <b>response to cadmium ion</b>                                  | BP | GPI, HSPA8, SOD2                                        | 3 | 0,039746496 |
| <b>protein nitrosylation</b>                                    | BP | S100A8, S100A9                                          | 2 | 0,039746496 |
| <b>peptidyl-cysteine S-nitrosylation</b>                        | BP | S100A8, S100A9                                          | 2 | 0,039746496 |
| <b>chaperone-mediated autophagy</b>                             | BP | HSP90AA1, HSPA8                                         | 2 | 0,039746496 |
| <b>collagen biosynthetic process</b>                            | BP | COL1A1, COL5A1, VIM                                     | 3 | 0,04115296  |
| <b>granulocyte activation</b>                                   | BP | CD177, GRN, PLA2G2A                                     | 3 | 0,04115296  |
| <b>response to heat</b>                                         | BP | HSP90AA1, HSP90AB1, HSPA8, YWHAE                        | 4 | 0,041354636 |

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| <b>cellular response to oxidative stress</b>                                        | BP | HSPA8, IL18BP, MPO, SIRPA, SOD2, TRAP1                                                                                                                                                                                             | 6  | 0,043281215 |
| <b>nucleoside diphosphate catabolic process</b>                                     | BP | ALDOA, COL6A1, GPI, PGK1                                                                                                                                                                                                           | 4  | 0,043281215 |
| <b>positive regulation of tumor necrosis factor production</b>                      | BP | DDT, LBP, MMP8, ORM1                                                                                                                                                                                                               | 4  | 0,043281215 |
| <b>low-density lipoprotein particle remodeling</b>                                  | BP | MPO, PLA2G2A                                                                                                                                                                                                                       | 2  | 0,043281215 |
| <b>regulation of receptor binding</b>                                               | BP | B2M, MMP9                                                                                                                                                                                                                          | 2  | 0,043281215 |
| <b>axon regeneration</b>                                                            | BP | GRN, SPP1, TNC                                                                                                                                                                                                                     | 3  | 0,044059946 |
| <b>lung morphogenesis</b>                                                           | BP | COL6A1, CTSZ, TNC                                                                                                                                                                                                                  | 3  | 0,046152521 |
| <b>carbohydrate catabolic process</b>                                               | BP | ALDOA, COL6A1, GPI, PGD, PGK1                                                                                                                                                                                                      | 5  | 0,047284739 |
| <b>opsonization</b>                                                                 | BP | CRP, LBP                                                                                                                                                                                                                           | 2  | 0,047284739 |
| <b>negative regulation of macrophage activation</b>                                 | BP | GRN, VSIG4                                                                                                                                                                                                                         | 2  | 0,047284739 |
| <b>positive regulation of tumor necrosis factor superfamily cytokine production</b> | BP | DDT, LBP, MMP8, ORM1                                                                                                                                                                                                               | 4  | 0,047284739 |
| <b>response to amyloid-beta</b>                                                     | BP | ICAM1, MMP9, VCAM1                                                                                                                                                                                                                 | 3  | 0,047284739 |
| <b>purine nucleotide metabolic process</b>                                          | BP | ALDOA, COL6A1, GPI, HSPA8, PGD, PGK1, TALDO1, TKT                                                                                                                                                                                  | 8  | 0,049841848 |
| <b>osteoblast differentiation</b>                                                   | BP | COL1A1, COL6A1, RRBP1, SPP1, TNC, VCAN                                                                                                                                                                                             | 6  | 0,049841848 |
| <b>collagen-containing extracellular matrix</b>                                     | CC | CALR, CCN2, COL11A2, COL1A1, COL1A2, COL2A1, COL5A1, COL6A1, CTSB, CTSD, CTSL, CTSZ, FGL2, HSP90AA1, ICAM1, LAMB1, LAMC1, LGALS3BP, LTBP2, MMP8, MMP9, NID1, ORM1, PSAP, S100A8, S100A9, SERPINA3, SERPINB1, TIMP1, TNC, VCAN, VWF | 32 | 9,46E-25    |

|                                    |    |                                                                                                                                                                                             |    |          |
|------------------------------------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----|----------|
| <b>secretory granule lumen</b>     | CC | ALDOA, B2M, CHI3L1, CTSD, CTSZ, F8, GPI, GRN, HSP90AA1, HSP90AB1, HSPA8, ITIH3, LCN2, LGALS3BP, LRG1, MMP8, MPO, NPC2, ORM1, PSMA5, S100A12, S100A8, S100A9, SERPINA3, SERPINB1, TIMP1, VWF | 27 | 3,45E-22 |
| <b>cytoplasmic vesicle lumen</b>   | CC | ALDOA, B2M, CHI3L1, CTSD, CTSZ, F8, GPI, GRN, HSP90AA1, HSP90AB1, HSPA8, ITIH3, LCN2, LGALS3BP, LRG1, MMP8, MPO, NPC2, ORM1, PSMA5, S100A12, S100A8, S100A9, SERPINA3, SERPINB1, TIMP1, VWF | 27 | 3,45E-22 |
| <b>vesicle lumen</b>               | CC | ALDOA, B2M, CHI3L1, CTSD, CTSZ, F8, GPI, GRN, HSP90AA1, HSP90AB1, HSPA8, ITIH3, LCN2, LGALS3BP, LRG1, MMP8, MPO, NPC2, ORM1, PSMA5, S100A12, S100A8, S100A9, SERPINA3, SERPINB1, TIMP1, VWF | 27 | 3,45E-22 |
| <b>endoplasmic reticulum lumen</b> | CC | B2M, CALR, COL11A2, COL1A1, COL1A2, COL2A1, COL5A1, COL6A1, CST3, CTSZ, F8, FSTL1, GANAB, GOLM1, IGFBP4, LAMB1, LAMC1, NUCB1, PDIA4, PRKCSH, SPP1, TIMP1, TNC, VCAN                         | 24 | 5,87E-19 |
| <b>proteasome core complex</b>     | CC | PSMA1, PSMA3, PSMA4, PSMA5, PSMA6, PSMA7, PSMB2, PSMB3, PSMB4                                                                                                                               | 9  | 2,49E-14 |



|                                     |    |                                                                                                      |    |          |
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| <b>ficolin-1-rich granule lumen</b> | CC | ALDOA, CST3, CTSB, CTSD, CTSZ, FGL2, GPI, HSP90AA1, HSP90AB1, HSPA8, LRG1, LTA4H, MMP9, PSMA5        | 14 | 3,05E-13 |
| <b>ficolin-1-rich granule</b>       | CC | ALDOA, CST3, CTSB, CTSD, CTSZ, FGL2, GPI, HSP90AA1, HSP90AB1, HSPA8, LRG1, LTA4H, MMP9, PSMA5, SIRPA | 15 | 4,01E-12 |
| <b>tertiary granule lumen</b>       | CC | ALDOA, B2M, CST3, CTSD, LRG1, LTA4H, MMP8, MMP9, ORM1                                                | 9  | 5,33E-10 |
| <b>proteasome complex</b>           | CC | PSMA1, PSMA3, PSMA4, PSMA5, PSMA6, PSMA7, PSMB2, PSMB3, PSMB4                                        | 9  | 1,99E-09 |
| <b>specific granule lumen</b>       | CC | B2M, CHI3L1, CTSD, CTSZ, LCN2, LRG1, MMP8, ORM1                                                      | 8  | 4,20E-08 |
| <b>tertiary granule</b>             | CC | ALDOA, B2M, CD177, CST3, CTSD, LRG1, LTA4H, MMP8, MMP9, ORM1, SIRPA                                  | 11 | 4,20E-08 |
| <b>fibrillar collagen trimer</b>    | CC | COL11A2, COL1A1, COL1A2, COL2A1, COL5A1                                                              | 5  | 6,33E-08 |
| <b>banded collagen fibril</b>       | CC | COL11A2, COL1A1, COL1A2, COL2A1, COL5A1                                                              | 5  | 6,33E-08 |
| <b>endopeptidase complex</b>        | CC | PSMA1, PSMA3, PSMA4, PSMA5, PSMA6, PSMA7, PSMB2, PSMB3, PSMB4                                        | 9  | 6,47E-08 |
| <b>vacuolar lumen</b>               | CC | CTSB, CTSD, CTSB, GRN, HSP90AA1, HSPA8, MPO, NPC2, PSAP, SERPINA3, VCAN                              | 11 | 7,46E-08 |
| <b>peptidase complex</b>            | CC | PSMA1, PSMA3, PSMA4, PSMA5, PSMA6, PSMA7, PSMB2, PSMB3, PSMB4                                        | 9  | 6,21E-07 |
| <b>basement membrane</b>            | CC | COL2A1, COL5A1, COL6A1, LAMB1, LAMC1, NID1, TIMP1, TNC                                               | 8  | 6,21E-07 |

|                                                         |    |                                                                       |    |             |
|---------------------------------------------------------|----|-----------------------------------------------------------------------|----|-------------|
| <b>lysosomal lumen</b>                                  | CC | CTSB, CTSD, CTSL, HSP90AA1, HSPA8, NPC2, PSAP, VCAN                   | 8  | 9,67E-07    |
| <b>complex of collagen trimers</b>                      | CC | COL11A2, COL1A1, COL1A2, COL2A1, COL5A1                               | 5  | 1,09E-06    |
| <b>endocytic vesicle lumen</b>                          | CC | CALR, CTSL, HSP90AA1, MPO, SAA1                                       | 5  | 1,71E-06    |
| <b>melanosome</b>                                       | CC | CTSB, CTSD, GANAB, HSP90AA1, HSP90AB1, HSPA8, PDIA4, YWHAE            | 8  | 2,26E-06    |
| <b>pigment granule</b>                                  | CC | CTSB, CTSD, GANAB, HSP90AA1, HSP90AB1, HSPA8, PDIA4, YWHAE            | 8  | 2,26E-06    |
| <b>specific granule</b>                                 | CC | B2M, CD177, CHI3L1, CTSD, CTSZ, LCN2, LRG1, MMP8, ORM1                | 9  | 2,89E-06    |
| <b>platelet alpha granule lumen</b>                     | CC | ALDOA, F8, ORM1, SERPINA3, TIMP1, VWF                                 | 6  | 1,83E-05    |
| <b>protein complex involved in cell-matrix adhesion</b> | CC | LAMB1, LAMC1, NID1, TNC                                               | 4  | 1,83E-05    |
| <b>collagen trimer</b>                                  | CC | COL11A2, COL1A1, COL1A2, COL2A1, COL5A1, COL6A1                       | 6  | 7,53E-05    |
| <b>platelet alpha granule</b>                           | CC | ALDOA, F8, ORM1, SERPINA3, TIMP1, VWF                                 | 6  | 0,000100624 |
| <b>proteasome core complex, beta-subunit complex</b>    | CC | PSMB2, PSMB3, PSMB4                                                   | 3  | 0,000210441 |
| <b>focal adhesion</b>                                   | CC | B2M, CALR, HSPA8, ICAM1, IL1RL1, LCP1, MARCKS, TNC, VIM, YWHAE, YWHAG | 11 | 0,000210441 |
| <b>cell-substrate junction</b>                          | CC | B2M, CALR, HSPA8, ICAM1, IL1RL1, LCP1, MARCKS, TNC, VIM, YWHAE, YWHAG | 11 | 0,00025183  |
| <b>endosome lumen</b>                                   | CC | B2M, CTSB, CTSD, CTSL                                                 | 4  | 0,000420189 |
| <b>protein complex involved in cell adhesion</b>        | CC | LAMB1, LAMC1, NID1, TNC                                               | 4  | 0,002146759 |

|                                                                      |    |                                                  |   |             |
|----------------------------------------------------------------------|----|--------------------------------------------------|---|-------------|
| <b>endocytic vesicle</b>                                             | CC | B2M, CALR, CD163, CTSL, HSP90AA1, MPO, SAA1, VIM | 8 | 0,006087241 |
| <b>perisynaptic extracellular matrix</b>                             | CC | TNC, VCAN                                        | 2 | 0,010477486 |
| <b>azurophil granule lumen</b>                                       | CC | GRN, MPO, NPC2, SERPINA3                         | 4 | 0,010744609 |
| <b>primary lysosome</b>                                              | CC | GRN, MPO, NPC2, PSAP, SERPINA3                   | 5 | 0,010821846 |
| <b>azurophil granule</b>                                             | CC | GRN, MPO, NPC2, PSAP, SERPINA3                   | 5 | 0,010821846 |
| <b>synapse-associated extracellular matrix</b>                       | CC | TNC, VCAN                                        | 2 | 0,011241772 |
| <b>dendrite terminus</b>                                             | CC | HSP90AA1, HSP90AB1                               | 2 | 0,012905764 |
| <b>platelet dense granule lumen</b>                                  | CC | ITIH3, LGALS3BP                                  | 2 | 0,014286821 |
| <b>cytolytic granule</b>                                             | CC | CALR, SERPINB1                                   | 2 | 0,014286821 |
| <b>endoplasmic reticulum protein-containing complex</b>              | CC | B2M, CALR, GANAB, PRKCSH                         | 4 | 0,021635957 |
| <b>platelet dense granule</b>                                        | CC | ITIH3, LGALS3BP                                  | 2 | 0,030060211 |
| <b>nuclear matrix</b>                                                | CC | BASP1, LMNB1, PSMA6, VIM                         | 4 | 0,030060211 |
| <b>endoplasmic reticulum-Golgi intermediate compartment</b>          | CC | CALR, CTSZ, F8, NUCB1                            | 4 | 0,034446994 |
| <b>external side of plasma membrane</b>                              | CC | B2M, CALR, CD163, CTSB, ICAM1, IL1RL1, VCAM1     | 7 | 0,039110243 |
| <b>blood microparticle</b>                                           | CC | HSPA8, LGALS3BP, ORM1, SERPINA3                  | 4 | 0,041233789 |
| <b>phagocytic vesicle</b>                                            | CC | B2M, CALR, MPO, VIM                              | 4 | 0,041360625 |
| <b>high-density lipoprotein particle</b>                             | CC | SAA1, SAA2                                       | 2 | 0,044123642 |
| <b>endolysosome</b>                                                  | CC | CTSB, CTSL                                       | 2 | 0,045678155 |
| <b>endoplasmic reticulum-Golgi intermediate compartment membrane</b> | CC | CALR, CTSZ, F8                                   | 3 | 0,045678155 |
| <b>nuclear periphery</b>                                             | CC | BASP1, LMNB1, PSMA6, VIM                         | 4 | 0,04796847  |

|                                                                                |    |                                                                                                          |    |             |
|--------------------------------------------------------------------------------|----|----------------------------------------------------------------------------------------------------------|----|-------------|
| <b>extracellular matrix structural constituent</b>                             | MF | CHI3L1, COL11A2, COL1A1, COL1A2, COL2A1, COL5A1, COL6A1, FGL2, LAMB1, LAMC1, LTBP2, NID1, TNC, VCAN, VWF | 15 | 1,99E-11    |
| <b>platelet-derived growth factor binding</b>                                  | MF | COL1A1, COL1A2, COL2A1, COL5A1, COL6A1                                                                   | 5  | 4,45E-07    |
| <b>integrin binding</b>                                                        | MF | CALR, CCN2, CD177, COL5A1, ICAM1, LCP1, SPP1, TNC, VCAM1, VWF                                            | 10 | 4,37E-06    |
| <b>proteoglycan binding</b>                                                    | MF | COL2A1, COL5A1, CTSB, CTSL, NID1, TNC                                                                    | 6  | 5,71E-06    |
| <b>extracellular matrix structural constituent conferring tensile strength</b> | MF | COL11A2, COL1A1, COL1A2, COL2A1, COL5A1, COL6A1                                                          | 6  | 1,54E-05    |
| <b>MHC class II protein complex binding</b>                                    | MF | B2M, HSP90AA1, HSP90AB1, HSPA8, YWHAЕ                                                                    | 5  | 2,40E-05    |
| <b>carbohydrate binding</b>                                                    | MF | ALDOA, CALR, CHI3L1, GALNT2, GANAB, GPI, MRC1, REG1A, REG1B, TALDO1, VCAN                                | 11 | 4,00E-05    |
| <b>growth factor binding</b>                                                   | MF | CCN2, COL1A1, COL1A2, COL2A1, COL5A1, COL6A1, IGFBP4, LTBP2                                              | 8  | 4,59E-05    |
| <b>glycosaminoglycan binding</b>                                               | MF | CCN2, COL11A2, COL5A1, FSTL1, LTBP2, MPO, REG1A, REG1B, SAA1, VCAN                                       | 10 | 7,28E-05    |
| <b>MHC protein complex binding</b>                                             | MF | B2M, HSP90AA1, HSP90AB1, HSPA8, YWHAЕ                                                                    | 5  | 7,42E-05    |
| <b>collagen binding</b>                                                        | MF | COL6A1, CTSB, CTSL, MMP9, NID1, VWF                                                                      | 6  | 9,16E-05    |
| <b>ATP-dependent protein folding chaperone</b>                                 | MF | HSP90AA1, HSP90AB1, HSPA4, HSPA8, TRAP1                                                                  | 5  | 9,20E-05    |
| <b>protein folding chaperone</b>                                               | MF | CALR, HSP90AA1, HSP90AB1, HSPA4, HSPA8, TRAP1                                                            | 6  | 0,000126419 |

|                                             |    |                                                     |   |             |
|---------------------------------------------|----|-----------------------------------------------------|---|-------------|
| <b>RAGE receptor binding</b>                | MF | S100A12, S100A8, S100A9                             | 3 | 0,000660987 |
| <b>scaffold protein binding</b>             | MF | CD163, HSP90AA1, PSAP, VIM, YWHAE                   | 5 | 0,0011722   |
| <b>heparin binding</b>                      | MF | CCN2, COL11A2, COL5A1, FSTL1, LTBP2, MPO, SAA1      | 7 | 0,001628295 |
| <b>protease binding</b>                     | MF | CD177, COL1A1, COL1A2, CST3, PSAP, VWF              | 6 | 0,002801831 |
| <b>opsonin binding</b>                      | MF | CALR, CRP, VSIG4                                    | 3 | 0,003957337 |
| <b>sulfur compound binding</b>              | MF | CCN2, COL11A2, COL5A1, FSTL1, LTBP2, MPO, SAA1, TKT | 8 | 0,003957337 |
| <b>molecular sequestering activity</b>      | MF | CALR, LCN2, YWHAE, YWHAG                            | 4 | 0,00427553  |
| <b>complement binding</b>                   | MF | CALR, CRP, VSIG4                                    | 3 | 0,006500552 |
| <b>endopeptidase inhibitor activity</b>     | MF | CAST, CST3, ITIH3, SERPINA3, SERPINB1, TIMP1        | 6 | 0,006608907 |
| <b>peptidase regulator activity</b>         | MF | CAST, CST3, CTSL, ITIH3, SERPINA3, SERPINB1, TIMP1  | 7 | 0,006608907 |
| <b>extracellular matrix binding</b>         | MF | ADAMTSL2, LTBP2, NID1, SPP1                         | 4 | 0,007249274 |
| <b>peptidase inhibitor activity</b>         | MF | CAST, CST3, ITIH3, SERPINA3, SERPINB1, TIMP1        | 6 | 0,007559764 |
| <b>unfolded protein binding</b>             | MF | CALR, HSP90AA1, HSP90AB1, HSPA8, TRAP1              | 5 | 0,009036921 |
| <b>endopeptidase regulator activity</b>     | MF | CAST, CST3, ITIH3, SERPINA3, SERPINB1, TIMP1        | 6 | 0,010130214 |
| <b>monosaccharide binding</b>               | MF | ALDOA, GPI, MRC1, TALDO1                            | 4 | 0,010130214 |
| <b>calcium-dependent protein binding</b>    | MF | CD177, S100A12, S100A8, S100A9                      | 4 | 0,012480842 |
| <b>cysteine-type endopeptidase activity</b> | MF | CTSB, CTSD, CTSL, CTSZ                              | 4 | 0,015478668 |
| <b>disulfide oxidoreductase activity</b>    | MF | GSTO1, PDIA4, PGK1                                  | 3 | 0,015478668 |

|                                                                    |    |                                                     |   |             |
|--------------------------------------------------------------------|----|-----------------------------------------------------|---|-------------|
| <b>antioxidant activity</b>                                        | MF | GSTO1, MPO, S100A9, SOD2                            | 4 | 0,015478668 |
| <b>lipopolysaccharide binding</b>                                  | MF | LBP, PSMA1, PSMB4                                   | 3 | 0,015882203 |
| <b>ubiquitin protein ligase binding</b>                            | MF | CALR, GPI, HSP90AA1, HSP90AB1, HSPA8, PSMA3, YWHAE  | 7 | 0,018657237 |
| <b>Toll-like receptor binding</b>                                  | MF | S100A8, S100A9                                      | 2 | 0,020924335 |
| <b>ubiquitin-like protein ligase binding</b>                       | MF | CALR, GPI, HSP90AA1, HSP90AB1, HSPA8, PSMA3, YWHAE  | 7 | 0,025176116 |
| <b>protein kinase C binding</b>                                    | MF | MARCKS, PRKCSH, YWHAG                               | 3 | 0,027253845 |
| <b>carbon-carbon lyase activity</b>                                | MF | ALDOA, DDT, GOT1                                    | 3 | 0,027253845 |
| <b>intramolecular oxidoreductase activity</b>                      | MF | DDT, GPI, PDIA4                                     | 3 | 0,028025955 |
| <b>cadherin binding</b>                                            | MF | ALDOA, ARHGAP1, CAST, HSP90AB1, HSPA8, PLIN3, YWHAE | 7 | 0,02814708  |
| <b>oxidoreductase activity, acting on a sulfur group of donors</b> | MF | GSTO1, PDIA4, PGK1                                  | 3 | 0,029232093 |
| <b>long-chain fatty acid binding</b>                               | MF | S100A8, S100A9                                      | 2 | 0,029232093 |
| <b>oligosaccharide binding</b>                                     | MF | REG1A, REG1B                                        | 2 | 0,029232093 |
| <b>insulin-like growth factor binding</b>                          | MF | CCN2, IGFBP4                                        | 2 | 0,034846567 |
| <b>peptidoglycan binding</b>                                       | MF | REG1A, REG1B                                        | 2 | 0,034846567 |
| <b>DNA polymerase binding</b>                                      | MF | HSP90AA1, HSP90AB1                                  | 2 | 0,041157181 |
| <b>cargo receptor activity</b>                                     | MF | CD163, LGALS3BP, MRC1                               | 3 | 0,041157181 |

**Table S5a.** Showing enriched gene ontologies from upregulated DEPs in sepsis compared to control. BP=biological processes, CC=cellular compartments, MF=molecular functions. Ontologies classified as significantly altered if exhibiting an adjusted p-value < 0.05.

Table S5b – Gene Ontology Sepsis vs Control Down

| Description              | Ontology | geneID                                                                                                                                                              | Protein Count | Adjusted P-value |
|--------------------------|----------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------|------------------|
| <b>blood coagulation</b> | BP       | ADAMTS13, APOH, CPB2, F10, F11, F12, F13A1, F2, FAP, HGFAC, HRG, ITGB3, KLKB1, KNG1, MYH9, PLEK, PLG, PROC, PROS1, PROZ, PTPRJ, SERPINC1, SERPIND1, SERPINF2, TUBB1 | 25            | 4,82E-21         |
| <b>hemostasis</b>        | BP       | ADAMTS13, APOH, CPB2, F10, F11, F12, F13A1, F2, FAP, HGFAC, HRG, ITGB3, KLKB1, KNG1, MYH9, PLEK, PLG, PROC, PROS1, PROZ, PTPRJ, SERPINC1, SERPIND1, SERPINF2, TUBB1 | 25            | 4,82E-21         |

|                                        |    |                                                                                                                                                                                       |    |          |
|----------------------------------------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----|----------|
| <b>coagulation</b>                     | BP | ADAMTS13, APOH, CPB2, F10, F11, F12, F13A1, F2, FAP, HGFAC, HRG, ITGB3, KLKB1, KNG1, MYH9, PLEK, PLG, PROC, PROS1, PROZ, PTPRJ, SERPINC1, SERPIND1, SERPINF2, TUBB1                   | 25 | 4,82E-21 |
| <b>wound healing</b>                   | BP | ADAMTS13, APOH, CPB2, ENG, F10, F11, F12, F13A1, F2, FAP, HGFAC, HRG, ITGB1, ITGB3, KLKB1, KNG1, MCAM, MYH9, PLEK, PLG, PROC, PROS1, PROZ, PTPRJ, SERPINC1, SERPIND1, SERPINF2, TUBB1 | 28 | 4,67E-18 |
| <b>regulation of body fluid levels</b> | BP | ADAMTS13, APOH, CPB2, F10, F11, F12, F13A1, F2, FAP, HGFAC, HRG, ITGB3, KLKB1, KNG1, MYH9, PLEK, PLG, PROC, PROS1, PROZ, PTPRJ, SERPINC1, SERPIND1, SERPINF2, TUBB1, UMOD             | 26 | 1,53E-17 |



|                                                 |    |                                                                                       |    |          |
|-------------------------------------------------|----|---------------------------------------------------------------------------------------|----|----------|
| <b>complement activation</b>                    | BP | C1QA, C1QB, C1RL, C3, C5, C6, C8A, C8B, C8G, CFH, CFI, CLU, COLEC10, FCN3, MASP1      | 15 | 2,40E-17 |
| <b>regulation of fibrinolysis</b>               | BP | APOH, CPB2, F11, F12, F2, FAP, HRG, KLKB1, PLG, SERPINF2                              | 10 | 6,56E-16 |
| <b>negative regulation of blood coagulation</b> | BP | APOH, CPB2, F11, F12, F2, FAP, HRG, KLKB1, KNG1, PLG, PROC, PROS1, SERPINF2           | 13 | 6,81E-16 |
| <b>negative regulation of hemostasis</b>        | BP | APOH, CPB2, F11, F12, F2, FAP, HRG, KLKB1, KNG1, PLG, PROC, PROS1, SERPINF2           | 13 | 7,34E-16 |
| <b>fibrinolysis</b>                             | BP | APOH, CPB2, F11, F12, F2, FAP, HRG, KLKB1, PLG, PROS1, SERPINF2                       | 11 | 7,34E-16 |
| <b>regulation of blood coagulation</b>          | BP | APOH, CPB2, F11, F12, F2, FAP, HRG, KLKB1, KNG1, PLG, PROC, PROS1, SERPINC1, SERPINF2 | 14 | 1,07E-15 |
| <b>negative regulation of coagulation</b>       | BP | APOH, CPB2, F11, F12, F2, FAP, HRG, KLKB1, KNG1, PLG, PROC, PROS1, SERPINF2           | 13 | 1,39E-15 |
| <b>regulation of hemostasis</b>                 | BP | APOH, CPB2, F11, F12, F2, FAP, HRG, KLKB1, KNG1, PLG, PROC, PROS1, SERPINC1, SERPINF2 | 14 | 1,40E-15 |
| <b>regulation of coagulation</b>                | BP | APOH, CPB2, F11, F12, F2, FAP, HRG, KLKB1, KNG1, PLG, PROC, PROS1, SERPINC1, SERPINF2 | 14 | 3,61E-15 |
| <b>complement activation, classical pathway</b> | BP | C1QA, C1QB, C1RL, C3, C5, C6, C8A, C8B, C8G, CFI, CLU                                 | 11 | 1,49E-13 |
| <b>negative regulation of wound healing</b>     | BP | APOH, CPB2, F11, F12, F2, FAP, HRG, KLKB1, KNG1,                                      | 13 | 1,84E-13 |

|                                                                       |    |                                                                                                                     |    |          |
|-----------------------------------------------------------------------|----|---------------------------------------------------------------------------------------------------------------------|----|----------|
|                                                                       |    | PLG, PROC, PROS1, SERPINF2                                                                                          |    |          |
| <b>regulation of wound healing</b>                                    | BP | APOH, CPB2, F11, F12, F2, FAP, HRG, ITGB1, KLKB1, KNG1, PLG, PROC, PROS1, SERPINC1, SERPINF2                        | 15 | 9,29E-13 |
| <b>protein processing</b>                                             | BP | ACE, ADAMTS13, APOH, BCHE, C1RL, CLEC3B, CPB2, DPP4, ENPEP, F11, F12, GSN, HGFAC, KLKB1, MASP1, MYH9, PLG, SERPINF2 | 18 | 1,29E-12 |
| <b>humoral immune response mediated by circulating immunoglobulin</b> | BP | C1QA, C1QB, C1RL, C3, C5, C6, C8A, C8B, C8G, CFI, CLU                                                               | 11 | 3,81E-12 |
| <b>negative regulation of response to wounding</b>                    | BP | APOH, CPB2, F11, F12, F2, FAP, HRG, KLKB1, KNG1, PLG, PROC, PROS1, SERPINF2                                         | 13 | 4,84E-12 |
| <b>regulation of response to wounding</b>                             | BP | APOH, CPB2, F11, F12, F2, FAP, HRG, ITGB1, KLKB1, KNG1, PLG, PROC, PROS1, SERPINC1, SERPINF2                        | 15 | 3,46E-11 |
| <b>humoral immune response</b>                                        | BP | C1QA, C1QB, C1RL, C3, C5, C6, C8A, C8B, C8G, CFH, CFI, CLU, COLEC10, F2, FCN3, HRG, KNG1, MASP1                     | 18 | 5,63E-11 |
| <b>zymogen activation</b>                                             | BP | APOH, C1RL, CLEC3B, CPB2, F11, F12, HGFAC, KLKB1, MASP1, SERPINF2                                                   | 10 | 1,94E-10 |

|                                                   |    |                                                                                                                              |    |          |
|---------------------------------------------------|----|------------------------------------------------------------------------------------------------------------------------------|----|----------|
| <b>negative regulation of peptidase activity</b>  | BP | ECM1, FETUB, ITIH1, ITIH2, ITIH4, KNG1, PI16, SERPINA4, SERPINA5, SERPINA6, SERPINA7, SERPINC1, SERPIND1, SERPINF2           | 14 | 1,69E-09 |
| <b>negative regulation of hydrolase activity</b>  | BP | APOC1, ECM1, FETUB, ITIH1, ITIH2, ITIH4, KNG1, PI16, SERPINA4, SERPINA5, SERPINA6, SERPINA7, SERPINC1, SERPIND1, SERPINF2    | 15 | 3,45E-09 |
| <b>negative regulation of proteolysis</b>         | BP | CPB2, ECM1, F2, FETUB, ITIH1, ITIH2, ITIH4, KNG1, PI16, SERPINA4, SERPINA5, SERPINA6, SERPINA7, SERPINC1, SERPIND1, SERPINF2 | 16 | 4,25E-09 |
| <b>negative regulation of fibrinolysis</b>        | BP | APOH, CPB2, F2, HRG, PLG, SERPINF2                                                                                           | 6  | 6,28E-09 |
| <b>positive regulation of blood coagulation</b>   | BP | APOH, CPB2, F12, F2, HRG, PLG, SERPINF2                                                                                      | 7  | 1,59E-08 |
| <b>plasminogen activation</b>                     | BP | APOH, CLEC3B, CPB2, F11, F12, KLKB1, SERPINF2                                                                                | 7  | 1,59E-08 |
| <b>positive regulation of hemostasis</b>          | BP | APOH, CPB2, F12, F2, HRG, PLG, SERPINF2                                                                                      | 7  | 1,59E-08 |
| <b>positive regulation of coagulation</b>         | BP | APOH, CPB2, F12, F2, HRG, PLG, SERPINF2                                                                                      | 7  | 4,46E-08 |
| <b>complement activation, alternative pathway</b> | BP | C3, C5, C8A, C8B, C8G, CFH                                                                                                   | 6  | 5,59E-08 |

|                                                  |    |                                                                                                                                               |    |          |
|--------------------------------------------------|----|-----------------------------------------------------------------------------------------------------------------------------------------------|----|----------|
| <b>negative regulation of catalytic activity</b> | BP | ADIPOQ, APOC1, ECM1, ENG, FETUB, ITIH1, ITIH2, ITIH4, KNG1, PI16, PTPRJ, SERPINA4, SERPINA5, SERPINA6, SERPINA7, SERPINC1, SERPIND1, SERPINF2 | 18 | 6,15E-08 |
| <b>lipid transport</b>                           | BP | ACE, ADIPOQ, APOA4, APOB, APOC1, APOC4, APOD, APOF, APOH, APOM, CETP, CLU, ITGB3, LCAT, PON1, RBP4, SERPINA5                                  | 17 | 1,83E-07 |
| <b>regulation of peptidase activity</b>          | BP | ECM1, FETUB, GSN, ITIH1, ITIH2, ITIH4, KNG1, PI16, SERPINA4, SERPINA5, SERPINA6, SERPINA7, SERPINC1, SERPIND1, SERPINF2                       | 15 | 2,00E-07 |
| <b>immunoglobulin mediated immune response</b>   | BP | C1QA, C1QB, C1RL, C3, C5, C6, C8A, C8B, C8G, CFI, CLU, IGHV3-7                                                                                | 12 | 3,63E-07 |
| <b>leukocyte mediated immunity</b>               | BP | ACE, C1QA, C1QB, C1RL, C3, C5, C6, C8A, C8B, C8G, CFI, CLU, DBH, F2, IGHV3-7, KIT, LAMP1                                                      | 17 | 3,84E-07 |
| <b>positive regulation of wound healing</b>      | BP | APOH, CPB2, F12, F2, HRG, ITGB1, PLG, SERPINF2                                                                                                | 8  | 3,84E-07 |
| <b>B cell mediated immunity</b>                  | BP | C1QA, C1QB, C1RL, C3, C5, C6, C8A, C8B, C8G, CFI, CLU, IGHV3-7                                                                                | 12 | 3,93E-07 |

|                                                             |    |                                                                                               |    |          |
|-------------------------------------------------------------|----|-----------------------------------------------------------------------------------------------|----|----------|
| <b>negative regulation of response to external stimulus</b> | BP | ADIPOQ, APOH, C5, CPB2, DPP4, F11, F12, F2, FAP, HRG, KLKB1, KNG1, PLG, PROC, PROS1, SERPINF2 | 16 | 5,60E-07 |
| <b>positive regulation of response to wounding</b>          | BP | APOH, CPB2, F12, F2, HRG, ITGB1, PLG, SERPINF2                                                | 8  | 1,85E-06 |
| <b>protein-lipid complex remodeling</b>                     | BP | APOA4, APOB, APOC1, APOM, CETP, LCAT                                                          | 6  | 2,30E-06 |
| <b>plasma lipoprotein particle remodeling</b>               | BP | APOA4, APOB, APOC1, APOM, CETP, LCAT                                                          | 6  | 2,30E-06 |
| <b>high-density lipoprotein particle remodeling</b>         | BP | APOA4, APOC1, APOM, CETP, LCAT                                                                | 5  | 2,32E-06 |
| <b>cholesterol transport</b>                                | BP | ADIPOQ, APOA4, APOB, APOC1, APOM, CETP, CLU, LCAT, PON1                                       | 9  | 3,13E-06 |
| <b>protein-containing complex remodeling</b>                | BP | APOA4, APOB, APOC1, APOM, CETP, LCAT                                                          | 6  | 3,13E-06 |
| <b>regulation of plasma lipoprotein particle levels</b>     | BP | ADIPOQ, APOA4, APOB, APOC1, APOM, CETP, GPLD1, LCAT                                           | 8  | 4,04E-06 |
| <b>reverse cholesterol transport</b>                        | BP | APOA4, APOM, CETP, CLU, LCAT                                                                  | 5  | 5,15E-06 |
| <b>protein activation cascade</b>                           | BP | APOH, F12, F13A1, ITGB3, KLKB1                                                                | 5  | 5,15E-06 |
| <b>sterol transport</b>                                     | BP | ADIPOQ, APOA4, APOB, APOC1, APOM, CETP, CLU, LCAT, PON1                                       | 9  | 5,26E-06 |
| <b>regulation of protein processing</b>                     | BP | CLEC3B, CPB2, F12, GSN, KLKB1, MYH9, SERPINF2                                                 | 7  | 7,48E-06 |
| <b>phagocytosis</b>                                         | BP | ADIPOQ, AHSG, BIN2, C3, COLEC10, FCN3, GSN, ITGB1, ITGB3, MYH9, PTPRJ                         | 11 | 1,06E-05 |
| <b>regulation of protein maturation</b>                     | BP | CLEC3B, CPB2, F12, GSN, KLKB1, MYH9, SERPINF2                                                 | 7  | 1,31E-05 |
| <b>cholesterol efflux</b>                                   | BP | ADIPOQ, APOA4, APOB, APOC1, APOM, CETP, PON1                                                  | 7  | 1,41E-05 |
| <b>positive regulation of protein processing</b>            | BP | CLEC3B, F12, GSN, KLKB1, MYH9                                                                 | 5  | 1,53E-05 |

|                                                               |    |                                                                            |    |          |
|---------------------------------------------------------------|----|----------------------------------------------------------------------------|----|----------|
| <b>plasma lipoprotein particle assembly</b>                   | BP | APOA4, APOB, APOC1, APOM, LCAT                                             | 5  | 2,23E-05 |
| <b>positive regulation of protein maturation</b>              | BP | CLEC3B, F12, GSN, KLKB1, MYH9                                              | 5  | 2,23E-05 |
| <b>plasma lipoprotein particle organization</b>               | BP | APOA4, APOB, APOC1, APOM, CETP, LCAT                                       | 6  | 2,25E-05 |
| <b>cell killing</b>                                           | BP | C3, C5, C6, C8A, C8B, C8G, CFH, F2, HRG, KNG1, LAMP1                       | 11 | 2,51E-05 |
| <b>lymphocyte mediated immunity</b>                           | BP | C1QA, C1QB, C1RL, C3, C5, C6, C8A, C8B, C8G, CFI, CLU, IGHV3-7, LAMP1      | 13 | 2,57E-05 |
| <b>protein-lipid complex organization</b>                     | BP | APOA4, APOB, APOC1, APOM, CETP, LCAT                                       | 6  | 3,05E-05 |
| <b>killing of cells of another organism</b>                   | BP | C5, C6, C8A, C8B, C8G, F2, HRG, KNG1                                       | 8  | 3,31E-05 |
| <b>disruption of cell in another organism</b>                 | BP | C5, C6, C8A, C8B, C8G, F2, HRG, KNG1                                       | 8  | 3,31E-05 |
| <b>protein-lipid complex assembly</b>                         | BP | APOA4, APOB, APOC1, APOM, LCAT                                             | 5  | 3,45E-05 |
| <b>disruption of anatomical structure in another organism</b> | BP | C5, C6, C8A, C8B, C8G, F2, HRG, KNG1                                       | 8  | 3,84E-05 |
| <b>leukocyte migration</b>                                    | BP | APOD, C5, DBH, DPP4, ECM1, ITGB1, ITGB3, KIT, MYH9, PLG, PTPRJ, SELL, UMOD | 13 | 3,89E-05 |
| <b>synapse pruning</b>                                        | BP | C1QA, C1QB, C3, ITGB1                                                      | 4  | 5,74E-05 |
| <b>organic hydroxy compound transport</b>                     | BP | ADIPOQ, APOA4, APOB, APOC1, APOM, CETP, CLU, ITGB3, LCAT, PON1, RBP4       | 11 | 5,85E-05 |
| <b>blood coagulation, fibrin clot formation</b>               | BP | APOH, F12, F13A1, ITGB3                                                    | 4  | 7,39E-05 |
| <b>regulation of lipid localization</b>                       | BP | ADIPOQ, APOA4, APOB, APOC1, APOC4, C3, CETP, ITGB3, PON1                   | 9  | 7,42E-05 |
| <b>platelet activation</b>                                    | BP | ADAMTS13, F2, HRG, ITGB3, MYH9, PLEK, PTPRJ, TUBB1                         | 8  | 7,74E-05 |

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| <b>lipoprotein metabolic process</b>                                                                                             | BP | APOA4, APOB, APOC1, APOD, APOM, ITGB3, LCAT                                         | 7  | 9,43E-05    |
| <b>regulation of plasminogen activation</b>                                                                                      | BP | CLEC3B, CPB2, F12, SERPINF2                                                         | 4  | 0,000116369 |
| <b>triglyceride metabolic process</b>                                                                                            | BP | APOA4, APOB, APOC1, APOH, C3, CETP, GPLD1                                           | 7  | 0,000134488 |
| <b>biological process involved in symbiotic interaction</b>                                                                      | BP | DPP4, F2, FCN3, GSN, HRG, ITGB1, ITGB3, LAMP1, NCAM1, PGLYRP2, PLG                  | 11 | 0,000135842 |
| <b>negative regulation of endopeptidase activity</b>                                                                             | BP | FETUB, SERPINA4, SERPINA5, SERPINA6, SERPINA7, SERPIND1, SERPINF2                   | 7  | 0,000139235 |
| <b>acute inflammatory response</b>                                                                                               | BP | AHSG, C3, F12, F2, ITIH4, KLKB1, SERPINF2                                           | 7  | 0,000146032 |
| <b>adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains</b> | BP | C1QA, C1QB, C1RL, C3, C5, C6, C8A, C8B, C8G, CFI, CLU, IGHV3-7                      | 12 | 0,000178398 |
| <b>chemotaxis</b>                                                                                                                | BP | BIN2, C5, CDH13, COLEC10, DPP4, ENG, GPNMB, HRG, ITGB3, KIT, MEGF8, PTPRJ, SERPIND1 | 13 | 0,000178843 |
| <b>taxis</b>                                                                                                                     | BP | BIN2, C5, CDH13, COLEC10, DPP4, ENG, GPNMB, HRG, ITGB3, KIT, MEGF8, PTPRJ, SERPIND1 | 13 | 0,000184826 |
| <b>phosphatidylcholine metabolic process</b>                                                                                     | BP | APOA4, APOC1, CETP, GPLD1, LCAT, PON1                                               | 6  | 0,000210505 |
| <b>regulation of collagen metabolic process</b>                                                                                  | BP | ENG, F2, FAP, ITGB1, SERPINF2                                                       | 5  | 0,000214547 |
| <b>endothelial cell migration</b>                                                                                                | BP | APOH, CDH13, DPP4, FAP, GPLD1, HRG, ITGB1, ITGB3, MYH9, PLG                         | 10 | 0,000286496 |

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| <b>alcohol metabolic process</b>                            | BP | APOA4, APOB, APOC1, APOF, CETP, DBH, LCAT, MINPP1, PLEK, PON1, RBP4 | 11 | 0,000375104 |
| <b>regulation of endocytosis</b>                            | BP | ADIPOQ, AHSG, APOC1, C3, CDH13, CLU, COLEC10, FCN3, ITGB3, PTPRJ    | 10 | 0,000500791 |
| <b>acylglycerol metabolic process</b>                       | BP | APOA4, APOB, APOC1, APOH, C3, CETP, GPLD1                           | 7  | 0,00050176  |
| <b>neutral lipid metabolic process</b>                      | BP | APOA4, APOB, APOC1, APOH, C3, CETP, GPLD1                           | 7  | 0,000520293 |
| <b>plasma lipoprotein particle clearance</b>                | BP | ADIPOQ, APOB, APOC1, APOM, GPLD1                                    | 5  | 0,000542212 |
| <b>tissue remodeling</b>                                    | BP | ACE, DBH, GPNMB, HRG, ITGB3, PLG, SPP2, UMOD                        | 8  | 0,000573908 |
| <b>cell junction disassembly</b>                            | BP | C1QA, C1QB, C3, ITGB1                                               | 4  | 0,000602465 |
| <b>cholesterol metabolic process</b>                        | BP | APOA4, APOB, APOC1, APOF, CETP, LCAT, PON1                          | 7  | 0,000857588 |
| <b>complement activation, lectin pathway</b>                | BP | COLEC10, FCN3, MASP1                                                | 3  | 0,000862241 |
| <b>biological process involved in interaction with host</b> | BP | DPP4, FCN3, GSN, ITGB1, ITGB3, LAMP1, NCAM1, PGLYRP2                | 8  | 0,000879381 |
| <b>regulation of phagocytosis</b>                           | BP | ADIPOQ, AHSG, C3, COLEC10, FCN3, PTPRJ                              | 6  | 0,000910195 |
| <b>steroid metabolic process</b>                            | BP | APOA4, APOB, APOC1, APOF, CETP, GC, KIT, LCAT, PON1, SERPINA6       | 10 | 0,000918327 |
| <b>extracellular matrix organization</b>                    | BP | ADAMTS13, CPB2, DPP4, ENG, FAP, ITGB1, ITGB3, LUM, PLG, SERPINF2    | 10 | 0,001029936 |
| <b>extracellular structure organization</b>                 | BP | ADAMTS13, CPB2, DPP4, ENG, FAP, ITGB1, ITGB3, LUM, PLG, SERPINF2    | 10 | 0,001044875 |
| <b>external encapsulating structure organization</b>        | BP | ADAMTS13, CPB2, DPP4, ENG, FAP, ITGB1, ITGB3, LUM, PLG, SERPINF2    | 10 | 0,00104793  |
| <b>triglyceride-rich lipoprotein particle remodeling</b>    | BP | APOA4, CETP, LCAT                                                   | 3  | 0,00104793  |



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| <b>very-low-density lipoprotein particle remodeling</b>                                 | BP | APOA4, CETP, LCAT                            | 3 | 0,00104793  |
| <b>regulation of macrophage derived foam cell differentiation</b>                       | BP | ADIPOQ, APOB, CETP, ITGB3                    | 4 | 0,00104793  |
| <b>sterol metabolic process</b>                                                         | BP | APOA4, APOB, APOC1, APOF, CETP, LCAT, PON1   | 7 | 0,001184937 |
| <b>symbiont entry into host cell</b>                                                    | BP | DPP4, FCN3, GSN, ITGB1, ITGB3, LAMP1, NCAM1  | 7 | 0,001184937 |
| <b>secondary alcohol metabolic process</b>                                              | BP | APOA4, APOB, APOC1, APOF, CETP, LCAT, PON1   | 7 | 0,001184937 |
| <b>peptide hormone processing</b>                                                       | BP | ACE, BCHE, DPP4, ENPEP                       | 4 | 0,001274087 |
| <b>negative regulation of platelet-derived growth factor receptor signaling pathway</b> | BP | ADIPOQ, APOD, PTPRJ                          | 3 | 0,001274087 |
| <b>glycosaminoglycan metabolic process</b>                                              | BP | B3GNT2, B4GAT1, ITIH1, ITIH2, ITIH4, PGLYRP2 | 6 | 0,001274087 |
| <b>collagen metabolic process</b>                                                       | BP | ENG, F2, FAP, ITGB1, PCOLCE, SERPINF2        | 6 | 0,001274087 |
| <b>symbiont entry into host</b>                                                         | BP | DPP4, FCN3, GSN, ITGB1, ITGB3, LAMP1, NCAM1  | 7 | 0,001375164 |
| <b>positive regulation of lipid localization</b>                                        | BP | ADIPOQ, APOB, APOC4, C3, CETP, PON1          | 6 | 0,001382105 |
| <b>negative regulation of macrophage derived foam cell differentiation</b>              | BP | ADIPOQ, CETP, ITGB3                          | 3 | 0,001541699 |
| <b>regulation of lipoprotein lipase activity</b>                                        | BP | APOA4, APOC1, APOH                           | 3 | 0,001541699 |
| <b>macrophage derived foam cell differentiation</b>                                     | BP | ADIPOQ, APOB, CETP, ITGB3                    | 4 | 0,001650291 |
| <b>positive regulation of phagocytosis</b>                                              | BP | AHSG, C3, COLEC10, FCN3, PTPRJ               | 5 | 0,001655908 |
| <b>foam cell differentiation</b>                                                        | BP | ADIPOQ, APOB, CETP, ITGB3                    | 4 | 0,001782928 |
| <b>signaling receptor ligand precursor processing</b>                                   | BP | ACE, BCHE, DPP4, ENPEP                       | 4 | 0,001782928 |

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| <b>regulation of smooth muscle cell proliferation</b> | BP | ADIPOQ, APOD, CDH13, DBH, IGFBP3, ITGB3, SERPINF2                      | 7  | 0,001858138 |
| <b>aminoglycan metabolic process</b>                  | BP | B3GNT2, B4GAT1, ITIH1, ITIH2, ITIH4, PGLYRP2                           | 6  | 0,001971539 |
| <b>regulation of sterol transport</b>                 | BP | ADIPOQ, APOA4, APOC1, CETP, PON1                                       | 5  | 0,002029514 |
| <b>regulation of cholesterol transport</b>            | BP | ADIPOQ, APOA4, APOC1, CETP, PON1                                       | 5  | 0,002029514 |
| <b>smooth muscle cell proliferation</b>               | BP | ADIPOQ, APOD, CDH13, DBH, IGFBP3, ITGB3, SERPINF2                      | 7  | 0,002070571 |
| <b>glycerolipid metabolic process</b>                 | BP | APOA4, APOB, APOC1, APOH, C3, CETP, GPLD1, LCAT, PLEK, PON1            | 10 | 0,002326457 |
| <b>regulation of endopeptidase activity</b>           | BP | FETUB, GSN, SERPINA4, SERPINA5, SERPINA6, SERPINA7, SERPIND1, SERPINF2 | 8  | 0,002604577 |
| <b>muscle cell proliferation</b>                      | BP | ADIPOQ, APOD, CDH13, DBH, IGFBP3, ITGB3, RBP4, SERPINF2                | 8  | 0,002869266 |
| <b>renal system process</b>                           | BP | ADIPOQ, GSN, MCAM, PON3, SERPINF2, UMOD                                | 6  | 0,002869266 |
| <b>phagocytosis, engulfment</b>                       | BP | BIN2, C3, GSN, MYH9                                                    | 4  | 0,003692887 |
| <b>acute-phase response</b>                           | BP | AHSG, F2, ITIH4, SERPINF2                                              | 4  | 0,003692887 |
| <b>peptide catabolic process</b>                      | BP | ACE, ADAMTS13, ENPEP                                                   | 3  | 0,00411332  |
| <b>mucopolysaccharide metabolic process</b>           | BP | B3GNT2, B4GAT1, ITIH1, ITIH2, ITIH4                                    | 5  | 0,004152156 |
| <b>regulation of lipid metabolic process</b>          | BP | ADIPOQ, APOA4, APOB, APOC1, APOD, C3, F2, GPLD1, KIT                   | 9  | 0,004549668 |
| <b>collagen biosynthetic process</b>                  | BP | ENG, F2, PCOLCE, SERPINF2                                              | 4  | 0,004888424 |
| <b>regulation of platelet activation</b>              | BP | F2, HRG, PLEK, PTPRJ                                                   | 4  | 0,005614253 |
| <b>regulation of lipid storage</b>                    | BP | APOB, APOC4, C3, ITGB3                                                 | 4  | 0,005980926 |

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|--------------------------------------------------------------------------------|----|-------------------------------------------------------|----|-------------|
| <b>regulation of complement activation</b>                                     | BP | C3, CFH, MASP1                                        | 3  | 0,006022946 |
| <b>positive regulation of cell-matrix adhesion</b>                             | BP | CDH13, HRG, ITGB3, PTPRJ                              | 4  | 0,006315866 |
| <b>regulation of lipid transport</b>                                           | BP | ADIPOQ, APOA4, APOC1, CETP, ITGB3, PON1               | 6  | 0,006498407 |
| <b>plasma membrane invagination</b>                                            | BP | BIN2, C3, GSN, MYH9                                   | 4  | 0,006606292 |
| <b>regulation of systemic arterial blood pressure by renin-angiotensin</b>     | BP | ACE, ENPEP, SERPINF2                                  | 3  | 0,006606292 |
| <b>regulation of platelet-derived growth factor receptor signaling pathway</b> | BP | ADIPOQ, APOD, PTPRJ                                   | 3  | 0,006606292 |
| <b>positive regulation of endocytosis</b>                                      | BP | AHSG, C3, CLU, COLEC10, FCN3, PTPRJ                   | 6  | 0,006986141 |
| <b>cellular component disassembly</b>                                          | BP | C1QA, C1QB, C3, DPP4, ENG, FAP, GSN, ITGB1, PLEK, PLG | 10 | 0,007002618 |
| <b>platelet formation</b>                                                      | BP | MYH9, PTPRJ, TUBB1                                    | 3  | 0,007285194 |
| <b>platelet-derived growth factor receptor signaling pathway</b>               | BP | ADIPOQ, APOD, ITGB3, PTPRJ                            | 4  | 0,007285194 |
| <b>cholesterol homeostasis</b>                                                 | BP | APOA4, APOB, APOM, CETP, LCAT                         | 5  | 0,007538265 |
| <b>sterol homeostasis</b>                                                      | BP | APOA4, APOB, APOM, CETP, LCAT                         | 5  | 0,007815379 |
| <b>negative regulation of cell migration</b>                                   | BP | ADIPOQ, APOD, APOH, C5, DPP4, ENG, HRG, IGFBP3, PTPRJ | 9  | 0,008788311 |
| <b>positive regulation of lipid storage</b>                                    | BP | APOB, APOC4, C3                                       | 3  | 0,008788311 |
| <b>positive regulation of collagen biosynthetic process</b>                    | BP | ENG, F2, SERPINF2                                     | 3  | 0,008788311 |
| <b>platelet morphogenesis</b>                                                  | BP | MYH9, PTPRJ, TUBB1                                    | 3  | 0,008788311 |
| <b>integrin-mediated signaling pathway</b>                                     | BP | ADAMTS13, ITGB1, ITGB3, MYH9, PLEK                    | 5  | 0,008933708 |

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| <b>axon guidance</b>                                     | BP | B3GNT2, B4GAT1, CHL1, CNTN1, MEGF8, NCAM1, PTPRJ           | 7  | 0,009212752 |
| <b>membrane invagination</b>                             | BP | BIN2, C3, GSN, MYH9                                        | 4  | 0,009322439 |
| <b>neuron projection guidance</b>                        | BP | B3GNT2, B4GAT1, CHL1, CNTN1, MEGF8, NCAM1, PTPRJ           | 7  | 0,009322439 |
| <b>positive regulation of collagen metabolic process</b> | BP | ENG, F2, SERPINF2                                          | 3  | 0,009419914 |
| <b>triglyceride catabolic process</b>                    | BP | APOA4, APOB, GPLD1                                         | 3  | 0,009419914 |
| <b>extracellular matrix disassembly</b>                  | BP | DPP4, ENG, FAP, PLG                                        | 4  | 0,009658739 |
| <b>cell-matrix adhesion</b>                              | BP | ADAMTS13, APOD, CDH13, HRG, ITGB1, ITGB3, PTPRJ            | 7  | 0,01002745  |
| <b>peptide metabolic process</b>                         | BP | ACE, ADAMTS13, ENPEP, PGLYRP2                              | 4  | 0,010040736 |
| <b>glycerolipid catabolic process</b>                    | BP | APOA4, APOB, APOC1, GPLD1                                  | 4  | 0,010040736 |
| <b>epithelial cell proliferation</b>                     | BP | APOH, CDH13, CPB2, DBH, ECM1, ENG, FAP, IGFBP3, ITGB3, KIT | 10 | 0,010495728 |
| <b>negative regulation of cell motility</b>              | BP | ADIPOQ, APOD, APOH, C5, DPP4, ENG, HRG, IGFBP3, PTPRJ      | 9  | 0,01053319  |
| <b>regulation of endothelial cell proliferation</b>      | BP | APOH, CDH13, DBH, ECM1, ENG, ITGB3                         | 6  | 0,011258728 |
| <b>lipid homeostasis</b>                                 | BP | APOA4, APOB, APOC4, APOM, CETP, LCAT                       | 6  | 0,011518686 |
| <b>regulation of immune effector process</b>             | BP | C3, CFH, COLEC10, FCN3, KIT, LAMP1, MASP1, PGLYRP2, RBP4   | 9  | 0,01274839  |
| <b>lamellipodium assembly</b>                            | BP | CDH13, HRG, ITGB1, KIT                                     | 4  | 0,013347948 |
| <b>positive chemotaxis</b>                               | BP | CDH13, COLEC10, GPNMB, PTPRJ                               | 4  | 0,013347948 |
| <b>regulation of cell-matrix adhesion</b>                | BP | APOD, CDH13, HRG, ITGB3, PTPRJ                             | 5  | 0,013724167 |

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| <b>negative regulation of locomotion</b>                                                         | BP | ADIPOQ, APOD, APOH, C5, DPP4, ENG, HRG, IGFBP3, PTPRJ | 9 | 0,013777051 |
| <b>heart trabecula morphogenesis</b>                                                             | BP | ADGRG6, ENG, RBP4                                     | 3 | 0,014072617 |
| <b>regulation of extracellular matrix organization</b>                                           | BP | CPB2, DPP4, FAP, ITGB3                                | 4 | 0,014441662 |
| <b>regulation of blood pressure</b>                                                              | BP | ACE, ADIPOQ, ENG, ENPEP, SERPINF2, UMOD               | 6 | 0,014523253 |
| <b>regulation of receptor-mediated endocytosis</b>                                               | BP | ADIPOQ, APOC1, C3, CLU, ITGB3                         | 5 | 0,014815773 |
| <b>hyaluronan metabolic process</b>                                                              | BP | ITIH1, ITIH2, ITIH4                                   | 3 | 0,015010831 |
| <b>positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction</b> | BP | ENG, F2, ITGB1, KIT, PROS1, PTPRJ                     | 6 | 0,015062279 |
| <b>glucose homeostasis</b>                                                                       | BP | ACE, ADIPOQ, CPB2, DBH, GPLD1, PTPRJ, RBP4            | 7 | 0,015639027 |
| <b>carbohydrate homeostasis</b>                                                                  | BP | ACE, ADIPOQ, CPB2, DBH, GPLD1, PTPRJ, RBP4            | 7 | 0,01589113  |
| <b>regulation of lipase activity</b>                                                             | BP | APOA4, APOC1, APOH                                    | 3 | 0,015976006 |
| <b>platelet aggregation</b>                                                                      | BP | ITGB3, MYH9, PLEK, TUBB1                              | 4 | 0,015995753 |
| <b>regulation of small molecule metabolic process</b>                                            | BP | ADIPOQ, APOA4, APOB, APOC1, GPLD1, IGFBP3, KIT, PLEK  | 8 | 0,016811184 |
| <b>positive regulation of sterol transport</b>                                                   | BP | ADIPOQ, CETP, PON1                                    | 3 | 0,016967763 |
| <b>positive regulation of cholesterol transport</b>                                              | BP | ADIPOQ, CETP, PON1                                    | 3 | 0,016967763 |
| <b>negative regulation of receptor-mediated endocytosis</b>                                      | BP | ADIPOQ, APOC1, ITGB3                                  | 3 | 0,018282189 |
| <b>receptor-mediated endocytosis</b>                                                             | BP | ADIPOQ, APOC1, C3, CLU, DPP4, ITGB1, ITGB3            | 7 | 0,018462705 |
| <b>endothelial cell proliferation</b>                                                            | BP | APOH, CDH13, DBH, ECM1, ENG, ITGB3                    | 6 | 0,018462705 |
| <b>regulation of systemic arterial blood pressure by hormone</b>                                 | BP | ACE, ENPEP, SERPINF2                                  | 3 | 0,019032327 |

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| <b>renal absorption</b>                                                    | BP | ADIPOQ, GSN, UMOD                                              | 3 | 0,019032327 |
| <b>regulation of angiotensin levels in blood</b>                           | BP | ACE, ENPEP                                                     | 2 | 0,019032327 |
| <b>positive regulation of phosphatase activity</b>                         | BP | GPLD1, PLEK                                                    | 2 | 0,019032327 |
| <b>peripheral nervous system axon regeneration</b>                         | BP | APOA4, APOD                                                    | 2 | 0,019032327 |
| <b>renal protein absorption</b>                                            | BP | ADIPOQ, GSN                                                    | 2 | 0,019032327 |
| <b>regulation of angiogenesis</b>                                          | BP | APOH, C3, ECM1, ENG, GPNMB, HRG, ITGB1, ITGB3                  | 8 | 0,019508259 |
| <b>cell-substrate adhesion</b>                                             | BP | ADAMTS13, APOD, CDH13, HRG, ITGB1, ITGB3, PLG, PTPRJ           | 8 | 0,019747094 |
| <b>detection of biotic stimulus</b>                                        | BP | FAP, PGLYRP2, PTPRJ                                            | 3 | 0,019892595 |
| <b>neutral lipid catabolic process</b>                                     | BP | APOA4, APOB, GPLD1                                             | 3 | 0,019892595 |
| <b>acylglycerol catabolic process</b>                                      | BP | APOA4, APOB, GPLD1                                             | 3 | 0,019892595 |
| <b>response to xenobiotic stimulus</b>                                     | BP | ACE, ADIPOQ, BCHE, CPB2, ENG, GPLD1, ITGB3, PON3, UMOD         | 9 | 0,02061089  |
| <b>regulation of collagen biosynthetic process</b>                         | BP | ENG, F2, SERPINF2                                              | 3 | 0,021086006 |
| <b>positive regulation of G protein-coupled receptor signaling pathway</b> | BP | C3, F2, ITGB3                                                  | 3 | 0,021086006 |
| <b>regulation of vasculature development</b>                               | BP | APOH, C3, ECM1, ENG, GPNMB, HRG, ITGB1, ITGB3                  | 8 | 0,021685228 |
| <b>positive regulation of dephosphorylation</b>                            | BP | GPLD1, PLEK                                                    | 2 | 0,021685228 |
| <b>cytolysis by host of symbiont cells</b>                                 | BP | F2, HRG                                                        | 2 | 0,021685228 |
| <b>complement-dependent cytotoxicity</b>                                   | BP | C3, CFH                                                        | 2 | 0,021685228 |
| <b>regulation of opsonization</b>                                          | BP | COLEC10, FCN3                                                  | 2 | 0,021685228 |
| <b>axonogenesis</b>                                                        | BP | B3GNT2, B4GAT1, CHL1, CNTN1, ITGB1, MEGF8, NCAM1, PTPRJ, RAB10 | 9 | 0,0223107   |

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| <b>regulation of mononuclear cell migration</b>                                     | BP | APOD, C5, ECM1, ITGB3, PTPRJ                | 5 | 0,022896831 |
| <b>regulation of chemotaxis</b>                                                     | BP | C5, CDH13, DPP4, HRG, MEGF8, PTPRJ          | 6 | 0,023128285 |
| <b>cell adhesion mediated by integrin</b>                                           | BP | DPP4, HRG, ITGB1, ITGB3                     | 4 | 0,023464228 |
| <b>glycerophospholipid metabolic process</b>                                        | BP | APOA4, APOC1, CETP, GPLD1, LCAT, PLEK, PON1 | 7 | 0,023751554 |
| <b>epiboly</b>                                                                      | BP | ITGB1, ITGB3, MEGF8                         | 3 | 0,024622682 |
| <b>very-low-density lipoprotein particle assembly</b>                               | BP | APOB, APOC1                                 | 2 | 0,024845921 |
| <b>thyroid hormone transport</b>                                                    | BP | SERPINA7, TUBB1                             | 2 | 0,024845921 |
| <b>lamellipodium organization</b>                                                   | BP | CDH13, HRG, ITGB1, KIT                      | 4 | 0,024845921 |
| <b>regulation of cell-substrate adhesion</b>                                        | BP | APOD, CDH13, HRG, ITGB3, PLG, PTPRJ         | 6 | 0,026229613 |
| <b>regulation of smooth muscle cell migration</b>                                   | BP | ACE, ADIPOQ, IGFBP3, ITGB3                  | 4 | 0,026597642 |
| <b>regulation of tube diameter</b>                                                  | BP | ACE, DBH, ITGB1, KNG1, SERPINF2             | 5 | 0,026597642 |
| <b>blood vessel diameter maintenance</b>                                            | BP | ACE, DBH, ITGB1, KNG1, SERPINF2             | 5 | 0,026597642 |
| <b>regulation of systemic arterial blood pressure mediated by a chemical signal</b> | BP | ACE, ENPEP, SERPINF2                        | 3 | 0,02665914  |
| <b>apoptotic cell clearance</b>                                                     | BP | C3, FCN3, ITGB3                             | 3 | 0,02665914  |
| <b>acylglycerol homeostasis</b>                                                     | BP | APOA4, APOC4, CETP                          | 3 | 0,02665914  |
| <b>cellular response to lipoprotein particle stimulus</b>                           | BP | APOB, CDH13, ITGB1                          | 3 | 0,02665914  |
| <b>regulation of tube size</b>                                                      | BP | ACE, DBH, ITGB1, KNG1, SERPINF2             | 5 | 0,026733608 |
| <b>cell recognition</b>                                                             | BP | COLEC10, CRTAC1, FCN3, FETUB, MEGF8         | 5 | 0,027283322 |
| <b>positive regulation of platelet activation</b>                                   | BP | PLEK, PTPRJ                                 | 2 | 0,027283322 |
| <b>regulation of triglyceride catabolic process</b>                                 | BP | APOA4, GPLD1                                | 2 | 0,027283322 |

|                                                                                      |    |                                            |   |             |
|--------------------------------------------------------------------------------------|----|--------------------------------------------|---|-------------|
| <b>high-density lipoprotein particle assembly</b>                                    | BP | APOM, LCAT                                 | 2 | 0,027283322 |
| <b>extracellular matrix constituent secretion</b>                                    | BP | CPB2, ENG                                  | 2 | 0,027283322 |
| <b>positive regulation of vascular associated smooth muscle cell differentiation</b> | BP | ENG, KIT                                   | 2 | 0,027283322 |
| <b>regulation of triglyceride metabolic process</b>                                  | BP | APOA4, C3, GPLD1                           | 3 | 0,027396918 |
| <b>cell-substrate junction assembly</b>                                              | BP | APOD, HRG, ITGB3, PTPRJ                    | 4 | 0,027930664 |
| <b>lipid storage</b>                                                                 | BP | APOB, APOC4, C3, ITGB3                     | 4 | 0,028800719 |
| <b>mononuclear cell migration</b>                                                    | BP | APOD, C5, ECM1, ITGB3, PLG, PTPRJ          | 6 | 0,028800719 |
| <b>regulation of systemic arterial blood pressure</b>                                | BP | ACE, ENG, ENPEP, SERPINF2                  | 4 | 0,029700857 |
| <b>regulation of acute inflammatory response</b>                                     | BP | C3, F12, KLKB1                             | 3 | 0,030019323 |
| <b>regulation of humoral immune response</b>                                         | BP | C3, CFH, MASP1                             | 3 | 0,030019323 |
| <b>trabecula morphogenesis</b>                                                       | BP | ADGRG6, ENG, RBP4                          | 3 | 0,030019323 |
| <b>negative regulation of cell adhesion</b>                                          | BP | ADIPOQ, APOD, CDH13, GPNMB, HRG, KNG1, PLG | 7 | 0,030111945 |
| <b>regulation of peptidyl-tyrosine phosphorylation</b>                               | BP | ADIPOQ, HRG, ITGB3, KIT, PTPRJ             | 5 | 0,030111945 |
| <b>positive regulation of systemic arterial blood pressure</b>                       | BP | ACE, ENG                                   | 2 | 0,030111945 |
| <b>phospholipid efflux</b>                                                           | BP | APOA4, APOC1                               | 2 | 0,030111945 |
| <b>regulation of leukocyte migration</b>                                             | BP | APOD, C5, DPP4, ECM1, ITGB3, PTPRJ         | 6 | 0,030749281 |
| <b>smooth muscle cell migration</b>                                                  | BP | ACE, ADIPOQ, IGFBP3, ITGB3                 | 4 | 0,030749281 |
| <b>regulation of cell adhesion mediated by integrin</b>                              | BP | DPP4, HRG, ITGB3                           | 3 | 0,030915166 |
| <b>homotypic cell-cell adhesion</b>                                                  | BP | ITGB3, MYH9, PLEK, TUBB1                   | 4 | 0,031606272 |
| <b>cell-cell adhesion mediated by cadherin</b>                                       | BP | CDH13, PLG, SERPINF2                       | 3 | 0,032342493 |



|                                                       |    |                                               |   |             |
|-------------------------------------------------------|----|-----------------------------------------------|---|-------------|
| <b>regulation of T cell migration</b>                 | BP | APOD, ECM1, ITGB3                             | 3 | 0,032342493 |
| <b>cellular response to peptide hormone stimulus</b>  | BP | ACE, ADIPOQ, AHSB, GPLD1, ITGB3, PTPRJ, RAB10 | 7 | 0,032684622 |
| <b>cell-substrate junction organization</b>           | BP | APOD, HRG, ITGB3, PTPRJ                       | 4 | 0,032820991 |
| <b>establishment of T cell polarity</b>               | BP | GSN, MYH9                                     | 2 | 0,032820991 |
| <b>complement receptor mediated signaling pathway</b> | BP | C3, GPLD1                                     | 2 | 0,032820991 |
| <b>positive regulation of fibroblast migration</b>    | BP | ITGB1, ITGB3                                  | 2 | 0,032820991 |
| <b>neuron remodeling</b>                              | BP | C1QA, C3                                      | 2 | 0,032820991 |
| <b>heart trabecula formation</b>                      | BP | ADGRG6, RBP4                                  | 2 | 0,032820991 |
| <b>viral life cycle</b>                               | BP | DPP4, FCN3, GSN, ITGB1, ITGB3, LAMP1, NCAM1   | 7 | 0,032878331 |
| <b>visual learning</b>                                | BP | DBH, ITGB1, KIT                               | 3 | 0,033000142 |
| <b>positive regulation of proteolysis</b>             | BP | CLEC3B, CLU, F12, GPLD1, GSN, KLKB1, MYH9     | 7 | 0,033738333 |
| <b>blood vessel remodeling</b>                        | BP | ACE, DBH, HRG                                 | 3 | 0,034459202 |
| <b>negative regulation of chemotaxis</b>              | BP | C5, DPP4, HRG                                 | 3 | 0,034459202 |
| <b>cell chemotaxis</b>                                | BP | BIN2, C5, DPP4, ENG, HRG, KIT, PTPRJ          | 7 | 0,035057099 |
| <b>establishment of lymphocyte polarity</b>           | BP | GSN, MYH9                                     | 2 | 0,035934028 |
| <b>renal sodium ion transport</b>                     | BP | PON3, UMOD                                    | 2 | 0,035934028 |
| <b>keratan sulfate biosynthetic process</b>           | BP | B3GNT2, B4GAT1                                | 2 | 0,035934028 |
| <b>low-density lipoprotein particle remodeling</b>    | BP | APOB, CETP                                    | 2 | 0,035934028 |
| <b>plasma membrane organization</b>                   | BP | BIN2, CLU, GSN, MYH9, SERPINA5                | 5 | 0,035934028 |
| <b>regulation of cholesterol efflux</b>               | BP | ADIPOQ, CETP, PON1                            | 3 | 0,037318875 |
| <b>opsonization</b>                                   | BP | COLEC10, FCN3                                 | 2 | 0,039655621 |

|                                                                                        |    |                                     |   |             |
|----------------------------------------------------------------------------------------|----|-------------------------------------|---|-------------|
| <b>regulation of lipoprotein metabolic process</b>                                     | BP | APOD, ITGB3                         | 2 | 0,039655621 |
| <b>actin filament severing</b>                                                         | BP | GSN, MYH9                           | 2 | 0,039655621 |
| <b>lactone metabolic process</b>                                                       | BP | PON1, PON3                          | 2 | 0,039655621 |
| <b>negative regulation of leukocyte migration</b>                                      | BP | APOD, C5, DPP4                      | 3 | 0,042636726 |
| <b>blood vessel endothelial cell migration</b>                                         | BP | GPLD1, HRG, ITGB1, MYH9, PLG        | 5 | 0,042991479 |
| <b>muscle cell migration</b>                                                           | BP | ACE, ADIPOQ, IGFBP3, ITGB3          | 4 | 0,042991479 |
| <b>regulation of systemic arterial blood pressure by circulatory renin-angiotensin</b> | BP | ACE, ENPEP                          | 2 | 0,042991479 |
| <b>regulation of extracellular matrix disassembly</b>                                  | BP | DPP4, FAP                           | 2 | 0,042991479 |
| <b>cell-cell adhesion mediated by integrin</b>                                         | BP | DPP4, ITGB1                         | 2 | 0,042991479 |
| <b>high-density lipoprotein particle clearance</b>                                     | BP | APOM, GPLD1                         | 2 | 0,042991479 |
| <b>keratan sulfate metabolic process</b>                                               | BP | B3GNT2, B4GAT1                      | 2 | 0,042991479 |
| <b>regulation of plasma membrane organization</b>                                      | BP | GSN, MYH9                           | 2 | 0,042991479 |
| <b>myeloid leukocyte mediated immunity</b>                                             | BP | ACE, C3, F2, KIT                    | 4 | 0,045185995 |
| <b>visual behavior</b>                                                                 | BP | DBH, ITGB1, KIT                     | 3 | 0,045272165 |
| <b>positive regulation of transforming growth factor beta production</b>               | BP | LUM, SERPINF2                       | 2 | 0,047345609 |
| <b>positive regulation of peptidyl-tyrosine phosphorylation</b>                        | BP | ADIPOQ, ITGB3, KIT, PTPRJ           | 4 | 0,047467341 |
| <b>glial cell differentiation</b>                                                      | BP | ADGRG6, C1QA, CLU, CNTN1, F2, PTPRJ | 6 | 0,047593988 |
| <b>positive regulation of angiogenesis</b>                                             | BP | C3, ECM1, ENG, ITGB1, ITGB3         | 5 | 0,048375671 |

|                                                 |    |                                                                                                                                                                                                 |    |          |
|-------------------------------------------------|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----|----------|
| <b>blood microparticle</b>                      | CC | A1BG, AFM, AHSG, APOA4, BCHE, C1QB, C3, C8A, C8G, CFH, CLU, ENG, F13A1, F2, FCN3, GC, GSN, HRG, IGHV3-7, ITIH1, ITIH2, ITIH4, KNG1, PLG, PON1, PROS1, SERPINC1, SERPINF2                        | 28 | 8,75E-33 |
| <b>collagen-containing extracellular matrix</b> | CC | A1BG, ADIPOQ, AHSG, APOA4, APOH, AZGP1, C1QA, C1QB, CDH13, CLEC3B, CLU, ECM1, F12, F13A1, F2, FCN3, HRG, ITIH1, ITIH2, ITIH4, KNG1, LUM, NCAM1, PCOLCE, PLG, SERPINA5, SERPINC1, SERPINF2, SPP2 | 29 | 1,07E-20 |
| <b>plasma lipoprotein particle</b>              | CC | APOA4, APOB, APOC1, APOC4, APOF, APOH, APOM, CETP, CLU, LCAT, PCYOX1, PON1                                                                                                                      | 12 | 8,99E-17 |
| <b>lipoprotein particle</b>                     | CC | APOA4, APOB, APOC1, APOC4, APOF, APOH, APOM, CETP, CLU, LCAT, PCYOX1, PON1                                                                                                                      | 12 | 8,99E-17 |
| <b>protein-lipid complex</b>                    | CC | APOA4, APOB, APOC1, APOC4, APOF, APOH, APOM, CETP, CLU, LCAT, PCYOX1, PON1                                                                                                                      | 12 | 2,14E-16 |

|                                          |    |                                                                                                                                              |    |          |
|------------------------------------------|----|----------------------------------------------------------------------------------------------------------------------------------------------|----|----------|
| <b>secretory granule lumen</b>           | CC | A1BG, AHSG, APOH, BIN2, C3, CLEC3B, CLU, CRISP3, DBH, ECM1, F13A1, GSN, HRG, ITIH4, KNG1, PLG, PROS1, SELENOP, SERPINA4, SERPINF2, SPP2, TTR | 22 | 7,65E-16 |
| <b>cytoplasmic vesicle lumen</b>         | CC | A1BG, AHSG, APOH, BIN2, C3, CLEC3B, CLU, CRISP3, DBH, ECM1, F13A1, GSN, HRG, ITIH4, KNG1, PLG, PROS1, SELENOP, SERPINA4, SERPINF2, SPP2, TTR | 22 | 8,46E-16 |
| <b>vesicle lumen</b>                     | CC | A1BG, AHSG, APOH, BIN2, C3, CLEC3B, CLU, CRISP3, DBH, ECM1, F13A1, GSN, HRG, ITIH4, KNG1, PLG, PROS1, SELENOP, SERPINA4, SERPINF2, SPP2, TTR | 22 | 8,46E-16 |
| <b>high-density lipoprotein particle</b> | CC | APOA4, APOC1, APOC4, APOF, APOH, APOM, CETP, CLU, LCAT, PON1                                                                                 | 10 | 6,51E-15 |

|                                                      |    |                                                                                                                        |    |          |
|------------------------------------------------------|----|------------------------------------------------------------------------------------------------------------------------|----|----------|
| <b>endoplasmic reticulum lumen</b>                   | CC | ADAMTS13, AHSG, APOA4, APOB, BCHE, C3, CLU, F10, F2, IGFBP3, ITIH2, KNG1, MINPP1, PROC, PROZ, SERPINC1, SERPIND1, SPP2 | 18 | 8,69E-12 |
| <b>platelet dense granule lumen</b>                  | CC | APOH, CLEC3B, ECM1, ITIH4, SELENOP, SERPINA4, SPP2                                                                     | 7  | 1,36E-11 |
| <b>platelet alpha granule</b>                        | CC | A1BG, AHSG, CLU, F13A1, HRG, ITGB3, KNG1, PLG, PROS1, SERPINA5, SERPINF2                                               | 11 | 1,09E-10 |
| <b>very-low-density lipoprotein particle</b>         | CC | APOA4, APOB, APOC1, APOC4, APOH, APOM, PCYOX1                                                                          | 7  | 3,27E-10 |
| <b>triglyceride-rich plasma lipoprotein particle</b> | CC | APOA4, APOB, APOC1, APOC4, APOH, APOM, PCYOX1                                                                          | 7  | 3,27E-10 |
| <b>platelet dense granule</b>                        | CC | APOH, CLEC3B, ECM1, ITIH4, SELENOP, SERPINA4, SPP2                                                                     | 7  | 3,27E-10 |
| <b>external side of plasma membrane</b>              | CC | ACE, AZGP1, CDH13, COLEC10, ENG, ENPEP, F10, F2, FCN3, ITGB1, ITGB3, KIT, LAMP1, MCAM, NCAM1, PLG, SELL, SERPINA5      | 18 | 4,15E-10 |
| <b>platelet alpha granule lumen</b>                  | CC | A1BG, AHSG, CLU, F13A1, HRG, KNG1, PLG, PROS1, SERPINF2                                                                | 9  | 2,61E-09 |
| <b>pore complex</b>                                  | CC | C5, C6, C8A, C8B, C8G                                                                                                  | 5  | 4,70E-06 |

|                                          |    |                                                             |    |             |
|------------------------------------------|----|-------------------------------------------------------------|----|-------------|
| <b>chylomicron</b>                       | CC | APOA4, APOB, APOC1, APOH                                    | 4  | 8,97E-06    |
| <b>low-density lipoprotein particle</b>  | CC | APOA4, APOB, APOF, APOM                                     | 4  | 1,61E-05    |
| <b>Golgi lumen</b>                       | CC | F10, F2, LUM, PROC, PROS1, PROZ, UMOD                       | 7  | 3,23E-05    |
| <b>collagen trimer</b>                   | CC | ADIPOQ, C1QA, C1QB, COLEC10, FCN3, LUM                      | 6  | 0,000116854 |
| <b>serine-type endopeptidase complex</b> | CC | CFH, COLEC10, FCN3                                          | 3  | 0,00169465  |
| <b>focal adhesion</b>                    | CC | CDH13, DPP4, ENG, FAP, GSN, ITGB1, ITGB3, MCAM, MYH9, RAB10 | 10 | 0,001899637 |
| <b>serine-type peptidase complex</b>     | CC | CFH, COLEC10, FCN3                                          | 3  | 0,002112675 |
| <b>cell-substrate junction</b>           | CC | CDH13, DPP4, ENG, FAP, GSN, ITGB1, ITGB3, MCAM, MYH9, RAB10 | 10 | 0,002112675 |
| <b>lamellipodium membrane</b>            | CC | DPP4, FAP, ITGB3                                            | 3  | 0,00226476  |
| <b>ruffle membrane</b>                   | CC | FAP, ITGB1, ITGB3, PLEK, PTPRJ                              | 5  | 0,00255434  |
| <b>leading edge membrane</b>             | CC | DPP4, FAP, ITGB1, ITGB3, PLEK, PTPRJ                        | 6  | 0,005532896 |
| <b>ruffle</b>                            | CC | FAP, ITGB1, ITGB3, MYH9, PLEK, PTPRJ                        | 6  | 0,005823916 |
| <b>cell projection membrane</b>          | CC | ACE, DPP4, FAP, ITGB1, ITGB3, PLEK, PTPRJ, UMOD             | 8  | 0,009033618 |
| <b>secretory granule membrane</b>        | CC | DBH, ITGB3, LAMP1, PTPRJ, RAB10, SELL, SERPINA5             | 7  | 0,019522125 |
| <b>chromaffin granule</b>                | CC | CLU, DBH                                                    | 2  | 0,019522125 |
| <b>brush border</b>                      | CC | ACE, ENPEP, MYH9, MYL12B                                    | 4  | 0,024857873 |
| <b>vacuolar lumen</b>                    | CC | APOB, C3, GC, LUM, TTR                                      | 5  | 0,024857873 |
| <b>cell leading edge</b>                 | CC | DPP4, FAP, GSN, ITGB1, ITGB3, MYH9, PLEK, PTPRJ             | 8  | 0,024857873 |
| <b>melanosome</b>                        | CC | GPNMB, ITGB1, ITGB3, LAMP1                                  | 4  | 0,024857873 |
| <b>pigment granule</b>                   | CC | GPNMB, ITGB1, ITGB3, LAMP1                                  | 4  | 0,024857873 |

|                                         |    |                                                                                                                                                      |    |             |
|-----------------------------------------|----|------------------------------------------------------------------------------------------------------------------------------------------------------|----|-------------|
| <b>lamellipodium</b>                    | CC | DPP4, FAP, GSN, ITGB1, ITGB3                                                                                                                         | 5  | 0,038781448 |
| <b>peptidase complex</b>                | CC | CFH, COLEC10, FAP, FCN3                                                                                                                              | 4  | 0,038781448 |
| <b>peptidase inhibitor activity</b>     | MF | AHSG, C3, C5, FETUB, HRG, ITIH1, ITIH2, ITIH4, KNG1, PI16, PROS1, SERPINA4, SERPINA5, SERPINA6, SERPINA7, SERPINC1, SERPIND1, SERPINF2, SPP2         | 19 | 4,55E-16    |
| <b>endopeptidase inhibitor activity</b> | MF | AHSG, C3, C5, FETUB, HRG, ITIH1, ITIH2, ITIH4, KNG1, PROS1, SERPINA4, SERPINA5, SERPINA6, SERPINA7, SERPINC1, SERPIND1, SERPINF2, SPP2               | 18 | 2,04E-15    |
| <b>peptidase regulator activity</b>     | MF | AHSG, C3, C5, FETUB, HRG, ITIH1, ITIH2, ITIH4, KNG1, PCOLCE, PI16, PROS1, SERPINA4, SERPINA5, SERPINA6, SERPINA7, SERPINC1, SERPIND1, SERPINF2, SPP2 | 20 | 2,04E-15    |

|                                           |    |                                                                                                                                        |    |          |
|-------------------------------------------|----|----------------------------------------------------------------------------------------------------------------------------------------|----|----------|
| <b>endopeptidase regulator activity</b>   | MF | AHSG, C3, C5, FETUB, HRG, ITIH1, ITIH2, ITIH4, KNG1, PROS1, SERPINA4, SERPINA5, SERPINA6, SERPINA7, SERPINC1, SERPIND1, SERPINF2, SPP2 | 18 | 9,21E-15 |
| <b>glycosaminoglycan binding</b>          | MF | APOB, APOH, CFH, CLEC3B, ENG, F11, F2, GPNMB, HABP2, HRG, ITIH1, ITIH2, KNG1, PCOLCE, PGLYRP2, SELL, SERPINA5, SERPINC1, SERPIND1      | 19 | 4,98E-14 |
| <b>serine-type peptidase activity</b>     | MF | ACE, C1RL, CFI, DPP4, F10, F11, F12, F2, FAP, HABP2, HGFAC, KLKB1, MASP1, PLG, PROC, PROZ                                              | 16 | 3,50E-12 |
| <b>serine hydrolase activity</b>          | MF | ACE, C1RL, CFI, DPP4, F10, F11, F12, F2, FAP, HABP2, HGFAC, KLKB1, MASP1, PLG, PROC, PROZ                                              | 16 | 4,12E-12 |
| <b>serine-type endopeptidase activity</b> | MF | C1RL, CFI, DPP4, F10, F11, F12, F2, FAP, HABP2, HGFAC, KLKB1, MASP1, PLG, PROC, PROZ                                                   | 15 | 1,12E-11 |



|                                                     |    |                                                                                                                                                     |    |          |
|-----------------------------------------------------|----|-----------------------------------------------------------------------------------------------------------------------------------------------------|----|----------|
| <b>enzyme inhibitor activity</b>                    | MF | AHSG, APOC1, C3, C5, FETUB, HRG, ITIH1, ITIH2, ITIH4, KNG1, PI16, PROS1, SERPINA4, SERPINA5, SERPINA6, SERPINA7, SERPINC1, SERPIND1, SERPINF2, SPP2 | 20 | 2,77E-11 |
| <b>heparin binding</b>                              | MF | APOB, APOH, CFH, CLEC3B, F11, F2, GPNMB, HRG, KNG1, PCOLCE, SELL, SERPINA5, SERPINC1, SERPIND1                                                      | 14 | 1,26E-10 |
| <b>serine-type endopeptidase inhibitor activity</b> | MF | HRG, ITIH1, ITIH2, ITIH4, SERPINA4, SERPINA5, SERPINA6, SERPINA7, SERPINC1, SERPIND1, SERPINF2                                                      | 11 | 9,01E-10 |
| <b>protease binding</b>                             | MF | CHL1, DPP4, ECM1, FAP, ITGB1, ITGB3, KIT, PLG, SELL, SERPINA5, SERPINC1, SERPINF2                                                                   | 12 | 1,12E-09 |
| <b>endopeptidase activity</b>                       | MF | ACE, ADAMTS13, ADGRG6, C1RL, CFI, DPP4, F10, F11, F12, F2, FAP, HABP2, HGFAC, KLKB1, MASP1, PLG, PROC, PROZ                                         | 18 | 1,30E-09 |
| <b>sulfur compound binding</b>                      | MF | APOB, APOH, CFH, CLEC3B, F11, F2, GPNMB, HRG, KNG1, PCOLCE, SELL, SERPINA5, SERPINC1, SERPIND1                                                      | 14 | 3,72E-08 |

|                                                       |    |                                                                      |    |             |
|-------------------------------------------------------|----|----------------------------------------------------------------------|----|-------------|
| <b>exopeptidase activity</b>                          | MF | ACE, CNDP1, CPB2, DPP4, ENPEP, F11, FAP                              | 7  | 6,39E-05    |
| <b>lipid transporter activity</b>                     | MF | APOA4, APOB, APOC4, APOD, APOF, APOM, CETP, RBP4                     | 8  | 0,000257283 |
| <b>phosphatidylcholine binding</b>                    | MF | APOA4, APOC1, CETP, SERPINA5                                         | 4  | 0,000527699 |
| <b>steroid binding</b>                                | MF | APOD, APOF, CETP, GC, SERPINA6, SHBG                                 | 6  | 0,000847889 |
| <b>carbohydrate binding</b>                           | MF | ATRN, CLEC3B, CNTN1, COLEC10, DBH, ENG, FCN3, ITIH1, SELL            | 9  | 0,000893233 |
| <b>cysteine-type endopeptidase inhibitor activity</b> | MF | AHSG, FETUB, HRG, KNG1                                               | 4  | 0,000936657 |
| <b>quaternary ammonium group binding</b>              | MF | APOA4, APOC1, CETP, SERPINA5                                         | 4  | 0,001357626 |
| <b>virus receptor activity</b>                        | MF | DPP4, ITGB1, ITGB3, LAMP1, NCAM1                                     | 5  | 0,001586869 |
| <b>exogenous protein binding</b>                      | MF | DPP4, ITGB1, ITGB3, LAMP1, NCAM1                                     | 5  | 0,001611061 |
| <b>insulin-like growth factor binding</b>             | MF | IGFALS, IGFBP3, ITGB3                                                | 3  | 0,002288939 |
| <b>alcohol binding</b>                                | MF | APOD, APOF, C8G, CETP, RBP4                                          | 5  | 0,002654511 |
| <b>phospholipid binding</b>                           | MF | APOA4, APOB, APOC1, APOH, APOM, BIN2, CETP, F10, GSN, PON1, SERPINA5 | 11 | 0,002654511 |
| <b>cholesterol transfer activity</b>                  | MF | APOA4, APOB, CETP                                                    | 3  | 0,004154158 |
| <b>integrin binding</b>                               | MF | ADAMTS13, FAP, GPNMB, ITGB1, ITGB3, MYH9                             | 6  | 0,004798583 |
| <b>complement binding</b>                             | MF | C8A, C8G, CFH                                                        | 3  | 0,004906186 |
| <b>coreceptor activity</b>                            | MF | ENG, IL1RAP, ITGB1, ITGB3                                            | 4  | 0,004906186 |
| <b>metalloexopeptidase activity</b>                   | MF | ACE, CNDP1, CPB2, ENPEP                                              | 4  | 0,006776003 |
| <b>fibronectin binding</b>                            | MF | IGFBP3, ITGB1, ITGB3                                                 | 3  | 0,006841758 |
| <b>collagen binding</b>                               | MF | ADGRG6, ITGB1, LUM, PCOLCE                                           | 4  | 0,007096925 |
| <b>sterol transfer activity</b>                       | MF | APOA4, APOB, CETP                                                    | 3  | 0,007096925 |

|                                                        |    |                                    |   |             |
|--------------------------------------------------------|----|------------------------------------|---|-------------|
| <b>growth factor binding</b>                           | MF | ENG, IGFALS, IGFBP3, ITGB3, KIT    | 5 | 0,010535385 |
| <b>proteoglycan binding</b>                            | MF | CFH, GPNMB, HRG                    | 3 | 0,011248671 |
| <b>dipeptidyl-peptidase activity</b>                   | MF | DPP4, FAP                          | 2 | 0,011248671 |
| <b>retinoid binding</b>                                | MF | C8G, RBP4, SERPINA5                | 3 | 0,011248671 |
| <b>isoprenoid binding</b>                              | MF | C8G, RBP4, SERPINA5                | 3 | 0,011248671 |
| <b>aminopeptidase activity</b>                         | MF | DPP4, ENPEP, F11                   | 3 | 0,012728906 |
| <b>serine-type exopeptidase activity</b>               | MF | ACE, F11                           | 2 | 0,015352877 |
| <b>vitamin binding</b>                                 | MF | AFM, C8G, DBH, GC, RBP4            | 5 | 0,015368238 |
| <b>insulin-like growth factor I binding</b>            | MF | IGFBP3, ITGB3                      | 2 | 0,017229929 |
| <b>carboxypeptidase activity</b>                       | MF | ACE, CNDP1, CPB2                   | 3 | 0,018399365 |
| <b>platelet-derived growth factor receptor binding</b> | MF | ITGB3, PTPRJ                       | 2 | 0,019129988 |
| <b>retinol binding</b>                                 | MF | C8G, RBP4                          | 2 | 0,023956799 |
| <b>misfolded protein binding</b>                       | MF | CLU, F12                           | 2 | 0,023956799 |
| <b>cholesterol binding</b>                             | MF | APOD, APOF, CETP                   | 3 | 0,024997163 |
| <b>dipeptidase activity</b>                            | MF | ACE, CNDP1                         | 2 | 0,025936973 |
| <b>apolipoprotein binding</b>                          | MF | LCAT, PLG                          | 2 | 0,028479333 |
| <b>metallopeptidase activity</b>                       | MF | ACE, ADAMTS13, CNDP1, CPB2, ENPEP  | 5 | 0,030481332 |
| <b>heparan sulfate proteoglycan binding</b>            | MF | CFH, HRG                           | 2 | 0,030481332 |
| <b>carboxylic acid binding</b>                         | MF | ADIPOQ, APOC1, DBH, SELL, SERPINA5 | 5 | 0,03100213  |
| <b>copper ion binding</b>                              | MF | AOC3, APOA4, DBH                   | 3 | 0,034159933 |
| <b>lipid transfer activity</b>                         | MF | APOA4, APOB, CETP                  | 3 | 0,034868013 |
| <b>carboxylic ester hydrolase activity</b>             | MF | BCHE, GPLD1, LCAT, PON1, PON3      | 5 | 0,034868013 |
| <b>extracellular matrix binding</b>                    | MF | ADGRG6, ITGB1, ITGB3               | 3 | 0,035277724 |
| <b>sialic acid binding</b>                             | MF | ADIPOQ, SELL                       | 2 | 0,035960396 |
| <b>organic acid binding</b>                            | MF | ADIPOQ, APOC1, DBH, SELL, SERPINA5 | 5 | 0,035960396 |
| <b>sterol binding</b>                                  | MF | APOD, APOF, CETP                   | 3 | 0,037936866 |

|                                                          |    |                        |   |             |
|----------------------------------------------------------|----|------------------------|---|-------------|
| <b>cell adhesion mediator activity</b>                   | MF | CNTN1, ITGB1, RAB10    | 3 | 0,038836224 |
| <b>hyaluronic acid binding</b>                           | MF | ITIH1, ITIH2           | 2 | 0,040432947 |
| <b>monosaccharide binding</b>                            | MF | COLEC10, DBH, ENG      | 3 | 0,045031029 |
| <b>immunoglobulin binding</b>                            | MF | HRG, UMOD              | 2 | 0,045031029 |
| <b>low-density lipoprotein particle receptor binding</b> | MF | APOB, CLU              | 2 | 0,045031029 |
| <b>myosin binding</b>                                    | MF | GSN, MYL12B, RAB10     | 3 | 0,045031029 |
| <b>cytokine binding</b>                                  | MF | ENG, ITGB1, ITGB3, KIT | 4 | 0,047600121 |
| <b>mitogen-activated protein kinase binding</b>          | MF | ACE, PTPRJ             | 2 | 0,049677292 |

**Table S5b.** Showing enriched gene ontologies from downregulated DEPs in sepsis compared to control. BP=biological processes, CC=cellular compartments, MF=molecular functions. Ontologies classified as significantly altered if exhibiting an adjusted p-value < 0.05.

**Table S6a – Gene Ontology Pancreatitis vs Control Up**

| <b>Description</b>                                           | <b>Ontology</b> | <b>geneID</b>                                                        | <b>Protein Count</b> | <b>Adjusted P-value</b> |
|--------------------------------------------------------------|-----------------|----------------------------------------------------------------------|----------------------|-------------------------|
| <b>acute-phase response</b>                                  | BP              | CRP, F8, LBP, ORM1, ORM2, SAA1, SAA2, SERPINA3                       | 8                    | 2,20E-10                |
| <b>acute inflammatory response</b>                           | BP              | CRP, F8, LBP, ORM1, ORM2, SAA1, SAA2, SERPINA3                       | 8                    | 1,07E-07                |
| <b>regulation of inflammatory response</b>                   | BP              | IL1RL1, LBP, MMP8, MMP9, PSMA1, PSMA6, S100A12, S100A8, S100A9, SAA1 | 10                   | 2,50E-05                |
| <b>collagen metabolic process</b>                            | BP              | COL6A1, CTSB, MMP8, MMP9, PRSS2, VIM                                 | 6                    | 6,76E-05                |
| <b>respiratory burst involved in inflammatory response</b>   | BP              | LBP, PRDX2, S100A9                                                   | 3                    | 0,000316302             |
| <b>neutrophil chemotaxis</b>                                 | BP              | LBP, S100A12, S100A8, S100A9, SAA1                                   | 5                    | 0,000316398             |
| <b>positive regulation of inflammatory response</b>          | BP              | IL1RL1, LBP, MMP8, S100A12, S100A8, S100A9                           | 6                    | 0,000355593             |
| <b>collagen catabolic process</b>                            | BP              | CTSB, MMP8, MMP9, PRSS2                                              | 4                    | 0,000523259             |
| <b>neutrophil migration</b>                                  | BP              | LBP, S100A12, S100A8, S100A9, SAA1                                   | 5                    | 0,000687732             |
| <b>respiratory burst involved in defense response</b>        | BP              | LBP, PRDX2, S100A9                                                   | 3                    | 0,000885594             |
| <b>regulation of macrophage activation</b>                   | BP              | IL1RL1, LBP, MMP8, VSIG4                                             | 4                    | 0,00113625              |
| <b>granulocyte chemotaxis</b>                                | BP              | LBP, S100A12, S100A8, S100A9, SAA1                                   | 5                    | 0,00113625              |
| <b>leukocyte migration involved in inflammatory response</b> | BP              | LBP, S100A8, S100A9                                                  | 3                    | 0,00113625              |
| <b>extracellular matrix disassembly</b>                      | BP              | LCP1, MMP8, MMP9, PRSS2                                              | 4                    | 0,001311467             |
| <b>response to lipopolysaccharide</b>                        | BP              | COL6A1, LBP, MMP8, MMP9, PRDX2, S100A8, VIM                          | 7                    | 0,001412143             |
| <b>regulation of endopeptidase activity</b>                  | BP              | CTSD, MMP9, S100A8, S100A9, SERPINA3, TIMP1                          | 6                    | 0,0017707               |
| <b>response to molecule of bacterial origin</b>              | BP              | COL6A1, LBP, MMP8, MMP9, PRDX2, S100A8, VIM                          | 7                    | 0,001801649             |

|                                                                                     |    |                                             |   |             |
|-------------------------------------------------------------------------------------|----|---------------------------------------------|---|-------------|
| <b>granulocyte migration</b>                                                        | BP | LBP, S100A12, S100A8, S100A9, SAA1          | 5 | 0,002041955 |
| <b>positive regulation of macrophage activation</b>                                 | BP | IL1RL1, LBP, MMP8                           | 3 | 0,00272215  |
| <b>respiratory burst</b>                                                            | BP | LBP, PRDX2, S100A9                          | 3 | 0,006102135 |
| <b>positive regulation of tumor necrosis factor production</b>                      | BP | LBP, MMP8, ORM1, ORM2                       | 4 | 0,006102135 |
| <b>macrophage activation</b>                                                        | BP | IL1RL1, LBP, MMP8, VSIG4                    | 4 | 0,006102135 |
| <b>positive regulation of tumor necrosis factor superfamily cytokine production</b> | BP | LBP, MMP8, ORM1, ORM2                       | 4 | 0,006102135 |
| <b>extracellular matrix organization</b>                                            | BP | COL6A1, LCP1, MMP8, MMP9, NID1, PRSS2       | 6 | 0,006102135 |
| <b>extracellular structure organization</b>                                         | BP | COL6A1, LCP1, MMP8, MMP9, NID1, PRSS2       | 6 | 0,006102135 |
| <b>external encapsulating structure organization</b>                                | BP | COL6A1, LCP1, MMP8, MMP9, NID1, PRSS2       | 6 | 0,006102135 |
| <b>astrocyte development</b>                                                        | BP | S100A8, S100A9, VIM                         | 3 | 0,006102135 |
| <b>regulation of peptidase activity</b>                                             | BP | CTSD, MMP9, S100A8, S100A9, SERPINA3, TIMP1 | 6 | 0,006357859 |
| <b>positive regulation of NF-kappaB transcription factor activity</b>               | BP | PSMA6, S100A12, S100A8, S100A9              | 4 | 0,007327278 |
| <b>cellular response to lipopolysaccharide</b>                                      | BP | LBP, MMP8, MMP9, PRDX2, VIM                 | 5 | 0,007327278 |
| <b>endodermal cell differentiation</b>                                              | BP | COL6A1, MMP8, MMP9                          | 3 | 0,008678051 |
| <b>leukocyte chemotaxis</b>                                                         | BP | LBP, S100A12, S100A8, S100A9, SAA1          | 5 | 0,008678051 |
| <b>cellular response to molecule of bacterial origin</b>                            | BP | LBP, MMP8, MMP9, PRDX2, VIM                 | 5 | 0,008678051 |
| <b>myeloid leukocyte migration</b>                                                  | BP | LBP, S100A12, S100A8, S100A9, SAA1          | 5 | 0,008678051 |
| <b>cellular response to UV-A</b>                                                    | BP | MMP9, TIMP1                                 | 2 | 0,008815081 |
| <b>myeloid leukocyte activation</b>                                                 | BP | IL1RL1, LBP, MMP8, S100A12, VSIG4           | 5 | 0,008815081 |
| <b>glial cell development</b>                                                       | BP | COL6A1, S100A8, S100A9, VIM                 | 4 | 0,008815081 |

|                                                                                         |    |                                        |   |             |
|-----------------------------------------------------------------------------------------|----|----------------------------------------|---|-------------|
| <b>glyceraldehyde-3-phosphate metabolic process</b>                                     | BP | TALDO1, TKT                            | 2 | 0,009841091 |
| <b>regulation of cysteine-type endopeptidase activity involved in apoptotic process</b> | BP | CTSD, MMP9, S100A8, S100A9             | 4 | 0,010389922 |
| <b>endoderm formation</b>                                                               | BP | COL6A1, MMP8, MMP9                     | 3 | 0,010762747 |
| <b>leukocyte aggregation</b>                                                            | BP | S100A8, S100A9                         | 2 | 0,010762747 |
| <b>cellular response to biotic stimulus</b>                                             | BP | LBP, MMP8, MMP9, PRDX2, VIM            | 5 | 0,011190162 |
| <b>response to UV-A</b>                                                                 | BP | MMP9, TIMP1                            | 2 | 0,011954045 |
| <b>response to UV</b>                                                                   | BP | CAT, COL6A1, MMP9, TIMP1               | 4 | 0,012599783 |
| <b>defense response to fungus</b>                                                       | BP | S100A12, S100A8, S100A9                | 3 | 0,012599783 |
| <b>protein nitrosylation</b>                                                            | BP | S100A8, S100A9                         | 2 | 0,012599783 |
| <b>peptidyl-cysteine S-nitrosylation</b>                                                | BP | S100A8, S100A9                         | 2 | 0,012599783 |
| <b>wound healing</b>                                                                    | BP | F8, LRG1, PRDX2, SAA1, TIMP1, VWF      | 6 | 0,014001442 |
| <b>response to peptide hormone</b>                                                      | BP | CAT, COL6A1, CTSD, LTA4H, REG1B, TIMP1 | 6 | 0,014041784 |
| <b>regulation of cysteine-type endopeptidase activity</b>                               | BP | CTSD, MMP9, S100A8, S100A9             | 4 | 0,014159409 |
| <b>opsonization</b>                                                                     | BP | CRP, LBP                               | 2 | 0,014638727 |
| <b>positive regulation of interleukin-1 production</b>                                  | BP | ORM1, ORM2, SAA1                       | 3 | 0,014638727 |
| <b>pyridine nucleotide metabolic process</b>                                            | BP | BPGM, COL6A1, TALDO1, TKT              | 4 | 0,014638727 |
| <b>nicotinamide nucleotide metabolic process</b>                                        | BP | BPGM, COL6A1, TALDO1, TKT              | 4 | 0,014638727 |
| <b>humoral immune response</b>                                                          | BP | PRSS2, REG1B, S100A12, S100A9, VSIG4   | 5 | 0,015758538 |
| <b>response to fungus</b>                                                               | BP | S100A12, S100A8, S100A9                | 3 | 0,015758538 |
| <b>pyridine-containing compound metabolic process</b>                                   | BP | BPGM, COL6A1, TALDO1, TKT              | 4 | 0,015758538 |
| <b>regulation of respiratory burst</b>                                                  | BP | LBP, S100A9                            | 2 | 0,016525685 |

|                                                                                                  |    |                                    |   |             |
|--------------------------------------------------------------------------------------------------|----|------------------------------------|---|-------------|
| <b>antimicrobial humoral response</b>                                                            | BP | PRSS2, REG1B, S100A12, S100A9      | 4 | 0,017431923 |
| <b>pentose-phosphate shunt</b>                                                                   | BP | TALDO1, TKT                        | 2 | 0,017431923 |
| <b>keratinocyte migration</b>                                                                    | BP | LRG1, MMP9                         | 2 | 0,017431923 |
| <b>tumor necrosis factor production</b>                                                          | BP | LBP, MMP8, ORM1, ORM2              | 4 | 0,01746395  |
| <b>regulation of tumor necrosis factor production</b>                                            | BP | LBP, MMP8, ORM1, ORM2              | 4 | 0,01746395  |
| <b>cell chemotaxis</b>                                                                           | BP | LBP, S100A12, S100A8, S100A9, SAA1 | 5 | 0,017514797 |
| <b>chronic inflammatory response</b>                                                             | BP | S100A8, S100A9                     | 2 | 0,017514797 |
| <b>regulation of integrin-mediated signaling pathway</b>                                         | BP | NID1, TIMP1                        | 2 | 0,017514797 |
| <b>neuroinflammatory response</b>                                                                | BP | BPGM, MMP8, MMP9                   | 3 | 0,017514797 |
| <b>tumor necrosis factor superfamily cytokine production</b>                                     | BP | LBP, MMP8, ORM1, ORM2              | 4 | 0,017514797 |
| <b>regulation of tumor necrosis factor superfamily cytokine production</b>                       | BP | LBP, MMP8, ORM1, ORM2              | 4 | 0,017514797 |
| <b>endoderm development</b>                                                                      | BP | COL6A1, MMP8, MMP9                 | 3 | 0,017514797 |
| <b>lung development</b>                                                                          | BP | CHI3L1, COL6A1, CTSZ, LTA4H        | 4 | 0,018763666 |
| <b>astrocyte differentiation</b>                                                                 | BP | S100A8, S100A9, VIM                | 3 | 0,018777935 |
| <b>defense response to bacterium</b>                                                             | BP | CRP, LBP, S100A12, S100A8, S100A9  | 5 | 0,018909315 |
| <b>NADPH regeneration</b>                                                                        | BP | TALDO1, TKT                        | 2 | 0,019045902 |
| <b>respiratory tube development</b>                                                              | BP | CHI3L1, COL6A1, CTSZ, LTA4H        | 4 | 0,019119036 |
| <b>positive regulation of DNA-binding transcription factor activity</b>                          | BP | PSMA6, S100A12, S100A8, S100A9     | 4 | 0,02100647  |
| <b>positive regulation of cysteine-type endopeptidase activity involved in apoptotic process</b> | BP | CTSD, S100A8, S100A9               | 3 | 0,02279305  |



|                                                                           |    |                                      |   |             |
|---------------------------------------------------------------------------|----|--------------------------------------|---|-------------|
| <b>cellular oxidant detoxification</b>                                    | BP | CAT, PRDX2, S100A9                   | 3 | 0,02279305  |
| <b>interleukin-8 production</b>                                           | BP | CHI3L1, CRP, LBP                     | 3 | 0,02605707  |
| <b>regulation of interleukin-8 production</b>                             | BP | CHI3L1, CRP, LBP                     | 3 | 0,02605707  |
| <b>respiratory system development</b>                                     | BP | CHI3L1, COL6A1, CTSZ, LTA4H          | 4 | 0,02605707  |
| <b>production of molecular mediator involved in inflammatory response</b> | BP | LBP, PRDX2, S100A9                   | 3 | 0,02605707  |
| <b>phagocytosis, recognition</b>                                          | BP | CRP, LBP                             | 2 | 0,02605707  |
| <b>glucose 6-phosphate metabolic process</b>                              | BP | TALDO1, TKT                          | 2 | 0,02605707  |
| <b>lung cell differentiation</b>                                          | BP | COL6A1, LTA4H                        | 2 | 0,02605707  |
| <b>lung epithelial cell differentiation</b>                               | BP | COL6A1, LTA4H                        | 2 | 0,02605707  |
| <b>negative regulation of endopeptidase activity</b>                      | BP | MMP9, SERPINA3, TIMP1                | 3 | 0,026893648 |
| <b>blood coagulation</b>                                                  | BP | F8, PRDX2, SAA1, VWF                 | 4 | 0,027851317 |
| <b>hydrogen peroxide catabolic process</b>                                | BP | CAT, PRDX2                           | 2 | 0,028749052 |
| <b>positive regulation of cysteine-type endopeptidase activity</b>        | BP | CTSD, S100A8, S100A9                 | 3 | 0,029527817 |
| <b>hemostasis</b>                                                         | BP | F8, PRDX2, SAA1, VWF                 | 4 | 0,029629878 |
| <b>coagulation</b>                                                        | BP | F8, PRDX2, SAA1, VWF                 | 4 | 0,029629878 |
| <b>reactive oxygen species metabolic process</b>                          | BP | CAT, COL6A1, CRP, PRDX2              | 4 | 0,029751586 |
| <b>leukocyte migration</b>                                                | BP | LBP, S100A12, S100A8, S100A9, SAA1   | 5 | 0,030360385 |
| <b>regulation of cell growth</b>                                          | BP | CDHR2, IGFBP4, PRSS2, S100A8, S100A9 | 5 | 0,031339863 |
| <b>leukotriene metabolic process</b>                                      | BP | CPA1, LTA4H                          | 2 | 0,032007142 |
| <b>peptidyl-cysteine modification</b>                                     | BP | S100A8, S100A9                       | 2 | 0,035159683 |
| <b>cellular detoxification</b>                                            | BP | CAT, PRDX2, S100A9                   | 3 | 0,035159683 |
| <b>carbohydrate derivative catabolic process</b>                          | BP | BPGM, CHI3L1, COL6A1, MAN1A1         | 4 | 0,035159683 |

|                                                                                |    |                                    |   |             |
|--------------------------------------------------------------------------------|----|------------------------------------|---|-------------|
| <b>intracellular zinc ion homeostasis</b>                                      | BP | S100A8, S100A9                     | 2 | 0,036309905 |
| <b>leukocyte cell-cell adhesion</b>                                            | BP | LRG1, PRDX2, S100A8, S100A9, VSIG4 | 5 | 0,036653577 |
| <b>regulation of toll-like receptor signaling pathway</b>                      | BP | S100A8, S100A9                     | 2 | 0,036653577 |
| <b>basement membrane organization</b>                                          | BP | COL6A1, NID1                       | 2 | 0,036653577 |
| <b>interleukin-1 production</b>                                                | BP | ORM1, ORM2, SAA1                   | 3 | 0,036653577 |
| <b>regulation of interleukin-1 production</b>                                  | BP | ORM1, ORM2, SAA1                   | 3 | 0,036653577 |
| <b>glial cell differentiation</b>                                              | BP | COL6A1, S100A8, S100A9, VIM        | 4 | 0,03710416  |
| <b>formation of primary germ layer</b>                                         | BP | COL6A1, MMP8, MMP9                 | 3 | 0,037291479 |
| <b>detection of biotic stimulus</b>                                            | BP | CDHR2, LBP                         | 2 | 0,037291479 |
| <b>response to toxic substance</b>                                             | BP | CAT, COL6A1, PRDX2, S100A9         | 4 | 0,037543505 |
| <b>cellular response to toxic substance</b>                                    | BP | CAT, PRDX2, S100A9                 | 3 | 0,03888695  |
| <b>antimicrobial humoral immune response mediated by antimicrobial peptide</b> | BP | REG1B, S100A12, S100A9             | 3 | 0,039339585 |
| <b>regulation of neuroinflammatory response</b>                                | BP | MMP8, MMP9                         | 2 | 0,039442012 |
| <b>positive regulation of endopeptidase activity</b>                           | BP | CTSD, S100A8, S100A9               | 3 | 0,039442012 |
| <b>cellular component disassembly</b>                                          | BP | COL6A1, LCP1, MMP8, MMP9, PRSS2    | 5 | 0,039626804 |
| <b>lung epithelium development</b>                                             | BP | COL6A1, LTA4H                      | 2 | 0,046360476 |
| <b>positive regulation of peptidase activity</b>                               | BP | CTSD, S100A8, S100A9               | 3 | 0,046743102 |
| <b>chemotaxis</b>                                                              | BP | LBP, S100A12, S100A8, S100A9, SAA1 | 5 | 0,047163041 |
| <b>NADP metabolic process</b>                                                  | BP | TALDO1, TKT                        | 2 | 0,047163041 |
| <b>taxis</b>                                                                   | BP | LBP, S100A12, S100A8, S100A9, SAA1 | 5 | 0,047206373 |

|                                                 |    |                                                                                                                  |    |          |
|-------------------------------------------------|----|------------------------------------------------------------------------------------------------------------------|----|----------|
| <b>secretory granule lumen</b>                  | CC | CAT, CHI3L1, CTSD, CTSZ, F8, LRG1, MMP8, ORM1, ORM2, PRSS2, PSMB7, S100A12, S100A8, S100A9, SERPINA3, TIMP1, VWF | 17 | 1,42E-17 |
| <b>cytoplasmic vesicle lumen</b>                | CC | CAT, CHI3L1, CTSD, CTSZ, F8, LRG1, MMP8, ORM1, ORM2, PRSS2, PSMB7, S100A12, S100A8, S100A9, SERPINA3, TIMP1, VWF | 17 | 1,42E-17 |
| <b>vesicle lumen</b>                            | CC | CAT, CHI3L1, CTSD, CTSZ, F8, LRG1, MMP8, ORM1, ORM2, PRSS2, PSMB7, S100A12, S100A8, S100A9, SERPINA3, TIMP1, VWF | 17 | 1,42E-17 |
| <b>collagen-containing extracellular matrix</b> | CC | COL6A1, CTSB, CTSD, CTSZ, MMP8, MMP9, NID1, ORM1, ORM2, S100A8, S100A9, SERPINA3, TIMP1, VWF                     | 14 | 1,32E-11 |
| <b>specific granule lumen</b>                   | CC | CHI3L1, CTSD, CTSZ, LRG1, MMP8, ORM1, ORM2                                                                       | 7  | 2,11E-09 |
| <b>ficolin-1-rich granule lumen</b>             | CC | CAT, CTSB, CTSD, CTSZ, LRG1, LTA4H, MMP9, PSMB7                                                                  | 8  | 6,93E-09 |
| <b>tertiary granule lumen</b>                   | CC | CTSD, LRG1, LTA4H, MMP8, MMP9, ORM1                                                                              | 6  | 4,47E-08 |
| <b>ficolin-1-rich granule</b>                   | CC | CAT, CTSB, CTSD, CTSZ, LRG1, LTA4H, MMP9, PSMB7                                                                  | 8  | 1,17E-07 |
| <b>platelet alpha granule lumen</b>             | CC | F8, ORM1, ORM2, SERPINA3, TIMP1, VWF                                                                             | 6  | 1,17E-07 |
| <b>platelet alpha granule</b>                   | CC | F8, ORM1, ORM2, SERPINA3, TIMP1, VWF                                                                             | 6  | 6,76E-07 |
| <b>specific granule</b>                         | CC | CHI3L1, CTSD, CTSZ, LRG1, MMP8, ORM1, ORM2                                                                       | 7  | 7,67E-07 |
| <b>tertiary granule</b>                         | CC | CTSD, LRG1, LTA4H, MMP8, MMP9, ORM1                                                                              | 6  | 1,84E-05 |

|                                                             |    |                                                   |   |             |
|-------------------------------------------------------------|----|---------------------------------------------------|---|-------------|
| <b>endoplasmic reticulum lumen</b>                          | CC | APOA5, COL6A1, CTSZ, F8, IGFBP4, NUCB1, TIMP1     | 7 | 5,97E-05    |
| <b>proteasome core complex</b>                              | CC | PSMA1, PSMA6, PSMB7                               | 3 | 9,98E-05    |
| <b>high-density lipoprotein particle</b>                    | CC | APOA5, SAA1, SAA2                                 | 3 | 0,000236369 |
| <b>vacuolar lumen</b>                                       | CC | CTSB, CTSD, ORM2, PRSS2, SERPINA3                 | 5 | 0,000373655 |
| <b>plasma lipoprotein particle</b>                          | CC | APOA5, SAA1, SAA2                                 | 3 | 0,000514866 |
| <b>lipoprotein particle</b>                                 | CC | APOA5, SAA1, SAA2                                 | 3 | 0,000514866 |
| <b>protein-lipid complex</b>                                | CC | APOA5, SAA1, SAA2                                 | 3 | 0,00061723  |
| <b>endoplasmic reticulum-Golgi intermediate compartment</b> | CC | CTSZ, F8, MAN1A1, NUCB1                           | 4 | 0,001441161 |
| <b>proteasome complex</b>                                   | CC | PSMA1, PSMA6, PSMB7                               | 3 | 0,002265608 |
| <b>azurophil granule lumen</b>                              | CC | ORM2, PRSS2, SERPINA3                             | 3 | 0,005960351 |
| <b>basement membrane</b>                                    | CC | COL6A1, NID1, TIMP1                               | 3 | 0,005960351 |
| <b>endopeptidase complex</b>                                | CC | PSMA1, PSMA6, PSMB7                               | 3 | 0,006851705 |
| <b>peptidase complex</b>                                    | CC | PSMA1, PSMA6, PSMB7                               | 3 | 0,014381388 |
| <b>endosome lumen</b>                                       | CC | CTSB, CTSD                                        | 2 | 0,014659162 |
| <b>blood microparticle</b>                                  | CC | ORM1, ORM2, SERPINA3                              | 3 | 0,017538691 |
| <b>peroxisome</b>                                           | CC | CAT, TKT, VIM                                     | 3 | 0,017538691 |
| <b>microbody</b>                                            | CC | CAT, TKT, VIM                                     | 3 | 0,017538691 |
| <b>primary lysosome</b>                                     | CC | ORM2, PRSS2, SERPINA3                             | 3 | 0,019374906 |
| <b>azurophil granule</b>                                    | CC | ORM2, PRSS2, SERPINA3                             | 3 | 0,019374906 |
| <b>collagen binding</b>                                     | MF | COL6A1, CTSB, MMP9, NID1, VWF                     | 5 | 0,000100477 |
| <b>RAGE receptor binding</b>                                | MF | S100A12, S100A8, S100A9                           | 3 | 0,000158884 |
| <b>endopeptidase activity</b>                               | MF | CTSB, CTSD, CTSZ, MMP8, MMP9, PRSS2, PSMA6, PSMB7 | 8 | 0,000260913 |
| <b>metallopeptidase activity</b>                            | MF | CPA1, LTA4H, MMP8, MMP9, PRSS2                    | 5 | 0,00309335  |
| <b>Toll-like receptor binding</b>                           | MF | S100A8, S100A9                                    | 2 | 0,012748451 |
| <b>extracellular matrix structural constituent</b>          | MF | CHI3L1, COL6A1, NID1, VWF                         | 4 | 0,015752396 |
| <b>long-chain fatty acid binding</b>                        | MF | S100A8, S100A9                                    | 2 | 0,015752396 |

|                                                          |    |                               |   |             |
|----------------------------------------------------------|----|-------------------------------|---|-------------|
| <b>calcium-dependent protein binding</b>                 | MF | S100A12, S100A8, S100A9       | 3 | 0,015752396 |
| <b>cysteine-type endopeptidase activity</b>              | MF | CTSB, CTSD, CTSZ              | 3 | 0,015752396 |
| <b>opsonin binding</b>                                   | MF | CRP, VSIG4                    | 2 | 0,015752396 |
| <b>antioxidant activity</b>                              | MF | CAT, PRDX2, S100A9            | 3 | 0,015752396 |
| <b>complement binding</b>                                | MF | CRP, VSIG4                    | 2 | 0,020019344 |
| <b>low-density lipoprotein particle receptor binding</b> | MF | APOA5, CRP                    | 2 | 0,020019344 |
| <b>exopeptidase activity</b>                             | MF | CPA1, CTSZ, LTA4H             | 3 | 0,02077495  |
| <b>metalloendopeptidase activity</b>                     | MF | MMP8, MMP9, PRSS2             | 3 | 0,023091608 |
| <b>lipoprotein particle receptor binding</b>             | MF | APOA5, CRP                    | 2 | 0,023091608 |
| <b>proteoglycan binding</b>                              | MF | CTSB, NID1                    | 2 | 0,030837826 |
| <b>quaternary ammonium group binding</b>                 | MF | APOA5, TKT                    | 2 | 0,033760771 |
| <b>lipopolysaccharide binding</b>                        | MF | LBP, PSMA1                    | 2 | 0,033760771 |
| <b>carbohydrate binding</b>                              | MF | CHI3L1, GALNT2, REG1B, TALDO1 | 4 | 0,03430252  |
| <b>carboxypeptidase activity</b>                         | MF | CPA1, CTSZ                    | 2 | 0,038080168 |
| <b>fatty acid binding</b>                                | MF | S100A8, S100A9                | 2 | 0,038080168 |

**Table S6a.** Showing enriched gene ontologies from upregulated DEPs in pancreatitis compared to control. BP=biological processes, CC=cellular compartments, MF=molecular functions. Ontologies classified as significantly altered if exhibiting an adjusted p-value < 0.05.

Table S6b – Gene Ontology Pancreatitis vs Control Down

| Description                                      | Ontology | geneID                                                       | Protein Count | Adjusted P-value |
|--------------------------------------------------|----------|--------------------------------------------------------------|---------------|------------------|
| <b>regulation of fibrinolysis</b>                | BP       | F12, FAP, HRG, KLKB1                                         | 4             | 3,44E-05         |
| <b>negative regulation of peptidase activity</b> | BP       | ECM1, FETUB, ITIH1, ITIH2, SERPINA4, SERPINA5, SERPIND1      | 7             | 3,78E-05         |
| <b>positive regulation of protein processing</b> | BP       | CLEC3B, F12, GSN, KLKB1                                      | 4             | 3,78E-05         |
| <b>fibrinolysis</b>                              | BP       | F12, FAP, HRG, KLKB1                                         | 4             | 3,78E-05         |
| <b>positive regulation of protein maturation</b> | BP       | CLEC3B, F12, GSN, KLKB1                                      | 4             | 3,78E-05         |
| <b>regulation of peptidase activity</b>          | BP       | ECM1, FETUB, GSN, ITIH1, ITIH2, SERPINA4, SERPINA5, SERPIND1 | 8             | 3,78E-05         |
| <b>blood coagulation</b>                         | BP       | F12, F13A1, FAP, HGFAC, HRG, KLKB1, SERPIND1                 | 7             | 3,78E-05         |
| <b>hemostasis</b>                                | BP       | F12, F13A1, FAP, HGFAC, HRG, KLKB1, SERPIND1                 | 7             | 3,78E-05         |
| <b>coagulation</b>                               | BP       | F12, F13A1, FAP, HGFAC, HRG, KLKB1, SERPIND1                 | 7             | 3,78E-05         |
| <b>negative regulation of hydrolase activity</b> | BP       | ECM1, FETUB, ITIH1, ITIH2, SERPINA4, SERPINA5, SERPIND1      | 7             | 4,60E-05         |
| <b>negative regulation of proteolysis</b>        | BP       | ECM1, FETUB, ITIH1, ITIH2, SERPINA4, SERPINA5, SERPIND1      | 7             | 0,000143413      |
| <b>negative regulation of blood coagulation</b>  | BP       | F12, FAP, HRG, KLKB1                                         | 4             | 0,000206271      |
| <b>negative regulation of hemostasis</b>         | BP       | F12, FAP, HRG, KLKB1                                         | 4             | 0,000206321      |
| <b>negative regulation of coagulation</b>        | BP       | F12, FAP, HRG, KLKB1                                         | 4             | 0,000241442      |
| <b>zymogen activation</b>                        | BP       | CLEC3B, F12, HGFAC, KLKB1                                    | 4             | 0,000300638      |
| <b>protein processing</b>                        | BP       | ACE, CLEC3B, F12, GSN, HGFAC, KLKB1                          | 6             | 0,000396342      |

|                                                      |    |                                                         |   |             |
|------------------------------------------------------|----|---------------------------------------------------------|---|-------------|
| <b>protein activation cascade</b>                    | BP | F12, F13A1, KLKB1                                       | 3 | 0,000396342 |
| <b>regulation of body fluid levels</b>               | BP | F12, F13A1, FAP, HGFAC, HRG, KLKB1, SERPIND1            | 7 | 0,000396342 |
| <b>regulation of protein processing</b>              | BP | CLEC3B, F12, GSN, KLKB1                                 | 4 | 0,000423453 |
| <b>regulation of blood coagulation</b>               | BP | F12, FAP, HRG, KLKB1                                    | 4 | 0,000452466 |
| <b>regulation of hemostasis</b>                      | BP | F12, FAP, HRG, KLKB1                                    | 4 | 0,000482977 |
| <b>regulation of protein maturation</b>              | BP | CLEC3B, F12, GSN, KLKB1                                 | 4 | 0,000515007 |
| <b>regulation of coagulation</b>                     | BP | F12, FAP, HRG, KLKB1                                    | 4 | 0,000578248 |
| <b>negative regulation of wound healing</b>          | BP | F12, FAP, HRG, KLKB1                                    | 4 | 0,000614404 |
| <b>plasminogen activation</b>                        | BP | CLEC3B, F12, KLKB1                                      | 3 | 0,000724751 |
| <b>wound healing</b>                                 | BP | F12, F13A1, FAP, HGFAC, HRG, KLKB1, SERPIND1            | 7 | 0,00073923  |
| <b>negative regulation of catalytic activity</b>     | BP | ECM1, FETUB, ITIH1, ITIH2, SERPINA4, SERPINA5, SERPIND1 | 7 | 0,001268936 |
| <b>negative regulation of response to wounding</b>   | BP | F12, FAP, HRG, KLKB1                                    | 4 | 0,001459976 |
| <b>negative regulation of endopeptidase activity</b> | BP | FETUB, SERPINA4, SERPINA5, SERPIND1                     | 4 | 0,001899481 |
| <b>regulation of endopeptidase activity</b>          | BP | FETUB, GSN, SERPINA4, SERPINA5, SERPIND1                | 5 | 0,003541566 |
| <b>regulation of wound healing</b>                   | BP | F12, FAP, HRG, KLKB1                                    | 4 | 0,00468999  |
| <b>peripheral nervous system axon regeneration</b>   | BP | APOA4, APOD                                             | 2 | 0,00483189  |
| <b>regulation of triglyceride catabolic process</b>  | BP | APOA4, GPLD1                                            | 2 | 0,0080916   |
| <b>positive regulation of proteolysis</b>            | BP | CLEC3B, F12, GPLD1, GSN, KLKB1                          | 5 | 0,010943162 |
| <b>regulation of response to wounding</b>            | BP | F12, FAP, HRG, KLKB1                                    | 4 | 0,011072057 |
| <b>blood coagulation, fibrin clot formation</b>      | BP | F12, F13A1                                              | 2 | 0,011369264 |

|                                                              |    |                                   |   |             |
|--------------------------------------------------------------|----|-----------------------------------|---|-------------|
| <b>regulation of plasminogen activation</b>                  | BP | CLEC3B, F12                       | 2 | 0,014069441 |
| <b>negative regulation of bone mineralization</b>            | BP | AHSG, ECM1                        | 2 | 0,018733702 |
| <b>positive regulation of triglyceride metabolic process</b> | BP | APOA4, GPLD1                      | 2 | 0,020054061 |
| <b>regulation of cell-substrate adhesion</b>                 | BP | ABI3BP, APOD, CDH13, HRG          | 4 | 0,021192554 |
| <b>positive regulation of blood coagulation</b>              | BP | F12, HRG                          | 2 | 0,027818066 |
| <b>positive regulation of hemostasis</b>                     | BP | F12, HRG                          | 2 | 0,027818066 |
| <b>acute inflammatory response</b>                           | BP | AHSG, F12, KLKB1                  | 3 | 0,027818066 |
| <b>glycosaminoglycan metabolic process</b>                   | BP | ITIH1, ITIH2, PGLYRP2             | 3 | 0,027903666 |
| <b>triglyceride catabolic process</b>                        | BP | APOA4, GPLD1                      | 2 | 0,02823175  |
| <b>negative regulation of biomineral tissue development</b>  | BP | AHSG, ECM1                        | 2 | 0,031704796 |
| <b>positive regulation of coagulation</b>                    | BP | F12, HRG                          | 2 | 0,033129603 |
| <b>aminoglycan metabolic process</b>                         | BP | ITIH1, ITIH2, PGLYRP2             | 3 | 0,033548386 |
| <b>ossification</b>                                          | BP | AHSG, CLEC3B, ECM1, GPLD1, IGFBP3 | 5 | 0,034523308 |
| <b>regulation of cell-matrix adhesion</b>                    | BP | APOD, CDH13, HRG                  | 3 | 0,034523308 |
| <b>positive regulation of cell-substrate adhesion</b>        | BP | ABI3BP, CDH13, HRG                | 3 | 0,034625612 |
| <b>bone mineralization</b>                                   | BP | AHSG, CLEC3B, ECM1                | 3 | 0,034660388 |
| <b>hyaluronan metabolic process</b>                          | BP | ITIH1, ITIH2                      | 2 | 0,034660388 |
| <b>negative regulation of cell junction assembly</b>         | BP | ACE, APOD                         | 2 | 0,034660388 |
| <b>endothelial cell migration</b>                            | BP | CDH13, FAP, GPLD1, HRG            | 4 | 0,038931915 |
| <b>detection of biotic stimulus</b>                          | BP | FAP, PGLYRP2                      | 2 | 0,042363751 |
| <b>neutral lipid catabolic process</b>                       | BP | APOA4, GPLD1                      | 2 | 0,042363751 |
| <b>acylglycerol catabolic process</b>                        | BP | APOA4, GPLD1                      | 2 | 0,042363751 |



|                                                 |    |                                                                                          |    |             |
|-------------------------------------------------|----|------------------------------------------------------------------------------------------|----|-------------|
| <b>negative regulation of ossification</b>      | BP | AHSG, ECM1                                                                               | 2  | 0,045972955 |
| <b>negative regulation of cell adhesion</b>     | BP | APOD, CDH13, GPNMB, HRG                                                                  | 4  | 0,049347306 |
| <b>collagen-containing extracellular matrix</b> | CC | ABI3BP, AHSG, APOA4, CDH13, CLEC3B, ECM1, F12, F13A1, HRG, ITIH1, ITIH2, NCAM1, SERPINA5 | 13 | 3,45E-11    |
| <b>blood microparticle</b>                      | CC | AFM, AHSG, APOA4, F13A1, GSN, HRG, ITIH1, ITIH2                                          | 8  | 5,37E-09    |
| <b>secretory granule lumen</b>                  | CC | ADA2, AHSG, CLEC3B, CRISP3, ECM1, F13A1, GSN, HRG, SELENOP, SERPINA4                     | 10 | 5,37E-09    |
| <b>cytoplasmic vesicle lumen</b>                | CC | ADA2, AHSG, CLEC3B, CRISP3, ECM1, F13A1, GSN, HRG, SELENOP, SERPINA4                     | 10 | 5,37E-09    |
| <b>vesicle lumen</b>                            | CC | ADA2, AHSG, CLEC3B, CRISP3, ECM1, F13A1, GSN, HRG, SELENOP, SERPINA4                     | 10 | 5,37E-09    |
| <b>platelet dense granule lumen</b>             | CC | CLEC3B, ECM1, SELENOP, SERPINA4                                                          | 4  | 1,41E-07    |
| <b>platelet dense granule</b>                   | CC | CLEC3B, ECM1, SELENOP, SERPINA4                                                          | 4  | 7,18E-07    |
| <b>platelet alpha granule</b>                   | CC | AHSG, F13A1, HRG, SERPINA5                                                               | 4  | 0,000255803 |
| <b>platelet alpha granule lumen</b>             | CC | AHSG, F13A1, HRG                                                                         | 3  | 0,002314778 |
| <b>endoplasmic reticulum lumen</b>              | CC | AHSG, APOA4, IGFBP3, ITIH2, SERPIND1                                                     | 5  | 0,002314778 |
| <b>external side of plasma membrane</b>         | CC | ACE, CDH13, NCAM1, SELL, SERPINA5                                                        | 5  | 0,00684829  |
| <b>rough endoplasmic reticulum</b>              | CC | F12, HGFAC                                                                               | 2  | 0,037104849 |
| <b>glycosaminoglycan binding</b>                | MF | ADA2, CLEC3B, GPNMB, HRG, ITIH1, ITIH2, PGLYRP2, SELL, SERPINA5, SERPIND1                | 10 | 3,69E-09    |
| <b>endopeptidase inhibitor activity</b>         | MF | AHSG, FETUB, HRG, ITIH1, ITIH2, SERPINA4, SERPINA5, SERPIND1                             | 8  | 6,01E-08    |

|                                                       |    |                                                              |   |             |
|-------------------------------------------------------|----|--------------------------------------------------------------|---|-------------|
| <b>peptidase inhibitor activity</b>                   | MF | AHSG, FETUB, HRG, ITIH1, ITIH2, SERPINA4, SERPINA5, SERPIND1 | 8 | 6,01E-08    |
| <b>endopeptidase regulator activity</b>               | MF | AHSG, FETUB, HRG, ITIH1, ITIH2, SERPINA4, SERPINA5, SERPIND1 | 8 | 7,92E-08    |
| <b>peptidase regulator activity</b>                   | MF | AHSG, FETUB, HRG, ITIH1, ITIH2, SERPINA4, SERPINA5, SERPIND1 | 8 | 3,50E-07    |
| <b>serine-type endopeptidase inhibitor activity</b>   | MF | HRG, ITIH1, ITIH2, SERPINA4, SERPINA5, SERPIND1              | 6 | 7,57E-07    |
| <b>heparin binding</b>                                | MF | ADA2, CLEC3B, GPNMB, HRG, SELL, SERPINA5, SERPIND1           | 7 | 7,57E-07    |
| <b>sulfur compound binding</b>                        | MF | ADA2, CLEC3B, GPNMB, HRG, SELL, SERPINA5, SERPIND1           | 7 | 1,38E-05    |
| <b>enzyme inhibitor activity</b>                      | MF | AHSG, FETUB, HRG, ITIH1, ITIH2, SERPINA4, SERPINA5, SERPIND1 | 8 | 1,38E-05    |
| <b>protease binding</b>                               | MF | CHL1, ECM1, FAP, SELL, SERPINA5                              | 5 | 7,72E-05    |
| <b>serine-type peptidase activity</b>                 | MF | ACE, F12, FAP, HGFAC, KLKB1                                  | 5 | 0,000399724 |
| <b>serine hydrolase activity</b>                      | MF | ACE, F12, FAP, HGFAC, KLKB1                                  | 5 | 0,000403684 |
| <b>cysteine-type endopeptidase inhibitor activity</b> | MF | AHSG, FETUB, HRG                                             | 3 | 0,000424322 |
| <b>proteoglycan binding</b>                           | MF | ADA2, GPNMB, HRG                                             | 3 | 0,000428196 |
| <b>carbohydrate binding</b>                           | MF | ATR1, CLEC3B, CNTN1, ITIH1, SELL                             | 5 | 0,001610289 |
| <b>serine-type endopeptidase activity</b>             | MF | F12, FAP, HGFAC, KLKB1                                       | 4 | 0,002900575 |
| <b>dipeptidase activity</b>                           | MF | ACE, CNDP1                                                   | 2 | 0,003396334 |
| <b>hyaluronic acid binding</b>                        | MF | ITIH1, ITIH2                                                 | 2 | 0,006399086 |
| <b>exopeptidase activity</b>                          | MF | ACE, CNDP1, FAP                                              | 3 | 0,006399086 |

|                                                                              |    |                             |   |             |
|------------------------------------------------------------------------------|----|-----------------------------|---|-------------|
| <b>endopeptidase activity</b>                                                | MF | ACE, F12, FAP, HGFAC, KLKB1 | 5 | 0,006399086 |
| <b>phosphatidylcholine binding</b>                                           | MF | APOA4, SERPINA5             | 2 | 0,008653098 |
| <b>hydrolase activity, acting on carbon-nitrogen bonds</b>                   | MF | ADA2, BTD, PGLYRP2          | 3 | 0,012312174 |
| <b>quaternary ammonium group binding</b>                                     | MF | APOA4, SERPINA5             | 2 | 0,013991902 |
| <b>carboxypeptidase activity</b>                                             | MF | ACE, CNDP1                  | 2 | 0,018422734 |
| <b>metalloexopeptidase activity</b>                                          | MF | ACE, CNDP1                  | 2 | 0,035288508 |
| <b>hydrolase activity, acting on carbon-nitrogen bonds, in linear amides</b> | MF | BTD, PGLYRP2                | 2 | 0,038984086 |

**Table S6b.** Showing enriched gene ontologies from downregulated DEPs in pancreatitis compared to control. BP=biological processes, CC=cellular compartments, MF=molecular functions. Ontologies classified as significantly altered if exhibiting an adjusted p-value < 0.05.

Table S7a – Gene Ontology Sepsis vs Pancreatitis Up

| Description                              | Ontology | geneID                    | Protein Count | Adjusted P-value |
|------------------------------------------|----------|---------------------------|---------------|------------------|
| secretory granule lumen                  | CC       | COTL1, HSP90AA1, SERPINB1 | 3             | 0,002834878      |
| cytoplasmic vesicle lumen                | CC       | COTL1, HSP90AA1, SERPINB1 | 3             | 0,002834878      |
| vesicle lumen                            | CC       | COTL1, HSP90AA1, SERPINB1 | 3             | 0,002834878      |
| collagen-containing extracellular matrix | CC       | HSP90AA1, PSAP, SERPINB1  | 3             | 0,00464278       |
| lysosomal lumen                          | CC       | HSP90AA1, PSAP            | 2             | 0,005239032      |
| melanosome                               | CC       | GANAB, HSP90AA1           | 2             | 0,005239032      |
| pigment granule                          | CC       | GANAB, HSP90AA1           | 2             | 0,005239032      |
| ficolin-1-rich granule lumen             | CC       | COTL1, HSP90AA1           | 2             | 0,005612712      |
| site of polarized growth                 | CC       | COTL1, HSP90AA1           | 2             | 0,009017718      |
| vacuolar lumen                           | CC       | HSP90AA1, PSAP            | 2             | 0,009017718      |
| ficolin-1-rich granule                   | CC       | COTL1, HSP90AA1           | 2             | 0,009017718      |
| dendrite terminus                        | CC       | HSP90AA1                  | 1             | 0,019981997      |
| cytolytic granule                        | CC       | SERPINB1                  | 1             | 0,019981997      |
| sperm plasma membrane                    | CC       | HSP90AA1                  | 1             | 0,019981997      |
| cell cortex                              | CC       | COTL1, MARCKS             | 2             | 0,019981997      |
| female germ cell nucleus                 | CC       | MARCKS                    | 1             | 0,021050864      |
| endocytic vesicle                        | CC       | CD163, HSP90AA1           | 2             | 0,021050864      |
| endocytic vesicle lumen                  | CC       | HSP90AA1                  | 1             | 0,025458436      |
| axonal growth cone                       | CC       | HSP90AA1                  | 1             | 0,031425866      |
| myelin sheath                            | CC       | HSP90AA1                  | 1             | 0,047638326      |
| scaffold protein binding                 | MF       | CD163, HSP90AA1, PSAP     | 3             | 8,13E-05         |
| actin filament binding                   | MF       | COTL1, MARCKS             | 2             | 0,042244076      |
| glycosphingolipid binding                | MF       | PSAP                      | 1             | 0,042244076      |
| glucosidase activity                     | MF       | GANAB                     | 1             | 0,042244076      |
| ceramide binding                         | MF       | PSAP                      | 1             | 0,042244076      |
| DNA polymerase binding                   | MF       | HSP90AA1                  | 1             | 0,042244076      |
| scavenger receptor activity              | MF       | CD163                     | 1             | 0,042244076      |

|                                                |    |               |   |             |
|------------------------------------------------|----|---------------|---|-------------|
| <b>MHC class II protein complex binding</b>    | MF | HSP90AA1      | 1 | 0,042244076 |
| <b>sphingolipid binding</b>                    | MF | PSAP          | 1 | 0,042244076 |
| <b>disordered domain specific binding</b>      | MF | HSP90AA1      | 1 | 0,042244076 |
| <b>actin binding</b>                           | MF | COTL1, MARCKS | 2 | 0,042244076 |
| <b>glycolipid binding</b>                      | MF | PSAP          | 1 | 0,042244076 |
| <b>MHC protein complex binding</b>             | MF | HSP90AA1      | 1 | 0,049687986 |
| <b>ATP-dependent protein folding chaperone</b> | MF | HSP90AA1      | 1 | 0,049855891 |
| <b>tau protein binding</b>                     | MF | HSP90AA1      | 1 | 0,049998069 |

**Table S7a.** Showing enriched gene ontologies from upregulated DEPs in sepsis compared to pancreatitis. BP=biological processes, CC=cellular compartments, MF=molecular functions. Ontologies classified as significantly altered if exhibiting an adjusted p-value < 0.05.

Table S7b – Gene Ontology Sepsis vs Pancreatitis Down

| Description                                       | Ontology | geneID                                            | Protein Count | Adjusted P-value |
|---------------------------------------------------|----------|---------------------------------------------------|---------------|------------------|
| blood coagulation                                 | BP       | APOE, APOH, F2, F9, PLG, PRDX2, PROC, PTPRJ       | 8             | 3,56E-08         |
| regulation of blood coagulation                   | BP       | APOE, APOH, F2, PLG, PRDX2, PROC                  | 6             | 3,56E-08         |
| regulation of hemostasis                          | BP       | APOE, APOH, F2, PLG, PRDX2, PROC                  | 6             | 3,56E-08         |
| hemostasis                                        | BP       | APOE, APOH, F2, F9, PLG, PRDX2, PROC, PTPRJ       | 8             | 3,56E-08         |
| coagulation                                       | BP       | APOE, APOH, F2, F9, PLG, PRDX2, PROC, PTPRJ       | 8             | 3,56E-08         |
| regulation of coagulation                         | BP       | APOE, APOH, F2, PLG, PRDX2, PROC                  | 6             | 4,29E-08         |
| regulation of lipase activity                     | BP       | APOA5, APOC2, APOC3, APOH, SNCA                   | 5             | 6,28E-08         |
| triglyceride-rich lipoprotein particle remodeling | BP       | APOA5, APOC2, APOC3, APOE                         | 4             | 7,92E-08         |
| very-low-density lipoprotein particle remodeling  | BP       | APOA5, APOC2, APOC3, APOE                         | 4             | 7,92E-08         |
| wound healing                                     | BP       | APOE, APOH, F2, F9, LRG1, PLG, PRDX2, PROC, PTPRJ | 9             | 7,92E-08         |
| phospholipid efflux                               | BP       | APOA5, APOC2, APOC3, APOE                         | 4             | 1,12E-07         |
| regulation of lipoprotein lipase activity         | BP       | APOA5, APOC2, APOC3, APOH                         | 4             | 1,12E-07         |
| triglyceride homeostasis                          | BP       | APOA5, APOC2, APOC3, APOC4, APOE                  | 5             | 1,12E-07         |
| acylglycerol homeostasis                          | BP       | APOA5, APOC2, APOC3, APOC4, APOE                  | 5             | 1,17E-07         |
| negative regulation of blood coagulation          | BP       | APOE, APOH, F2, PLG, PROC                         | 5             | 1,89E-07         |
| negative regulation of hemostasis                 | BP       | APOE, APOH, F2, PLG, PROC                         | 5             | 1,96E-07         |
| negative regulation of coagulation                | BP       | APOE, APOH, F2, PLG, PROC                         | 5             | 2,48E-07         |

|                                                     |    |                                             |   |          |
|-----------------------------------------------------|----|---------------------------------------------|---|----------|
| <b>regulation of body fluid levels</b>              | BP | APOE, APOH, F2, F9, PLG, PRDX2, PROC, PTPRJ | 8 | 3,67E-07 |
| <b>neutral lipid metabolic process</b>              | BP | APOA5, APOC2, APOC3, APOE, APOH, SNCA       | 6 | 4,67E-07 |
| <b>regulation of wound healing</b>                  | BP | APOE, APOH, F2, PLG, PRDX2, PROC            | 6 | 5,28E-07 |
| <b>positive regulation of blood coagulation</b>     | BP | APOH, F2, PLG, PRDX2                        | 4 | 1,14E-06 |
| <b>positive regulation of hemostasis</b>            | BP | APOH, F2, PLG, PRDX2                        | 4 | 1,14E-06 |
| <b>negative regulation of wound healing</b>         | BP | APOE, APOH, F2, PLG, PROC                   | 5 | 1,20E-06 |
| <b>positive regulation of coagulation</b>           | BP | APOH, F2, PLG, PRDX2                        | 4 | 1,87E-06 |
| <b>regulation of response to wounding</b>           | BP | APOE, APOH, F2, PLG, PRDX2, PROC            | 6 | 1,96E-06 |
| <b>protein-lipid complex remodeling</b>             | BP | APOA5, APOC2, APOC3, APOE                   | 4 | 2,16E-06 |
| <b>plasma lipoprotein particle remodeling</b>       | BP | APOA5, APOC2, APOC3, APOE                   | 4 | 2,16E-06 |
| <b>protein-containing complex remodeling</b>        | BP | APOA5, APOC2, APOC3, APOE                   | 4 | 2,67E-06 |
| <b>negative regulation of response to wounding</b>  | BP | APOE, APOH, F2, PLG, PROC                   | 5 | 3,52E-06 |
| <b>triglyceride metabolic process</b>               | BP | APOA5, APOC2, APOC3, APOE, APOH             | 5 | 4,76E-06 |
| <b>regulation of triglyceride metabolic process</b> | BP | APOA5, APOC2, APOC3, APOE                   | 4 | 7,44E-06 |
| <b>plasma lipoprotein particle organization</b>     | BP | APOA5, APOC2, APOC3, APOE                   | 4 | 1,01E-05 |
| <b>protein-lipid complex organization</b>           | BP | APOA5, APOC2, APOC3, APOE                   | 4 | 1,18E-05 |
| <b>regulation of triglyceride catabolic process</b> | BP | APOA5, APOC2, APOC3                         | 3 | 1,18E-05 |
| <b>negative regulation of fibrinolysis</b>          | BP | APOH, F2, PLG                               | 3 | 1,18E-05 |
| <b>acylglycerol metabolic process</b>               | BP | APOA5, APOC2, APOC3, APOE, APOH             | 5 | 1,21E-05 |

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|---------------------------------------------------------|----|----------------------------------------------|---|-------------|
| <b>lipid transport</b>                                  | BP | APOA5, APOC2, APOC3, APOC4, APOE, APOF, APOH | 7 | 1,68E-05    |
| <b>positive regulation of wound healing</b>             | BP | APOH, F2, PLG, PRDX2                         | 4 | 2,64E-05    |
| <b>regulation of endocytosis</b>                        | BP | APOA5, APOC2, APOC3, APOE, PTPRJ, SNCA       | 6 | 2,83E-05    |
| <b>high-density lipoprotein particle clearance</b>      | BP | APOC2, APOC3, APOE                           | 3 | 2,87E-05    |
| <b>regulation of fibrinolysis</b>                       | BP | APOH, F2, PLG                                | 3 | 2,87E-05    |
| <b>cholesterol efflux</b>                               | BP | APOA5, APOC2, APOC3, APOE                    | 4 | 3,79E-05    |
| <b>reverse cholesterol transport</b>                    | BP | APOC2, APOC3, APOE                           | 3 | 3,82E-05    |
| <b>lipid homeostasis</b>                                | BP | APOA5, APOC2, APOC3, APOC4, APOE             | 5 | 4,11E-05    |
| <b>regulation of lipid metabolic process</b>            | BP | APOA5, APOC2, APOC3, APOE, F2, SNCA          | 6 | 4,75E-05    |
| <b>positive regulation of lipase activity</b>           | BP | APOA5, APOC2, APOH                           | 3 | 4,81E-05    |
| <b>positive regulation of response to wounding</b>      | BP | APOH, F2, PLG, PRDX2                         | 4 | 4,87E-05    |
| <b>regulation of plasma lipoprotein particle levels</b> | BP | APOA5, APOC2, APOC3, APOE                    | 4 | 7,61E-05    |
| <b>fibrinolysis</b>                                     | BP | APOH, F2, PLG                                | 3 | 8,55E-05    |
| <b>triglyceride catabolic process</b>                   | BP | APOA5, APOC2, APOC3                          | 3 | 9,38E-05    |
| <b>lipoprotein metabolic process</b>                    | BP | APOA5, APOC2, APOC3, APOE                    | 4 | 0,000112904 |
| <b>negative regulation of sterol transport</b>          | BP | APOC2, APOC3, APOE                           | 3 | 0,000119674 |
| <b>negative regulation of cholesterol transport</b>     | BP | APOC2, APOC3, APOE                           | 3 | 0,000119674 |
| <b>phospholipid transport</b>                           | BP | APOA5, APOC2, APOC3, APOE                    | 4 | 0,000119674 |
| <b>cholesterol homeostasis</b>                          | BP | APOA5, APOC2, APOC3, APOE                    | 4 | 0,000122013 |
| <b>sterol homeostasis</b>                               | BP | APOA5, APOC2, APOC3, APOE                    | 4 | 0,000124393 |



|                                                                |    |                                  |   |             |
|----------------------------------------------------------------|----|----------------------------------|---|-------------|
| <b>regulation of fatty acid metabolic process</b>              | BP | APOA5, APOC2, APOC3, SNCA        | 4 | 0,000126815 |
| <b>negative regulation of response to external stimulus</b>    | BP | APOE, APOH, F2, PLG, PRDX2, PROC | 6 | 0,000145974 |
| <b>cholesterol transport</b>                                   | BP | APOA5, APOC2, APOC3, APOE        | 4 | 0,000205198 |
| <b>neutral lipid catabolic process</b>                         | BP | APOA5, APOC2, APOC3              | 3 | 0,000212664 |
| <b>acylglycerol catabolic process</b>                          | BP | APOA5, APOC2, APOC3              | 3 | 0,000212664 |
| <b>receptor-mediated endocytosis</b>                           | BP | APOA5, APOC2, APOC3, APOE, SNCA  | 5 | 0,000230445 |
| <b>sterol transport</b>                                        | BP | APOA5, APOC2, APOC3, APOE        | 4 | 0,000250046 |
| <b>positive regulation of lipid metabolic process</b>          | BP | APOA5, APOC2, APOE, F2           | 4 | 0,000250046 |
| <b>organic hydroxy compound transport</b>                      | BP | APOA5, APOC2, APOC3, APOE, SNCA  | 5 | 0,000293547 |
| <b>negative regulation of lipid transport</b>                  | BP | APOC2, APOC3, APOE               | 3 | 0,000393282 |
| <b>regulation of cellular ketone metabolic process</b>         | BP | APOA5, APOC2, APOC3, SNCA        | 4 | 0,000420711 |
| <b>positive regulation of small molecule metabolic process</b> | BP | APOA5, APOC2, APOE, SNCA         | 4 | 0,000420711 |
| <b>positive regulation of endocytosis</b>                      | BP | APOA5, APOE, PTPRJ, SNCA         | 4 | 0,000482101 |
| <b>regulation of platelet activation</b>                       | BP | APOE, F2, PTPRJ                  | 3 | 0,000490341 |
| <b>regulation of fatty acid biosynthetic process</b>           | BP | APOA5, APOC2, APOC3              | 3 | 0,000490341 |
| <b>plasma lipoprotein particle clearance</b>                   | BP | APOC2, APOC3, APOE               | 3 | 0,000511043 |
| <b>regulation of small molecule metabolic process</b>          | BP | APOA5, APOC2, APOC3, APOE, SNCA  | 5 | 0,000605865 |
| <b>organophosphate ester transport</b>                         | BP | APOA5, APOC2, APOC3, APOE        | 4 | 0,000625279 |
| <b>glycerolipid catabolic process</b>                          | BP | APOA5, APOC2, APOC3              | 3 | 0,000841788 |
| <b>regulation of lipid localization</b>                        | BP | APOC2, APOC3, APOC4, APOE        | 4 | 0,000841788 |

|                                                                                         |    |                                 |   |             |
|-----------------------------------------------------------------------------------------|----|---------------------------------|---|-------------|
| <b>regulation of lipid catabolic process</b>                                            | BP | APOA5, APOC2, APOC3             | 3 | 0,000864743 |
| <b>negative regulation of lipid localization</b>                                        | BP | APOC2, APOC3, APOE              | 3 | 0,000892386 |
| <b>glycerolipid metabolic process</b>                                                   | BP | APOA5, APOC2, APOC3, APOE, APOH | 5 | 0,00090488  |
| <b>regulation of lipid biosynthetic process</b>                                         | BP | APOA5, APOC2, APOC3, APOE       | 4 | 0,000940264 |
| <b>regulation of sterol transport</b>                                                   | BP | APOC2, APOC3, APOE              | 3 | 0,001230659 |
| <b>regulation of cholesterol transport</b>                                              | BP | APOC2, APOC3, APOE              | 3 | 0,001230659 |
| <b>negative regulation of platelet-derived growth factor receptor signaling pathway</b> | BP | PTPRJ, SNCA                     | 2 | 0,00129087  |
| <b>positive regulation of cellular catabolic process</b>                                | BP | APOA5, APOC2, APOE, SNCA        | 4 | 0,001805733 |
| <b>cellular ketone metabolic process</b>                                                | BP | APOA5, APOC2, APOC3, SNCA       | 4 | 0,001843612 |
| <b>positive regulation of lipid biosynthetic process</b>                                | BP | APOA5, APOC2, APOE              | 3 | 0,002070105 |
| <b>Cdc42 protein signal transduction</b>                                                | BP | APOC3, APOE                     | 2 | 0,002070105 |
| <b>high-density lipoprotein particle remodeling</b>                                     | BP | APOC3, APOE                     | 2 | 0,002070105 |
| <b>negative regulation of triglyceride metabolic process</b>                            | BP | APOC3, APOE                     | 2 | 0,002070105 |
| <b>regulation of cellular catabolic process</b>                                         | BP | APOA5, APOC2, APOC3, APOE, SNCA | 5 | 0,002070105 |
| <b>regulation of hydrogen peroxide metabolic process</b>                                | BP | PRDX2, SNCA                     | 2 | 0,002227947 |
| <b>regulation of phospholipase activity</b>                                             | BP | APOC2, SNCA                     | 2 | 0,002227947 |
| <b>negative regulation of platelet activation</b>                                       | BP | APOE, F2                        | 2 | 0,002227947 |
| <b>lipoprotein catabolic process</b>                                                    | BP | APOC2, APOE                     | 2 | 0,002227947 |
| <b>negative regulation of vascular permeability</b>                                     | BP | APOE, PTPRJ                     | 2 | 0,002733767 |

|                                                                                |    |                           |   |             |
|--------------------------------------------------------------------------------|----|---------------------------|---|-------------|
| <b>negative regulation of lipoprotein particle clearance</b>                   | BP | APOC2, APOC3              | 2 | 0,00298796  |
| <b>positive regulation of triglyceride metabolic process</b>                   | BP | APOA5, APOC2              | 2 | 0,003250589 |
| <b>positive regulation of fatty acid biosynthetic process</b>                  | BP | APOA5, APOC2              | 2 | 0,003521368 |
| <b>negative regulation of lipid metabolic process</b>                          | BP | APOC2, APOC3, APOE        | 3 | 0,00360675  |
| <b>regulation of platelet-derived growth factor receptor signaling pathway</b> | BP | PTPRJ, SNCA               | 2 | 0,003762021 |
| <b>regulation of receptor-mediated endocytosis</b>                             | BP | APOA5, APOC2, APOC3       | 3 | 0,004487768 |
| <b>biological process involved in interaction with symbiont</b>                | BP | APOE, F2, PLG             | 3 | 0,004546162 |
| <b>plasma lipoprotein particle assembly</b>                                    | BP | APOC3, APOE               | 2 | 0,004635192 |
| <b>positive regulation of lipid catabolic process</b>                          | BP | APOA5, APOC2              | 2 | 0,004940279 |
| <b>positive regulation of hydrolase activity</b>                               | BP | APOA5, APOC2, APOH, SNCA  | 4 | 0,005324636 |
| <b>protein-lipid complex assembly</b>                                          | BP | APOC3, APOE               | 2 | 0,005570151 |
| <b>platelet activation</b>                                                     | BP | APOE, F2, PTPRJ           | 3 | 0,005619671 |
| <b>hydrogen peroxide catabolic process</b>                                     | BP | PRDX2, SNCA               | 2 | 0,005839935 |
| <b>maintenance of location</b>                                                 | BP | APOC4, APOE, F2, SNCA     | 4 | 0,005993878 |
| <b>cholesterol metabolic process</b>                                           | BP | APOA5, APOE, APOF         | 3 | 0,006279263 |
| <b>lipid catabolic process</b>                                                 | BP | APOA5, APOC2, APOC3, APOE | 4 | 0,006279263 |
| <b>regulation of reactive oxygen species metabolic process</b>                 | BP | F2, PRDX2, SNCA           | 3 | 0,006809545 |
| <b>alcohol metabolic process</b>                                               | BP | APOA5, APOE, APOF, SNCA   | 4 | 0,006947232 |
| <b>negative regulation of protein kinase activity</b>                          | BP | APOE, PTPRJ, SNCA         | 3 | 0,006947232 |
| <b>regulation of lipid transport</b>                                           | BP | APOC2, APOC3, APOE        | 3 | 0,007016593 |

|                                                                               |    |                           |   |             |
|-------------------------------------------------------------------------------|----|---------------------------|---|-------------|
| <b>regulation of lipoprotein particle clearance</b>                           | BP | APOC2, APOC3              | 2 | 0,007226732 |
| <b>sterol metabolic process</b>                                               | BP | APOA5, APOE, APOF         | 3 | 0,007226732 |
| <b>secondary alcohol metabolic process</b>                                    | BP | APOA5, APOE, APOF         | 3 | 0,007226732 |
| <b>negative regulation of receptor-mediated endocytosis</b>                   | BP | APOC2, APOC3              | 2 | 0,00755924  |
| <b>fatty acid biosynthetic process</b>                                        | BP | APOA5, APOC2, APOC3       | 3 | 0,007911344 |
| <b>negative regulation of kinase activity</b>                                 | BP | APOE, PTPRJ, SNCA         | 3 | 0,007984376 |
| <b>positive regulation of fatty acid metabolic process</b>                    | BP | APOA5, APOC2              | 2 | 0,008617313 |
| <b>negative regulation of MAP kinase activity</b>                             | BP | APOE, PTPRJ               | 2 | 0,008979275 |
| <b>fatty acid metabolic process</b>                                           | BP | APOA5, APOC2, APOC3, SNCA | 4 | 0,009583614 |
| <b>regulation of endothelial cell proliferation</b>                           | BP | APOE, APOH, LRG1          | 3 | 0,009609342 |
| <b>positive regulation of release of sequestered calcium ion into cytosol</b> | BP | F2, SNCA                  | 2 | 0,009639192 |
| <b>amyloid fibril formation</b>                                               | BP | APOE, SNCA                | 2 | 0,010469981 |
| <b>negative regulation of transferase activity</b>                            | BP | APOE, PTPRJ, SNCA         | 3 | 0,011141386 |
| <b>regulation of vascular permeability</b>                                    | BP | APOE, PTPRJ               | 2 | 0,012709793 |
| <b>endothelial cell proliferation</b>                                         | BP | APOE, APOH, LRG1          | 3 | 0,01307686  |
| <b>regulation of kinase activity</b>                                          | BP | APOE, F2, PTPRJ, SNCA     | 4 | 0,01450296  |
| <b>hydrogen peroxide metabolic process</b>                                    | BP | PRDX2, SNCA               | 2 | 0,01500454  |
| <b>negative regulation of transport</b>                                       | BP | APOC2, APOC3, APOE, SNCA  | 4 | 0,015096626 |
| <b>negative regulation of cell activation</b>                                 | BP | APOE, F2, PRDX2           | 3 | 0,015980547 |
| <b>zymogen activation</b>                                                     | BP | APOH, F9                  | 2 | 0,016176745 |

|                                                                         |    |                          |   |             |
|-------------------------------------------------------------------------|----|--------------------------|---|-------------|
| <b>regulation of alcohol biosynthetic process</b>                       | BP | APOE, SNCA               | 2 | 0,016176745 |
| <b>platelet-derived growth factor receptor signaling pathway</b>        | BP | PTPRJ, SNCA              | 2 | 0,016428575 |
| <b>maintenance of location in cell</b>                                  | BP | APOE, F2, SNCA           | 3 | 0,016428575 |
| <b>monocarboxylic acid biosynthetic process</b>                         | BP | APOA5, APOC2, APOC3      | 3 | 0,016428575 |
| <b>negative regulation of catalytic activity</b>                        | BP | APOC3, APOE, PTPRJ, SNCA | 4 | 0,016588536 |
| <b>regulation of neuronal synaptic plasticity</b>                       | BP | APOE, SNCA               | 2 | 0,0166841   |
| <b>regulation of endothelial cell migration</b>                         | BP | APOE, APOH, PLG          | 3 | 0,018428098 |
| <b>negative regulation of protein phosphorylation</b>                   | BP | APOE, PTPRJ, SNCA        | 3 | 0,018520961 |
| <b>cellular lipid catabolic process</b>                                 | BP | APOA5, APOC2, APOC3      | 3 | 0,018837699 |
| <b>reactive oxygen species metabolic process</b>                        | BP | F2, PRDX2, SNCA          | 3 | 0,019612239 |
| <b>protein processing</b>                                               | BP | APOH, F9, PLG            | 3 | 0,020402727 |
| <b>negative regulation of lipid biosynthetic process</b>                | BP | APOC3, APOE              | 2 | 0,020481009 |
| <b>negative regulation of phosphorylation</b>                           | BP | APOE, PTPRJ, SNCA        | 3 | 0,022524172 |
| <b>receptor metabolic process</b>                                       | BP | APOE, SNCA               | 2 | 0,023565846 |
| <b>positive regulation of reactive oxygen species metabolic process</b> | BP | F2, SNCA                 | 2 | 0,023565846 |
| <b>regulation of protein serine/threonine kinase activity</b>           | BP | APOE, PTPRJ, SNCA        | 3 | 0,023565846 |
| <b>negative regulation of endocytosis</b>                               | BP | APOC2, APOC3             | 2 | 0,02464243  |
| <b>negative regulation of endothelial cell proliferation</b>            | BP | APOE, APOH               | 2 | 0,026410129 |
| <b>tissue regeneration</b>                                              | BP | APOA5, PLG               | 2 | 0,028223218 |

|                                                                           |    |                     |   |             |
|---------------------------------------------------------------------------|----|---------------------|---|-------------|
| <b>regulation of release of sequestered calcium ion into cytosol</b>      | BP | F2, SNCA            | 2 | 0,028529345 |
| <b>negative regulation of protein serine/threonine kinase activity</b>    | BP | APOE, PTPRJ         | 2 | 0,028529345 |
| <b>regulation of amide metabolic process</b>                              | BP | APOE, SNCA          | 2 | 0,028835058 |
| <b>regulation of Rho protein signal transduction</b>                      | BP | APOC3, APOE         | 2 | 0,028835058 |
| <b>endothelial cell migration</b>                                         | BP | APOE, APOH, PLG     | 3 | 0,028900767 |
| <b>positive regulation of calcium ion transmembrane transport</b>         | BP | F2, SNCA            | 2 | 0,029140358 |
| <b>neuroinflammatory response</b>                                         | BP | BPGM, SNCA          | 2 | 0,029628132 |
| <b>intracellular calcium ion homeostasis</b>                              | BP | APOE, F2, SNCA      | 3 | 0,033099507 |
| <b>positive regulation of transferase activity</b>                        | BP | APOE, F2, SNCA      | 3 | 0,033099507 |
| <b>negative regulation of phosphorus metabolic process</b>                | BP | APOE, PTPRJ, SNCA   | 3 | 0,033300184 |
| <b>negative regulation of phosphate metabolic process</b>                 | BP | APOE, PTPRJ, SNCA   | 3 | 0,033300184 |
| <b>lipid storage</b>                                                      | BP | APOC4, APOE         | 2 | 0,03632503  |
| <b>cellular oxidant detoxification</b>                                    | BP | APOE, PRDX2         | 2 | 0,037567174 |
| <b>biological process involved in symbiotic interaction</b>               | BP | APOE, F2, PLG       | 3 | 0,037673502 |
| <b>negative regulation of endothelial cell migration</b>                  | BP | APOE, APOH          | 2 | 0,037853719 |
| <b>calcium ion homeostasis</b>                                            | BP | APOE, F2, SNCA      | 3 | 0,039511883 |
| <b>carboxylic acid biosynthetic process</b>                               | BP | APOA5, APOC2, APOC3 | 3 | 0,039943935 |
| <b>steroid metabolic process</b>                                          | BP | APOA5, APOE, APOF   | 3 | 0,040477789 |
| <b>organic acid biosynthetic process</b>                                  | BP | APOA5, APOC2, APOC3 | 3 | 0,040477789 |
| <b>production of molecular mediator involved in inflammatory response</b> | BP | F2, PRDX2           | 2 | 0,041915558 |

|                                                            |    |                                                      |   |             |
|------------------------------------------------------------|----|------------------------------------------------------|---|-------------|
| <b>negative regulation of protein modification process</b> | BP | APOE, PTPRJ, SNCA                                    | 3 | 0,042712561 |
| <b>long-term synaptic potentiation</b>                     | BP | APOE, SNCA                                           | 2 | 0,043715032 |
| <b>positive regulation of lipid localization</b>           | BP | APOC4, APOE                                          | 2 | 0,045786459 |
| <b>plasma lipoprotein particle</b>                         | CC | APOA5, APOC2, APOC3, APOC4, APOE, APOF, APOH, PCYOX1 | 8 | 6,41E-16    |
| <b>lipoprotein particle</b>                                | CC | APOA5, APOC2, APOC3, APOC4, APOE, APOF, APOH, PCYOX1 | 8 | 6,41E-16    |
| <b>protein-lipid complex</b>                               | CC | APOA5, APOC2, APOC3, APOC4, APOE, APOF, APOH, PCYOX1 | 8 | 8,50E-16    |
| <b>very-low-density lipoprotein particle</b>               | CC | APOA5, APOC2, APOC3, APOC4, APOE, APOH, PCYOX1       | 7 | 1,04E-15    |
| <b>triglyceride-rich plasma lipoprotein particle</b>       | CC | APOA5, APOC2, APOC3, APOC4, APOE, APOH, PCYOX1       | 7 | 1,04E-15    |
| <b>high-density lipoprotein particle</b>                   | CC | APOA5, APOC2, APOC3, APOC4, APOE, APOF, APOH         | 7 | 6,57E-15    |
| <b>chylomicron</b>                                         | CC | APOA5, APOC2, APOC3, APOE, APOH                      | 5 | 1,20E-11    |
| <b>low-density lipoprotein particle</b>                    | CC | APOC2, APOE, APOF                                    | 3 | 4,33E-06    |
| <b>collagen-containing extracellular matrix</b>            | CC | APOC3, APOE, APOH, F2, F9, PLG                       | 6 | 3,94E-05    |
| <b>blood microparticle</b>                                 | CC | AFM, APOE, F2, PLG                                   | 4 | 0,000113378 |
| <b>endoplasmic reticulum lumen</b>                         | CC | APOA5, APOE, F2, F9, PROC                            | 5 | 0,000118359 |
| <b>Golgi lumen</b>                                         | CC | F2, F9, PROC                                         | 3 | 0,001145663 |
| <b>early endosome</b>                                      | CC | APOA5, APOC2, APOC3, APOE                            | 4 | 0,006206798 |
| <b>platelet alpha granule</b>                              | CC | PLG, SNCA                                            | 2 | 0,021097672 |
| <b>secretory granule lumen</b>                             | CC | APOH, LRG1, PLG                                      | 3 | 0,021207717 |
| <b>cytoplasmic vesicle lumen</b>                           | CC | APOH, LRG1, PLG                                      | 3 | 0,021207717 |

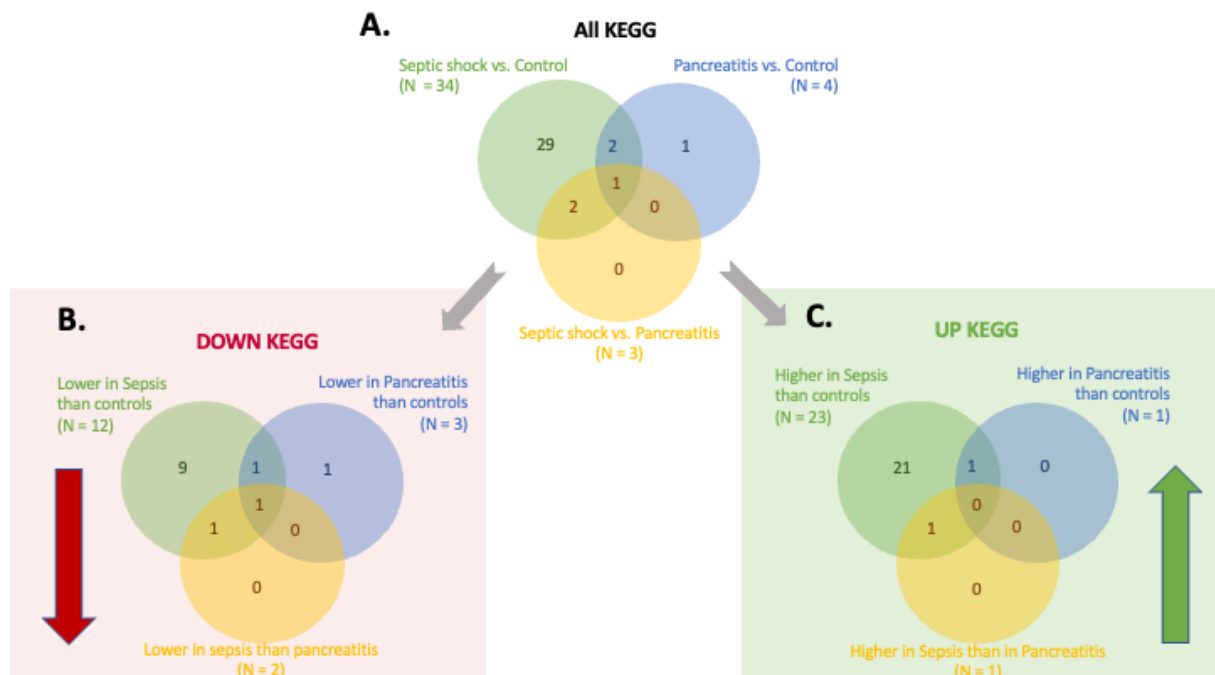
|                                                          |    |                                |   |             |
|----------------------------------------------------------|----|--------------------------------|---|-------------|
| <b>vesicle lumen</b>                                     | CC | APOH, LRG1, PLG                | 3 | 0,021207717 |
| <b>specific granule</b>                                  | CC | LRG1, PTPRJ                    | 2 | 0,048687102 |
| <b>serine-type endopeptidase activity</b>                | MF | F2, F9, HABP2, PLG, PROC       | 5 | 6,94E-05    |
| <b>serine-type peptidase activity</b>                    | MF | F2, F9, HABP2, PLG, PROC       | 5 | 6,94E-05    |
| <b>lipase activator activity</b>                         | MF | APOA5, APOC2, APOH             | 3 | 6,94E-05    |
| <b>serine hydrolase activity</b>                         | MF | F2, F9, HABP2, PLG, PROC       | 5 | 6,94E-05    |
| <b>lipoprotein particle receptor binding</b>             | MF | APOA5, APOC3, APOE             | 3 | 0,000117455 |
| <b>glycosaminoglycan binding</b>                         | MF | APOA5, APOE, APOH, F2, HABP2   | 5 | 0,000130113 |
| <b>heparin binding</b>                                   | MF | APOA5, APOE, APOH, F2          | 4 | 0,000598357 |
| <b>lipid transporter activity</b>                        | MF | APOA5, APOC4, APOE, APOF       | 4 | 0,000598357 |
| <b>endopeptidase activity</b>                            | MF | F2, F9, HABP2, PLG, PROC       | 5 | 0,000933536 |
| <b>lipase inhibitor activity</b>                         | MF | APOC2, APOC3                   | 2 | 0,001485397 |
| <b>phospholipid binding</b>                              | MF | APOA5, APOC3, APOE, APOH, SNCA | 5 | 0,001957969 |
| <b>sulfur compound binding</b>                           | MF | APOA5, APOE, APOH, F2          | 4 | 0,002194067 |
| <b>cholesterol transfer activity</b>                     | MF | APOA5, APOE                    | 2 | 0,002613098 |
| <b>low-density lipoprotein particle receptor binding</b> | MF | APOA5, APOE                    | 2 | 0,00285317  |
| <b>sterol transfer activity</b>                          | MF | APOA5, APOE                    | 2 | 0,003796558 |
| <b>tau protein binding</b>                               | MF | APOE, SNCA                     | 2 | 0,006853181 |
| <b>cholesterol binding</b>                               | MF | APOC3, APOF                    | 2 | 0,010141958 |
| <b>lipid transfer activity</b>                           | MF | APOA5, APOE                    | 2 | 0,013398801 |
| <b>sterol binding</b>                                    | MF | APOC3, APOF                    | 2 | 0,014302606 |
| <b>antioxidant activity</b>                              | MF | APOE, PRDX2                    | 2 | 0,021524238 |
| <b>alcohol binding</b>                                   | MF | APOC3, APOF                    | 2 | 0,02288578  |
| <b>steroid binding</b>                                   | MF | APOC3, APOF                    | 2 | 0,030454775 |
| <b>protein-folding chaperone binding</b>                 | MF | PLG, SNCA                      | 2 | 0,040670992 |
| <b>mannosyl-oligosaccharide mannosidase activity</b>     | MF | MAN1A1                         | 1 | 0,040670992 |



|                                                                                        |    |                    |   |             |
|----------------------------------------------------------------------------------------|----|--------------------|---|-------------|
| <b>intramolecular phosphotransferase activity</b>                                      | MF | BPGM               | 1 | 0,040670992 |
| <b>delta-catenin binding</b>                                                           | MF | PTPRJ              | 1 | 0,040670992 |
| <b>enzyme inhibitor activity</b>                                                       | MF | APOC2, APOC3, SNCA | 3 | 0,040670992 |
| <b>type II transforming growth factor beta receptor binding</b>                        | MF | LRG1               | 1 | 0,040670992 |
| <b>oxidoreductase activity, acting on a sulfur group of donors, oxygen as acceptor</b> | MF | PCYOX1             | 1 | 0,040670992 |
| <b>type I transforming growth factor beta receptor binding</b>                         | MF | LRG1               | 1 | 0,040670992 |
| <b>gamma-catenin binding</b>                                                           | MF | PTPRJ              | 1 | 0,042913092 |
| <b>platelet-derived growth factor receptor binding</b>                                 | MF | PTPRJ              | 1 | 0,048446482 |

**Table S7b.** Showing enriched gene ontologies from downregulated DEPs in sepsis compared to pancreatitis. BP=biological processes, CC=cellular compartments, MF=molecular functions. Ontologies classified as significantly altered if exhibiting an adjusted p-value < 0.05.

Figure S4 – KEGG pathways



**Figure S4.** Venn diagrams showing the distribution of KEGG pathways in plain numbers for the comparisons Septic shock vs. Control (green circles), Pancreatitis vs. Control (blue circles) and Septic shock vs. Pancreatitis (yellow circles). Numbers in the overlapping areas representing terms significantly altered in multiple comparisons. **A.** Terms enriched from all significantly altered proteins. **B.** Terms enriched from significantly downregulated proteins. **C.** Terms enriched from significantly upregulated proteins.

Table S8a – KEGG Sepsis vs Control Up

| Description                                        | ID       | geneID                                                                             | Protein count | Adjusted p-value |
|----------------------------------------------------|----------|------------------------------------------------------------------------------------|---------------|------------------|
| <b>PI3K-Akt signaling pathway</b>                  | hsa04151 | COL1A1/COL1A2/COL2A1/COL6A1/HSP90AA1/HSP90AB1/LAMB1/LAMC1/SPP1/TNC/VWF/YWHAЕ/YWHAG | 13            | 0,00048542       |
| <b>Prion disease</b>                               | hsa05020 | HSPA8/LAMC1/PSMA1/PSMA3/PSMA4/PSMA5/PSMA6/PSMA7/PSMB2/PSMB3/PSMB4                  | 11            | 0,00070699       |
| <b>Parkinson disease</b>                           | hsa05012 | PSMA1/PSMA3/PSMA4/PSMA5/PSMA6/PSMA7/PSMB2/PSMB3/PSMB4/TRAP1                        | 10            | 0,00183748       |
| <b>Huntington disease</b>                          | hsa05016 | PSMA1/PSMA3/PSMA4/PSMA5/PSMA6/PSMA7/PSMB2/PSMB3/PSMB4/SOD2                         | 10            | 0,00429124       |
| <b>Proteasome</b>                                  | hsa03050 | PSMA1/PSMA3/PSMA4/PSMA5/PSMA6/PSMA7/PSMB2/PSMB3/PSMB4                              | 9             | 3,667E-08        |
| <b>ECM-receptor interaction</b>                    | hsa04512 | COL1A1/COL1A2/COL2A1/COL6A1/LAMB1/LAMC1/SPP1/TNC/VWF                               | 9             | 7,6768E-06       |
| <b>Spinocerebellar ataxia</b>                      | hsa05017 | PSMA1/PSMA3/PSMA4/PSMA5/PSMA6/PSMA7/PSMB2/PSMB3/PSMB4                              | 9             | 0,00018219       |
| <b>Focal adhesion</b>                              | hsa04510 | COL1A1/COL1A2/COL2A1/COL6A1/LAMB1/LAMC1/SPP1/TNC/VWF                               | 9             | 0,00126365       |
| <b>Lipid and atherosclerosis</b>                   | hsa05417 | HSP90AA1/HSP90AB1/HSPA4/HSPA8/ICAM1/LBP/MMP9/SOD2/VCAM1                            | 9             | 0,00183748       |
| <b>Cytoskeleton in muscle cells</b>                | hsa04820 | COL11A2/COL1A1/COL1A2/COL5A1/COL6A1/LMNB1/NID1/VCAN/VIM                            | 9             | 0,00238044       |
| <b>Human papillomavirus infection</b>              | hsa05165 | COL1A1/COL1A2/COL2A1/COL6A1/LAMB1/LAMC1/SPP1/TNC/VWF                               | 9             | 0,02209993       |
| <b>Amyotrophic lateral sclerosis</b>               | hsa05014 | PSMA1/PSMA3/PSMA4/PSMA5/PSMA6/PSMA7/PSMB2/PSMB3/PSMB4                              | 9             | 0,04258769       |
| <b>Antigen processing and presentation</b>         | hsa04612 | B2M/CALR/CTSB/CTSL/HSP90AA1/HSP90AB1/HSPA4/HSPA8                                   | 8             | 3,2655E-05       |
| <b>Fluid shear stress and atherosclerosis</b>      | hsa05418 | CTSL/GSTO1/HSP90AA1/HSP90AB1/ICAM1/IL1R2/MMP9/VCAM1                                | 8             | 0,00070699       |
| <b>Protein processing in endoplasmic reticulum</b> | hsa04141 | CALR/GANAB/HSP90AA1/HSP90AB1/HSPA8/PDIA4/PRKCSH/RRBP1                              | 8             | 0,00183748       |

|                                         |          |                                            |   |            |
|-----------------------------------------|----------|--------------------------------------------|---|------------|
| <b>Biosynthesis of amino acids</b>      | hsa01230 | ACY1/ALDOA/ASL/GOT1/PGK1/TALDO1/TKT        | 7 | 0,00018219 |
| <b>Carbon metabolism</b>                | hsa01200 | ALDOA/GOT1/GPI/PGD/PGK1/TALDO1/TKT         | 7 | 0,00126365 |
| <b>IL-17 signaling pathway</b>          | hsa04657 | HSP90AA1/HSP90AB1/LCN2/MMP9/S100A8/S100A9  | 6 | 0,00217537 |
| <b>Protein digestion and absorption</b> | hsa04974 | COL11A2/COL1A1/COL1A2/COL2A1/COL5A1/COL6A1 | 6 | 0,003303   |
| <b>Lysosome</b>                         | hsa04142 | CTSB/CTSD/CTSL/CTSZ/NPC2/PSAP              | 6 | 0,00974493 |
| <b>Pentose phosphate pathway</b>        | hsa00030 | ALDOA/GPI/PGD/TALDO1/TKT                   | 5 | 0,00019503 |
| <b>Amoebiasis</b>                       | hsa05146 | COL1A1/COL1A2/IL1R2/LAMB1/LAMC1            | 5 | 0,01708147 |
| <b>Arginine biosynthesis</b>            | hsa00220 | ACY1/ASL/GOT1                              | 3 | 0,00864517 |

**Table S8a.** Showing enriched KEGG pathways from upregulated DEPs in sepsis compared to control. Pathways classified as significantly altered if exhibiting an adjusted p-value < 0.05.

**Table S8b – KEGG Sepsis vs Control Down**

| <b>Description</b>                         | <b>ID</b> | <b>geneID</b>                                                                                                                            | <b>Protein count</b> | <b>Adjusted p-value</b> |
|--------------------------------------------|-----------|------------------------------------------------------------------------------------------------------------------------------------------|----------------------|-------------------------|
| <b>Complement and coagulation cascades</b> | hsa04610  | C1QA/C1QB/C3/C5/C6/C8A/C8B/C8G/CFH/CFI/CLU/CPB2/F10/F11/F12/F13A1/F2/KLKB1/KNG1/MASP1/PLG/PROC/PROS1/SERPINA5/SERPINC1/SERPIND1/SERPINF2 | 27                   | 5,9863E-36              |
| <b>Regulation of actin cytoskeleton</b>    | hsa04810  | C5/C6/C8A/C8B/C8G/F2/GSN/ITGB1/ITGB3/KNG1/MYH9/MYL12B                                                                                    | 12                   | 8,0335E-06              |
| <b>Coronavirus disease - COVID-19</b>      | hsa05171  | ACE/C1QA/C1QB/C3/C5/C6/C8A/C8B/C8G/F13A1/F2/MASP1                                                                                        | 12                   | 8,0335E-06              |
| <b>Prion disease</b>                       | hsa05020  | C1QA/C1QB/C5/C6/C8A/C8B/C8G/NCAM1/TUBB1                                                                                                  | 9                    | 0,00422142              |
| <b>Staphylococcus aureus infection</b>     | hsa05150  | C1QA/C1QB/C3/C5/CFH/CFI/MASP1/PLG                                                                                                        | 8                    | 2,87E-05                |
| <b>Systemic lupus erythematosus</b>        | hsa05322  | C1QA/C1QB/C3/C5/C6/C8A/C8B/C8G                                                                                                           | 8                    | 0,00025455              |
| <b>Cholesterol metabolism</b>              | hsa04979  | APOA4/APOB/APOC1/APOH/CETP/LCAT                                                                                                          | 6                    | 5,2704E-05              |
| <b>Pertussis</b>                           | hsa05133  | C1QA/C1QB/C3/C5/ITGB1                                                                                                                    | 5                    | 0,00461874              |
| <b>Chagas disease</b>                      | hsa05142  | ACE/C1QA/C1QB/C3/KNG1                                                                                                                    | 5                    | 0,0132211               |
| <b>Platelet activation</b>                 | hsa04611  | ADAMTS13/F2/ITGB1/ITGB3/MYL12B                                                                                                           | 5                    | 0,02928658              |
| <b>Alcoholic liver disease</b>             | hsa04936  | ADIPOQ/C1QA/C1QB/C3/C5                                                                                                                   | 5                    | 0,04757178              |
| <b>Vitamin digestion and absorption</b>    | hsa04977  | APOA4/APOB/BTD                                                                                                                           | 3                    | 0,01296529              |

**Table S8b.** Showing enriched KEGG pathways from downregulated DEPs in sepsis compared to control. Pathways classified as significantly altered if exhibiting an adjusted p-value < 0.05.

Table S9a – KEGG Pancreatitis vs Control Up

| Description       | ID       | geneID            | Protein count | Adjusted p-value |
|-------------------|----------|-------------------|---------------|------------------|
| <b>Proteasome</b> | hsa03050 | PSMA1/PSMA6/PSMB7 | 3             | 0,03415958       |

**Table S9a.** Showing enriched KEGG pathways from upregulated DEPs in pancreatitis compared to control. Pathways classified as significantly altered if exhibiting an adjusted p-value < 0.05.

Table S9b – KEGG Pancreatitis vs Control Down

| Description                                | ID       | geneID                            | Protein count | Adjusted p-value |
|--------------------------------------------|----------|-----------------------------------|---------------|------------------|
| <b>Complement and coagulation cascades</b> | hsa04610 | F12/F13A1/KLKBI/SERPINA5/SERPIND1 | 5             | 9,29575E-06      |
| <b>Cell adhesion molecules</b>             | hsa04514 | CNTN1/NCAM1/SELL                  | 3             | 0,024458582      |
| <b>Vitamin digestion and absorption</b>    | hsa04977 | APOA4/BTD                         | 2             | 0,013063128      |

**Table S9b.** Showing enriched KEGG pathways from downregulated DEPs in pancreatitis compared to control. Pathways classified as significantly altered if exhibiting an adjusted p-value < 0.05.

Table S10a – KEGG Sepsis vs Pancreatitis Up

| Description                                        | ID       | geneID         | Protein count | Adjusted p-value |
|----------------------------------------------------|----------|----------------|---------------|------------------|
| <b>Protein processing in endoplasmic reticulum</b> | hsa04141 | GANAB/HSP90AA1 | 2             | 0,04109991       |

**Table S10a.** Showing enriched KEGG pathways from upregulated DEPs in sepsis compared to pancreatitis. Pathways classified as significantly altered if exhibiting an adjusted p-value < 0.05.

Table S10b – KEGG Sepsis vs Pancreatitis Down

| Description                         | ID       | geneID                | Protein count | Adjusted p-value |
|-------------------------------------|----------|-----------------------|---------------|------------------|
| Complement and coagulation cascades | hsa04610 | C6/F2/F9/PLG/PROC     | 5             | 8,95146E-06      |
| Cholesterol metabolism              | hsa04979 | APOC2/APOC3/APOE/APOH | 4             | 2,18387E-05      |

**Table S10b.** Showing enriched KEGG pathways from upregulated DEPs in sepsis compared to pancreatitis. Pathways classified as significantly altered if exhibiting an adjusted p-value < 0.05.