

Proteomic study revealed cellular assembly and lipid metabolism dysregulation in sepsis secondary to community-acquired pneumonia

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Supplementary data

Fig. S1. Gene ontology annotation for molecular function and biological processes for differentially expressed proteins after D7.

Fig. S2. IPA generated protein-protein interaction network to identify altered functional categories in septic patients.

Table S1. Quantitative proteomics data with protein description, number of peptides matched, Mascot score and fold changes in septic patients.

Table S2. Detailed gene ontology annotations for septic patients for molecular function, biological processes and cellular components.

Table S3. IPA-generated functional interaction network based on scores for septic patients.

Table S4. Altered functions with their activation and inhibition z-scores in septic patients.

Table S5. IPA-identified canonical pathways in septic patients.

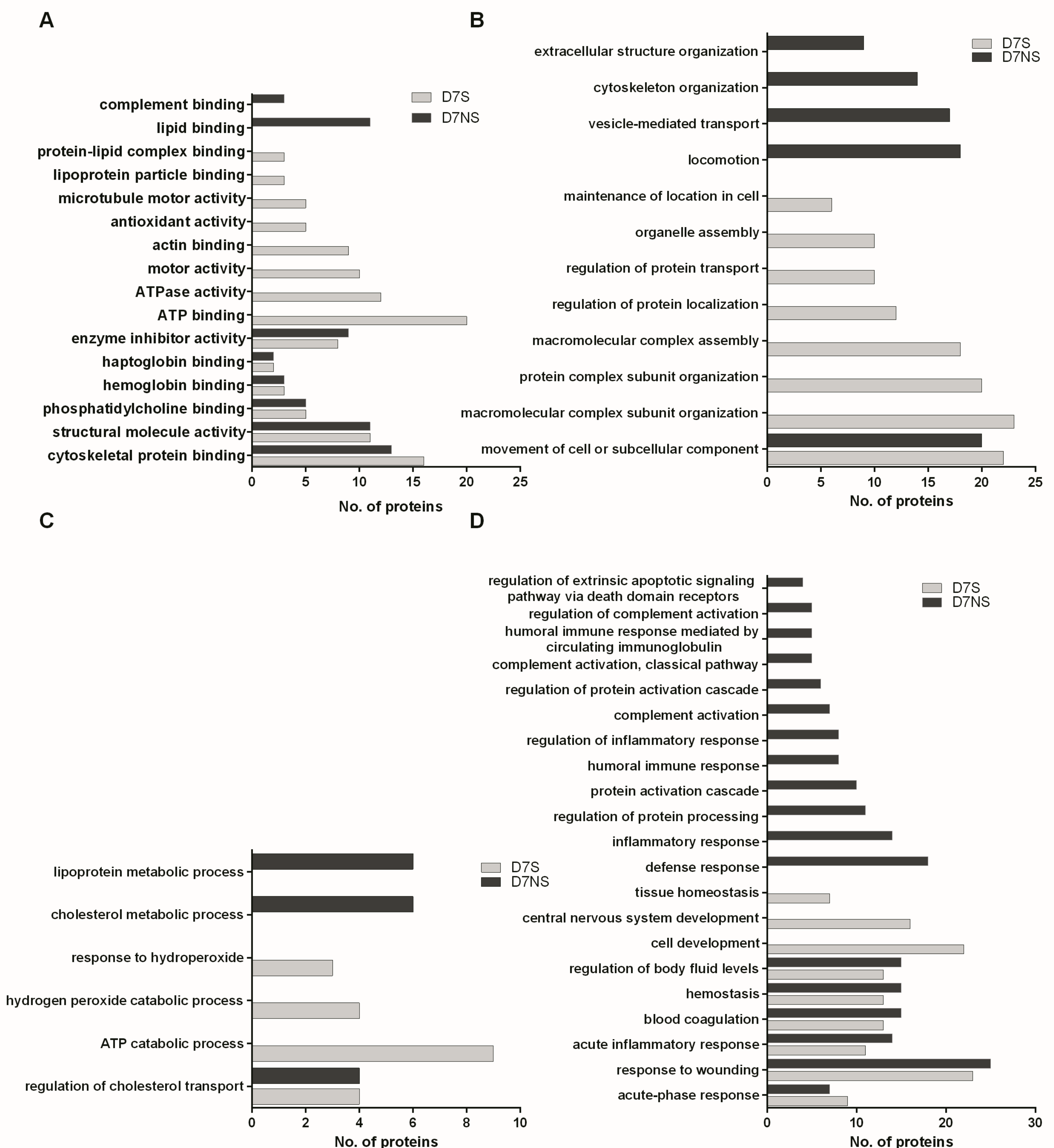


Fig. S1: Gene ontology annotation for molecular function and biological processes for differentially expressed proteins after D7. A refers to altered molecular functions between septic survivors and non-survivors. Biological processes were further categorized accordingly to the biological process: associated cellular organization and movement (B); alteration associated to metabolism (C) and to immune response related altered processes (D).

Fig. S2. IPA generated protein-protein interaction network to identified altered functional categories in septic patients.

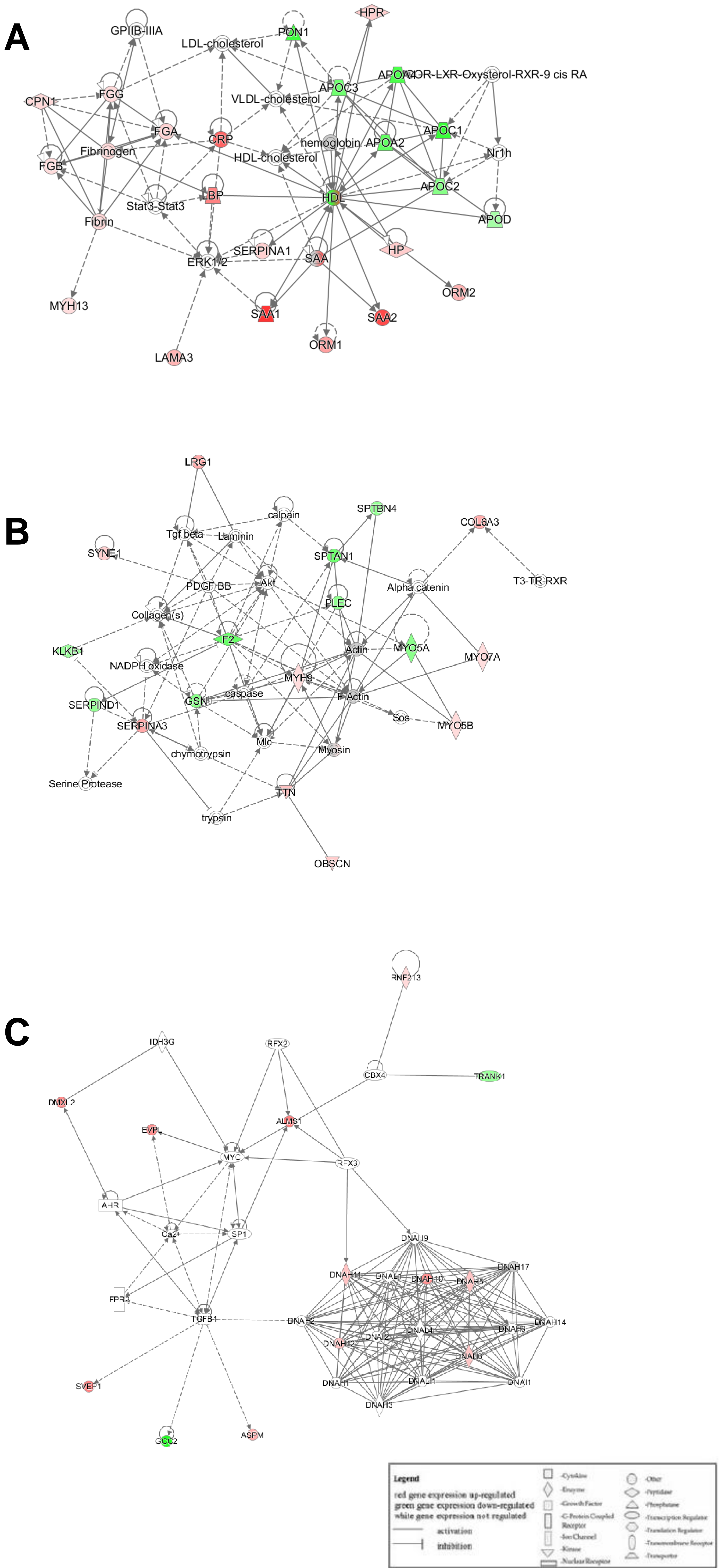


Fig. S2_1. Interaction network for day 0 survivors (D0S) where, A denote Metabolic Disease, Lipid Metabolism, Small Molecule Biochemistry, B, Cellular Assembly and Organization, Cellular Function and Maintenance, Cellular Movement and, C, developmental Disorder, Hereditary Disorder, Respiratory Disease. The green color represent down-regulation, red color represent up-regulation.

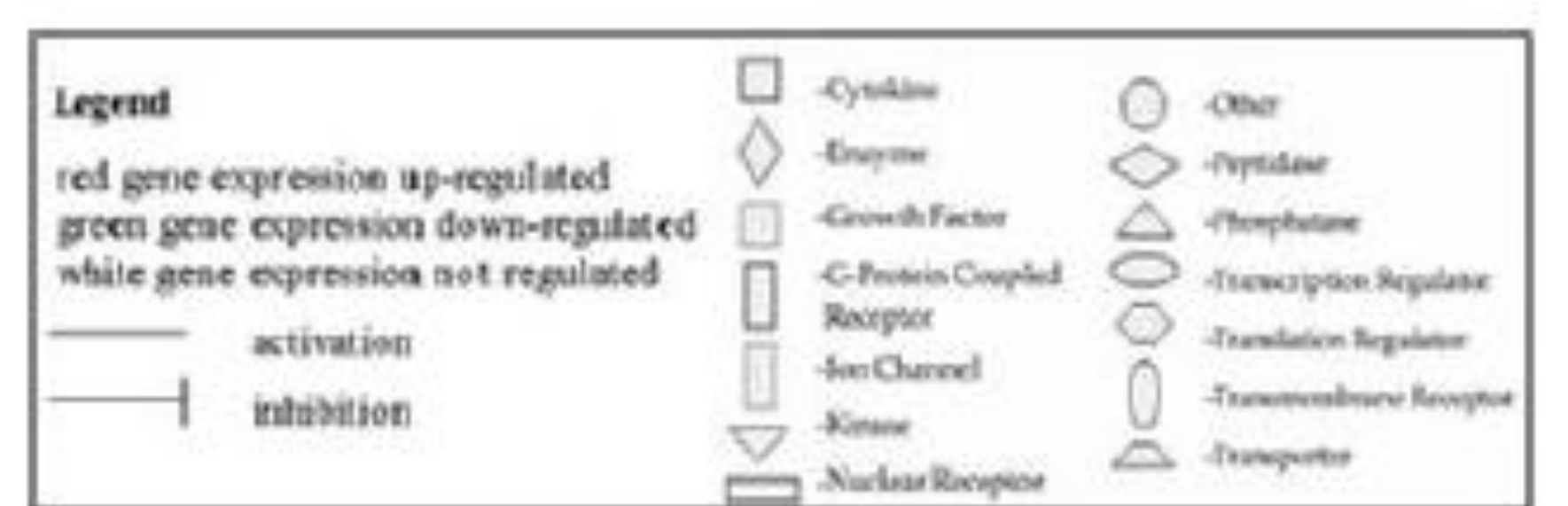
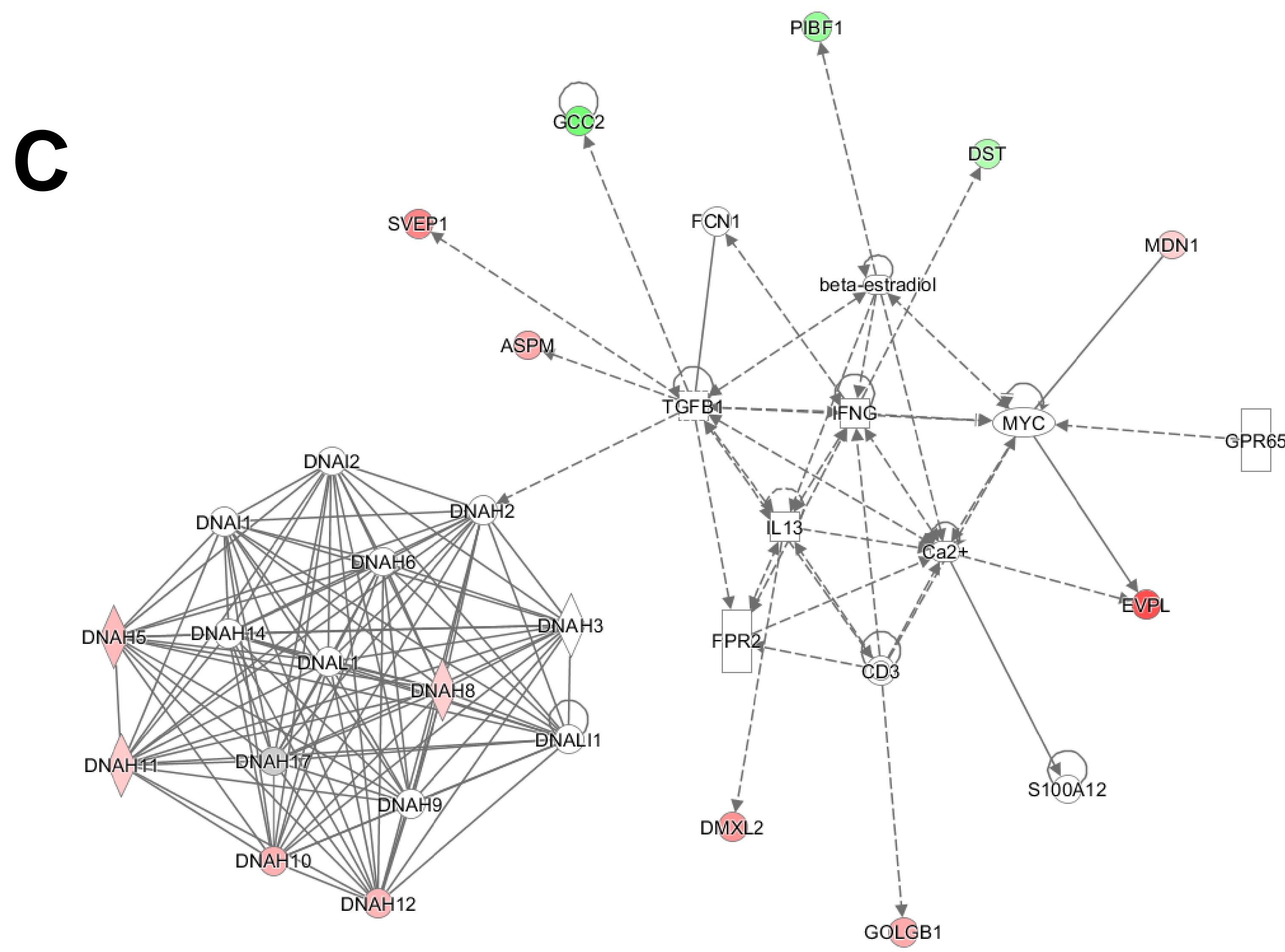
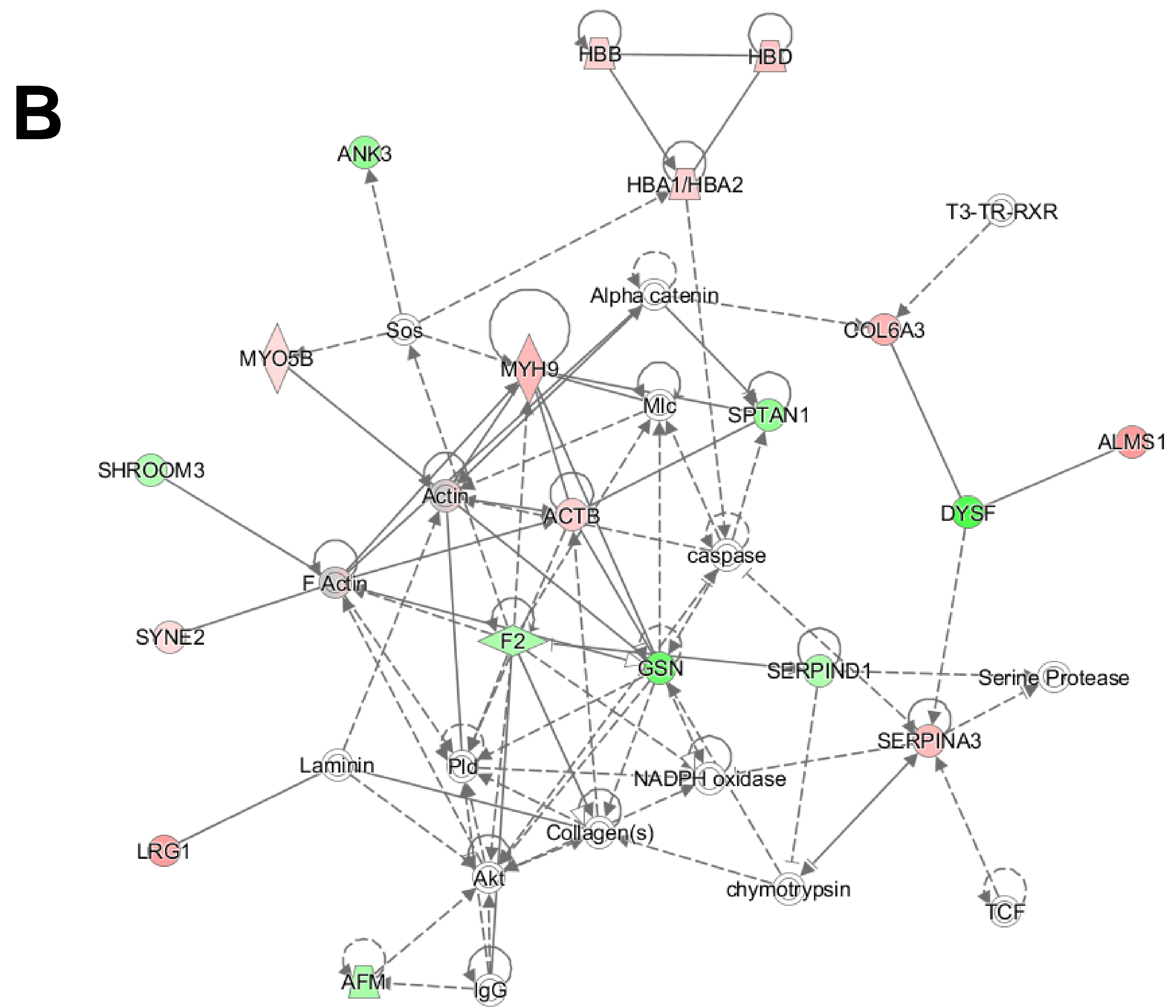
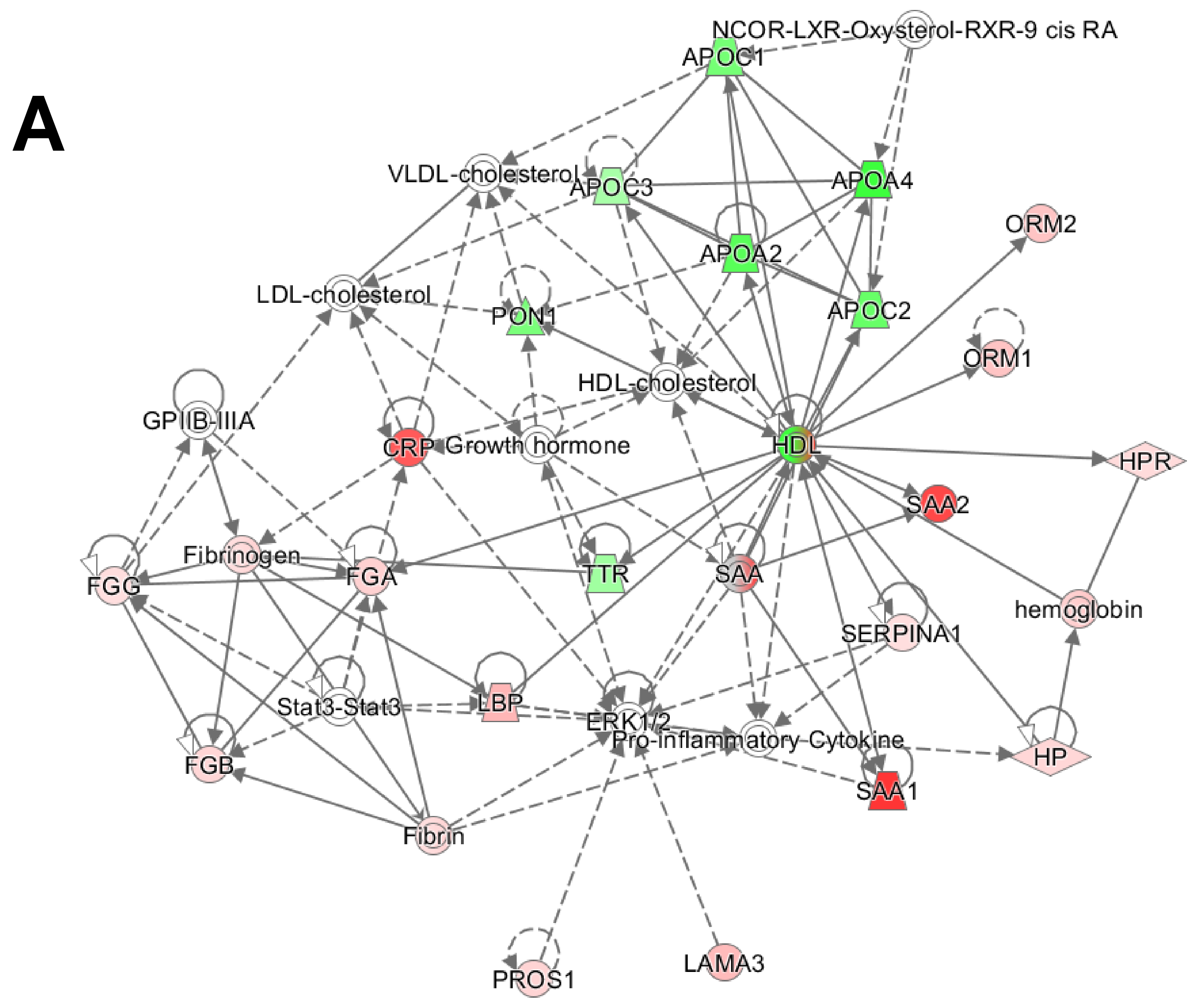


Fig.S2_2. Interaction network for day 0 non-survivors (DONS) where, A denote Metabolic Disease, lipid Metabolism, Molecular Transport, B, Cell-to Cell Signaling and Interaction, Cellular Assembly and Organization, Connective Tissue Disorders, C, Developmental Disorder, Hereditary Disorder, Respiratory Disease. The green color represent down-regulation, red color represent up-regulation.

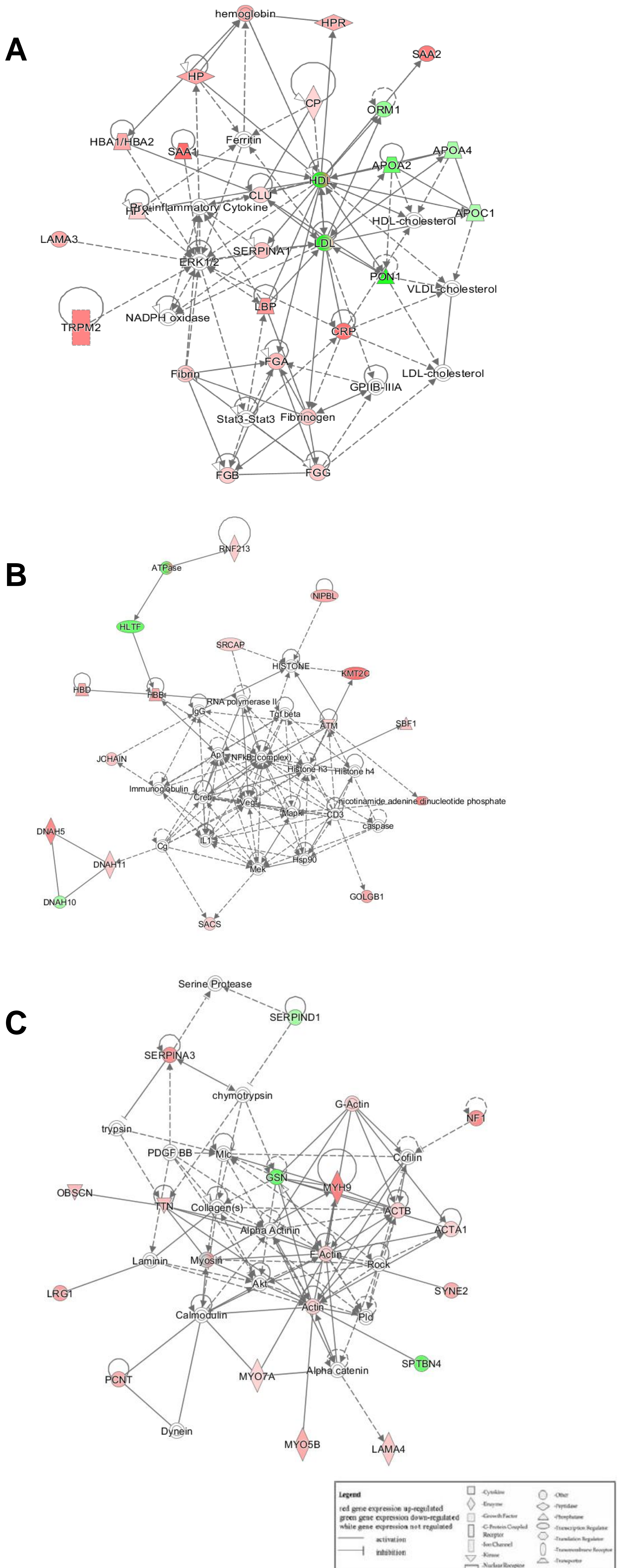


Fig.S2_3. Interaction network for day 7 survivors (D7S) where, A denote Metabolic Disease, Cardiovascular Disease, Developmental Disorder, B, Cancer, Organismal Injury and Abnormalities, Endocrine System Disorders, C, Cellular Assembly and Organization, Cellular Development, Cellular Growth and Proliferation. The green color represent down-regulation, red color represent up-regulation.

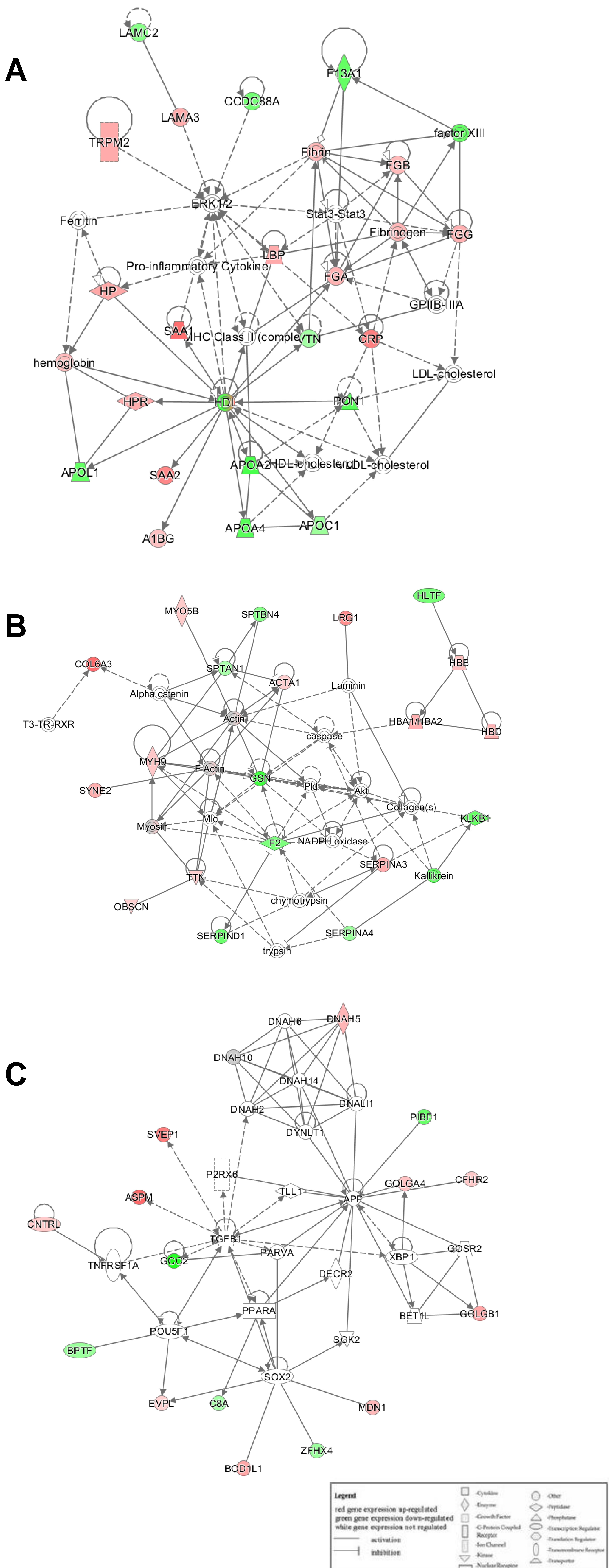


Fig.S2_4. Interaction network for day 7 non-survivors (D7NS) where, A denote Developmental Disorder, Hematological Disease, Hereditary Disorder, B, Cellular Assembly and Organization, Cellular Development, Cellular Growth and Proliferation, C, Cellular Development, Tissue Development, Cancer. The green color represent down-regulation, red color represent up-regulation.

Table S1. Quantitative proteomics data with protein description, number of peptides matched, Mascot score and fold changes in septic patients.

| Protein Groups | Acces | Gene name | Protein description | Peptides matched | Score | D0A | D0D | D7A | D7D |
|----------------------------------|--------|-----------|--|------------------|-------|----------|-----------|----------|----------|
| CO3_HUMAN | P01024 | C3 | Complement C3 | 780 | 22992 | -0.37707 | -0.37707 | -0.25154 | -0.37707 |
| A1AT_HUMAN | P01009 | SERPINA1 | Alpha-1-antitrypsin | 897 | 19469 | 0.565597 | 0.389567 | 0.613532 | 0.263034 |
| APOA1_HUMAN | P02647 | APOA1 | Apolipoprotein A-I | 725 | 13962 | -0.2863 | -0.34008 | 0.163499 | -0.05889 |
| FIBA_HUMAN | P02671 | FGA | Fibrinogen alpha chain | 379 | 9810 | 0.536053 | 0.545968 | 0.695994 | 0.678072 |
| SAA1_HUMAN | P0DJ18 | SAA1 | Serum amyloid A-1 protein | 218 | 8379 | 2.462052 | 2.451541 | 1.475085 | 1.257011 |
| CO4B_HUMAN | P0C0L5 | C4B | Complement C4-B | 323 | 8217 | -0.34008 | -0.34008 | -0.32193 | -0.37707 |
| CO4A_HUMAN | P0C0L4 | C4A | Complement C4-A | 322 | 8014 | -0.34008 | -0.34008 | -0.32193 | -0.37707 |
| SAA2_HUMAN | P0DJ19 | SAA2 | Serum amyloid A-2 protein | 223 | 7805 | 2.179511 | 2.204767 | 1.286881 | 1.035624 |
| A2MG_HUMAN | P01023 | A2M | Alpha-2-macroglobulin | 360 | 7199 | -0.21759 | 0.163499 | -0.20091 | 0.286881 |
| FIBB_HUMAN | P02675 | FBG | Fibrinogen beta chain | 215 | 5741 | 0.422233 | 0.485427 | 0.485427 | 0.594549 |
| CERU_HUMAN | P00450 | CP | Ceruloplasmin | 217 | 5622 | -0.13606 | 0.014355 | 0.411426 | 0.378512 |
| TRFE_HUMAN | P02787 | TF | Serotransferrin | 213 | 4252 | -0.05889 | -0.34008 | -0.02915 | -0.30401 |
| AACT_HUMAN | P01011 | SERPINA3 | Alpha-1-antichymotrypsin | 169 | 3946 | 1.035624 | 0.807355 | 1.111031 | 0.713696 |
| APOB_HUMAN | P04114 | APOB | Apolipoprotein B-100 | 201 | 3797 | -0.35845 | -0.18442 | -0.30401 | 0 |
| ITIH4_HUMAN | Q14624 | ITIH4 | Inter-alpha-trypsin inhibitor heavy chain H4 | 143 | 3563 | 0.097611 | 0.189034 | 0.344828 | 0.189034 |
| APOA4_HUMAN | P06727 | APOA4 | Apolipoprotein A-IV | 160 | 3136 | -0.81097 | -0.97143 | -0.4344 | -0.78588 |
| CFAH_HUMAN | P08603 | CFH | Complement factor H | 164 | 2916 | 0.176323 | -0.08927 | 0.321928 | 0.201634 |
| HPT_HUMAN | P00738 | HP | Haptoglobin | 205 | 2778 | 0.613532 | 0.475085 | 0.895303 | 0.748461 |
| VTNC_HUMAN | P04004 | VTN | Vitronectin | 103 | 2761 | -0.04394 | 0.056584 | -0.02915 | -0.4344 |
| A2GL_HUMAN | P02750 | LRG1 | Leucine-rich alpha-2-glycoprotein | 115 | 2688 | 0.992768 | 1.163499 | 0.918386 | 0.978196 |
| APOE_HUMAN | P02649 | APOE | Apolipoprotein E | 82 | 2465 | -0.26882 | -0.152 | -0.074 | -0.21759 |
| FIBG_HUMAN | P02679 | FGG | Fibrinogen gamma chain | 127 | 2103 | 0.443607 | 0.389567 | 0.555816 | 0.678072 |
| CFAB_HUMAN | P00751 | CFB | Complement factor B | 102 | 2086 | 0.15056 | -0.08927 | 0.097611 | -0.08927 |
| ANGT_HUMAN | P01019 | AGT | Angiotensinogen | 59 | 2061 | -0.02915 | 0.028569 | 0.189034 | 0 |
| ANT3_HUMAN | P01008 | SERPINC1 | Antithrombin-III | 106 | 2039 | 0 | 0.042644 | 0.333424 | 0.214125 |
| HPTR_HUMAN | P00739 | HPR | Haptoglobin-related protein | 130 | 1917 | 0.594549 | 0.422233 | 0.815575 | 0.713696 |
| THRB_HUMAN | P00734 | F2 | Prothrombin | 85 | 1867 | -0.68966 | -0.41504 | -0.68966 | -0.62149 |
| PLMN_HUMAN;PLGB_HUMAN | P00747 | PLG | Plasminogen | 79 | 1826 | -0.08927 | -0.18442 | 0.137504 | 0.028569 |
| CLUS_HUMAN | P10909 | CLU | Clusterin | 65 | 1808 | -0.13606 | -0.05889 | 0.389567 | 0.176323 |
| TTYH_HUMAN | P02766 | TTR | Transthyretin | 53 | 1609 | -0.37707 | -0.47393 | -0.1047 | -0.0145 |
| HBB_HUMAN;HBE_HUMAN | P68871 | HBB | Hemoglobin subunit beta | 71 | 1590 | -0.16812 | 0.545968 | 0.871844 | 0.555816 |
| HEMO_HUMAN | P02790 | HPX | Hemopexin | 99 | 1558 | 0.097611 | -0.05889 | 0.464668 | 0.137504 |
| APOC3_HUMAN | P02656 | APOC3 | Apolipoprotein C-III | 51 | 1549 | -0.64386 | -0.4344 | -0.152 | -0.25154 |
| CRP_HUMAN | P02741 | CRP | C-reactive protein | 113 | 1512 | 1.85599 | 1.974529 | 1.400538 | 1.097611 |
| PON1_HUMAN | P27169 | PON1 | Serum paraoxonase/arylesterase 1 | 56 | 1500 | -0.8625 | -0.66658 | -1.08927 | -0.78588 |
| IGLL5_HUMAN;LAC1_HUMAN | B9A064 | IGLL5 | Immunoglobulin lambda-like polypeptide 5 | 68 | 1490 | 0.15056 | 0 | 0.226509 | 0.176323 |
| CBPB_HUMAN | P15169 | CPB1 | Carboxypeptidase N catalytic chain | 132 | 1362 | 0.454176 | 0.028569 | 0.137504 | -0.074 |
| APOA2_HUMAN | P02652 | APOA2 | Apolipoprotein A-II | 125 | 1318 | -0.71312 | -0.8365 | -0.73697 | -0.8625 |
| SAMP_HUMAN | P02743 | APCS | Serum amyloid P-component | 86 | 1277 | -0.074 | -0.32193 | 0.15056 | -0.13606 |
| GELS_HUMAN | P06396 | GSN | Gelsolin | 48 | 1058 | -0.53533 | -0.73697 | -0.76121 | -0.91594 |
| APOD_HUMAN | P05090 | APOD | Apolipoprotein D | 50 | 970 | -0.39593 | -0.05889 | 0 | 0.189034 |
| A1BG_HUMAN | P04217 | A1BG | Alpha-1B-glycoprotein | 40 | 969 | 0.226509 | 0.201634 | 0.214125 | 0.536053 |
| CO5_HUMAN | P01031 | C5 | Complement C5 | 53 | 953 | -0.25154 | -0.152 | 0.214125 | -0.02915 |
| HBD_HUMAN | P02042 | HBD | Hemoglobin subunit delta | 37 | 828 | -0.08927 | 0.704872 | 0.879706 | 0.659925 |
| FHR1_HUMAN | Q03591 | CFHR1 | Complement factor H-related protein 1 | 33 | 743 | 0.124328 | -0.02915 | 0.367371 | 0.378512 |
| APOC2_HUMAN | P02655 | APOC2 | Apolipoprotein C-II | 35 | 740 | -0.53533 | -0.76121 | -0.18442 | -0.37707 |
| PZP_HUMAN | P20742 | PZP | Pregnancy zone protein | 55 | 718 | -0.30401 | 0.15056 | -0.30401 | 0.250962 |
| C4BPA_HUMAN | P04003 | C4BPA | C4b-binding protein alpha chain | 36 | 716 | 0.238787 | -0.333424 | -0.1047 | 0.137504 |
| FBLN1_HUMAN | P23142 | FBLN1 | Fibulin-1 | 26 | 651 | 0.042644 | -0.02915 | 0.214125 | 0.163499 |
| LBP_HUMAN | P18428 | LBP | Lipopolysaccharide-binding protein | 22 | 631 | 1.505891 | 0.871844 | 1.042644 | 0.722466 |
| VTDB_HUMAN | P02774 | GC | Vitamin D-binding protein | 39 | 602 | 0.201634 | 0.124328 | 0.201634 | 0.250962 |
| AMBP_HUMAN | P02760 | AMBP | Protein AMBP | 12 | 470 | -0.30401 | -0.152 | -0.12029 | -0.18442 |
| CD14_HUMAN | P08571 | CD14 | Monocyte differentiation antigen CD14 | 8 | 399 | 0.226509 | 0.111031 | 0.226509 | -0.04394 |
| IGJ_HUMAN | P01591 | JCHAIN | Immunoglobulin J chain | 13 | 378 | 0.163499 | 0.356144 | 0.594549 | 0.389567 |
| CO2_HUMAN | P06681 | C2 | Complement C2 | 14 | 372 | 0.028569 | -0.12029 | -0.13606 | 0.124328 |
| A2AP_HUMAN | P08697 | SERPINF2 | Alpha-2-antiplasmin | 18 | 341 | -0.0145 | -0.18442 | 0.189034 | 0.070389 |
| QSOX1_HUMAN | O00391 | QSOX1 | Sulfhydryl oxidase 1 | 17 | 336 | 0.189034 | 0.378512 | 0.422233 | 0.176323 |
| ITIH2_HUMAN | P19823 | ITIH2 | Inter-alpha-trypsin inhibitor heavy chain H2 | 16 | 335 | -0.30401 | 0.014355 | -0.08927 | -0.1047 |
| APOC1_HUMAN | P02654 | APOC1 | Apolipoprotein C-I | 37 | 330 | -0.88897 | -0.68966 | -0.39593 | -0.47393 |
| CO8G_HUMAN | P07360 | C8G | Complement component C8 gamma chain | 15 | 328 | 0 | 0.084064 | -0.25154 | -0.30401 |
| CO6_HUMAN | P13671 | C6 | Complement component C6 | 7 | 313 | 0.263034 | 0.042644 | 1.275007 | 0.286881 |
| ITIH1_HUMAN | P19827 | ITIH1 | Inter-alpha-trypsin inhibitor heavy chain H1 | 19 | 300 | -0.13606 | -0.074 | 0.163499 | -0.18442 |
| CO9_HUMAN | P02748 | C9 | Complement component C9 | 25 | 291 | 0.097611 | 0.321928 | 0.367371 | 0.389567 |
| CE350_HUMAN | Q5VT06 | CEP350 | Centrosome-associated protein 350 | 24 | 290 | -0.18442 | -0.20091 | 0.263034 | 0.028569 |
| HRG_HUMAN | P04196 | HRG | Histidine-rich glycoprotein | 11 | 284 | 0.124328 | -0.05889 | 0.097611 | 0.124328 |
| TLN1_HUMAN | Q9Y490 | TLN1 | Talin-1 | 27 | 275 | -0.08927 | -0.05889 | 0.263034 | -0.152 |
| DYH8_HUMAN | Q96181 | DNAH8 | Dynein heavy chain 8, axonemal | 21 | 270 | 0.669027 | 0.565597 | 0.124328 | 0.014355 |
| CO8A_HUMAN | P07357 | C8A | Complement component C8 alpha chain | 10 | 267 | -0.04394 | -0.08927 | -0.25154 | -0.41504 |
| OBSN_HUMAN | Q5V5T9 | OBSN | Obscurin | 20 | 252 | 0.613532 | 0.31034 | 0.659925 | 0.411426 |
| A1AG1_HUMAN | P02763 | ORM1 | Alpha-1-acid glycoprotein 1 | 19 | 243 | 1.144046 | 0.704872 | -0.51457 | -0.074 |
| ACTB_HUMAN;ACTG_HUMAN;ACTG_HUMAN | P60709 | ACTB | Actin, cytoplasmic 1 | 9 | 241 | 0.344828 | 0.565597 | 0.495695 | 0.163499 |
| LAMA3_HUMAN | Q16787 | LAMA3 | Laminin subunit alpha-3 | 13 | 233 | 0.903038 | 0.807355 | 0.871844 | 0.704872 |
| MYO5B_HUMAN | Q9ULV0 | MYO5B | Unconventional myosin-Vb | 16 | 228 | 0.411426 | 0.411426 | 0.807355 | 0.454176 |
| APOL1_HUMAN | O14791 | APOL1 | Apolipoprotein L1 | 11 | 224 | -0.20091 | -0.32193 | 0.15056 | -0.73697 |
| DYH5_HUMAN | Q8TE73 | DNAH5 | Dynein heavy chain 5, axonemal | 21 | 215 | 0.704872 | 0.815575 | 1.124328 | 0.641546 |
| DYST_HUMAN | Q03001 | DST | Dystonin | 28 | 213 | -0.35845 | -0.39593 | 0.070389 | -0.23447 |
| HEP2_HUMAN | P05546 | SERPIND1 | Heparin cofactor 2 | 14 | 210 | -0.47393 | -0.39593 | -0.45403 | -0.68966 |
| FHR2_HUMAN | P36980 | CFHR2 | Complement factor H-related protein 2 | 21 | 209 | 0.137504 | 0.028569 | 0.400538 | 0.464668 |
| SYNE1_HUMAN | Q8NF91 | SYNE1 | Nesprin-1 | 18 | 203 | 0.555816 | 0.111031 | 0.333424 | 0.097611 |
| LUM_HUMAN | P51884 | LUM | Lumican | 14 | 202 | -0.04394 | -0.16812 | 0.097611 | -0.08927 |
| TITIN_HUMAN | Q8WZ42 | TTN | Titin | 18 | 197 | 0.731183 | 0.367371 | 0.678072 | 0.432959 |
| PEDF_HUMAN | P36955 | SERPINF1 | Pigment epithelium-derived factor | 12 | 194 | 0.097611 | -0.02915 | -0.0145 | 0 |
| KNG1_HUMAN | P01042 | KNG1 | Kininogen-1 | 8 | 188 | 0.084064 | 0.028569 | 0.111031 | -0.0145 |
| ITIH3_HUMAN | Q06033 | ITIH3 | Inter-alpha-trypsin inhibitor heavy chain H3 | 8 | 176 | -0.0145 | 0.097611 | 0.042644 | -0.05889 |
| C1R_HUMAN | P00736 | C1R | Complement C1r subcomponent | 7 | 171 | 0.263034 | 0.632268 | 0.263034 | 0.286881 |
| C1S_HUMAN | P09871 | C1S | Complement C1s subcomponent | 10 | 169 | 0.124328 | 0.056584 | 0.226509 | 0.263034 |
| IC1_HUMAN | P05155 | SERPING1 | Plasma protease C1 inhibitor | 10 | 169 | 0.163499 | 0.378512 | -0.074 | 0.378512 |
| CFAI_HUMAN | P05156 | CFI | Complement factor I | 8 | 164 | -0.05889 | -0.04394 | 0.189034 | 0.485427 |
| DYH17_HUMAN | Q9UHF2 | DNAH17 | Dynein heavy chain 17, axonemal | 17 | 160 | -0.35845 | -0.2863 | 0.250962 | -0.05889 |
| GPX3_HUMAN;GPX6_HUMAN | P22352 | GPX3 | Glutathione peroxidase 3 | 23 | 159 | 0.333424 | 0.137504 | 0.432959 | 0.189034 |
| SPTA1_HUMAN | P02549 | SPTA1 | Spectrin alpha chain, erythrocytic 1 | 9 | 154 | -0.2863 | -0.30401 | 0.333424 | 0.084064 |
| VP13B_HUMAN | Q7Z7G8 | VPS13B | Vacuolar protein sorting-associated protein 13B | 8 | 151 | -0.18442 | -0.34008 | 0 | 0 |
| SAA4_HUMAN | P35542 | SAA4 | Serum amyloid A-4 protein | 14 | 151 | -0.16812 | 0.084064 | -0.02915 | -0.152 |
| HLTF_HUMAN | Q14527 | HLTF | Helicase-like transcription factor | 18 | 146 | 0.056584 | -0.21759 | -0.76121 | -0.64386 |
| CE290_HUMAN | Q15078 | CEP290 | Centrosomal protein of 290 kDa | 21 | 142 | 0.042644 | 0.070389 | 0.378512 | -0.08927 |
| HBA_HUMAN;HBAZ_HUMAN | P69905 | HBA1 | Hemoglobin subunit alpha | 15 | 142 | -0.20091 | 0.565597 | 0.85599 | 0.687061 |
| CO8B_HUMAN | P07358 | C8B | Complement component C8 beta chain | 6 | 138 | -0.0145 | -0.12029 | -0.30401 | -0.20091 |
| PROS_HUMAN | P07225 | PROS1 | Vitamin K-dependent protein 5 | 7 | 137 | 0.084064 | 0.505891 | 0.286881 | -0.08927 |
| GOLGB1_HUMAN | Q14789 | GOLGB1 | Golgin subfamily B member 1 | 9 | 135 | 0.632268 | 1.007196 | 0.879706 | 0.773996 |
| CNTRL_HUMAN | Q7Z7A1 | CNTRL | Centriolin | 6 | 134 | 0.014355 | 0.111031 | 0.443607 | 0.454176 |
| SMC3_HUMAN | Q9UQF7 | SMC3 | Structural maintenance of chromosomes protein 3 | 6 | 131 | 0.454176 | 0.014355 | 0.201634 | 0.189034 |
| SACS_HUMAN | Q9NZJ4 | SACS | Sacsin | 10 | 126 | -0.25154 | -0.35845 | 0.495695 | 0.263034 |
| RN213_HUMAN | Q63HN8 | RNF213 | E3 ubiquitin-protein ligase RNF213 | 10 | 122 | 0.443607 | 0.250962 | 0.505891 | 0.275007 |
| KAIN_HUMAN | P29622 | SERPINA4 | Kallistatin | 6 | 118 | -0.21759 | -0.2863 | -0.0145 | -0.47393 |
| CE112_HUMAN | Q8N8E3 | CEP112 | Centrosomal protein of 112 kDa | 6 | 113 | -0.1047 | 0.070389 | -0.21759 | -0.2863 |
| PERQ1_HUMAN | O75420 | GIGYF1 | PERQ amino acid-rich with GYF domain-containing protein 1 | 8 | 103 | -0.20091 | -0.152 | -0.30401 | -0.35845 |
| DMXL2_HUMAN | Q8TDJ6 | DMXL2 | DmX-like protein 2 | 7 | 102 | 1.372952 | 1.298658 | 0.879706 | 1.042644 |
| MACF1_HUMAN | Q9UPN3 | MACF1 | Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 | 9 | 99 | 0.201634 | 0 | 0.15056 | 0.097611 |
| K1109_HUMAN | Q2LD37 | KIAA1109 | Uncharacterized protein KIAA1109 | 5 | 90 | 0.594549 | -0.05889 | 0.321928 | 0.124328 |
| DYSF_HUMAN | O75923 | DYSF | Dysferlin | 5 | 90 | -0.04394 | -0.88897 | -0.18442 | -0.32193 |
| NF1_HUMAN | P21359 | NF1 | Neurofibromin | 7 | 89 | 1.232661 | 1.333424 | 1.104337 | 1.042644 |
| LAMC2_HUMAN | Q13753 | LAMC2 | Laminin subunit gamma-2 | 7 | 89 | -0.35845 | 0.028569 | -0.30401 | -0.57777 |
| DYH11_HUMAN | Q96DT5 | DNAH11 | Dynein heavy chain 11, axon | | | | | | |

Table S2. Detailed gene ontology annotations for septic patients for molecular function, biological processes and cellular components.

Table S2.1 Survivors patients D0 samples.

| Category | ID | Name | p-value | q-value Bonferroni | q-value FDR B&H | q-value FDR B&Y | Hit Count in Query List | Hit Count in Query List | Hit in Query List |
|------------------------|------------|--|----------|--------------------|-----------------|-----------------|-------------------------|-------------------------|--|
| GO: Molecular Function | GO:0003774 | motor activity | 3.86E-16 | 8.61E-14 | 8.61E-14 | 5.36E-13 | 13 | 130 | MHY9,DNAH12,KIF27,MHY13,DNAH10,MYO5A,MYO5B,SMC3,CENPE,MYO7A,DNAH5,DNAH8,DNAH11 |
| GO: Molecular Function | GO:0003777 | microtubule motor activity | 1.88E-10 | 4.22E-08 | 2.10E-08 | 1.26E-07 | 8 | 77 | DNAH12,KIF27,DNAH10,SMC3,CENPE,DNAH5,DNAH8,DNAH11 |
| GO: Molecular Function | GO:0008092 | cytoskeletal protein binding | 6.42E-10 | 1.43E-07 | 4.77E-08 | 2.86E-07 | 17 | 792 | SPBTBNA,MHY9,NF1,KIF27,MHY13,ALMS1,MYO5A,MYO5B,CENPE,MYO7A,SYNE1,SPTAN1,NUMA1,OBSCN,PLEC,TTN,GSN |
| GO: Molecular Function | GO:0005516 | calmodulin binding | 7.06E-09 | 1.57E-06 | 3.27E-07 | 1.96E-06 | 9 | 175 | MHY9,MHY13,MYO5A,MYO5B,MYO7A,SPTAN1,OBSCN,ASPM,TTN |
| GO: Molecular Function | GO:0000146 | microfilament motor activity | 7.34E-09 | 1.64E-06 | 3.27E-07 | 1.96E-06 | 5 | 21 | MHY9,MHY13,MYO5A,MYO5B,MYO7A |
| GO: Molecular Function | GO:0017111 | nucleoside-triphosphatase activity | 3.48E-08 | 7.77E-06 | 1.29E-06 | 7.75E-06 | 15 | 781 | MHY9,DNAH12,KIF27,MHY13,DNAH10,MYO5A,MYO5B,SMC3,CENPE,MYO7A,RNF213,SRCAP,DNAH5,DNAH8,DNAH11 |
| GO: Molecular Function | GO:0043178 | alcohol binding | 4.80E-08 | 1.07E-05 | 1.45E-06 | 8.68E-06 | 7 | 101 | NF1,APOA2,APOA4,APOC1,APOC2,APOC3,CRP |
| GO: Molecular Function | GO:0018462 | hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides | 6.71E-08 | 1.50E-05 | 1.45E-06 | 8.68E-06 | 17 | 821 | MHY9,DNAH12,KIF27,MHY13,DNAH10,MYO5A,MYO5B,SMC3,CENPE,MYO7A,RNF213,SRCAP,DNAH5,DNAH8,DNAH11 |
| GO: Molecular Function | GO:0016818 | hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides | 6.93E-08 | 1.55E-05 | 1.45E-06 | 8.68E-06 | 15 | 823 | MHY9,DNAH12,KIF27,MHY13,DNAH10,MYO5A,MYO5B,SMC3,CENPE,MYO7A,RNF213,SRCAP,DNAH5,DNAH8,DNAH11 |
| GO: Molecular Function | GO:0003779 | actin binding | 7.13E-08 | 1.59E-05 | 1.45E-06 | 8.68E-06 | 11 | 392 | SPBTBNA,MHY9,MHY13,MYO5A,MYO5B,MYO7A,SYNE1,SPTAN1,PLEC,TTN,GSN |
| GO: Molecular Function | GO:0018817 | hydrolase activity, acting on acid anhydrides | 7.15E-08 | 1.60E-05 | 1.45E-06 | 8.68E-06 | 15 | 825 | MHY9,DNAH12,KIF27,MHY13,DNAH10,MYO5A,MYO5B,SMC3,CENPE,MYO7A,RNF213,SRCAP,DNAH5,DNAH8,DNAH11 |
| GO: Molecular Function | GO:0005997 | quaternary ammonium group binding | 1.51E-07 | 3.36E-05 | 2.80E-06 | 1.68E-05 | 5 | 37 | NF1,APOA2,APOA4,APOC1,CRP |
| GO: Molecular Function | GO:0005524 | ATP binding | 2.17E-07 | 4.85E-05 | 3.73E-06 | 2.23E-05 | 19 | 1476 | MHY9,TRANX1,DNAH12,KIF27,MHY13,DNAH10,MYO5A,MYO5B,SMC3,CENPE,MYO7A,OBSCN,RNF213,ATM,SRCAP,DNAH5,DNAH8,TTN,DNAH11 |
| GO: Molecular Function | GO:0031210 | phosphate/diacylglycerol binding | 2.73E-07 | 6.10E-05 | 4.36E-06 | 2.61E-05 | 4 | 17 | NF1,APOA2,APOA4,APOC3 |
| GO: Molecular Function | GO:0032559 | adenyl ribonucleotide binding | 3.33E-07 | 7.42E-05 | 4.81E-06 | 2.88E-05 | 19 | 1517 | MHY9,TRANX1,DNAH12,KIF27,MHY13,DNAH10,MYO5A,MYO5B,SMC3,CENPE,MYO7A,OBSCN,RNF213,ATM,SRCAP,DNAH5,DNAH8,TTN,DNAH11 |
| GO: Molecular Function | GO:0055102 | lipase inhibitor activity | 3.51E-07 | 7.82E-05 | 4.81E-06 | 2.88E-05 | 4 | 18 | APOA2,APOA4,APOC2,APOC3 |
| GO: Molecular Function | GO:0060228 | phosphatidylcholine-sterol O-acyltransferase activity | 3.67E-07 | 8.18E-05 | 4.81E-06 | 2.88E-05 | 3 | 5 | APOA2,APOA4,APOC1 |
| GO: Molecular Function | GO:0003554 | adenyl nucleotide binding | 4.03E-07 | 8.99E-05 | 4.98E-06 | 2.99E-05 | 10 | 1538 | MHY9,TRANX1,DNAH12,KIF27,MHY13,DNAH10,MYO5A,MYO5B,SMC3,CENPE,MYO7A,OBSCN,RNF213,ATM,SRCAP,DNAH5,DNAH8,TTN,DNAH11 |
| GO: Molecular Function | GO:0018887 | ATPase activity | 1.00E-06 | 2.24E-04 | 1.18E-05 | 7.05E-05 | 10 | 407 | MHY9,DNAH12,KIF27,DNAH10,CENPE,MYO7A,RNF213,DNAH5,DNAH8,DNAH11 |
| GO: Molecular Function | GO:0004857 | enzyme inhibitor activity | 2.20E-06 | 4.91E-04 | 2.46E-05 | 1.47E-04 | 9 | 34 | SERPINA3,COL6A3,SERPINA1,APOA2,APOC1,APOC2,APOC3,SERPIND1,HEXIM1 |
| GO: Molecular Function | GO:0035639 | purine ribonucleoside triphosphate binding | 4.79E-06 | 1.07E-03 | 5.05E-04 | 3.04E-04 | 9 | 1810 | MHY9,TRANX1,DNAH12,KIF27,MHY13,DNAH10,MYO5A,MYO5B,SMC3,CENPE,MYO7A,OBSCN,RNF213,ATM,SRCAP,DNAH5,DNAH8,TTN,DNAH11 |
| GO: Molecular Function | GO:0032550 | purine ribonucleoside binding | 5.32E-06 | 1.19E-03 | 5.10E-05 | 3.06E-04 | 9 | 1828 | MHY9,TRANX1,DNAH12,KIF27,MHY13,DNAH10,MYO5A,MYO5B,SMC3,CENPE,MYO7A,OBSCN,RNF213,ATM,SRCAP,DNAH5,DNAH8,TTN,DNAH11 |
| GO: Molecular Function | GO:0001883 | purine nucleoside binding | 5.45E-06 | 1.22E-03 | 5.10E-05 | 3.06E-04 | 19 | 1823 | MHY9,TRANX1,DNAH12,KIF27,MHY13,DNAH10,MYO5A,MYO5B,SMC3,CENPE,MYO7A,OBSCN,RNF213,ATM,SRCAP,DNAH5,DNAH8,TTN,DNAH11 |
| GO: Molecular Function | GO:0032549 | ribonucleoside binding | 5.49E-06 | 1.23E-03 | 5.10E-05 | 3.06E-04 | 19 | 1827 | MHY9,TRANX1,DNAH12,KIF27,MHY13,DNAH10,MYO5A,MYO5B,SMC3,CENPE,MYO7A,OBSCN,RNF213,ATM,SRCAP,DNAH5,DNAH8,TTN,DNAH11 |
| GO: Molecular Function | GO:0001882 | nucleoside binding | 5.95E-06 | 1.33E-03 | 5.31E-05 | 3.18E-04 | 19 | 1837 | MHY9,TRANX1,DNAH12,KIF27,MHY13,DNAH10,MYO5A,MYO5B,SMC3,CENPE,MYO7A,OBSCN,RNF213,ATM,SRCAP,DNAH5,DNAH8,TTN,DNAH11 |
| GO: Molecular Function | GO:0008289 | lipid binding | 6.34E-06 | 1.41E-03 | 5.46E-05 | 3.26E-04 | 11 | 610 | SPBTBNA,NF1,PON1,APOA2,APOA4,APOC1,APOC2,APOC3,LRP,APOD,CRP |
| GO: Molecular Function | GO:0032555 | purine ribonucleotide binding | 6.97E-06 | 1.55E-03 | 5.76E-05 | 3.45E-04 | 19 | 1857 | MHY9,TRANX1,DNAH12,KIF27,MHY13,DNAH10,MYO5A,MYO5B,SMC3,CENPE,MYO7A,OBSCN,RNF213,ATM,SRCAP,DNAH5,DNAH8,TTN,DNAH11 |
| GO: Molecular Function | GO:0032556 | phospholipid efflux | 7.90E-06 | 1.76E-03 | 6.18E-05 | 3.78E-04 | 19 | 1878 | MHY9,TRANX1,DNAH12,KIF27,MHY13,DNAH10,MYO5A,MYO5B,SMC3,CENPE,MYO7A,OBSCN,RNF213,ATM,SRCAP,DNAH5,DNAH8,TTN,DNAH11 |
| GO: Molecular Function | GO:0015485 | cholesterol binding | 8.04E-06 | 1.79E-03 | 6.18E-05 | 3.78E-04 | 4 | 38 | APOA2,APOC3,APOD,CRP |
| GO: Molecular Function | GO:0017076 | purine nucleoside binding | 8.34E-06 | 1.86E-03 | 6.20E-05 | 3.71E-04 | 19 | 1880 | MHY9,TRANX1,DNAH12,KIF27,MHY13,DNAH10,MYO5A,MYO5B,SMC3,CENPE,MYO7A,OBSCN,RNF213,ATM,SRCAP,DNAH5,DNAH8,TTN,DNAH11 |
| GO: Molecular Function | GO:0005198 | structural molecule activity | 8.82E-06 | 1.97E-03 | 6.35E-05 | 3.80E-04 | 11 | 641 | SPBTBNA,SPTAN1,NUMA1,OBSCN,FGA,FGB,LAMA3,EVPL,FGG,PLEC,TTN |
| GO: Molecular Function | GO:0029294 | steroid binding | 1.21E-05 | 2.69E-03 | 8.41E-05 | 5.04E-04 | 4 | 42 | APOA2,APOA4,APOC1,APOC2,CRP |
| GO: Molecular Function | GO:0070653 | high-density lipoprotein particle receptor binding | 3.37E-05 | 7.52E-03 | 2.28E-04 | 1.36E-03 | 2 | 3 | APOA2,APOC3 |
| GO: Molecular Function | GO:0030506 | ankyrin binding | 4.70E-05 | 1.05E-02 | 3.08E-04 | 1.84E-03 | 3 | 21 | SPBTBNA,OBSCN,PLEC |
| GO: Molecular Function | GO:0005543 | phospholipid binding | 8.38E-05 | 1.87E-02 | 5.34E-04 | 3.20E-03 | 7 | 311 | SPBTBNA,NF1,PON1,APOA2,APOA4,APOC1,APOC2 |
| GO: Molecular Function | GO:0071813 | lipoprotein particle binding | 9.07E-05 | 2.02E-02 | 5.47E-04 | 3.27E-03 | 3 | 26 | PON1,APOA2,CRP |
| GO: Molecular Function | GO:0071814 | protein-lipid complex binding | 9.07E-05 | 2.02E-02 | 5.47E-04 | 3.27E-03 | 3 | 26 | PON1,APOA2,CRP |
| GO: Molecular Function | GO:0030325 | glycosylated protein binding | 9.38E-05 | 2.14E-02 | 5.54E-04 | 3.33E-03 | 3 | 23 | SPBTBNA,MHY9,SPTAN1 |
| GO: Molecular Function | GO:0046983 | protein dimerization activity | 1.23E-04 | 2.74E-02 | 7.03E-04 | 4.21E-03 | 13 | 1172 | MHY9,MYO5A,SMC3,MYO7A,HP,SYNE1,SPTAN1,PON1,APOA2,APOA4,APOC2,ATM,CRP |
| GO: Molecular Function | GO:0030234 | enzyme regulator activity | 2.10E-04 | 4.67E-02 | 1.17E-03 | 6.96E-03 | 11 | 909 | SERPINA3,COL6A3,SERPINA1,NF1,APOA2,APOA4,APOC1,APOC2,APOC3,SERPIND1,HEXIM1 |
| GO: Molecular Function | GO:0032403 | protein complex binding | 2.41E-04 | 5.38E-02 | 1.31E-03 | 7.69E-03 | 11 | 924 | MHY9,NF1,KIF27,SMC3,CENPE,MYO7A,SYNE1,SPTAN1,NUMA1,ATM,TTN |
| GO: Molecular Function | GO:0005496 | steroid binding | 2.55E-04 | 5.68E-02 | 1.35E-03 | 8.10E-03 | 4 | 91 | APOA2,APOC3,APOD,CRP |
| GO: Molecular Function | GO:0030492 | hemoglobin binding | 3.11E-04 | 6.94E-02 | 1.58E-03 | 9.48E-03 | 2 | 8 | HP,HRP |
| GO: Molecular Function | GO:0004867 | serine-type endopeptidase inhibitor activity | 3.13E-04 | 6.97E-02 | 1.58E-03 | 9.48E-03 | 4 | 96 | SERPINA3,COL6A3,SERPINA1,SERPIND1 |
| GO: Molecular Function | GO:0006953 | acute-phase response | 8.78E-16 | 1.75E-12 | 1.75E-12 | 1.43E-11 | 10 | 49 | SERPINA3,ORM1,ORM2,SA1,SERPINA1,SA2,HP,LRP,F2,CRP |
| GO: Biological Process | GO:0005256 | acute inflammatory response | 5.19E-14 | 1.03E-10 | 5.17E-11 | 4.22E-10 | 12 | 144 | SERPINA3,ORM1,ORM2,SA1,SERPINA1,SA2,HP,LRP,F2,CRP |
| GO: Biological Process | GO:0006111 | response to wounding | 8.51E-11 | 1.69E-07 | 5.05E-08 | 4.67E-07 | 22 | 125 | SERPINA3,ORM1,ORM2,SA1,SERPINA1,SA2,HP,LRP,F2,CRP |
| GO: Biological Process | GO:0032555 | lipoprotein particle receptor binding | 3.37E-05 | 7.52E-03 | 2.28E-04 | 1.36E-03 | 2 | 3 | APOA2,APOC3 |
| GO: Biological Process | GO:0033234 | regulation of cholesterol transport | 2.04E-09 | 4.05E-06 | 6.76E-07 | 5.52E-06 | 6 | 35 | PON1,APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0023271 | regulation of sterol transport | 2.04E-09 | 4.05E-06 | 6.76E-07 | 5.52E-06 | 6 | 35 | PON1,APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0033344 | cholesterol efflux | 4.75E-09 | 9.46E-06 | 1.35E-06 | 1.10E-05 | 6 | 40 | PON1,APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0006954 | inflammatory response | 1.30E-08 | 2.60E-05 | 2.47E-06 | 2.02E-05 | 14 | 599 | SERPINA3,ORM1,ORM2,SA1,SERPINA1,SA2,HP,LRP,F2,CRP |
| GO: Biological Process | GO:0034369 | plasma lipoprotein particle remodeling | 1.36E-08 | 2.71E-05 | 2.47E-06 | 2.02E-05 | 5 | 23 | APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0034368 | protein-lipid complex remodeling | 1.36E-08 | 2.71E-05 | 2.47E-06 | 2.02E-05 | 5 | 23 | APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0034367 | macromolecular complex remodeling | 1.36E-08 | 2.71E-05 | 2.47E-06 | 2.02E-05 | 5 | 23 | APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0042157 | lipoprotein metabolic process | 1.63E-08 | 3.25E-05 | 2.70E-06 | 2.21E-05 | 8 | 131 | PON1,APOA2,APOA4,APOC1,APOC2,ATM,APOC3,APOD |
| GO: Biological Process | GO:0034372 | very-low-density lipoprotein particle remodeling | 4.24E-08 | 8.44E-05 | 6.03E-06 | 4.93E-05 | 4 | 11 | APOA2,APOA4,APOC2,APOC3 |
| GO: Biological Process | GO:0033379 | plasma lipoprotein particle remodeling | 4.24E-08 | 8.44E-05 | 6.03E-06 | 4.93E-05 | 4 | 11 | APOA2,APOA4,APOC2,APOC3 |
| GO: Biological Process | GO:0042060 | wound healing | 6.47E-08 | 1.29E-04 | 8.59E-06 | 7.02E-05 | 14 | 681 | SA1,SERPINA1,NF1,CENPE,FGA,FGB,FGG,APOD,F2,TTN,KLK11,SERPIND1,GSN,CRP |
| GO: Biological Process | GO:0032372 | negative regulation of sterol transport | 9.13E-08 | 1.82E-04 | 1.04E-05 | 8.46E-05 | 4 | 13 | APOA2,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0032375 | negative regulation of cholesterol transport | 9.13E-08 | 1.82E-04 | 1.04E-05 | 8.46E-05 | 4 | 13 | APOA2,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0071827 | plasma lipoprotein particle organization | 9.35E-08 | 1.86E-04 | 1.04E-05 | 8.46E-05 | 5 | 33 | APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0010876 | lipid localization | 1.07E-07 | 2.13E-04 | 1.09E-05 | 8.90E-05 | 10 | 311 | KIAA1109,PON1,APOA2,APOA4,APOC1,APOC2,APOC3,LRP,APOD,CRP |
| GO: Biological Process | GO:0015918 | sterol transport | 1.15E-07 | 2.29E-04 | 1.09E-05 | 8.90E-05 | 6 | 67 | PON1,APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0030301 | cholesterol transport | 1.15E-07 | 2.29E-04 | 1.09E-05 | 8.90E-05 | 6 | 67 | PON1,APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0034375 | high-density lipoprotein particle remodeling | 1.28E-07 | 2.54E-04 | 1.16E-05 | 9.44E-05 | 4 | 14 | APOA2,APOA4,APOC1,APOC3 |
| GO: Biological Process | GO:0039228 | movement of cell or subcellular component | 1.31E-07 | 2.66E-04 | 1.16E-05 | 9.46E-05 | 21 | 170 | SPBTBNA,COL6A3,SA1,MHY9,DNAH12,NF1,KIF27,DNAH10,MYO5A,CENPE,MYO7A,SPTAN1,ASPM,LAMA3,LRP,APOD,F2,DNAH5,DNAH8,TTN,DNAH11 |
| GO: Biological Process | GO:0037825 | protein-lipid complex subunit organization | 1.47E-07 | 2.94E-04 | 1.24E-05 | 1.01E-04 | 3 | 12 | APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0034443 | negative regulation of lipoprotein oxidation | 1.58E-07 | 3.15E-04 | 1.17E-05 | 9.53E-05 | 3 | 4 | PON1,APOA4,APOD |
| GO: Biological Process | GO:0010915 | regulation of very-low-density lipoprotein particle | 1.58E-07 | 3.15E-04 | 1.17E-05 | 9.53E-05 | 3 | 4 | APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0010916 | negative regulation of very-low-density lipoprotein particle | 1.58E-07 | 3.15E-04 | 1.17E-05 | 9.53E-05 | 3 | 4 | APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0046503 | glycerolipid catabolic process | 2.23E-07 | 4.45E-04 | 1.59E-05 | 1.30E-04 | 5 | 39 | APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0034361 | reverse cholesterol transport | 3.01E-07 | 5.99E-04 | 2.07E-05 | 1.69E-04 | 4 | 17 | APOA2,APOA4,APOC2,APOC3 |
| GO: Biological Process | GO:0016192 | vesicle-mediated transport | 3.58E-07 | 7.13E-04 | 2.38E-05 | 1.94E-04 | 17 | 118 | SPBTBNA,SERPINA1,MYO5A,MYO5B,MYO7A,GCC2,SYNE1,FGA,FGB,APOD,APOC1,APOC2,APOC3,LRP,FGG,TTN,GSN,CRP |
| GO: Biological Process | GO:0034442 | regulation of lipoprotein oxidation | 3.94E-07 | 7.85E-04 | 2.45E-05 | 2.01E-04 | 3 | 5 | PON1,APOA4,APOD |
| GO: Biological Process | GO:0010901 | regulation of very-low-density lipoprotein particle | 3.94E-07 | 7.85E-04 | 2.45E-05 | 2.01E-04 | 3 | 5 | APOA2,APOC2,APOC3 |
| GO: Biological Process | GO:0007017 | microtubule-based process | 4.08E-07 | 8.12E-04 | 2.46E-05 | 2.01E-04 | 12 | 559 | MHY9,DNAH12,KIF27,DNAH10,SMC3,CENPE,GCC2,NUMA1,ASPM,DNAH5,DNAH8,DNAH11 |
| GO: Biological Process | GO:0034378 | plasma lipoprotein particle assembly | 4.21E-07 | 8.37E-04 | 2.46E-05 | 2.01E-04 | 13 | 19 | APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0050994 | regulation of lipid catabolic process | 5.82E-07 | 1.16E-03 | 3.31E-05 | 2.71E-04 | 5 | 47 | APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0032368 | regulation of lipid transport | 7.67E-07 | 1.53E-03 | 4.02E-05 | 3.28E-04 | 6 | 92 | PON1,APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0034447 | very-low-density lipoprotein particle clearance | 7.86E-07 | 1.57E-03 | 4.02E-05 | 3.28E-04 | 3 | 6 | APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0042160 | lipoprotein modification | 7.86E-07 | 1.57E-03 | 4.02E-05 | 3.28E-04 | 3 | 6 | PON1,APOA4,APOD |
| GO: Biological Process | GO:0042161 | lipoprotein oxidation | 7.86E-07 | 1.57E-03 | 4.02E-05 | 3.28E-04 | 3 | 6 | PON1,APOA4,APOD |
| GO: Biological Process | GO:0005005 | protein-lipid complex assembly | 9.13E-07 | 1.82E-03 | 4.55E-05 | 3.72E-04 | 4 | 22 | APOA2,APOA4,APOC1,APOC3 |
| GO: Biological Process | GO:0097006 | regulation of plasma lipoprotein particle levels | 1.18E-06 | 2.35E-03 | 5.73E-05 | 4.68E-04 | 5 | 54 | APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0010985 | | | | | | | | |

Table S2.2 Non-survivors patients D0 samples.

| Category | ID | Name | p-value | q-value Bonferroni | q-value FDR B&H | q-value FDR B&Y | HIT Count in Query List | HIT Count in Hit in Query List | Genome |
|------------------------|------------|--|----------|--------------------|-----------------|-----------------|-------------------------|--------------------------------|--|
| GO: Molecular Function | GO:0004857 | enzyme inhibitor activity | 3.14E-09 | 7.40E-07 | 7.40E-07 | 4.47E-06 | 12 | 344 | SERPINA3,COL6A3,SERPINA1,SBF1,SERPING1,APOA2,APOC1,APOC2,APOC3,SERPIND1,HEXIM1,PROS1 |
| GO: Molecular Function | GO:0003774 | motor activity | 2.10E-08 | 4.95E-06 | 2.48E-06 | 1.50E-05 | 8 | 130 | MYS8,DNAH12,KIF27,DNAH10,MYO5B,DNAH5,DNAH8,DNAH11 |
| GO: Molecular Function | GO:0050997 | quaternary ammonium group binding | 2.07E-07 | 4.89E-05 | 1.52E-05 | 9.21E-05 | 5 | 37 | NF1,APOA2,APOA4,APOC1,CRP |
| GO: Molecular Function | GO:0003777 | microtubule motor activity | 3.36E-07 | 7.92E-05 | 1.52E-05 | 9.21E-05 | 6 | 77 | DNAH12,KIF27,DNAH10,DNAH5,DNAH8,DNAH11 |
| GO: Molecular Function | GO:0031210 | phosphatidylcholine binding | 3.53E-07 | 8.32E-05 | 1.52E-05 | 9.21E-05 | 4 | 17 | NF1,APOA2,APOA4,APOC1 |
| GO: Molecular Function | GO:0060228 | activator activity | 4.44E-07 | 1.05E-04 | 1.52E-05 | 9.21E-05 | 3 | 5 | APOA2,APOA4,APOC1 |
| GO: Molecular Function | GO:0055102 | lipase inhibitor activity | 4.52E-07 | 1.07E-04 | 1.52E-05 | 9.21E-05 | 4 | 18 | APOA2,APOC1,APOC2,APOC3 |
| GO: Molecular Function | GO:0043178 | alcohol binding | 1.68E-06 | 3.96E-04 | 4.95E-05 | 2.99E-04 | 6 | 101 | NF1,APOA2,APOA4,APOC1,APOC3,CRP |
| GO: Molecular Function | GO:0030492 | hemoglobin binding | 2.47E-06 | 5.82E-04 | 6.47E-05 | 3.91E-04 | 3 | 8 | HP,HPR,HBB |
| GO: Molecular Function | GO:0030234 | enzyme regulator activity | 3.43E-06 | 8.09E-04 | 8.09E-05 | 4.89E-04 | 14 | 90 | SERPINA3,COL6A3,SERPINA1,NF1,SBF1,SERPING1,APOA2,APOA4,APOC1,APOC2,APOC3,SERPIND1,HEXIM1,PROS1 |
| GO: Molecular Function | GO:0008092 | cytoskeletal protein binding | 4.07E-06 | 9.61E-04 | 8.74E-05 | 5.28E-04 | 13 | 792 | SHROOM3,MYS9,DST,NF1,KIF27,ANK3,ALMS1,MYO5B,SPTAN1,SYNE2,ACTB,NUMA1,GSN |
| GO: Molecular Function | GO:0004867 | serine-type endopeptidase inhibitor activity | 2.47E-05 | 5.82E-03 | 4.85E-04 | 2.93E-03 | 5 | 96 | SERPINA3,COL6A3,SERPINA1,SERPING1,SERPIND1 |
| GO: Molecular Function | GO:0004866 | endopeptidase inhibitor activity | 2.83E-05 | 6.67E-03 | 5.13E-04 | 3.10E-03 | 6 | 165 | SERPINA3,COL6A3,SERPINA1,SERPING1,SERPIND1,PROS1 |
| GO: Molecular Function | GO:0061135 | endopeptidase regulator activity | 3.46E-05 | 8.16E-03 | 5.31E-04 | 3.21E-03 | 6 | 171 | SERPINA3,COL6A3,SERPINA1,SERPING1,SERPIND1,PROS1 |
| GO: Molecular Function | GO:0030414 | peptidase inhibitor activity | 3.57E-05 | 8.43E-03 | 5.31E-04 | 3.21E-03 | 6 | 172 | SERPINA3,COL6A3,SERPINA1,SERPING1,SERPIND1,PROS1 |
| GO: Molecular Function | GO:0070653 | high-density lipoprotein particle receptor binding | 3.82E-05 | 9.02E-03 | 5.31E-04 | 3.21E-03 | 2 | 3 | APOA2,APOC3 |
| GO: Molecular Function | GO:0031270 | haptoglobin binding | 3.82E-05 | 9.02E-03 | 5.31E-04 | 3.21E-03 | 2 | 3 | HBA1,HBB |
| GO: Molecular Function | GO:0008289 | lipid binding | 6.89E-05 | 1.63E-02 | 9.03E-04 | 5.46E-03 | 10 | 619 | NF1,PON1,APOA2,APOA4,APOC1,APOC2,APOC3,LBP,DYF,CRP |
| GO: Molecular Function | GO:0016887 | ATPase activity | 1.03E-04 | 2.43E-02 | 1.23E-03 | 7.43E-03 | 8 | 407 | MYS8,DNAH12,MDM1,KIF27,DNAH10,DNAH5,DNAH8,DNAH11 |
| GO: Molecular Function | GO:0071813 | lipoprotein particle binding | 1.09E-04 | 2.58E-02 | 1.23E-03 | 7.43E-03 | 3 | 26 | PON1,APOA2,CRP |
| GO: Molecular Function | GO:0071814 | protein-lipid complex binding | 1.09E-04 | 2.58E-02 | 1.23E-03 | 7.43E-03 | 3 | 26 | PON1,APOA2,CRP |
| GO: Molecular Function | GO:0061134 | peptidase regulator activity | 1.17E-04 | 2.76E-02 | 1.25E-03 | 7.57E-03 | 6 | 213 | SERPINA3,COL6A3,SERPINA1,SERPING1,SERPIND1,PROS1 |
| GO: Molecular Function | GO:0005543 | phospholipid binding | 1.25E-04 | 2.96E-02 | 1.29E-03 | 7.76E-03 | 7 | 311 | NF1,PON1,APOA2,APOA4,APOC1,APOC3,DYF |
| GO: Molecular Function | GO:0031827 | oxidant activity | 1.31E-04 | 3.10E-02 | 1.31E-03 | 8.09E-03 | 7 | 72 | HP,HPA,HBA1,HBB |
| GO: Molecular Function | GO:0030574 | protein binding, bridging | 1.49E-04 | 3.51E-02 | 1.41E-03 | 8.49E-03 | 5 | 140 | ANK3,FGA,FGB,EVL,PLGG |
| GO: Molecular Function | GO:0005509 | calcium ion binding | 1.76E-04 | 4.16E-02 | 1.60E-03 | 9.67E-03 | 10 | 694 | DST,SPTAN1,PON1,CIR,F2,DYF,SVEP1,GSN,CRP,PROS1 |
| GO: Biological Process | GO:0006953 | acute-phase response | 1.67E-15 | 3.00E-12 | 3.00E-12 | 2.42E-11 | 10 | 49 | SERPINA3,ORM1,ORM2,SAI1,SERPINA1,SAI2,HP,LRP,F2,CRP |
| GO: Biological Process | GO:0002526 | acute inflammatory response | 3.37E-15 | 6.05E-12 | 3.02E-12 | 2.44E-11 | 13 | 140 | SERPINA3,ORM1,ORM2,SAI1,SERPINA1,SAI2,HP,SERPING1,APOA2,LBP,F2,CRP,PROS1 |
| GO: Biological Process | GO:0009611 | response to wounding | 7.72E-13 | 1.38E-09 | 4.61E-10 | 3.72E-09 | 25 | 1255 | SERPINA3,ORM1,ORM2,SAI1,SERPINA1,SAI2,DST,NF1,HP,ACTB,FGA,FGB,SERPING1,APOA2,APOC3,LBP,FGG,F2,HBB,DYF,HBD,SERPIND1,GSN,CRP,PROS1 |
| GO: Biological Process | GO:0033700 | phospholipid efflux | 4.51E-10 | 8.08E-07 | 2.02E-07 | 1.63E-06 | 5 | 12 | APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0042060 | wound healing | 2.99E-09 | 4.29E-06 | 7.57E-07 | 6.11E-06 | 16 | 681 | SAI1,SERPINA1,NF1,ACTB,FGA,FGB,SERPING1,FGG,F2,HBB,DYF,HBD,SERPIND1,GSN,CRP,PROS1 |
| GO: Biological Process | GO:0032374 | regulation of cholesterol transport | 2.96E-09 | 5.30E-06 | 7.57E-07 | 6.11E-06 | 6 | 35 | PON1,APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0032371 | regulation of steryl transport | 2.96E-09 | 5.30E-06 | 7.57E-07 | 6.11E-06 | 6 | 35 | PON1,APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0033344 | cholesterol efflux | 6.89E-09 | 1.24E-05 | 1.54E-06 | 1.25E-05 | 6 | 40 | PON1,APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0034369 | plasma lipoprotein particle remodeling | 1.86E-08 | 3.33E-05 | 3.03E-06 | 2.44E-05 | 5 | 23 | APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0034368 | protein-lipid complex remodeling | 1.86E-08 | 3.33E-05 | 3.03E-06 | 2.44E-05 | 5 | 23 | APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0034367 | macromolecular complex remodeling | 1.86E-08 | 3.33E-05 | 3.03E-06 | 2.44E-05 | 5 | 23 | APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0006954 | inflammatory response | 2.98E-08 | 5.34E-05 | 4.45E-06 | 3.59E-05 | 14 | 599 | SERPINA3,ORM1,ORM2,SAI1,SERPINA1,SAI2,HP,SERPING1,APOA2,APOC3,LBP,F2,CRP,PROS1 |
| GO: Biological Process | GO:0034372 | very-low-density lipoprotein particle remodeling | 5.42E-08 | 9.73E-05 | 6.95E-06 | 5.61E-05 | 4 | 11 | APOA2,APOA4,APOC2,APOC3 |
| GO: Biological Process | GO:0034370 | triglyceride-rich lipoprotein particle remodeling | 5.42E-08 | 9.73E-05 | 6.95E-06 | 5.61E-05 | 4 | 11 | APOA2,APOA4,APOC2,APOC3 |
| GO: Biological Process | GO:0032372 | negative regulation of steryl transport | 1.17E-07 | 2.10E-04 | 1.31E-05 | 1.06E-04 | 4 | 13 | APOA2,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0032375 | negative regulation of cholesterol transport | 1.17E-07 | 2.10E-04 | 1.31E-05 | 1.06E-04 | 4 | 13 | APOA2,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0018227 | plasma lipoprotein particle organization | 1.27E-07 | 2.28E-04 | 1.31E-05 | 1.08E-04 | 4 | 14 | APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0034375 | high-density lipoprotein particle remodeling | 1.63E-07 | 2.92E-04 | 1.49E-05 | 1.20E-04 | 4 | 14 | APOA2,APOA4,APOC1,APOC3 |
| GO: Biological Process | GO:0015918 | sterol transport | 1.66E-07 | 2.97E-04 | 1.49E-05 | 1.20E-04 | 6 | 67 | PON1,APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0030301 | cholesterol transport | 1.66E-07 | 2.97E-04 | 1.49E-05 | 1.20E-04 | 6 | 67 | PON1,APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0010915 | regulation of very-low-density lipoprotein particle clearance | 1.90E-07 | 3.41E-04 | 1.55E-05 | 1.25E-04 | 3 | 4 | APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0010916 | negative regulation of very-low-density lipoprotein particle clearance | 1.90E-07 | 3.41E-04 | 1.55E-05 | 1.25E-04 | 3 | 4 | APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0071825 | protein-lipid complex subunit organization | 2.00E-07 | 3.59E-04 | 1.56E-05 | 1.26E-04 | 5 | 36 | APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0046503 | glycerolipid catabolic process | 3.03E-07 | 5.44E-04 | 2.27E-05 | 1.83E-04 | 5 | 39 | APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0043691 | reverse cholesterol transport | 3.89E-07 | 6.90E-04 | 2.76E-05 | 2.23E-04 | 6 | 17 | APOA2,APOA4,APOC2,APOC3 |
| GO: Biological Process | GO:0006928 | movement of cell or subcellular component | 4.26E-07 | 7.63E-04 | 2.94E-05 | 2.37E-04 | 21 | 1703 | COL6A3,SAI1,MYS8,DNAH12,DST,NF1,KIF27,ANK3,DNAH10,SPTAN1,SYNE2,ACTB,ASPM,LAMA3,LBP,F2,DNAH5,DNAH8,PROS1,PCNT,DNAH11 |
| GO: Biological Process | GO:0007596 | blood coagulation | 4.52E-07 | 8.11E-04 | 2.97E-05 | 2.40E-04 | 12 | 529 | SAI1,SERPINA1,ACTB,FGA,FGB,SERPING1,FGG,F2,HBB,HBD,SERPIND1,PROS1 |
| GO: Biological Process | GO:0010901 | regulation of very-low-density lipoprotein particle remodeling | 4.74E-07 | 8.50E-04 | 2.97E-05 | 2.40E-04 | 3 | 5 | APOA2,APOC2,APOC3 |
| GO: Biological Process | GO:0050817 | coagulation | 4.80E-07 | 8.61E-04 | 2.97E-05 | 2.40E-04 | 12 | 532 | SAI1,SERPINA1,ACTB,FGA,FGB,SERPING1,FGG,F2,HBB,HBD,SERPIND1,PROS1 |
| GO: Biological Process | GO:0007599 | hemostasis | 5.00E-07 | 8.96E-04 | 2.99E-05 | 2.41E-04 | 12 | 534 | SAI1,SERPINA1,ACTB,FGA,FGB,SERPING1,FGG,F2,HBB,HBD,SERPIND1,PROS1 |
| GO: Biological Process | GO:0034377 | plasma lipoprotein particle assembly | 6.23E-07 | 1.12E-03 | 3.61E-05 | 2.91E-04 | 4 | 19 | APOA2,APOA4,APOC1,APOC3 |
| GO: Biological Process | GO:0043086 | negative regulation of catalytic activity | 6.52E-07 | 1.17E-03 | 3.66E-05 | 2.95E-04 | 14 | 771 | SERPINA3,COL6A3,SERPINA1,NF1,SBF1,HP,SERPING1,APOA2,APOC1,APOC2,APOC3,SERPIND1,HEXIM1,PROS1 |
| GO: Biological Process | GO:0002576 | platelet degranulation | 6.89E-07 | 1.24E-03 | 3.79E-05 | 3.02E-04 | 6 | 85 | SERPINA1,FGA,FGB,SERPING1,FGG,PROS1 |
| GO: Biological Process | GO:0050994 | microtubule-based process | 7.90E-07 | 1.42E-03 | 4.15E-05 | 3.35E-04 | 5 | 47 | APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0007017 | microtubule-based process | 8.10E-07 | 1.45E-03 | 4.15E-05 | 3.35E-04 | 12 | 559 | MYS8,DNAH12,DST,KIF27,DNAH10,GCC2,NUMA1,ASPM,DNAH5,DNAH8,PCNT,DNAH11 |
| GO: Biological Process | GO:0016192 | vesicle-mediated transport | 9.14E-07 | 1.64E-03 | 4.55E-05 | 3.67E-04 | 17 | 1184 | SERPINA1,ANK3,MYS8,GCC2,ACTB,FGA,FGB,SERPING1,APOC1,APOC2,APOC3,LBP,FGG,DYF,GSN,CRP,PROS1 |
| GO: Biological Process | GO:0034447 | very-low-density lipoprotein particle clearance | 9.45E-07 | 1.70E-03 | 4.58E-05 | 3.70E-04 | 3 | 6 | APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0072376 | protein activation cascade | 1.03E-06 | 1.85E-03 | 4.88E-05 | 3.93E-04 | 6 | 91 | FGA,SERPING1,CIR,F2,CRP,PROS1 |
| GO: Biological Process | GO:0032368 | regulation of lipid transport | 1.10E-06 | 1.98E-03 | 5.07E-05 | 4.09E-04 | 6 | 92 | PON1,APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0065005 | protein-lipid complex assembly | 1.17E-06 | 2.09E-03 | 5.23E-05 | 4.22E-04 | 4 | 22 | APOA2,APOA4,APOC1,APOC3 |
| GO: Biological Process | GO:0040011 | locomotion | 1.49E-06 | 2.67E-03 | 6.52E-05 | 5.26E-04 | 19 | 1522 | COL6A3,SAI1,MYS8,DST,NF1,ANK3,SPTAN1,SYNE2,ACTB,ASPM,LAMA3,LBP,F2,DNAH5,DNAH8,SERPIND1,PROS1,PCNT,DNAH11 |
| GO: Biological Process | GO:0057006 | regulation of plasma lipoprotein particle levels | 1.60E-06 | 2.87E-03 | 6.58E-05 | 5.31E-04 | 5 | 54 | APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0010285 | negative regulation of lipoprotein particle clearance | 1.65E-06 | 2.96E-03 | 6.58E-05 | 5.31E-04 | 3 | 7 | APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0071830 | triglyceride-rich lipoprotein particle clearance | 1.65E-06 | 2.96E-03 | 6.58E-05 | 5.31E-04 | 3 | 7 | APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0034382 | chylomicron remnant clearance | 1.65E-06 | 2.96E-03 | 6.58E-05 | 5.31E-04 | 3 | 7 | APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0015914 | phospholipid transport | 2.10E-06 | 3.76E-03 | 8.18E-05 | 6.60E-04 | 5 | 57 | APOA2,APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0030168 | platelet activation | 2.18E-06 | 3.91E-03 | 8.33E-05 | 6.72E-04 | 8 | 233 | SAI1,SERPINA1,FGA,FGB,SERPING1,FGG,F2,PROS1 |
| GO: Biological Process | GO:0010873 | positive regulation of cholesterol esterification | 2.63E-06 | 4.72E-03 | 9.74E-05 | 7.86E-04 | 3 | 8 | APOA2,APOA4,APOC1 |
| GO: Biological Process | GO:0010035 | response to inorganic substance | 2.66E-06 | 4.77E-03 | 9.74E-05 | 7.86E-04 | 10 | 415 | SERPINA1,HP,FGA,FGB,PON1,APOA4,FGG,HBB,GSN,CRP |
| GO: Biological Process | GO:0032369 | negative regulation of lipid transport | 3.21E-06 | 5.76E-03 | 1.11E-04 | 8.94E-04 | 4 | 28 | APOA2,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0046464 | acylglycerol catabolic process | 3.21E-06 | 5.76E-03 | 1.11E-04 | 8.94E-04 | 4 | 28 | APOA2,APOA4,APOC2,APOC3 |
| GO: Biological Process | GO:0046461 | neutral lipid catabolic process | 3.21E-06 | 5.76E-03 | 1.11E-04 | 8.94E-04 | 4 | 28 | APOA2,APOA4,APOC2,APOC3 |
| GO: Biological Process | GO:0034384 | high-density lipoprotein particle clearance | 3.94E-06 | 7.07E-03 | 1.31E-04 | 1.06E-03 | 3 | 9 | APOA2,APOC2,APOC3 |
| GO: Biological Process | GO:0034115 | positive regulation of lipoprotein lipase activity | 3.94E-06 | 7.07E-03 | 1.31E-04 | 1.06E-03 | 3 | 9 | FGA,FGG,FGG |
| GO: Biological Process | GO:0034381 | plasma lipoprotein particle clearance | 4.89E-06 | 8.78E-03 | 1.60E-04 | 1.29E-03 | 4 | 31 | APOA2,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0050878 | regulation of body fluid levels | 5.29E-06 | 9.49E-03 | 1.69E-04 | 1.37E-03 | 12 | 670 | SAI1,SERPINA1,ACTB,FGA,FGB,SERPING1,FGG,F2,HBB,HBD,SERPIND1,PROS1 |
| GO: Biological Process | GO:0042304 | regulation of fatty acid biosynthetic process | 5.58E-06 | 1.00E-02 | 1.71E-04 | 1.38E-03 | 4 | 32 | APOA4,APOC1,APOC2,APOC3 |
| GO: Biological Process | GO:0010872 | regulation of cholesterol esterification | 5.61E-06 | 1.01E-02 | 1.71E-04 | 1.38E-03 | 3 | 10 | APOA2,APOA4,APOC1 |
| GO: Biological Process | GO:0 | | | | | | | | |

Table S2.3 Survivors patients D7 samples.

| Category | ID | Name | p-value | q-value Bonferroni | q-value FDR B&H | q-value FDR B&Y | Hit Count in Query List | Hit Count in Genome | Hit in Query List |
|------------------------|------------|---|----------|--------------------|-----------------|-----------------|-------------------------|---------------------|---|
| GO: Molecular Function | GO:0003774 | motor activity | 1.46E-10 | 4.48E-08 | 4.48E-08 | 2.83E-07 | 10 | 130 | MH9,KIF27,MH13,DNAH10,MYO5B,CENPE,MYO7A,MYO9A,DNAH5,DNAH11 |
| GO: Molecular Function | GO:0031210 | phosphatidylcholine binding | 6.39E-09 | 1.96E-06 | 8.94E-07 | 5.64E-06 | 5 | 17 | NF1,JCHAIN,APOA2,APOA4,APOC1 |
| GO: Molecular Function | GO:0050997 | quaternary ammonium group binding | 8.73E-09 | 2.68E-06 | 8.94E-07 | 5.64E-06 | 6 | 37 | NF1,JCHAIN,APOA2,APOA4,APOC1,CRP |
| GO: Molecular Function | GO:0016462 | pyrophosphatase activity | 3.18E-08 | 9.76E-06 | 1.75E-06 | 1.10E-05 | 17 | 821 | BPTF,MYH9,MDN1,KIF27,MH13,DNAH10,MYO5B,CENPE,CLU,MYO7A,MYO9A,TRPM2,HLTF,RFN213,SRCAP,DNAH5,DNAH11 |
| GO: Molecular Function | GO:0016818 | phosphorus-containing anhydrides | 3.30E-08 | 1.01E-05 | 1.75E-06 | 1.10E-05 | 17 | 823 | BPTF,MYH9,MDN1,KIF27,MH13,DNAH10,MYO5B,CENPE,CLU,MYO7A,MYO9A,TRPM2,HLTF,RFN213,SRCAP,DNAH5,DNAH11 |
| GO: Molecular Function | GO:0016817 | hydrolase activity, acting on acid anhydrides | 3.41E-08 | 1.05E-05 | 1.75E-06 | 1.10E-05 | 17 | 825 | BPTF,MYH9,MDN1,KIF27,MH13,DNAH10,MYO5B,CENPE,CLU,MYO7A,MYO9A,TRPM2,HLTF,RFN213,SRCAP,DNAH5,DNAH11 |
| GO: Molecular Function | GO:0017111 | nucleoside-triphosphatase activity | 1.00E-07 | 3.08E-05 | 4.05E-06 | 2.55E-05 | 16 | 781 | BPTF,MYH9,MDN1,KIF27,MH13,DNAH10,MYO5B,CENPE,CLU,MYO7A,MYO9A,HLTF,RFN213,SRCAP,DNAH5,DNAH11 |
| GO: Molecular Function | GO:0001887 | ATPase activity | 1.05E-07 | 3.24E-05 | 4.05E-06 | 2.55E-05 | 12 | 407 | BPTF,MYH9,MDN1,KIF27,MH13,DNAH10,MYO5B,CENPE,CLU,MYO7A,HLTF,RFN213,DNAH5,DNAH11 |
| GO: Molecular Function | GO:0008092 | cytoskeletal protein binding | 1.22E-07 | 3.73E-05 | 4.14E-06 | 2.61E-05 | 16 | 792 | SPTBN4,MYH9,NF1,KIF27,MH13,MYO5B,CENPE,MYO7A,MYO9A,SYNE2,CEP290,ACTA1,ACTB,OBSCN,TTN,GSN |
| GO: Molecular Function | GO:0005516 | calmodulin binding | 6.39E-07 | 1.96E-04 | 1.90E-05 | 1.20E-04 | 8 | 175 | MYH9,MH13,MYO5B,MYO7A,OBSCN,ASPM,TTN,PCNT |
| GO: Molecular Function | GO:0060228 | phosphatidylcholine-sterol O-acyltransferase activator activity | 6.81E-07 | 2.09E-04 | 1.90E-05 | 1.20E-04 | 3 | 5 | APOA2,APOA4,APOC1 |
| GO: Molecular Function | GO:0000146 | microfilament motor activity | 1.55E-06 | 4.76E-04 | 3.74E-05 | 2.36E-04 | 4 | 21 | MYH9,MH13,MYO5B,MYO7A |
| GO: Molecular Function | GO:0005524 | ATP binding | 1.58E-06 | 4.86E-04 | 3.74E-05 | 2.36E-04 | 20 | 1476 | MYH9,MDN1,KIF27,MH13,DNAH10,MYO5B,SACS,CENPE,MYO7A,MYO9A,ACTA1,ACTB,OBSCN,HLTF,RFN213,ATM,SRCAP,DNAH5,TTN,DNAH11 |
| GO: Molecular Function | GO:0032559 | adenyl ribonucleotide binding | 2.42E-06 | 7.42E-04 | 5.30E-05 | 3.34E-04 | 20 | 1517 | MYH9,MDN1,KIF27,MH13,DNAH10,MYO5B,SACS,CENPE,MYO7A,MYO9A,ACTA1,ACTB,OBSCN,HLTF,RFN213,ATM,SRCAP,DNAH5,TTN,DNAH11 |
| GO: Molecular Function | GO:0030554 | adenyl nucleotide binding | 2.93E-06 | 8.98E-04 | 5.99E-05 | 3.78E-04 | 20 | 1536 | MYH9,MDN1,KIF27,MH13,DNAH10,MYO5B,SACS,CENPE,MYO7A,MYO9A,ACTA1,ACTB,OBSCN,HLTF,RFN213,ATM,SRCAP,DNAH5,TTN,DNAH11 |
| GO: Molecular Function | GO:0004992 | hemoglobin binding | 3.78E-06 | 1.16E-03 | 6.97E-05 | 4.40E-03 | 3 | 8 | HP,HRP,HBB |
| GO: Molecular Function | GO:0034378 | alcohol binding | 3.86E-06 | 1.19E-03 | 6.97E-05 | 4.40E-03 | 2 | 101 | NF1,JCHAIN,APOA2,APOA4,APOC1,CRP |
| GO: Molecular Function | GO:0016209 | antioxidant activity | 1.21E-05 | 3.71E-03 | 2.06E-04 | 1.30E-03 | 5 | 72 | HP,GPX3,APOA4,HBA1,HBB |
| GO: Molecular Function | GO:0003777 | microtubule motor activity | 1.68E-05 | 5.16E-03 | 2.72E-04 | 1.71E-03 | 5 | 77 | KIF27,DNAH10,CENPE,DNAH5,DNAH11 |
| GO: Molecular Function | GO:0035639 | purine ribonucleoside triphosphate binding | 3.36E-05 | 1.03E-02 | 4.92E-04 | 3.10E-03 | 20 | 1810 | MYH9,MDN1,KIF27,MH13,DNAH10,MYO5B,SACS,CENPE,MYO7A,MYO9A,ACTA1,ACTB,OBSCN,HLTF,RFN213,ATM,SRCAP,DNAH5,TTN,DNAH11 |
| GO: Molecular Function | GO:0037779 | actin binding | 3.44E-05 | 1.06E-02 | 4.92E-04 | 3.10E-03 | 9 | 392 | SPTBN4,MYH9,MH13,MYO5B,MYO7A,MYO9A,SYNE2,TTN,GSN |
| GO: Molecular Function | GO:0032550 | purine ribonucleoside binding | 3.73E-05 | 1.14E-02 | 4.92E-04 | 3.10E-03 | 20 | 1826 | MYH9,MDN1,KIF27,MH13,DNAH10,MYO5B,SACS,CENPE,MYO7A,MYO9A,ACTA1,ACTB,OBSCN,HLTF,RFN213,ATM,SRCAP,DNAH5,TTN,DNAH11 |
| GO: Molecular Function | GO:0001883 | purine nucleoside binding | 3.81E-05 | 1.17E-02 | 4.92E-04 | 3.10E-03 | 20 | 1823 | SPTBN4,MYH9,MH13,DNAH10,MYO5B,SACS,CENPE,MYO7A,MYO9A,ACTA1,ACTB,OBSCN,HLTF,RFN213,ATM,SRCAP,DNAH5,TTN,DNAH11 |
| GO: Molecular Function | GO:0034549 | ribonucleoside binding | 3.84E-05 | 1.18E-02 | 4.92E-04 | 3.10E-03 | 20 | 1827 | MYH9,MDN1,KIF27,MH13,DNAH10,MYO5B,SACS,CENPE,MYO7A,MYO9A,ACTA1,ACTB,OBSCN,HLTF,RFN213,ATM,SRCAP,DNAH5,TTN,DNAH11 |
| GO: Molecular Function | GO:0001882 | nucleoside binding | 4.16E-05 | 1.33E-02 | 5.10E-04 | 3.22E-03 | 20 | 1837 | SPTBN4,MYH9,MH13,DNAH10,MYO5B,SACS,CENPE,MYO7A,MYO9A,ACTA1,ACTB,OBSCN,HLTF,RFN213,ATM,SRCAP,DNAH5,TTN,DNAH11 |
| GO: Molecular Function | GO:0032555 | purine nucleoside binding | 4.85E-05 | 1.49E-02 | 5.73E-04 | 3.61E-03 | 20 | 1857 | MYH9,MDN1,KIF27,MH13,DNAH10,MYO5B,SACS,CENPE,MYO7A,MYO9A,ACTA1,ACTB,OBSCN,HLTF,RFN213,ATM,SRCAP,DNAH5,TTN,DNAH11 |
| GO: Molecular Function | GO:0031720 | haptoglobin binding | 5.09E-05 | 1.55E-02 | 5.77E-04 | 3.64E-03 | 2 | 3 | HBA1,HBB |
| GO: Molecular Function | GO:0032553 | ribonucleotide binding | 5.48E-05 | 1.68E-02 | 6.01E-04 | 3.76E-03 | 20 | 1873 | MYH9,MDN1,KIF27,MH13,DNAH10,MYO5B,SACS,CENPE,MYO7A,MYO9A,ACTA1,ACTB,OBSCN,HLTF,RFN213,ATM,SRCAP,DNAH5,TTN,DNAH11 |
| GO: Molecular Function | GO:0017076 | purine nucleotide binding | 5.78E-05 | 1.77E-02 | 6.11E-04 | 3.82E-03 | 20 | 1880 | MYH9,MDN1,KIF27,MH13,DNAH10,MYO5B,SACS,CENPE,MYO7A,MYO9A,ACTA1,ACTB,OBSCN,HLTF,RFN213,ATM,SRCAP,DNAH5,TTN,DNAH11 |
| GO: Molecular Function | GO:0005198 | structural molecule activity | 6.38E-05 | 1.96E-02 | 6.53E-04 | 4.16E-03 | 11 | 61 | SPTBN4,ACTA1,ACTB,OBSCN,FGA,FBG,LAMA3,LAMC2,EVP1,FGG,TTN |
| GO: Molecular Function | GO:0004857 | enzyme inhibitor activity | 8.83E-05 | 2.71E-02 | 8.74E-04 | 5.51E-03 | 3 | 34 | SERPINA3,COL6A3,SERPINA1,SBF1,APOA2,APOC1,SERPIND1,HEXIM1 |
| GO: Molecular Function | GO:0071813 | lipoprotein particle binding | 1.66E-04 | 5.11E-02 | 1.55E-03 | 9.76E-03 | 8 | 26 | PON1,APOA2,CRP |
| GO: Molecular Function | GO:0071814 | protein-lipid complex binding | 1.66E-04 | 5.11E-02 | 1.55E-03 | 9.76E-03 | 3 | 26 | PON1,APOA2,CRP |
| GO: Biological Process | GO:0006953 | acute-phase response | 4.73E-13 | 1.01E-09 | 1.01E-09 | 8.32E-09 | 9 | 49 | SERPINA3,ORM1,SA1,SERPINA1,SA2,HP,LRP,F2,CRP |
| GO: Biological Process | GO:0002526 | acute inflammatory response | 1.60E-11 | 3.41E-08 | 1.70E-08 | 1.41E-07 | 11 | 140 | SERPINA3,ORM1,SA1,SERPINA1,SA2,HP,LRP,F2,CRP |
| GO: Biological Process | GO:0009511 | response to wounding | 1.03E-09 | 2.20E-06 | 7.35E-07 | 6.06E-06 | 23 | 125 | SERPINA3,ORM1,SA1,SERPINA1,SA2,NF1,CENPE,CLU,HP,ACTB,FGA,FBG,APOA2,LRP,C6,FGG,F2,HBB,HBD,TTN,SERPIND1,GSN,CRP |
| GO: Biological Process | GO:0010035 | response to inorganic substance | 1.46E-09 | 3.94E-06 | 8.84E-07 | 8.11E-06 | 14 | 415 | SERPINA1,HP,ACTA1,GPX3,FGA,FBG,PON1,CP,APOA4,FGG,HBB,TTN,GSN,CRP |
| GO: Biological Process | GO:0042060 | wound healing | 1.98E-08 | 4.23E-05 | 8.47E-06 | 6.98E-05 | 16 | 681 | SA1,SERPINA1,NF1,CENPE,CLU,ACTB,FGA,FBG,FGG,F2,HBB,HBD,TTN,SERPIND1,GSN,CRP |
| GO: Biological Process | GO:0007596 | blood coagulation | 3.01E-07 | 6.42E-04 | 8.93E-05 | 5.36E-04 | 13 | 529 | SA1,SERPINA1,CENPE,CLU,ACTB,FGA,FBG,FGG,F2,HBB,HBD,TTN,SERPIND1 |
| GO: Biological Process | GO:0050817 | coagulation | 3.21E-07 | 6.84E-04 | 8.93E-05 | 5.36E-04 | 13 | 532 | SA1,SERPINA1,CENPE,CLU,ACTB,FGA,FBG,FGG,F2,HBB,HBD,TTN,SERPIND1 |
| GO: Biological Process | GO:0007599 | hemostasis | 3.35E-07 | 7.14E-04 | 8.93E-05 | 5.36E-04 | 13 | 534 | SA1,SERPINA1,CENPE,CLU,ACTB,FGA,FBG,FGG,F2,HBB,HBD,TTN,SERPIND1 |
| GO: Biological Process | GO:0007417 | central nervous system development | 4.73E-07 | 1.01E-03 | 1.09E-04 | 9.01E-04 | 23 | 1859 | SPTBN4,POTE,PTF,NF1,KIF27,CLU,CEP290,ACTB,ASPM,ATM,F2,DNAH5,NIPBL,PCML,GSN,PCNT |
| GO: Biological Process | GO:0034933 | macromolecular complex subunit organization | 5.12E-07 | 1.09E-03 | 1.09E-04 | 9.01E-04 | 26 | 1752 | SPTBN4,CDC8B,MYH9,NF1,MDN1,CENPE,CLU,JCHAIN,ACTA1,GPX3,ASPM,FGA,FBG,APOA2,APOA4,APOC1,FGG,HBB,TTN,PCML,GSN,CRP,PCNT |
| GO: Biological Process | GO:0006928 | movement of cell or subcellular component | 1.29E-06 | 2.75E-03 | 2.50E-04 | 2.06E-03 | 22 | 1703 | SPTBN4,COL6A3,SA1,MYH9,NF1,KIF27,DNAH10,CENPE,MYO7A,SYNE2,ACTA1,ACTB,ASPM,LAMA3,LAMA4,LRP,F2,DNAH5,TTN,PCML,PCNT,DNAH11 |
| GO: Biological Process | GO:0002576 | platelet degranulation | 1.56E-06 | 3.33E-03 | 2.77E-04 | 2.29E-03 | 6 | 85 | SERPINA1,CLU,FGA,FBG,FGG |
| GO: Biological Process | GO:0042744 | hydrolytic catabolic process | 2.03E-06 | 4.33E-03 | 3.33E-04 | 2.74E-03 | 4 | 22 | HP,GPX3,APOA4,HBB |
| GO: Biological Process | GO:0010038 | response to metal ion | 2.70E-06 | 5.77E-03 | 4.12E-04 | 3.42E-03 | 9 | 280 | SERPINA1,ACTA1,FGA,FBG,CP,FGG,TTN,GSN,CRP |
| GO: Biological Process | GO:0032989 | cellular component morphogenesis | 3.08E-06 | 6.57E-03 | 4.26E-04 | 3.50E-03 | 18 | 1242 | SPTBN4,COL6A3,MYH9,KIF27,CLU,MYO7A,CEP290,ACTA1,ACTB,OBSCN,FGA,FBG,FGG,F2,TTN,PCML,GSN,PCNT |
| GO: Biological Process | GO:0007925 | organelle assembly | 3.20E-06 | 6.82E-03 | 4.26E-04 | 3.52E-03 | 10 | 367 | KIF27,CENPE,MYO7A,CEP290,ACTA1,OBSCN,ASPM,TTN,PCML,PCNT |
| GO: Biological Process | GO:0032880 | regulation of protein localization | 3.41E-06 | 7.28E-03 | 4.28E-04 | 3.53E-03 | 12 | 555 | SA1,NF1,MYO5B,CENPE,GCC2,CEP290,FGA,FBG,APOA2,FGG,PCML,PCNT |
| GO: Biological Process | GO:0010873 | positive regulation of cholesterol esterification | 3.99E-06 | 8.51E-03 | 4.70E-04 | 3.88E-03 | 3 | 8 | APOA2,APOA4,APOC1 |
| GO: Biological Process | GO:0005878 | regulation of body fluid levels | 4.19E-06 | 8.93E-03 | 4.70E-04 | 3.88E-03 | 3 | 670 | SA1,SERPINA1,CENPE,CLU,ACTB,FGA,FBG,FGG,F2,HBB,HBD,TTN,SERPIND1 |
| GO: Biological Process | GO:0071822 | protein complex subunit organization | 5.54E-06 | 1.18E-02 | 5.91E-04 | 4.87E-03 | 20 | 1570 | SPTBN4,CDC8B,MYH9,NF1,MDN1,CENPE,CLU,JCHAIN,ACTA1,GPX3,ASPM,FGA,FBG,FGG,HBB,TTN,PCML,GSN,CRP,PCNT |
| GO: Biological Process | GO:0034116 | positive regulation of heterotypic cell-cell adhesion | 5.96E-06 | 1.27E-02 | 6.02E-04 | 4.97E-03 | 3 | 9 | FGA,FBG,FGG |
| GO: Biological Process | GO:0030168 | platelet activation | 6.21E-06 | 1.33E-02 | 6.02E-04 | 4.97E-03 | 8 | 233 | SA1,SERPINA1,CLU,FGA,FBG,FGG,F2,TTN |
| GO: Biological Process | GO:0051223 | regulation of protein transport | 7.46E-06 | 1.59E-02 | 6.54E-04 | 5.30E-03 | 10 | 404 | SA1,NF1,GCC2,CEP290,FGA,FBG,APOA2,FGG,PCML,PCNT |
| GO: Biological Process | GO:0001895 | retina homeostasis | 7.97E-06 | 1.70E-02 | 6.54E-04 | 5.30E-03 | 5 | 65 | POTE,POTE,JCHAIN,ACTB,POTEI |
| GO: Biological Process | GO:0006200 | ATP catabolic process | 7.99E-06 | 1.70E-02 | 6.54E-04 | 5.30E-03 | 9 | 320 | BPTF,MYH9,MDN1,DNAH10,MYO7A,HLTF,RFN213,DNAH5,DNAH11 |
| GO: Biological Process | GO:0010872 | regulation of cholesterol esterification | 8.50E-06 | 1.81E-02 | 6.54E-04 | 5.30E-03 | 3 | 10 | APOA2,APOA4,APOC1 |
| GO: Biological Process | GO:0015918 | sterol transport | 9.26E-06 | 1.98E-02 | 6.54E-04 | 5.30E-03 | 5 | 67 | CLU,PON1,APOA2,APOA4,APOC1 |
| GO: Biological Process | GO:0030301 | cholesterol transport | 9.26E-06 | 1.98E-02 | 6.54E-04 | 5.30E-03 | 5 | 67 | CLU,PON1,APOA2,APOA4,APOC1 |
| GO: Biological Process | GO:0009158 | ribonucleoside monophosphate catabolic process | 9.27E-06 | 1.98E-02 | 6.54E-04 | 5.30E-03 | 9 | 326 | BPTF,MYH9,MDN1,DNAH10,MYO7A,HLTF,RFN213,DNAH5,DNAH11 |
| GO: Biological Process | GO:0009169 | purine ribonucleoside monophosphate catabolic process | 9.27E-06 | 1.98E-02 | 6.54E-04 | 5.30E-03 | 9 | 326 | BPTF,MYH9,MDN1,DNAH10,MYO7A,HLTF,RFN213,DNAH5,DNAH11 |
| GO: Biological Process | GO:0009128 | purine nucleoside monophosphate catabolic process | 9.50E-06 | 2.03E-02 | 6.54E-04 | 5.30E-03 | 9 | 327 | BPTF,MYH9,MDN1,DNAH10,MYO7A,HLTF,RFN213,DNAH5,DNAH11 |
| GO: Biological Process | GO:0009125 | nucleoside monophosphate catabolic process | 9.98E-06 | 2.13E-02 | 6.65E-04 | 5.48E-03 | 9 | 329 | BPTF,MYH9,MDN1,DNAH10,MYO7A,HLTF,RFN213,DNAH5,DNAH11 |
| GO: Biological Process | GO:0065003 | macromolecular complex assembly | 1.14E-05 | 2.44E-02 | 7.38E-04 | 6.09E-03 | 18 | 1365 | SPTBN4,CDC8B,MDN1,CENPE,CLU,JCHAIN,GPX3,ASPM,FGA,FBG,APOA2,APOA4,APOC1,FGG,HBB,TTN,GSN,CRP |
| GO: Biological Process | GO:0048468 | cell development | 1.39E-05 | 2.97E-02 | 8.06E-04 | 6.65E-03 | 22 | 1970 | SPTBN4,COL6A3,MYH9,NF1,CLU,MYO7A,CEP290,ACTA1,ACTB,OBSCN,ASPM,FGA,FBG,ATM,FGG,HBA1,F2,TTN,NIPBL,PCML,GSN,CRP |
| GO: Biological Process | GO:0032374 | regulation of cholesterol transport | 1.39E-05 | 2.97E-02 | 8.06E-04 | 6.65E-03 | 4 | 35 | PON1,APOA2,APOA4,APOC1 |
| GO: Biological Process | GO:0032371 | regulation of sterol transport | 1.39E-05 | 2.97E-02 | 8.06E-04 | 6.65E-03 | 4 | 35 | PON1,APOA2,APOA4,APOC1 |
| GO: Biological Process | GO:0051651 | maintenance of location in cell | 1.40E-05 | 2.98E-02 | 8.06E-04 | 6.65E-03 | 6 | 124 | SPTBN4,CENPE,GCC2,SYNE2,ASPM,PCML |
| GO: Biological Process | GO:0035700 | phospholipid efflux | 1.55E-05 | 3.30E-02 | 8.64E-04 | 7.13E-03 | 3 | 12 | APOA2,APOA4,APOC1 |
| GO: Biological Process | GO:0014774 | brain development | 1.59E-05 | 3.37E-02 | 8.64E-04 | 7.13E-03 | 12 | 646 | POTE,POTE,NF1,KIF27,CEP290,ACTB,ASPM,ATM,DNAH5,NIPBL,PCML,PCNT |
| GO: Biological Process | GO:0024433 | sterol esterification | 2.01E-05 | 4.28E-02 | 9.96E-04 | 8.21E-03 | 3 | 13 | APOA2,APOA4,APOC1 |
| GO: Biological Process | GO:0033194 | response to hydrogen peroxide | 2.01E-05 | 4.28E-02 | 9.96E-04 | 8.21E-03 | 3 | 13 | TRPM2,GPX3,APOA4 |
| GO: Biological Process | GO:0034435 | cholesterol esterification | 2.01E-05 | 4.28E-02 | 9.96E-04 | 8.21E-03 | 3 | 13 | APOA2,APOA4,APOC1 |
| GO: Biological Process | GO:0034434 | sterol esterification | 2.01E-05 | 4.28E-02 | 9.96E-04 | 8.21E-03 | 3 | 13 | |

Table S3. IPA-generated functional interaction network based on scores for septic patients.

| ID | Molecules in Network | Score | Focus Molecules | Top Diseases and Functions |
|---|--|-------|-----------------|---|
| IPA generated functional interaction network with based of score for septic survivor patients after day 0 (D0S). Green down arrow represent down-regulated proteins and red up arrow represent up-regulation. The bold symbols are the proteins, identified in the present study. | | | | |
| 1 | ↓APOA2, ↓APOA4, ↓APOC1, ↓APOC2, ↓APOC3, ↓APOD, ↑CPN1, ↑CRP, ERK1/2, ↑FGA, ↑FGB, ↑FGG, Fibrin, Fibrinogen, GPIIB-IIIa, HDL, HDL-cholesterol, hemoglobin, ↑HP, ↑HPR, ↑LAMA3, ↑LBP, LDL-cholesterol, ↑MYH13, NCOR-LXR-Oxysterol-RXR-9 cis RA, Nr1h, ↑ORM1, ↑ORM2, ↓PON, SAA, ↑SAA1, ↑SAA2, ↑SERPINA1, Stat3-Stat3, VLDL-cholesterol | 48 | 22 | Metabolic Disease, Lipid Metabolism, Small Molecule Biochemistry |
| 2 | Actin, Akt, Alpha catenin, calpain, caspase, chymotrypsin, ↑COL6A3, Collagen(s), ↓F2, F Actin, ↓GSN, ↓KLKB1, Laminin, ↑LRG1, Mic, ↑MYH9, ↓MYO5A, ↑MYO5B, ↑MYO7A, Myosin, NADPH oxidase, ↑OBSCN, PDGF BB, ↓PLEC, SerineProtease, ↑SERPINA3, ↓SERPIND1, Sos, ↓SPTAN1, ↓SPTBN4, ↑SYNE1, T3-TR-RXR, Tgf beta, trypsin, ↑TTN | 33 | 17 | Cellular Assembly and Organization, Cellular Function and Maintenance, Cellular Movement |
| 3 | AHR, ↑ALMS1, ↑ASPM, Ca2+, CBX4, ↑DMXL2, DNAH1, DNAH2, DNAH3, ↑DNAH5, DNAH6, ↑DNAH8, DNAH9, ↑DNAH10, ↑DNAH11, ↑DNAH12, DNAH14, ↓DNAH17, DNAH1, DNAI2, DNAL1, DNAL4, DNAL11, ↑EVPL, FPR2, ↓GCC2, IDH3G, MYC, RFX2, RFX3, ↑RNF2I3, SP1, ↑SVEP1, TGFB1, ↓TRANK1 | 26 | 13 | Developmental Disorder, Hereditary Disorder, Respiratory Disease |
| IPA generated functional interaction network with based of score for septic non-survivors patients after day 0 (D0NS). | | | | |
| 1 | ↓APOA2, ↓APOA4, ↓APOC1, ↓APOC2, ↓APOC3, ↑CRP, ERK1/2, ↑FGA, ↑FGB, ↑FGG, Fibrin, Fibrinogen, GPIIB-IIIa, Growth hormone, HDL, HDL-cholesterol, hemoglobin, ↑HP, ↑HPR, ↑LAMA3, ↑LBP, IDL-cholesterol, NCOR-LXR-Oxysterol-RXR-9 cis RA, ↑ORM1, ↑ORM2, ↓PON, Pro-inflammatory Cytokine, ↑PROS1, ↑SAA1, ↑SAA2, ↑SERPINA1, Stat3-Stat3, ↓TTR, VLDL-cholesterol | 45 | 21 | Metabolic Disease, lipid Metabolism, Molecular Transport |
| 2 | ↑ACTB, Actin, ↓AFM, Akt, ↑ALMS1, Alpha catenin, ↓ANK3, caspase, chymotrypsin, ↑COL6A3, Collagen(s), ↓DYSE, ↓F2, F Actin, ↓GSN, ↑HBA1/HBA2, ↑HBB, ↑HBD, IgG, Laminin, ↑LRG1, Mic, ↑MYH9, ↑MYO5B, NADPH oxidase, PId, Serine Protease, ↑SERPINA3, ↓SERPIND1, ↓SHROOM3, Sos, ↓SPTAN1, ↑SYNE2, T3-TR-RXR, TCF | 38 | 19 | Cell-to-Cell Signaling and Interaction, Cellular Assembly and Organization, Connective Tissue Disorders |
| 3 | ↑ASPM, beta-estradiol, Ca2+, CD3, ↑DMXL2, DNAH2, DNAH3, ↑DNAH5, DNAH6, ↑DNAH8, DNAH9, ↑DNAH10, ↑DNAH11, ↑DNAH12, DNAH14, ↓DNAH17, DNAH1, DNAI2, DNAL1, DNAL11, ↓DST, ↑EVPL, FCN1, FPR2, ↓GCC2, ↑GOLGB1, GPR65, IFNG, IL13, ↑MDN1, MYC, ↓PIBFI, S100A12, ↑SVEPI, TGFB1 | 28 | 14 | Developmental Disorder, Hereditary Disorder, Respiratory Disease |
| IPA generated functional interaction network with based of score for septic survivors patients after day 7 (D7S). | | | | |
| 1 | ↓APOA2, ↓APOA4, ↓APOC1, ↑CLU, ↑CP, ↑CRP, ERK1/2, Ferritin, ↑FGA, ↑FGB, ↑FGG, Fibrin, Fibrinogen, GPIIB-IIIa, ↑HBA1/HBA2, HDL, HDL-cholesterol, hemoglobin, ↑HP, ↑HPR, ↑HPX, ↑LAMA3, ↑LBP, LDL-cholesterol, NADPH oxidase, ↑ORM1, ↓PON, Pro-inflammatory Cytokine, ↑SAA1, ↑SAA2, ↑SERPINA1, Stat3-Stat3, ↑TRMP2, VLDL-cholesterol | 43 | 21 | Metabolic Disease, Cardiovascular Disease, Developmental Disorder |
| 2 | Apl, ↑ATM, ATPase, caspase, CD3, Cg, Creb, ↑DNAH5, ↓DNAH10, ↑DNAH11, ↑GOLGB1, ↑HBB, ↑HBD, HISTONE, Histoneh3, Histoneh4, ↓HLTF, Hsp90, IgG, IL1, Immunoglobulin, ↑JCHAIN, ↑KMT2C, Mapk, Mek, NFkB (complex), ↑nikotinamide adenine dinucleotide phosphate, ↑NIPBL, RNA polymerase II, ↑RNF213, ↑SACS, ↑SBFI, ↑SRCAP, Tgf beta, Vegf | 32 | 16 | Cancer, Organismal Injury and Abnormalities, Endocrine System Disorders |
| 3 | ↑ACTA1, ↑ACTB, Actin, Akt, Alpha Actinin, Alpha catenin, Calmodulin, chymotrypsin, Cofilin, Collagen(s), Dynein, F Actin, G-Actin, ↓GSN, ↑LAMA4, Laminin, ↑LRG1, Mic, ↑MYH9, ↑MYO5B, ↑MYO7A, Myosin, ↑NFI, ↑OBSCN, ↑PCNT, PDGF-BB, PId, Rock, Serine Protease, ↑SERPINA3, ↓SERPIND1, ↓SPTBN4, ↑SYNE2, trypsin, ↑TTN | 30 | 16 | Cellular Assembly and Organization, Cellular Development, Cellular Growth and Proliferation |
| IPA generated functional interaction network with based of score for septic non-survivors patients after day 7 (D7NS). | | | | |
| 1 | ↑AIBG, ↓APOA2, ↓APOA4, ↓APOC1, ↓APOLI, ↓CCDC88A, ↑CRP, ERK1/2, ↑F13A1, factor XIII, Ferritin, ↑FGA, ↑FGB, ↑FGG, Fibrin, Fibrinogen, GPIIB-IIIa, HDL, HDL-cholesterol, hemoglobin, ↑HP, ↑HPR, ↑LAMA3, ↓LAMC2, ↑LBP, LDL-cholesterol, MHC Class II (complex), ↓PONI, Pro inflammatory Cytokine, ↑SAA1, ↑SAA2, Stat3-Stat3, ↑TRPM2, VLDL-cholesterol, ↓VTN | 43 | 21 | Developmental Disorder, Hematological Disease, Hereditary Disorder |
| 2 | ↑ACTA1, Actin, Akt, Alpha catenin, caspase, chymotrypsin, ↑COL6A3, Collagen(s), ↓F2, F Actin, ↓GSN, ↑HBA1/HBA2, ↑HBB, ↑HBD, ↓HLTF, Kallikrein, ↓KLKB1, Laminin, ↑LRG1, Mic, ↑MYH9, ↑MYO5B, Myosin, NADPH oxidase, ↑OBSCN, PId, ↑SERPINA3, ↓SERPINA4, ↓SERPIND1, ↓SPTAN1, ↓SPTBN4, ↑SYNE2, T3-TR-RXR, trypsin, ↑TTN | 39 | 20 | Cellular Assembly and Organization, Cellular Development, Cellular Growth and Proliferation |
| 3 | APP, ↑ASPM, BET1L, ↑BODIL1, ↓BPTF, ↓C8A, ↑CFHR2, ↑CNTRL, DECR2, DNAH2, ↑DNAH5, DNAH6, ↓DNAH10, DNAH14, DNAL1, DYNLT1, ↑EVPL, ↓GCC2, ↑GOLGA4, ↑GOLGB1, GOSR2, ↑MDN1, P2RX6, PARVA, ↓PIBFI, POU5F1, PPARA, SGK2, SOX2, ↑SVEPI, TGFB1, TLL1, TNFRSP1A, XBP1, ↓ZFHX4 | 29 | 15 | Cellular Development, Tissue Development, Cancer |

Table S4. Altered functions with their activation and inhibition z scores in septic patients.

| S. No. | Categories | Diseases or Functions Annotation | p-Value | Predicted Activation State | Activation z-score | # Molecules |
|--------|---|--|----------|----------------------------|--------------------|-------------|
| 1 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | transport of phospholipid | 1.47E-07 | Decreased | -2.236 | 6 |
| 2 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | efflux of phospholipid | 5.60E-08 | Decreased | -2 | 5 |
| 3 | Cardiac Hypertrophy, Cardiovascular Disease, Developmental Disorder, Organismal Injury and Abnormalities | hypertrophy of heart | 3.82E-02 | | -1.977 | 4 |
| 4 | Molecular Transport | export of molecule | 3.46E-05 | | -1.703 | 8 |
| 5 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | quantity of steroid | 1.35E-04 | | -1.509 | 9 |
| 6 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | efflux of cholesterol | 2.13E-07 | | -1.429 | 7 |
| 7 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | transport of lipid | 5.28E-08 | | -1.336 | 10 |
| 8 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | concentration of cholesterol | 1.45E-04 | | -1.298 | 7 |
| 9 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | concentration of fatty acid | 1.07E-03 | | -1.266 | 6 |
| 10 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | transport of steroid | 1.43E-07 | | -1.254 | 8 |
| 11 | Cardiovascular System Development and Function, Cell-To-Cell Signaling and Interaction | activation of vascular endothelial cells | 2.58E-06 | | -1.217 | 4 |
| 12 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | concentration of sterol | 2.98E-05 | | -1.199 | 8 |
| 13 | Lipid Metabolism, Small Molecule Biochemistry | fatty acid metabolism | 6.10E-05 | | -1.17 | 11 |
| 14 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | concentration of lipid | 4.70E-05 | | -1.04 | 13 |
| 15 | Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response | chemotaxis of mononuclear leukocytes | 5.49E-04 | | -1 | 5 |
| 16 | Organismal Injury and Abnormalities | Bleeding | 4.03E-06 | | -0.95 | 10 |
| 17 | Cellular Movement | chemotaxis of cells | 2.56E-04 | | -0.931 | 9 |
| 18 | Protein Synthesis | quantity of protein lipid complex in blood | 6.34E-06 | | -0.931 | 5 |
| 19 | Cardiovascular System Development and Function, Cellular Development, Cellular Growth and Proliferation, Organismal Development, Tissue Development | proliferation of endothelial cells | 1.30E-03 | | -0.842 | 6 |
| 20 | Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking | cell movement of leukocytes | 3.75E-04 | | -0.836 | 11 |
| 21 | Cardiovascular Disease | atherosclerosis | 2.86E-09 | | -0.695 | 14 |
| 22 | Cardiovascular System Development and Function, Cell-To-Cell Signaling and Interaction | activation of endothelial cells | 2.72E-06 | | -0.69 | 5 |
| 23 | Free Radical Scavenging | metabolism of reactive oxygen species | 2.88E-03 | | -0.62 | 8 |
| 24 | Molecular Transport | transport of molecule | 1.20E-05 | | -0.555 | 20 |
| 25 | Lipid Metabolism, Small Molecule Biochemistry | synthesis of fatty acid | 2.46E-03 | | -0.544 | 6 |
| 26 | Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response | cell movement of phagocytes | 4.25E-04 | | -0.543 | 9 |
| 27 | Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking | cell movement of myeloid cells | 4.02E-04 | | -0.529 | 9 |
| 28 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response | activation of myeloid cells | 4.94E-04 | | -0.439 | 7 |
| 29 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response | activation of phagocytes | 7.76E-04 | | -0.439 | 7 |
| 30 | Inflammatory Response | inflammatory response | 3.73E-06 | | -0.429 | 14 |
| 31 | Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response | cell movement of neutrophils | 1.05E-03 | | -0.391 | 6 |
| 32 | Cell-To-Cell Signaling and Interaction | adhesion of blood cells | 3.26E-06 | | -0.381 | 10 |
| 33 | Cellular Movement | cell movement | 1.09E-06 | | -0.372 | 25 |
| 34 | Cell-To-Cell Signaling and Interaction | aggregation of cells | 7.73E-06 | | -0.353 | 9 |
| 35 | Molecular Transport | secretion of molecule | 9.99E-05 | | -0.343 | 10 |
| 36 | Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response | chemotaxis of phagocytes | 1.42E-05 | | -0.254 | 8 |
| 37 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking | adhesion of immune cells | 1.05E-05 | | -0.253 | 9 |
| 38 | Cardiovascular Disease | vascular lesion | 1.76E-05 | | -0.243 | 7 |
| 39 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response | adhesion of phagocytes | 1.74E-03 | | -0.205 | 4 |
| 40 | Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response | chemotaxis of myeloid cells | 1.37E-05 | | -0.128 | 8 |
| 41 | Cellular Assembly and Organization, Cellular Function and Maintenance | organization of cytoskeleton | 2.35E-06 | | -0.055 | 19 |
| 42 | Cellular Assembly and Organization, Cellular Function and Maintenance | microtubule dynamics | 4.21E-06 | | 0.116 | 17 |
| 43 | Cardiovascular Disease | atherosclerotic lesion | 1.60E-05 | | 0.13 | 6 |
| 44 | Molecular Transport | quantity of metal | 1.93E-03 | | 0.156 | 8 |
| 45 | Hematological System Development and Function | hemostasis | 2.21E-05 | | 0.191 | 7 |
| 46 | Hematological System Development and Function | coagulation | 9.54E-05 | | 0.192 | 6 |
| 47 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Inflammatory Response | aggregation of blood platelets | 1.20E-06 | | 0.335 | 8 |
| 48 | Cardiovascular Disease, Hematological Disease | Thrombosis | 3.09E-04 | | 0.613 | 5 |
| 49 | Cellular Assembly and Organization | quantity of filaments | 2.45E-07 | | 0.655 | 7 |
| 50 | Cell-To-Cell Signaling and Interaction, Cellular Function and Maintenance, Inflammatory Response | phagocytosis of cells | 6.75E-04 | | 0.676 | 6 |
| 51 | Cellular Function and Maintenance, Inflammatory Response | phagocytosis | 1.71E-04 | | 0.961 | 7 |

Functional interaction network annotation of differentially expressed proteins in septic survival patients at day 0 (D0S) in order to Z-scores.

| | | | | | | |
|----|---|---------------------|----------|--|-------|---|
| 52 | Cellular Function and Maintenance Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | engulfment of cells | 1.23E-03 | | 1.02 | 7 |
| 53 | Molecule Biochemistry | uptake of lipid | 5.49E-05 | | 1.387 | 6 |

Functional interaction network annotation of differentially expressed proteins in septic nonsurvival patients at day 0 (D0NS) in order to Z-scores.

| | | | | | | |
|----|--|---|-----------|-----------|--------|----|
| 1 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | transport of phospholipid | 1.77E-07 | Decreased | -2.236 | 6 |
| 2 | Cellular Assembly and Organization, Tissue Development | fibrogenesis | 3.288E-05 | Decreased | -2.17 | 9 |
| 3 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | efflux of phospholipid | 6.55E-08 | Decreased | -2 | 5 |
| 4 | Molecular Transport | export of molecule | 5.41 E-06 | | -1.953 | 9 |
| 5 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | concentration of lipid | 2.76E-04 | | -1.688 | 12 |
| 6 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | quantity of steroid | 1.72E-04 | | -1.509 | 9 |
| 7 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | efflux of cholesterol | 2.64E-07 | | -1.429 | 7 |
| 8 | Lipid Metabolism, Small Molecule Biochemistry | fatty acid metabolism | 8.17E-05 | | -1.369 | 11 |
| 9 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | transport of lipid | 7.16E-08 | | -1.336 | 10 |
| 10 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | concentration of cholesterol | 1.76E-04 | | -1.298 | 7 |
| 11 | Molecular Transport | transport of molecule | 5.30E-06 | | -1.271 | 21 |
| 12 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | transport of steroid | 1.83E-07 | | -1.254 | 8 |
| 13 | Free Radical Scavenging | metabolism of reactive oxygen species | 3.64E-05 | | -1.246 | 11 |
| 14 | Free Radical Scavenging | synthesis of reactive oxygen species | 1.39E-04 | | -1.246 | 10 |
| 15 | Tissue Development | development of epithelial tissue | 1.22E-03 | | -1.234 | 8 |
| 16 | Cardiovascular System Development and Function, Cellular Development, Cellular Growth and Proliferation, Organismal Development, Tissue Development | proliferation of endothelial cells | 2.42E-04 | | -1.234 | 7 |
| 17 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | concentration of sterol | 3.74E-05 | | -1.199 | 8 |
| 18 | Cardiovascular System Development and Function, Cellular Development, Cellular Growth and Proliferation, Organismal Development, Tissue Development | proliferation of vascular endothelial | 1.91 E-03 | | -1.154 | 4 |
| 19 | Free Radical Scavenging | production of reactive oxygen species | 4.24E-04 | | -1.056 | 8 |
| 20 | Protein Synthesis | quantity of protein lipid concentration | 7.38E-06 | | -0.931 | 5 |
| 21 | Lipid Metabolism, Small Molecule Biochemistry | hydrolysis of lipid | 1.188E-03 | | -0.865 | 5 |
| 22 | Lipid Metabolism, Small Molecule Biochemistry | synthesis of fatty acid | 2.88E-03 | | -0.84 | 6 |
| 23 | Lipid Metabolism, Small Molecule Biochemistry | synthesis of lipid | 5.36E-03 | | -0.717 | 9 |
| 24 | Cardiovascular Disease | atherosclerosis | 4.39E-09 | | -0.695 | 14 |
| 25 | Cellular Movement | chemotaxis of cells | 1.52E-03 | | -0.657 | 8 |
| 26 | Cellular Movement, Hematological System Development and Function, Immune C | cell movement of phagocyt | 2.34E-03 | | -0.543 | 8 |
| 27 | Cellular Movement, Hematological System Development and Function, Immune C | cell movement of myeloid c | 2.23E-03 | | -0.529 | 8 |
| 28 | Cellular Movement, Hematological System Development and Function, Immune C | cell movement of neutrophil | 1.23E-03 | | -0.391 | 6 |
| 29 | Cell-To-Cell Signaling and Interaction | aggregation of cells | 1.19E-06 | | -0.353 | 10 |
| 30 | Molecular Transport | secretion of molecule | 1.30E-04 | | -0.343 | 10 |
| 31 | Cellular Assembly and Organization | quantity of filaments | 1.03E-03 | | -0.277 | 4 |
| 32 | Cellular Movement, Hematological System Development and Function, Immune C | chemotaxis of phagocytes | 1.43E-04 | | -0.254 | 7 |
| 33 | Cell-To-Cell Signaling and Interaction | binding of cells | 1.11E-03 | | -0.245 | 8 |
| 34 | Cardiovascular Disease | vascular lesion | 2.16E-05 | | -0.243 | 7 |
| 35 | Cellular Movement, Hematological System Development and Function, Immune C | cell movement of leukocyte | 4.93E-04 | | -0.239 | 11 |
| 36 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Cell-To-Cell Signaling and Inte | adhesion of phagocytes | 1.95E-03 | | -0.205 | 4 |
| 37 | Cardiovascular System Development and Function, Cell-To-Cell Signaling and Inte | activation of endothelial cell | 7.88E-05 | | -0.174 | 4 |
| 38 | Cell-To-Cell Signaling and Interaction | adhesion of blood cells | 3.14E-05 | | -0.143 | 9 |
| 39 | Cellular Movement, Hematological System Development and Function, Immune C | chemotaxis of myeloid cells | 1.38E-04 | | -0.128 | 7 |
| 40 | Cardiovascular System Development and Function, Organismal Development | vasculogenesis | 2.56E-04 | | -0.1 | 11 |
| 41 | Cell-To-Cell Signaling and Interaction | activation of cells | 4.11E-03 | | -0.071 | 11 |
| 42 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Cell-To-Cell Signaling and Interaction, Hematological System Development and Function | aggregation of blood platelets | 1.18E-07 | | -0.028 | 9 |
| 43 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Cell-To-Cell Signaling and Interaction, Hematological System Development and Function | adhesion of immune cells | 9.67E-05 | | -0.008 | 8 |
| 44 | Cardiovascular Disease | atherosclerotic lesion | 1.91E-05 | | 0.13 | 6 |
| 45 | Cardiovascular System Development and Function, Organismal Development | angiogenesis | 4.28E-04 | | 0.227 | 12 |
| 46 | Molecular Transport | quantity of metal | 1.10E-04 | | 0.228 | 10 |
| 47 | Cellular Movement | cell movement | 7.75E-06 | | 0.228 | 24 |
| 48 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Cell-To-Cell Signaling and Interaction, Hematological System Development and Function | activation of macrophages | 2.60E-03 | | 0.294 | 5 |
| 49 | Cell Signaling, Molecular Transport, Vitamin and Mineral Metabolism | quantity of Ca2+ | 6.91E-04 | | 0.506 | 8 |
| 50 | Hematological System Development and Function | homeostasis | 2.70E-05 | | 0.564 | 7 |
| 51 | Hematological System Development and Function | coagulation | 1.13E-04 | | 0.565 | 6 |
| 52 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Cell-To-Cell Signaling and Interaction, Hematological System Development and Function | activation of myeloid cells | 3.23E-03 | | 0.596 | 6 |
| 53 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Cell-To-Cell Signaling and Interaction, Hematological System Development and Function | activation of phagocytes | 4.68E-03 | | 0.596 | 6 |
| 54 | Inflammatory Response | inflammatory response | 1.25E-02 | | 0.619 | 12 |
| 55 | Cell-To-Cell Signaling and Interaction, Cellular Function and Maintenance, Inflammation, Phagocytosis of cells | Phagocytosis of cells | 7.95E-04 | | 0.676 | 6 |
| 56 | Cellular Function and Maintenance | engulfment of cells | 1.48E-03 | | 1.02 | 7 |
| 57 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | uptake of lipid | 6.54E-05 | | 1.387 | 6 |

Functional interaction network annotation of differentially expressed proteins in septic survival patients after day 7 (D7S) in order to Z-scores.

| | | | | | | |
|---|--|----------------------|----------|-----------|--------|---|
| 1 | Organismal Injury and Abnormalities | Fibrosis | 8.61E-04 | Decreased | -2.213 | 9 |
| 2 | Cardiac Hypertrophy, Cardiovascular Disease, Developmental Disorder, Organismal Injury and Abnormalities | hypertrophy of heart | 3.99E-03 | Decreased | -2.211 | 6 |
| 3 | Organismal Injury and Abnormalities | Bleeding | 1.17E-04 | | -1.687 | 9 |

| | | | | | |
|--|---|--|----------|--------|----|
| 4 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | concentration of sterol | 1.04E-04 | -1.431 | 8 |
| 5 | Free Radical Scavenging | metabolism of reactive oxygen species | 2.85E-05 | -1.167 | 12 |
| 6 | Free Radical Scavenging | synthesis of reactive oxygen species | 4.51E-04 | -1.167 | 10 |
| 7 | Free Radical Scavenging | production of reactive oxygen species | 1.10E-03 | -0.968 | 8 |
| 8 | Protein Synthesis | quantity of protein lipid complex in blood | 1.48E-05 | -0.931 | 5 |
| 9 | Lipid Metabolism, Small Molecule Biochemistry | fatty acid metabolism | 1.19E-03 | -0.886 | 10 |
| 10 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response, Nervous System | activation of microglia | 1.07E-03 | -0.817 | 4 |
| 11 | Molecular Transport | quantity of metal | 3.62E-04 | -0.644 | 10 |
| 12 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | transport of steroid | 7.11E-06 | -0.516 | 7 |
| 13 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Inflammatory Response | aggregation of blood platelets | 3.30E-08 | -0.484 | 10 |
| 14 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | transport of lipid | 2.76E-06 | -0.447 | 9 |
| 15 | Tissue Development | development of epithelial tissue | 3.02E-03 | -0.416 | 8 |
| 16 | Cardiovascular Disease | atherosclerosis | 3.55E-09 | -0.416 | 15 |
| 17 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | efflux of cholesterol | 1.11E-05 | -0.415 | 6 |
| 18 | Cardiovascular Disease, Hematological Disease | Thrombosis | 6.84E-04 | -0.343 | 5 |
| 19 | Cardiovascular Disease | vascular lesion | 5.44E-05 | -0.243 | 7 |
| 20 | Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response | cell movement of phagocytes | 1.50E-03 | -0.227 | 9 |
| 21 | Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking | cell movement of myeloid cells | 1.43E-03 | -0.211 | 9 |
| 22 | Molecular Transport | export of molecule | 1.20E-04 | -0.183 | 8 |
| 23 | Cellular Movement, Hair and Skin Development and Function | cell movement of epithelial cell lines | 1.01E-03 | -0.152 | 4 |
| 24 | Neurological Disease | damage of central nervous system | 2.03E-03 | -0.152 | 5 |
| 25 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function | aggregation of blood cells | 2.36E-08 | -0.023 | 11 |
| 26 | Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response | cell movement of neutrophils | 4.50E-04 | 0 | 7 |
| 27 | Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking | cell movement of leukocytes | 4.64E-04 | 0.026 | 12 |
| 28 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response | activation of macrophages | 7.93E-04 | 0.104 | 6 |
| 29 | Cell-To-Cell Signaling and Interaction | aggregation of cells | 6.55E-09 | 0.112 | 13 |
| 30 | Cellular Movement, Immune Cell Trafficking | leukocyte migration | 4.45E-04 | 0.127 | 13 |
| 31 | Cardiovascular Disease | atherosclerotic lesion | 4.29E-03 | 0.13 | 6 |
| 32 | Cardiovascular System Development and Function, Organismal Development | angiogenesis | 4.65E-04 | 0.248 | 13 |
| 33 | Cellular Movement | cell movement | 1.03E-06 | 0.364 | 28 |
| 34 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response | activation of myeloid cells | 1.39E-03 | 0.392 | 7 |
| 35 | Inflammatory Response | inflammatory response | 1.27E-02 | 0.482 | 13 |
| 36 | Molecular Transport | transport of molecule | 5.00E-06 | 0.739 | 23 |
| 37 | Cell-To-Cell Signaling and Interaction | adhesion of blood cells | 1.58E-05 | 0.83 | 10 |
| 38 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking | adhesion of immune cells | 4.30E-05 | 0.972 | 9 |
| 39 | Organismal Survival | lifespan of organism | 2.59E-03 | 1.067 | 4 |
| 40 | Cellular Assembly and Organization | quantity of filaments | 1.63E-04 | 1.213 | 5 |
| 41 | Cellular Movement | migration of cells | 5.16E-05 | 1.219 | 23 |
| 42 | Organismal Injury and Abnormalities, Tissue Morphology | size of lesion | 1.38E-04 | 1.342 | 7 |
| Functional interaction network annotation of differentially expressed proteins in septic nonsurvival patients after day 7 (D/NS) in order to Z-scores | | | | | |
| 1 | Cardiac Hypertrophy, Cardiovascular Disease, Developmental Disorder, Organismal Injury and Abnormalities | hypertrophy of heart | 5.25E-02 | -1.977 | 4 |
| 2 | Cellular Movement | chemotaxis of cells | 1.16E-04 | -1.612 | 10 |
| 3 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | quantity of steroid | 1.42E-03 | -1.509 | 8 |
| 4 | Lipid Metabolism, Small Molecule Biochemistry | fatty acid metabolism | 6.93E-04 | -1.37 | 10 |
| 5 | Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response | chemotaxis of leukocytes | 2.10E-05 | -1.299 | 9 |
| 6 | Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response | chemotaxis of phagocytes | 3.08E-05 | -1.299 | 8 |
| 7 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | concentration of cholesterol | 2.78E-04 | -1.298 | 7 |
| 8 | Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response | chemotaxis of myeloid cells | 2.97E-05 | -1.254 | 8 |
| 9 | Cardiovascular System Development and Function, Cell-To-Cell Signaling and Interaction | activation of vascular endothelial cells | 3.91E-06 | -1.217 | 4 |
| 10 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response, Nervous system | activation of microglia | 6.35E-05 | -1.216 | 5 |
| 11 | Cellular Assembly and Organization, Tissue Development | fibrogenesis | 5.92E-05 | -1.211 | 9 |
| 12 | Molecular Transport | export of molecule | 2.68E-03 | -1.145 | 6 |
| 13 | Free Radical Scavenging | metabolism of reactive oxygen species | 3.44E-04 | -1.053 | 10 |
| 14 | Free Radical Scavenging | synthesis of reactive oxygen species | 1.13E-03 | -1.053 | 9 |
| 15 | Cellular Assembly and Organization | quantity of actin filaments | 4.87E-06 | -1 | 5 |

| | | | | | |
|----|---|--|----------|--------|----|
| 16 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | concentration of lipid | 1.94E-03 | -0.998 | 11 |
| 17 | Free Radical Scavenging | production of reactive oxygen species | 3.23E-03 | -0.968 | 7 |
| 18 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | transport of steroid | 5.34E-05 | -0.952 | 6 |
| 19 | Protein Synthesis | quantity of protein lipid complex in blood | 1.06E-05 | -0.931 | 5 |
| 20 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | transport of lipid | 1.44E-05 | -0.915 | 8 |
| 21 | Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | efflux of cholesterol | 1.07E-04 | -0.875 | 5 |
| 22 | Cardiovascular System Development and Function, Cellular Development, Cellular Growth and Proliferation, Organismal Development, Tissue Development | proliferation of endothelial cells | 2.22E-03 | -0.842 | 6 |
| 23 | Organismal Injury and Abnormalities | Bleeding | 6.82E-05 | -0.833 | 9 |
| 24 | Cardiovascular Disease | atherosclerosis | 1.30E-09 | -0.695 | 15 |
| 25 | Inflammatory Response | inflammatory response | 2.69E-06 | -0.616 | 15 |
| 26 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response | activation of myeloid cells | 2.44E-05 | -0.393 | 9 |
| 27 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response | activation of phagocytes | 4.42E-05 | -0.393 | 9 |
| 28 | Cardiovascular System Development and Function, Cell-To-Cell Signaling and Interaction | activation of endothelial cells | 1.61E-07 | -0.355 | 6 |
| 29 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response | activation of macrophages | 7.20E-05 | -0.354 | 7 |
| 30 | Cell-To-Cell Signaling and Interaction | aggregation of cells | 2.38E-06 | -0.353 | 10 |
| 31 | Cellular Movement, Immune Cell Trafficking | leukocyte migration | 5.55E-05 | -0.348 | 14 |
| 32 | Cellular Movement | cell movement | 7.70E-07 | -0.304 | 27 |
| 33 | Molecular Transport | transport of molecule | 1.88E-05 | -0.262 | 21 |
| 34 | Cardiovascular Disease | vascular lesion | 3.49E-05 | -0.243 | 7 |
| 35 | Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking | cell movement of leukocytes | 5.75E-05 | -0.239 | 13 |
| 36 | Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response | cell movement of phagocytes | 2.04E-04 | -0.227 | 10 |
| 37 | Cellular Assembly and Organization | quantity of filaments | 5.04E-07 | -0.218 | 7 |
| 38 | Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking | cell movement of myeloid cells | 1.91E-04 | -0.211 | 10 |
| 39 | Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response | cell movement of neutrophils | 2.96E-04 | -0.115 | 7 |
| 40 | Cell-To-Cell Signaling and Interaction, Inflammatory Response | immune response of macrophages | 2.50E-03 | 0 | 4 |
| 41 | Cellular Movement, Hair and Skin Development and Function | cell movement of epithelial cell lines | 7.85E-04 | 0 | 4 |
| 42 | Gastrointestinal Disease, Hepatic System Disease, Liver Damage, Organismal Injury and Abnormalities | damage of liver | 1.04E-03 | 0 | 6 |
| 43 | Cardiovascular Disease | atherosclerotic lesion | 2.91E-05 | 0.13 | 6 |
| 44 | Carbohydrate Metabolism | activation of carbohydrate | 2.37E-07 | 0.152 | 4 |
| 45 | Hematological System Development and Function | hemostasas | 3.31E-08 | 0.191 | 10 |
| 46 | Hematological System Development and Function | coagulation | 1.26E-07 | 0.192 | 9 |
| 47 | Cell-To-Cell Signaling and Interaction, Cellular Function and Maintenance, Hematological System Development and Function, Inflammatory Res | phagocytosis of myeloid cells | 1.89E-03 | 0.278 | 4 |
| 48 | Cell-To-Cell Signaling and Interaction, Cellular Function and Maintenance, Inflammatory Response | phagocytosis of phagocytes | 1.89E-03 | 0.278 | 4 |
| 49 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Inflammatory Response | aggregation of blood platelets | 2.26E-05 | 0.335 | 9 |
| 50 | Cell-To-Cell Signaling and Interaction | adhesion of blood cells | 5.67E-05 | 0.349 | 9 |
| 51 | Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking | adhesion of immune cells | 1.63E-04 | 0.506 | 8 |
| 52 | Cell-To-Cell Signaling and Interaction, Inflammatory Response | immune response of phagocytes | 1.28E-01 | 0.603 | 5 |
| 53 | Cell-To-Cell Signaling and Interaction | response of myeloid cells | 1.58E-03 | 0.603 | 5 |
| 54 | Cardiovascular Disease, Hematological Disease | Thrombosis | 4.92E-05 | 0.613 | 6 |
| 55 | Cardiovascular Disease | Infarction | 6.11E-04 | 0.686 | 7 |
| 56 | Cardiovascular Disease, Organismal Injury and Abnormalities, Tissue Morphology | size of infarct | 4.57E-03 | 0.686 | 4 |
| 57 | Cell-To-Cell Signaling and Interaction, Cellular Function and Maintenance, Inflammatory Response | phagocytosis of cells | 1.17E-03 | 0.789 | 6 |
| 58 | Organismal Injury and Abnormalities, Tissue Morphology | size of lesion | 6.60E-04 | 1 | 6 |
| 59 | Cellular Function and Maintenance | engulfment of cells | 2.27E-03 | 1.109 | 7 |
| 60 | Embryonic Development, Organismal Development, Tissue Development | growth of embryonic tissue | 4.94E-03 | 1.131 | 5 |

Table S5. IPA-identified canonical pathways in septic patients.

| S. No. | Name of Canonical Pathway | No. of molecules | Total molecules | Ratio | Z Score | (-LOG B-H-p value | B-H-p value |
|---|---|------------------|-----------------|-------|---------|-------------------|-------------|
| IPA identified canonical pathways in septic survivor patients at day 0 (D0S). | | | | | | | |
| 1 | LXR/RXR Activation | 15 | 128 | 0.117 | -2.58 | 17.476 | 3.34E-18 |
| 2 | Acute Phase Response Signaling | 16 | 171 | 0.094 | 2.828 | 17.476 | 3.34E-18 |
| 3 | FXR/RXR Signaling | 14 | 138 | 0.101 | NaN | 15.711 | 1.95E-16 |
| 4 | IL-12 Signaling and Production in Macrophages | 11 | 138 | 0.08 | NaN | 11 | 1E-11 |
| 5 | Clathrin-mediated Endocytosis Signaling | 12 | 188 | 0.064 | NaN | 11 | 1E-11 |
| 6 | Atherosclerosis Signaling | 10 | 125 | 0.08 | NaN | 10.006 | 9.85E-11 |
| 7 | Production of Nitric Oxide and Reactive Oxygen Species in Macrophages | 11 | 186 | 0.059 | -0.905 | 9.753 | 1.76E-10 |
| 8 | Coagulation System | 7 | 35 | 0.2 | 0.378 | 9.695 | 2.02E-10 |
| 9 | Intrinsic Prothrombin Activation Pathway | 5 | 30 | 0.167 | NaN | 6.273 | 5.33E-07 |
| 10 | Extrinsic Prothrombin Activation Pathway | 4 | 18 | 0.222 | 1 | 5.415 | 3.84E-06 |
| 11 | Actin Cytoskeleton Signaling | 7 | 221 | 0.032 | 1.342 | 4.18 | 6.61E-05 |
| 12 | Role of Tissue Factor in Cancer | 5 | 112 | 0.045 | NaN | 3.505 | 0.000313 |
| 13 | TR/RXR Activation | 4 | 92 | 0.043 | NaN | 2.639 | 0.0023 |
| 14 | Hepatic Fibrosis/Hepatic Stellate Cell Activation | 4 | 187 | 0.021 | NaN | 1.515 | 0.0306 |
| IPA identified canonical pathways in septic non-survivor patients at day 0 (D0NS). | | | | | | | |
| 1 | Acute Phase Response Signaling | 17 | 171 | 0.099 | 3 | 19.068 | 8.56E-20 |
| 2 | LXR/RXR Activation | 15 | 128 | 0.117 | -0.258 | 17.995 | 1.01E-18 |
| 3 | FXR/RXR Signaling | 14 | 138 | 0.101 | NaN | 15.96 | 1.1E-16 |
| 4 | Clathrin-mediated Endocytosis Signaling | 11 | 188 | 0.059 | NaN | 9.847 | 1.42E-10 |
| 5 | Coagulation System | 7 | 35 | 0.2 | 0.378 | 9.847 | 1.42E-10 |
| 6 | Atherosclerosis Signaling | 9 | 125 | 0.072 | NaN | 8.803 | 1.57E-09 |
| 7 | IL-12 Signaling and Production in Macrophages | 9 | 138 | 0.065 | NaN | 8.484 | 3.28E-09 |
| 8 | Extrinsic Prothrombin Activation Pathway | 5 | 18 | 0.278 | 0.447 | 7.816 | 1.53E-08 |
| 9 | Production of Nitric Oxide and Reactive Oxygen Species in Macrophages | 9 | 186 | 0.048 | -1 | 7.446 | 3.58E-08 |
| 10 | Intrinsic Prothrombin Activation Pathway | 5 | 30 | 0.167 | NaN | 6.704 | 1.98E-07 |
| 11 | Role of Tissue Factor in Cancer | 4 | 112 | 0.036 | NaN | 2.64 | 0.00299 |
| 12 | Actin Cytoskeleton Signaling | 5 | 221 | 0.023 | 1 | 2.507 | 0.00311 |
| 13 | TR/RXR Activation | 3 | 92 | 0.033 | NaN | 1.845 | 0.0143 |
| IPA identified canonical pathways in septic survival patients after day 7 (D7S). | | | | | | | |
| 1 | Acute Phase Response Signaling | 16 | 171 | 0.094 | 3.162 | 15.722 | 1.9E-16 |
| 2 | LXR/RXR Activation | 13 | 128 | 0.102 | 2.77 | 13.11 | 7.76E-14 |
| 3 | FXR/RXR Signaling | 12 | 138 | 0.087 | NaN | 11.309 | 4.91E-12 |
| 4 | Clathrin-mediated Endocytosis Signaling | 11 | 188 | 0.059 | NaN | 8.469 | 3.39E-09 |
| 5 | Coagulation System | 6 | 35 | 0.171 | 0.816 | 6.932 | 1.17E-07 |
| 6 | IL-12 Signaling and Production in Macrophages | 8 | 138 | 0.058 | NaN | 5.914 | 1.22E-06 |
| 7 | Atherosclerosis Signaling | 7 | 125 | 0.056 | NaN | 5.037 | 9.19E-06 |
| 8 | Production of Nitric Oxide and Reactive Oxygen Species in Macrophages | 8 | 186 | 0.043 | -0.707 | 5.037 | 9.19E-06 |
| 9 | Extrinsic Prothrombin Activation Pathway | 4 | 18 | 0.222 | 1 | 4.924 | 1.19E-05 |
| 10 | Actin Cytoskeleton Signaling | 8 | 221 | 0.036 | 1.633 | 4.566 | 2.72E-05 |
| 11 | Intrinsic Prothrombin Activation Pathway | 4 | 30 | 0.133 | NaN | 4.073 | 8.45E-05 |
| 12 | Role of Tissue Factor in Cancer | 5 | 112 | 0.045 | NaN | 2.999 | 0.001 |
| 13 | Germ Cell-Sertoli Cell Junction Signaling | 5 | 163 | 0.031 | NaN | 2.266 | 0.00542 |
| 14 | TR/RXR Activation | 4 | 92 | 0.043 | NaN | 2.24 | 0.00575 |
| 15 | MSP-RON Signaling Pathway | 3 | 47 | 0.064 | NaN | 1.978 | 0.0105 |
| 16 | Epithelial Adherens Junction Signaling | 4 | 148 | 0.027 | NaN | 1.525 | 0.0298 |
| 17 | Role of BRCA1 in DNA Damage Response | 3 | 78 | 0.038 | NaN | 1.395 | 0.0403 |
| IPA identified canonical pathways in septic non-survivor patients after day 7 (D7NS). | | | | | | | |
| 1 | LXR/RXR Activation | 12 | 128 | 0.094 | -0.577 | 11.841 | 1.44E-12 |
| 2 | Acute Phase Response Signaling | 13 | 171 | 0.076 | 2.646 | 11.841 | 1.44E-12 |
| 3 | FXR/RXR Signaling | 11 | 138 | 0.08 | NaN | 10.129 | 7.43E-11 |
| 4 | Coagulation System | 7 | 35 | 0.2 | 0.378 | 8.906 | 1.24E-09 |
| 5 | Intrinsic Prothrombin Activation Pathway | 6 | 30 | 0.2 | NaN | 7.526 | 2.98E-08 |
| 6 | Extrinsic Prothrombin Activation Pathway | 5 | 18 | 0.278 | 1 | 6.914 | 1.22E-07 |
| 7 | Clathrin-mediated Endocytosis Signaling | 8 | 188 | 0.043 | NaN | 5.157 | 6.97E-06 |
| 8 | IL-12 Signaling and Production in Macrophages | 6 | 138 | 0.043 | NaN | 3.689 | 0.000205 |
| 9 | Actin Cytoskeleton Signaling | 7 | 221 | 0.032 | 1.342 | 3.626 | 0.000236 |
| 10 | Production of Nitric Oxide and Reactive Oxygen Species in Macrophages | 6 | 186 | 0.032 | -1.633 | 3.085 | 0.000822 |
| 11 | Role of Tissue Factor in Cancer | 5 | 112 | 0.045 | NaN | 3.085 | 0.000822 |
| 12 | Atherosclerosis Signaling | 5 | 125 | 0.04 | NaN | 2.895 | 0.00127 |
| 13 | TR/RXR Activation | 4 | 92 | 0.043 | NaN | 2.303 | 0.00498 |
| 14 | MSP-RON Signaling Pathway | 3 | 47 | 0.064 | NaN | 2.016 | 0.00964 |