**Supplementary data**

Supplementary Table 1: List of significant differentially expressed proteins with properties in patients with HF.

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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Uniprot Accession | Protein Name | Gene | Peptide count | Unique peptide | Confidence score | Fold Change | Expression | P value |
| P51665 | 26S proteasome non-ATPase regulatory subunit 7 | PSMD7 | 8 | 2 | 46 | 0.18 | Down | 0.0252 |
| P62266 | 40S ribosomal protein S23 | RPS23 | 4 | 2 | 27 | 0.19 | Down | 0.0378 |
| P62851 | 40S ribosomal protein S25 | RPS25 | 6 | 3 | 42 | 0.32 | Down | 0.0148 |
| P49189 | 4-trimethylaminobutyraldehyde dehydrogenase | ALDH9A1 | 15 | 7 | 86 | 0.29 | Down | 0.0351 |
| P35268 | 60S ribosomal protein L22 | RPL22 | 10 | 8 | 65 | 0.48 | Down | 0.0488 |
| P36578 | 60S ribosomal protein L4 | RPL4 | 25 | 17 | 137 | 4.00 | Up | 0.0438 |
| Q8N6G6 | ADAMTS-like protein 1 | ADAMTSL1 | 7 | 5 | 41 | 3.09 | Up | 0.0359 |
| Q8N142 | Adenylosuccinate synthetase isozyme 1 | ADSSL1 | 5 | 2 | 39 | 4.71 | Up | 0.0225 |
| P12235 | ADP/ATP translocase 1 | SLC25A4 | 16 | 3 | 116 | 0.39 | Down | 0.0457 |
| O75366 | Advillin | AVIL | 2 | 2 | 10 | 0.36 | Down | 0.0089 |
| Q53LP3 | Ankyrin repeat domain-containing protein SOWAHC | SOWAHC | 3 | 2 | 20 | 2.26 | Up | 0.0488 |
| P08133 | Annexin A6 | ANXA6 | 64 | 39 | 597 | 0.24 | Down | 0.0067 |
| Q96PC3 | AP-1 complex subunit sigma-3 | AP1S3 | 1 | 1 | 6 | 0.25 | Down | 0.0244 |
| Q86UQ4 | ATP-binding cassette sub-family A member 13 | ABCA13 | 44 | 14 | 218 | 0.39 | Down | 0.0097 |
| P49662 | Caspase-4 | CASP4 | 1 | 1 | 5 | 0.32 | Down | 0.0098 |
| Q14839 | Chromodomain-helicase-DNA-binding protein 4 | CHD4 | 15 | 6 | 84 | 3.35 | Up | 0.0397 |
| P12109 | Collagen alpha-1(VI) chain | COL6A1 | 35 | 25 | 298 | 3.10 | Up | 0.0213 |
| P02746 | Complement C1q subcomponent subunit B | C1QB | 8 | 4 | 55 | 2.29 | Up | 0.0443 |
| Q96FN4 | Copine-2 | CPNE2 | 9 | 2 | 50 | 11.40 | Up | 0.0292 |
| Q69YN2 | CWF19-like protein 1 | CWF19L1 | 3 | 1 | 19 | 0.40 | Down | 0.0228 |
| P09622 | Dihydrolipoyl dehydrogenase\_ mitochondrial | DLD | 20 | 12 | 118 | 4.02 | Up | 0.0175 |
| P33991 | DNA replication licensing factor MCM4 | MCM4 | 13 | 8 | 91 | 7.51 | Up | 0.0004 |
| Q99615 | DnaJ homolog subfamily C member 7 | DNAJC7 | 3 | 1 | 16 | 12.48 | Up | 0.0002 |
| Q9P2D7 | Dynein heavy chain 1\_ axonemal | DNAH1 | 37 | 11 | 190 | 0.40 | Down | 0.0373 |
| Q96JB1 | Dynein heavy chain 8\_ axonemal | DNAH8 | 39 | 11 | 225 | 0.18 | Down | 0.0499 |
| O75923 | Dysferlin | DYSF | 18 | 6 | 95 | 12.47 | Up | 0.0412 |
| Q9UBQ5 | Eukaryotic translation initiation factor 3 subunit K | EIF3K | 4 | 2 | 24 | 3.05 | Up | 0.0424 |
| Q9NV70 | Exocyst complex component 1 | EXOC1 | 5 | 2 | 27 | 0.11 | Down | 0.0012 |
| Q9UPT5 | Exocyst complex component 7 | EXOC7 | 5 | 3 | 27 | 4.07 | Up | 0.0122 |
| Q6ZUT3 | FERM domain-containing protein 7 | FRMD7 | 5 | 3 | 28 | 0.10 | Down | 0.0141 |
| P35555 | Fibrillin-1 | FBN1 | 55 | 40 | 352 | 0.30 | Down | 0.0291 |
| Q05397 | Focal adhesion kinase 1 | PTK2 | 15 | 2 | 84 | 2.81 | Up | 0.0478 |
| Q8WWL7 | G2/mitotic-specific cyclin-B3 | CCNB3 | 9 | 5 | 42 | 0.35 | Down | 0.0332 |
| O75223 | Gamma-glutamylcyclotransferase | GGCT | 3 | 2 | 17 | 0.31 | Down | 0.0263 |
| P46439 | Glutathione S-transferase Mu 5 | GSTM5 | 9 | 4 | 55 | 6.24 | Up | 0.0190 |
| P06737 | Glycogen phosphorylase\_ liver form | PYGL | 32 | 11 | 219 | 3.33 | Up | 0.0048 |
| Q5JWF2 | Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas | GNAS | 18 | 10 | 114 | 0.38 | Down | 0.0166 |
| Q9HAV0 | Guanine nucleotide-binding protein subunit beta-4 | GNB4 | 5 | 1 | 45 | 3.68 | Up | 0.0013 |
| P34931 | Heat shock 70 kDa protein 1-like | HSPA1L | 31 | 4 | 204 | 0.37 | Down | 0.0147 |
| O14558 | Heat shock protein beta-6 | HSPB6 | 6 | 4 | 64 | 0.21 | Down | 0.0259 |
| P26927 | Hepatocyte growth factor-like protein | MST1 | 20 | 9 | 106 | 0.23 | Down | 0.0087 |
| P52272 | Heterogeneous nuclear ribonucleoprotein M | HNRNPM | 43 | 30 | 366 | 0.30 | Down | 0.0112 |
| P37235 | Hippocalcin-like protein 1 | HPCAL1 | 9 | 4 | 59 | 6.45 | Up | 0.0089 |
| Q6YN16 | Hydroxysteroid dehydrogenase-like protein 2 | HSDL2 | 6 | 3 | 30 | 0.11 | Down | 0.0000 |
| Q04760 | Lactoylglutathione lyase | GLO1 | 12 | 10 | 100 | 2.17 | Up | 0.0448 |
| P42167 | Lamina-associated polypeptide 2\_ isoforms beta/gamma | TMPO | 25 | 7 | 178 | 0.27 | Down | 0.0151 |
| P48740 | Mannan-binding lectin serine protease 1 | MASP1 | 31 | 3 | 210 | 2.65 | Up | 0.0309 |
| P14780 | Matrix metalloproteinase-9 | MMP9 | 2 | 1 | 9 | 0.06 | Down | 0.0464 |
| O15480 | Melanoma-associated antigen B3 | MAGEB3 | 6 | 4 | 36 | 0.46 | Down | 0.0418 |
| O14880 | Microsomal glutathione S-transferase 3 | MGST3 | 2 | 2 | 16 | 0.42 | Down | 0.0436 |
| Q765P7 | MTSS1-like protein | MTSS1L | 2 | 1 | 10 | 6.92 | Up | 0.0009 |
| Q8TDD5 | Mucolipin-3 | MCOLN3 | 3 | 2 | 22 | 0.07 | Down | 0.0285 |
| Q99836 | Myeloid differentiation primary response protein MyD88 | MYD88 | 4 | 2 | 20 | 2.94 | Up | 0.0091 |
| Q6ZS30 | Neurobeachin-like protein 1 | NBEAL1 | 11 | 5 | 65 | 2.02 | Up | 0.0021 |
| Q6ZNJ1 | Neurobeachin-like protein 2 | NBEAL2 | 7 | 3 | 37 | 0.47 | Down | 0.0211 |
| Q9UNZ2 | NSFL1 cofactor p47 | NSFL1C | 10 | 3 | 59 | 0.37 | Down | 0.0079 |
| Q8N987 | N-terminal EF-hand calcium-binding protein 1 | NECAB1 | 2 | 1 | 11 | 0.37 | Down | 0.0004 |
| P52948 | Nuclear pore complex protein Nup98-Nup96 | NUP98 | 8 | 2 | 60 | 20.43 | Up | 0.0462 |
| Q9GZY0 | Nuclear RNA export factor 2 | NXF2 | 8 | 2 | 40 | 5.06 | Up | 0.0198 |
| Q9NR30 | Nucleolar RNA helicase 2 | DDX21 | 18 | 8 | 111 | 15.30 | Up | 0.0137 |
| Q00688 | Peptidyl-prolyl cis-trans isomerase FKBP3 | FKBP3 | 12 | 5 | 90 | 6.92 | Up | 0.0493 |
| Q92569 | Phosphatidylinositol 3-kinase regulatory subunit gamma | PIK3R3 | 2 | 1 | 11 | 2.60 | Up | 0.0219 |
| P02776 | Platelet factor 4 | PF4 | 5 | 4 | 43 | 2.25 | Up | 0.0094 |
| P07359 | Platelet glycoprotein Ib alpha chain | GP1BA | 5 | 3 | 29 | 0.38 | Down | 0.0291 |
| P51805 | Plexin-A3 | PLXNA3 | 5 | 1 | 29 | 3.34 | Up | 0.0303 |
| P0CG38 | POTE ankyrin domain family member I | POTEI | 30 | 1 | 263 | 2.20 | Up | 0.0165 |
| Q6UN15 | Pre-mRNA 3'-end-processing factor FIP1 | FIP1L1 | 6 | 3 | 40 | 2.82 | Up | 0.0040 |
| P17844 | Probable ATP-dependent RNA helicase DDX5 | DDX5 | 36 | 12 | 291 | 2.18 | Up | 0.0073 |
| Q8TF62 | Probable phospholipid-transporting ATPase IM | ATP8B4 | 2 | 1 | 9 | 0.16 | Down | 0.0353 |
| P13674 | Prolyl 4-hydroxylase subunit alpha-1 | P4HA1 | 18 | 10 | 140 | 9.74 | Up | 0.0259 |
| Q96JJ7 | Protein disulfide-isomerase TMX3 | TMX3 | 8 | 3 | 59 | 2.23 | Up | 0.0328 |
| Q9NUQ9 | Protein FAM49B | FAM49B | 9 | 2 | 56 | 26.91 | Up | 0.0043 |
| Q8TBQ9 | Protein kish-A | TMEM167A | 2 | 2 | 14 | 5.60 | Up | 0.0068 |
| Q96C90 | Protein phosphatase 1 regulatory subunit 14B | PPP1R14B | 2 | 1 | 20 | 33.57 | Up | 0.0130 |
| Q13123 | Protein Red | IK | 10 | 5 | 65 | 0.15 | Down | 0.0120 |
| P61457 | Pterin-4-alpha-carbinolamine dehydratase | PCBD1 | 1 | 1 | 7 | 0.43 | Down | 0.0398 |
| Q96DA2 | Ras-related protein Rab-39B | RAB39B | 5 | 3 | 32 | 5.31 | Up | 0.0383 |
| O43665 | Regulator of G-protein signaling 10 | RGS10 | 4 | 3 | 31 | 0.10 | Down | 0.0386 |
| Q9HB40 | Retinoid-inducible serine carboxypeptidase | SCPEP1 | 4 | 2 | 24 | 4.95 | Up | 0.0055 |
| P42224 | Signal transducer and activator of transcription 1-alpha/beta | STAT1 | 33 | 22 | 271 | 0.49 | Down | 0.0281 |
| Q96R06 | Sperm-associated antigen 5 | SPAG5 | 2 | 2 | 8 | 2.53 | Up | 0.0426 |
| P19623 | Spermidine synthase | SRM | 11 | 6 | 71 | 0.20 | Down | 0.0237 |
| Q9UJZ1 | Stomatin-like protein 2\_ mitochondrial | STOML2 | 15 | 8 | 114 | 0.17 | Down | 0.0169 |
| Q14683 | Structural maintenance of chromosomes protein 1A | SMC1A | 49 | 17 | 281 | 2.37 | Up | 0.0225 |
| Q99973 | Telomerase protein component 1 | TEP1 | 7 | 1 | 40 | 8.83 | Up | 0.0000 |
| Q8NDW8 | Tetratricopeptide repeat protein 21A | TTC21A | 9 | 1 | 44 | 4.65 | Up | 0.0037 |
| Q16881 | Thioredoxin reductase 1\_ cytoplasmic | TXNRD1 | 32 | 13 | 236 | 2.75 | Up | 0.0423 |
| Q9H1E5 | Thioredoxin-related transmembrane protein 4 | TMX4 | 2 | 2 | 11 | 5.58 | Up | 0.0347 |
| Q9UPV9 | Trafficking kinesin-binding protein 1 | TRAK1 | 4 | 1 | 21 | 22.27 | Up | 0.0281 |
| P63272 | Transcription elongation factor SPT4 | SUPT4H1 | 1 | 1 | 5 | 79.28 | Up | 0.0144 |
| P43403 | Tyrosine-protein kinase ZAP-70 | ZAP70 | 4 | 1 | 28 | 0.15 | Down | 0.0494 |
| O43172 | U4/U6 small nuclear ribonucleoprotein Prp4 | PRPF4 | 3 | 2 | 16 | 3.94 | Up | 0.0132 |
| O14933 | Ubiquitin/ISG15-conjugating enzyme E2 L6 | UBE2L6 | 9 | 6 | 54 | 0.34 | Down | 0.0069 |
| P61077 | Ubiquitin-conjugating enzyme E2 D3 | UBE2D3 | 2 | 1 | 21 | 2.44 | Up | 0.0369 |
| Q9NYU2 | UDP-glucose:glycoprotein glucosyltransferase 1 | UGGT1 | 24 | 14 | 142 | 0.24 | Down | 0.0444 |
| O75083 | WD repeat-containing protein 1 | WDR1 | 32 | 17 | 253 | 0.15 | Down | 0.0063 |
| Q5FWF6 | Zinc finger protein 789 | ZNF789 | 4 | 2 | 21 | 0.48 | Down | 0.0191 |

**Fold change:** Ratio of HF with death/rehospitalisation: HF with no events.

**Supplementary Figure 1: Schematic of the proteomic workflow to discover significant differentially expressed proteins in patients with HF.**

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| --- | --- |
| **Sample preparation** |  |
| **Sample analysis** |
| **Data analysis** |

**Supplementary Figure 2: Heatmap showing the expression profiles of 97 significant differentially expressed proteins in comparing between both HF groups (death/rehospitalisation vs no events) (Experiment performed in triplicate).**



Accession numbers corresponds to protein and gene names that are presented in *Supplementary Table 1*.