## Supplementary materials

## Olink biomarkers

The following Olink biomarker panels were used: Cardiovascular II (CVII), CVD III, Immune response and Oncology II. Across the panels there were several duplicates; B-natriuretic peptide (BNP) and N-terminal pro-B-type natriuretic peptide (NT-proBNP) in CVDII and CVDIII panels; amphiregulin (AREG) in the Immune response and Oncology II panel; stem cell factor (SCF) in oncology II and CVDIII; and interleukin 6 in CVDII, Immune response and Oncology II panels. Detailed information about the 363 biomarkers used in this analysis can be found online(1-4). Figure S1 and S2 show that the biomarker set used encompassed biomarkers from a wide range of biological processes and diseases.

## Cluster analysis

The aim of this study was to identify mutually exclusive HFpEF clusters based on biomarker profiles. Supplementary figure 4 summarises the statistical approach used. Due to the large set of biomarkers, we sought to reduce the dimension of the data using principle component analysis (PCA). PCA was performed on all 363 biomarkers using the prcomp package in R. Fifty-nine principle components (PCs) with a minimum eigenvalue of 1 were used as input for the cluster analysis. The optimal number of clusters was determined using the NbClust package in R. NbClust uses 30 indices to determine the optimal cluster number by picking the number of clusters that is calculated in the majority of these indices(5). NbClust determined 6 to be the optimal number of clusters (Supplementary figure 4). A hierarchical cluster analysis using complete linkage was performed using the 59 PCs as input.

Cluster 5 and 6 were small clusters and therefore not included in the downstream analyses. Table SI shows an overview of these patients characteristics.

Table S1. Characteristics of cluster 5 and 6

|  | Cluster 5 | Cluster 6 |
| :---: | :---: | :---: |
| N | 3 | 2 |
| Age > 75 years (\%) | 1 (33.3\%) | 1(50\%) |
| Male (\%) | 2 (66.7\%) | 2 (100\%) |
| BMI (kg/m ${ }^{2}$ ) | 25.2 (3.67) | 35.0 (3.04) |
| NYHA, $n(\%)$ |  |  |
| I | 0 (0\%) | 0 (0\%) |
| II | 2 (66.6\%) | 0 (0\%) |
| III | 1 (33.3\%) | 1 (50\%) |
| IV | 0 (0\%) | 1 (50\%) |
| Haemoglobin, (g/dl) | 13.7 (2.90) | 14.2 (1.34) |
| Creatinine, $(\mu \mathrm{mol} / \mathrm{L})$ | 113 (13.5) | 89.0 (4.24) |
| NT-proBNP, (pg/L) | 408 []334;1022] | 3548 [1886;5211] |
| GDF-15, (pg/mL) | 3716 [2564;4020] | 11386 [6392;16380] |

Table S2. Differentially expressed proteins in Cluster 1

| Protein | Symbol | Description | $\operatorname{logFC}$ | $\underset{\mathbf{r}}{\underset{\text { AveExp }}{ }}$ | t | P.Value | adj.P.Val | Up/downregulated |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 095971 | CD160 | CD160 molecule [CD160] | $\begin{array}{r} 0.8049 \\ 19 \end{array}$ | $\begin{array}{r} 7.34782 \\ 8 \end{array}$ | $\begin{array}{r} 8.32830 \\ 2 \end{array}$ | $\begin{array}{r} 1.14 \mathrm{E}- \\ 15 \end{array}$ | 8.96E-15 | Up-regulated |
| $\begin{aligned} & \text { Q8WXI } \\ & 8 \end{aligned}$ | $\begin{aligned} & \text { CLEC4 } \\ & \mathrm{D} \end{aligned}$ | C-type lectin domain family 4 member D [CLEC4D] | $\begin{array}{r} 0.9124 \\ 16 \end{array}$ | $\begin{array}{r} 4.86834 \\ 2 \end{array}$ | $\begin{array}{r} 9.13485 \\ 8 \end{array}$ | $\begin{array}{r} 2.69 \mathrm{E}- \\ 18 \end{array}$ | $3.48 \mathrm{E}-17$ | Up-regulated |
| $\begin{aligned} & \text { Q9BXN } \\ & 2 \end{aligned}$ | $\begin{aligned} & \text { CLEC7 } \\ & \text { A } \end{aligned}$ | C-type lectin domain containing 7A [CLEC7A] | $\begin{array}{r} 1.0027 \\ 67 \end{array}$ | 4.52783 | $\begin{array}{r} 9.40662 \\ 4 \end{array}$ | $\begin{array}{r} 3.22 \mathrm{E}- \\ 19 \end{array}$ | $5.32 \mathrm{E}-18$ | Up-regulated |
| P15086 | CPB1 | carboxypept idase B1 [CPB1] | $\begin{array}{r} 0.8115 \\ 7 \end{array}$ | $\begin{array}{r} 3.78332 \\ 6 \end{array}$ | $\begin{array}{r} 6.48797 \\ 6 \end{array}$ | $\begin{array}{r} 2.42 \mathrm{E}- \\ 10 \end{array}$ | $8.22 \mathrm{E}-10$ | Up-regulated |
| P04080 | CSTB | cystatin B [CSTB] | $\begin{array}{r} 0.9111 \\ 33 \end{array}$ | $\begin{array}{r} 5.19877 \\ 7 \end{array}$ | $\begin{array}{r} 7.97962 \\ 6 \end{array}$ | $\begin{array}{r} 1.38 \mathrm{E}- \\ 14 \end{array}$ | 8.32E-14 | Up-regulated |
| P78310 | CXADR | CXADR Ig- | 0.8325 | 3.56822 | 8.85513 | $2.28 \mathrm{E}-$ | $2.59 \mathrm{E}-16$ | Up-regulated |


|  |  | like cell adhesion molecule [CXADR] | 13 | 9 | 8 | 17 |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| P15090 | FABP4 | fatty acid binding protein 4 [FABP4] | $\begin{array}{r} 0.9387 \\ 81 \end{array}$ | $\begin{array}{r} 6.11966 \\ 3 \end{array}$ | 6.17449 | $\begin{array}{r} 1.55 \mathrm{E}- \\ 09 \end{array}$ | 4.69E-09 | Up-regulated |
| $\begin{aligned} & \text { Q9NSA } \\ & 1 \end{aligned}$ | FGF21 | fibroblast growth <br> factor 21 <br> [FGF21] | $\begin{array}{r} 1.3287 \\ 39 \end{array}$ | $\begin{array}{r} 9.06590 \\ 7 \end{array}$ | $\begin{array}{r} 5.84122 \\ 2 \end{array}$ | $\begin{array}{r} 1.03 \mathrm{E}- \\ 08 \end{array}$ | $2.75 \mathrm{E}-08$ | Up-regulated |
| $\begin{aligned} & \text { Q9GZV } \\ & 9 \end{aligned}$ | FGF23 | fibroblast growth factor 23 [FGF23] | $\begin{array}{r} 1.1934 \\ 86 \end{array}$ | $\begin{array}{r} 6.80004 \\ 6 \end{array}$ | $\begin{array}{r} 5.49195 \\ 8 \end{array}$ | $\begin{array}{r} 6.85 \mathrm{E}- \\ 08 \end{array}$ | 1.61E-07 | Up-regulated |
| Q99988 | GDF15 | growth <br> differentiati <br> on factor 15 <br> [GDF15] | $\begin{array}{r} 0.9074 \\ 49 \end{array}$ | $\begin{array}{r} 5.61169 \\ 9 \end{array}$ | $\begin{array}{r} 7.91597 \\ 8 \end{array}$ | $\begin{array}{r} 2.15 \mathrm{E}- \\ 14 \end{array}$ | 1.26E-13 | Up-regulated |
| P08833 | IGFBP1 | insulin like <br> growth <br> factor <br> binding <br> protein 1 <br> [IGFBP1] | $\begin{array}{r} 1.1435 \\ 93 \end{array}$ | $\begin{array}{r} 4.59369 \\ 2 \end{array}$ | $\begin{array}{r} 5.91236 \\ 9 \end{array}$ | $\begin{array}{r} 6.93 \mathrm{E}- \\ 09 \end{array}$ | 1.91E-08 | Up-regulated |
| Q16270 | IGFBP7 | insulin like <br> growth <br> factor <br> binding <br> protein 7 <br> [IGFBP7] | $\begin{array}{r} 0.8304 \\ 34 \end{array}$ | $\begin{array}{r} 4.19883 \\ 2 \end{array}$ | $\begin{array}{r} 8.99453 \\ 1 \end{array}$ | 7.9E-18 | $9.56 \mathrm{E}-17$ | Up-regulated |
| 095998 | IL18BP | interleukin 18 binding protein [IL18BP] | $\begin{array}{r} 0.8427 \\ 36 \end{array}$ | $\begin{array}{r} 6.44924 \\ 6 \end{array}$ | $\begin{array}{r} 10.6387 \\ 8 \end{array}$ | $\begin{array}{r} 1.35 \mathrm{E}- \\ 23 \end{array}$ | $9.79 \mathrm{E}-22$ | Up-regulated |
| P01589 | IL2RA | interleukin <br> 2 receptor <br> subunit <br> alpha <br> [IL2RA] | $\begin{array}{r} 0.8371 \\ 03 \end{array}$ | $\begin{array}{r} 4.35455 \\ 9 \end{array}$ | $\begin{array}{r} 8.78591 \\ 6 \end{array}$ | $\begin{array}{r} 3.85 \mathrm{E}- \\ 17 \end{array}$ | 3.99E-16 | Up-regulated |
| P18627 | LAG3 | lymphocyte activating 3 [LAG3] | $\begin{array}{r} 0.8203 \\ 26 \end{array}$ | $\begin{array}{r} 3.69981 \\ 8 \end{array}$ | $\begin{array}{r} 10.1167 \\ 3 \end{array}$ | $\begin{array}{r} 1.06 \mathrm{E}- \\ 21 \end{array}$ | 4.26E-20 | Up-regulated |
| $\begin{aligned} & \text { Q8NHJ } \\ & 6 \end{aligned}$ | LILRB4 | leukocyte immunoglo bulin like receptor B4 [LILRB4] | $\begin{array}{r} 0.8364 \\ 2 \end{array}$ | $\begin{array}{r} 4.67922 \\ 4 \end{array}$ | 8.53106 | $\begin{array}{r} 2.57 \mathrm{E}- \\ 16 \end{array}$ | $2.13 \mathrm{E}-15$ | Up-regulated |
| $\begin{aligned} & \text { Q8WXI } \\ & 7 \end{aligned}$ | MUC16 | mucin 16, cell surface associated [MUC16] | $\begin{array}{r} 0.8982 \\ 5 \end{array}$ | $\begin{array}{r} 6.84115 \\ 3 \end{array}$ | $\begin{array}{r} 4.15347 \\ 9 \end{array}$ | $\begin{array}{r} 3.96 \mathrm{E}- \\ 05 \end{array}$ | $6.3 \mathrm{E}-05$ | Up-regulated |
| 076036 | NCR1 | natural | 0.8374 | 4.45856 | 9.53834 | $1.14 \mathrm{E}-$ | 2.29E-18 | Up-regulated |


|  |  | cytotoxicity triggering receptor 1 [NCR1] | 97 | 6 | 3 | 19 |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| P19957 | PI3 | peptidase inhibitor 3 [PI3] | $\begin{array}{r} 0.8329 \\ 41 \end{array}$ | $\begin{array}{r} 3.77257 \\ 3 \end{array}$ | $\begin{array}{r} 6.53699 \\ 6 \end{array}$ | $1.8 \mathrm{E}-10$ | $6.22 \mathrm{E}-10$ | Up-regulated |
| Q03405 | PLAUR | plasminoge <br> n activator, urokinase receptor [PLAUR] | $\begin{array}{r} 0.8148 \\ 71 \end{array}$ | $\begin{array}{r} 4.70634 \\ 7 \end{array}$ | $\begin{array}{r} 9.89228 \\ 8 \end{array}$ | $\begin{array}{r} 6.63 \mathrm{E}- \\ 21 \end{array}$ | 2.19E-19 | Up-regulated |
| $\begin{aligned} & \text { Q9BXY } \\ & 4 \end{aligned}$ | RSPO3 | $\begin{aligned} & \text { R-spondin } 3 \\ & \text { [RSPO3] } \end{aligned}$ | $\begin{array}{r} 0.8278 \\ 91 \end{array}$ | $\begin{array}{r} 6.45588 \\ 2 \end{array}$ | 6.82658 | $\begin{array}{r} 3.01 \mathrm{E}- \\ 11 \end{array}$ | $1.23 \mathrm{E}-10$ | Up-regulated |
| $\begin{aligned} & \text { Q9Y6Q } \\ & 6 \end{aligned}$ | TNFRS <br> F11A | TNF <br> receptor superfamily member 11a <br> [TNFRSF1 1A] | $\begin{array}{r} 1.0444 \\ 83 \end{array}$ | $\begin{array}{r} 7.08572 \\ 5 \end{array}$ | $\begin{array}{r} 10.6651 \\ 9 \end{array}$ | $\begin{array}{r} 1.08 \mathrm{E}- \\ 23 \end{array}$ | $9.78 \mathrm{E}-22$ | Up-regulated |
| Q92956 | TNFRS F14 | TNF receptor superfamily member 14 [TNFRSF1 4] | $\begin{array}{r} 0.8579 \\ 86 \end{array}$ | $\begin{array}{r} 4.82143 \\ 4 \end{array}$ | $\begin{array}{r} 9.17877 \\ 5 \end{array}$ | $\begin{array}{r} 1.91 \mathrm{E}- \\ 18 \end{array}$ | $2.78 \mathrm{E}-17$ | Up-regulated |
| Q9NS68 | TNFRS <br> F19 | TNF receptor superfamily member 19 [TNFRSF1 9] | $\begin{array}{r} 0.9135 \\ 89 \end{array}$ | $\begin{array}{r} 6.04489 \\ 8 \end{array}$ | 8.59774 | $\begin{array}{r} 1.57 \mathrm{E}- \\ 16 \end{array}$ | 1.36E-15 | Up-regulated |
| P19438 | TNFRS F1A | TNF receptor superfamily member 1A [TNFRSF1 A] | $\begin{array}{r} 0.8820 \\ 84 \end{array}$ | $\begin{array}{r} 5.63058 \\ 7 \end{array}$ | $\begin{array}{r} 9.14973 \\ 5 \end{array}$ | $\begin{array}{r} 2.39 \mathrm{E}- \\ 18 \end{array}$ | $3.22 \mathrm{E}-17$ | Up-regulated |
| P20333 | TNFRS F1B | TNF receptor superfamily member 1B [TNFRSF1 B] | $\begin{array}{r} 0.9869 \\ 61 \end{array}$ | $\begin{array}{r} 5.15987 \\ 9 \end{array}$ | $\begin{array}{r} 10.3878 \\ 5 \end{array}$ | $\begin{array}{r} 1.11 \mathrm{E}- \\ 22 \end{array}$ | $5.78 \mathrm{E}-21$ | Up-regulated |
| P43489 | TNFRS F4 | TNF receptor superfamily member 4 [TNFRSF4] | $\begin{array}{r} 1.0077 \\ 05 \end{array}$ | $\begin{array}{r} 5.73468 \\ 8 \end{array}$ | $\begin{array}{r} 11.0032 \\ 8 \end{array}$ | $\begin{array}{r} 5.96 \mathrm{E}- \\ 25 \end{array}$ | $1.08 \mathrm{E}-22$ | Up-regulated |
| 095407 | TNFRS <br> F6B | TNF <br> receptor superfamily member 6b | $\begin{array}{r} 1.0537 \\ 24 \end{array}$ | $\begin{array}{r} 7.30737 \\ 1 \end{array}$ | $\begin{array}{r} 9.16504 \\ 7 \end{array}$ | $\begin{array}{r} 2.13 \mathrm{E}- \\ 18 \end{array}$ | $2.97 \mathrm{E}-17$ | Up-regulated |

[TNFRSF6
$\mathrm{B}]$

Table S3. Differentially expressed proteins in Cluster 3

| Protein | Symbol | Description | $\operatorname{logFC}$ | AveEx pr | t | P.value | adj.P.Val | Up/downregulated |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| P36222 | CHI3L1 | chitinase 3 <br> like 1 <br> [CHI3L1] | $0.8592$ | $\begin{array}{r} 6.4501 \\ 91 \end{array}$ | -8.69879 | 7.4E-17 | $2.89 \mathrm{E}-16$ | Downregulated |
| Q07065 | CKAP4 | cytoskeleto n associated protein 4 [CKAP4] | $\begin{array}{r} 0.8173 \\ 2 \end{array}$ | $\begin{array}{r} 6.5563 \\ 4 \end{array}$ | -15.8032 | $\begin{array}{r} 1.36 \mathrm{E}- \\ 44 \end{array}$ | 4.94E-43 | Downregulated |
| $\begin{aligned} & \text { Q9BXN } \\ & 2 \end{aligned}$ | $\begin{aligned} & \text { CLEC7 } \\ & \text { A } \end{aligned}$ | C-type lectin domain containing 7A <br> [CLEC7A] | $0.8949$ | $\begin{array}{r} 4.5278 \\ 3 \end{array}$ | -12.7184 | $\begin{array}{r} 1.25 \mathrm{E}- \\ 31 \end{array}$ | $1.19 \mathrm{E}-30$ | Downregulated |
| P04080 | CSTB | cystatin B [CSTB] | $0.9439$ | $\begin{array}{r} 5.1987 \\ 77 \end{array}$ | -12.8849 | $\begin{array}{r} 2.65 \mathrm{E}- \\ 32 \end{array}$ | $2.67 \mathrm{E}-31$ | Downregulated |
| P15090 | FABP4 | fatty acid binding protein 4 [FABP4] | 1.0203 | $\begin{array}{r} 6.1196 \\ 63 \end{array}$ | $-10.1573$ | $\begin{array}{r} 7.57 \mathrm{E}- \\ 22 \end{array}$ | $3.77 \mathrm{E}-21$ | Downregulated |
| $\begin{aligned} & \text { Q9NSA } \\ & 1 \end{aligned}$ | FGF21 | fibroblast growth factor 21 [FGF21] | $0.9533$ | $\begin{array}{r} 9.0659 \\ 07 \end{array}$ | -5.94774 | $\begin{array}{r} 5.68 \mathrm{E}- \\ 09 \end{array}$ | $1.17 \mathrm{E}-08$ | Downregulated |
| $\begin{aligned} & \text { Q9GZV } \\ & 9 \end{aligned}$ | FGF23 | fibroblast growth factor 23 [FGF23] | $1.0416$ $9$ | $\begin{array}{r} 6.8000 \\ 46 \end{array}$ | -6.9249 | $\begin{array}{r} 1.62 \mathrm{E}- \\ 11 \end{array}$ | $4.02 \mathrm{E}-11$ | Downregulated |
| Q99988 | GDF15 | growth differentiati on factor 15 [GDF15] | 0.8648 | $\begin{array}{r} 5.6116 \\ 99 \end{array}$ | -11.4077 | $\begin{array}{r} 1.75 \mathrm{E}- \\ 26 \end{array}$ | $1.22 \mathrm{E}-25$ | Downregulated |
| P08833 | IGFBP1 | insulin like growth factor binding protein 1 <br> [IGFBP1] | $1.0895$ | $\begin{array}{r} 4.5936 \\ 92 \end{array}$ | -8.26778 | $\begin{array}{r} 1.76 \mathrm{E}- \\ 15 \end{array}$ | 6.14E-15 | Downregulated |
| P08727 | KRT19 | keratin 19 <br> [KRT19] | $0.9018$ | $\begin{array}{r} 3.0610 \\ 24 \end{array}$ | -10.2735 | $\begin{array}{r} 2.89 \mathrm{E}- \\ 22 \end{array}$ | $1.52 \mathrm{E}-21$ | Downregulated |
| $\begin{aligned} & \text { Q8NHJ } \\ & 6 \end{aligned}$ | LILRB4 | leukocyte immunoglo bulin like receptor B4 | $\begin{array}{r} 0.8560 \\ 3 \end{array}$ | $\begin{array}{r} 4.6792 \\ 24 \end{array}$ | -13.7411 | $\begin{array}{r} 8.13 \mathrm{E}- \\ 36 \end{array}$ | $1.23 \mathrm{E}-34$ | Downregulated |


|  |  | [LILRB4] |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| $\begin{aligned} & \text { Q8WXI } \\ & 7 \end{aligned}$ | MUC16 | mucin 16 , cell surface associated [MUC16] | $\begin{array}{r} 0.8922 \\ 8 \end{array}$ | $\begin{array}{r} 6.8411 \\ 53 \end{array}$ | -5.96745 | $\begin{array}{r} 5.08 \mathrm{E}- \\ 09 \end{array}$ | $1.05 \mathrm{E}-08$ | Downregulated |
| $\begin{aligned} & \text { Q96NY } \\ & 8 \end{aligned}$ | $\begin{aligned} & \text { NECTI } \\ & \text { N4 } \end{aligned}$ | nectin cell adhesion molecule 4 [NECTIN4] | $\begin{array}{r} 0.8476 \\ 8 \end{array}$ | $\begin{array}{r} 7.1985 \\ 72 \end{array}$ | -15.6614 | $\begin{array}{r} 5.61 \mathrm{E}- \\ 44 \end{array}$ | $1.45 \mathrm{E}-42$ | Downregulated |
| P16860 | NPPB | natriuretic peptide B [NPPB] | $0.8793$ $4$ | $\begin{array}{r} 3.7369 \\ 58 \end{array}$ | -5.55119 | 5E-08 | $9.41 \mathrm{E}-08$ | Downregulated |
| P19957 | PI3 | peptidase <br> inhibitor 3 <br> [PI3] | $\begin{array}{r} 0.9097 \\ 2 \end{array}$ | $\begin{array}{r} 3.7725 \\ 73 \end{array}$ | -10.9132 | $1.3 \mathrm{E}-24$ | $7.71 \mathrm{E}-24$ | Downregulated |
| $\begin{aligned} & \text { Q9BXY } \\ & 4 \end{aligned}$ | RSPO3 | R-spondin 3 [RSPO3] | $\begin{array}{r} 0.9935 \\ 8 \end{array}$ | $\begin{array}{r} 6.4558 \\ 82 \end{array}$ | -13.043 | $\begin{array}{r} 6.05 \mathrm{E}- \\ 33 \end{array}$ | 6.65E-32 | Downregulated |
| Q07654 | TFF3 | trefoil <br> factor 3 <br> [TFF3] | $\begin{array}{r} 0.9730 \\ 7 \end{array}$ | $\begin{array}{r} 5.9291 \\ 7 \end{array}$ | -13.8915 | $\begin{array}{r} 1.92 \mathrm{E}- \\ 36 \end{array}$ | 3.17E-35 | Downregulated |
| 014763 | TNFRS F10B | TNF receptor superfamily member 10b [TNFRSF1 0B] | $\begin{array}{r} 0.8393 \\ 2 \end{array}$ | $\begin{array}{r} 7.3542 \\ 25 \end{array}$ | -15.2089 | $\begin{array}{r} 5.03 \mathrm{E}- \\ 42 \end{array}$ | $1.14 \mathrm{E}-40$ | Downregulated |
| $\begin{aligned} & \text { Q9Y6Q } \\ & 6 \end{aligned}$ | TNFRS <br> F11A | TNF receptor superfamily member 11a [TNFRSF1 1A] | $0.9914$ | $\begin{array}{r} 7.0857 \\ 25 \end{array}$ | -16.2108 | $\begin{array}{r} 2.29 \mathrm{E}- \\ 46 \end{array}$ | $1.66 \mathrm{E}-44$ | Downregulated |
| Q92956 | TNFRS F14 | TNF receptor superfamily member 14 [TNFRSF1 4] | $\begin{array}{r} 0.9084 \\ 8 \end{array}$ | $\begin{array}{r} 4.8214 \\ 34 \end{array}$ | -15.8857 | $\begin{array}{r} 5.97 \mathrm{E}- \\ 45 \end{array}$ | $2.41 \mathrm{E}-43$ | Downregulated |
| Q9NS68 | TNFRS F19 | TNF receptor superfamily member 19 [TNFRSF1 9] | $\begin{array}{r} 1.0420 \\ 4 \end{array}$ | $\begin{array}{r} 6.0448 \\ 98 \end{array}$ | -16.3847 | $\begin{array}{r} 3.97 \mathrm{E}- \\ 47 \end{array}$ | $3.6 \mathrm{E}-45$ | Downregulated |
| P19438 | TNFRS <br> F1A | TNF receptor superfamily member 1A [TNFRSF1 A] | $0.9397$ | $\begin{array}{r} 5.6305 \\ 87 \end{array}$ | -15.9731 | $\begin{array}{r} 2.49 \mathrm{E}- \\ 45 \end{array}$ | $1.29 \mathrm{E}-43$ | Downregulated |
| P20333 | TNFRS F1B | TNF receptor | $0.9287$ | $\begin{array}{r} 5.1598 \\ 79 \end{array}$ | -15.4661 | $\begin{array}{r} 3.92 \mathrm{E}- \\ 43 \end{array}$ | $9.49 \mathrm{E}-42$ | Downregulated |


|  |  | superfamily member 1B [TNFRSF1 B] | 1 |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| P43489 | $\begin{aligned} & \text { TNFRS } \\ & \text { F4 } \end{aligned}$ | TNF receptor superfamily member 4 [TNFRSF4] | $\begin{array}{r} 0.8366 \\ 2 \end{array}$ | $\begin{array}{r} 5.7346 \\ 88 \end{array}$ | -13.7211 | $\begin{array}{r} 9.84 \mathrm{E}- \\ 36 \end{array}$ | $1.43 \mathrm{E}-34$ | Downregulated |
| 095407 | $\begin{aligned} & \text { TNFRS } \\ & \text { F6B } \end{aligned}$ | TNF receptor superfamily member 6b [TNFRSF6 B] | $\begin{array}{r} 0.9773 \\ 6 \end{array}$ | $\begin{array}{r} 7.3073 \\ 71 \end{array}$ | -13.0209 | $\begin{array}{r} 7.43 \mathrm{E}- \\ 33 \end{array}$ | 7.94E-32 | Downregulated |

Table S4. Differentially expressed proteins in Cluster 4

| Protein | Symbol | Description | $\operatorname{logFC}$ | AveEx pr | t | P.Value | adj.P.Val | Up/downregulated |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Q15389 | $\begin{aligned} & \text { ANGPT } \\ & 1 \end{aligned}$ | angiopoieti n 1 <br> [ANGPT1] | 1.043379 | $\begin{array}{r} 7.3016 \\ 49 \end{array}$ | $\begin{array}{r} 6.4455 \\ 98 \end{array}$ | $3.13 \mathrm{E}-10$ | $2.22 \mathrm{E}-09$ | Upregulated |
| P42574 | CASP3 | caspase 3 <br> [CASP3] | 1.504064 | $\begin{array}{r} 6.3530 \\ 16 \end{array}$ | $\begin{array}{r} 10.319 \\ 29 \end{array}$ | 1.97E-22 | $3.58 \mathrm{E}-21$ | regulated |
| P29965 | $\begin{aligned} & \text { CD40L } \\ & \text { G } \end{aligned}$ | CD40 <br> ligand <br> [CD40LG] | 1.312199 | $\begin{array}{r} 4.3474 \\ 95 \end{array}$ | $\begin{array}{r} 10.068 \\ 01 \end{array}$ | $1.58 \mathrm{E}-21$ | $2.72 \mathrm{E}-20$ | regulated |
| P38936 | $\begin{aligned} & \text { CDKN1 } \\ & \text { A } \end{aligned}$ | cyclin dependent kinase inhibitor 1A [CDKN1A] | 1.1699 | $\begin{array}{r} 3.8499 \\ 87 \end{array}$ | $\begin{array}{r} 9.5269 \\ 49 \end{array}$ | $1.24 \mathrm{E}-19$ | 1.81E-18 | regulated |
| P09341 | CXCL1 | C-X-C motif chemokine ligand 1 [CXCL1] | 1.147292 | $\begin{array}{r} 8.8021 \\ 1 \end{array}$ | $\begin{array}{r} 7.6962 \\ 25 \end{array}$ | $9.88 \mathrm{E}-14$ | $9.43 \mathrm{E}-13$ | regulated |
| $\begin{aligned} & \text { Q9UN1 } \\ & 9 \end{aligned}$ | DAPP1 | dual adaptor of phosphotyr osine and 3phosphoino sitides 1 [DAPP1] | 2.154514 | $\begin{array}{r} 4.6248 \\ 69 \end{array}$ | $\begin{array}{r} 10.427 \\ 86 \end{array}$ | 7.97E-23 | $1.61 \mathrm{E}-21$ | regulated |
| Q14203 | DCTN1 | dynactin subunit 1 <br> [DCTN1] | 0.832109 | $\begin{array}{r} 4.6700 \\ 96 \end{array}$ | $\begin{array}{r} 8.4635 \\ 49 \end{array}$ | $4.23 \mathrm{E}-16$ | $4.65 \mathrm{E}-15$ | $\begin{aligned} & \text { Up- } \\ & \text { regulated } \end{aligned}$ |
| Q16698 | DECR1 | 2,4-dienoylCoA reductase 1 [DECR1] | 1.761809 | $\begin{array}{r} 5.4729 \\ 35 \end{array}$ | $\begin{array}{r} 12.476 \\ 73 \end{array}$ | 1.16E-30 | $1.4 \mathrm{E}-28$ | regulated |


| 094907 | DKK1 | dickkopf WNT signaling pathway inhibitor 1 [DKK1] | 0.827601 | $\begin{array}{r} 9.1265 \\ 66 \end{array}$ | $\begin{array}{r} 7.4533 \\ 5 \end{array}$ | 5.13E-13 | $4.54 \mathrm{E}-12$ | regulated |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| P01133 | EGF | epidermal <br> growth <br> factor <br> [EGF] | 1.616315 | $\begin{array}{r} 6.9227 \\ 69 \end{array}$ | $\begin{array}{r} 8.5355 \\ 7 \end{array}$ | $2.49 \mathrm{E}-16$ | $2.82 \mathrm{E}-15$ | regulated |
| Q04637 | EIF4G1 | eukaryotic translation initiation factor 4 gamma 1 [EIF4G1] | 1.53699 | $\begin{array}{r} 4.4613 \\ 54 \end{array}$ | $\begin{array}{r} 11.893 \\ 89 \end{array}$ | $2.32 \mathrm{E}-28$ | $1.2 \mathrm{E}-26$ | regulated |
| P09038 | FGF2 | fibroblast growth factor 2 [FGF2] | 0.883794 | $\begin{array}{r} 1.4374 \\ 25 \end{array}$ | $\begin{array}{r} 11.216 \\ 86 \end{array}$ | $9.32 \mathrm{E}-26$ | $3.08 \mathrm{E}-24$ | regulated |
| P14317 | HCLS 1 | hematopoiet ic cellspecific Lyn substrate 1 [HCLS1] | 1.230829 | $\begin{array}{r} 5.9391 \\ 95 \end{array}$ | $\begin{array}{r} 10.717 \\ 22 \end{array}$ | $6.92 \mathrm{E}-24$ | $1.65 \mathrm{E}-22$ | regulated |
| 094992 | HEXIM <br> 1 | HEXIM P- <br> TEFb complex subunit 1 [HEXIM1] | 1.185035 | $\begin{array}{r} 5.5832 \\ 11 \end{array}$ | $\begin{array}{r} 11.471 \\ 12 \end{array}$ | 1E-26 | $4.04 \mathrm{E}-25$ | regulated |
| $\begin{aligned} & \text { Q9Y6K } \\ & 9 \end{aligned}$ | IKBKG | inhibitor of nuclear <br> factor <br> kappa B <br> kinase regulatory subunit gamma <br> [IKBKG] | 1.131863 | $\begin{array}{r} 4.5205 \\ 84 \end{array}$ | $\begin{array}{r} 12.007 \\ 82 \end{array}$ | 8.3E-29 | $5.02 \mathrm{E}-27$ | regulated |
| $\begin{aligned} & \text { Q9NW } \\ & \text { Z3 } \end{aligned}$ | IRAK4 | interleukin 1 receptor associated kinase 4 [IRAK4] | 1.616846 | $\begin{array}{r} 3.0026 \\ 74 \end{array}$ | $\begin{array}{r} 12.132 \\ 42 \end{array}$ | $2.69 \mathrm{E}-29$ | $2.44 \mathrm{E}-27$ | regulated |
| $\begin{aligned} & \text { Q9UKP } \\ & 3 \end{aligned}$ | $\begin{aligned} & \text { ITGB1B } \\ & \text { P2 } \end{aligned}$ | integrin subunit beta 1 binding protein 2 [ITGB1BP2 ] | 1.66077 | $\begin{array}{r} 4.6353 \\ 37 \end{array}$ | $\begin{array}{r} 11.581 \\ 1 \end{array}$ | $3.78 \mathrm{E}-27$ | $1.72 \mathrm{E}-25$ | regulated |
| P07948 | LYN | LYN protooncogene, Src family | 0.920128 | $\begin{array}{r} 4.5662 \\ 85 \end{array}$ | $\begin{array}{r} 10.766 \\ 99 \end{array}$ | $4.52 \mathrm{E}-24$ | $1.17 \mathrm{E}-22$ | regulated |


|  |  | lyrosine <br> kinase <br> [LYN] |  |  |  |  |  |
| :--- | :--- | :--- | ---: | ---: | ---: | ---: | ---: |


|  |  | [SRC] |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| P78362 | SRPK2 | SRSF <br> protein <br> kinase 2 <br> [SRPK2] | 1.074254 | $\begin{array}{r} 1.7413 \\ 13 \end{array}$ | $\begin{array}{r} 12.089 \\ 28 \end{array}$ | $3.97 \mathrm{E}-29$ | $2.88 \mathrm{E}-27$ | $\begin{aligned} & \mathrm{Up}- \\ & \text { regulated } \end{aligned}$ |
| Q13043 | STK4 | serine/threo nine kinase <br> 4 [STK4] | 1.387621 | $\begin{array}{r} 4.1260 \\ 16 \end{array}$ | $\begin{array}{r} 9.0804 \\ 06 \end{array}$ | $4.08 \mathrm{E}-18$ | $4.78 \mathrm{E}-17$ | $\begin{aligned} & \text { Up- } \\ & \text { regulated } \end{aligned}$ |
| P 40222 | TXLNA | taxilin <br> alpha <br> [TXLNA] | 1.311471 | $\begin{array}{r} 5.6051 \\ 38 \end{array}$ | $\begin{array}{r} 11.248 \\ 59 \end{array}$ | 7.07E-26 | $2.57 \mathrm{E}-24$ | regulated |
| Q05516 | ZBTB16 | zinc finger and BTB domain containing 16 <br> [ZBTB16] | 1.365525 | $\begin{array}{r} 1.9971 \\ 67 \end{array}$ | $\begin{array}{r} 15.081 \\ 15 \end{array}$ | $1.77 \mathrm{E}-41$ | $6.42 \mathrm{E}-39$ | regulated |
| P27352 | CBLIF | cobalamin binding intrinsic factor [CBLIF] | -0.80701 | $\begin{array}{r} 8.5001 \\ 53 \end{array}$ | $3.6794$ | 0.000264 | 0.001029 | Downregulated |

Table S5. Survival all-cause mortality and/or hospitalisation at 2 years

|  | Cluster 1 | Cluster 2 | Cluster 3 | Cluster 4 |
| :---: | :---: | :---: | :---: | :---: |
| All-cause mortality and/or hospitalisation at 24 months |  |  |  |  |
|  | HR ( $95 \%$ CI) $p$ value | HR (95\% CI) $p$-value | HR (95\% CI) $p$-value | HR (95\% CI) $p$-value |
| Univariate | Reference | 0.64 (0.43-0.95) 0.026* | $\begin{aligned} & 0.27(0.17-0.42) \\ & <0.001^{* * *} \end{aligned}$ | $\begin{aligned} & 0.92(0.56-1.52) \\ & 0.745 \end{aligned}$ |
| Model 1 | Reference | 0.61 (0.41-0.90) 0.014* | $\begin{aligned} & 0.31(0.20-0.49) \\ & <0.001 * * * \end{aligned}$ | $\begin{aligned} & 0.93(0.56-1.53) \\ & 0.777 \end{aligned}$ |


| Model 2 | Reference | $0.59(0.39-0.89) 0.011^{*}$ | $0.31(0.20-0.49)$ <br> $<0.001^{* * *}$ | $0.94(0.57-1.55)$ <br>  <br> Model 3 Reference |
| :--- | :--- | :--- | :--- | :--- |
|  | $0.58(0.39-0.87)$ <br> $0.008^{* *}$ | $0.30(0.19-0.48)$ <br> $<0.001^{* * *}$ | $0.84(0.51-1.40)$ |  |
| Model 1 = adjusts for Age and Sex |  |  |  |  |
| Model 2 = Model 1 + adjusts HF hospitalisation in the previous year |  |  |  |  |
| Model 3 = Model 2 + adjusts for NYHA class |  |  |  |  |

Figure S1. Overview of GO biological processes of Olink biomarker proteins


Figure S2. Pie chart depicting the proportion of Olink biomarkers involved in each disease area.


Figure S3: Variance explained for the top 10 principle components.


Figure S4. NbClust: optimal number of clusters according to indices.


Figure S5. Flow chart of cluster analysis

- Biomarkers were scaled

> 363 biomarkers of 429 HFpEF patients

- To reduce dimensions and redundancy
- All compomonents with an Eigenvalue > 1.00 are retained (59)

- Optimal cluster number of 6 calculated by NbClust

Table S6. Overview of cluster analyses studies and their findings

| Article/reference | Year | Cohort size | Based on | Validation group | Phenotypes/clusters |
| :---: | :---: | :---: | :---: | :---: | :---: |
| Shah et al. (6) | 2015 | 397 | Clinical features | Yes | 1. Younger patients with moderate diastolic dysfunction, relatively normal BNP. <br> 2. Obese, diabetic with high prevalence of sleep apnoea. <br> 3. Older patients with CKD, RV dysfunction, poorest outcomes. |
| Segar et al. (7) | 2019 | 654 | Clinical features \& echo data | Yes | 1. Higher BNP, severe symptoms, DM and increased creatinine. <br> 2. Lower prevalence of DM \& HF symptoms <br> 3. Low BMI , intermediate risk |
| Kao et al. (8) | 2015 | 3023 | Clinical features | Yes | Multiple clusters. <br> Subgroup C \& E clusters of patients with poor renal function and poorest outcomes. |
| Tromp et al. (9) | 2018 | 6480 | Clinical features | Yes | 3 HFpEF clusters <br> 1. Elderly/AF cluster <br> 2. Metabolic cluster: Obese, hypertension, diabetes <br> 3. Lean diabetic: DM \& low BMI |
| Hedman et al. (10) | 2020 | 320 | Biomarkers \& echo data | No | 2 worse faring clusters <br> 1. Hypertension, coronary artery disease, CKD, diabetes, anaemia <br> 2. AF, COPD, old age, CKD |
| Cohen et al. (11) | 2020 | 3442 | Clinical features | No | 1. Younger higher prevalence smoking, best prognosis <br> 2. Older, AF <br> 3. Obesity, DM, CKD, worst prognosis. |

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