# Replication Proteome Heart Map (PXD006675)

Ines Assum

July 12, 2021

```
## [1] "Genes in fibrosis score: "
```

```
##  [1] "ELN"      "FGF10"    "JAG1"     "KIAA1199" "CPXM2"    "FOSB"     "FCRL2"
##  [8] "SCN7A"    "NOV"      "ARHGAP20" "CILP"     "FRAS1"    "DCDC2"    "NRG1"
## [15] "CLEC3B"   "AFAP1L2"  "COL14A1"  "ITGBL1"
```

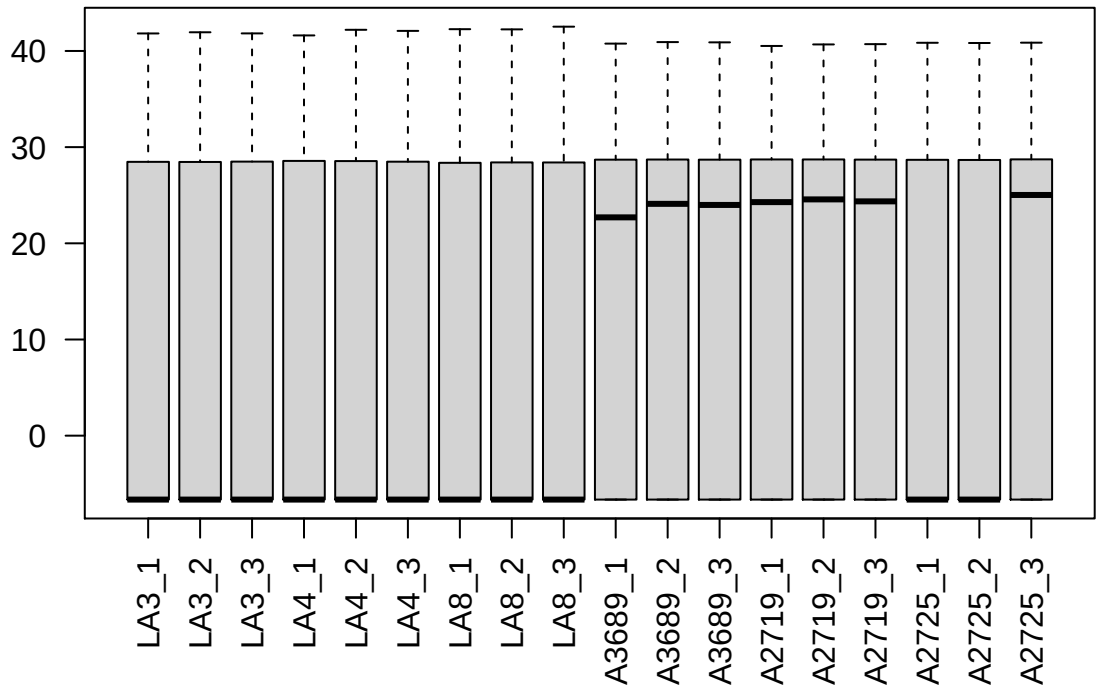
## 0.1 Replication: Left atrium AF vs. healthy

Data was downloaded from PXD006675. LFQ protein intensities were extracted using the file `PXD006675/txtAFibNewSearch/proteinGroups.txt`

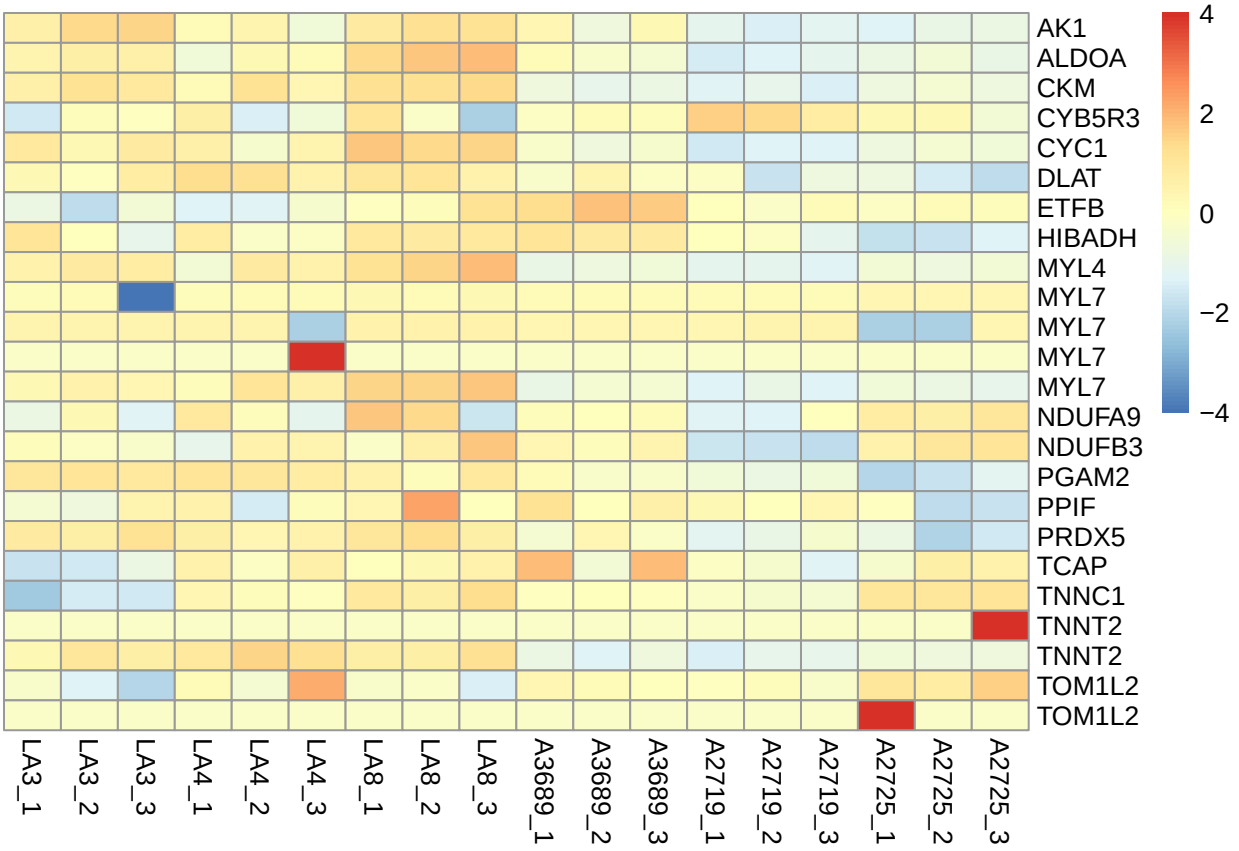
```
## [1] "Data column names:"
```

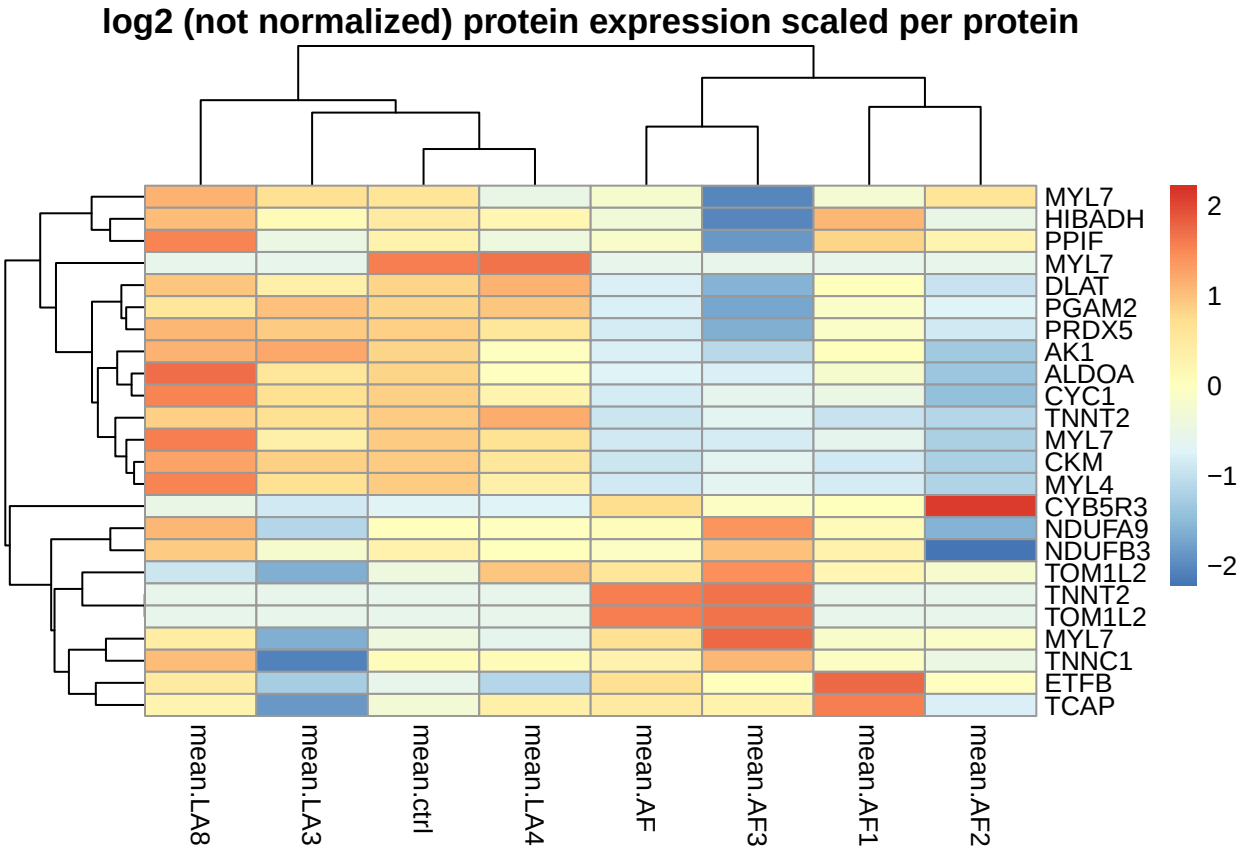
```
##  [1] "Protein.IDs"                "Protein.names"
##  [3] "Gene.names"                 "Majority.protein.IDs"
##  [5] "A3689"                      "A3689_161111143554"
##  [7] "A3689_161111164237"         "LA3"
##  [9] "LA3BoxCar1"                 "LA3BoxCar2"
## [11] "LA3BoxCar3"                 "LA3.frac1"
## [13] "LA3.frac2"                  "LA3.frac3"
## [15] "LA3.frac4"                  "LA3.frac5"
## [17] "LA3.frac6"                  "LA3.frac7"
## [19] "LA3.frac8"                  "LA4"
## [21] "LA4BoxCar1"                 "LA4BoxCar2"
## [23] "LA4BoxCar3"                 "LA4.frac1"
## [25] "LA4.frac2"                  "LA4.frac3"
## [27] "LA4.frac4"                  "LA4.frac5"
## [29] "LA4.frac6"                  "LA4.frac7"
## [31] "LA4.frac8"                  "LA8"
## [33] "LA8bisBoxCar1"              "LA8BoxCar1"
## [35] "LA8BoxCar3"                 "LA8combiBoxCar1"
## [37] "LA8.frac1"                  "LA8.frac2"
## [39] "LA8.frac3"                  "LA8.frac4"
## [41] "LA8.frac5"                  "LA8.frac6"
## [43] "LA8.frac7"                  "LA8.frac8"
## [45] "LCproto_A2719"              "LCproto_A2719_161111205623"
## [47] "LCproto_A2719_161111230316" "LCproto_A2725"
## [49] "LCproto_A2725_161112031716" "LCproto_A2725_161112052429"
```

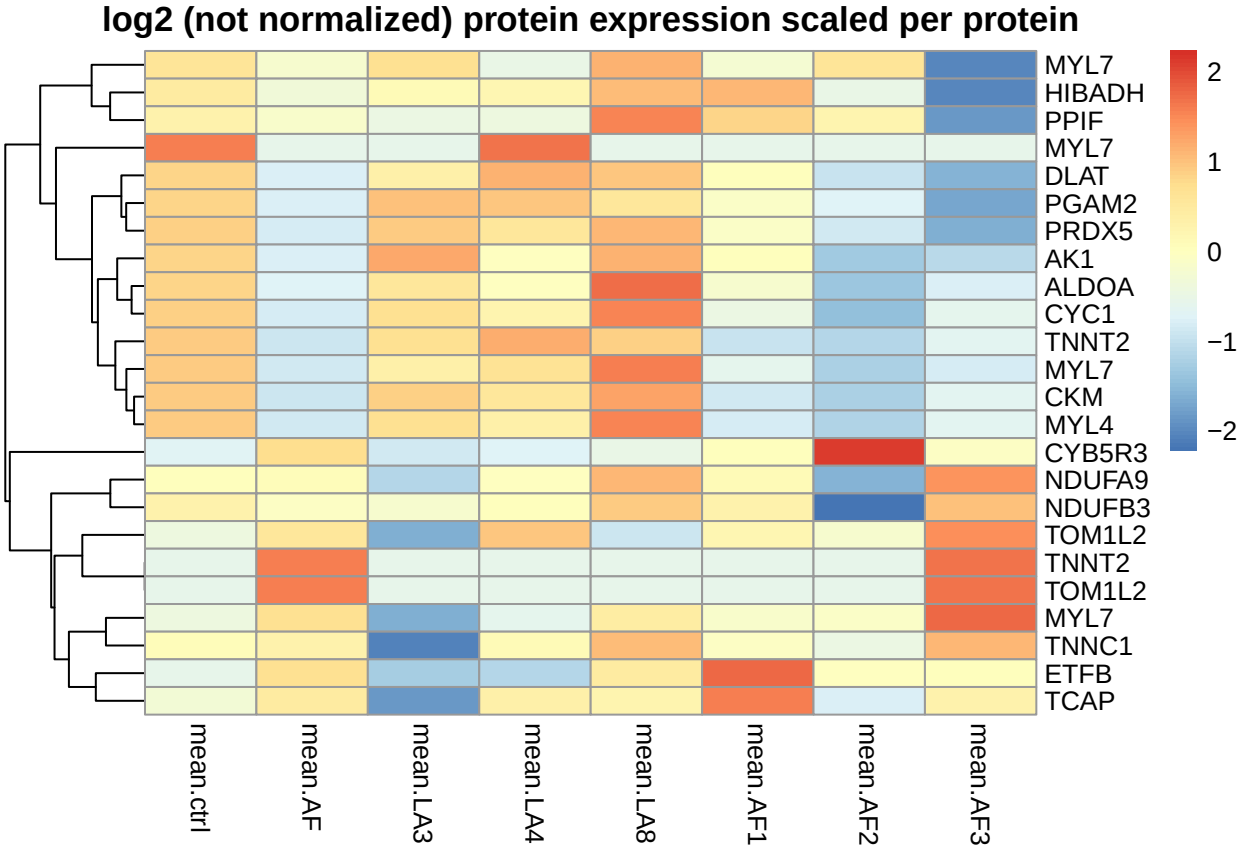
```
## [1] "without additional normalization:"
```



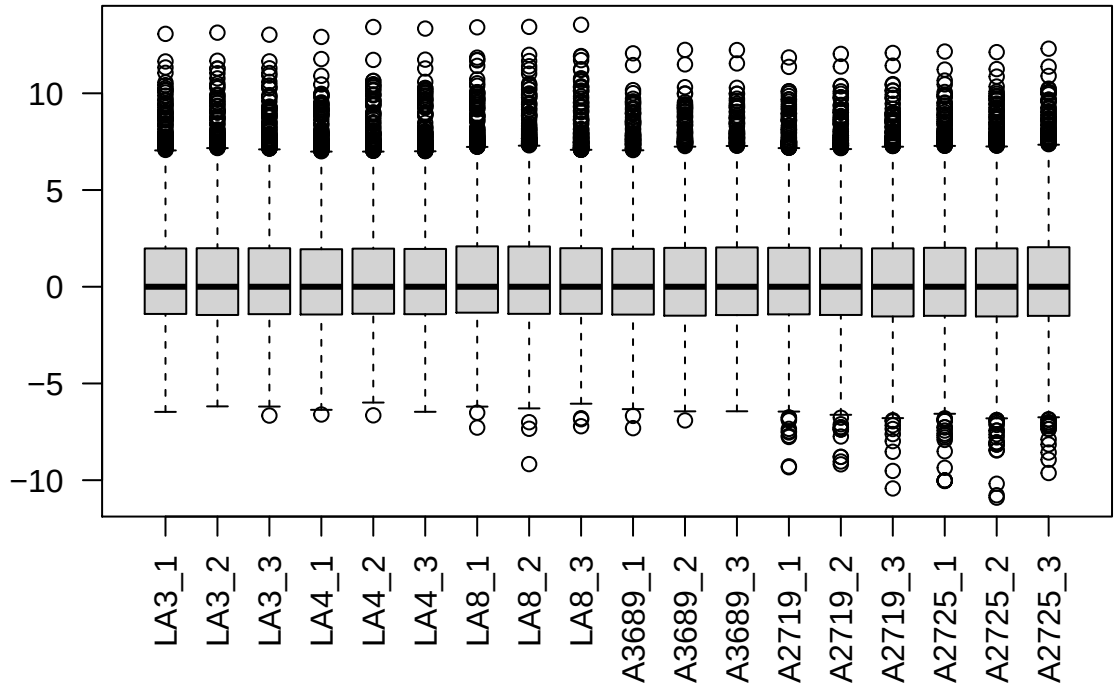

```
## [1] "Sample A2719 seems to have much more high LFQ intensities than all other samples."
```



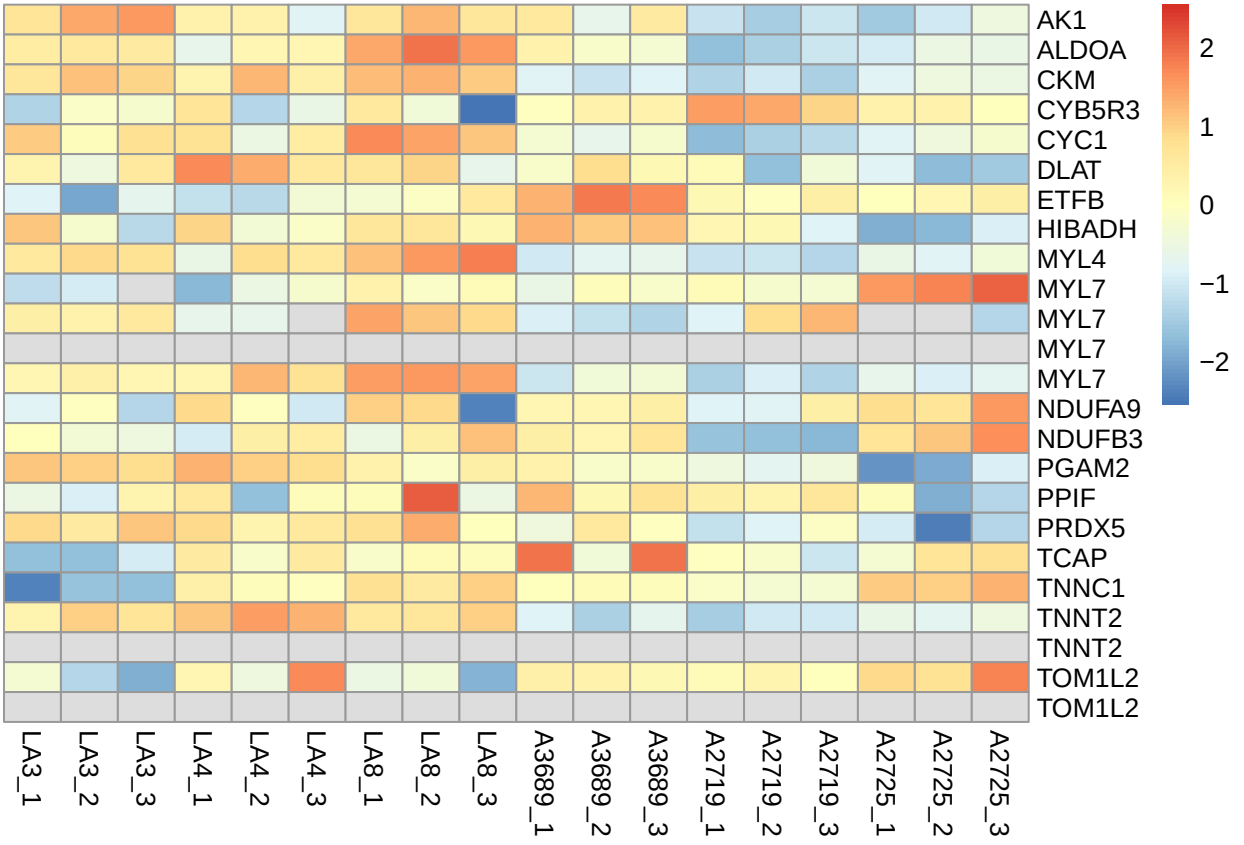

log2 (not normalized) protein expression scaled per protein
MYL7
HIBADH
PPIF
MYL7
DLAT
PGAM2
PRDX5
AK1
ALDOA
CYC1
TNNT2
MYL7
CKM
MYL4
CYB5R3
NDUFA9
NDUFB3
TOM1L2
TNNT2
TOM1L2
MYL7
TNNC1
ETFB
TCAP
mean.LA8
mean.LA3
mean.ctrl
mean.LA4
mean.AF
mean.AF3
mean.AF1
mean.AF2
2
1
0
−1
−2

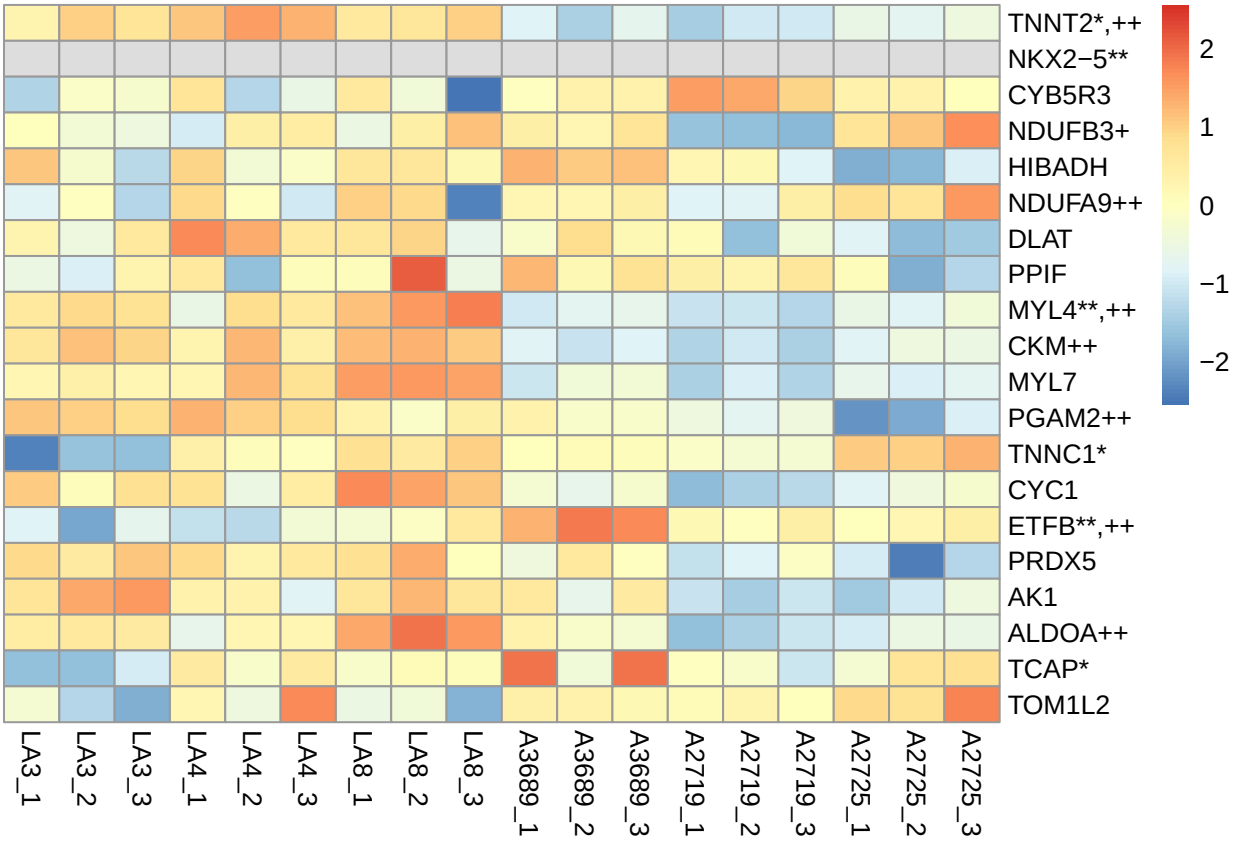

log2 (not normalized) protein expression scaled per protein
MYL7
HIBADH
PPIF
MYL7
DLAT
PGAM2
PRDX5
AK1
ALDOA
CYC1
TNNT2
MYL7
CKM
MYL4
CYB5R3
NDUFA9
NDUFB3
TOM1L2
TNNT2
TOM1L2
MYL7
TNNC1
ETFB
TCAP
mean.ctrl
mean.AF
mean.LA3
mean.LA4
mean.LA8
mean.AF1
mean.AF2
mean.AF3
2
1
0
−1
−2

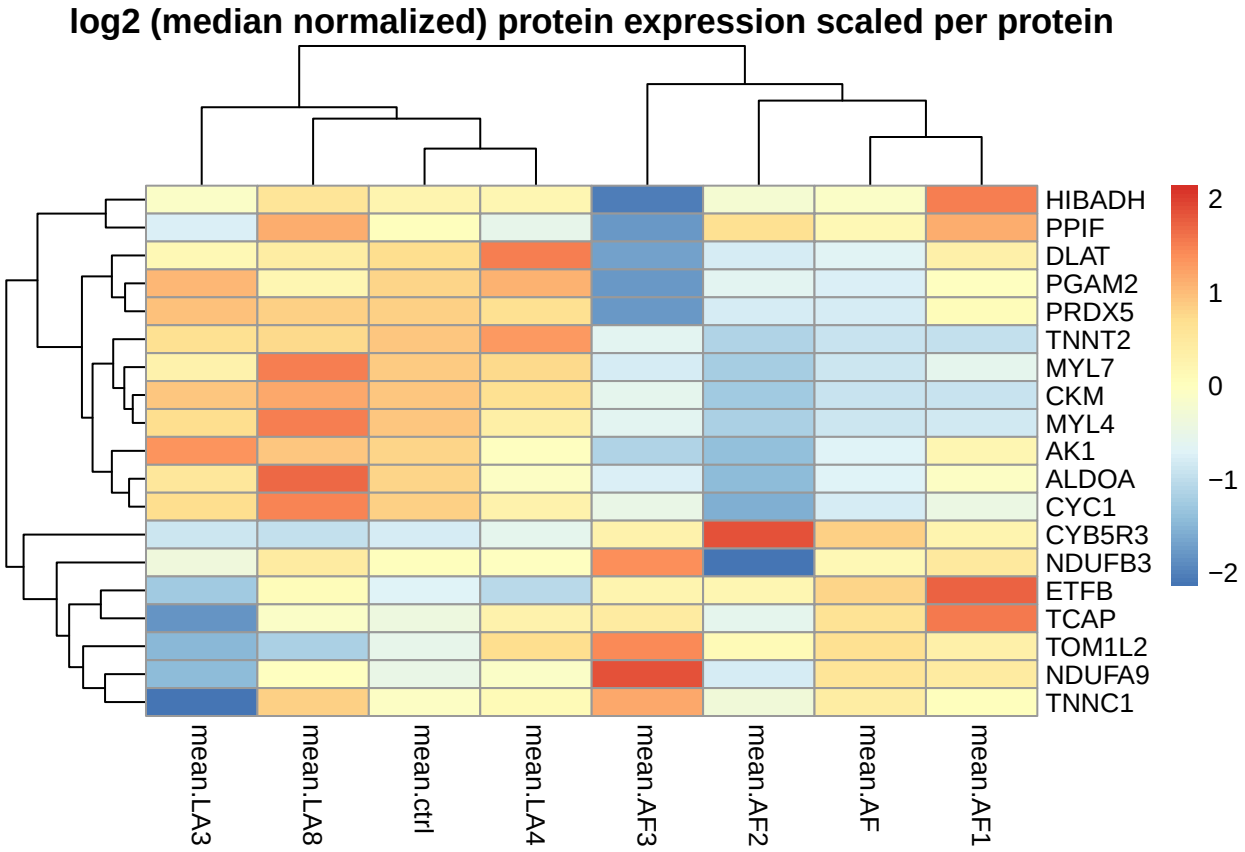
```
## [1] "Median normalization per sample:"
```

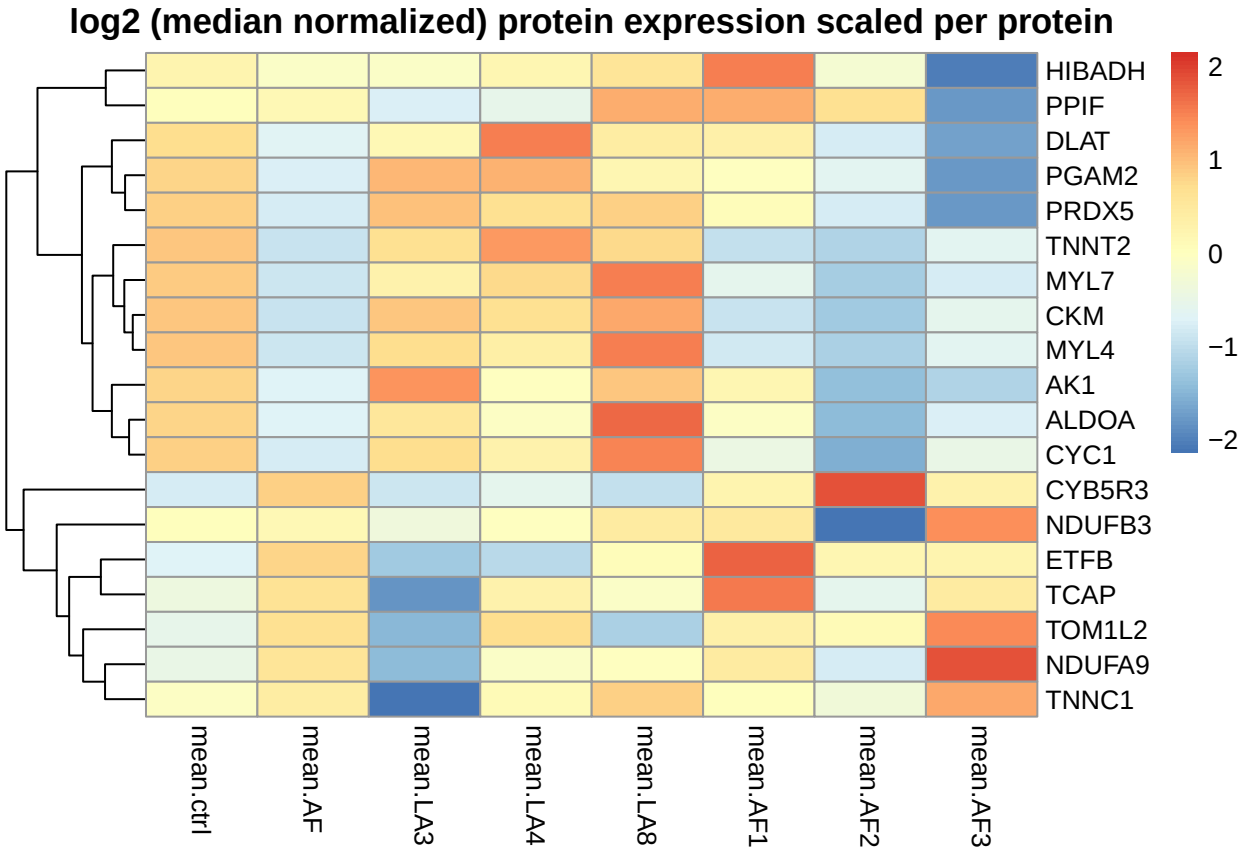



```
##  [1] "AK1:P00568_Q5T9B7_H0Y4J6_H0YID2_Q9Y6K8-2"
##  [2] "ALDOA:P04075_P04075-2_J3KPS3_H3BQN4_H3BPS8_H3BUH7_H3BR04_H3BMQ8_H3BU78_H3BR68"
##  [3] "CKM:P06732"
##  [4] "CYB5R3:P00387_P00387-2_P00387-3_B1AHF3"
##  [5] "CYC1:P08574"
##  [6] "DLAT:P10515_E9PEJ4_H0YDD4"
##  [7] "ETFB:P38117_P38117-2_M0QY67"
##  [8] "HIBADH:P31937_H7BZL2"
##  [9] "MYL4:P12829_I3L1K6_I3L532_I3L4B1_I3L3U1_I3L1R3"
## [10] "MYL7:C9JEG4"
## [11] "MYL7:H7BZE4_H7C3E3_H7C1B1"
## [12] "MYL7:H7C482"
## [13] "MYL7:Q01449_H7C243"
## [14] "NDUFA9:Q16795_F5GY40_H3BRM9_F5H0J3"
## [15] "NDUFB3:O43676_C9JKQ2"
## [16] "PGAM2:P15259"
## [17] "PPIF:P30405_R4GN99_H0Y548_P30405-2"
## [18] "PRDX5:P30044_P30044-2_P30044-3_P30044-4"
## [19] "TCAP:O15273_J3KT40"
## [20] "TNNC1:P63316_C9JDI3"
## [21] "TNNT2_HNTN1:P45379_E7EPW4_A0A0A0MRJ5_A0A0A0MRJ4_P45379-7_P45379-11_P45379-6_P45379-8_P45379-10_
## [22] "TNNT2:C9JDF8"
## [23] "TOM1L2:Q6ZVM7_Q6ZVM7-2_Q6ZVM7-3_B7Z2U2_Q6ZVM7-4_K7ENB0"
## [24] "TOM1L2:Q6ZVM7-5_F5H3S6"
```


AK1
ALDOA
CKM
CYB5R3
CYC1
DLAT
ETFB
HIBADH
MYL4
MYL7
MYL7
MYL7
MYL7
NDUFA9
NDUFB3
PGAM2
PPIF
PRDX5
TCAP
TNNC1
TNNT2
TNNT2
TOM1L2
TOM1L2
2
1
0
−1
−2
LA3_1
LA3_2
LA3_3
LA4_1
LA4_2
LA4_3
LA8_1
LA8_2
LA8_3
A3689_1
A3689_2
A3689_3
A2719_1
A2719_2
A2719_3
A2725_1
A2725_2
A2725_3


TNNT2*,++
NKX2−5**
CYB5R3
NDUFB3+
HIBADH
NDUFA9++
DLAT
PPIF
MYL4**,++
CKM++
MYL7
PGAM2++
TNNC1*
CYC1
ETFB**,++
PRDX5
AK1
ALDOA++
TCAP*
TOM1L2
2
1
0
−1
−2
LA3_1
LA3_2
LA3_3
LA4_1
LA4_2
LA4_3
LA8_1
LA8_2
LA8_3
A3689_1
A3689_2
A3689_3
A2719_1
A2719_2
A2719_3
A2725_1
A2725_2
A2725_3


log2 (median normalized) protein expression scaled per protein
HIBADH
PPIF
DLAT
PGAM2
PRDX5
TNNT2
MYL7
CKM
MYL4
AK1
ALDOA
CYC1
CYB5R3
NDUFB3
ETFB
TCAP
TOM1L2
NDUFA9
TNNC1
mean.LA3
mean.LA8
mean.ctrl
mean.LA4
mean.AF3
mean.AF2
mean.AF
mean.AF1
2
1
0
−1
−2

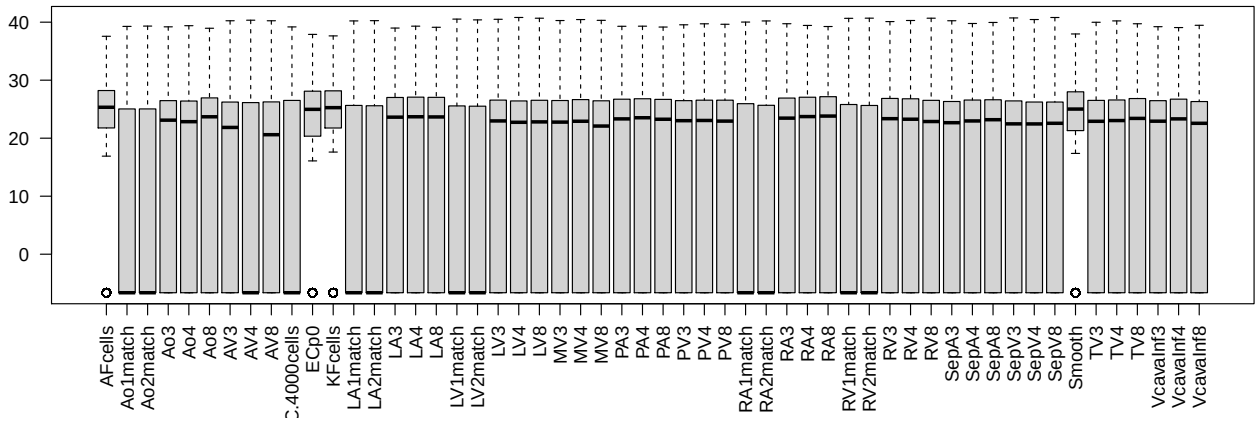

log2 (median normalized) protein expression scaled per protein
HIBADH
PPIF
DLAT
PGAM2
PRDX5
TNNT2
MYL7
CKM
MYL4
AK1
ALDOA
CYC1
CYB5R3
NDUFB3
ETFB
TCAP
TOM1L2
NDUFA9
TNNC1
mean.ctrl
mean.AF
mean.LA3
mean.LA4
mean.LA8
mean.AF1
mean.AF2
mean.AF3
2
1
0
−1
−2

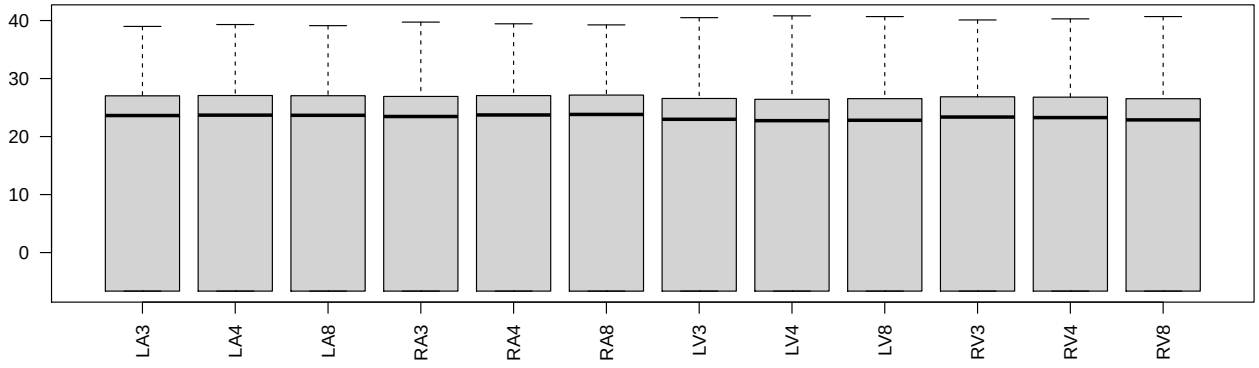
## 0.2 Human Heart Map (left and right atrium)

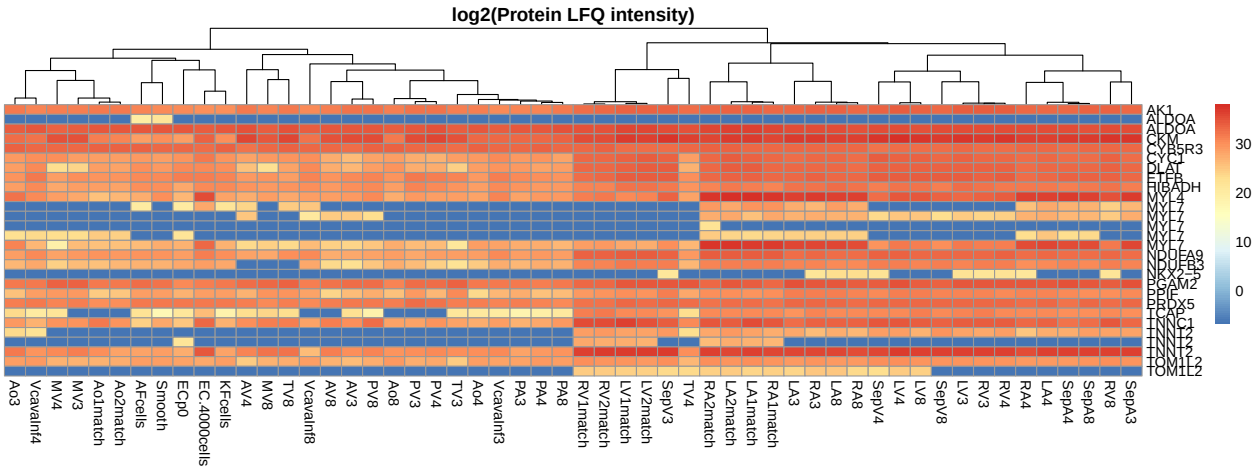
### 0.2.1 QC and genes of interest

```
## [1] "Usable samples:"

##  [1] "AFcells"      "Ao1match"     "Ao2match"     "Ao3"          "Ao4"
##  [6] "Ao8"          "AV3"          "AV4"          "AV8"          "EC.4000cells"
## [11] "ECp0"         "KFcells"      "LA1match"     "LA2match"     "LA3"
## [16] "LA4"          "LA8"          "LV1match"     "LV2match"     "LV3"
## [21] "LV4"          "LV8"          "MV3"          "MV4"          "MV8"
## [26] "PA3"          "PA4"          "PA8"          "PV3"          "PV4"
## [31] "PV8"          "RA1match"     "RA2match"     "RA3"          "RA4"
## [36] "RA8"          "RV1match"     "RV2match"     "RV3"          "RV4"
## [41] "RV8"          "SepA3"        "SepA4"        "SepA8"        "SepV3"
## [46] "SepV4"        "SepV8"        "Smooth"       "TV3"          "TV4"
## [51] "TV8"          "VcavaInf3"    "VcavaInf4"    "VcavaInf8"
```

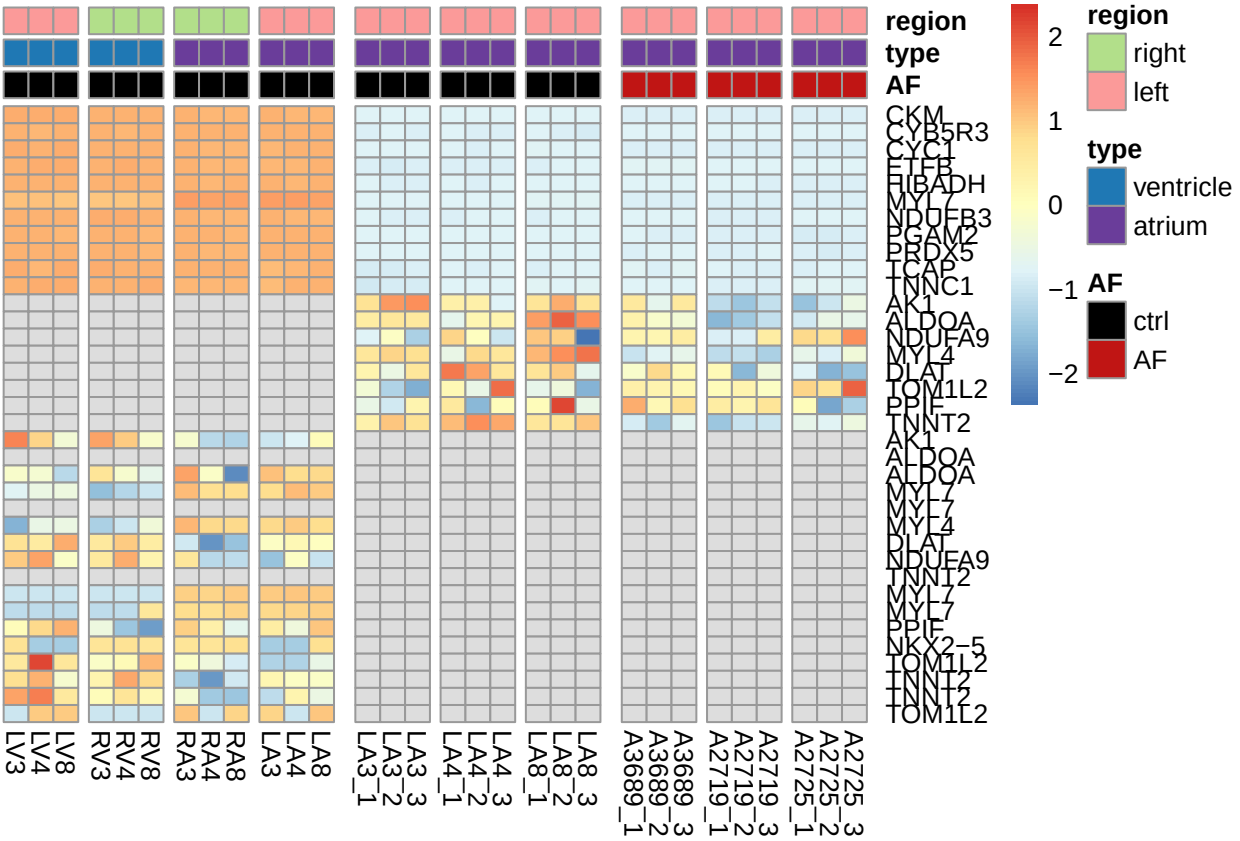





## 0.3 Comparison with AF case-ctrl data

Left atrial samples were measured with different measurement techniques!




## 0.4 GSEA on AFib data

### 0.4.1 Summary statistics

### 0.4.2 GSEA analysis

```
## [1] "GSEA with direction of effect (signed P-value):"
```

```
##            pathway         pval         padj         ES       NES size
```

```
## 1: NKX2-5_targets 6.96937e-05 0.0001469168 -0.783872 -2.197056   13
```

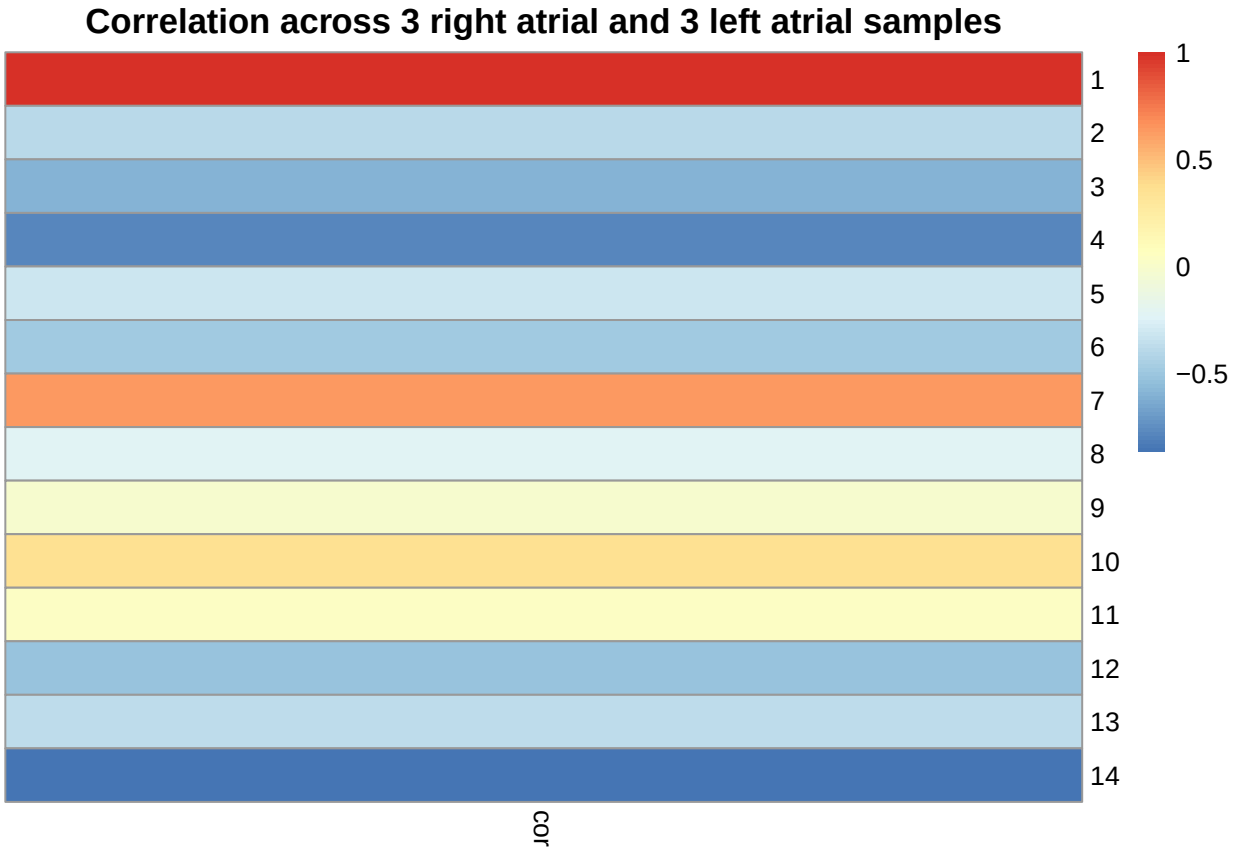
```
## [1] "GSEA with direction of effect (signed P-value, incl. FC cutoff):"
```

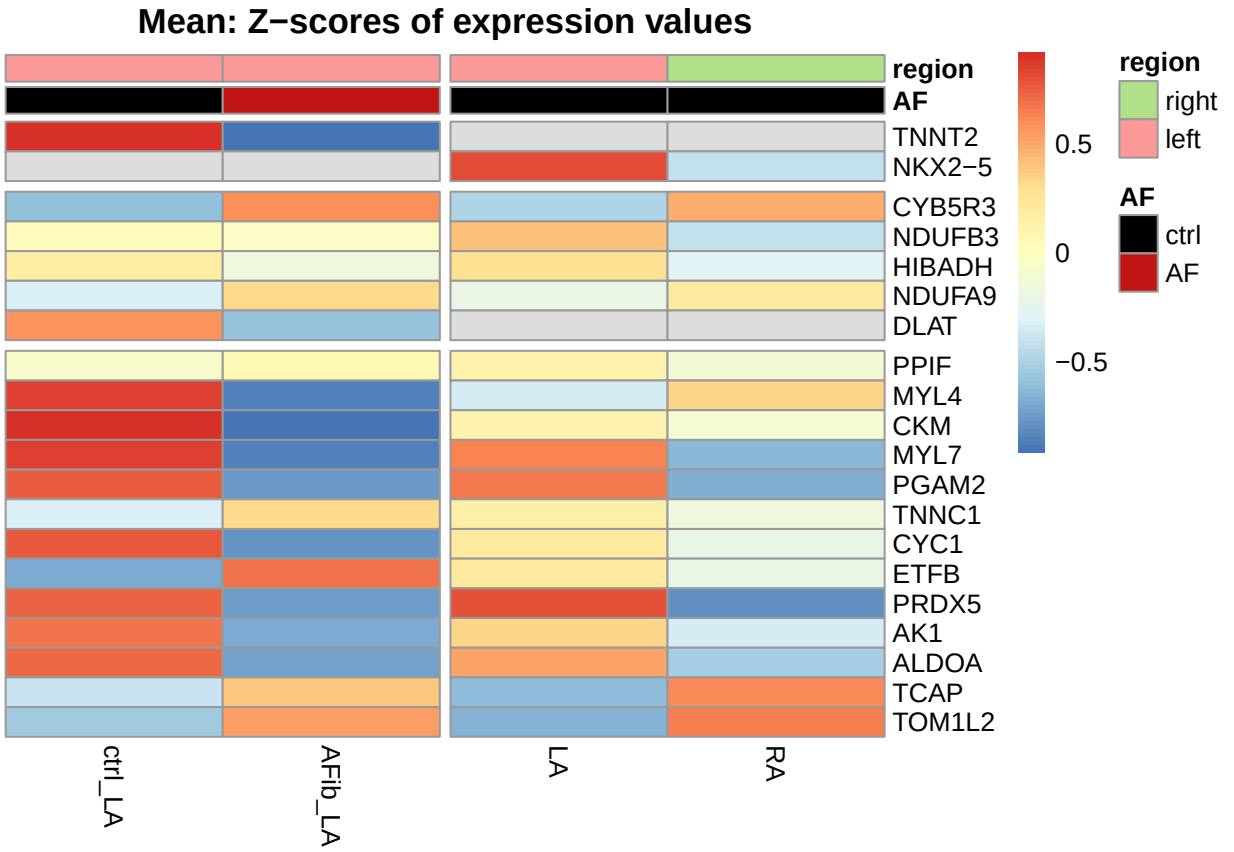
```
##                pathway         pval        padj         ES       NES size
## 1: Atrial_fibrillation 3.575131e-05 0.000109529 -0.5902873 -2.368059   23
```

```
## [1] "KEGG GSEA with direction of effect (signed P-value, incl. FC cutoff):"
```

```
##                                          pathway         pval        padj         ES
##  1:                                KEGG_RIBOSOME 1.219155e-05 0.001460638  0.4967743
##  2:         KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM 4.355590e-05 0.001460638 -0.4620744
##  3:              KEGG_CARDIAC_MUSCLE_CONTRACTION 4.372923e-05 0.001460638 -0.6062822
##  4:            KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS 4.832786e-05 0.001460638 -0.4408180
##  5:                      KEGG_PARKINSONS_DISEASE 6.171697e-05 0.001460638 -0.4825086
##  6:               KEGG_OXIDATIVE_PHOSPHORYLATION 6.239860e-05 0.001460638 -0.4523059
##  7:                     KEGG_ALZHEIMERS_DISEASE 6.835270e-05 0.001460638 -0.4068488
##  8:                    KEGG_HUNTINGTONS_DISEASE 7.105805e-05 0.001460638 -0.3437734
##  9:                 KEGG_DILATED_CARDIOMYOPATHY 8.504125e-05 0.001573263 -0.4900678
## 10:                              NKX2-5_targets 1.512310e-04 0.002543431 -0.7179327
## 11:               KEGG_ECM_RECEPTOR_INTERACTION 1.681732e-04 0.002592670 -0.4456353
## 12:   KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION 2.263859e-04 0.003221646  0.5228449
## 13:                KEGG_CITRATE_CYCLE_TCA_CYCLE 3.326680e-04 0.004395970 -0.5024848
## 14:                      KEGG_SULFUR_METABOLISM 5.759895e-04 0.007103870  0.8719487
## 15: KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION 1.846997e-03 0.021355904 -0.6382211
## 16:                  KEGG_FATTY_ACID_METABOLISM 5.379582e-03 0.058542506 -0.3829846
## 17:                KEGG_SMALL_CELL_LUNG_CANCER 5.729282e-03 0.058884289 -0.4214470
## 18:    KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION 8.295961e-03 0.080776465  0.3927033
## 19:                              KEGG_PROTEASOME 1.254447e-02 0.116036346  0.4240405
## 20:                              KEGG_PEROXISOME 1.850737e-02 0.155766209 -0.3464595
## 21:           KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY 1.880789e-02 0.155766209  0.5628262
##                                          pathway         pval        padj         ES
##           NES size
##  1:  2.179002   73
##  2: -2.213113   44
##  3: -2.921618   45
##  4: -2.241332   56
##  5: -2.703630   88
##  6: -2.537870   89
##  7: -2.336914  101
##  8: -2.001131  108
##  9: -2.319763   42
## 10: -2.391031   13
## 11: -2.098614   41
## 12:  1.987695   36
## 13: -2.132155   28
## 14:  1.858726    5
## 15: -2.064730   12
## 16: -1.742920   36
## 17: -1.788294   28
## 18:  1.622965   53
## 19:  1.622757   37
## 20: -1.576698   36
## 21:  1.636841   13
##           NES size
```

# 1 Overall summary




Mean: Z−scores of expression values
region
AF
TNNT2
NKX2−5
CYB5R3
NDUFB3
HIBADH
NDUFA9
DLAT
PPIF
MYL4
CKM
MYL7
PGAM2
TNNC1
CYC1
ETFB
PRDX5
AK1
ALDOA
TCAP
TOM1L2
ctrl_LA
AFib_LA
LA
RA
0.5
0
−0.5
region
right
left
AF
ctrl
AF