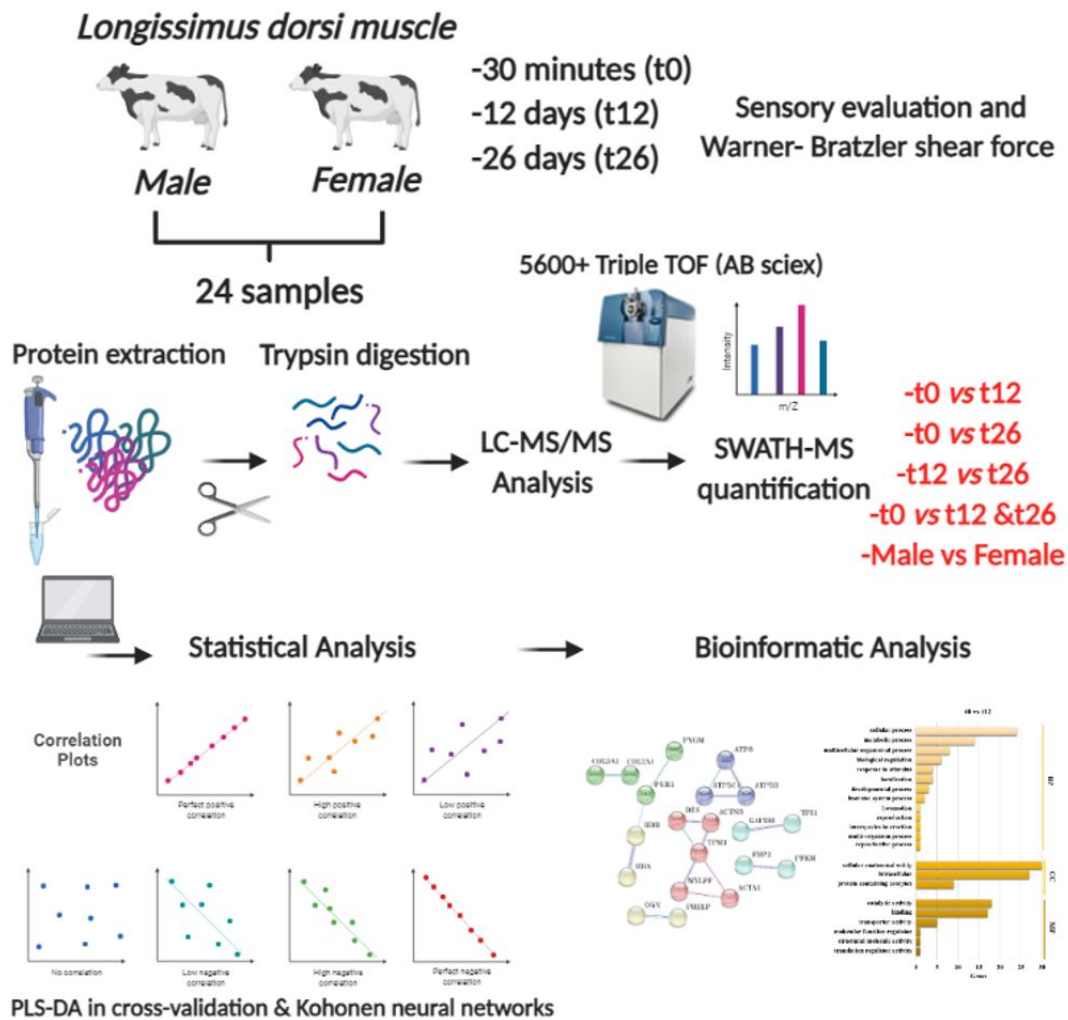


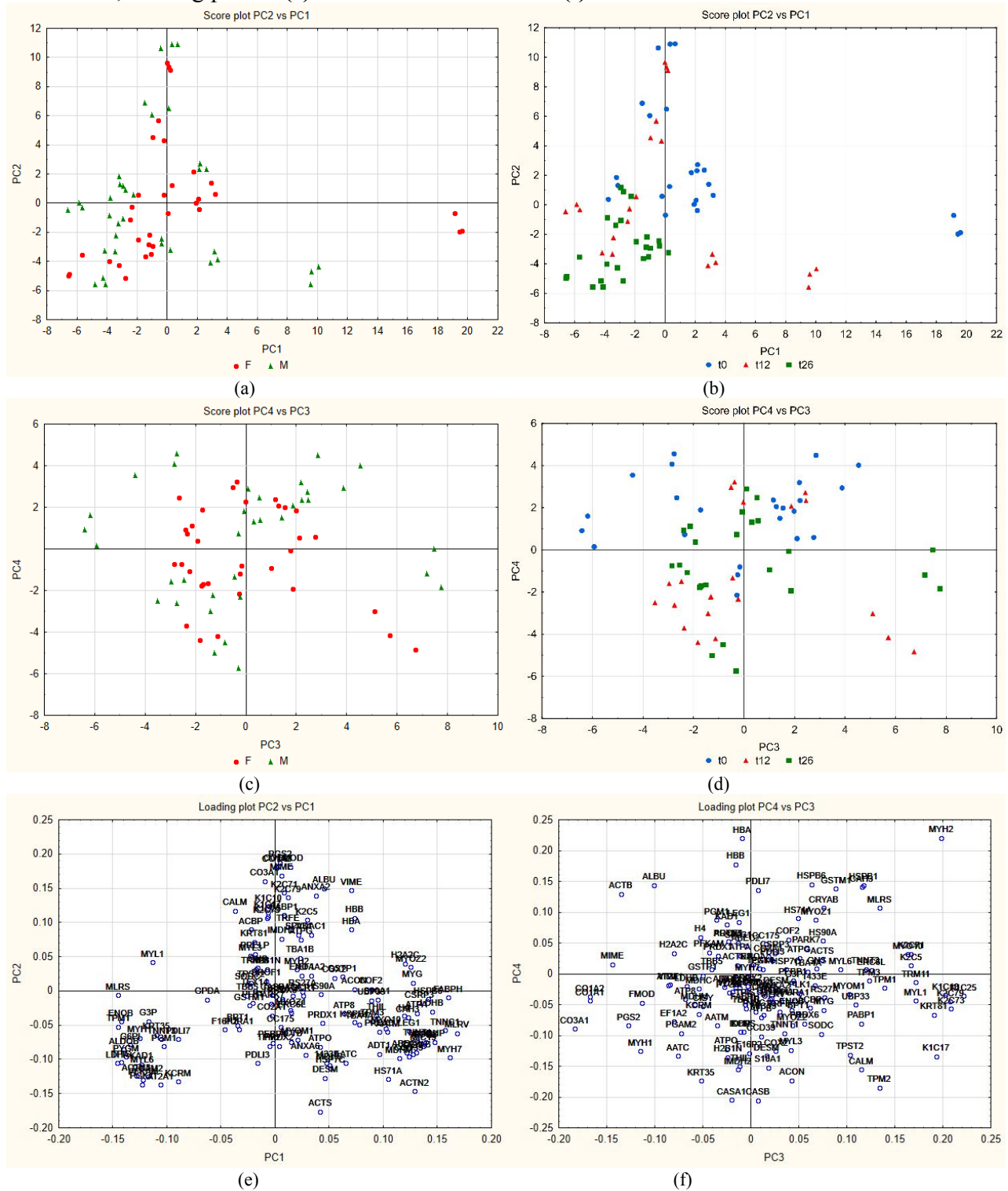
Supplementary Figure 1

Experimental workflow and overview of the gel-free proteomics, statistical and bioinformatics analyses. The figure was created with BioRender.com.



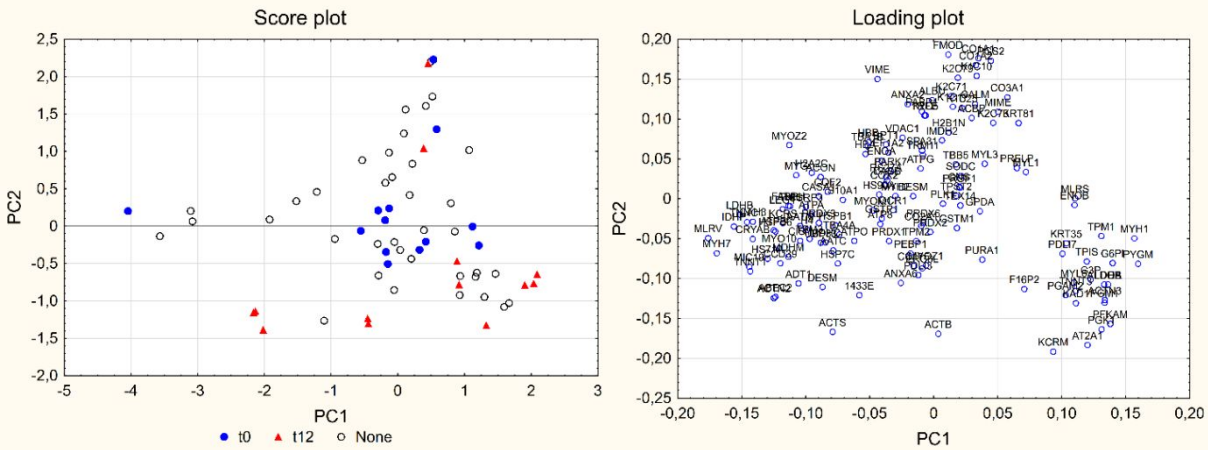
Supplementary Figure 2

Results of PCA carried out on the overall dataset consisting of 69 samples (24 t0 samples, 21 t12 samples and 24 t26 samples) described by 138 variables (protein signals): score plot of the first two PCs with the samples labelled according to **(a)** the gender and **(b)** the time of maturation; score plot of the PC3 and PC4 with the samples labelled according to **(c)** the gender and **(d)** the time of maturation; loading plot of **(e)** the first two PCs and of **(f)** PC3 and PC4.

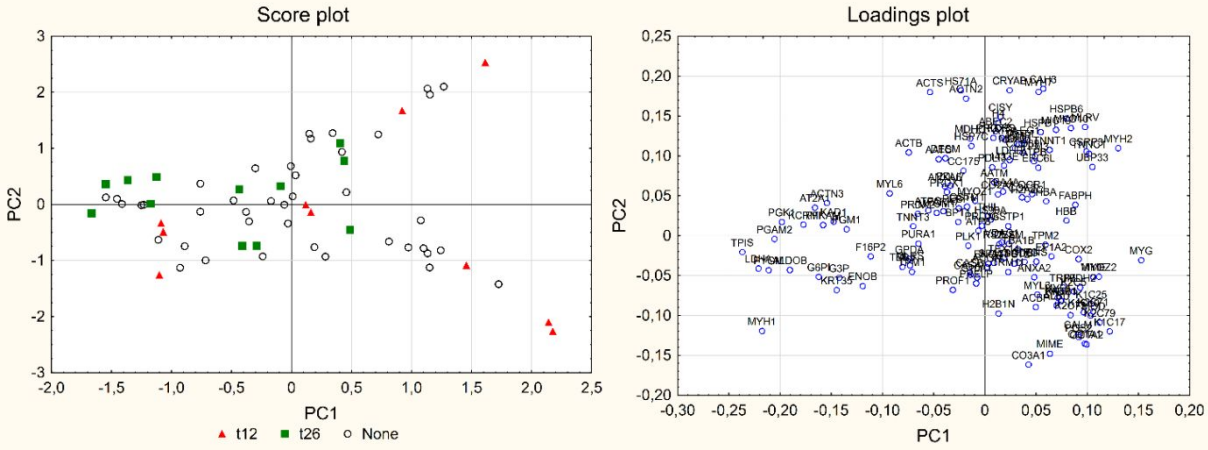


Supplementary Figure 3

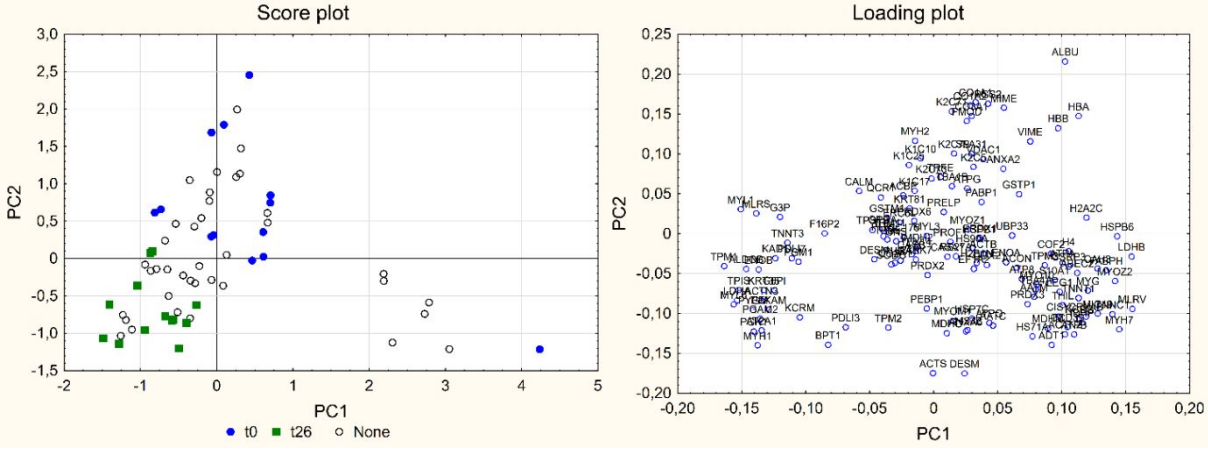
Results of PCA carried out on the weights of the neurons of the Kohonen's top map; score plot and loading plot of the first two PCs for: early **(a)**, late **(b)**, long **(c)**, general **(d)** aging. Neurons in the score plot are labelled according to the class of samples they contain; if the neurons do not contain samples, they are indicated as black circles.



(a)



(b)



(c)

Supplementary Figure 4

The protein-protein interaction networks as analysed by String software for proteins having altered abundance after (a) early, (b) late, (c) long, and (d) general ageing. A pink line indicates experimental evidence, while a light blue line indicates database evidence.

