Glycation Isotopic Labelling (GIL) with ^{13}C-reducing Sugars for Quantitative Analysis of Glycated Proteins in Human Plasma*

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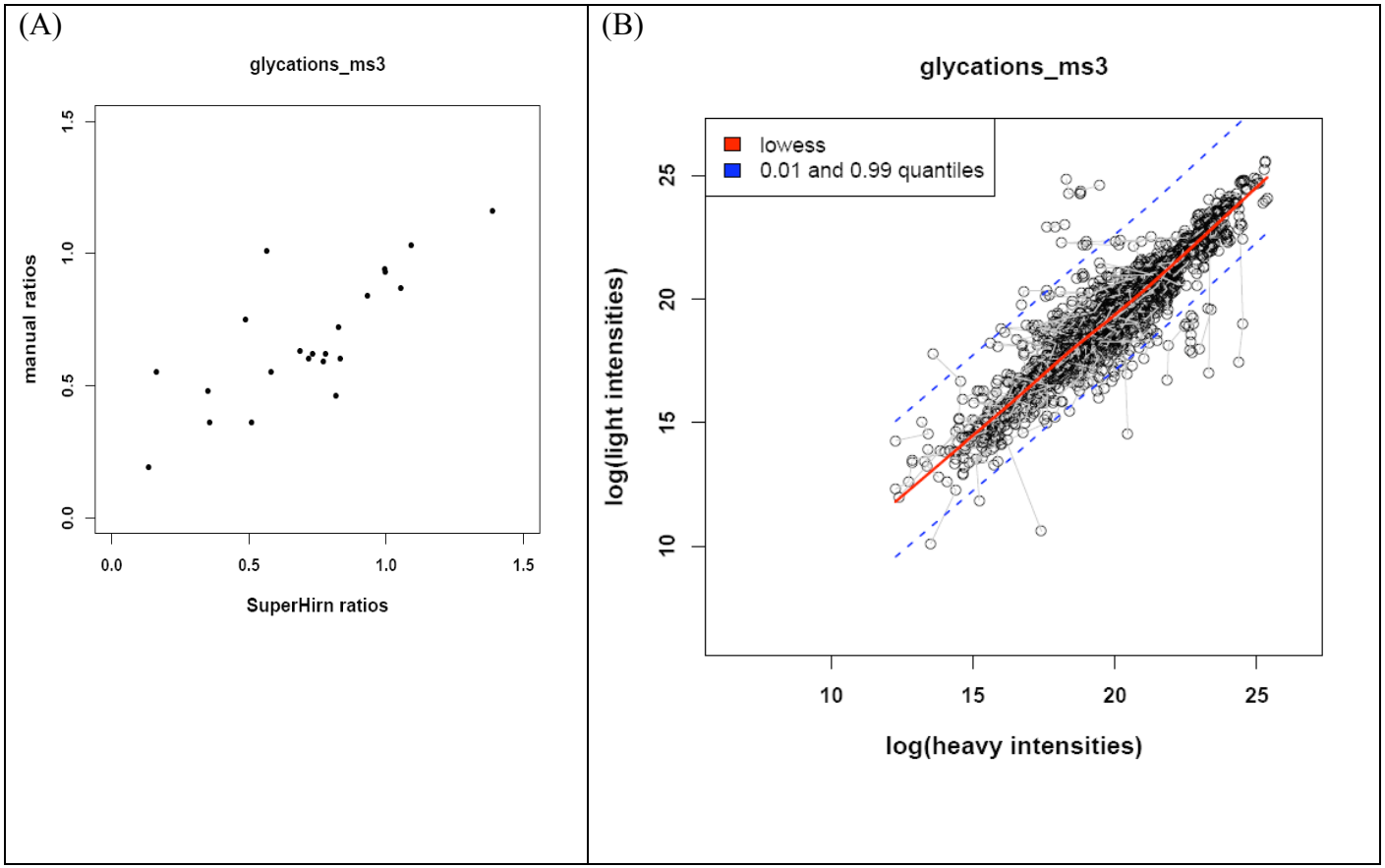
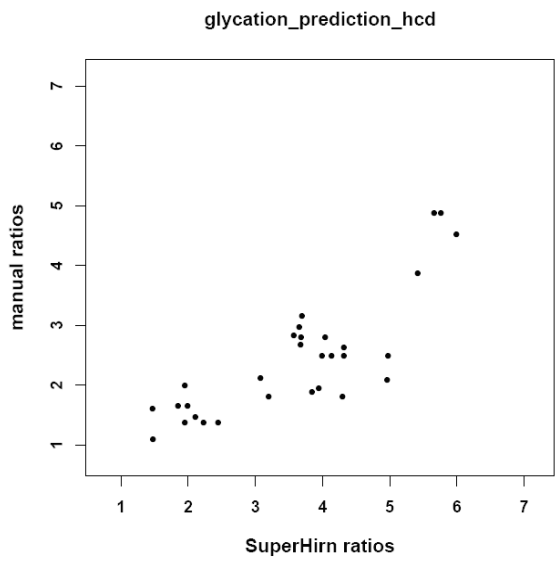
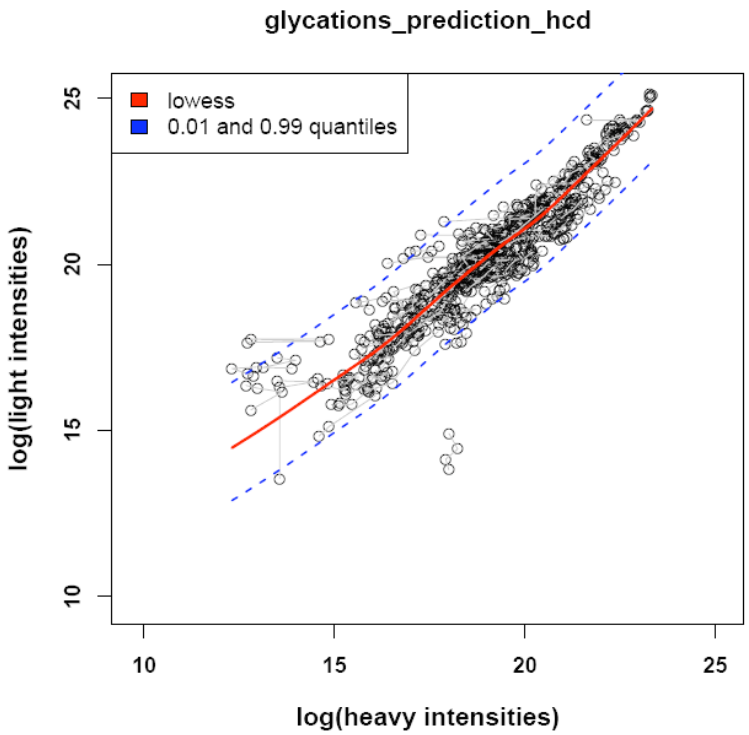
Supplementary Figure 1: Scatterplots obtained after application of SuperHirn for the experiments CID-MS3 assessing the real glycaemic state, HCD-MS2 for predictive analysis and CID-MS3 for predictive analysis. (A) Scatterplot for the SuperHirn and manually determined ratios between peak areas provided by the *in vivo* and *in vitro* labelled peptides for the experiment assessing the real glycaemic state. B) Scatterplot of the log-intensities of the light and heavy features, which can be detected in all 3 replicates. Replicates of the same features are connected by a light grey line. The regression lines show the lowest fit and the dashed lines above and below it indicate the 0.01 and 0.99 quantiles of the residues to the lowest fit.



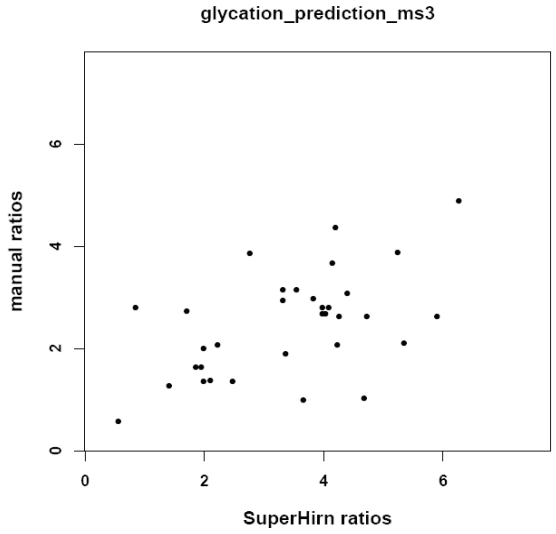
(A)


glycation_prediction_hcd
manual ratios
SuperHirn ratios
1
2
3
4
5
6
7

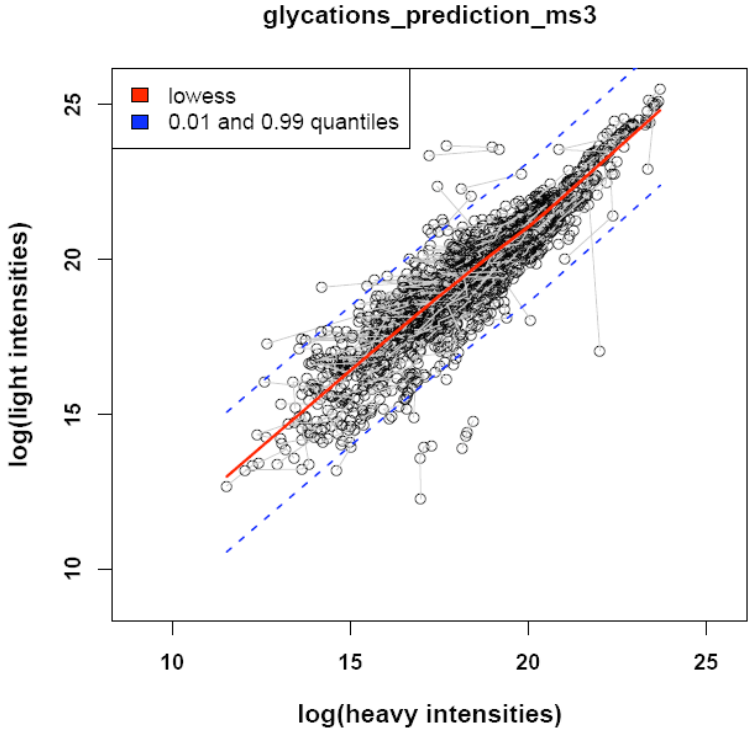
(B)


glycations_prediction_hcd
lowess
0.01 and 0.99 quantiles
log(light intensities)
log(heavy intensities)
10
15
20
25

(A)


glycation_prediction_ms3
manual ratios
SuperHirn ratios
0
2
4
6

(B)


glycations_prediction_ms3
lowess
0.01 and 0.99 quantiles
log(light intensities)
log(heavy intensities)
10
15
20
25

Supplementary Figure 2: Approach used for predictive analysis of the glycation site state as response to glucose stimuli.