

Proteome- and Transcriptome-Driven Reconstruction of the Human Myocyte Metabolic Network and Its Use for Identification of Markers for Diabetes

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Within the subject characteristic data that we received and reported in the originally published version of Table 1, the ages were unfortunately slightly wrong (a deviance of 1, 3, 3, 6, 1, and 1 year, respectively). This was due to missing information about the sampling dates at the time of writing the paper. We have now received this information and have therefore updated Table 1 with the correct values. The ages did not influence our analysis or results in any way. The corrected table is shown below, and the article has been corrected online as well.

The authors regret this error.

Table 1. Characteristics of the Six Subjects

	Female 1	Female 2	Female 3	Male 1	Male 2	Male 3
Age (years)	49	48	63	55	50	50
Body mass index (kg/m ²)	23.0	24.0	24.8	23.7	23.9	24.4
Plasma glucose (mmol/l)	4.9	5.0	5.5	5.6	6.4	4.9
Plasma insulin (pmol/l)	25	17	36	26	24	20
HOMA-IR	0.47	0.38 ^a	0.69	0.5	0.48	0.38
Plasma total cholesterol (mmol/l)	5.0	6.2	5.4	4.3	5.0	6.8
Plasma HDL cholesterol (mmol/l)	2.0	3.0	1.7	1.0	1.3	2.0
Plasma LDL cholesterol (mmol/l)	2.7	3.0	3.1	2.7	3.2	4.2
Plasma triglyceride (mmol/l)	1.16	0.72	0.97	1.20	1.38	1.40
Sequencing depth (M pair-end reads)	48.0	84.9	62.6	45.8	68.9	49.5

Phenotypic characteristics, selected plasma levels, and sequencing depth for the six samples.

^aThe minimum allowed input (20 pmol/l) for plasma insulin was used for HOMA-IR calculation.