**Table S4:** *Correlation between DNA methylation of cg17901584 and cg23011663 and phenotypes representing glucose metabolism in a pooled cohort of ANDIS and ANDiU (n=361).*

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | **TargetID** | **Gene** | **R** | **HbA1c p-value** | **HOMA2-B p-value** | **HOMA2-IR p-value** |
| **Model 1 (all variables)** | cg17901584 | *DHCR24* | 0.082 | 0.018\* | 0.173 | 0.003\* |
| cg23011663 | *ARIH2* | 0.063 | 0.338 | 0.698 | 0.436 |
| **Model 2 (HbA1c)** | cg17901584 | *DHCR24* | 0.058 | 0.003\* |  |  |
| cg23011663 | *ARIH2* | 0.058 | 0.591 |  |  |
| **Model 3 (HOMA2-B)** | cg17901584 | *DHCR24* | 0.030 |  | 0.165 |  |
| cg23011663 | *ARIH2* | 0.058 |  | 0.753 |  |
| **Model 4 (HOMA2-IR)** | cg17901584 | *DHCR24* | 0.064 |  |  | 3e-04\* |
| cg23011663 | *ARIH2* | 0.061 |  |  | 0.316 |

Linear regression was performed on the sites cg17901584 and cg23011663 in order to assess whether DNA methylation of these sites identified to be associated with statin therapy, are further associated with phenotypes representing glucose metabolism. For this analysis, the *ANDIS discovery* and *ANDiU replication cohort* were pooled into one cohort (n=361) to increase power. We considered HbA1c, HOMA2-B and HOMA2-IR as indicators of glucose metabolism. Due to possible dependency between the variables, we conducted 1 model containing all variables in question (Model 1), and one model only including HbA1c (Model 2), one only including HOMA2-B (Model 3) and one only including HOMA2-IR (Model 4), to ascertain whether observed associations are influenced by the other variables. For models including HOMA2, we could only use 318 patients due to lack of HOMA2 baseline measurements. All regression analyses were further adjusted for age, sex and statin therapy and p<0.05 was considered significant. Only HbA1c and HOMA2-IR show a significant association with methylation on cg17901584, both in the single models and the combined model.