Description of Additional Supplementary Files

Supplementary Data 1. List of non-genomic molecular traits measured along with list of RNA deployed to conduct MBH

Supplementary Data 2. GGM. Association statistics and residuals were computed using the linear model "lm(OMICS ~ AGE + SEX + BMI + DIAB + genoPC1 + genoPC2 + genoPC3 + somaPC1 + somaPC2 + somaPC3)". Platform-wise Bonferroni significant correlations (p-value < 0.05 / (NPLAT*(NPLAT-1)/2)), where NPLAT represents the number of traits measured on the respective platform, were retained

Supplementary Data 3. Correlation levels of statistically significant MBH. Spearman correlation coefficients between unscaled raw omics data were computed. Platform-pairwise Bonferroni significance cutoffs (p < 0.05 / (nPLTA1 * nPLAT2 / 2)) were obtained after cross-platform correlation.

Supplementary Data 4. Associations between gene SNPs and methylation levels (meQTL's). Expression data was log-scaled, with all values off-set by the smallest occurring value in the dataset in order to avoid taking the log of zero, and z-scored. Methylation d(CpG) were b-values. The following linear model was used to compute the associations: meQTL: lm(CpG ~ SNP + AGE + SEX + BMI + DIAB + genoPC1 + genoPC2 + genoPC3). A significance cut-off of p-value <5x10-8 was used.

Supplementary Data 5. Associations between methylation levels and mRNA (eQTM's). Expression data was log-scaled, with all values off-set by the smallest occurring value in the dataset in order to avoid taking the log of zero, and z-scored. Methylation d(CpG) were *b*-values. The following linear model was used to compute the associations: eQTM: lm(transcriptomics ~ *CpG* + *SNP* + *AGE* + *SEX* + *BMI* + *DIAB* + *genoPC1* + *genoPC2* + *genoPC3*). A significance cut-off of *p*-value <$5x10^{-8}$ was used.

Supplementary Data 6. Associations between gene SNPs and mRNA (eQTL's). Expression data was log-scaled, with all values off-set by the smallest occurring value in the dataset in order to avoid taking the log of zero, and z-scored. The following linear model was used to compute the associations: eQTL: lm(transcriptomics ~ *SNP* + *AGE* + *SEX* + *BMI* + *DIAB* + *genoPC1* + *genoPC2* + *genoPC3*)

Supplementary Data 7. Multiomics GWAS. Omicsdata was inverse-normal scaled and residual were computed using the linear model "lm(Omicsdata ~ SEX + AGE + BMI + DIAB + genoPC1 + genoPC2 + genoPC3 + somaPC1 + somaPC2 + somaPC3)". After QC, excluding non-autosomal SNPs, MAF<5%, HWE pvalue<10-6, or genotyping rate <98%18, 1,221,345 SNPs for 353 samples were available

Supplementary Data 8. Multiomics EWAS. Residuals of methylation beta values (CpG) were computed using the linear model "lm (CpG ~ *AGE* + *SEX* + *BMI* + *DIAB* + *Gran* + *NK* + *CD4T* + *CD8T* + *Mono* + *Bcell* + *genoPC1* + *genoPC2* + *genoPC3*)" and then z-scored. Saliva and urine metabolites were first normalized by saliva and urine osmolality, respectively. All omics variables were then inverse normal-scaled and

residuals computed using the linear model "lm (Omicsdata ~ *AGE* + *SEX* + *BMI* + *DIAB* + genoPC1 + genoPC2 + genoPC3)" and then z-scored. Association statistics were then computed using the linear model "lm(CpG_residual ~ Omicsdata_residual)". Associations reaching an ad hoc significance level of $5x10^{-8}$ were retained. CpG sites were annotated for gene names and CpG position relative to the genes using the Illumina provided HumanMethylation 450k annotation file.

Supplementary Data 9. Multiomics TWAS. RNA expression data with less than 100 valid data points or median expression levels below 1 TPM were removed. Expression data was log-scaled, with all values off-set by the smallest occurring value in the dataset in order to avoid taking the log of zero, and z-scored. Saliva and urine metabolites were normalized by saliva osmolality and urine creatinine obtained from the respective platform, respectively. The comicsdata was then inverse-normal scaled. Metabolites and then samples with more than 50% missing values were removed. Association statistics were then computed using the linear model "lm(OMICS ~ transcriptomics + *AGE* + *SEX* + *BMI* + *DIAB* + *genoPC1* + *genoPC2* + *genoPC3* + *CD8* + *CD4* + *NK* + *Bcell* + *Mono* + *Gran* + *Eos*)". Associations reaching an ad hoc significance level of $5x10^{-8}$ were retained.

Supplementary Data 10. Correlation levels of molecules measured on both SOMA and OLINK. Spearman correlation coefficients between unscaled raw omics data were computed. Platform-pairwise Bonferroni significance cutoffs ($p < 0.05 / (nPLTA1 * nPLAT2 / 2)$) were obtained after cross-platform correlation.

Supplementary Data 11. Molecules assocaietd with AGE. Association statistics were computed using the linear model "lm(OMICS ~ *AGE* + *SEX* + *BMI* + *DIAB* + *genoPC1* + *genoPC2* + *genoPC3*)". Associations reaching an ad hoc significance level of $5x10^{-8}$ were retained.

Supplementary Data 12. Molecules assocaietd with SEX. Association statistics were computed using the linear model "lm(OMICS ~ SEX + AGE + BMI + DIAB + genoPC1 + genoPC2 + genoPC3)". Associations reaching an ad hoc significance level of 5x10-8 were retained.

Supplementary Data 13. Molecules assocaietd with BMI. Association statistics were computed using the linear model "lm(OMICS ~ BMI + SEX + AGE + DIAB + genoPC1 + genoPC2 +)". Associations reaching an ad hoc significance level of $5x10^{-8}$ were retained.

Supplementary Data 14. Molecules assocaietd with T2D. Association statistics were computed using the linear model "lm(OMICS ~ DIAB + BMI + SEX + AGE + genoPC1 + genoPC2 + genoPC3)". Associations reaching an ad hoc significance level of $5x10^{-8}$ were retained.

Supplementary Data 15. The gene transcripts associated with CXCL11 and CXCL10 overlap with molecules involved in responses to viral infection

Supplementary Data 16. List of metabolic and proteinlist of metabolic and protein signatures defining T2D subgroups, detected in our previous study, and overlapping with our multiomics dataset

Supplementary Data 17. List of molecules forming multiomics MARD cluster

Supplementary Data 18. List of molecules forming multiomics MOD cluster

Supplementary Data 19. List of molecules forming multiomics SIRD cluster

Supplementary Data 20. List of molecules forming multiomics SIDD cluster