Table S5. Genetic and residual correlations between MetS traits in the ARIC population among unrelated individuals based on simultaneous analysis of all traits.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | BMI | WHR | GLU | INS | TG | HDL | SBP |
| BMI |  | 0.90 (0.16)\* | 0.18 (0.25) | 0.61 (0.19)\* | 0.30 (0.20) | -0.23 (0.24) | 0.13 (0.19) |
| WHR | 0.43 (0.04)\* |  | 0.16 (0.25) | 0.46 (0.22) | 0.37 (0.19) | -0.14 (0.25) | 0.18 (0.19) |
| GLU | 0.25 (0.04)\* | 0.17 (0.04)\* |  | 0.40 (0.25) | 0.24 (0.23) | -0.24 (0.27) | 0.04 (0.21) |
| INS | 0.50 (0.03)\* | 0.38 (0.04)\* | 0.35 (0.04)\* |  | 0.32 (0.22) | -0.34 (0.26) | 0.15 (0.21) |
| TG | 0.30 (0.04)\* | 0.32 (0.04)\* | 0.18 (0.04)\* | 0.42 (0.04)\* |  | -0.61 (0.16)\* | 0.06 (0.18) |
| HDL | -0.34 (0.04)\* | -0.34 (0.04)\* | -0.14 (0.04)\* | -0.50 (0.03)\* |  |  | -0.02 (0.21) |
| SBP | 0.26 (0.05)\* | 0.17 (0.05)\* | 0.18 (0.05)\* | 0.23 (0.05)\* | 0.20 (0.05)\* | -0.05 (0.05)\* |  |

Mean and standard error of the Pearson correlation coefficient for genetic correlations (upper triangle) and residual correlations (lower triangle). An asterisk indicates significance with p<0.05 adjusted for 21 hypotheses using the two-tailed hypothesis test and normal distribution of the Fisher transformed correlation coefficient.