**Table S3. Variance contributions of *PIK3CA-KCNMB3* variants and their interaction with dietary n-3: n-6 PUFA ratio for HOMA-IR in GOLDN1**

|  |  |  |
| --- | --- | --- |
| SNPs | Main genetic effect on HOMA-IR, % | Interaction with dietary n-3: n-6 PUFA ratio on HOMA-IR, % |
| rs3975506 | 0.30 | 0.14 |
| rs4855094 | 0.03 | <0.01 |
| rs6443624 | 0.30 | 0.07 |
| rs2677760 | 1.14 | 0.39 |
| rs2677764 | 0.04 | 0.03 |
| rs7645550 | 0.41 | 0.95 |
| rs1170672 | 0.19 | <0.01 |
| rs1183319 | 0.25 | 1.02 |
| rs7642066 | <0.01 | 0.19 |

1 R software (version 2.15.0) GWAF package was used in the estimation of variance contribution. Among these nine SNPs, six independent SNPs (rs3975506, rs2677760, rs2677764, rs1170672, rs1183319, and rs7642066), with r2 < 0.20, were selected to estimate the total portion of HOMA-IR variation explained by the *PIK3CA-KCNMB3* variants and their interactions with diet. Total portion of HOMA-IR variation explained by these six independent SNPs was 1.91%, and explained by the interaction of these SNPs with dietary n-3: n-6 PUFA ratio was 1.78%. The statistical model was adjusted for age, sex, waist circumference, alcohol drinking, smoking status, physical activity, type 2 diabetes, study center and family relationships.