|  |  |  |  |
| --- | --- | --- | --- |
| **Variant 1 (*T2D-joint* set)** | **Variant 2 (*genome set*)** | **Interaction effect (OR)** | **Interaction p-value** |
| **Variant ID** | **Chr** | **Nearest gene** | **Variant ID\*** | **Chr** | **Nearest gene** |
| rs184509201 | 10 | *TCF7L2* | rs10885397 | 10 | *TCF7L2* | 1.55 | 2.24 x 10-9 |
| rs1948770 | 5 | *LINC02112* | rs4887198 | 15 | *AGBL1* | 1.20 | 2.40 x 10-9 |
| rs73025299 | 11 | *KCNJ5* | rs1919295 | 11 | *SPON1* | 1.23 | 7.25 x 10-9 |
| rs73025299 | 11 | *KCNJ5* | rs4757219 | 11 | *SPON1* | 1.23 | 8.37 x 10-9 |
| rs73025299 | 11 | *KCNJ5* | rs4756773 | 11 | *SPON1* | 1.23 | 9.21 x 10-9 |
| [rs11257655](https://www.ncbi.nlm.nih.gov/snp/rs11257655) | 10 | *CDC123/CAMK1D* | rs4635275 | 14 | *C14orf177* | 1.12 | 1.32 x 10-8 |
| [rs11257655](https://www.ncbi.nlm.nih.gov/snp/rs11257655) | 10 | *CDC123/CAMK1D* | rs75416827 | 14 | *C14orf177* | 1.12 | 1.32 x 10-8 |
| [rs11257655](https://www.ncbi.nlm.nih.gov/snp/rs11257655) | 10 | *CDC123/CAMK1D* | rs11160481 | 14 | *C14orf177* | 1.12 | 1.41 x 10-8 |
| [rs11257655](https://www.ncbi.nlm.nih.gov/snp/rs11257655) | 10 | *CDC123/CAMK1D* | rs75389111 | 14 | *C14orf177* | 1.12 | 1.49 x 10-8 |
| rs2197973 | 12 | *USP44* | rs7231810 | 18 | *L3MBTL4* | 1.10 | 1.57 x 10-8 |

 **Supplemental Table 4: Summary of the interactions between variants in the *T2D-joint* *set* and the *genome set* with**
 **the** **strongest association p-values**
 An interaction analysis was performed between variants in the *T2D-joint set* (which comprised of the variants from the
 *T2D-risk set* and the *T2D-variance set*) and a subset of variants from the genome (MAF ≥ 10%), selected based on prior
 power calculations. The table provides the association statistics for the interactions between variants in the *T2D-joint* *set* and the *genome set* with the strongest p-values.

 (Chr = Chromosome; OR = Odds ratio)

 \*All variants at a locus, including those in LD, have been listed