|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Supplementary Table 7. Association of genetically-predicted smoke initiation with NAFLD in MR† ‡** | | | | | |
| **Number of used SNPs** | **Method** | **OR (95%CI)** | ***p-*value** | ***p*-value for heterogeneity** | ***p*-value for pleiotropy** |
| **102** | Inverse-variance weighted | 1.76 (1.29,2.41) | 3.65E-04 | 0.218 | **-** |
| 102 | MR Egger | 0.47 (0.10,2.16) | 0.337 | - | 0.086 |
| 102 | Weighted median | 1.53 (0.99,2.35) | 0.055 | - | - |
| 102 | MR-PRESSO**‡** | NA | NA | - | 0.239 |
| CI, confidence interval; IVW, inverse-variance weighted; MR, Mendelian randomization; MR-PRESSO, Mendelian Randomization Pleiotropy RESidual Sum and Outlier; OR, odds ratio; SNPs, single nucleotide polymorphisms. | | | | | |
| **†**Outlier-corrected estimate. NA, not available (if no outliers were detected). The *p*-value was estimated by global test.  **‡***P*-value for heterogeneity was tested by IVW, *p*-values for pleiotropy were only tested by MR Egger and MR-PRESSO, “-” represents that this method does not work for this test. | | | | | |