|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| MR method | Parameter | OR (95%CI) \* | P-value\* | OR (95%CI) \*\* | P-value\*\* |
| IVW (FE) | OR | 0.90 (0.86-0.95) | <0.001 | 0.93 (0.88-0.97) | 0.001 |
| IVW (RE) | OR | 0.90 (0.85-0.96) | 0.001 | 0.93 (0.86-0.99) | 0.030 |
| MR-egger (RE) | intercept | 1.00 (0.99-1.01) | 0.558 | 1.00 (0.99-1.01) | 0.960 |
| OR | 0.93 (0.83-1.04) | 0.196 | 0.93 (0.81-1.05) | 0.217 |
| weighted median | OR | 0.91 (0.85-0.98) | 0.008 | 0.92 (0.86-0.98) | 0.011 |

Table 1. Mendelian Randomization results for the 18 CRP-associated SNPs defined by the authors as ‘liberal’ 1 for risk factor of schizophrenia.

Abbreviations: CRP=C-reactive protein, FE= fixed effects, RE= random effects, IVW=inverse variance weighting, SNP, single nucleotide polymorphism, OR=odds ratio with 2-fold increment, 95%CI= 95% confident intervals with 2-fold increment. We left out MR Egger regression with FE because heterogeneity between the causal estimates is expected, so we think random effects are preferred2.

\*Results of our two analysis pipelines (consistent between the R packages and our own scripts) when considering the G allele as the effect allele (as per Hartwig et al). The highlighted parts are consistent with findings of Hartwig et al.

\*\*Results of our two analysis pipelines (consistent between the R packages and our own scripts) when considering the A allele as the effect allele (as per Prins et al).

1 Dehghan, A. *et al.* Meta-analysis of genome-wide association studies in >80 000 subjects identifies multiple loci for C-reactive protein levels. *Circulation* **123**, 731-738, doi:10.1161/CIRCULATIONAHA.110.948570 (2011).

2 Burgess, S. & Thompson, S. G. Interpreting findings from Mendelian randomization using the MR-Egger method. *Eur J Epidemiol* **32**, 377-389, doi:10.1007/s10654-017-0255-x (2017).