**Supplementalry Table 1.** Genetic instruments of *HMGCR* and *PCSK9* variants

| Gene | SNP | Effect allele frequency | Effect allele | Other allele | Beta | Standard error | p-value |
|---|---|---|---|---|---|---|---|
| *HMGCR* | rs12916 | 0.57 | T | C | −0.06061 | 0.003 | 7.79E-78 |
| | rs17238484 | 0.75 | G | T | −0.05184 | 0.005 | 1.35E-21 |
| | rs5909 | 0.90 | G | A | −0.05102 | 0.007 | 4.93E-13 |
| | rs2303152 | 0.88 | G | A | −0.03498 | 0.005 | 1.04E-09 |
| | rs10066707 | 0.58 | G | A | −0.04110 | 0.005 | 2.97E-19 |
| | rs2006760 | 0.81 | C | G | −0.04407 | 0.006 | 1.67E-13 |
| *PCSK9* | rs11206510 | 0.15 | C | T | −0.06871 | 0.001 | 2.38E-53 |
| | rs2479409 | 0.67 | A | G | −0.05309 | 0.001 | 2.52E-50 |
| | rs2149041 | 0.84 | C | G | −0.05259 | 0.001 | 1.44E-35 |
| | rs2479394 | 0.72 | A | G | −0.03192 | 0.001 | 1.58E-19 |
| | rs10888897 | 0.40 | T | C | −0.04192 | 0.001 | 8.43E-31 |
| | rs7552841 | 0.63 | C | T | −0.04589 | 0.001 | 5.40E-15 |
| | rs562556 | 0.19 | G | A | −0.05292 | 0.002 | 6.16E-21 |

The presented original effect sizes were toward LDL cholesterol (continuous increase, mmol/L) from the genetic instruments introduced from previous studies (PMID: 27959767, 33886544).
After calculation of the causal estimates, the effect sizes were transformed toward eGFR % change by 50 mg/dL decrease in LDL cholesterol, calculated by [exponential (beta × −50/38.7) − 1] × 100 (%).
eGFR, estimated glomerular filtration rate; LDL, low-density lipoprotein; SNP, single nucleotide polymorphism.