**Table S2.** Sensitivity analysis of the genotypic model of AC versus AA.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Omitted study | OR(95%CI) | *P*(Z)a | *P*bheterogeneity | *I*2(%) |
| Tenesa A (Scotland 1) | 1.18 (1.12-1.25) | 0.000 | 0.005 | 48.5 |
| Tenesa A (Scotland 2) | 1.18 (1.12-1.24) | 0.000 | 0.006 | 48.0 |
| Tenesa A (Canada) | 1.18 (1.12-1.24) | 0.000 | 0.006 | 48.1 |
| Tenesa A (DACHS) | 1.18 (1.12-1.24) | 0.000 | 0.006 | 48.1 |
| Tenesa A (England) | 1.19 (1.13-1.25) | 0.000 | 0.016 | 43.1 |
| Tenesa A (Israel) | 1.18 (1.12-1.24) | 0.000 | 0.005 | 48.6 |
| Tenesa A (Japan) | 1.19 (1.13-1.25) | 0.000 | 0.019 | 41.9 |
| Tenesa A (Kiel) | 1.18 (1.12-1.24) | 0.000 | 0.006 | 48.1 |
| Tenesa A (Spain) | 1.19 (1.13-1.24) | 0.000 | 0.008 | 46.8 |
| Pittman AM (CORGI) | 1.18 (1.13-1.24) | 0.000 | 0.006 | 48.1 |
| Pittman AM (DFCCS) | 1.17 (1.12-1.23) | 0.000 | 0.015 | 43.2 |
| Pittman AM (EPICOLON) | 1.18 (1.12-1.24) | 0.000 | 0.005 | 48.7 |
| Pittman AM (FCCPS) | 1.18 (1.12-1.24) | 0.000 | 0.006 | 47.9 |
| Pittman AM (MCCS) | 1.18 (1.12-1.24) | 0.000 | 0.005 | 48.5 |
| Pittman AM (NSCCG1) | 1.18 (1.12-1.24) | 0.000 | 0.006 | 48.0 |
| Pittman AM (NSCCG2) | 1.19 (1.13-1.25) | 0.000 | 0.006 | 48.2 |
| Pittman AM (VCQ) | 1.19 (1.13-1.25) | 0.000 | 0.009 | 45.9 |
| Wijnen JT | 1.18 (1.12-1.24) | 0.000 | 0.005 | 48.4 |
| [Von Holst S](http://www.ncbi.nlm.nih.gov/pubmed?term=%22von%20Holst%20S%22%5BAuthor%5D) | 1.19 (1.13-1.25) | 0.000 | 0.012 | 44.7 |
| Xiong F | 1.17 (1.11-1.22) | 0.000 | 0.027 | 39.8 |
| [Talseth-Palmer BA](http://www.ncbi.nlm.nih.gov/pubmed?term=%22Talseth-Palmer%20BA%22%5BAuthor%5D) | 1.18 (1.13-1.24) | 0.000 | 0.005 | 48.2 |
| Ho JW | 1.18 (1.12-1.24) | 0.000 | 0.006 | 47.8 |
| Mates IN | 1.18 (1.12-1.24) | 0.000 | 0.005 | 48.7 |
| Current study  | 1.16 (1.12-1.21) | 0.000 | 0.115 | 27.0 |

aZ-test used to determine the significance of the overall OR.

bCochran’s *x*2-based Q statistic test used to assess the heterogeneity.