

Table 1. Genotype distribution for the H324Q (C→A) SNP in *LARS2* in four different cohorts.

| Cohort | NGT | | T2DM | | <i>P</i> | <i>P</i> _{adj} | OR _{adj} (95% CI) |
|---------------------------------|------|--------------|------|------------|----------|-------------------------|----------------------------|
| | CC | CA+AA | CC | CA+AA | | | |
| Hoorn Study | 323 | 13 (0.039) | 193 | 18 (0.085) | 0.04 | 0.05 | 2.19 (1.00 – 4.85) |
| ERGO (R'dam) Study | 432 | 25 (0.055) | 422 | 35 (0.077) | 0.23 | 0.27 | 1.37 (0.77 – 2.42) |
| DK1, Steno case-control study | 491 | 23 (0.045) | 667 | 39 (0.055) | 0.43 | 0.11 | 1.58 (0.90 – 2.78) |
| DK2, Inter99 case-control study | 4248 | 253 (0.056)* | 605 | 49 (0.075) | 0.06 | 0.05 | 1.43 (1.00 – 2.05) |

*P*_{adj} and OR_{adj} values were obtained after regression analysis with adjustment for age and gender. * including 3 AA homozygotes.