**Web table F** Association of genotypes with triglyceride levels (mmol/l) (phase 3 and phase 7)

| Gene | Genotype | Number | Phase 3 | Phase 7 | Beta-value (standard error) all years combined |
|---|---|---|---|---|---|
| *ADAMTS9* | GG | 2878 | 1.22 (0.68) | 1.23 (0.64) | 0 |
| | GA | 1857 | 1.22 (0.66) | 1.19 (0.59) | -0.013 (0.014) |
| | AA | 297 | 1.19 (0.61) | 1.20 (0.55) | -0.022 (0.028) |
| | P value[1] | | 0.66 | 019 | |
| | P value[2] | | 0.60 | 0.17 | 0.45 |
| *BCL11A* | AA | 2728 | 1.23 (0.68) | 1.23 (0.62) | 0 |
| | AG | 1909 | 1.21 (0.66) | 1.19 (0.60) | -0.021 (0.014) |
| | GG | 380 | 1.20 (0.63) | 1.23 (0.67) | -0.010 (0.025) |
| | P value[1] | | 0.55 | 0.17 | |
| | P value[2] | | 0.57 | 0.22 | 0.23 |
| *CALPN10* | GG | 2945 | 1.24 (0.70) | 1.22 (0.62) | 0 |
| | GA | 2150 | 1.22 (0.67) | 1.22 (0.63) | -0.002 (0.013) |
| | AA | 378 | 1.18 (0.60) | 1.18 (0.60) | -0.029 (0.026) |
| | P value[1] | | 0.22 | 0.61 | |
| | P value[2] | | 0.39 | 0.70 | 0.27* |
| *CDC123, CAMK1D* | AA | 3464 | 1.21 (0.66) | 1.20 (0.61) | 0 |
| | AG | 1448 | 1.24 (0.70) | 1.24 (0.63) | 0.027 (0.015) |
| | GG | 124 | 1.12 (0.57) | 1.11 (0.58) | -0.069 (0.043) |
| | P value[1] | | 0.09 | 0.03 | |
| | P value[2] | | 0.12 | 0.03 | 0.20 |
| *CDKALI* | GG | 4463 | 1.22 (0.67) | 1.21 (0.62) | 0 |
| | GA | 543 | 1.22 (0.68) | 1.22 (0.62) | 0.003 (0.021) |
| | AA | 24 | 1.22 (0.64) | 1.31 (0.49) | 0.042 (0.095) |
| | P value[1] | | 0.997 | 0.71 | |
| | P value[2] | | 0.98 | 0.70 | 0.78 |
| *CDKN* | AA | 3257 | 1.22 (0.66) | 1.20 (0.62) | 0 |
| | AG | 1543 | 1.22 (0.68) | 1.23 (0.61) | 0.014 (0.014) |
| | GG | 149 | 1.23 (0.72) | 1.19 (0.61) | 0.011 (0.039) |
| | P value[1] | | 0.97 | 0.36 | |
| | P value[2] | | 0.97 | 0.37 | 0.70 |
| *FTO* | TT | 1953 | 1.22 (0.68) | 1.22 (0.62) | 0 |
| | TC | 2716 | 1.20 (0.66) | 1.20 (0.61) | -0.018 (0.014) |
| | CC | 938 | 1.27 (0.70) | 1.23 (0.63) | 0.016 (0.018) |
| | P value[1] | | 0.05 | 0.24 | |
| | P value[2] | | 0.05 | 0.21 | 0.73 |
| *HHEX* | GG | 2635 | 1.22 (0.67) | 1.22 (0.61) | 0 |
| | GA | 1968 | 1.23 (0.67) | 1.20 (0.62) | -0.016 (0.014) |
| | AA | 405 | 1.19 (0.66) | 1.20 (0.63) | -0.025 (0.025) |
| | P value[1] | | 0.62 | 0.58 | |
| | P value[2] | | 0.69 | 0.47 | 0.35 |

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|---|---|---|---|---|---|
| *HNF1A* | CC | 5106 | 1.23 (0.68) | 1.22 (0.62) | 0 |
| | CT | 301 | 1.20 (0.60) | 1.18 (0.58) | -0.023 (0.028) |
| | TT | 5 | 1.86 (0.54) | 1.55 (0.23) | 0.340 (0.213) |
| | P value[1] | | 0.27 | 0.36 | |
| | P value[2] | | 0.15 | 0.32 | 0.11* |
| *IGF2BP2* | CC | 2362 | 1.21 (0.66) | 1.20 (0.60) | 0 |
| | AC | 2182 | 1.24 (0.70) | 1.23 (0.65) | 0.027 (0.014) |
| | AA | 485 | 1.17 (0.61) | 1.16 (0.54) | -0.023 (0.023) |
| | P value[1] | | 0.04 | 0.03 | |
| | P value[2] | | 0.06 | 0.04 | 0.20 |
| *JAZF1* | AA | 1269 | 1.23 (0.70) | 1.22 (0.63) | 0 |
| | AG | 2453 | 1.21 (0.66) | 1.21 (0.62) | -0.001 (0.016) |
| | GG | 1304 | 1.23 (0.65) | 1.22 (0.60) | 0.004 (0.018) |
| | P value[1] | | 0.57 | 0.73 | |
| | P value[2] | | 0.47 | 0.74 | 0.74 |
| *KCNJ11* | CC | 2313 | 1.23 (0.67) | 1.21 (0.61) | 0 |
| | CT | 2478 | 1.22 (0.67) | 1.22 (0.63) | 0.009 (0.013) |
| | TT | 720 | 1.24 (0.72) | 1.20 (0.61) | 0.004 (0.020) |
| | P value[1] | | 0.76 | 0.70 | |
| | P value[2] | | 0.93 | 0.61 | 0.65 |
| *NOTCH2* | CC | 4024 | 1.21 (0.67) | 1.21 (0.62) | 0 |
| | AC | 949 | 1.25 (0.66) | 1.22 (0.59) | 0.015 (0.017) |
| | AA | 62 | 1.09 (0.64) | 1.11 (0.53) | -0.074 (0.060) |
| | P value[1] | | 0.09 | 0.37 | |
| | P value[2] | | 0.11 | 0.44 | 0.34 |
| *PPARG* | CC | 4290 | 1.22 (0.68) | 1.22 (0.62) | 0 |
| | CG | 1138 | 1.24 (0.67) | 1.21 (0.62) | 0.001(0.016) |
| | GG | 86 | 1.14 (0.60) | 1.14 (0.56) | -0.066 (0.051) |
| | P value[1] | | 0.38 | 0.47 | |
| | P value[2] | | 0.22 | 0.47 | 0.58 |
| *SLC30A8* | GG | 2416 | 1.21 (0.67) | 1.21 (0.62) | 0 |
| | GA | 2177 | 1.23 (0.68 ) | 1.21 (0.62) | 0.006 (0.014) |
| | AA | 428 | 1.22 (0.64) | 1.23 (0.62) | 0.010 (0.024) |
| | P value[1] | | 0.39 | 0.79 | |
| | P value[2] | | 0.44 | 0.84 | 0.72 |
| *TCF2 (HNF1B)* | AA | 1395 | 1.20 (0.67) | 1.20 (0.61) | 0 |
| | AG | 2446 | 1.23 (0.69) | 1.22 (0.62) | 0.016 (0.016) |
| | GG | 1154 | 1.21 (0.65) | 1.22 (0.61) | 0.006 (0.019) |
| | P value[1] | | 0.39 | 0.79 | |
| | P value[2] | | 0.21 | 0.72 | 0.84 |
| *TCF7L2* | AA | 2365 | 1.21 (0.68) | 1.22 (0.63) | 0 |
| | AG | 2173 | 1.23 (0.67) | 1.21 (0.62) | 0.004 (0.014) |
| | GG | 467 | 1.18 (0.61) | 1.18 (0.55) | -0.030 (0.024) |
| | P value[1] | | 0.26 | 0.41 | |
| | P value[2] | | 0.33 | 0.47 | 0.46 |
| *THADA* | AA | 3953 | 1.23 (0.68) | 1.21 (0.62) | 0 |

| | | | | | |
|---|---|---|---|---|---|
| | AG | 1003 | 1.19 (0.64) | 1.22 (0.61) | 0.000 (0.016) |
| | GG | 75 | 1.15 (0.63) | 1.17 (0.67) | -0.060 (0.054) |
| | P value[1] | | 0.24 | 0.71 | |
| | P value[2] | | 0.21 | 0.77 | 0.30 |
| *TSPAN8, LGR5* | AA | 1762 | 1.21 (0.66) | 1.21 (0.61) | 0 |
| | AG | 2424 | 1.23 (0.67) | 1.22 (0.63) | 0.015 (0.015) |
| | GG | 838 | 1.22 (0.69) | 1.19 (0.59) | -0.007 (0.019) |
| | P value[1] | | 0.55 | 0.31 | |
| | P value[2] | | 0.61 | 0.34 | 0.44 |
| *VEGFA* | GG | 2611 | 1.23 (0.68) | 1.21 (0.63) | 0 |
| | GA | 2008 | 1.22 (0.66) | 1.22 (0.61) | -0.002 (0.014) |
| | AA | 400 | 1.18 (0.66) | 1.21 (0.58) | -0.013 (0.025) |
| | P value[1] | | 0.42 | 0.90 | |
| | P value[2] | | 0.27 | 0.91 | 0.65 |

Results are geometric mean (approximate SD)

[1] ANOVA, unadjusted

[2] ANOVA, adjusted for age and gender.

*recessive model

B(se) is the coefficient for overall genotype effect estimated from a mixed model with age at phase1 and gender included as fixed covariates. The change in cholesterol over time is allowed to vary between subjects.