**FILE S1**

Table S1. Associations between 32 risk variants of higher body mass index and mean telomere length (*z*-score), Nurses’ Health Study, 1989-1990

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **SNP** | **Gene**  | **Chr** | **Risk** | **Risk** | **Per** | **SE** | ***P* b,c** |
|  |  | **region** |  | **allele** | **allele** | **allele** |  |  |
|  |  |  |  |  | **freq** | **βa** |  |  |
|  | rs1514175 | *TNNI3K* | 1 | A | 0.41 | -0.003 | 0.023 | 0.899 |
|  | rs1555543 | *PTBP2* | 1 | C | 0.59 | 0.028 | 0.023 | 0.231 |
|  | rs2815752 | *NEGR1* | 1 | A | 0.64 | -0.031 | 0.023 | 0.174 |
|  | rs543874 | *SEC16B* | 1 | G | 0.19 | 0.013 | 0.028 | 0.639 |
|  | rs2867125 | *TMEM18* | 2 | C | 0.82 | 0.004 | 0.029 | 0.891 |
|  | rs2890652 | *LRP1B* | 2 | C | 0.17 | 0.008 | 0.030 | 0.800 |
|  | rs713586 | *RBJ* | 2 | C | 0.48 | -0.011 | 0.022 | 0.618 |
|  | rs887912 | *FANCL* | 2 | T | 0.29 | -0.041 | 0.025 | 0.096 |
|  | rs13078807 | *CADM2* | 3 | G | 0.21 | 0.036 | 0.027 | 0.183 |
|  | rs9816226 | *ETV5* | 3 | T | 0.82 | -0.014 | 0.029 | 0.638 |
|  | rs10938397 | *GNPDA2* | 4 | G | 0.44 | -0.044 | 0.023 | 0.050 |
| § | rs13107325 | *SLC39A8* | 4 | T | 0.07 | -0.057 | 0.043 | 0.187 |
|  | rs2112347 | *FLJ35779* | 5 | T | 0.64 | -0.005 | 0.023 | 0.826 |
|  | rs4836133 | *ZNF608* | 5 | A | 0.49 | 0.036 | 0.022 | 0.113 |
|  | rs206936 | *NUDT3* | 6 | G | 0.20 | 0.026 | 0.028 | 0.359 |
|  | rs987237 | *TFAP2B* | 6 | G | 0.19 | -0.024 | 0.029 | 0.398 |
|  | rs10968576 | *LRRN6C* | 9 | G | 0.30 | -0.006 | 0.024 | 0.802 |
|  | rs10767664 | *BDNF* | 11 | A | 0.78 | 0.023 | 0.027 | 0.386 |
|  | rs3817334 | *MTCH2* | 11 | T | 0.42 | -0.031 | 0.023 | 0.168 |
|  | rs4929949 | *RPL27A* | 11 | C | 0.51 | -0.044 | 0.022 | 0.045 |
|  | rs7138803 | *FAIM2* | 12 | A | 0.38 | 0.040 | 0.023 | 0.083 |
|  | rs4771122 | *MTIF3* | 13 | G | 0.21 | -0.001 | 0.027 | 0.982 |
|  | rs10150332 | *NRXN3* | 14 | C | 0.22 | -0.014 | 0.027 | 0.611 |
|  | rs11847697 | *PRKD1* | 14 | T | 0.04 | -0.005 | 0.056 | 0.927 |
|  | rs2241423 | *MAP2K5* | 15 | G | 0.78 | -0.001 | 0.027 | 0.984 |
|  | rs12444979 | *GPRC5B* | 16 | C | 0.86 | 0.008 | 0.033 | 0.810 |
|  | rs1558902 | *FTO* | 16 | A | 0.41 | 0.002 | 0.023 | 0.942 |
|  | rs7359397 | *SH2B1* | 16 | T | 0.39 | -0.025 | 0.023 | 0.265 |
|  | rs571312 | *MC4R* | 18 | A | 0.24 | -0.001 | 0.026 | 0.980 |
| ‡ | rs2287019 | *QPCTL* | 19 | C | 0.82 | 0.017 | 0.030 | 0.575 |
|  | rs29941 | *KCTD15* | 19 | G | 0.68 | 0.003 | 0.024 | 0.886 |
| § | rs3810291 | *TMEM160* | 19 | A | 0.69 | 0.025 | 0.024 | 0.315 |

Abbreviations: SNP, single nucleotide polymorphism; Chr., chromosome; freq., frequency; SE, standard error

aAdjusted for age in years (continuous), case status (case, control)

b*P* values are 2-sided; calculated using the additive genetic model

cAll SNPs nonsignificant after False Discovery Rate correction for multiple testing

§SNPs imputed with 0.6 < MACH Rsq < 0.8

‡SNPs imputed with MACH Rsq ≤ 0.6

Table S2. Associations between 36 risk variants of type 2 diabetes and mean telomere length (*z*-score), Nurses’ Health Study, 1989-1990

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **SNP** | **Gene** | **Chr** | **Risk** | **Risk** | **Per** | **SE** | ***P* b,c** |
|  |  | **region** |  | **allele** | **allele** | **allele** |  |  |
|  |  |  |  |  | **freq** | **βa** |  |  |
|  | rs10923931 | *NOTCH2* | 1 | T | 0.10 | 0.006 | 0.037 | 0.865 |
|  | rs340874 | *PROX1* | 1 | C | 0.55 | 0.020 | 0.023 | 0.372 |
|  | rs243021 | *BCL11A* | 2 | A | 0.46 | 0.043 | 0.022 | 0.057 |
|  | rs2943641 | *IRS1* | 2 | C | 0.63 | 0.006 | 0.023 | 0.796 |
|  | rs7578597 | *THADA* | 2 | T | 0.89 | -0.009 | 0.036 | 0.797 |
|  | rs7593730 | *RBMS1-ITGB6* | 2 | C | 0.78 | -0.057 | 0.027 | 0.034 |
|  | rs780094 | *GCKR* | 2 | C | 0.59 | -0.004 | 0.023 | 0.879 |
|  | rs11708067 | *ADCY5* | 3 | A | 0.78 | 0.024 | 0.027 | 0.367 |
|  | rs1801282 | *PPARG* | 3 | C | 0.88 | -0.009 | 0.035 | 0.784 |
|  | rs4402960 | *IGF2BP2* | 3 | T | 0.32 | 0.018 | 0.024 | 0.460 |
|  | rs4607103 | *ADAMTS9* | 3 | C | 0.75 | -0.021 | 0.026 | 0.417 |
|  | rs10010131 | *WFS1* | 4 | G | 0.60 | -0.032 | 0.023 | 0.168 |
| § | rs4457053 | *ZBED3* | 5 | G | 0.30 | -0.004 | 0.025 | 0.871 |
|  | rs10946398 | *CDKAL1* | 6 | C | 0.32 | 0.009 | 0.024 | 0.688 |
|  | rs2191349 | *DGKB-TMEM195* | 7 | T | 0.55 | -0.029 | 0.023 | 0.206 |
|  | rs4607517 | *GCK* | 7 | A | 0.17 | -0.001 | 0.030 | 0.986 |
|  | rs864745 | *JAZF1* | 7 | T | 0.49 | -0.026 | 0.022 | 0.244 |
| § | rs972283 | *KLF14* | 7 | G | 0.52 | -0.025 | 0.022 | 0.258 |
|  | rs13266634 | *SLC30A8* | 8 | C | 0.70 | -0.016 | 0.024 | 0.510 |
|  | rs896854 | *TP53INP1* | 8 | T | 0.49 | -0.027 | 0.022 | 0.228 |
|  | rs10811661 | *CDKN2A-B* | 9 | T | 0.83 | 0.037 | 0.030 | 0.218 |
|  | rs13292136 | *CHCHD9* | 9 | C | 0.93 | 0.038 | 0.045 | 0.394 |
|  | rs1111875 | *HHEX-IDE* | 10 | C | 0.59 | 0.001 | 0.023 | 0.958 |
|  | rs12779790 | *CDC123-CAMK1D* | 10 | G | 0.19 | 0.050 | 0.029 | 0.082 |
|  | rs7903146 | *TCF7L2* | 10 | T | 0.29 | 0.009 | 0.025 | 0.716 |
| § | rs10830963 | *MTNR1B* | 11 | G | 0.29 | 0.027 | 0.025 | 0.277 |
|  | rs1552224 | *CENTD2* | 11 | A | 0.86 | -0.036 | 0.032 | 0.260 |
|  | rs2237892 | *KCNQ1* | 11 | C | 0.94 | 0.030 | 0.048 | 0.529 |
| § | rs231362 | *KCNQ1* | 11 | G | 0.52 | 0.024 | 0.023 | 0.282 |
|  | rs5215 | *KCNJ11* | 11 | C | 0.36 | 0.002 | 0.023 | 0.926 |
|  | rs1531343 | *HMGA2* | 12 | C | 0.09 | 0.060 | 0.038 | 0.117 |
|  | rs7957197 | *HNF1A* | 12 | T | 0.80 | -0.006 | 0.028 | 0.823 |
|  | rs7961581 | *TSPAN8-LGR5* | 12 | C | 0.28 | -0.046 | 0.025 | 0.067 |
| § | rs11634397 | *ZFAND6* | 15 | G | 0.67 | -0.046 | 0.024 | 0.053 |
|  | rs8042680 | *PRC1* | 15 | A | 0.32 | -0.020 | 0.024 | 0.408 |
| ‡ | rs757210 | *HNF1B-TCF2* | 17 | T | 0.38 | -0.015 | 0.024 | 0.520 |

Abbreviations: SNP, single nucleotide polymorphism; Chr., chromosome; freq., frequency; SE, standard error

aAdjusted for age in years (continuous), case status (case, control)

b*P* values are 2-sided; calculated using the additive genetic model

cAll SNPs nonsignificant after False Discovery Rate correction for multiple testing

§SNPs imputed with 0.6 < MACH Rsq < 0.8

‡SNPs imputed with MACH Rsq ≤ 0.6

 Figure S1.



*P* interaction = 0.11