Supplemental Table 1. Demographic and weight characteristics for those who lost 3% or more at year 1.

|  |  |  |  |
| --- | --- | --- | --- |
| Characteristic | Total (N= 2,022) | DSE  (N=477) | ILI  (N=1,545) |
|  |  | | |
|  | Number (%) | | |
| Women | 1,151(56.9) | 287 (60.2) | 864 (55.9) |
| Ethnicity |  |  |  |
| African American | 300 (14.8) | 64 (13.4) | 236 (15.3) |
| American Indian/Alaskan Nativea | 8 (0.4) | 2 (0.4) | 6 (0.4) |
| Asian/Pacific Islander | 21 (1.0) | 3 (0.6) | 18 (1.2) |
| Hispanic/Latino | 145 (7.2) | 39 (8.2) | 106 (6.9) |
| Non-Hispanic White | 1,511(74.7) | 360 (75.5) | 1151 (74.5) |
| Other (multiple) | 37 (1.8) | 9 (1.9) | 28 (1.8) |
|  |  | | |
|  | Mean ± Standard Deviation | | |
| Age at Y1 (years) | 61.0±6.9 | 61.1±6.8 | 61.0±6.9 |
| BMI at Y1 (kg/m2) |  |  |  |
| Women | 33.2±5.9 | 34.9±6.0 | 32.6±5.8 |
| Men | 31.7±5.5 | 33.2±5.0 | 31.3±5.5 |
| Waist circumference at Y1 (cm) |  |  |  |
| Women | 103.6±13.4 | 107.4±13.3 | 102.4±13.2 |
| Men | 109.3±14.0 | 114.1±12.9 | 107.9±14.1 |
| Weight at Y1 (kg) |  |  |  |
| Women | 87.4±16.5 | 91.3±17.3 | 86.1±16.0 |
| Men | 98.5±18.0 | 104.2±17.0 | 96.9±18.0 |
| Weight at Y4 (kg) |  |  |  |
| Women | 91.1±17.4 | 91.8±17.2 | 90.8±17.4 |
| Men | 103.3±19.1 | 106.6±17.6 | 102.4±19.4 |
| Weight Change Y4-Y1 (kg) |  |  |  |
| Women | 3.7±8.2 | 0.5±9.1 | 4.7±7.6 |
| Men | 4.8±7.8 | 2.4±7.0 | 5.5±7.8 |
|  |  |  |  |
|  |  | Number (%) |  |
| Weight Regain Y4-Y1 |  |  |  |
| Women | 834 (72.5) | 157 (54.7) | 677 (78.4) |
| Men | 684 (78.5) | 123 (64.7) | 561 (82.4) |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |

aThe number of American Indian participants included in this study is less than that of

the parent Look AHEAD trial due to limitations in genetic consent.

Supplemental Table 2. Single nucleotide polymorphisms associated with year 1 weight change within ILI Shading denotes gene regions achieving chip-wide significance.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| SNP | Chr | Closest gene | Minor allele | MAF (%)a | Betab | SE | P valuec | Q valued |
| rs484066 | 2 | *ABCB11* | T | 39.79 | 1.159 | 0.222 | 1.89E-07 | 0.003 |
| rs569805 | 2 | *ABCB11* | T | 31.15 | 1.237 | 0.237 | 1.92E-07 | 0.003 |
| rs17069904 | 18 | *TNFRSF11A* | A | 9.76 | -1.703 | 0.358 | 1.97E-06 | 0.018 |
| rs12452844 | 17 | *AANAT* | A | 28.51 | -1.105 | 0.237 | 3.12E-06 | 0.022 |
| rs494874 | 2 | *ABCB11* | A | 30.15 | 1.102 | 0.239 | 4.23E-06 | 0.023 |
| rs519887 | 2 | *ABCB11* | G | 49.53 | -0.979 | 0.216 | 6.03E-06 | 0.028 |
| rs149157 | 1 | *RAB4A* | A | 22.86 | -1.117 | 0.264 | 2.33E-05 | 0.071 |
| rs1826909 | 4 | *ADH1A* | A | 34.13 | -0.971 | 0.230 | 2.36E-05 | 0.071 |
| rs1946293 | 12 | *TBX5* | G | 30.74 | -0.993 | 0.235 | 2.43E-05 | 0.071 |
| rs1105297 | 1 | *SLC2A1* | A | 40.35 | -0.994 | 0.236 | 2.57E-05 | 0.071 |
| rs2012390 | 11 | *MMP8* | G | 23.79 | 1.027 | 0.248 | 3.54E-05 | 0.081 |
| rs2544367 | 2 | *ABCB11* | A | 49.13 | 0.891 | 0.218 | 4.42E-05 | 0.081 |
| rs473351 | 2 | *ABCB11* | A | 41.77 | 0.888 | 0.219 | 4.91E-05 | 0.081 |
| rs10916461 | 1 | *RAB4A* | A | 19.98 | -1.118 | 0.276 | 5.11E-05 | 0.081 |
| rs2041992 | 19 | *PGLYRP1* | A | 35.28 | -0.889 | 0.220 | 5.17E-05 | 0.081 |
| rs10185661 | 2 | *GTDC1* | A | 43.94 | -0.891 | 0.220 | 5.23E-05 | 0.081 |
| rs752261 | 6 | *MICAL1* | A | 6.14 | -1.807 | 0.447 | 5.39E-05 | 0.081 |
| rs797195 | 13 | *STARD13* | G | 40.7 | 0.894 | 0.222 | 5.51E-05 | 0.081 |
| rs7231887 | 18 | *TNFRSF11A* | A | 10.15 | -1.422 | 0.354 | 5.93E-05 | 0.081 |
| rs853778 | 2 | *ABCB11* | A | 47.13 | 0.867 | 0.216 | 6.02E-05 | 0.081 |
| rs10067048 | 5 | *PDE4D* | A | 39.64 | 0.913 | 0.228 | 6.41E-05 | 0.081 |
| rs853787 | 2 | *ABCB11* | C | 30.35 | 0.954 | 0.239 | 6.41E-05 | 0.081 |
| rs8099140 | 18 | *BCL2* | G | 5.74 | -1.922 | 0.484 | 7.31E-05 | 0.088 |
| rs1318379 | 20 | *BMP7* | C | 15.36 | 1.512 | 0.383 | 7.95E-05 | 0.092 |
| rs467300 | 5 | *PDE4D* | G | 11.69 | 1.326 | 0.338 | 8.97E-05 | 0.092 |
| rs2904254 | 20 | *CEBPB* | A | 16.21 | 1.140 | 0.291 | 9.05E-05 | 0.092 |
| rs11700258 | 20 | *PTGIS* | G | 8.53 | 1.541 | 0.395 | 9.46E-05 | 0.092 |
| rs2279027 | 4 | *TBC1D1* | A | 37.37 | 0.875 | 0.225 | 9.77E-05 | 0.092 |
| rs7818199 | 8 | *NRG1* | T | 47.59 | 0.846 | 0.217 | 9.92E-05 | 0.092 |
| rs11791416 | 9 | *Intergenic* | G | 25.08 | -0.988 | 0.255 | 0.000107 | 0.092 |
| rs11647415 | 16 | *A2BP1* | A | 13.09 | -1.260 | 0.325 | 0.000109 | 0.092 |
| rs9069 | 1 | *SPHAR* | T | 21.78 | -1.027 | 0.266 | 0.000114 | 0.092 |
| rs11909995 | 21 | *ATP5J* | A | 23.56 | 1.031 | 0.267 | 0.000117 | 0.092 |
| rs1962082 | 11 | *MMP20* | A | 29.89 | -0.904 | 0.235 | 0.00012 | 0.092 |
| rs10811659 | 9 | *Intergenic* | G | 20.24 | -1.056 | 0.275 | 0.000122 | 0.092 |
| rs10093667 | 8 | *ADRA1A* | A | 12.95 | -1.203 | 0.313 | 0.000124 | 0.092 |
| rs2369521 | 14 | *BDKRB2* | G | 27.44 | -0.910 | 0.237 | 0.000125 | 0.092 |
| rs6140526 | 20 | *ANGPT4* | A | 19.31 | -1.062 | 0.277 | 0.000126 | 0.092 |
| rs797224 | 13 | *STARD13* | A | 38.13 | -0.878 | 0.229 | 0.00013 | 0.092 |
| rs153982 | 5 | *PDE4D* | A | 25.99 | 0.952 | 0.249 | 0.000133 | 0.092 |
| rs6410 | 8 | *CYP11B1* | A | 46.74 | 0.809 | 0.213 | 0.000143 | 0.097 |
| rs10507246 | 12 | *TBX5* | A | 8.91 | -1.448 | 0.382 | 0.000153 | 0.101 |
| rs797226 | 13 | *STARD13* | A | 34.78 | -0.866 | 0.230 | 0.000173 | 0.112 |
| rs1597253 | 2 | *TGFA* | G | 17.41 | 1.100 | 0.293 | 0.000178 | 0.112 |
| rs853789 | 2 | *ABCB11* | A | 29.14 | 0.904 | 0.243 | 0.000206 | 0.127 |
| rs4678013 | 3 | *CASR* | A | 19.99 | -0.977 | 0.264 | 0.00022 | 0.129 |
| rs17650274 | 3 | *MYL3* | A | 6.21 | -1.635 | 0.443 | 0.000223 | 0.129 |
| rs882210 | 1 | *PDZK1* | G | 6.05 | -1.681 | 0.456 | 0.000226 | 0.129 |
| rs347272 | 1 | *NOS1AP* | A | 14.83 | -1.131 | 0.307 | 0.000227 | 0.129 |
| rs1029035 | 9 | *PCSK5* | C | 46.5 | -0.792 | 0.215 | 0.000234 | 0.129 |
| rs10078079 | 5 | *CTNNA1* | A | 26.78 | -0.882 | 0.240 | 0.000237 | 0.129 |
| rs4804063 | 19 | *FBN3* | G | 19.83 | -0.994 | 0.271 | 0.000242 | 0.129 |
| rs1972041 | 15 | *TPM1* | A | 37.35 | -0.807 | 0.220 | 0.000249 | 0.130 |
| rs1427463 | 17 | *DDX5* | A | 20.41 | 1.182 | 0.323 | 0.000252 | 0.130 |
| rs10509561 | 10 | *FAS* | A | 33 | 0.830 | 0.228 | 0.000267 | 0.133 |
| rs7546522 | 1 | *PCSK9* | A | 13.11 | 1.149 | 0.315 | 0.000268 | 0.133 |
| rs8005195 | 14 | *BDKRB2* | G | 26.76 | -0.875 | 0.241 | 0.000287 | 0.136 |
| rs12980641 | 19 | *PGLYRP1* | A | 28.41 | -0.864 | 0.238 | 0.00029 | 0.136 |
| rs901561 | 8 | *NRG1* | G | 30.45 | 0.860 | 0.237 | 0.000291 | 0.136 |
| rs11604561 | 11 | *PIK3C2A* | G | 12.52 | 1.167 | 0.322 | 0.000293 | 0.136 |
| rs8078510 | 17 | *GIP* | A | 27.27 | -0.835 | 0.231 | 0.000312 | 0.142 |
| rs10110519 | 8 | *IL7* | A | 14.45 | -1.136 | 0.316 | 0.000318 | 0.142 |
| rs3813572 | 15 | *PSMA4* | G | 35.29 | 0.821 | 0.228 | 0.000324 | 0.142 |
| rs853779 | 2 | *ABCB11* | C | 48.83 | 0.778 | 0.217 | 0.000328 | 0.142 |
| rs11749163 | 5 | *CTNNA1* | G | 29.96 | -0.831 | 0.232 | 0.000341 | 0.145 |
| rs3786527 | 19 | *LTBP4* | A | 18.55 | -0.992 | 0.278 | 0.000357 | 0.150 |
| rs986639 | 1 | *DDAH1* | C | 14.85 | -1.062 | 0.298 | 0.000369 | 0.152 |
| rs36232 | 16 | *RAB26* | A | 21.28 | 0.927 | 0.261 | 0.00038 | 0.152 |
| rs258281 | 16 | *RAB26* | A | 22.25 | 0.956 | 0.269 | 0.000382 | 0.152 |
| rs487820 | 9 | *SURF5* | A | 48.77 | -0.760 | 0.214 | 0.000383 | 0.152 |
| rs17111495 | 1 | *PCSK9* | G | 16.59 | 1.041 | 0.294 | 0.000404 | 0.156 |
| rs16868917 | 5 | *MASS1* | G | 7.17 | 1.502 | 0.425 | 0.000407 | 0.156 |
| rs8114057 | 20 | *HNF4A* | A | 47.13 | -0.773 | 0.219 | 0.00041 | 0.156 |
| rs922734 | 8 | *ADRA1A* | G | 13.93 | -1.062 | 0.302 | 0.000442 | 0.164 |
| rs8089829 | 18 | *TNFRSF11A* | G | 45.77 | -0.743 | 0.212 | 0.000446 | 0.164 |
| rs4918258 | 10 | *SORCS1* | T | 30.49 | -0.821 | 0.234 | 0.00045 | 0.164 |
| rs17320616 | 8 | *TRIB1* | G | 19.81 | -0.952 | 0.272 | 0.000458 | 0.165 |
| rs6433 | 8 | *CYP11B2* | G | 36.39 | 0.797 | 0.228 | 0.000472 | 0.165 |
| rs6544647 | 2 | *THADA* | G | 46.13 | -0.747 | 0.214 | 0.000472 | 0.165 |
| rs8069501 | 17 | *POLR2A* | G | 7.84 | 1.352 | 0.387 | 0.000477 | 0.165 |
| rs10482771 | 1 | *TGFB2* | A | 10.92 | 1.211 | 0.347 | 0.000482 | 0.165 |
| rs10489985 | 2 | *TGFA* | G | 16.92 | 0.991 | 0.284 | 0.000489 | 0.165 |
| rs1382243 | 1 | *RGS7* | G | 43.97 | 0.743 | 0.214 | 0.000507 | 0.169 |
| rs1356410 | 15 | *PLA2G4F* | A | 29.53 | 0.829 | 0.239 | 0.000525 | 0.173 |
| rs11077820 | 17 | *AANAT* | G | 42.75 | -0.760 | 0.219 | 0.000539 | 0.175 |
| rs2154328 | 1 | *Intergenic* | A | 37.88 | -0.760 | 0.220 | 0.00057 | 0.175 |
| rs4792717 | 17 | *NCOR1* | A | 41.23 | -0.743 | 0.216 | 0.00057 | 0.175 |
| rs6753702 | 2 | *Intergenic* | G | 25.74 | -0.862 | 0.250 | 0.000573 | 0.175 |
| rs178831 | 17 | *NCOR1* | A | 37.64 | -0.775 | 0.225 | 0.00058 | 0.175 |
| rs10811466 | 9 | *IFNB1* | A | 15.05 | -1.026 | 0.298 | 0.000581 | 0.175 |
| rs37250 | 5 | *F2R* | A | 33.83 | -0.806 | 0.234 | 0.000582 | 0.175 |
| rs11215545 | 11 | *IGSF4* | A | 33.91 | -0.804 | 0.234 | 0.000586 | 0.175 |
| rs1896509 | 10 | *NRG3* | G | 11.95 | -1.144 | 0.333 | 0.000588 | 0.175 |
| rs12138754 | 1 | *WNT2B* | A | 18.14 | -0.970 | 0.283 | 0.00061 | 0.177 |
| rs893182 | 19 | *A1BG* | A | 9.94 | 1.294 | 0.378 | 0.000611 | 0.177 |
| rs12450199 | 17 | *GAA* | C | 36.1 | 0.759 | 0.222 | 0.000614 | 0.177 |
| rs6704061 | 1 | *PCSK9* | A | 7.2 | -1.354 | 0.397 | 0.000653 | 0.187 |
| rs2995920 | 4 | *TBC1D1* | A | 33.73 | 0.791 | 0.232 | 0.000665 | 0.187 |
| rs725937 | 5 | *SPARC* | A | 40.03 | 0.747 | 0.220 | 0.000677 | 0.187 |
| rs2017116 | 2 | *ALMS1* | G | 12.31 | 1.111 | 0.327 | 0.000678 | 0.187 |
| rs1321129 | 20 | *C20orf28* | A | 48.06 | 0.735 | 0.216 | 0.000682 | 0.187 |
| rs3917225 | 2 | *IL1R1* | G | 38.36 | -0.770 | 0.227 | 0.000697 | 0.189 |
| rs12145922 | 1 | *PKN2* | C | 44.17 | 0.730 | 0.215 | 0.000708 | 0.189 |
| rs2855122 | 11 | *HBG2* | G | 49.59 | 0.716 | 0.211 | 0.00071 | 0.189 |
| rs2715817 | 17 | *MAP2K6* | G | 44.17 | 0.723 | 0.214 | 0.000721 | 0.190 |
| rs2869961 | 20 | *Intergenic* | A | 10.26 | 1.198 | 0.355 | 0.000732 | 0.192 |
| rs1695365 | 15 | *NRG4* | G | 6.2 | -1.629 | 0.483 | 0.000745 | 0.192 |
| rs7195066 | 16 | *FANCA* | A | 39.14 | -0.795 | 0.236 | 0.000748 | 0.192 |
| rs7747989 | 6 | *CDKAL1* | C | 30.04 | 0.792 | 0.235 | 0.000762 | 0.192 |
| rs1019731 | 12 | *IGF1* | A | 11.75 | -1.121 | 0.333 | 0.000763 | 0.192 |
| rs6699866 | 1 | *HTR6* | A | 21.4 | -0.894 | 0.266 | 0.00077 | 0.192 |
| rs7207463 | 17 | *NCOR1* | A | 44.35 | -0.723 | 0.215 | 0.000778 | 0.193 |
| rs4144707 | 3 | *GHSR* | G | 33.43 | -0.778 | 0.232 | 0.000804 | 0.194 |
| rs11084332 | 19 | *LAIR1* | G | 36.31 | -0.756 | 0.226 | 0.000811 | 0.194 |
| rs10817128 | 9 | *EDG2* | A | 29.07 | -0.785 | 0.235 | 0.000812 | 0.194 |
| rs1731902 | 17 | *NAGS* | G | 41.88 | 0.732 | 0.219 | 0.000823 | 0.194 |
| rs17720953 | 18 | *TNFRSF11A* | A | 23.14 | 0.833 | 0.249 | 0.000825 | 0.194 |
| rs4886571 | 15 | *PSMA4* | G | 37.43 | 0.744 | 0.223 | 0.000844 | 0.194 |
| rs797213 | 13 | *STARD13* | A | 45.89 | 0.721 | 0.216 | 0.000844 | 0.194 |
| rs9671808 | 14 | *C14orf50* | A | 5.96 | 1.388 | 0.416 | 0.000849 | 0.194 |
| rs2764628 | 13 | *STARD13* | A | 21.64 | 0.861 | 0.258 | 0.00085 | 0.194 |
| rs2304677 | 2 | *PER2* | A | 6.56 | -1.446 | 0.434 | 0.000855 | 0.194 |
| rs6028505 | 20 | *Intergenic* | A | 48.09 | -0.738 | 0.222 | 0.000862 | 0.194 |
| rs4793621 | 17 | *MYST2* | G | 31.56 | -0.830 | 0.249 | 0.000873 | 0.194 |
| rs7125819 | 11 | *IGSF4* | A | 35.49 | -0.768 | 0.231 | 0.000876 | 0.194 |
| rs4892117 | 18 | *Intergenic* | G | 32.62 | -0.774 | 0.233 | 0.000882 | 0.194 |
| rs2071406 | 1 | *AGT* | G | 10 | 1.215 | 0.365 | 0.000886 | 0.194 |
| rs6470355 | 8 | *TRIB1* | G | 24.15 | -0.855 | 0.257 | 0.000894 | 0.194 |
| rs2239140 | 12 | *VWF* | A | 41.05 | 0.765 | 0.231 | 0.000908 | 0.195 |
| rs561510 | 9 | *EDG2* | C | 19.23 | 0.914 | 0.276 | 0.000923 | 0.197 |
| rs1265956 | 19 | *A1BG* | A | 11.32 | 1.207 | 0.364 | 0.000932 | 0.197 |
| rs4726484 | 7 | *MGAM* | A | 27.32 | 0.818 | 0.247 | 0.000945 | 0.197 |
| rs12731764 | 1 | *PDE4B* | G | 20.92 | 0.880 | 0.266 | 0.000949 | 0.197 |
| rs6094631 | 20 | *PRKCBP1* | A | 34.6 | 0.778 | 0.235 | 0.000951 | 0.197 |

aMinor allele frequency in full sample

bEffect of each copy of the minor allele on year 1 weight change in ILI (in kgs)

c Shading denotes gene regions with at least one SNP achieving chip-wide significance (p < 2.96E-06).

d Ranking based on q-values (FDR < 20%).