Table S3

1. Cox regressions of 34 genome-wide index-SNPs associated with FG predicting CRC risk

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **SNP** | **Chr** | **Position¥** | **Allele** | **HR¶ (95% CI)** | **SE** | ***p*** |
| **Ref** | **Alt** |
| rs11264743 | 1 | 153941514 | T | C | 0.948 (0.574 - 1.567) | 0.2563 | 0.8347 |
| rs1260326 | 2 | 27730940 | C | T | 1.362 (0.821 - 2.258) | 0.2580 | 0.2315 |
| rs780094 | 2 | 27741237 | C | T | 1.172 (0.752 - 1.826) | 0.2263 | 0.4839 |
| rs6753534 | 2 | 27752871 | T | C | 1.084 (0.754 - 1.557) | 0.1849 | 0.6630 |
| rs11678685 | 2 | 169710607 | A | G | 1.034 (0.680 - 1.570) | 0.2133 | 0.8768 |
| rs1402837 | 2 | 169757354 | T | C | 1.065 (0.749 - 1.516) | 0.1798 | 0.7244 |
| rs17539351 | 2 | 169766560 | C | T | 4.876 (0.459 - 51.855) | 1.2062 | 0.1890 |
| rs518598 | 2 | 169776914 | C | T | 1.313 (0.823 - 2.095) | 0.2383 | 0.2529 |
| rs853777 | 2 | 169812217 | C | T | 1.904 (0.879 - 4.123) | 0.3943 | 0.1026 |
| rs11708067 | 3 | 123065778 | A | G | 0.761 (0.506 - 1.143) | 0.2075 | 0.1876 |
| rs10934647 | 3 | 123130684 | C | T | 1.257 (0.735 - 2.152) | 0.2742 | 0.4035 |
| rs17085593 | 5 | 95630705 | C | G | 0.713 (0.451 - 1.125) | 0.2330 | 0.1461 |
| rs10040098 | 5 | 95674266 | C | T | 0.798 (0.550 - 1.157) | 0.1900 | 0.2339 |
| rs7722200 | 5 | 95717440 | T | C | 0.739 (0.518 - 1.054) | 0.1812 | 0.0949 |
| rs13169290 | 5 | 95729406 | G | A | 0.627 (0.423 - 0.930) | 0.2012 | 0.0204 |
| rs193069188 | 5 | 95736557 | C | T | 0.697 (0.499 - 0.972) | 0.1699 | 0.0333 |
| rs76323047 | 7 | 44185955 | G | A | 1.335 (0.660 - 2.702) | 0.3596 | 0.4213 |
| rs2908294 | 7 | 44204426 | T | C | 1.416 (0.927 - 2.162) | 0.2159 | 0.1072 |
| rs2971672 | 7 | 44205906 | C | A | 1.113 (0.790 - 1.570) | 0.1753 | 0.5406 |
| rs2908292 | 7 | 44210710 | T | C | 1.318 (0.879 - 1.978) | 0.2069 | 0.1817 |
| rs2908290 | 7 | 44216137 | A | G | 1.112 (0.793 - 1.558) | 0.1723 | 0.5390 |
| rs730497 | 7 | 44223721 | A | G | 1.602 (1.107 - 2.319) | 0.1886 | 0.0124 |
| rs2971667 | 7 | 44245060 | C | T | 1.309 (0.913 - 1.877) | 0.1838 | 0.1425 |
| rs4548554 | 10 | 113029377 | G | A | 1.072 (0.758 - 1.515) | 0.1766 | 0.6956 |
| rs174537 | 11 | 61552680 | G | T | 0.875 (0.516 - 1.486) | 0.2699 | 0.6218 |
| rs174546 | 11 | 61569830 | C | T | 0.873 (0.515 - 1.480) | 0.2693 | 0.6145 |
| rs174555 | 11 | 61579760 | T | C | 0.851 (0.494 - 1.464) | 0.2769 | 0.5590 |
| rs1535 | 11 | 61597972 | A | G | 1.069 (0.654 - 1.745) | 0.2501 | 0.7910 |
| rs12222793 | 11 | 92667047 | G | A | 0.994 (0.709 - 1.394) | 0.1726 | 0.9731 |
| rs11020107 | 11 | 92667730 | C | G | 1.181 (0.850 - 1.641) | 0.1677 | 0.3215 |
| rs12792753 | 11 | 92668975 | C | T | 1.054 (0.762 - 1.458) | 0.1657 | 0.7523 |
| rs10466351 | 11 | 92697981 | T | C | 0.778 (0.545 - 1.110) | 0.1813 | 0.1658 |
| rs10830963 | 11 | 92708710 | G | C | 0.941 (0.494 - 1.790) | 0.3282 | 0.8525 |
| rs954750 | 13 | 28463938 | T | C | 0.887 (0.540 - 1.456) | 0.2529 | 0.6353 |

Alt, alternative; Chr, chromosome; CI, confidence interval; CRC, colorectal cancer; FG, fasting glucose; HR, hazard ratio; Ref, reference; SE, standard error; SNP, single-nucleotide polymorphism.

¥ GRCh 37 coordinated.

¶ Regression was adjusted for 10 genetic principal components as well as age.

Table S3

1. Cox regressions of 4 genome-wide index-SNPs associated with FI predicting CRC risk

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **SNP** | **Chr** | **Position¥** | **Allele** | **HR¶ (95%CI)** | **SE** | ***p*** |
| **Ref** | **Alt** |
| rs1260326 | 2 | 27730940 | C | T | 1.362 (0.821 - 2.258) | 0.2580 | 0.2315 |
| rs780094 | 2 | 27741237 | C | T | 1.172 (0.752 - 1.826) | 0.2263 | 0.4839 |
| rs6450176 | 5 | 53298025 | A | G | 0.981 (0.683 - 1.409) | 0.1848 | 0.9182 |
| rs459193 | 5 | 55806751 | G | A | 0.970 (0.695 - 1.354) | 0.1701 | 0.8592 |

Alt, alternative; Chr, chromosome; CI, confidence interval; CRC, colorectal cancer; FI, fasting insulin; HR, hazard ratio; Ref, reference; SE, standard error; SNP, single-nucleotide polymorphism.

¥ GRCh 37 coordinated.

¶ Regression was adjusted for 10 genetic principal components as well as age.