

Supplemental Data

Identification of *KCNJ15* as a Susceptibility Gene

in Asian Patients with Type 2 Diabetes Mellitus

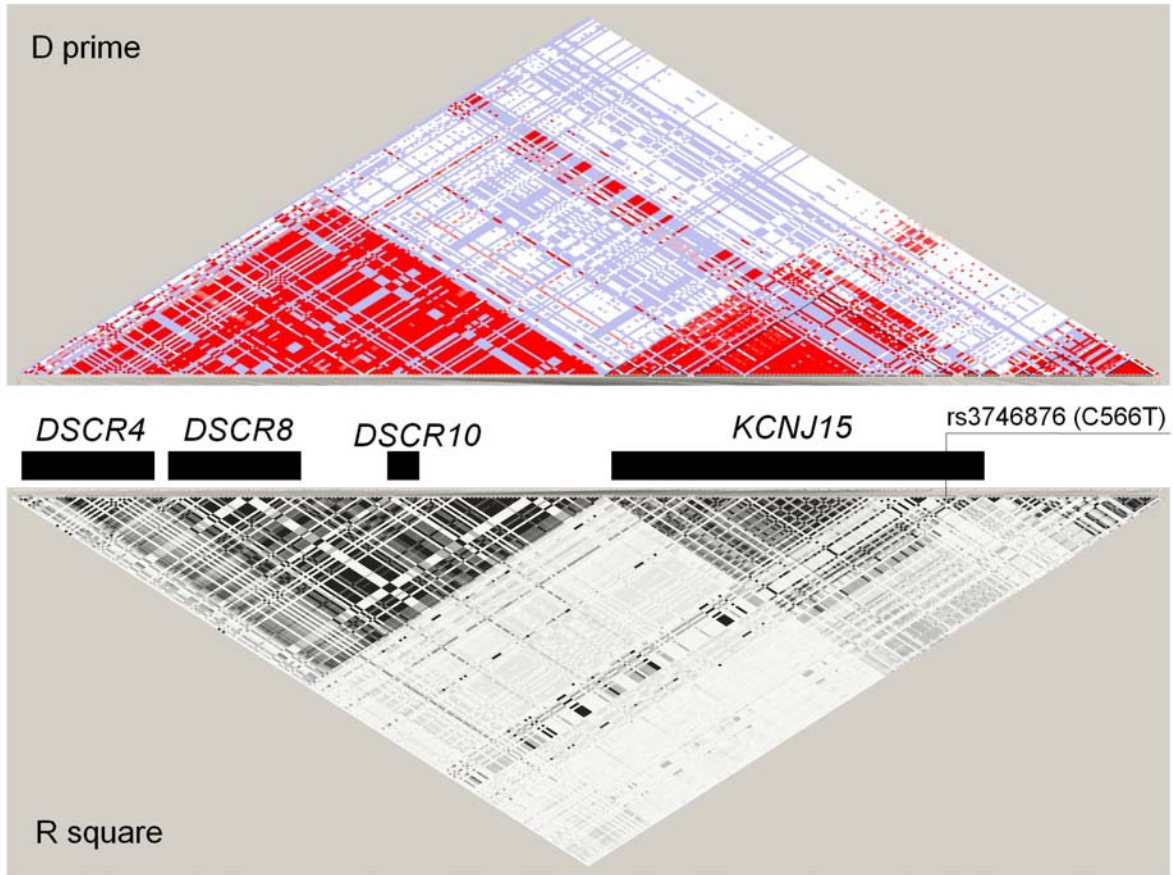
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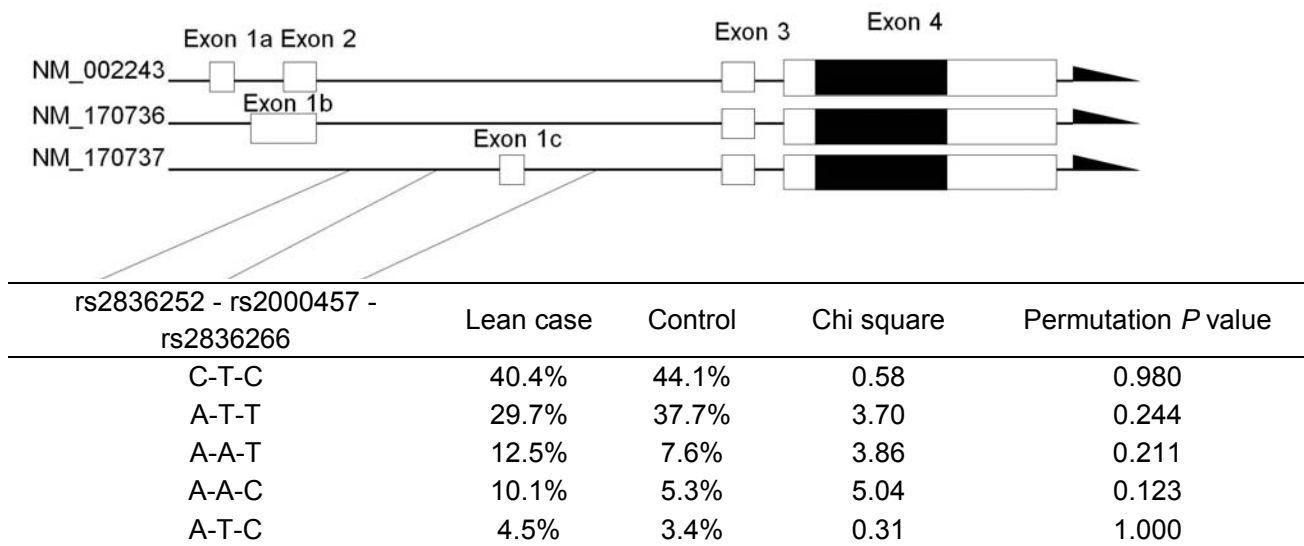
The Danish case-control study was supported by the Lundbeck Foundation Centre of Applied Medical Genomics for Personalized Disease Prediction, Prevention and Care (LUCAMP), and the Danish Diabetes Association. The Inter99 study was supported by the Danish Research Council, The Danish Centre for Health Technology Assessment, Novo Nordisk Inc., Research Foundation of Copenhagen County, Ministry of Internal Affairs and Health, The Danish Heart Foundation, The Danish Pharmaceutical Association, The Augustinus Foundation, and The Ib Henriksen Foundation. The Inter99 intervention was initiated by: Torben Jørgensen (PI), Knut Borch-Johnsen (co-PI), Hans Ibsen and Troels F. Thomsen. The steering committee comprises the former two and Charlotta Pisinger. The ADDITION study Denmark was supported by the National Health Services in the counties of Copenhagen, Aarhus, Ringkøbing, Ribe and South Jutland, together with the Danish Research Foundation for General Practice, Danish Centre for Evaluation and Health Technology Assessment, the diabetes fund of the National Board of Health, the Danish Medical Research Council, the Aarhus University Research Foundation and the Novo Nordisk Foundation. The study received unrestricted grants from Novo Nordisk, Novo Nordisk Scandinavia, Astra Denmark, Pfizer Denmark, GlaxoSmithKline Pharma Denmark, Servier Denmark and HemoCue Denmark.

Figure S1. LD Block Structure of the Target Region Extracted from HapMap Japanese Data



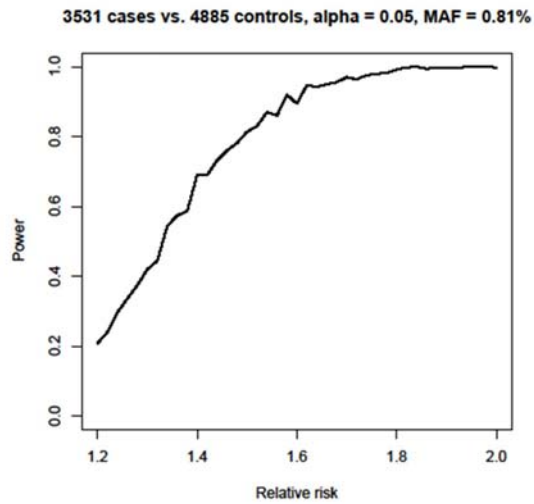
Haplotype structure and gene annotation. The plot includes pairwise r^2 values and D prime from the HapMap database for the JPT population.

Figure S2. Estimated Haplotype Frequencies in Intron 2 in Case and Control Samples



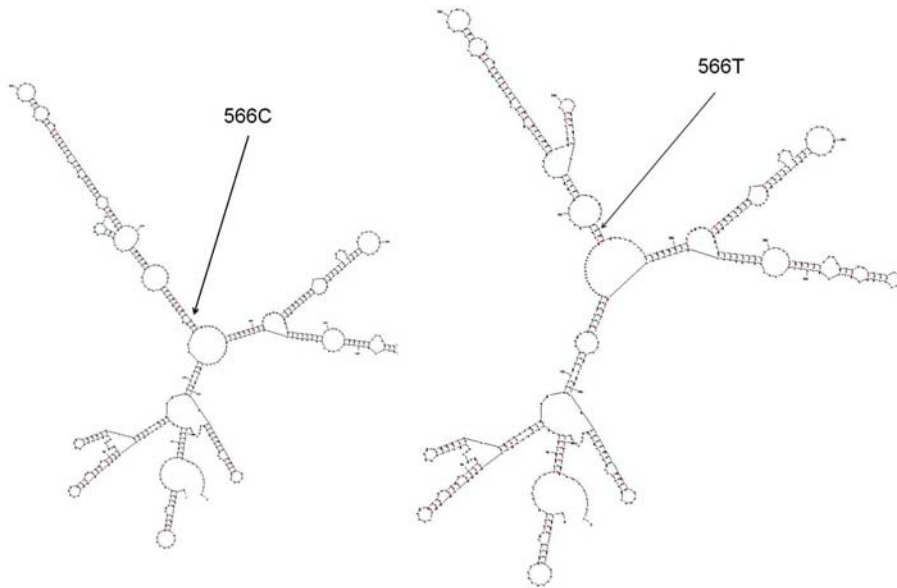
Structure of *KCNJ15* and SNPs used for haplotype analysis. Black blocks represent coding regions and white blocks are the untranslated regions. Three SNPs (rs2836252, rs2000457, rs2836266) were selected for haplotype estimation. Haplotypes with frequencies of less than 3% were excluded. The permutation *p* value was calculated by Haploview ver. 4.1 with 10,000 permutations.

Figure S3. Statistical Power in the Danish Case-Control Study for Different Effect Sizes



A plot of the statistical power in the Danish case-control study for different effect sizes. The analyses are based on an additive model, a minor allele frequency of 0.81, a significance level of 0.05 and a disease prevalence of 8%.

Figure S4. Examples of *KCNJ15* mRNA Folding Structures Predicted by MFOLD



KCNJ15 mRNA sequence carrying C566T synonymous SNP was used for secondary folding structure model building by the use of the computer program MFOLD. Note an obvious change of folding patterns between the 566C and the 566T *KCNJ15* mRNA.

Table S1. Basic Characteristics of Subjects

| | | N | Sex (M:F) | Age | BMI | Diabetes duration |
|-------------------------------|-------------------------|-------|-----------|-----------|----------|-------------------|
| Japanese screening sample | Control | 200 | 94:106 | 54.0±8.2 | N.A. | N.A. |
| | All case | 149 | 68:81 | 59.9±9.7 | 23.1±2.1 | 13.7±8.7 |
| | Case Lean case | 96 | 46:50 | 59.8±9.9 | 21.4±1.7 | 14.8±8.8 |
| | Lifelong lean case | 36 | 13:23 | 56.1±11.6 | 20.4±1.4 | 13.0±8.6 |
| Japanese replication sample A | Control | 500 | 353:147 | 37.3±6.3 | N.A. | N.A. |
| | All case | 419 | 244:175 | 50.3±7.8 | 23.1±3.2 | 9.9±6.9 |
| | Case Lean case | 269 | 140:129 | 50.4±7.6 | 21.2±1.8 | 10.3±7.2 |
| | Lifelong lean case | 98 | 51:47 | 50.8±7.9 | 20.3±1.9 | 8.2±7.6 |
| Japanese replication sample B | Control | 1,000 | 502:498 | 64.6±11.6 | 24.0±3.8 | N.A. |
| | All case | 1,000 | 583:417 | 59.7±10.3 | 24.2±3.9 | 12.0±10.1 |
| | Case Lean case | 510 | 314:196 | 61.6±9.4 | 21.3±1.9 | 13.5±10.9 |
| | Lifelong lean case | 151 | 98:53 | 63.1±9.7 | 20.5±2.2 | 14.3±9.7 |
| Danish replication sample | Control | 4,885 | 2264:2621 | 46.4±8.8 | 25.5±4.1 | N.A. |
| | All case | 3,531 | 2097:1434 | 60.4±19.7 | 30.7±5.5 | N.A. |
| | Case Relative lean case | 1,748 | 1105:643 | 61.3±10.0 | 26.4±2.6 | N.A. |
| | Absolute lean case | 454 | 238:216 | 62.0±11.2 | 22.9±1.8 | N.A. |

Japanese lean case was defined as the body mass index ≤ 24 at the time of sampling.

Japanese lifelong lean case was defined as the body mass index ≤ 24 for lifelong time.

Danish relative lean case was defined as the body mass index ≤ 30.0 as 50 percentile of type 2 diabetes mellitus cases

Danish absolute lean case was defined as the body mass index ≤ 25.0 as population based control samples 50 percentile

Values are means \pm standard deviation, NA: not available.

Table S2. Specific Primer Pairs for Pooled CE-SSCP

| SNP ID | Sequence | | Product (bp) | Annealing temperature (°) | Temperature of SSCP (°) |
|------------|-----------------------------|-----------------------------|-----------------|--------------------------------|------------------------------|
| | Forward primer | Reverse primer | | | |
| rs2070995 | 5'-ACTGCATGGGTGAAAAGAC-3' | 5'-GCTACCGGGTCATCACAGAT-3' | 163 | 63 | 20 |
| rs2836154 | 5'-GATCAGAAGGTCCCAGTGG-3' | 5'-GGGTTAGGAGAGAGCCATCC-3' | 221 | 66 | 25 |
| rs743296 | 5'-TTCTGCACAGCACTTTGCTT-3' | 5'-CCAGCCTCCTGCAGAGTAAG-3' | 303 | 61 | 25 |
| rs461155 | 5'-TCTGCCTCAATAAGCCAACC-3' | 5'-AGAAACACCTCGGTGAATG-3' | 209 | 61 | 20 |
| rs1541101 | 5'-TATTGCCAAGCTGCCTTTCT-3' | 5'-GAGCCATGGAGAAAAATGGA-3' | 283 | 61 | 20 |
| rs3787927 | 5'-GCTGGACTTTGAGCACTTCC-3' | 5'-CTGTGCATCTCCACCCAGT-3' | 195 | 66 | 25 |
| rs666085 | 5'-AAGTCAATGGCAAGGATGG-3' | 5'-GGGAATGGTCAAGGCAAGTA-3' | 203 | 66 | 25 |
| rs914162 | 5'-GTGGCAGGCTCTGTTCTAGG-3' | 5'-GCTCAAGGCTGAATGGAGAG-3' | 214 | 66 | 25 |
| rs914172 | 5'-TGATCTGACCAACCCTCCTC-3' | 5'-GACAGGGAAGGAATTGTCCA-3' | 251 | 61 | 25 |
| rs2210277 | 5'-TATAGCAGGGTTGGCAGAC-3' | 5'-TCTAAGCCTTCGGATGGAAA-3' | 289 | 60 | 25 |
| rs12149 | 5'-CTGCTCCAGATGCCTTCTA-3' | 5'-GAGAAGAGAACGAGCCAAGG-3' | 217 | 63 | 20 |
| rs398800 | 5'-AGCAAGGATAAGCCTGTGA-3' | 5'-GTACTTTGGGGCTCCTAGC-3' | 194 | 63 | 20 |
| rs462574 | 5'-GTGCCAACTGTTTCCAAGGT-3' | 5'-CTCTCTGTGGTCCCTTCCAA-3' | 265 | 63 | 20 |
| rs11203151 | 5'-GATGGTGATGGCAGAGGAAT-3' | 5'-GGTGCTCAGAACTTTCCAC-3' | 150 | 63 | 20 |
| rs2838111 | 5'-GGCATCCAAAATGTCAGCTT-3' | 5'-GGTTTACCAGAGTCTCCA-3' | 269 | 66 | 20 |
| rs2236692 | 5'-CACCTGGCAGGAAATAGCAT-3' | 5'-CAGAAATCCCAGTGGAAAGAA-3' | 183 | 61 | 20 |
| rs2839392 | 5'-GCAAAATGACAGAGGAAAA-3' | 5'-GTGAGAAGACCTTCCGCATC-3' | 201 | 61 | 25 |
| rs220159 | 5'-CTCCAATAAGGCCAGTTCA-3' | 5'-AGAGCCTCGAACCGTAACAA-3' | 184 | 61 | 20 |
| rs225361 | 5'-GACCCTGCTCAGAAGACACC-3' | 5'-TGCAGGAGAAAAACCCTGAC-3' | 163 | 63 | 20 |
| rs2839497 | 5'-AGCAGGAGTCCGAGAAAAACA-3' | 5'-CCCACGAAGCCTACAACATT-3' | 260 | 63 | 20 |
| rs11203201 | 5'-ACTTCTCCTCCGCTTCTTC-3' | 5'-CAGCGTCCACCAATCCTAAC-3' | 152 | 63 | 20 |
| rs1893592 | 5'-TTGAAAACGATCCCCATTA-3' | 5'-GCCACTTCTTGTGTGTGA-3' | 244 | 59 | 25 |
| rs884339 | 5'-TAAGCTGGACTTGCTCATGC-3' | 5'-GGTCTGAGTGAGGCTGTA-3' | 195 | 63 | 25 |
| rs1788448 | 5'-ATTTCCAGCAATCTGCACT-3' | 5'-TTTAGCCACACCATGTGCTC-3' | 242 | 61 | 25 |
| rs869725 | 5'-GGTGATCCAGGAGGCTACAA-3' | 5'-CTCTCTCAGCCCTGGAGGT-3' | 290 | 63 | 30 |
| rs2839629 | 5'-CTCTCTGCAATGGTGCTTT-3' | 5'-CGAAATCTTAGAGGGGTCA-3' | 166 | 63 | 20 |
| rs234784 | 5'-CCATGGGTCTCAGCTGATCT-3' | 5'-TTCTTCCCAGGAAGGTTTT-3' | 151 | 57 | 25 |
| rs870137 | 5'-CCACCCAGCACCTCATAAAC-3' | 5'-AGCCTGTGGAATGAGGTCAC-3' | 218 | 66 | 25 |
| rs229351 | 5'-TGTGAGAGGCAGAAATGCAA-3' | 5'-GAATGAGCCTGCCTGAGAAC-3' | 177 | 61 | 30 |
| rs162385 | 5'-CCCAGAACTGAAGGAAGTG-3' | 5'-TGACTGCGTCATTGTTAGGG-3' | 150 | 59 | 25 |
| rs229341 | 5'-TAGGGAGTGAGCCTCCTCTG-3' | 5'-CTTCCGGTGTCAATTGCTCTC-3' | 224 | 63 | 25 |
| rs762400 | 5'-CCTCAGTGATCCCATTTGGT-3' | 5'-ACGGCGAATACGGTAATGAG-3' | 170 | 63 | 30 |
| rs1107204 | 5'-TCTTCTCCTCAGTCCTCA-3' | 5'-TTGGTTCCAGACTTGACAG-3' | 155 | 61 | 30 |
| rs11701801 | 5'-CTGTGAGGGGAAGAGAGTG-3' | 5'-CTAAGCTGTGACAGGCCCA-3' | 180 | 63 | 25 |
| rs915770 | 5'-TTGCCTCTGTGACGTCTCTC-3' | 5'-CAAGAAAGGGCAACTCCAAG-3' | 185 | 61 | 20 |
| rs915876 | 5'-GAAAGCGCTTCTGAAACAGC-3' | 5'-AGAGAGGCTTCGTGCATCAT-3' | 192 | 61 | 30 |
| rs1051981 | 5'-CATGAATGCTTCTGCCTTTT-3' | 5'-GCTGCAAATTCCTTGCTTTT-3' | 232 | 61 | 20 |
| rs2073435 | 5'-TTCCTGATGAAGCAGAAGCA-3' | 5'-TGGTCTGTGACCCAGCAATA-3' | 238 | 63 | 30 |
| rs2026880 | 5'-GAGGCGTTCACTCATGTTCA-3' | 5'-CTGTGCTCGAATCACAGGAA-3' | 181 | 59 | 25 |
| rs1800522 | 5'-AACGATGGCCATGATTCTGT-3' | 5'-GGAGGTGTCTTCTCAGCAC-3' | 199 | 63 | 25 |
| rs1057034 | 5'-CCTACAACCTGGTCCAGCAC-3' | 5'-AAACCCAGGGCCTACAGT-3' | 161 | 66 | 20 |
| rs11911937 | 5'-ATGCTCCGTGGGAGAAG-3' | 5'-GCTCTGGCCTAGGGAGTAGG-3' | 166 | 66 | 25 |
| rs458178 | 5'-CCAGGCTGATCTCAAACCTCC-3' | 5'-CTGGCATGTGCATTAACACC-3' | 208 | 66 | 25 |
| rs2838624 | 5'-GCTGCCTGTGAGTGAAGTA-3' | 5'-GGAGAAACAAACCGTGAAG-3' | 162 | 63 | 25 |
| rs1883039 | 5'-AGCTGATCGATGTGACGATG-3' | 5'-CAAAAAGTCCAAGCAGCTC-3' | 219 | 63 | 30 |
| rs235312 | 5'-GGACGAAGACCCGACCTTACA-3' | 5'-AGCAGCCATCAAAATTGGAC-3' | 215 | 63 | 20 |
| rs235280 | 5'-AGAAAATGCACCAGGACCAAG-3' | 5'-ACCGTAGCGTAGGTTGAGA-3' | 161 | 66 | 20 |
| rs760458 | 5'-GGAAGAAAGGACAGCCACAG-3' | 5'-GGTTCTGCCCTCATCAAATC-3' | 230 | 63 | 30 |
| rs928311 | 5'-GACTTTGCTGCTTTGGGATG-3' | 5'-AACACAAGCCACAGGACTC-3' | 179 | 63 | 30 |
| rs10854467 | 5'-CCGGAAGTCAGACACCTTTT-3' | 5'-TTCTACGACTCTGCCCTGGT-3' | 245 | 63 | 30 |

| | | | | | |
|------------|-------------------------------|-----------------------------|-----|----|----------|
| rs2236445 | 5'-AAAAGCACCTTCTGCACACA-3' | 5'-ATCGTCAGGAGGCATTTGAG-3' | 184 | 63 | 20 |
| rs2255761 | 5'-GGCCATACTGCCATCTCCTA-3' | 5'-CATCAGGACACCACCTTCTGC-3' | 199 | 63 | 20 |
| rs2297291 | 5'-ATGGCTGATCCAGCTCACT-3' | 5'-AGAGCTGAGCAGAGCCACTC-3' | 171 | 63 | 30 |
| rs9306142 | 5'-TGCCTAAAATCGAGCTAGGG-3' | 5'-CTTTCCTCAGGACCACTCCA-3' | 228 | 61 | 20 or 25 |
| rs1736421 | 5'-GAGGGGCAGGGAGATACTTC-3' | 5'-AAGATGCCAACATCCAGGAG-3' | 218 | 63 | 25 |
| rs13047753 | 5'-TGTGCAGCCTGTTCTTGTTTC-3' | 5'-TCAGAACTGCTCCCTTCGAT-3' | 197 | 61 | 25 |
| rs12626197 | 5'-GGTCTGCGGTACGAAGTCAG-3' | 5'-GTTCTCTGTGCGCAGCACGTA-3' | 183 | 66 | 30 |
| rs9637215 | 5'-GAAGGGAGCTCACAGGATTG-3' | 5'-GGCAGGCAGCAGTTGTAGTT-3' | 236 | 66 | 30 |
| rs2280957 | 5'-CTATGGCTCTGCTCCCAAAG-3' | 5'-GGGTGAGGGAGAGACTAGCA-3' | 248 | 63 | 30 |
| rs2839171 | 5'-CCAAAAGTTTCTTTAAGGGGAAA-3' | 5'-AGGGACACAAATCCAAACCA-3' | 185 | 59 | 20 |
| rs2839181 | 5'-AAATGCAGCTAGTCCCCTCA-3' | 5'-GTGTCAGTCGGGGAAATTGT-3' | 196 | 63 | 20 |
| rs2249057 | 5'-GCACCTCTCGTGTGGAAGAT-3' | 5'-TGGAAGTCTTTGCTTACCC-3' | 217 | 61 | 25 |
| rs2839302 | 5'-AGCAAGCAGCTGTTTTGACA-3' | 5'-AGAGTGTGGTGTGGGAGCAT-3' | 155 | 63 | 20 |
| rs1107065 | 5'-TCCTCTCTCGCAGGAACAGT-3' | 5'-AGCCTCCCACTCACAGACTC-3' | 250 | 63 | 25 |
| rs9722 | 5'-CCGTTAAAACAGCCTTTGGA-3' | 5'-ACTACTGCCTGCCACGAGTT-3' | 213 | 61 | 20 |

Table S3. Specific Primer Pairs for the Variation Screening

| Region | Forward primer | Reverse primer |
|--------------------|----------------------------------|----------------------------------|
| Promoter | 5'-CAGAGATCTCCATTAGAACCT-3' | 5'-ATTTGGTTCTTCTGGATCATGGA-3' |
| Exon 1a | 5'-TCCATGATCCAGAAGAACCAAAT-3' | 5'-CTGAGAAAGGAGACCATGATGTCAGC-3' |
| Exon 2& exon1b | 5'-CTGGATGCCCACTAGAATCCTGTG-3' | 5'-TGTCCCATCATTAAAGTAAATCCC-3' |
| Exon 1c | 5'-ATGAGGGCAGCTGGGCGGTGGGAC-3' | 5'-CCAGAAATCTCCTTTAAGGTC-3' |
| Exon 3 | 5'-GAACCTTTACCCTATTCTGTGCAC-3' | 5'-GAAAGAGAGCAGCTGGCACTCAGC-3' |
| Exon 4 (section 1) | 5'-AGAATTCTCCTTTCTTGTAATTC-3' | 5'-CAGAGAGCTGGCACTGAATCAA-3' |
| Exon 4 (section 2) | 5'-TTGATTCAGTGCCAGCTCTCTG-3' | 5'-GCTTGCAGGGTTAAACCTGGATGGC-3' |
| Exon 4 (section 3) | 5'-GCCATCCAGGTTTAAACCCTGCAAGC-3' | 5'-CATTGTGTAGGTTCCACAGTTGT-3' |
| Exon 4 (section 4) | 5'-ACAACCTGTGAAACCTACACAAATG-3' | 5'-TGACTGAGACAACAATTACTCTCAAG-3' |
| Exon 4 (section 5) | 5'-CTTGAGAGTAATTGTTGTCTCAGTCA-3' | 5'-ATGTATGCAGGGGCTGAATATTCA-3' |

Table S4. Specific Primers for Quantitative Real-Time PCR

| Gene name | Direction | Sequence |
|----------------------------|-----------|--------------------------------|
| Human KCNJ15 | Sense | 5'-GGAATGTCCTCATGCCATCT-3' |
| | Antisense | 5'-TTCTGCTTGGTGATGACTGC-3' |
| Rat kcnj15 | Sense | 5'-CCGTTCCATCACAGAGGAGT-3' |
| | Antisense | 5'-GCTTTTTGGGTCTTGCAATC-3' |
| Rat kir6.2 | Sense | 5'-GCCATGCTGTCCCGAAAGGG-3' |
| | Antisense | 5'-GGCCAGGGGACATTCCTCTGT-3' |
| Rat glut2 | Sense | 5'-ATGTCAGAAGACAAGATCACCGGA-3' |
| | Antisense | 5'-CCCGAGCCACCCACCAAAGAAT-3' |
| Rat preproinsulin | Sense | 5'-TGCCCGGGCTTTTGTCAAAC-3' |
| | Antisense | 5'-CTCCAGTGCCAAGGTCTGAA-3' |
| Human & rat β -actin | Sense | 5'-CGCACCCTGGCATTGTCAT-3' |
| | Antisense | 5'-TTCTCCTTGATGTCACGCAC-3' |
| GFP | Sense | 5'-ACGTAAACGGCCACAAGTTC-3' |
| | Antisense | 5'-AAGTCGTGCTGCTTCATGTG-3' |

Table S5. Estimated Allele Frequencies by Pooled CE-SSCP and Allele and Genotype Frequencies Determined by Individual Typing

| SNP ID | Pooled sample | | | Individual sample | | | Control (%) | |
|-----------|---------------|-------------|-------------|-------------------|---------------|--------------------------|--------------------------|------------|
| | All case | Lean case | Control | All case (%) | Lean case (%) | | | |
| rs743296 | Allele | n.s. | $P = 0.039$ | Allele | $P = 0.042$ | $P = 0.013$ | | |
| | C | 66.2% | 68.4% | 58.9% | C | 218 (75.7) | 143 (78.6) | 238 (68.4) |
| | G | 33.8% | 31.6% | 41.1% | G | 70 (24.3) | 70 (21.4) | 110 (31.6) |
| | | | | | Genotype | $P = 2.7 \times 10^{-3}$ | $P = 4.2 \times 10^{-4}$ | |
| | | | | | CC | 88 (61.1) | 61 (67.0) | 77 (44.3) |
| | | | | | CG | 42 (29.2) | 21 (23.1) | 84 (48.3) |
| | | | | | GG | 14 (9.7) | 9 (9.9) | 13 (7.5) |
| rs869725 | Allele | $P = 0.036$ | n.s. | Allele | $P = 0.037$ | n.s. | | |
| | T | 67.6% | 67.6% | 59.2% | T | 181 (63.7) | 118 (64.1) | 239 (60.4) |
| | C | 32.4% | 32.4% | 40.8% | C | 103 (36.3) | 66 (35.9) | 157 (39.6) |
| | | | | | Genotype | n.s. | n.s. | |
| | | | | | TT | 59 (41.5) | 37 (40.2) | 74 (37.4) |
| | | | | | TC | 63 (44.4) | 44 (47.8) | 91 (46.0) |
| | | | | | CC | 20 (14.1) | 11 (12.0) | 33 (16.7) |
| rs162385 | Allele | $P = 0.042$ | n.s. | Allele | n.s. | n.s. | | |
| | A | 49.7% | 51.2% | 56.7% | A | 146 (51.4) | 96 (53.3) | 207 (52.8) |
| | G | 50.3% | 48.8% | 43.3% | G | 138 (48.6) | 84 (46.7) | 185 (47.2) |
| | | | | | Genotype | n.s. | n.s. | |
| | | | | | AA | 38 (26.8) | 25 (27.8) | 52 (26.5) |
| | | | | | AG | 70 (49.3) | 46 (51.1) | 103 (52.6) |
| | | | | | GG | 34 (23.9) | 19 (21.1) | 41 (21.1) |
| rs2297291 | Allele | n.s. | $P = 0.035$ | Allele | n.s. | n.s. | | |
| | A | 61.3% | 62.7% | 52.5% | A | 164 (57.3) | 105 (57.7) | 191 (50.5) |
| | G | 38.7% | 37.3% | 47.5% | G | 122 (42.7) | 77 (42.3) | 187 (49.5) |
| | | | | | Genotype | n.s. | n.s. | |
| | | | | | AA | 43 (30.1) | 30 (33.0) | 50 (26.5) |
| | | | | | AG | 78 (54.5) | 45 (49.5) | 91 (48.1) |
| | | | | | GG | 22 (15.4) | 16 (17.6) | 48 (25.4) |
| rs2280957 | Allele | n.s. | $P = 0.026$ | Allele | $P = 0.043$ | $P = 0.019$ | | |
| | G | 75.7% | 73.5% | 81.9% | G | 216 (76.1) | 134 (71.3) | 320 (80.0) |
| | A | 24.3% | 26.5% | 18.1% | A | 68 (23.9) | 54 (28.7) | 80 (20.0) |
| | | | | | Genotype | n.s. | $P = 8.8 \times 10^{-3}$ | |
| | | | | | GG | 76 (53.5) | 45 (47.9) | 128 (64.0) |
| | | | | | GA | 64 (45.1) | 44 (46.8) | 64 (32.0) |
| | | | | | AA | 2 (1.4) | 5 (5.3) | 8 (4.0) |

Lower p value based on genotype frequencies with recessive or dominant model
Lean case was defined as the body mass index ≥ 24 at the time of sampling.
Lifelong lean case was defined as the body mass index ≥ 24 for lifelong time.

Table S6. Clinical Characteristics Associated with C566T

| | Japanese panel [#] | | | Danish panel | | |
|--------------------|-----------------------------|-----------------------|-----------------------|----------------------------|----------------------------|---------|
| | CC | CT | TT | CC | CT | TT |
| N (men/women) | 492 | 53 | 3 | 5690 (2824/2866) | 93 (46/47) | 0 (0/0) |
| Age (years) | 49.4±8.8 | 50.0±8.2 | 46.5±10.0 | 46.2 ± 7.9 | 44.7 ± 8.1 | - |
| BMI at enrollment | 23.2±3.2 | 22.7±2.9 | 20.8±1.6 | 26.2 ± 4.6 | 25.6 ± 3.7 | - |
| Maximal BMI | 26.4±4.0 | 50.0±3.4 | 46.5±1.2* | N.A. | N.A. | - |
| Insulin deficiency | 40.4 ^{##} | 59.3 ^{##,**} | 66.7 ^{##,**} | 49.5 ± 70.4 ^{###} | 64.8 ± 51.3 ^{###} | - |
| HOMA-IR | 2.7±2.0 | 2.9±3.7 | - | 4.8 ± 5.5 | 4.2 ± 2.5 | - |

*: C/T + T/T p value < 0.05 compared with CC.

** : T/T p value < 0.05 compared with CC.

: Cases followed up more than 10 years

: Insulin deficiency was defined as require insulin therapy or HOMA-β < 10 within 10 years after diagnosis

: HOMA-B (fasting plasma insulin (U/ml) × 20 / (fasting plasma glucose (mmol/l) -3.5) data at enrollment was documented.

HOMA-IR: fasting insulin (μU/ml) x fasting glucose (mg/dl) / 405.

Values are means ± S.D