

Online appendix Table 1. Hardy-Weinberg equilibrium, genotyping success rate , and statistical power of each genetic variant.

Gene	SNP	Minor Allele	Major Allele	Hardy-Weinberg equilibrium						Genotyping success rate (%)	Statistical power <sup>†</sup>	Statistical power <sup>‡</sup>
				Total (n=1501)		GDM (n=869)		Control (n=632)				
				mm/mM/MM*	P value	mm/mM/MM*	P value	mm/mM/MM*	P value			
KCNQ1	rs2074196	T	<b>G</b>	232/718/536	0.787	123/411/326	0.773	109/307/210	0.935	99.7	0.659	0.588
	rs2237892	T	<b>C</b>	196/679/602	0.822	96/390/367	0.648	100/289/235	0.502	99.1	0.913	0.865
	rs2237895	<b>C</b>	A	131/677/672	0.036	77/410/369	0.016	54/267/303	0.704	99.3	0.465	0.405

mm/mM/MM\*, m and M represents minor allele and major allele, respectively.

<sup>†</sup>[Assuming prevalence of GDM as 10 % in additive model.](#)

<sup>‡</sup>[Assuming prevalence of GDM as 2.2% in additive model.](#)

Risk alleles are shown in bold type.

### **Onlin Appendix Figure Legend**

Online Supplemental Figure 1. Linkage disequilibrium(LD) pattern of the tested SNPs in *KCNQ1* along with its genomic location of RefSeq genes with intron and exon structure is visualized by Haploview (<http://www.broadinstitute.org/haploview>). Pairwise  $r^2$  values are shown with its corresponding color: dark represents high LD and light represents low LD. Since rs2074196 and rs2237892 were in strong LD only one LD block (rs2237893-rs2237895) were formed.

