

Supplementary Tables and Figures

Supplementary Table 1. Individual SNPs in the fasting glucose genetic risk score and their association with fasting glucose

SNP	Gene region	risk allele	other allele	β per risk allele	risk allele frequency	% additional variance in glucose explained by SNP*
rs780094	<i>GCKR</i>	C	T	.0463 mmol/L	.603	0.38
rs560887	<i>G6PC2</i>	C	T	.0685 mmol/L	.704	0.84
rs4607517	<i>GCK</i>	A	G	.0673 mmol/L	.172	0.51
rs13266634	<i>SLC30A8</i>	C	T	.0433 mmol/L	.684	0.34
rs10830963	<i>MTNR1B</i>	G	C	.0796 mmol/L	.278	0.86

*after adjustment for age, sex, and study center

Supplementary Table 2. Associations of intima-media thickness (IMT) with individual SNPs used to construct the fasting glucose genetic risk score

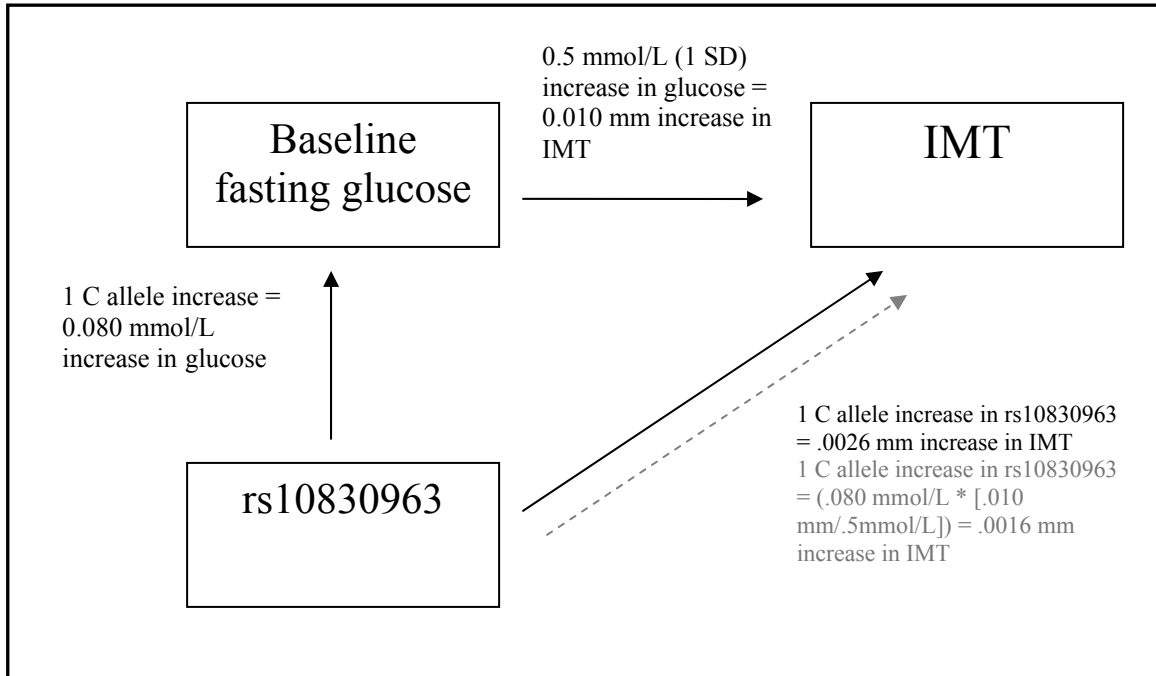
SNP	<i>Linear regression adjusted for age, sex, and study center</i>		<i>Linear regression models additional adjusted for baseline fasting glucose</i>	
	β^* (SE) for association with IMT (mm)	p-value	β^* (SE) for association with IMT (mm)	p-value
rs10830963	.0026 (.0030)	.38	.0011(.0030)	.73
rs560887	.0080 (.0029)	.0055	.0066 (.0029)	.022
rs4607517	.0068 (.0035)	.052	.0055 (.0035)	.12
rs13266634	.0014 (.0028)	.49	.0005 (.0028)	.85
rs780094	-.0020 (.0027)	.46	-.0029 (.0027)	.27

* *linear regression. Betas represent a 1 allele increase in the risk (glucose-raising) allele*

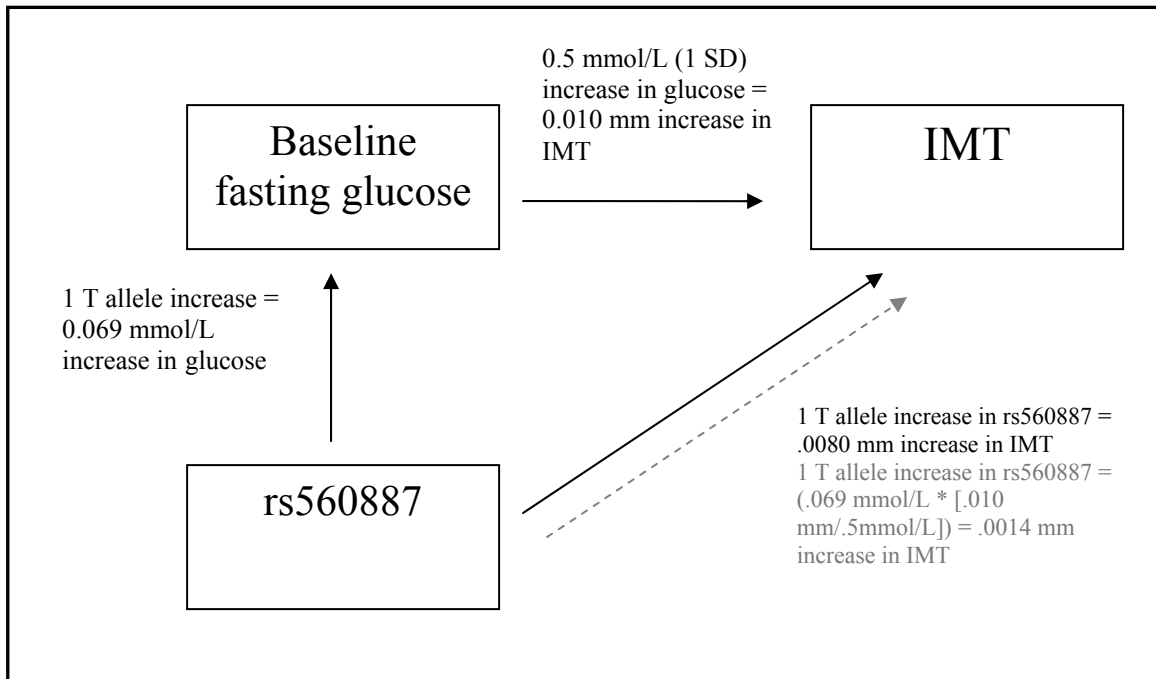
Supplementary Figure 1 (A-E). Observed vs. expected associations between the fasting glucose genetic risk score (FGGRS) and intima-media thickness (IMT)

Associations determined from observed regression equations are described in black. All regressions adjusted for age, sex, and center. Predicted associations are described in gray.

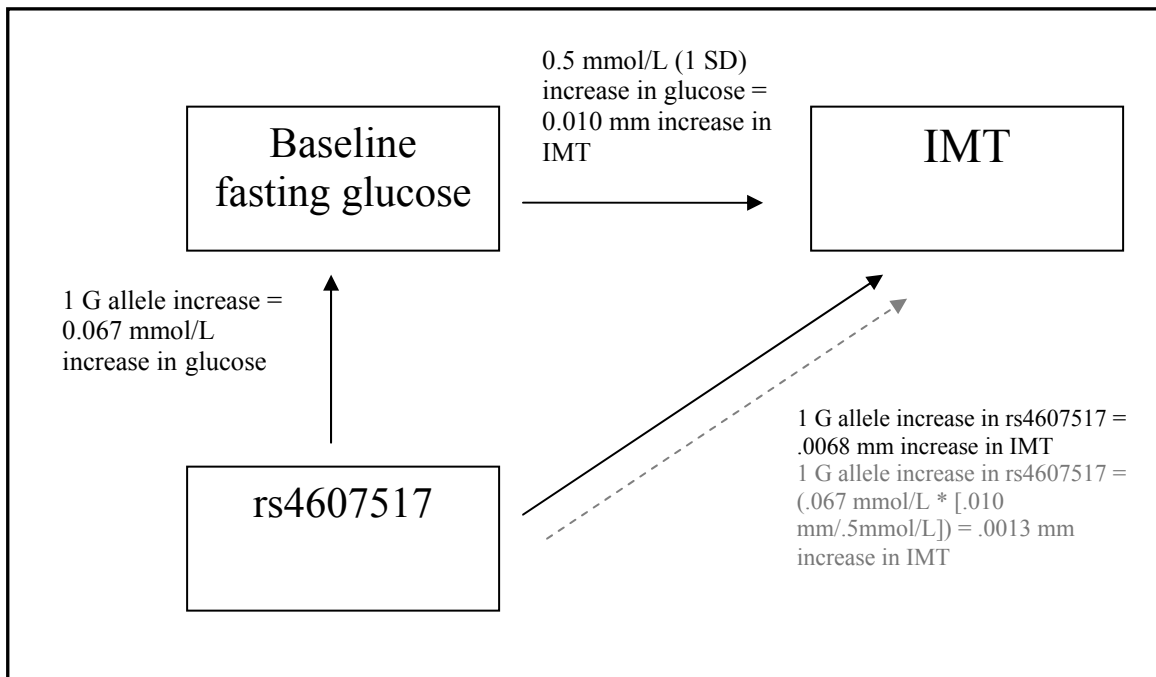
A) rs10839063



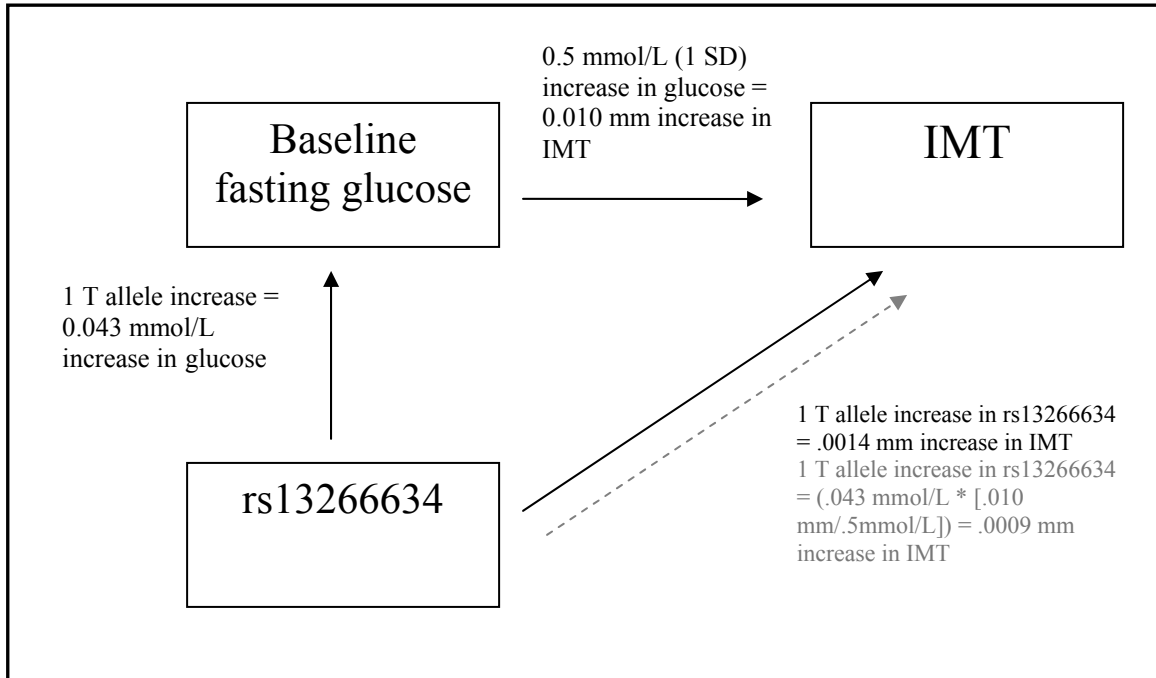
B) rs560887



C) rs4607517



D) rs13266634



E) rs780094

