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**Supplemental Table 1:** Comparison of ROC models where fasting time is included or is not included as a covariate

	ROC AUC	$\chi^2$ value (comparison with null distribution)	<i>P</i> -value (comparison with null distribution)
Genetic model (1)	0.5805	80.9	<1.0x10 <sup>-20</sup>
Genetic model (2)	0.5933	108.8	<1.0x10 <sup>-20</sup>
NGRS_1 model (1)	0.5667	56.0	7.4x10 <sup>-14</sup>
NGRS_1 model (2)	0.5796	78.5	<1.0x10 <sup>-20</sup>
NGRS_2 model (1)	0.6452	226.9	<1.0x10 <sup>-20</sup>
NGRS_2 model (2)	0.6536	255.0	<1.0x10 <sup>-20</sup>
NGRS_1 + genetic model (1)	0.6070	144.8	<1.0x10 <sup>-20</sup>
NGRS_1 + genetic model (2)	0.6133	162.4	<1.0x10 <sup>-20</sup>
NGRS_2 + genetic model (1)	0.6621	291.0	<1.0x10 <sup>-20</sup>
NGRS_2 + genetic model (2)	0.6677	312.3	<1.0x10 <sup>-20</sup>

Model (1) is unadjusted for fasting time, whereas model (2) is. ROC AUC: Receiver operator characteristic area under the curve. NGRS\_1 comprised of age, sex, and type 2 diabetes family history. NGRS\_2 comprised of NGRS\_1 + baseline fasting and 2-hr glucose concentrations, triglycerides, diastolic and systolic blood pressures, and BMI. Genetic model comprised of fasting glucose and type 2 diabetes loci, as described in the Methods section.