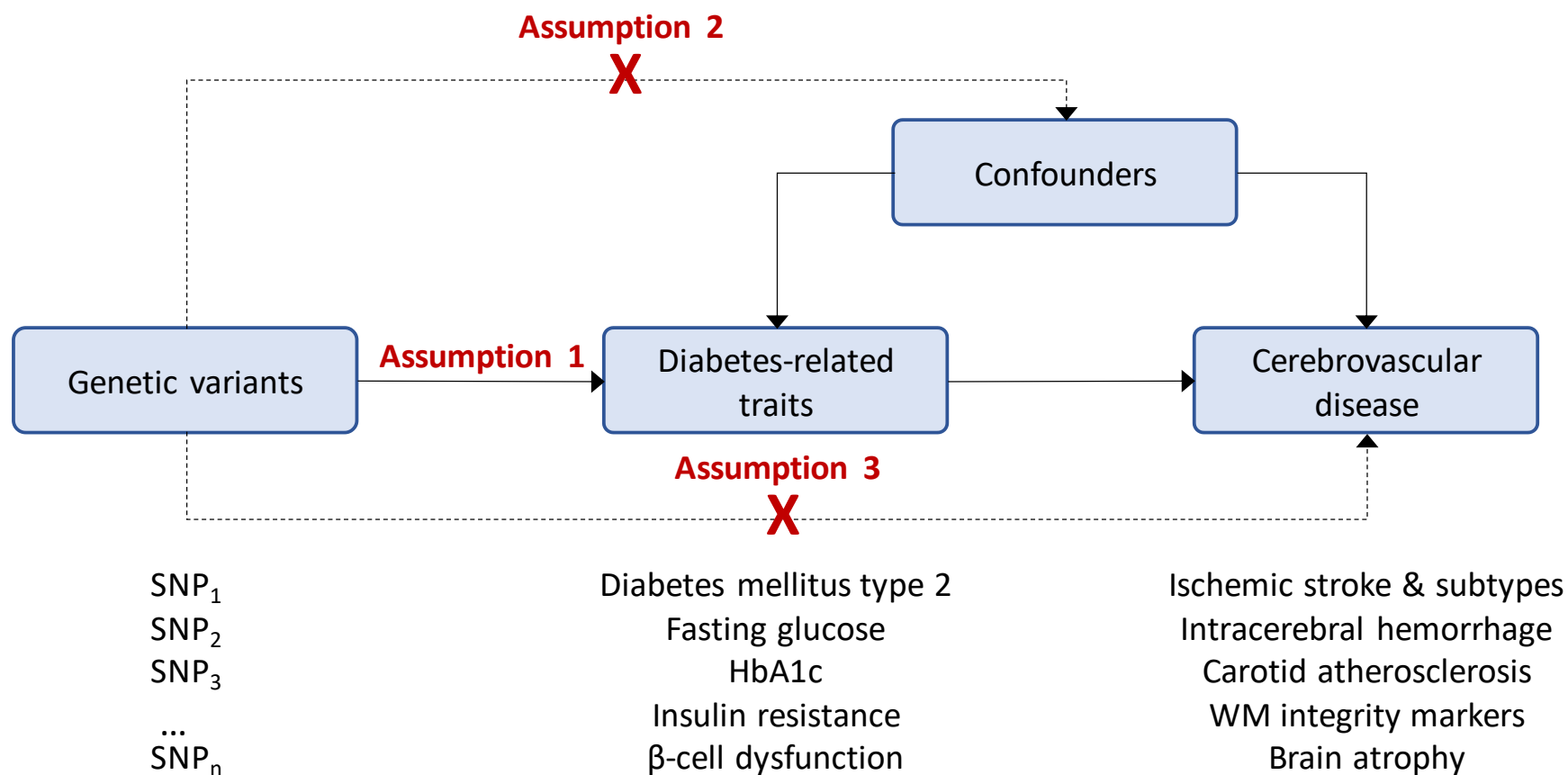
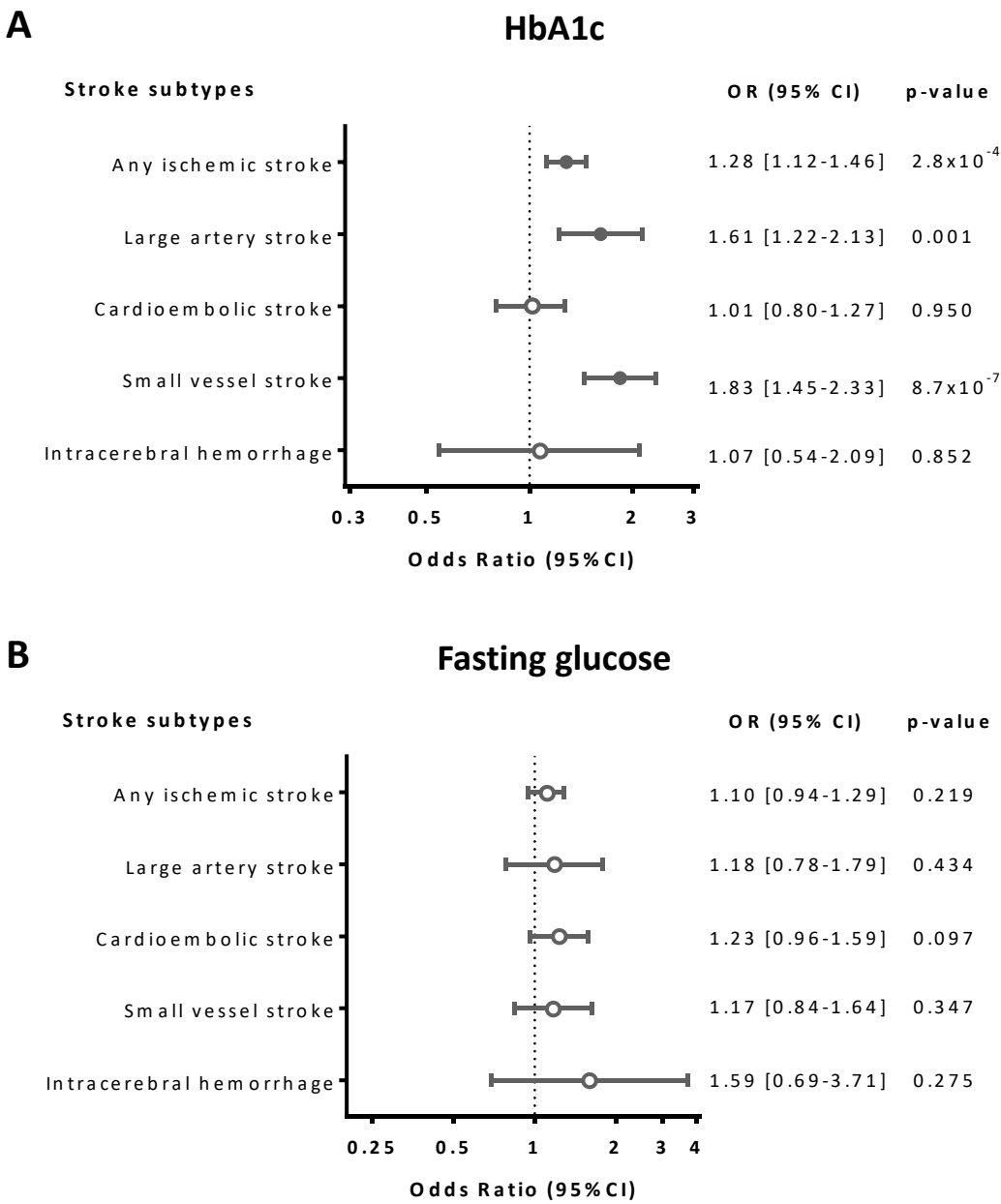


**Figure e-1. Schematic representation of our study design and assumptions of Mendelian randomization (MR) analyses.** The assumptions of the MR study design include the following: the genetic variants (instruments) must be associated with the exposure (assumption 1); the variants must not be associated with confounders (assumption 2); the variants must influence the outcome only through the risk factor under study (assumption 3).



*Abbreviations.* HbA1c, Glycated hemoglobin; SNP, single nucleotide polymorphism; WM, white matter.

**Figure e-2. Mendelian Randomization associations of genetic predisposition to (A) HbA1c levels, and (B) fasting glucose among non-diabetic individuals with stroke subtypes.** Results derived from random-effects inverse-variance weighted analyses.



Full circles correspond to statistically significant association estimates at an FDR-adjusted p-value<0.05.

*Abbreviations.* HbA1c, Glycated hemoglobin.