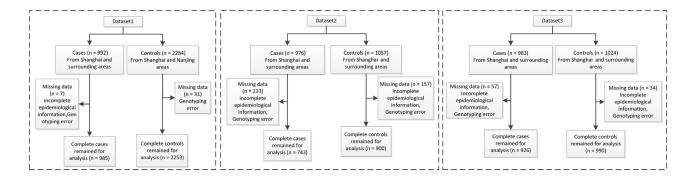
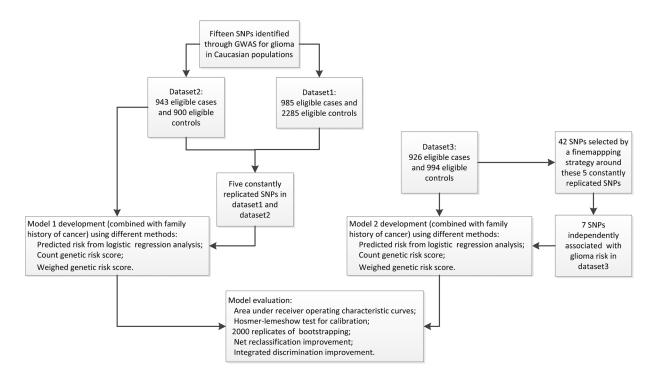
### Development of risk prediction models for glioma based on genome-wide association study findings and comprehensive evaluation of predictive performances

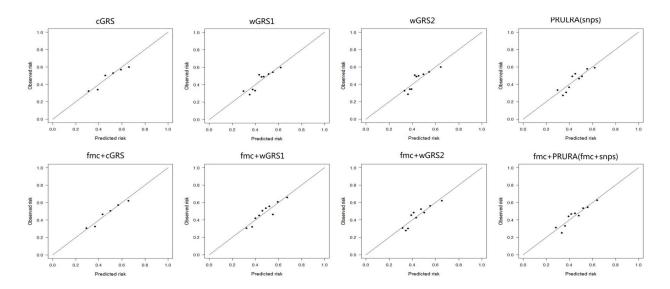
#### **SUPPLEMENTARY DATA**



Supplementary Figure 1: Participant flow diagrams of the three datasets in this study.

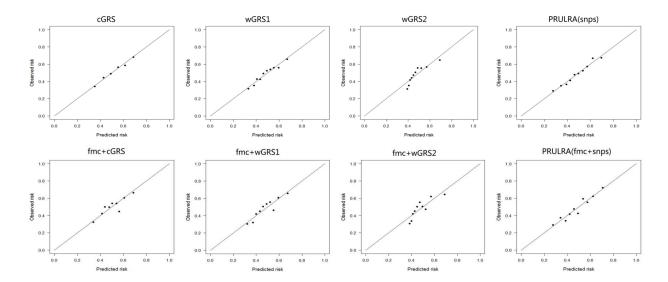


Supplementary Figure 2: Flow chart of the study design.



Supplementary Figure 3: Calibration plots in dataset2.

fmc: family history of caner; cGRS: count genetic risk score; wGRS: weighed genetic risk score; PRFLR: predicted risks from logistic regression analysis.



Supplementary Figure 4: Calibration plots in dataset3.

fmc: family history of caner; cGRS: count genetic risk score; wGRS: weighed genetic risk score; PRFLR: predicted risks from logistic regression analysis.

Supplementary Table 1: Basic epidemiological information of the study subjects

See Supplementary File: 1

### Supplementary Table 2: Univariate logistic regression analysis of family history of caner with glioma risk

Epidemiological variable	Dataset2		Dataset3	
	OR (95%CI)	P	OR (95%CI)	P
Family history of cancer	1.63(1.24-2.15)	0.001	1.47(1.13-1.91)	0.004

Supplementary Table 3: Associations between SNPs selected from previous GWAS and gioma risk in datasets 1 and
See Supplementary File: 1
Supplementary Table 4: Associations between selected SNPs and glioma risk in dataset3
Supplementary Table 4. Associations between selected 51v1 8 and ghoma 11sk in datasets
See Supplementary File: 1
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# $Supplementary\ Table\ 5:\ Interaction\ test\ P\ values\ for\ all\ combinations\ of\ 5\ SNPs\ used\ for\ model\ development\ in\ dataset 2$

SNP1	SNP2	Interaction P
rs2736100	rs2736100	0.326
rs2736100	rs2157719	0.536
rs2736100	rs498872	0.782
rs2736100	rs6010620	0.546
rs1077236	rs2157719	0.769
rs1077236	rs498872	0.831
rs1077236	rs6010620	0.237
rs2157719	rs498872	0.386
rs2157719	rs6010620	0.499
rs498872	rs6010620	0.228

# $Supplementary\ Table\ 6: Interaction\ test\ P\ values\ for\ all\ combinations\ of\ 7\ SNPs\ used\ for\ model\ development\ in\ dataset 3$

SNP1	SNP2	Interaction P	
rs2853677	rs2735948	0.531	
rs2853677	rs6589664	0.427	
rs2853677	rs494560	0.785	
rs2853677	rs17748	0.342	
rs2853677	rs3761121	0.196	
rs2853677	rs1058319	0.261	
rs2735948	rs6589664	0.125	
rs2735948	rs494560	0.715	
rs2735948	rs17748	0.700	
rs2735948	rs3761121	0.031	
rs2735948	rs1058319	0.199	
rs6589664	rs494560	0.746	
rs6589664	rs17748	0.333	
rs6589664	rs3761121	0.436	
rs6589664	rs1058319	0.055	
rs494560	rs17748	0.351	
rs494560	rs3761121	0.311	
rs494560	rs1058319	0.380	
rs17748	rs3761121	0.963	
rs17748	rs1058319	0.949	
rs3761121	rs1058319	0.059	