

Influence of obesity-related risk factors in the aetiology of glioma

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LIST OF ABBREVIATIONS

GBM Glioblastoma

MR Mendelian Randomization

IV Instrumental Variable

GWAS Genome-wide Association Study

GICC Glioma Case-Control Consortium

SNP Single nucleotide Polymorphism

BMI Body Mass Index

WHR Waist-Hip Ratio

GIANT Genetic Investigation of ANthropometric Traits

HDL High-Density Lipoprotein Cholesterol

LDL Low-Density Lipoprotein Cholesterol

GLGC Global Lipids Genetic Consortium

MAGIC Meta-Analysis of Glucose and Insulin related traits Consortium

SD Standard Deviations

LD Linkage Disequilibrium

WHO World Health Organisation

OR Odds Ratio

GSMR Generalised Summary-data-based Mendelian Randomisation

CI Confidence Interval

ABSTRACT

Background: Obesity and related factors have been implicated as possible aetiological factors for the development of glioma in epidemiological observation studies. We used genetic markers in a Mendelian randomization framework to examine if obesity-related traits influence glioma risk. This methodology reduces bias from confounding and is not affected by reverse causation.

Methods: Genetic instruments were identified for 10 key obesity-related risk factors, and their association with glioma risk was evaluated using data from a genome-wide association study of 12,488 glioma patients and 18,169 controls. The estimated odds ratio of glioma associated with each of the genetically defined obesity-related traits was used to infer evidence for a causal relationship.

Results: No convincing association with glioma risk was seen for genetic instruments for body mass index, waist-to-hip ratio, lipids, type-2 diabetes, hyperglycaemia or insulin resistance. Similarly we found no evidence to support a relationship between obesity-related traits with subtypes of glioma – glioblastoma (GBM) or non-GBM tumours.

Conclusions: This study provides no evidence to implicate obesity-related factors as causes of glioma.

INTRODUCTION

Glioma is the most common primary intracranial tumour, accounting for around 80% of all malignant brain tumours [1]. Thus far, few established risk factors for the development of glioma have been robustly identified [2].

Obesity-related factors are increasingly being recognised as risk determinants for the development many of common cancers, such as those of the breast and colorectum [3]. Evidence from epidemiological observational studies, for obesity-related traits being a risk factor for the development of glioma have, however been inconsistent, with only a subset of studies reporting a significant association [4-9]. Furthermore, in contrast to most cancers, some studies have reported diabetes to be protective against glioma [10-13]. Obesity-related exposures are however inherently interrelated [14, 15], and in traditional epidemiological studies it can be problematic to isolate specific risk factors that may exert a causal influence on disease from those that are merely associated with an underlying causal factor (i.e. confounded). Additionally, findings can be affected by reverse causation.

Mendelian randomization (MR) is an analytical approach to the traditional epidemiological study whereby genetic markers are used as proxies or instrumental variables (IVs) of environmental and lifestyle-related risk factors [16]. Such genetic markers cannot be influenced by reverse causation and can act as unconfounded markers of exposures provided the variants are not associated with the disease through an alternative mechanism [16]. Under these circumstances, the association between a genetic variant (or set of variants) and outcome of interest implies a causal relationship between the risk factor and outcome. MR has therefore been compared to a natural randomised controlled trial, circumventing some of the limitations of epidemiological observational studies [17]. However, as IVs used in MR often explain a small proportion of the exposure phenotypic variance, large sample sizes are required to have sufficient power [18].

To gain insight into the aetiology of glioma we have examined the role of obesity-related risk factors in glioma using an MR-based framework. Specifically, we identified genetic variants associated with 10 key obesity-related risk factors from external genetic association studies. We implemented two-sample MR [19] to estimate associations between these genetic variants with glioma risk using genome-wide association study (GWAS) data from the Glioma International Case-Control Consortium study (GICC) [20].

MATERIALS AND METHODS

Two-sample MR was undertaken using GWAS data. Ethical approval was not sought for this specific project because all data came from the summary statistics of published GWAS, and no individual-level data were used.

Genetic instruments for obesity and related risk factors

Genetic instruments were identified as a panel of single nucleotide polymorphisms (SNPs) identified from recent meta-analyses or largest studies published to date. Specifically: (i) SNPs for body mass index (BMI) and waist-to-hip ratio (WHR) were identified from the Genetic Investigation of ANthropometric Traits (GIANT) consortium [21, 22]; (ii) SNPs for circulating high-density and low-density lipoprotein cholesterol (HDL and LDL), total cholesterol and triglycerides, were identified from the Global Lipids Genetic Consortium (GLGC) [23]; (iii) SNPs for factors related to hyperglycemia and hyperinsulinemia - fasting glucose, fasting insulin, and 2-hour post-challenge glucose, were obtained from the Meta-Analysis of Glucose and Insulin related traits Consortium (MAGIC) [24] and (iv) SNPs for type-2 diabetes were identified from Gaulton *et al.* [25]. For each SNP, we recovered the chromosome position, the effect estimate expressed in standard deviations (SD) of the trait per-allele along with the corresponding standard error (**Supplementary Table 1**). We restricted our analysis to SNPs associated at genome-wide significance (*i.e.* $P \leq 5.0 \times 10^{-8}$) in individuals with European ancestry. To avoid collinearity between SNPs for each trait, we excluded SNPs that were correlated (*i.e.* $r^2 \geq 0.01$) within each trait, and only considered the SNPs with the strongest effect on the trait for inclusion in genetic risk scores (**Supplementary Table 2**). For type-2 diabetes, linkage disequilibrium (LD) scores with rs140730081 were calculated via a proxy SNP rs2259835 ($r^2=0.48$). After imposing these criteria we obtained 7 SNPs for 2-hour post-challenge glucose, 75 for BMI, 33 for fasting glucose, 13 for fasting insulin, 54 for HDL cholesterol, 26 for LDL cholesterol, 38 for type-2 diabetes, 39 for total cholesterol, 25 for triglycerides, and 33 for WHR.

Glioma association results

To evaluate the association of each genetic instrument with glioma risk, we made use of data from the most recent meta-analysis of GWAS in glioma, comprising >10 million genetic variants (after imputation) in 12,488 glioma patients and 18,169 controls from eight independent GWAS datasets of individuals of European descent (**Supplementary Table 3**) [20]. Comprehensive details of the genotyping and quality control of the seven GWAS have been previously reported [20]. To limit the effects of cryptic population stratification, association test statistics for six of the glioma GWAS were generated using principal components as previously detailed [20]. Gliomas are heterogeneous and different tumour subtypes, defined in part by malignancy grade (*e.g.* pilocytic astrocytoma World Health Organization (WHO) grade I, diffuse 'low-grade' glioma WHO grade II, anaplastic glioma WHO grade III and GBM WHO grade IV) can be distinguished [26]. For the sake of diagnostic brevity we considered gliomas as being either GBM or non-GBM tumours.

Statistical analysis

The odds ratios (OR) of glioma per unit of SD increment for each obesity-related trait, were estimated using Generalised Summary-data-based Mendelian Randomisation (GSMR) [27]. This approach performs a multi-SNP MR analysis, which is more powerful than other existing summary-data-based MR methodologies [28]. Separation of signals of causality from horizontal pleiotropy (a single locus influencing affecting multiple phenotypes, also referred to as type-II pleiotropy) is a recognized issue in MR analyses and we therefore used a HEIDI-outlier test [27] to detect and eliminate genetic instruments that have apparent pleiotropic effects on both the obesity-related trait and glioma. A *P*-value threshold of 0.01 for the HEIDI-outlier test was utilised as recommended by Zhu *et al.* The HEIDI-outlier test may also in theory detect additional violations of the assumptions of MR such as the exclusion restriction assumption..

For each statistical test we considered a global significance level of $P < 0.05$ as being satisfactory to derive conclusions. To assess the robustness of our conclusions, we imposed a Bonferroni-corrected significance threshold of 0.0017 (*i.e.* 0.05/30, to correct for testing 10 traits over

three outcomes). We considered a P value >0.05 as non-significant (*i.e.* no association), a P value ≤ 0.05 as evidence for a potential causal association, and a P value ≤ 0.0017 as significant evidence for an association. Additionally, we defined the Bayesian False Null Probability (BFNP) using the Bayesian False Discovery Probability (BFDP) as per Wakefield[29] by $BFNP=1-BFDP$. Then to assess if null results found could be considered reliable we calculated the minimum prior probability of the alternative hypothesis for which the Bayesian False Null Probability was $>10\%$. The power of an MR investigation depends greatly on the proportion of variance in the risk factor that is explained by the respective IV. We estimated study power *a priori* using the methodology of Burgess *et al* [30]. Statistical analyses were undertaken using R software (Version 3.1.2).

RESULTS

In our data sets, there were missing data for one fasting insulin SNP (rs1530559), four type-2 diabetes SNPs (rs2972156, rs34706136, rs11257658, rs144613775) and one total cholesterol SNP (rs7570971). These SNPs were excluded from our analysis. Performing HEIDI-outlier analysis on the instruments for each trait identified two SNPs as violating the assumptions of MR with respect to horizontal pleiotropy, rs11603023 for total cholesterol and rs5756931 for triglyceride, which were further excluded. Both SNPs are in LD with the lead SNP in glioma risk loci.

Subsequently, **Table 1** details the number of SNPs used as an IV for each of the obesity-related traits, the mean and SD of the risk factor in the original discovery study, and the proportion of variance explained for each factor by the corresponding genetic instruments. Effect estimates for each SNP used as genetic instruments for each risk factor and disease risk are detailed in **Supplementary Table 1**. For BMI and LDL, the SNPs rs12016871 and rs9411489 have since merged with the SNPs rs9581854 and rs635634 respectively, and it is from these subsequent SNPs the associations with glioma were derived. **Figure 1** shows the statistical power of genetic instruments for different levels of predicted ORs for each obesity-related trait.

Figure 2 shows a plot of the association of each IV with exposure against the association with glioma, together with the resulting GSMR estimate of the log OR. For each of the obesity-related traits under investigation an approximately null estimate for effect was obtained, with the strongest association being shown by fasting insulin. Setting a threshold of $P \leq 0.05$, no statistically significant associations were shown for 2-hour post-challenge glucose ($OR_{SD}=1.25$, 95% confidence interval (CI)=0.93-1.67), BMI ($OR_{SD}=0.91$, 95% CI=0.77-1.07), fasting glucose ($OR_{SD}=1.00$, 95%CI=0.78-1.3), fasting insulin ($OR_{SD}=1.32$, 95% CI=0.71-2.46), HDL cholesterol ($OR_{SD}=1.01$, 95% CI=0.98-1.05), LDL cholesterol ($OR_{SD}=1.00$, 95% CI=0.95-1.05), type-2 diabetes ($OR_{SD}=1.04$, 95% CI=0.97-1.11), total cholesterol ($OR_{SD}=0.98$, 95% CI=0.88-1.09), triglycerides ($OR_{SD}=1.01$, 95% CI=0.97-1.06) and WHR ($OR_{SD}=1.11$, 95% CI=0.84-1.46).

We explored the possibility that a relationship between an obesity-related trait and glioma might be subtype-specific, considering GBM and non-GBM separately. **Figures 3** and **Figure 4** show corresponding plots of the association of each IV with exposure against the association with GBM and non-GBM glioma. The strongest association was provided by the relationship between increased triglyceride level and risk of non-GBM glioma ($OR_{SD}=1.07$, 95% CI=1.00-1.13, $P=0.044$), albeit non-significant after adjustment for multiple testing (**Table 2**). **Table 3** presents the minimum prior probabilities of an association required for each trait in order to have a $BFNP \geq 0.1$. Where possible, the maximum likely OR has been taken from the largest value reported in observational studies[6, 11, 31]. In the event that this was not possible, an upper bound of 2 was chosen. If the “true” maximum likely OR were lower, then the smallest required prior probability would in fact be lower. There is no current precedent for what value should be taken for the prior probability of an association, indeed attempting to sample published papers would produce an over estimation due to winners curse, but it is noted that a value of 10% would ensure all the results reported would have significance.

DISCUSSION

There is an abundance of studies that have implicated obesity and related traits (notably diabetes), as risk factors for all of the major common cancers, including breast, colorectal, oesophageal, pancreatic, ovarian, and renal [3]. Furthermore, there is increasing evidence that obesity is likely to also be a risk factor for many of the less common tumours, such as those of the haematopoietic system [3, 32]. The mechanistic basis of how obesity and diabetes affects an increased cancer risk is poorly understood. The long-term metabolic consequences of obesity and its related traits are complex and several mechanisms have been suggested, including increased insulin and insulin-like growth factor signalling, chronic inflammation and signalling via adipokines [33]. Such mechanisms would be compatible with obesity and related traits having a generic effect on cancer risk.

Evidence for obesity influencing risk of glioma from previous observational studies has been mixed [4, 5, 8]. Intriguingly, in contrast to other cancers, an inverse relationship between both diabetes and increased HbA1c with risk of glioma has been reported in some but not all studies [4-8]. Furthermore, in so far as it has been studied, anti-diabetic treatment has been reported to not influence glioma risk [11]. In terms of the wider spectrum of the metabolic syndrome a study has linked elevated levels of triglyceride to risk of developing glioma [4].

Our findings do not support a causal role for higher BMI and related metabolic risk factors, including diagnosis of type-2 diabetes and blood lipid levels, in influencing glioma risk. An important strength of our analysis is that by utilising the random allocation of genetic variants, we were able to overcome potential confounding, for example from other inter-related traits [14, 15]. Furthermore, reverse causation and selection bias may have biased estimates from previously published observational studies. By exploiting data from large genetic consortia for multiple obesity-related traits and glioma risk has enabled us to more precisely test study hypotheses than if we had been reliant on individual-level data from a small study. The only obesity-related trait with a first-stage F-statistic <10 was WHR ($F=6.75$) and therefore weak

instrument bias for other traits is unlikely [34]. Additionally, given that a poor outcome from glioma is almost universal, it is unlikely that survival bias will have influenced study findings materially. Finally, we have employed a Bayesian approach to interpret the significance of the null results whilst comparing our findings to published observational epidemiological studies. There is currently no precedent within the MR community as to what value is an accurate representation of the prior probability of association. If the true value is approximately 20% then the null findings for 2 hour post-challenge glucose, BMI, fasting glucose, fasting insulin, and WHR all have a greater than 10% chance of being false.

There are however potential limitations in our analysis which warrant further discussion. Firstly, the use of summary test statistics in two-sample MR analyses requires consideration of sample overlap the winner's curse and genotype uncertainty [35, 36]. Sample overlap between the association studies of the exposure traits and outcome trait has the potential of inflating the Type I error rate. The number of controls shared between the glioma GWAS and the anthropometric and lipid GWAS are, however less than 2% of the respective exposure sample size. While we are unable to calculate an exact number of glioma cases sampled in the exposure GWAS r given lifetime risk of glioma of is only 0.24%, at best very few numbers of glioma cases will have been analysed in the exposure trait studies. Hence such sample overlap is unlikely to contribute to Type I error rate inflation [36]. As the instrumental variables were discovered in the data used in this two-sample MR analysis, weak instrument bias will be accentuated due to winner's curse, thus attenuating the causal effect estimate towards the null [36]. Uncertainty with respect to genotyping or disease associations may diminish causal effect estimates [36]. However IVs used in this analysis are robust and only SNPs passing stringent quality control thresholds were used in the analysis. Secondly, MR is limited in the extent to which it can explore different life course models, such as when an exposure has a temporal relationship to the outcome risk [35]. , Thirdly, in the case of a binary exposure such as type 2 diabetes, a ratio estimator may not provide fully recapulate an estimate of the causal OR.[37]. Finally, our study does have limitations related to power. However, based on the relatively

sizable fraction of variance explained by the genetic instruments for the majority of the obesity-related factors (**Table 1**), typically there was sufficient statistical power (>80%) to detect even modest odds ratios of 1.43, and close to complete statistical power (99%) to detect relative risks of 1.72 (**Figure 1**).

In conclusion, our findings shed light on an issue for which the evidence to date has been mixed. Specifically, they provide evidence against obesity and related traits as significant risk factors for the development of glioma.

DECLARATIONS

Ethics approval and consent to participate

Two-sample MR was undertaken using GWAS data. Ethical approval was not sought for this specific project because all data came from the summary statistics of published GWAS, and no individual-level data were used.

Consent for publication

Not applicable

Availability of data and material

Genotype data from the GICC GWAS are available from the database of Genotypes and Phenotypes (dbGaP) under accession phs001319.v1.p1. Additionally, genotypes from the GliomaScan GWAS can be accessed through dbGaP accession phs000652.v1.p1.

Competing interests

The authors declare that they have no competing interests

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Author contributions

R.S.H., A.S. and A.J.C. managed the project. L.D-H., A.S., P.J.L., A.J.C., and R.S.H. drafted the manuscript. L.D-H. performed statistical analyses. B.K., K.L., A.J.S. and R.H.S. provided U.K. data. M. Simon, P.H., M.M.N. and K.-H.J. provided German data. Q.T.O., J.E.E.-P., G.N.A., E.B.C., D.I., J.S., J.S.B.-S., S.H.O., J.L.B., R.K.L., C.J., R.B.J., B.S.M., M.R.W., M.L.B. and R.S.H. provided GICC data. S.C. and P.R. provided National Cancer Institute (NCI) data. M. Sanson provided French data. All authors reviewed the final manuscript.

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TABLES AND FIGURES

Figure 1: Study power against OR for each obesity-related trait and all glioma ($P=0.05$, two-sided). A line indicating a power of 80% is shown. OR, odds ratio; BMI, body mass index; HDL, high-density lipoprotein; LDL, low-density lipoprotein.

Figure 2: SNP-specific effects for risk of all glioma. For each figure, the effect size of the respective measure for (a) 2-hour post-challenge glucose, (b) BMI, (c) fasting glucose, (d) fasting insulin, (e) HDL cholesterol, (f) LDL cholesterol, (g) type-2 diabetes, (h) total cholesterol, (i) triglycerides and (j) WHR is plotted against the effect for all glioma. Error bars represent one SD. The GSMR estimate is plotted as a dashed line for reference. BMI, body mass index; GSMR, generalised summary-data-based Mendelian randomisation; HDL, high-density lipoprotein; LDL, low-density lipoprotein; SD, standard deviation; WHR, waist-hip ratio.

Figure 3: SNP-specific effects for risk of GBM glioma. For each figure, the effect size of the respective measure for (a) 2-hour post-challenge glucose, (b) BMI, (c) fasting glucose, (d) fasting insulin, (e) HDL cholesterol, (f) LDL cholesterol, (g) type-2 diabetes, (h) total cholesterol, (i) triglycerides and (j) WHR is plotted against the effect for GBM glioma. Error bars represent one SD. The GSMR estimate is plotted as a dashed line for reference. BMI, body mass index; GBM, glioblastoma multiforme; GSMR, generalised summary-data-based Mendelian randomisation; HDL, high-density lipoprotein; LDL, low-density lipoprotein; SD, standard deviation; WHR, waist-hip ratio.

Figure 4: SNP-specific effects for risk of non-GBM glioma. For each figure, the effect size of the respective measure for (a) 2-hour post-challenge glucose, (b) BMI, (c) fasting glucose, (d) fasting insulin, (e) HDL cholesterol, (f) LDL cholesterol, (g) type-2 diabetes, (h) total cholesterol, (i) triglycerides and (j) WHR, is plotted against the effect for non-GBM glioma. Error bars represent one SD. The GSMR estimate is plotted as a dashed line for reference. BMI, body mass index; GBM, glioblastoma multiforme; GSMR, generalised summary-data-based Mendelian

randomisation; HDL, high-density lipoprotein; LDL, low-density lipoprotein; SD, standard deviation; WHR, waist-hip ratio.

Table 1: Metabolic risk factors for which genetic instruments were developed and evaluated in relation to disease risk.

BMI, body mass index; HDL, high-density lipoprotein; LDL, low-density lipoprotein; PVE, proportion of variance explained; SD, standard deviation; SNP, single nucleotide polymorphism; WHR, waist-hip ratio.

Table 2: GSMR results for the combined obesity-related IVs.

BMI, body mass index; CI, confidence interval; GBM, glioblastoma multiforme; GSMR, generalised summary-data-based Mendelian randomisation; HDL, high-density lipoprotein; IV, instrumental variable; LDL, low-density lipoprotein; OR, odds ratio; SD, standard deviation; WHR, waist-hip ratio.

Table 3: Prior probability of association required for BFNP>0.1, for the combined obesity-related IVs.

BFNP; Bayesian false null probability; BMI, body mass index; HDL, high-density lipoprotein; IV, instrumental variable; LDL, low-density lipoprotein; WHR, waist-hip ratio; OR, odds ratio; N/A, no observational data to inform maximum likely OR, value of 2 taken.

Supplementary Table 1: Effect allele, frequencies, effect on each obesity-related trait and strength of association with glioma for SNPs used as genetic instruments.

BMI, body mass index; CI, confidence interval; GBM, glioblastoma multiforme; GSMR, generalised summary-data-based Mendelian randomisation; HDL, high-density lipoprotein; IV, instrumental variable; LDL, low-density lipoprotein; MAF, minor allele frequency; OR, odds ratio; SD, standard deviation; WHR, waist-hip ratio.

Supplementary Table 2: Pairwise r^2 calculations for the SNPs used as genetic instruments.

BMI, body mass index; HDL, high-density lipoprotein; LDL, low-density lipoprotein; WHR, waist-hip ratio.

Supplementary Table 3: Summary of the eight glioma genome wide association studies (GWAS).

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Figure 1: Study power against OR for each obesity-related trait and all glioma ($P=0.05$, two-sided). A line indicating a power of 80% is shown.

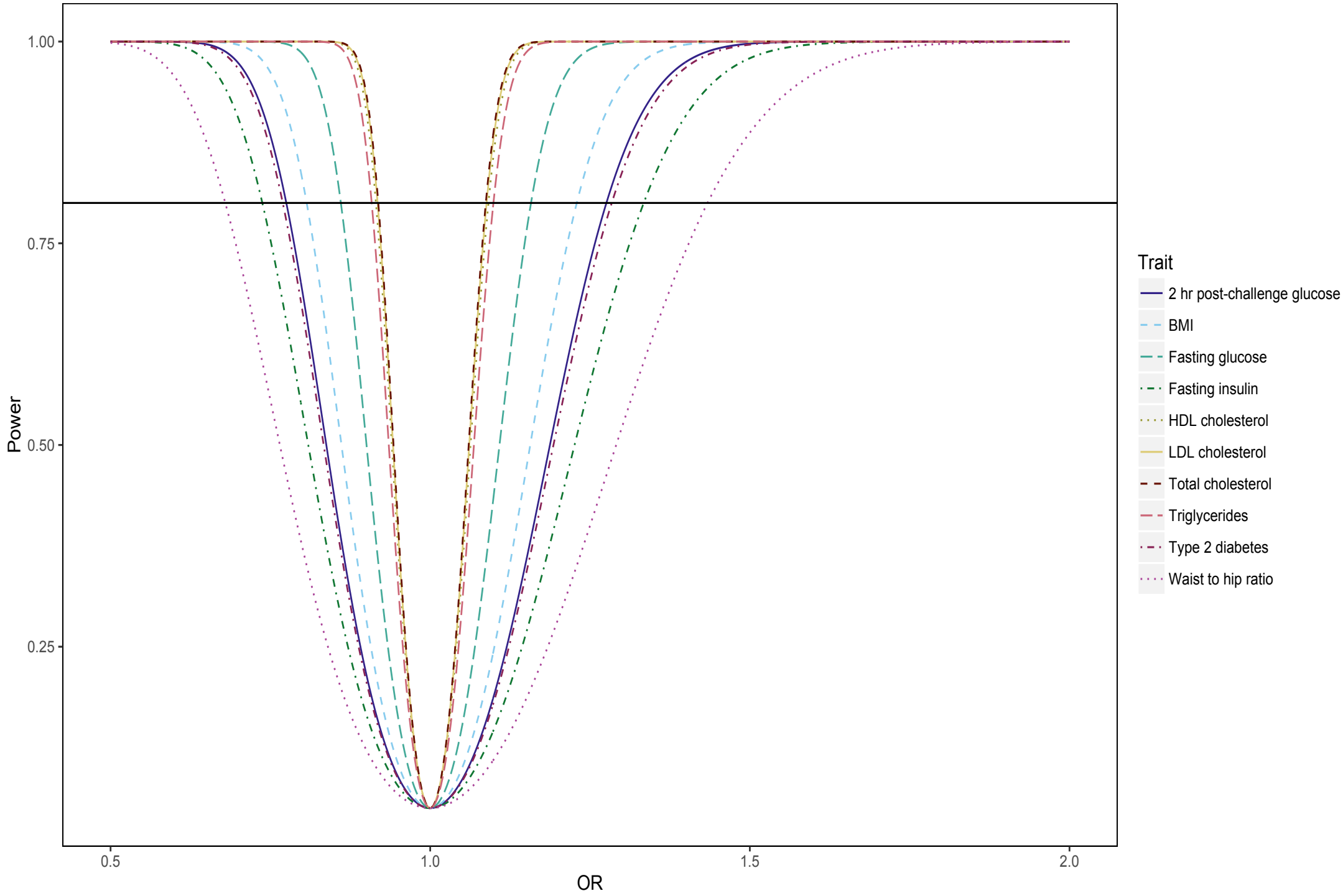


Figure 2: SNP-specific effects for risk of all glioma. For each figure, the effect size of the respective measure for (a) 2-hour post-challenge glucose, (b) BMI, (c) fasting glucose, (d) fasting insulin, (e) HDL, (f) LDL, (g) type-2 diabetes, (h) total cholesterol, (i) triglycerides and (j) WHR is plotted against the effect of all glioma. Error bars represent one SD. The GSMR estimate is plotted as a dashed line for reference.

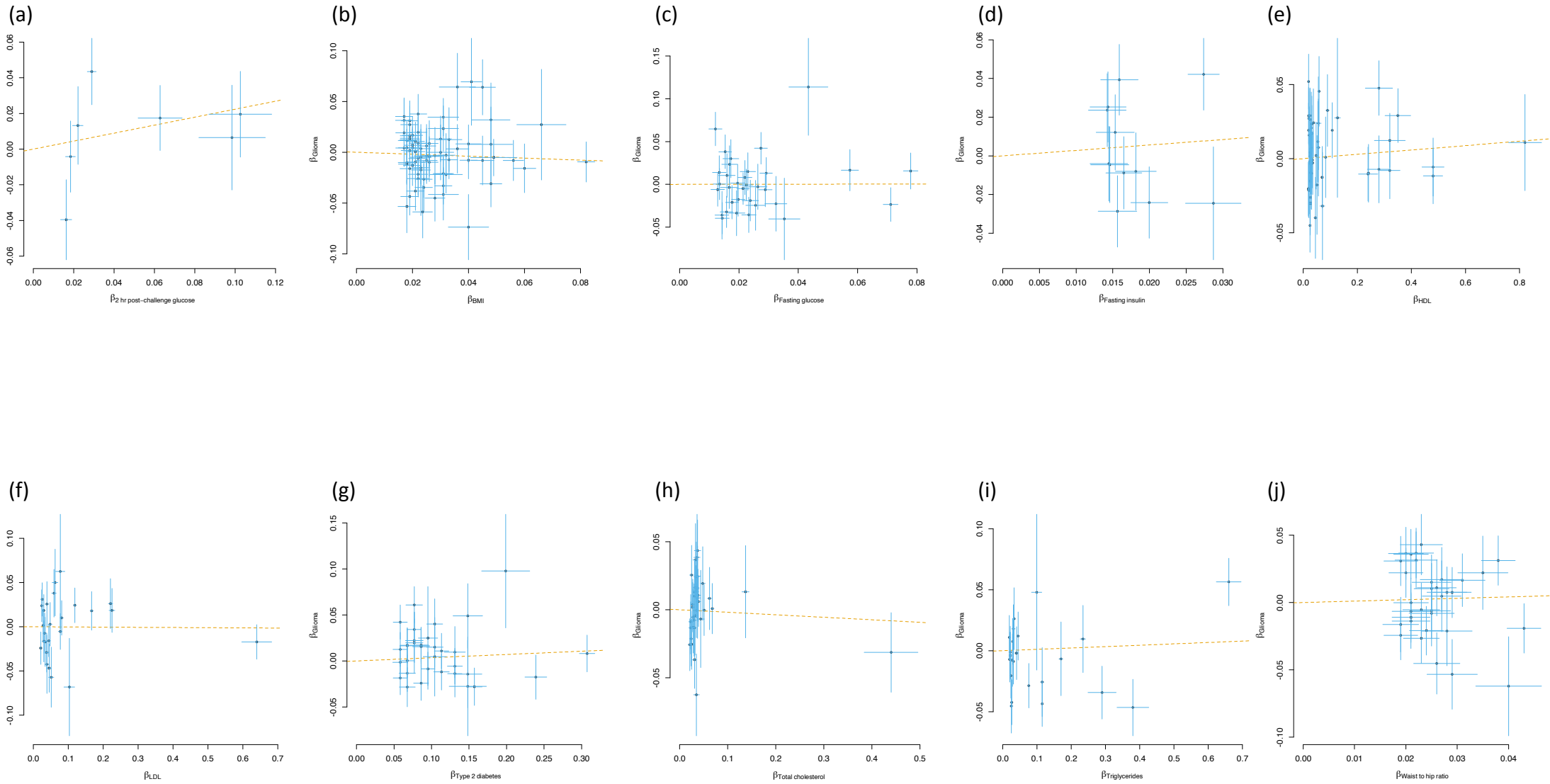


Figure 3: SNP-specific effects for risk of GBM glioma. For each figure, the effect size of the respective measure for (a) 2-hour post-challenge glucose, (b) BMI, (c) fasting glucose, (d) fasting insulin, (e) HDL, (f) LDL, (g) type-2 diabetes, (h) total cholesterol, (i) triglycerides and (j) WHR is plotted against the effect of GBM glioma. Error bars represent one standard deviation. The GSMR estimate is plotted as a dashed line for reference.

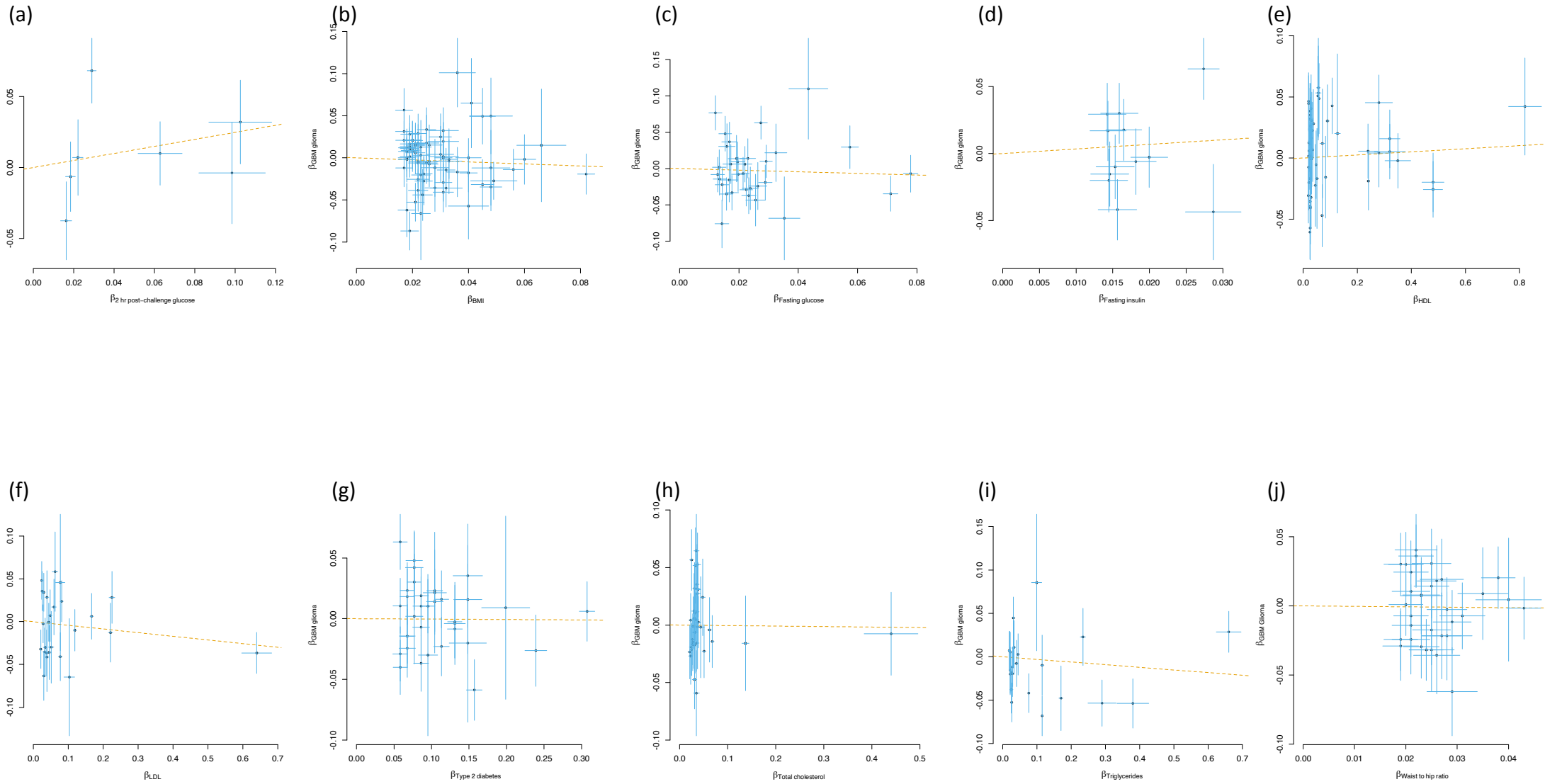


Figure 4: SNP-specific effects for risk of non-GBM glioma. For each figure, the effect size of the respective measure for (a) 2-hour post-challenge glucose, (b) BMI, (c) fasting glucose, (d) fasting insulin, (e) HDL, (f) LDL, (g) type-2 diabetes, (h) total cholesterol, (i) triglycerides and (j) WHR is plotted against the effect of non-GBM glioma. Error bars represent one standard deviation. The GSMR estimate is plotted as a dashed line for reference.

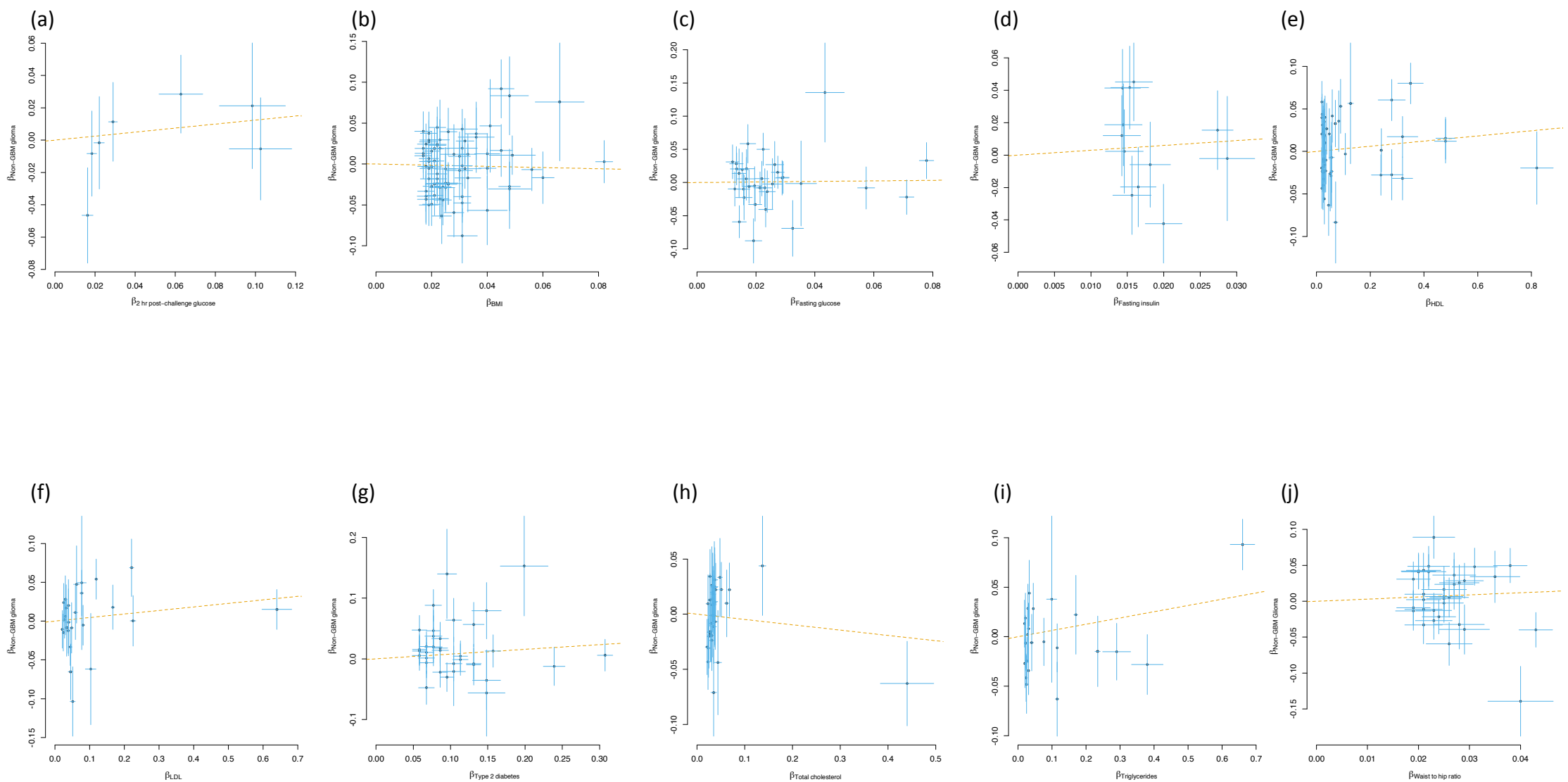


Table 1: Metabolic risk factors for which genetic instruments were developed and evaluated in relation to disease risk.

Trait	SNPs*	Mean (SD)	Units	PVE (%)	Reference
2-hour post-challenge glucose	7	5.6 (1.7)	mmol/l	1.7	Scott <i>et al.</i> 2012
BMI	75	27.0 (4.6)	kg/m ²	2.4	Locke <i>et al.</i> 2015
Fasting glucose	33	5.2 (0.8)	mmol/l	4.8	Scott <i>et al.</i> 2012
Fasting insulin	12	56.9 (44.4)	pmol/l	1.2	Scott <i>et al.</i> 2012
HDL cholesterol	54	53.3 (15.5)	mg/dl	13.7	Willer <i>et al.</i> 2013
LDL cholesterol	26	133.6 (38.0)	mg/dl	14.6	Willer <i>et al.</i> 2013
Type-2 diabetes	34	-	-	1.6	Gaulton <i>et al.</i> 2015
Total cholesterol	37	213.3 (42.6)	mg/dl	15.0	Willer <i>et al.</i> 2013
Triglycerides	24	140.9 (87.8)	mg/dl	11.7	Willer <i>et al.</i> 2013
WHR	33	1.1 (0.1)	cm/cm	0.7	Shungin <i>et al.</i> 2015

*Number of SNPs used after quality control.

BMI, body mass index; HDL, high-density lipoprotein; LDL, low-density lipoprotein; PVE; proportion of variance explained; SD, standard deviation; SNP, single nucleotide polymorphism; WHR, waist-hip ratio.

Table 2: GSMR results for the combined obesity-related IVs.

Trait	All glioma		GBM		Non-GBM	
	OR (95% CI)	P value	OR (95% CI)	P value	OR (95% CI)	P value
2-hour post-challenge glucose	1.25 (0.93-1.67)	0.132	1.28 (0.90-1.83)	0.173	1.13 (0.77-1.66)	0.525
BMI	0.91 (0.77-1.07)	0.247	0.89 (0.73-1.08)	0.237	0.93 (0.75-1.15)	0.510
Fasting glucose	1.00 (0.78-1.3)	0.974	0.89 (0.66-1.22)	0.484	1.04 (0.75-1.45)	0.809
Fasting insulin	1.32 (0.71-2.46)	0.374	1.41 (0.66-3.00)	0.377	1.35 (0.60-3.04)	0.471
HDL Cholesterol	1.01 (0.98-1.05)	0.375	1.01 (0.97-1.05)	0.532	1.03 (0.99-1.08)	0.167
LDL Cholesterol	1.00 (0.95-1.05)	0.939	0.96 (0.90-1.02)	0.197	1.05 (0.98-1.12)	0.195
Type-2 diabetes	1.04 (0.97-1.11)	0.290	1.00 (0.92-1.08)	0.933	1.08 (0.99-1.18)	0.076
Total cholesterol	0.98 (0.88-1.09)	0.736	1.00 (0.87-1.14)	0.949	0.95 (0.83-1.10)	0.505
Triglycerides	1.01 (0.97-1.06)	0.637	0.97 (0.92-1.03)	0.291	1.07 (1.00-1.13)	0.044
WHR	1.11 (0.84-1.46)	0.456	0.97 (0.69-1.35)	0.847	1.34 (0.94-1.93)	0.109

BMI, body mass index; CI, confidence interval; GBM, glioblastoma multiforme; GSMR, generalised summary-data-based Mendelian randomisation; HDL, high-density lipoprotein; IV, instrumental variable; LDL, low-density lipoprotein; OR, odds ratio; SD, standard deviation; WHR, waist-hip ratio.

Table 3: Prior probability of association required for BFNP>0.1, for the combined obesity-related IVs.

Trait	Glioma		Reference
	Maximum likely OR	Minimum required prior probability	
2 hr post-challenge glucose	2.00	0.10	N/A
BMI	1.27	0.11	Dai <i>et al.</i> 2015
Fasting glucose	1.57	0.18	Derr <i>et al.</i> 2009
Fasting insulin	2.00	0.12	N/A
HDL Cholesterol	200	0.64	N/A
LDL Cholesterol	2.00	0.61	N/A
Type 2 diabetes	0.60	0.31	Seliger <i>et al.</i> 2016
Total cholesterol	2.00	0.41	N/A
Triglycerides	2.00	0.60	N/A
WHR	2.00	0.19	N/A

BFNP; Bayesian false null probability; BMI, body mass index; HDL, high-density lipoprotein; IV, instrumental variable; LDL, low-density lipoprotein; WHR, waist-hip ratio; OR, odds ratio; N/A, no observational data to inform maximum likely OR, value of 2 taken.

Supplementary Table 1: Effect allele, frequency, effect on obesity-related trait and strength of association with glioma for SNPs used as genetic instruments.

2-hour post-challenge glucose

Chromosome	SNP	Base pair position*	Alleles**	MAF	2-hour post-challenge glucose	All glioma	GBM	Non-GBM
					OR (95% CI)	OR (95% CI)	OR (95% CI)	OR (95% CI)
2	rs1260326	27730940	T/C	T=0.378	1.03 (1.03-1.03)	1.04 (1.01-1.08)	1.07 (1.02-1.12)	1.01 (0.96-1.06)
3	rs11717195	123082398	C/T	C=0.210	1.02 (1.02-1.03)	1.01 (0.97-1.06)	1.01 (0.96-1.06)	1 (0.94-1.06)
5	rs1019503	96254817	G/A	A=0.483	1.06 (1.04-1.09)	1.02 (0.98-1.05)	1.01 (0.97-1.06)	1.03 (0.98-1.08)
7	rs6975024	44231886	T/C	C=0.150	1.11 (1.07-1.14)	1.02 (0.97-1.07)	1.03 (0.97-1.09)	0.99 (0.93-1.06)
8	rs11782386	9201787	T/C	T=0.103	1.10 (1.07-1.14)	1.01 (0.95-1.07)	1.00 (0.93-1.07)	1.02 (0.95-1.10)
10	rs12255372	114808902	G/T	T=0.236	1.02 (1.01-1.02)	1.00 (0.96-1.04)	0.99 (0.95-1.04)	0.99 (0.94-1.04)
19	rs11672660	46180184	T/C	T=0.220	1.02 (1.01-1.02)	0.96 (0.92-1.00)	0.96 (0.91-1.02)	0.95 (0.90-1.01)

BMI

Chromosome	SNP	Base pair position *	Alleles**	MAF	BMI	All glioma	GBM	Non-GBM
					OR (95% CI)	OR (95% CI)	OR (95% CI)	OR (95% CI)
1	rs543874	177889480	A/G	G=0.193	1.05 (1.04-1.06)	0.97 (0.93-1.01)	0.97 (0.91-1.02)	0.97 (0.92-1.03)
1	rs3101336	72751185	T/C	T=0.387	1.03 (1.03-1.04)	0.99 (0.96-1.03)	1.00 (0.95-1.04)	1.01 (0.96-1.06)
1	rs12566985	75002193	A/G	G=0.446	1.02 (1.02-1.03)	0.97 (0.94-1.01)	0.98 (0.94-1.02)	0.97 (0.93-1.02)
1	rs17024393	110154688	T/C	C=0.040	1.07 (1.05-1.09)	1.03 (0.92-1.14)	1.01 (0.89-1.16)	1.08 (0.94-1.24)
1	rs11165643	96924097	C/T	C=0.417	1.02 (1.02-1.03)	1.02 (0.98-1.06)	1.02 (0.97-1.06)	1.02 (0.98-1.07)
1	rs12401738	78446761	G/A	A=0.352	1.02 (1.01-1.03)	1.01 (0.97-1.05)	1.02 (0.97-1.06)	1.02 (0.97-1.07)
1	rs657452	49589847	G/A	A=0.394	1.02 (1.02-1.03)	0.98 (0.95-1.02)	1.00 (0.96-1.05)	0.96 (0.91-1.01)
1	rs2820292	201784287	A/C	A=0.445	1.02 (1.01-1.03)	1.01 (0.97-1.04)	1.01 (0.97-1.05)	1.02 (0.97-1.06)
2	rs13021737	632348	A/G	A=0.172	1.06 (1.05-1.07)	0.98 (0.94-1.03)	1.00 (0.94-1.06)	0.98 (0.92-1.05)
2	rs10182181	25150296	A/G	G=0.462	1.03 (1.03-1.04)	0.97 (0.93-1.00)	0.97 (0.93-1.01)	0.95 (0.91-1.00)
2	rs1016287	59305625	C/T	T=0.287	1.02 (1.02-1.03)	0.94 (0.90-0.99)	0.96 (0.9-1.02)	0.94 (0.88-1.00)
2	rs2121279	143043285	C/T	T=0.152	1.03 (1.02-1.03)	1.00 (0.94-1.05)	1.02 (0.95-1.09)	0.98 (0.91-1.05)
2	rs7599312	213413231	A/G	A=0.276	1.02 (1.02-1.03)	0.99 (0.95-1.03)	0.99 (0.95-1.04)	0.98 (0.93-1.04)
2	rs11126666	26928811	G/A	A=0.283	1.02 (1.01-1.03)	1.00 (0.96-1.04)	1.01 (0.96-1.06)	1.00 (0.95-1.06)
2	rs1528435	181550962	C/T	C=0.369	1.02 (1.01-1.02)	1.01 (0.97-1.05)	1.00 (0.96-1.05)	1.02 (0.98-1.08)
2	rs11688816	63053048	A/G	A=0.475	1.02 (1.01-1.02)	1.00 (0.97-1.04)	0.99 (0.95-1.03)	1.02 (0.97-1.07)
3	rs1516725	185824004	T/C	T=0.128	1.05 (1.04-1.06)	1.07 (1.01-1.12)	1.05 (0.98-1.12)	1.10 (1.02-1.18)
3	rs13078960	85807590	T/G	G=0.196	1.03 (1.02-1.04)	1.01 (0.97-1.06)	1.03 (0.97-1.08)	1.01 (0.95-1.07)
3	rs2365389	61236462	T/C	T=0.418	1.02 (1.01-1.03)	1.00 (0.97-1.04)	1.02 (0.98-1.07)	0.97 (0.93-1.02)
3	rs16851483	141275436	G/T	T=0.066	1.05 (1.03-1.07)	1.01 (0.94-1.08)	1.05 (0.96-1.15)	0.97 (0.88-1.07)
3	rs6804842	25106437	A/G	A=0.425	1.02 (1.01-1.03)	1.03 (0.99-1.07)	1.03 (0.98-1.07)	1.03 (0.98-1.08)
3	rs3849570	81792112	C/A	A=0.359	1.02 (1.01-1.03)	1.01 (0.98-1.05)	1.01 (0.97-1.06)	1.00 (0.96-1.05)
4	rs10938397	45182527	A/G	G=0.434	1.04 (1.03-1.05)	0.99 (0.96-1.03)	0.98 (0.94-1.03)	0.99 (0.95-1.04)
4	rs13107325	103188709	C/T	T=0.072	1.05 (1.04-1.06)	1.03 (0.96-1.11)	0.99 (0.91-1.08)	1.09 (0.99-1.19)
4	rs17001654	77129568	C/G	G=0.153	1.03 (1.02-1.04)	0.96 (0.91-1.01)	1.00 (0.94-1.06)	0.92 (0.86-0.98)
4	rs11727676	145659064	C/T	C=0.090	1.04 (1.02-1.05)	1.07 (1.00-1.14)	1.11 (1.02-1.20)	1.03 (0.95-1.12)
5	rs2112347	75015242	G/T	G=0.371	1.03 (1.02-1.03)	0.99 (0.95-1.03)	1.00 (0.95-1.04)	0.98 (0.93-1.02)
6	rs2207139	50845490	A/G	G=0.177	1.05 (1.04-1.05)	0.99 (0.95-1.04)	0.97 (0.91-1.03)	1.02 (0.96-1.08)
6	rs205262	34563164	A/G	G=0.273	1.02 (1.02-1.03)	0.98 (0.94-1.02)	0.96 (0.92-1.01)	0.99 (0.94-1.04)
6	rs13191362	163033350	G/A	G=0.121	1.03 (1.02-1.04)	1.00 (0.94-1.05)	0.99 (0.92-1.06)	1.01 (0.94-1.09)
6	rs2033529	40348653	A/G	G=0.293	1.02 (1.01-1.03)	1.02 (0.98-1.06)	1.02 (0.97-1.07)	1.03 (0.98-1.08)
6	rs9400239	108977663	C/T	T=0.312	1.02 (1.01-1.03)	0.99 (0.95-1.03)	1.01 (0.96-1.06)	0.95 (0.90-1.00)
7	rs1167827	75163169	G/A	A=0.447	1.02 (1.01-1.03)	0.98 (0.94-1.01)	0.96 (0.92-1.01)	0.99 (0.95-1.04)
7	rs2245368	76608143	T/C	C=0.180	1.03 (1.02-1.04)	1.01 (0.96-1.06)	1.00 (0.94-1.06)	1.02 (0.96-1.09)
8	rs17405819	76806584	C/T	C=0.300	1.02 (1.02-1.03)	1.01 (0.97-1.05)	1.00 (0.95-1.05)	1.01 (0.96-1.06)
8	rs2033732	85079709	C/T	T=0.253	1.02 (1.01-1.03)	1.01 (0.97-1.05)	1.03 (0.98-1.09)	0.97 (0.92-1.03)
9	rs10968576	28414339	G/A	G=0.320	1.03 (1.02-1.03)	1.03 (0.99-1.07)	1.01 (0.96-1.06)	1.04 (0.99-1.09)
9	rs1928295	120378483	C/T	C=0.452	1.02 (1.01-1.03)	1.00 (0.97-1.04)	1.01 (0.97-1.06)	1.00 (0.95-1.04)
9	rs4740619	15634326	C/T	C=0.458	1.02 (1.01-1.02)	1.02 (0.98-1.06)	1.02 (0.98-1.07)	1.01 (0.97-1.06)
9	rs10733682	129460914	G/A	A=0.478	1.02 (1.01-1.02)	1.04 (1.00-1.07)	1.03 (0.99-1.08)	1.04 (0.99-1.09)
9	rs6477694	111932342	T/C	C=0.365	1.02 (1.01-1.02)	1.00 (0.97-1.04)	0.98 (0.94-1.03)	1.03 (0.98-1.08)
10	rs7903146	114758349	T/C	T=0.287	1.02 (1.02-1.03)	0.99 (0.95-1.03)	0.99 (0.95-1.04)	0.99 (0.94-1.05)
10	rs17094222	102395440	C/T	C=0.211	1.03 (1.02-1.03)	1.02 (0.98-1.07)	1.03 (0.98-1.09)	1.02 (0.96-1.08)
10	rs11191560	104869038	C/T	C=0.089	1.03 (1.02-1.04)	0.93 (0.87-0.99)	0.94 (0.87-1.02)	0.94 (0.87-1.03)
10	rs7899106	87410904	G/A	G=0.052	1.04 (1.03-1.06)	1.07 (0.99-1.17)	1.07 (0.96-1.18)	1.05 (0.94-1.17)
11	rs11030104	27684517	G/A	G=0.208	1.04 (1.03-1.05)	1.01 (0.97-1.05)	0.99 (0.94-1.05)	1.04 (0.98-1.10)
11	rs3817334	47650993	T/C	T=0.407	1.03 (1.02-1.03)	0.96 (0.93-1.00)	0.95 (0.91-0.99)	0.96 (0.92-1.01)
11	rs4256980	8673939	G/C	C=0.354	1.02 (1.01-1.03)	1.04 (1.00-1.08)	1.03 (0.98-1.08)	1.05 (1.00-1.10)
11	rs12286929	115022404	G/A	A=0.477	1.02 (1.02-1.03)	1.02 (0.98-1.05)	1.02 (0.98-1.07)	1.00 (0.95-1.04)
11	rs2176598	43864278	C/T	T=0.251	1.02 (1.01-1.03)	1.00 (0.96-1.04)	0.99 (0.94-1.04)	1.03 (0.97-1.09)
12	rs7138803	50247468	A/G	A=0.384	1.03 (1.03-1.04)	1.04 (1.00-1.07)	1.02 (0.98-1.07)	1.04 (0.99-1.09)
12	rs11057405	122781897	A/G	A=0.099	1.03 (1.02-1.04)	1.01 (0.95-1.08)	1.00 (0.92-1.07)	0.98 (0.91-1.07)
13	rs12429545	54102206	A/G	A=0.133	1.03 (1.02-1.04)	1.00 (0.95-1.05)	1.00 (0.94-1.07)	0.99 (0.93-1.06)
13	rs12016871	28017782	T/C	T=0.203	1.03 (1.02-1.04)	0.97 (0.92-1.01)	0.97 (0.92-1.03)	0.96 (0.90-1.02)

14	rs17141420	79899454	T/C	C=0.473	1.02 (1.02-1.03)	0.99 (0.96-1.03)	0.97 (0.93-1.02)	1.01 (0.96-1.06)
14	rs11847697	30515112	T/C	T=0.042	1.05 (1.03-1.07)	0.98 (0.90-1.07)	0.94 (0.84-1.04)	1.02 (0.91-1.14)
14	rs10132280	25928179	A/C	A=0.318	1.02 (1.02-1.03)	0.99 (0.95-1.03)	1.02 (0.97-1.07)	0.98 (0.93-1.03)
14	rs12885454	29736838	A/C	A=0.358	1.02 (1.01-1.03)	0.98 (0.94-1.02)	0.96 (0.92-1.01)	1.00 (0.95-1.05)
15	rs16951275	68077168	C/T	C=0.216	1.03 (1.02-1.04)	0.99 (0.95-1.03)	1.00 (0.95-1.05)	0.96 (0.91-1.01)
15	rs3736485	51748610	G/A	A=0.454	1.02 (1.01-1.02)	0.99 (0.95-1.03)	0.98 (0.94-1.03)	1.00 (0.95-1.05)
16	rs1558902	53803574	A/T	A=0.415	1.09 (1.08-1.09)	0.98 (0.94-1.02)	1.00 (0.96-1.05)	0.96 (0.92-1.01)
16	rs3888190	28889486	A/C	A=0.403	1.03 (1.03-1.04)	1.01 (0.97-1.05)	1.00 (0.96-1.05)	1.01 (0.96-1.06)
16	rs12446632	19935389	A/G	A=0.135	1.04 (1.03-1.05)	0.99 (0.95-1.05)	1.01 (0.95-1.08)	0.97 (0.91-1.04)
16	rs758747	3627358	T/C	T=0.265	1.02 (1.02-1.03)	1.00 (0.96-1.04)	1.01 (0.96-1.06)	0.98 (0.93-1.04)
16	rs9925964	31129895	G/A	G=0.380	1.02 (1.01-1.03)	0.99 (0.95-1.03)	1.01 (0.96-1.05)	0.97 (0.92-1.02)
17	rs12940622	78615571	A/G	A=0.425	1.02 (1.01-1.02)	0.96 (0.92-0.99)	0.92 (0.88-0.96)	0.99 (0.95-1.04)
17	rs1000940	5283252	G/A	G=0.32	1.02 (1.01-1.03)	0.99 (0.95-1.03)	0.99 (0.94-1.03)	0.99 (0.94-1.05)
18	rs6567160	57829135	C/T	C=0.236	1.06 (1.05-1.07)	1.03 (0.99-1.08)	1.06 (1.01-1.11)	1.01 (0.96-1.07)
18	rs1808579	21104888	T/C	T=0.466	1.02 (1.01-1.02)	0.97 (0.94-1.01)	0.97 (0.93-1.02)	0.98 (0.93-1.02)
18	rs7243357	56883319	G/T	G=0.188	1.02 (1.01-1.03)	1.00 (0.96-1.05)	0.98 (0.93-1.04)	1.04 (0.98-1.10)
19	rs2287019	46202172	T/C	T=0.196	1.04 (1.03-1.05)	0.96 (0.91-1.00)	0.96 (0.91-1.02)	0.94 (0.89-1.00)
19	rs3810291	47569003	A/G	G=0.334	1.03 (1.02-1.04)	1.00 (0.96-1.03)	1.02 (0.97-1.06)	0.98 (0.93-1.03)
19	rs2075650	45395619	G/A	G=0.152	1.03 (1.02-1.04)	0.95 (0.90-1.00)	0.94 (0.88-1.00)	0.96 (0.90-1.03)
19	rs29941	34309532	G/A	A=0.331	1.02 (1.01-1.02)	0.98 (0.95-1.02)	1.01 (0.97-1.06)	0.95 (0.91-1.00)

Fasting glucose

Chromosome	SNP	Base pair position *	Alleles**	MAF	Fasting glucose	All glioma	GBM	Non-GBM
					OR (95% CI)	OR (95% CI)	OR (95% CI)	OR (95% CI)
1	rs340874	214159256	T/C	T=0.479	1.01 (1.01-1.02)	1.00 (0.97-1.04)	0.99 (0.94-1.03)	1.02 (0.97-1.07)
2	rs780094	27741237	T/C	T=0.390	1.03 (1.02-1.03)	1.04 (1.01-1.08)	1.07 (1.02-1.11)	1.02 (0.97-1.07)
2	rs560887	169763148	T/C	T=0.296	1.07 (1.07-1.08)	0.98 (0.94-1.02)	0.97 (0.92-1.01)	0.98 (0.93-1.03)
3	rs7651090	185513392	A/G	G=0.306	1.01 (1.01-1.02)	0.99 (0.96-1.03)	0.99 (0.95-1.04)	0.99 (0.94-1.04)
3	rs11715915	49455330	T/C	T=0.325	1.01 (1.01-1.02)	1.07 (1.03-1.11)	1.08 (1.03-1.13)	1.03 (0.98-1.08)
3	rs11708067	123065778	G/A	G=0.210	1.02 (1.02-1.03)	1.02 (0.97-1.06)	1.01 (0.96-1.07)	0.99 (0.94-1.05)
3	rs1280	170713290	C/T	C=0.136	1.03 (1.02-1.03)	1.00 (0.95-1.05)	0.98 (0.92-1.04)	1.03 (0.96-1.10)
5	rs4869272	95539448	C/T	C=0.311	1.02 (1.01-1.02)	0.98 (0.94-1.02)	0.97 (0.92-1.01)	0.99 (0.95-1.05)
6	rs9368222	20686996	C/A	A=0.283	1.01 (1.01-1.02)	0.96 (0.91-1.02)	0.93 (0.87-0.99)	1.01 (0.94-1.09)
7	rs6943153	50791579	C/T	T=0.335	1.02 (1.01-1.02)	1.04 (1.00-1.08)	1.05 (1.00-1.10)	1.02 (0.97-1.07)
7	rs2191349	15064309	G/T	G=0.474	1.03 (1.03-1.03)	1.01 (0.98-1.05)	1.01 (0.97-1.06)	1.01 (0.96-1.06)
7	rs2908289	44223942	G/A	A=0.163	1.06 (1.05-1.07)	1.02 (0.97-1.07)	1.03 (0.97-1.09)	0.99 (0.93-1.06)
8	rs983309	9177732	G/T	T=0.117	1.03 (1.02-1.03)	0.98 (0.92-1.03)	0.96 (0.89-1.03)	1.00 (0.93-1.08)
8	rs11558471	118185733	G/A	G=0.319	1.03 (1.02-1.03)	0.99 (0.96-1.03)	0.98 (0.94-1.03)	1.01 (0.96-1.06)
9	rs10811661	22134094	C/T	C=0.180	1.02 (1.02-1.03)	0.98 (0.94-1.03)	0.97 (0.92-1.03)	0.99 (0.93-1.05)
9	rs16913693	111680359	G/T	G=0.027	1.04 (1.03-1.06)	1.12 (1.00-1.25)	1.12 (0.97-1.28)	1.15 (0.99-1.33)
9	rs3829109	139256766	A/G	A=0.293	1.02 (1.01-1.02)	1.03 (0.99-1.08)	1.01 (0.95-1.06)	1.06 (1.00-1.12)
9	rs10814916	4293150	A/C	A=0.492	1.02 (1.01-1.02)	0.97 (0.93-1.00)	0.97 (0.92-1.01)	0.99 (0.94-1.04)
10	rs11195502	113039667	T/C	T=0.087	1.03 (1.03-1.04)	0.98 (0.92-1.04)	1.02 (0.95-1.10)	0.93 (0.86-1.01)
10	rs7903146	114758349	C/T	T=0.280	1.02 (1.02-1.03)	1.01 (0.97-1.05)	1.01 (0.96-1.06)	1.01 (0.96-1.06)
11	rs11603334	72432985	A/G	A=0.167	1.02 (1.01-1.03)	0.97 (0.92-1.02)	1.01 (0.95-1.08)	0.92 (0.86-0.98)
11	rs11607883	45839709	A/G	G=0.482	1.02 (1.02-1.03)	1.00 (0.96-1.03)	0.99 (0.95-1.04)	0.99 (0.95-1.04)
11	rs11039182	47346723	C/T	C=0.270	1.02 (1.02-1.03)	0.96 (0.93-1.00)	0.96 (0.92-1.01)	0.96 (0.91-1.01)
11	rs174576	61603510	A/C	A=0.348	1.02 (1.02-1.02)	0.98 (0.95-1.02)	0.99 (0.95-1.04)	0.97 (0.92-1.02)
11	rs10830963	92708710	C/G	G=0.290	1.08 (1.08-1.09)	1.02 (0.97-1.06)	0.99 (0.94-1.04)	1.03 (0.98-1.09)
12	rs10747083	133041618	G/A	G=0.337	1.01 (1.01-1.02)	1.01 (0.98-1.05)	1.00 (0.96-1.05)	1.03 (0.98-1.08)
13	rs11619319	28487599	A/G	G=0.226	1.02 (1.01-1.02)	1.00 (0.96-1.05)	1.01 (0.96-1.06)	1.00 (0.94-1.05)
13	rs576674	33554302	A/G	G=0.154	1.02 (1.01-1.02)	1.00 (0.95-1.05)	0.98 (0.93-1.04)	1.01 (0.94-1.07)
14	rs3783347	100839261	T/G	T=0.211	1.02 (1.01-1.02)	1.02 (0.98-1.07)	1.04 (0.98-1.09)	1.02 (0.97-1.08)
15	rs4502156	62383155	C/T	C=0.448	1.02 (1.02-1.03)	1.00 (0.96-1.04)	0.97 (0.93-1.02)	1.05 (1.00-1.10)
19	rs2302593	46196634	G/C	G=0.497	1.01 (1.01-1.02)	0.96 (0.93-1.00)	0.98 (0.94-1.02)	0.94 (0.90-0.99)
20	rs6113722	22557099	A/G	A=0.043	1.04 (1.03-1.05)	0.96 (0.87-1.05)	0.93 (0.84-1.04)	1.00 (0.88-1.13)
20	rs6072275	39743905	G/A	A=0.165	1.02 (1.01-1.02)	1.01 (0.96-1.06)	1.03 (0.97-1.10)	0.98 (0.92-1.04)

Fasting insulin

Chromosome	SNP	Base pair position *	Alleles**	MAF	Fasting insulin	All glioma	GBM	Non-GBM
					OR (95% CI)	OR (95% CI)	OR (95% CI)	OR (95% CI)
1	rs2820436	219640680	A/C	A=0.329	1.02 (1.01-1.02)	1.01 (0.97-1.05)	0.99 (0.94-1.04)	1.04 (0.99-1.10)
2	rs10195252	165513091	C/T	C=0.407	1.02 (1.01-1.02)	1.04 (1.00-1.08)	1.03 (0.99-1.08)	1.05 (1.00-1.10)
2	rs2972143	227116365	A/G	A=0.376	1.01 (1.01-1.02)	1.02 (0.99-1.06)	1.03 (0.98-1.08)	1.01 (0.96-1.06)
2	rs780094	27741237	T/C	T=0.393	1.03 (1.02-1.03)	1.04 (1.01-1.08)	1.07 (1.02-1.11)	1.02 (0.97-1.07)
4	rs9884482	106081636	T/C	C=0.390	1.02 (1.01-1.02)	0.99 (0.96-1.03)	1.02 (0.97-1.06)	0.98 (0.93-1.03)
5	rs4865796	53272664	G/A	G=0.327	1.01 (1.01-1.02)	1.00 (0.96-1.03)	0.98 (0.94-1.03)	1.00 (0.95-1.05)
6	rs2745353	127452935	C/T	C=0.492	1.01 (1.01-1.02)	1.03 (0.99-1.06)	1.02 (0.97-1.06)	1.04 (0.99-1.09)
7	rs1167800	75176196	G/A	G=0.457	1.02 (1.01-1.02)	0.97 (0.94-1.01)	0.96 (0.92-1.00)	0.98 (0.93-1.02)
8	rs983309	9177732	G/T	T=0.116	1.03 (1.02-1.04)	0.98 (0.92-1.03)	0.96 (0.89-1.03)	1.00 (0.93-1.08)
10	rs7903146	114758349	T/C	T=0.281	1.02 (1.01-1.02)	0.99 (0.95-1.03)	0.99 (0.95-1.04)	0.99 (0.94-1.05)
16	rs1421085	53800954	T/C	C=0.417	1.02 (1.02-1.03)	0.98 (0.94-1.01)	1.00 (0.95-1.04)	0.96 (0.91-1.01)

19	rs731839	33899065	A/G	G=0.357	1.01 (1.01-1.02)	1.00 (0.96-1.05)	0.98 (0.94-1.03)	1.02 (0.97-1.07)
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HDL cholesterol

Chromosome	SNP	Base pair position *	Alleles**	MAF	HDL	All glioma	GBM	Non-GBM
					OR (95% CI)	OR (95% CI)	OR (95% CI)	OR (95% CI)
1	rs12748152	27138393	T/C	T=0.090	1.05 (1.04-1.07)	0.98 (0.92-1.05)	0.98 (0.91-1.07)	0.97 (0.89-1.06)
1	rs12145743	156700651	T/G	G=0.340	1.02 (1.01-1.03)	1.03 (0.99-1.07)	1.05 (1.00-1.10)	1.02 (0.97-1.07)
1	rs4650994	178515312	A/G	G=0.490	1.02 (1.01-1.03)	1.03 (0.99-1.06)	1.01 (0.97-1.06)	1.04 (1.00-1.09)
1	rs4660293	40028180	G/A	G=0.240	1.04 (1.03-1.04)	1.00 (0.96-1.04)	1.01 (0.96-1.06)	0.99 (0.94-1.05)
1	rs1689800	182168885	G/A	G=0.350	1.03 (1.03-1.04)	1.00 (0.96-1.04)	1.02 (0.98-1.07)	0.98 (0.93-1.03)
1	rs4846914	230295691	G/A	G=0.410	1.62 (1.51-1.73)	0.99 (0.95-1.03)	0.97 (0.93-1.02)	1.02 (0.97-1.07)
2	rs12328675	165540800	T/C	C=0.130	1.05 (1.03-1.06)	0.96 (0.91-1.01)	0.98 (0.92-1.04)	0.94 (0.88-1.01)
2	rs2972146	227100698	G/T	G=0.370	1.03 (1.02-1.04)	1.02 (0.99-1.06)	1.03 (0.99-1.08)	1.01 (0.96-1.06)
3	rs2606736	11400249	T/C	C=0.390	1.03 (1.02-1.03)	1.03 (0.99-1.07)	1.04 (0.99-1.09)	1.02 (0.98-1.08)
3	rs2290547	47061183	A/G	A=0.200	1.03 (1.02-1.04)	1.02 (0.97-1.07)	1.02 (0.96-1.08)	1.02 (0.96-1.08)
3	rs2013208	50129399	C/T	T=0.500	1.03 (1.02-1.03)	0.96 (0.92-0.99)	0.94 (0.90-0.98)	0.98 (0.93-1.02)
3	rs13326165	52532118	G/A	A=0.210	1.03 (1.02-1.04)	1.00 (0.96-1.04)	1.04 (0.99-1.10)	0.95 (0.89-1.00)
4	rs10019888	26062990	G/A	G=0.180	1.03 (1.02-1.04)	0.99 (0.94-1.04)	0.96 (0.91-1.02)	1.03 (0.97-1.09)
4	rs3822072	89741269	A/G	A=0.460	1.03 (1.02-1.03)	1.00 (0.96-1.04)	0.98 (0.94-1.03)	1.02 (0.97-1.07)
4	rs2602836	100014805	G/A	A=0.440	1.02 (1.01-1.03)	0.98 (0.94-1.02)	0.97 (0.93-1.01)	0.98 (0.94-1.03)
4	rs13107325	103188709	T/C	T=0.080	1.07 (1.06-1.09)	0.97 (0.90-1.04)	1.01 (0.93-1.10)	0.92 (0.84-1.01)
5	rs6450176	53298025	A/G	A=0.260	1.03 (1.02-1.03)	1.03 (0.99-1.07)	1.03 (0.98-1.09)	1.03 (0.97-1.08)
6	rs1936800	127436064	T/C	C=0.490	1.02 (1.01-1.03)	0.98 (0.95-1.02)	0.99 (0.95-1.04)	0.96 (0.91-1.00)
6	rs605066	139829666	C/T	C=0.420	1.32 (1.20-1.46)	1.05 (1.01-1.09)	1.05 (1.00-1.09)	1.06 (1.01-1.11)
7	rs702485	6449272	A/G	G=0.450	1.02 (1.02-1.03)	1.00 (0.96-1.03)	1.01 (0.97-1.06)	0.98 (0.94-1.03)
7	rs4142995	17919258	T/G	T=0.380	1.03 (1.02-1.03)	0.97 (0.94-1.01)	0.96 (0.92-1.00)	0.98 (0.93-1.02)
7	rs4917014	50305863	T/G	G=0.320	1.02 (1.01-1.03)	1.02 (0.98-1.06)	1.01 (0.96-1.05)	1.03 (0.98-1.08)
7	rs4731702	130433384	C/T	T=0.490	1.03 (1.02-1.04)	1.01 (0.97-1.04)	1.00 (0.96-1.05)	1.02 (0.97-1.07)
8	rs9987289	9183358	A/G	A=0.100	2.27 (2.02-2.56)	1.01 (0.95-1.08)	1.04 (0.97-1.13)	0.98 (0.90-1.07)
8	rs2293889	116599199	T/G	T=0.410	1.03 (1.02-1.04)	0.99 (0.94-1.04)	1.00 (0.94-1.06)	0.98 (0.92-1.05)
9	rs1883025	107664301	T/C	T=0.250	1.07 (1.06-1.08)	0.99 (0.95-1.03)	0.95 (0.91-1.00)	1.03 (0.98-1.09)
10	rs970548	46013277	A/C	C=0.260	1.03 (1.02-1.03)	1.00 (0.96-1.05)	1.04 (0.98-1.09)	0.97 (0.92-1.02)
11	rs12801636	65391317	G/A	A=0.230	1.02 (1.02-1.03)	0.98 (0.94-1.03)	1.00 (0.95-1.05)	0.96 (0.91-1.02)
11	rs499974	75455021	A/C	A=0.190	1.03 (1.02-1.04)	0.97 (0.93-1.02)	0.96 (0.91-1.02)	0.98 (0.92-1.04)
11	rs2923084	10388782	G/A	G=0.180	1.03 (1.02-1.04)	1.00 (0.95-1.04)	1.00 (0.95-1.06)	0.99 (0.93-1.05)
11	rs3136441	46743247	T/C	C=0.180	1.06 (1.05-1.07)	1.01 (0.96-1.07)	1.05 (0.99-1.12)	0.97 (0.91-1.04)
12	rs7134375	20473758	C/A	A=0.430	1.02 (1.01-1.03)	0.98 (0.94-1.01)	0.98 (0.94-1.02)	0.98 (0.93-1.02)
12	rs7134594	110000193	C/T	C=0.480	1.42 (1.29-1.56)	1.03 (0.99-1.07)	1.00 (0.95-1.04)	1.08 (1.03-1.14)
12	rs4759375	123796238	C/T	T=0.080	1.06 (1.04-1.08)	1.02 (0.96-1.09)	1.05 (0.98-1.14)	0.99 (0.92-1.08)
12	rs4765127	124460167	G/T	T=0.350	1.03 (1.02-1.04)	1.02 (0.98-1.06)	1.00 (0.95-1.05)	1.04 (0.99-1.09)
12	rs838880	125261593	T/C	C=0.340	1.62 (1.49-1.75)	0.99 (0.96-1.03)	0.98 (0.94-1.03)	1.01 (0.96-1.06)
14	rs4983559	105277209	A/G	G=0.400	1.02 (1.01-1.03)	1.05 (1.02-1.09)	1.05 (1.00-1.09)	1.06 (1.01-1.11)
15	rs1532085	58683366	G/A	A=0.400	1.11 (1.10-1.12)	1.02 (0.98-1.06)	1.04 (1.00-1.09)	1.00 (0.95-1.05)
15	rs2652834	63396867	A/G	A=0.210	1.32 (1.22-1.44)	0.99 (0.95-1.04)	1.00 (0.95-1.06)	0.97 (0.92-1.03)
16	rs1121980	53809247	A/G	A=0.430	1.02 (1.01-1.03)	1.02 (0.98-1.06)	1.00 (0.96-1.05)	1.04 (0.99-1.09)
16	rs3764261	56993324	C/A	A=0.320	1.27 (1.26-1.28)	0.99 (0.95-1.03)	0.98 (0.94-1.03)	1.00 (0.95-1.05)
16	rs16942887	67928042	G/A	A=0.140	1.09 (1.08-1.10)	1.00 (0.95-1.06)	0.98 (0.92-1.05)	1.04 (0.97-1.11)
17	rs11869286	37813856	G/C	G=0.350	1.38 (1.28-1.48)	0.99 (0.96-1.03)	1.02 (0.97-1.06)	0.97 (0.92-1.02)
17	rs4148008	66875294	G/C	G=0.330	1.03 (1.02-1.04)	1.00 (0.97-1.04)	1.03 (0.98-1.08)	0.99 (0.94-1.04)
17	rs4129767	76403984	G/A	G=0.480	1.27 (1.19-1.36)	0.99 (0.96-1.03)	1.01 (0.96-1.05)	0.97 (0.93-1.02)
18	rs7241918	47160953	G/T	G=0.190	1.09 (1.08-1.11)	1.03 (0.99-1.08)	1.03 (0.97-1.09)	1.05 (0.99-1.12)
18	rs12967135	57849023	A/G	A=0.250	1.03 (1.02-1.04)	0.97 (0.93-1.01)	0.94 (0.90-0.99)	0.99 (0.94-1.05)
19	rs17695224	52324216	A/G	A=0.260	1.03 (1.02-1.04)	1.00 (0.96-1.04)	0.97 (0.92-1.02)	1.04 (0.98-1.09)
19	rs7255436	8433196	C/A	C=0.470	1.38 (1.23-1.54)	1.01 (0.98-1.05)	1.01 (0.96-1.05)	1.02 (0.97-1.07)
19	rs737337	11347493	C/T	C=0.110	1.06 (1.04-1.07)	1.01 (0.95-1.07)	1.06 (0.98-1.15)	0.98 (0.90-1.06)
19	rs386000	54792761	G/C	C=0.260	1.05 (1.04-1.06)	1.00 (0.96-1.05)	0.99 (0.94-1.05)	1.02 (0.96-1.08)
20	rs1800961	43042364	T/C	T=0.050	1.14 (1.11-1.16)	1.03 (0.93-1.14)	1.02 (0.90-1.16)	1.06 (0.92-1.22)
20	rs6065906	44554015	C/T	C=0.190	1.06 (1.05-1.07)	1.05 (1.00-1.10)	1.05 (0.99-1.11)	1.04 (0.98-1.11)
22	rs181362	21932068	T/C	T=0.230	1.04 (1.03-1.05)	1.02 (0.98-1.07)	1.03 (0.97-1.09)	1.03 (0.97-1.09)

LDL cholesterol

Chromosome	SNP	Base pair position *	Alleles**	MAF	LDL	All glioma	GBM	Non-GBM
					OR (95% CI)	OR (95% CI)	OR (95% CI)	OR (95% CI)
1	rs2479409	55504650	A/G	G=0.320	1.90 (1.74-2.06)	0.98 (0.95-1.02)	0.96 (0.92-1.01)	1.02 (0.97-1.07)
1	rs629301	109818306	G/T	G=0.240	1.18 (1.17-1.19)	1.02 (0.98-1.06)	1.01 (0.95-1.06)	1.02 (0.96-1.08)
2	rs10490626	118835841	A/G	A=0.080	1.05 (1.04-1.07)	0.94 (0.88-1.01)	0.97 (0.89-1.05)	0.90 (0.83-0.98)
2	rs2030746	121309488	C/T	T=0.400	1.02 (1.01-1.03)	0.98 (0.94-1.01)	0.97 (0.93-1.01)	0.99 (0.94-1.04)
2	rs1367117	21263900	G/A	A=0.320	1.13 (1.12-1.14)	1.02 (0.99-1.06)	0.99 (0.94-1.04)	1.06 (1.00-1.11)
2	rs4299376	44072576	T/G	G=0.310	1.08 (1.07-1.09)	1.01 (0.97-1.05)	1.02 (0.98-1.07)	0.99 (0.95-1.05)
3	rs7640978	32533010	T/C	T=0.090	1.04 (1.03-1.05)	0.96 (0.90-1.02)	0.96 (0.89-1.04)	1.00 (0.92-1.09)
3	rs17404153	132163200	T/G	T=0.140	1.03 (1.02-1.05)	0.98 (0.93-1.04)	0.97 (0.91-1.04)	0.99 (0.92-1.07)
5	rs4530754	122855416	G/A	G=0.460	1.03 (1.02-1.04)	1.00 (0.97-1.04)	1.00 (0.95-1.04)	1.00 (0.96-1.05)

0	rs3757354	10127407	T/C	T=0.240	1.04 (1.05-1.05)	0.97 (0.95-1.01)	0.96 (0.91-1.02)	0.99 (0.93-1.05)
6	rs1800562	26093141	A/G	A=0.070	1.06 (1.05-1.08)	1.05 (0.98-1.13)	1.06 (0.97-1.16)	1.05 (0.95-1.16)
6	rs1564348	160578860	T/C	C=0.180	1.05 (1.04-1.06)	1.00 (0.96-1.05)	1.01 (0.95-1.07)	0.99 (0.93-1.06)
7	rs4722551	25991826	T/C	C=0.200	1.04 (1.03-1.05)	1.03 (0.98-1.08)	1.03 (0.97-1.09)	1.02 (0.96-1.09)
8	rs10102164	55421614	G/A	A=0.210	1.03 (1.02-1.04)	0.99 (0.95-1.04)	0.97 (0.91-1.02)	1.02 (0.96-1.08)
8	rs11136341	145043543	A/G	G=0.400	1.05 (1.03-1.06)	0.95 (0.90-1.01)	0.96 (0.91-1.03)	0.94 (0.87-1.00)
9	rs9411489	136155000	C/T	T=0.210	1.08 (1.07-1.09)	0.99 (0.96-1.03)	0.96 (0.91-1.01)	1.04 (0.98-1.10)
11	rs11220462	126243952	G/A	A=0.140	1.06 (1.05-1.07)	1.04 (0.99-1.10)	1.02 (0.95-1.08)	1.01 (0.94-1.08)
13	rs4942486	32953388	C/T	T=0.480	1.02 (1.02-1.03)	1.02 (0.99-1.06)	1.05 (1.00-1.10)	0.99 (0.94-1.03)
14	rs8017377	24883887	G/A	A=0.460	1.03 (1.02-1.04)	1.02 (0.98-1.06)	1.03 (0.99-1.08)	1.01 (0.96-1.05)
17	rs1801689	64210580	A/C	C=0.040	1.11 (1.08-1.14)	0.93 (0.84-1.04)	0.94 (0.82-1.07)	0.94 (0.82-1.08)
19	rs6511720	11202306	T/G	T=0.120	1.25 (1.23-1.26)	1.03 (0.97-1.08)	0.99 (0.92-1.06)	1.07 (1.00-1.15)
19	rs4420638	45422946	A/G	G=0.190	1.25 (1.23-1.27)	1.02 (0.97-1.07)	1.03 (0.97-1.09)	1.00 (0.94-1.07)
20	rs364585	12962718	A/G	A=0.380	1.03 (1.02-1.03)	1.03 (0.99-1.07)	1.04 (0.99-1.08)	1.02 (0.98-1.08)
20	rs2328223	17845921	A/C	C=0.210	1.03 (1.02-1.04)	0.98 (0.94-1.03)	0.94 (0.89-0.99)	1.03 (0.97-1.09)
20	rs6029526	39672618	T/A	A=0.470	1.04 (1.03-1.06)	0.98 (0.95-1.02)	1.00 (0.96-1.04)	0.97 (0.92-1.01)
22	rs5763662	30378703	C/T	T=0.040	1.08 (1.05-1.11)	1.06 (0.94-1.21)	1.05 (0.90-1.22)	1.05 (0.89-1.24)

Type-2 diabetes

Chromosome	SNP	Base pair position *	Alleles**	MAF	Type-2 diabetes	All glioma	GBM	Non-GBM
					OR (95% CI)	OR (95% CI)	OR (95% CI)	OR (95% CI)
1	rs340874	214159256	T/C	T=0.480	1.07 (1.05-1.09)	1.00 (0.97-1.04)	0.99 (0.94-1.03)	1.02 (0.97-1.07)
2	rs780094	27741237	T/C	T=0.389	1.06 (1.04-1.08)	1.04 (1.01-1.08)	1.07 (1.02-1.11)	1.02 (0.97-1.07)
2	rs77981966	43777964	T/C	T=0.066	1.16 (1.12-1.21)	1.05 (0.98-1.12)	1.04 (0.95-1.13)	1.08 (0.99-1.19)
2	rs243020	60585028	A/G	A=0.462	1.06 (1.04-1.08)	0.98 (0.95-1.02)	0.96 (0.92-1.00)	1.01 (0.97-1.06)
2	rs75297654	165545615	T/C	C=0.124	1.11 (1.09-1.13)	1.04 (0.99-1.10)	1.02 (0.96-1.09)	1.07 (0.99-1.14)
3	rs11712037	12344730	G/C	C=0.138	1.14 (1.11-1.17)	1.01 (0.96-1.07)	1.00 (0.93-1.06)	1.06 (0.98-1.14)
3	rs17676309	64730121	T/C	C=0.410	1.07 (1.05-1.09)	1.02 (0.98-1.05)	1.02 (0.97-1.07)	1.01 (0.96-1.06)
3	rs11708067	123065778	G/A	A=0.214	1.11 (1.09-1.13)	1.02 (0.97-1.06)	1.01 (0.96-1.07)	0.99 (0.94-1.05)
3	rs35510946	185518910	G/A	G=0.301	1.14 (1.12-1.16)	0.99 (0.96-1.03)	0.99 (0.95-1.04)	0.99 (0.94-1.04)
4	rs10937721	6306763	G/C	C=0.420	1.09 (1.07-1.11)	0.98 (0.94-1.01)	0.96 (0.92-1.01)	0.98 (0.93-1.03)
5	rs7732130	76435004	A/G	A=0.278	1.08 (1.06-1.10)	1.06 (1.02-1.10)	1.05 (1.00-1.10)	1.09 (1.04-1.15)
6	rs35261542	20675792	C/A	A=0.280	1.17 (1.15-1.19)	0.97 (0.93-1.01)	0.94 (0.90-0.99)	1.01 (0.96-1.07)
7	rs10276674	14922007	T/C	T=0.183	1.08 (1.06-1.10)	1.02 (0.96-1.09)	1.00 (0.93-1.08)	1.04 (0.95-1.13)
7	rs1974620	15065467	C/T	T=0.481	1.06 (1.04-1.08)	1.01 (0.98-1.05)	1.01 (0.97-1.06)	1.01 (0.96-1.05)
7	rs1513272	28200097	T/C	C=0.482	1.10 (1.08-1.12)	0.99 (0.96-1.03)	1.01 (0.97-1.06)	0.97 (0.93-1.02)
7	rs878521	44255643	G/A	G=0.235	1.07 (1.05-1.09)	0.97 (0.93-1.01)	0.99 (0.94-1.04)	0.95 (0.90-1.01)
8	rs13266634	118184783	T/C	C=0.324	1.12 (1.10-1.14)	0.99 (0.95-1.03)	0.98 (0.93-1.02)	1.00 (0.95-1.05)
9	rs10811660	22134068	A/G	G=0.170	1.27 (1.23-1.31)	0.98 (0.94-1.03)	0.97 (0.92-1.03)	0.99 (0.93-1.05)
10	rs11187140	94466910	A/G	G=0.368	1.12 (1.10-1.14)	1.01 (0.97-1.05)	1.02 (0.97-1.06)	1.00 (0.96-1.06)
10	rs7903146	114758349	C/T	C=0.260	1.36 (1.33-1.39)	1.01 (0.97-1.05)	1.01 (0.96-1.06)	1.01 (0.96-1.06)
11	rs2237895	2857194	A/C	A=0.428	1.07 (1.05-1.09)	0.99 (0.95-1.03)	0.98 (0.93-1.02)	1.00 (0.95-1.05)
11	rs5215	17408630	T/C	T=0.389	1.07 (1.05-1.09)	1.02 (0.98-1.06)	1.02 (0.98-1.07)	0.99 (0.95-1.04)
11	rs142489578	72460930	A/AT	AT=0.177	1.10 (1.07-1.13)	1.03 (0.92-1.14)	0.97 (0.85-1.11)	1.15 (1.00-1.33)
11	rs10830963	92708710	C/G	C=0.283	1.09 (1.07-1.11)	1.02 (0.97-1.06)	0.99 (0.94-1.04)	1.03 (0.98-1.09)
12	rs2583941	66204598	G/A	G=0.090	1.11 (1.08-1.14)	1.00 (0.92-1.09)	1.02 (0.93-1.13)	0.98 (0.88-1.09)
12	rs1169288	121416650	A/C	A=0.334	1.09 (1.07-1.11)	1.02 (0.98-1.06)	1.01 (0.96-1.06)	1.01 (0.96-1.07)
12	rs1800574	121416864	C/T	C=0.027	1.22 (1.15-1.30)	1.10 (0.98-1.24)	1.01 (0.87-1.17)	1.17 (0.99-1.37)
15	rs7161785	62395224	C/G	G=0.445	1.06 (1.04-1.08)	1.00 (0.96-1.04)	0.97 (0.93-1.02)	1.05 (1.00-1.10)
15	rs3803563	91531352	C/A	C=0.175	1.08 (1.06-1.11)	1.02 (0.98-1.07)	1.04 (0.99-1.10)	1.02 (0.96-1.08)
16	rs9927317	53820996	C/G	C=0.396	1.14 (1.12-1.16)	0.99 (0.94-1.04)	1.00 (0.94-1.06)	0.99 (0.93-1.06)
17	rs4430796	36098040	A/G	A=0.455	1.09 (1.07-1.11)	1.02 (0.98-1.06)	1.02 (0.97-1.07)	1.02 (0.97-1.07)
19	rs72999033	19366632	C/T	C=0.069	1.16 (1.12-1.20)	0.99 (0.92-1.06)	1.02 (0.93-1.11)	0.97 (0.88-1.06)
19	rs2238689	46178661	T/C	T=0.425	1.08 (1.06-1.10)	1.03 (1.00-1.07)	1.03 (0.99-1.08)	1.05 (1.00-1.10)
20	rs1800961	43042364	C/T	C=0.034	1.16 (1.10-1.22)	0.97 (0.88-1.08)	0.98 (0.86-1.11)	0.95 (0.82-1.09)

Total cholesterol

Chromosome	SNP	Base pair position *	Alleles**	MAF	Total cholesterol	All glioma	GBM	Non-GBM
					OR (95% CI)	OR (95% CI)	OR (95% CI)	OR (95% CI)
1	rs1077514	23766233	C/T	C=0.150	1.03 (1.02-1.04)	0.99 (0.94-1.05)	1.01 (0.95-1.08)	0.99 (0.93-1.06)
1	rs12027135	25775733	C/T	A=0.460	1.03 (1.02-1.04)	1.00 (0.97-1.04)	0.99 (0.95-1.03)	1.01 (0.97-1.06)
1	rs7515577	93009438	C/A	C=0.230	1.04 (1.02-1.05)	1.04 (1.00-1.09)	1.05 (1.00-1.11)	1.03 (0.97-1.09)
1	rs2642442	220973563	C/T	C=0.330	1.04 (1.02-1.05)	1.00 (0.96-1.04)	0.98 (0.94-1.03)	1.01 (0.96-1.06)
1	rs514230	234858597	C/T	A=0.480	1.04 (1.03-1.05)	1.01 (0.97-1.04)	1.00 (0.96-1.05)	1.02 (0.98-1.07)
2	rs2287623	169830155	A/G	G=0.410	1.03 (1.02-1.04)	1.00 (0.97-1.04)	0.98 (0.94-1.03)	1.03 (0.99-1.09)
2	rs11694172	203532304	C/G	G=0.250	1.03 (1.02-1.04)	0.99 (0.95-1.04)	1.00 (0.95-1.05)	0.98 (0.93-1.04)
2	rs11563251	234679384	C/T	T=0.120	1.04 (1.03-1.05)	1.01 (0.95-1.07)	1.00 (0.93-1.07)	1.01 (0.94-1.09)
3	rs13315871	58381287	A/G	A=0.100	1.04 (1.02-1.05)	1.04 (0.98-1.11)	1.03 (0.96-1.11)	1.02 (0.94-1.11)
3	rs2290159	12628920	C/G	C=0.230	1.04 (1.03-1.05)	1.02 (0.98-1.07)	1.03 (0.97-1.08)	1.03 (0.97-1.09)
5	rs12916	74656539	C/C	C=0.400	1.07 (1.06-1.08)	1.00 (0.97-1.04)	0.99 (0.94-1.03)	1.02 (0.97-1.07)
5	rs6882076	156390297	C/C	T=0.360	1.05 (1.04-1.06)	1.00 (0.96-1.04)	0.98 (0.93-1.02)	1.02 (0.97-1.07)
6	rs2758886	39250837	C/A	A=0.300	1.02 (1.01-1.03)	0.99 (0.95-1.03)	0.97 (0.93-1.02)	1.01 (0.96-1.06)

rs	rs93/6090	133411228	C/C	T=0.280	1.05 (1.02-1.05)	1.05 (0.98-1.07)	1.06 (1.00-1.11)	0.98 (0.93-1.04)
6	rs3177928	32412435	C/A	A=0.170	1.05 (1.04-1.06)	1.02 (0.97-1.08)	1.02 (0.96-1.09)	1.03 (0.96-1.11)
6	rs2814982	34546560	T/C	T=0.120	1.55 (1.39-1.73)	0.97 (0.92-1.03)	0.99 (0.92-1.07)	0.94 (0.87-1.01)
6	rs9488822	116312893	C/T	T=0.360	1.03 (1.02-1.05)	1.01 (0.98-1.05)	1.00 (0.96-1.05)	1.02 (0.97-1.07)
7	rs1997243	1083777	C/G	G=0.130	1.03 (1.02-1.04)	1.04 (0.98-1.09)	1.05 (0.99-1.12)	1.02 (0.95-1.09)
7	rs12670798	21607352	C/C	C=0.250	1.04 (1.03-1.05)	1.02 (0.97-1.06)	1.04 (0.98-1.09)	1.00 (0.94-1.06)
7	rs2072183	44579180	C/C	C=0.290	1.04 (1.03-1.05)	1.02 (0.97-1.06)	1.01 (0.96-1.07)	1.01 (0.95-1.07)
8	rs2081687	59388565	C/T	T=0.360	1.04 (1.03-1.05)	1.01 (0.97-1.05)	1.03 (0.98-1.08)	0.99 (0.95-1.04)
9	rs3780181	2640759	G/A	G=0.080	1.04 (1.03-1.06)	0.99 (0.93-1.07)	1.00 (0.92-1.09)	0.96 (0.87-1.05)
10	rs10904908	17260290	C/G	G=0.430	1.03 (1.02-1.03)	0.97 (0.94-1.01)	0.98 (0.94-1.02)	0.98 (0.94-1.03)
10	rs2255141	113933886	G/A	A=0.300	1.03 (1.02-1.04)	1.01 (0.96-1.06)	1.01 (0.95-1.07)	1.03 (0.96-1.10)
11	rs10128711	18632984	C/C	T=0.300	1.03 (1.02-1.04)	0.96 (0.92-1.00)	0.95 (0.91-1.00)	0.98 (0.93-1.03)
11	rs7941030	122522375	C/C	C=0.390	1.03 (1.02-1.04)	0.99 (0.95-1.02)	0.99 (0.94-1.03)	0.98 (0.94-1.03)
12	rs4883201	9082581	G/A	G=0.120	1.04 (1.02-1.05)	0.94 (0.89-1.00)	0.94 (0.88-1.01)	0.93 (0.86-1.01)
12	rs11065987	112072424	G/A	G=0.410	1.03 (1.02-1.04)	1.01 (0.98-1.05)	1.03 (0.99-1.08)	1.01 (0.96-1.06)
12	rs1169288	121416650	C/C	C=0.340	1.03 (1.02-1.04)	1.02 (0.98-1.06)	1.01 (0.96-1.06)	1.01 (0.96-1.07)
16	rs2000999	72108093	C/A	A=0.200	1.06 (1.05-1.07)	1.01 (0.96-1.05)	1.00 (0.94-1.05)	1.01 (0.95-1.07)
17	rs314253	7091650	C/T	C=0.370	1.02 (1.02-1.03)	0.99 (0.95-1.02)	1.00 (0.96-1.05)	0.96 (0.91-1.01)
19	rs10401969	19407718	C/T	C=0.090	1.15 (1.13-1.16)	1.01 (0.95-1.08)	0.98 (0.91-1.07)	1.04 (0.96-1.14)
19	rs492602	49206417	C/G	T=0.470	1.03 (1.02-1.04)	0.99 (0.95-1.03)	0.98 (0.94-1.03)	0.98 (0.93-1.03)
20	rs2277862	34152782	T/C	T=0.150	1.04 (1.02-1.05)	1.02 (0.97-1.08)	1.07 (1.00-1.13)	0.99 (0.93-1.06)
20	rs2902940	39091487	G/A	G=0.300	1.02 (1.02-1.03)	0.98 (0.94-1.02)	0.98 (0.93-1.03)	0.97 (0.92-1.02)
22	rs138777	35711098	G/A	A=0.360	1.02 (1.01-1.03)	0.97 (0.94-1.01)	0.98 (0.93-1.02)	0.97 (0.92-1.02)
22	rs4253772	46627603	C/T	T=0.110	1.03 (1.02-1.04)	1.00 (0.94-1.05)	0.99 (0.93-1.07)	1.00 (0.93-1.08)

Triglycerides

Chromosome	SNP	Base pair position *	Alleles**	MAF	Triglycerides	All glioma	GBM	Non-GBM
					OR (95% CI)	OR (95% CI)	OR (95% CI)	OR (95% CI)
1	rs2131925	63025942	G/T	G=0.340	1.93 (1.80-2.08)	1.06 (1.02-1.10)	1.03 (0.98-1.08)	1.10 (1.04-1.15)
2	rs1260326	27730940	C/T	T=0.390	1.12 (1.11-1.13)	0.96 (0.92-0.99)	0.93 (0.89-0.98)	0.99 (0.94-1.04)
3	rs645040	135926622	G/T	G=0.230	1.34 (1.23-1.45)	0.97 (0.93-1.01)	0.95 (0.90-1.00)	0.99 (0.93-1.04)
4	rs6831256	3473139	A/G	G=0.420	1.03 (1.02-1.03)	0.96 (0.92-0.99)	0.95 (0.91-0.99)	0.98 (0.93-1.02)
4	rs442177	88030261	G/T	G=0.420	1.03 (1.02-1.04)	0.99 (0.96-1.03)	1.01 (0.97-1.06)	0.97 (0.92-1.01)
5	rs9686661	55861786	C/T	T=0.200	1.46 (1.33-1.60)	0.95 (0.91-1.00)	0.95 (0.90-1.00)	0.97 (0.92-1.03)
6	rs998584	43757896	C/A	A=0.490	1.03 (1.02-1.04)	1.01 (0.97-1.05)	0.99 (0.95-1.03)	1.03 (0.98-1.08)
7	rs38855	116358044	G/A	G=0.470	1.02 (1.01-1.03)	1.01 (0.98-1.05)	1.01 (0.96-1.05)	1.01 (0.97-1.06)
7	rs17145738	72982874	T/C	T=0.130	1.12 (1.11-1.13)	0.97 (0.92-1.03)	0.99 (0.93-1.06)	0.94 (0.87-1.01)
8	rs11776767	10683929	G/C	C=0.370	1.02 (1.02-1.03)	1.00 (0.96-1.03)	1.01 (0.96-1.05)	0.99 (0.95-1.04)
8	rs1495741	18272881	A/G	G=0.260	1.04 (1.03-1.05)	1.00 (0.96-1.04)	0.99 (0.94-1.05)	0.99 (0.94-1.05)
8	rs12678919	19844222	G/A	G=0.130	1.19 (1.17-1.20)	0.99 (0.94-1.05)	0.95 (0.89-1.03)	1.02 (0.95-1.11)
8	rs2954029	126490972	T/A	T=0.470	1.08 (1.07-1.09)	0.97 (0.94-1.01)	0.96 (0.92-1.00)	0.99 (0.95-1.04)
10	rs1832007	5254847	G/A	G=0.180	1.03 (1.02-1.04)	1.03 (0.98-1.08)	1.01 (0.95-1.07)	1.04 (0.98-1.12)
10	rs10761731	65027610	T/A	T=0.440	1.03 (1.02-1.04)	1.02 (0.98-1.06)	1.05 (1.00-1.10)	1.01 (0.96-1.06)
10	rs2068888	94839642	A/G	A=0.450	1.02 (1.02-1.03)	0.98 (0.95-1.02)	0.98 (0.94-1.03)	0.96 (0.92-1.01)
11	rs174546	61569830	C/T	T=0.360	1.05 (1.04-1.05)	1.01 (0.97-1.05)	1.00 (0.96-1.05)	1.03 (0.98-1.08)
11	rs964184	116648917	C/G	G=0.160	1.26 (1.25-1.28)	1.01 (0.96-1.07)	1.02 (0.96-1.09)	0.99 (0.92-1.06)
12	rs11613352	57792580	T/C	T=0.260	1.03 (1.02-1.04)	0.99 (0.95-1.03)	0.98 (0.93-1.03)	1.00 (0.95-1.06)
15	rs2412710	42683787	G/A	A=0.040	1.10 (1.07-1.14)	1.05 (0.93-1.19)	1.09 (0.93-1.27)	1.04 (0.88-1.22)
16	rs3198697	15129940	T/C	T=0.430	1.02 (1.01-1.03)	0.99 (0.96-1.03)	1.01 (0.96-1.05)	0.97 (0.93-1.02)
17	rs8077889	41878166	A/C	C=0.220	1.03 (1.02-1.03)	0.96 (0.91-1.00)	0.96 (0.91-1.02)	0.95 (0.90-1.01)
19	rs7248104	7224431	A/G	A=0.420	1.02 (1.02-1.03)	1.00 (0.96-1.04)	0.98 (0.93-1.04)	0.99 (0.94-1.05)
19	rs731839	33899065	A/G	G=0.350	1.02 (1.01-1.03)	1.00 (0.96-1.03)	0.98 (0.94-1.03)	1.02 (0.97-1.07)

WHR

Chromosome	SNP	Position*	Alleles**	MAF	WHR	All glioma	GBM	Non-GBM
					OR (95% CI)	OR (95% CI)	OR (95% CI)	OR (95% CI)
1	rs2765539	119549418	C/T	C=0.292	1.03 (1.02-1.04)	1.00 (0.95-1.06)	0.98 (0.92-1.04)	1.02 (0.96-1.10)
1	rs1011731	172346548	A/G	G=0.458	1.02 (1.01-1.03)	0.98 (0.94-1.01)	0.98 (0.93-1.02)	0.99 (0.95-1.04)
1	rs1563355	219653101	T/C	T=0.314	1.03 (1.02-1.04)	1.02 (0.98-1.06)	0.99 (0.95-1.04)	1.05 (1.00-1.10)
2	rs929641	58792377	G/A	G=0.383	1.02 (1.01-1.03)	1.02 (0.99-1.06)	1.00 (0.96-1.05)	1.04 (0.99-1.09)
2	rs1128249	165528624	T/G	T=0.442	1.02 (1.01-1.03)	1.04 (1.00-1.07)	1.02 (0.98-1.07)	1.04 (1.00-1.09)
2	rs1569135	188115398	G/A	G=0.467	1.02 (1.02-1.03)	0.98 (0.95-1.01)	0.97 (0.93-1.01)	0.98 (0.93-1.03)
3	rs2972164	12334416	T/C	T=0.500	1.02 (1.01-1.03)	1.03 (0.99-1.07)	1.03 (0.99-1.08)	1.03 (0.98-1.08)
3	rs9860730	64701146	G/A	G=0.233	1.02 (1.02-1.03)	0.99 (0.96-1.03)	1.01 (0.96-1.06)	0.97 (0.93-1.02)
3	rs17451107	156797609	C/T	C=0.375	1.02 (1.02-1.03)	0.97 (0.94-1.01)	0.97 (0.93-1.02)	0.99 (0.94-1.04)
5	rs459193	55806751	G/A	A=0.217	1.03 (1.02-1.03)	1.01 (0.97-1.05)	1.02 (0.97-1.07)	1.01 (0.95-1.06)
6	rs1294421	6743149	T/G	T=0.400	1.03 (1.02-1.03)	1.01 (0.97-1.05)	1.01 (0.97-1.06)	1.00 (0.96-1.05)
6	rs11755724	7118990	A/G	A=0.300	1.02 (1.01-1.03)	0.98 (0.95-1.02)	0.97 (0.92-1.02)	0.99 (0.94-1.04)
6	rs998584	43757896	C/A	A=0.475	1.03 (1.02-1.04)	1.01 (0.97-1.05)	0.99 (0.95-1.03)	1.03 (0.98-1.08)
6	rs2207139	50845490	A/G	G=0.100	1.03 (1.02-1.03)	0.99 (0.95-1.04)	0.97 (0.91-1.03)	1.02 (0.96-1.08)
6	rs9491696	127452639	C/G	C=0.475	1.04 (1.03-1.05)	1.03 (1.00-1.07)	1.02 (0.98-1.07)	1.05 (1.00-1.10)
7	rs10245353	25858614	C/A	A=0.183	1.03 (1.02-1.04)	1.02 (0.97-1.07)	1.02 (0.96-1.08)	1.04 (0.98-1.10)

r	rs7801581	72223771	C/T	F=0.258	1.02 (1.01-1.03)	1.03 (0.99-1.08)	1.04 (0.99-1.10)	1.05 (0.99-1.11)
8	rs12549058	72492238	T/G	G=0.058	1.04 (1.03-1.05)	0.94 (0.87-1.01)	1.00 (0.92-1.10)	0.87 (0.79-0.96)
11	rs4929927	8658485	A/G	A=0.275	1.02 (1.01-1.03)	1.04 (1.00-1.08)	1.03 (0.98-1.08)	1.04 (0.99-1.10)
12	rs11048470	26487283	G/T	T=0.233	1.03 (1.02-1.03)	0.99 (0.95-1.03)	0.98 (0.94-1.03)	1.01 (0.95-1.06)
12	rs10783615	54349773	A/G	G=0.133	1.04 (1.03-1.05)	1.02 (0.97-1.08)	1.01 (0.95-1.08)	1.03 (0.96-1.11)
12	rs10876528	54421476	C/A	A=0.310	1.03 (1.02-1.04)	1.01 (0.97-1.05)	1.00 (0.95-1.04)	1.03 (0.98-1.08)
12	rs1316952	124399550	C/T	C=0.117	1.03 (1.02-1.04)	0.98 (0.93-1.03)	0.98 (0.92-1.04)	0.97 (0.91-1.04)
14	rs17109256	79939993	G/A	A=0.275	1.02 (1.02-1.03)	1.04 (1.00-1.09)	1.01 (0.95-1.06)	1.09 (1.03-1.16)
15	rs1440372	67033151	T/C	T=0.258	1.02 (1.01-1.03)	0.99 (0.96-1.03)	1.01 (0.96-1.06)	0.97 (0.92-1.02)
16	rs1121980	53809247	G/A	A=0.475	1.04 (1.04-1.05)	0.98 (0.95-1.02)	1.00 (0.96-1.04)	0.96 (0.92-1.01)
17	rs4640244	21284223	A/G	G=0.375	1.02 (1.01-1.03)	0.99 (0.95-1.03)	0.99 (0.94-1.03)	0.99 (0.94-1.04)
18	rs11663816	57876227	T/C	C=0.317	1.03 (1.02-1.03)	1.02 (0.98-1.06)	1.03 (0.98-1.08)	1.00 (0.95-1.05)
19	rs3786897	33893008	A/G	G=0.408	1.02 (1.02-1.03)	1.04 (1.00-1.08)	1.04 (0.99-1.08)	1.04 (0.99-1.09)
19	rs2075650	45395619	G/A	G=0.142	1.03 (1.02-1.04)	0.95 (0.90-1.00)	0.94 (0.88-1.00)	0.96 (0.90-1.03)
19	rs2287019	46202172	T/C	T=0.150	1.03 (1.02-1.04)	0.96 (0.91-1.00)	0.96 (0.91-1.02)	0.94 (0.89-1.00)
20	rs16996700	50981945	C/T	C=0.300	1.02 (1.01-1.03)	0.99 (0.95-1.03)	0.98 (0.93-1.02)	1.01 (0.96-1.06)
22	rs2179129	29450923	G/A	G=0.450	1.02 (1.01-1.03)	1.00 (0.96-1.04)	0.99 (0.95-1.04)	1.00 (0.96-1.05)

* NCBI build 37; ** Reference allele/effect allele; ORs are measured per unit of SD increment. BMI, body mass index; CI, confidence interval; GBM, glioblastoma multiforme; GSMR, generalised summary-data-based Mendelian randomisation; HDL, high-density lipoprotein; IV, instrumental variable; LDL, low-density lipoprotein; MAF, minor allele frequency; OR, odds ratio; SD, standard deviation; WHR, waist-hip ratio.

4	rs17001654	0	0	0	0	0	0	0	0
4	rs13107325	0	0	0	0	0	0	0	0
4	rs11727676	0	0	0	0	0	0	0	0
5	rs2112347	0	0	0	0	0	0	0	0
6	rs205262	0	0	0	0	0	0	0	0
6	rs2207139	0	0	0	0	0	0	0	0
6	rs9400239	0	0	0	0	0	0	0	0
6	rs13191362	0	0	0	0	0	0	0	0
7	rs1167827	0	0	0	0	0	0	0	0
7	rs2245368	0	0	0	0	0	0	0	0
8	rs17405819	0	0	0	0	0	0	0	0
8	rs2033732	0	0	0	0	0	0	0	0
9	rs4740619	0	0	0	0	0	0	0	0
9	rs10968576	0	0	0	0	0	0	0	0
9	rs6477694	0	0	0	0	0	0	0	0
9	rs1928295	0	0	0	0	0	0	0	0
9	rs10733682	0	0	0	0	0	0	0	0
10	rs7899106	0	0	0	0	0	0	0	0
10	rs17094222	0	0	0	0	0	0	0	0
10	rs11191560	0	0	0	0	0	0	0	0
10	rs7903146	0	0	0	0	0	0	0	0
11	rs4256980	0	0	0	0	0	0	0	0
11	rs11030104	0	0	0	0	0	0	0	0
11	rs2176598	0	0	0	0	0	0	0	0
11	rs3817334	0	0	0	0	0	0	0	0
11	rs12286929	0	0	0	0	0	0	0	0
12	rs7138803	0	0	0	0	0	0	0	0
12	rs11057405	0	0	0	0	0	0	0	0
13	rs9581854	0	0	0	0	0	0	0	0
13	rs12429545	0	0	0	0	0	0	0	0
14	rs10132280	0	0	0	0	0	0	0	0
14	rs12885454	0	0	0	0	0	0	0	0
14	rs11847697	0	0	0	0	0	0	0	0
14	rs7141420	0	0	0	0	0	0	0	0
15	rs3736485	0	0	0	0	0	0	0	0
15	rs16951275	0	0	0	0	0	0	0	0
16	rs758747	0	0	0	0	0	0	0	0
16	rs12446632	0	0	0	0	0	0	0	0
16	rs2650492	0	0	0	0	0	0	0	0
16	rs3888190	0	0	0	0	0	0	0	0

2	rs1047891	0	0	0	0	0	0	0.016	1
2	rs2972146	0	0	0	0	0	0	0.001	0.002
3	rs2606736	0	0	0	0	0	0	0	0
3	rs2290547	0	0	0	0	0	0	0	0
3	rs2013208	0	0	0	0	0	0	0	0
3	rs13326165	0	0	0	0	0	0	0	0
3	rs6805251	0	0	0	0	0	0	0	0
4	rs10019888	0	0	0	0	0	0	0	0
4	rs3822072	0	0	0	0	0	0	0	0
4	rs2602836	0	0	0	0	0	0	0	0
4	rs13107325	0	0	0	0	0	0	0	0
5	rs6450176	0	0	0	0	0	0	0	0
6	rs1936800	0	0	0	0	0	0	0	0
6	rs605066	0	0	0	0	0	0	0	0
7	rs702485	0	0	0	0	0	0	0	0
7	rs4142995	0	0	0	0	0	0	0	0
7	rs4917014	0	0	0	0	0	0	0	0
7	rs4731702	0	0	0	0	0	0	0	0
7	rs17173637	0	0	0	0	0	0	0	0
8	rs9987289	0	0	0	0	0	0	0	0
8	rs2293889	0	0	0	0	0	0	0	0
9	rs581080	0	0	0	0	0	0	0	0
9	rs1883025	0	0	0	0	0	0	0	0
10	rs970548	0	0	0	0	0	0	0	0
11	rs2923084	0	0	0	0	0	0	0	0
11	rs3136441	0	0	0	0	0	0	0	0
11	rs11246602	0	0	0	0	0	0	0	0
11	rs12801636	0	0	0	0	0	0	0	0
11	rs499974	0	0	0	0	0	0	0	0
12	rs7134375	0	0	0	0	0	0	0	0
12	rs7134594	0	0	0	0	0	0	0	0
12	rs4759375	0	0	0	0	0	0	0	0
12	rs4765127	0	0	0	0	0	0	0	0
12	rs838880	0	0	0	0	0	0	0	0
14	rs4983559	0	0	0	0	0	0	0	0
15	rs1532085	0	0	0	0	0	0	0	0
15	rs2652834	0	0	0	0	0	0	0	0
16	rs1121980	0	0	0	0	0	0	0	0
16	rs3764261	0	0	0	0	0	0	0	0
16	rs16942887	0	0	0	0	0	0	0	0

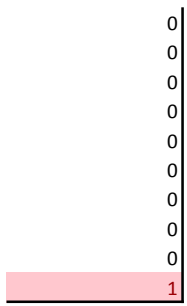
22 rs4253772	0	0	0	0	0	0	0	0	0
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WHR	Chromosome	1	1	1	2	2	2	3	3
Chromosome	rs ID	rs2765539	rs1011731	rs1563355	rs929641	rs1128249	rs1569135	rs2972164	rs904453
1	rs2765539	1	0	0	0	0	0	0	0
1	rs1011731	0	1	0	0	0	0	0	0
1	rs1563355	0	0	1	0	0	0	0	0
2	rs929641	0	0	0	1	0	0	0	0
2	rs1128249	0	0	0	0	1	0	0	0
2	rs1569135	0	0	0	0	0	1	0	0
3	rs2972164	0	0	0	0	0	0	1	0.011
3	rs904453	0	0	0	0	0	0	0.011	1
3	rs9860730	0	0	0	0	0	0	0	0.002
3	rs17451107	0	0	0	0	0	0	0	0.001
5	rs459193	0	0	0	0	0	0	0	0
6	rs1294421	0	0	0	0	0	0	0	0
6	rs11755724	0	0	0	0	0	0	0	0
6	rs998584	0	0	0	0	0	0	0	0
6	rs2207139	0	0	0	0	0	0	0	0
6	rs9491696	0	0	0	0	0	0	0	0
7	rs10245353	0	0	0	0	0	0	0	0
7	rs7801581	0	0	0	0	0	0	0	0
8	rs12549058	0	0	0	0	0	0	0	0
11	rs4929927	0	0	0	0	0	0	0	0
12	rs11048470	0	0	0	0	0	0	0	0
12	rs10783615	0	0	0	0	0	0	0	0
12	rs10876528	0	0	0	0	0	0	0	0
12	rs1316952	0	0	0	0	0	0	0	0
14	rs17109256	0	0	0	0	0	0	0	0
15	rs1440372	0	0	0	0	0	0	0	0
16	rs1121980	0	0	0	0	0	0	0	0
17	rs4640244	0	0	0	0	0	0	0	0
18	rs11663816	0	0	0	0	0	0	0	0
19	rs3786897	0	0	0	0	0	0	0	0
19	rs2075650	0	0	0	0	0	0	0	0
19	rs2287019	0	0	0	0	0	0	0	0
20	rs16996700	0	0	0	0	0	0	0	0
22	rs2179129	0	0	0	0	0	0	0	0

BMI, body mass index; HDL, high-density lipoprotein; LDL, low-density lipoprotein ; WHR, waist-hip ratio.

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

	9	10	10	10	10	11	11	11	11	11	11	11
rs3829109	rs11195502	rs10885122	rs4506565	rs7903146	rs11607883	rs11605924	rs11039182	rs174550	rs174576	rs11603334		
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0.001	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0.656	0	0	0	0	0	0	0	0	0	0
0	0.656	1	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0.878	0	0	0	0	0	0	0	0
0	0	0	0.878	1	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0.949	0	0	0	0	0	0



0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0.003	0	0	0	0	0
0	0	0	0	0	0	0	0.003	1	0	0	0	0
0	0	0	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	1	0.001	0
0	0	0	0	0	0	0	0	0	0	0	0.001	1
0	0	0	0	0	0	0	0	0	0	0	0	0.003
0	0	0	0	0	0	0	0	0	0	0.001	0	0.003

	0	0
	0	0
	0	0
	0	0
	0	0
	0	0
	0	0
	0	0
	0	0
	0	0.001
0.003		0.003
1		0.001
0.001	1	

Supplementary Table 3: Summary of the eight glioma genome wide association studies (GWAS).

Series	Study centre	Sampling	Cases	Controls
FRE	Groupe Hospitalier Pitié-Salpêtrière Paris	Patients with glioma were ascertained through the Service de Neurologie Mazarin, Groupe Hospitalier Pitié-Salpêtrière Paris. Controls were ascertained from the SU.VI.MAX (Supplementation en Vitamines et Minéraux Antioxydants) study.	1423	1190
GER	University of Bonn	Comprised of patients who had undergone surgery for a glioma at the Department of Neurosurgery, University of Bonn Medical Center, between 1996 and 2008. Control subjects were taken from three population studies: KORA (Co-operative Health Research in the Region of Augsburg); POPGEN (Population Genetic Cohort) and the Heinz Nixdorf Recall study.	846	1310
GICC	GLIOGENE Consortium	Comprise glioma cases and controls that were ascertained through Brigham and Women's Hospital (Boston, Massachusetts), Case Western Reserve University (Cleveland, Ohio), Columbia University (New York, New York), the Danish Cancer Society Research Centre (Copenhagen, Denmark), the Gertner Institute (Tel Hashomer, Israel), Duke University (Durham, North Carolina), the University of Texas MD Anderson Cancer Center (Houston, Texas), Memorial Sloan Kettering Cancer Center (New York, New York), the Mayo Clinic (Rochester, Minnesota), NorthShore HealthSystem (Chicago, Illinois), Umeå University (Umeå, Sweden), the University of California, San Francisco (San Francisco, California), the University of Southern California (Los Angeles, California), and the Institute of Cancer Research (London, United Kingdom). Cases had newly diagnosed glioma, and controls had no personal history of central nervous system tumor at the time of ascertainment	4564	3265
MDA	The University of Texas M.D. Anderson Cancer Center	Cases were ascertained through the MD Anderson Cancer Center, Texas, between 1990 and 2008. Individuals from the Cancer Genetic Markers of Susceptibility studies served as controls.	1175	2236
GiomaScan (NIH)	National Cancer Institute	Cases were newly diagnosed glioma (ICDO-3 codes 9380-9480 or equivalent), and controls were cancer-free at the time of glioma diagnosis.	1653	2725
UCSF-Mayo	Mayo Clinic	Comprised of Mayo cases, UCSF cases, and Mayo Clinic Biobank control data	1519	804
UCSF (SFAGS)	University of California, San Francisco	Cases were adults with newly diagnosed, histologically confirmed glioma. Population-based cases who were diagnosed between 1991 and 2009 and who were residing in the six San Francisco Bay area counties were ascertained using the Cancer Prevention Institute of California's early-case ascertainment system. Clinic-based cases who were diagnosed between 2002 and 2012 were recruited from the UCSF Neuro-oncology Clinic, regardless of the place of residence. From 1991 to 2010, population-based controls from the same residential area as the population-based cases were identified using random digit-dialing and were frequency matched to population-based cases for age, gender and ethnicity. Between 2010 and 2012, all controls were selected from the UCSF general medicine phlebotomy clinic. Clinic-based controls were matched to clinic-based glioma cases for age, gender and ethnicity.	677	3940
UK	INTERPHONE	Cases were ascertained through the INTERPHONE study. Individuals from the 1958 Birth Cohort served as a source of controls.	631	2699
Total			12488	18169