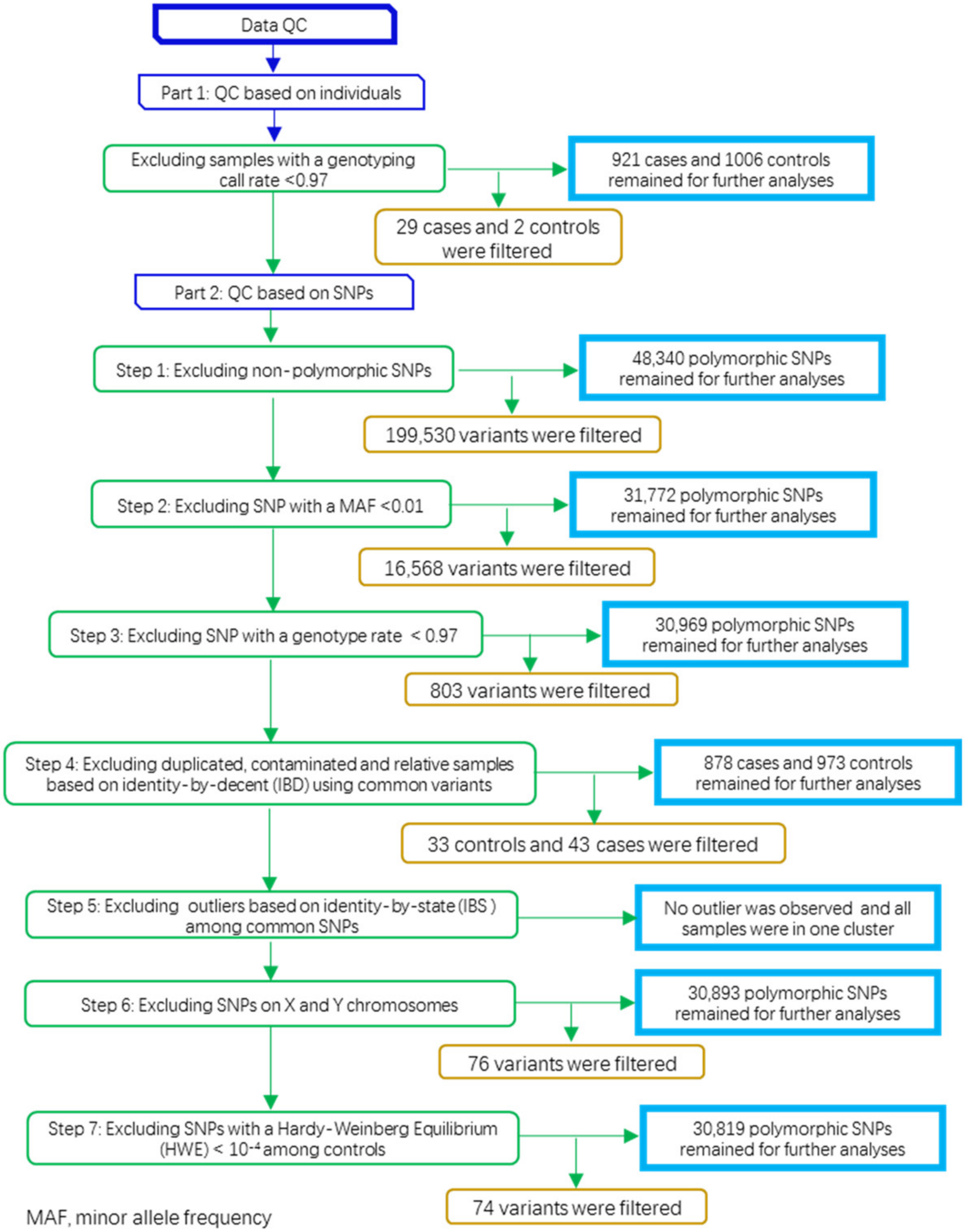


MAF, minor allele frequency

Supplementary Figure 1. Flowchart of data quality control (QC) steps in the exome-wide association analysis. The flowchart shows the steps used to filter study subjects and variants based on variants genotyped by Illumina HumanExome Beadchip v1.0.

Supplementary Table 1. Power for detecting associations in 1,000 cases vs 1,000 controls, *P* = 10E-06

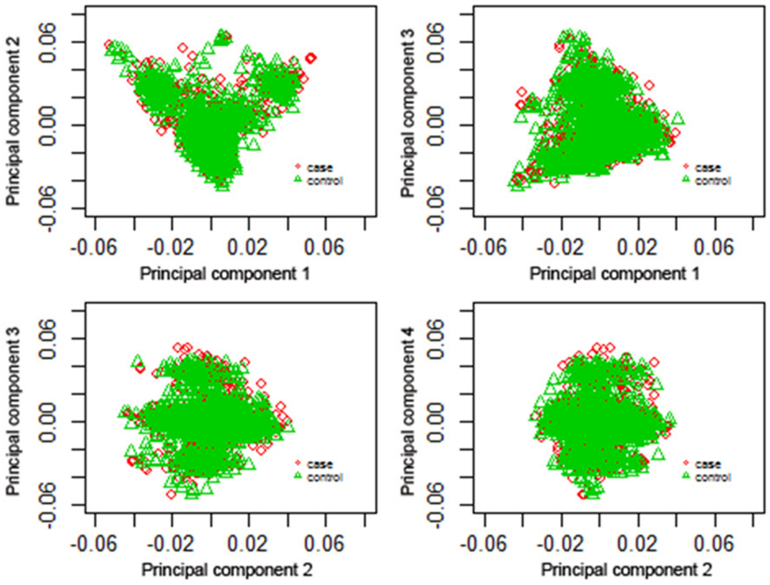
MAF	OR					
	2.0	2.4	2.8	3.2	3.6	4.0
0.01	0.01	0.07	0.23	0.48	0.72	0.88
0.02	0.10	0.45	0.82	0.97	>0.99	>0.99
0.03	0.31	0.81	0.98	>0.99	>0.99	>0.99
0.04	0.55	0.95	>0.99	>0.99	>0.99	>0.99
0.05	0.74	0.99	>0.99	>0.99	>0.99	>0.99

Supplementary Table 2. Constitutions of SNP passing QC according to their genomic contexts

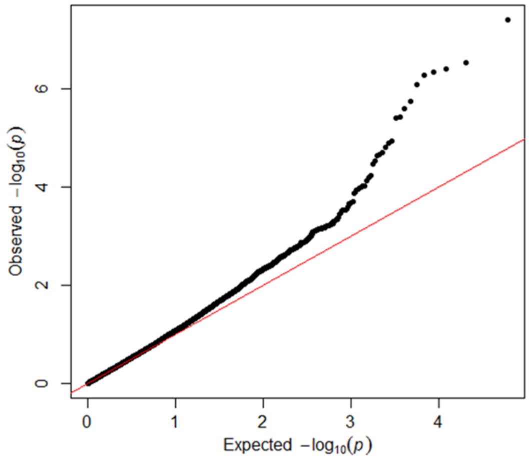
SNP Type	Number	Percentage
Missense	15,467	50.19
Intergenic	7,585	24.61
Intron	5,382	17.46
Silent	1,042	3.38
Coding	383	1.24
3'UTR	379	1.23
Non_coding_exon	140	0.45
5'UTR	125	0.41
Nonsense	121	0.39
Splicing	94	0.31
Missing data	92	0.30
Upstream gene variant	4	0.01
Downstream gene variant	2	0.01
5 prime UTR variant	1	0.00
Regulatory region variant	1	0.00
Synonymous variant	1	0.00
Total	30,819	100.00

Supplementary Table 3. Sequences of primers and oligonucleotides used for real-time PCR and plasmid construction

Primer name	Sense (5'-3')	Antisense (5'-3')
Primers for real-time PCR		
CDK2-qPCR	CATTCCTCTTCCCCTCATCA	TTTAAGGTCTCGGTGGAGGA
CDK6-qPCR	GAACTAGGCAAAGACCTACTTCTGA	GGTGGGAATCCAGGTTTTCT
E2F1-qPCR	TCTATGACATCACCAACGTCCT	CTGGGTCAACCCCTCAAG
Myc-qPCR	CACCAGCAGCGACTCTGA	GATCCAGACTCTGACCTTTTGC
Actin-qPCR	AGGCACCAGGGCGTGAT	GCCCACATAGGAATCCTTCTGAC
Primers for plasmid construction		
SLC2A4RG-rs8957-T-overlap	GGGAGGCAGGCAGAGCCTGATCAGAGTGATGGTGAGGAGGA	TCCTCCTCACCATCACTCTGATCAGGCTCTGCCTGCCTCCC
SLC2A4RG-N2-EGFP-OV	CCGCTCGAGGAGTCAGCCCTCGCCGCTGCA	CCGGAATTCGTCCAGGAACCGCTGGCAGGCT



Supplementary Figure 2. Pairwise MDS (multi-dimentional scaling) plot of the first 4 principal components.



Supplementary Figure 3. Quantile-Quantile (Q-Q) plot of observed versus expected *P* values in GBM exome chip-wide association analyses. The analysis was adjusted by the first 4 principal conponents. The genomic control lambda is 1.044.