

Supplemental Table 2.DNA methylation analysis of SLC16A1 in LGG

statistic	tissue	
	disease	normal
maximum	0.221	2.111
upper quartile	0.191	0.144
median	0.176	0
lower quartile	0.132	0.12
minimum	0.038	-1.816
P-valuse	2.20E-03	