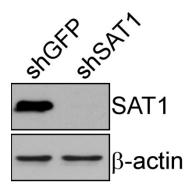
Supplementary Table:

Supplementary Table 1: List of 10 genes demonstrating at least 2-fold depletion in the shRNA screen in both LN229 and U87MG cell lines.

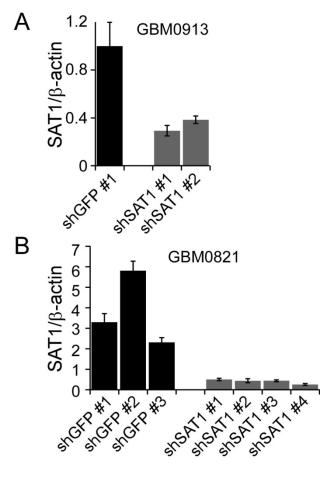
Gene	Function	LN229	U87
-	-	-1.18	-2.08
ARFGEF1	exocytosis regulation of ARF protein signal transduction	-1.02	-1.42
CAMK4	protein amino acid phosphorylation nucleocytoplasmic	-1.02	-1.54
	transport signal transduction nerve synaptic transmission		
CD9	cell motility cell adhesion fusion of sperm to egg plasma	-1.19	-2.07
	membrane platelet activation paranodal junction assembly		
GIT2	regulation of G-protein coupled receptor protein signaling	-1.77	-1.20
	pathway regulation of ARF GTPase activity		
GTF2H2	DNA repair transcription initiation regulation of	-1.09	-1.87
	transcription, DNA-dependent response to UV DNA repair		
PRKCQ	regulation of cell growth protein amino acid phosphorylation	-1.08	-2.48
	intracellular signaling cascade activation of NF-kappaB		
RAC1	cell motility cell adhesion small GTPase mediated signal	-1.06	-2.03
	transduction actin filament polymerization regulation of Rho		
RAD21	double-strand break repair apoptosis chromosome	-1.47	-2.22
	segregation mitosis meiotic recombination cell division		
SAT1	metabolic process	-1.05	-2.22

Supplementary Figures:

Supplementary Figure 1: shSAT1 effectively reduces SAT1 protein expression in denspermine treated D54MG cells.



Supplementary Figure 2: SAT1 expression in shGFP and shSAT1 GBM0821 (A) and GBM0913 (B) tumors from **Figure 3** measured by qRT-PCR after sacrifice. Error bars represent standard deviations.



Supplementary Figure 3: Flow cytometry of Hoechst 33342 stained D54MG shGFP and shSAT1 cells identifying populations sorted for cell cycle specific colony assays from **Figure 5C**.

