

Table W1. Summary of Methylation Frequencies, Mean Methylation Levels and *t* Test Results of *RANK/TNFRSF11A* in All Investigated Gliomas.

WHO Grade	Methylated Samples	Mean Methylation Level	<i>t</i> Test						
AII	8/14	24.5%	<table border="1"> <tr> <td></td> <td></td> </tr> <tr> <td></td> <td>*.0035</td> </tr> <tr> <td></td> <td>*.046</td> </tr> </table>				*.0035		*.046
	*.0035								
	*.046								
AAIII	17/22	28.9%							
sGBMIV	20/23	40.2%							
pGBMIV	81/97	33.3%							

.3767

*.026

For *t* test, the mean methylation levels of all investigated glioma entities were tested against each other.
 *Significant difference between the methylation levels in different WHO grades (*t* test): AII versus AAIII, *P* = .3767; AII + AAIII versus pGBMIV, *P* = .026; AII + AAIII versus sGBMIV, *P* = .0035; and pGBMIV versus sGBMIV, *P* = .046.

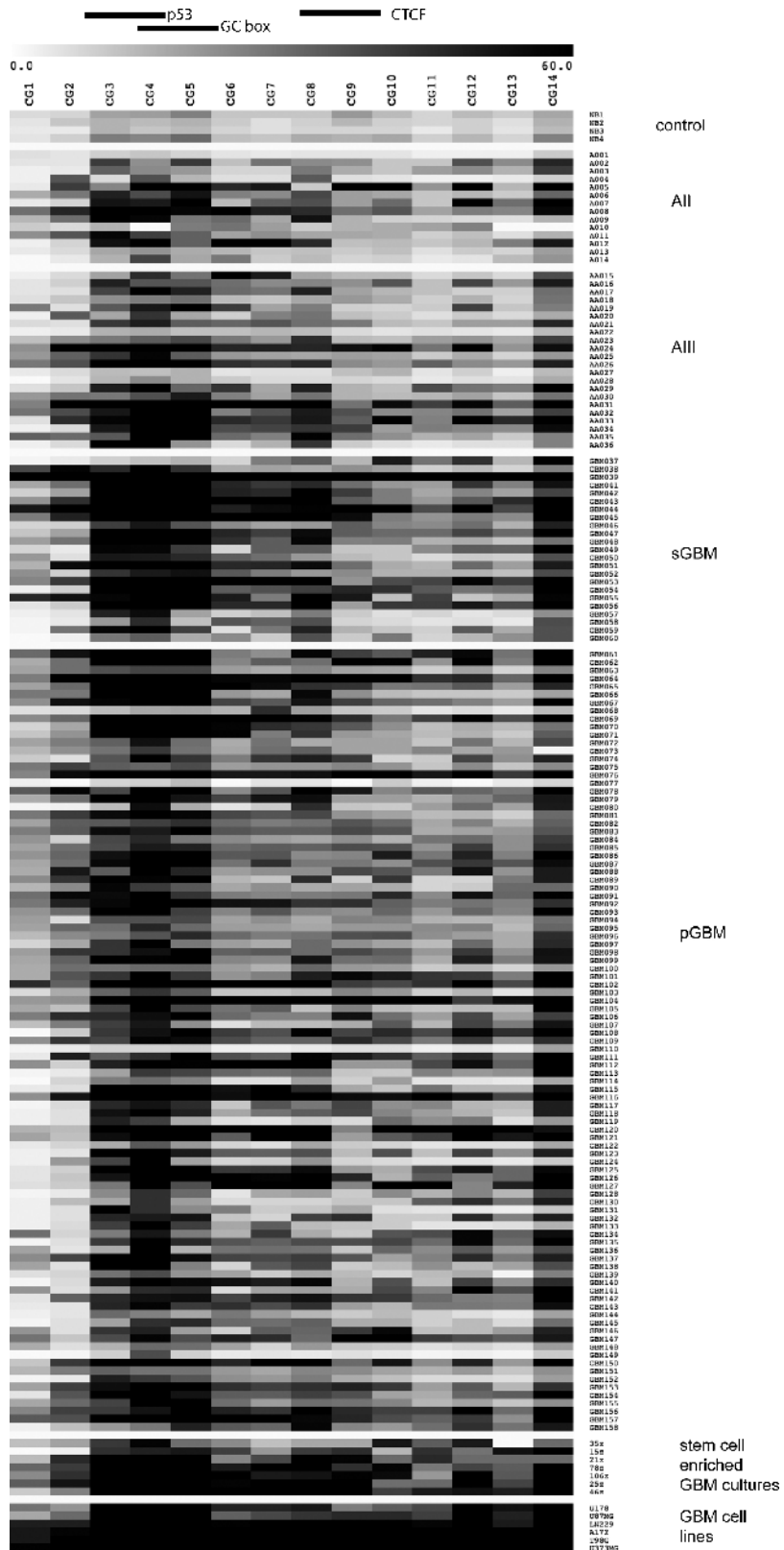


Figure W1. Quantitative methylation data of 156 primary glioma and all investigated cell cultures. The localization of the putative p53 and CTCF binding sites and a GC box are indicated. The color code shows the methylation range (0%-60%).

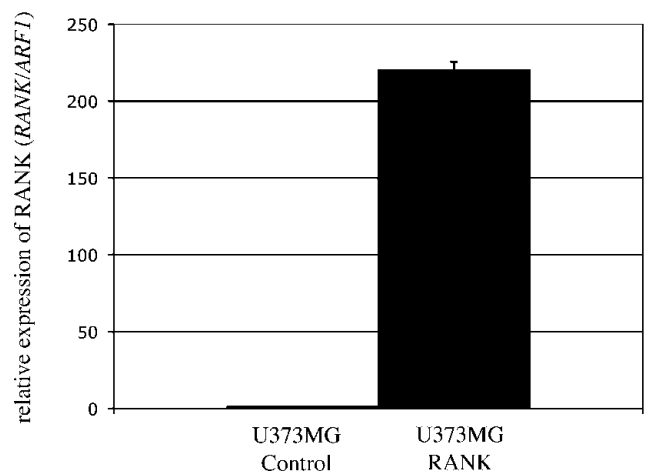
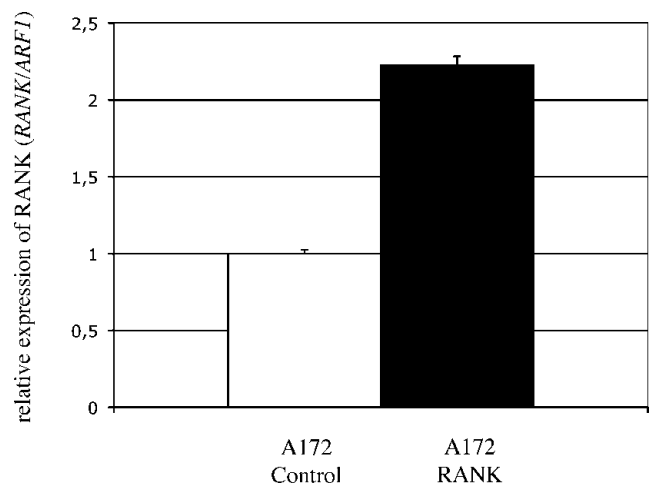
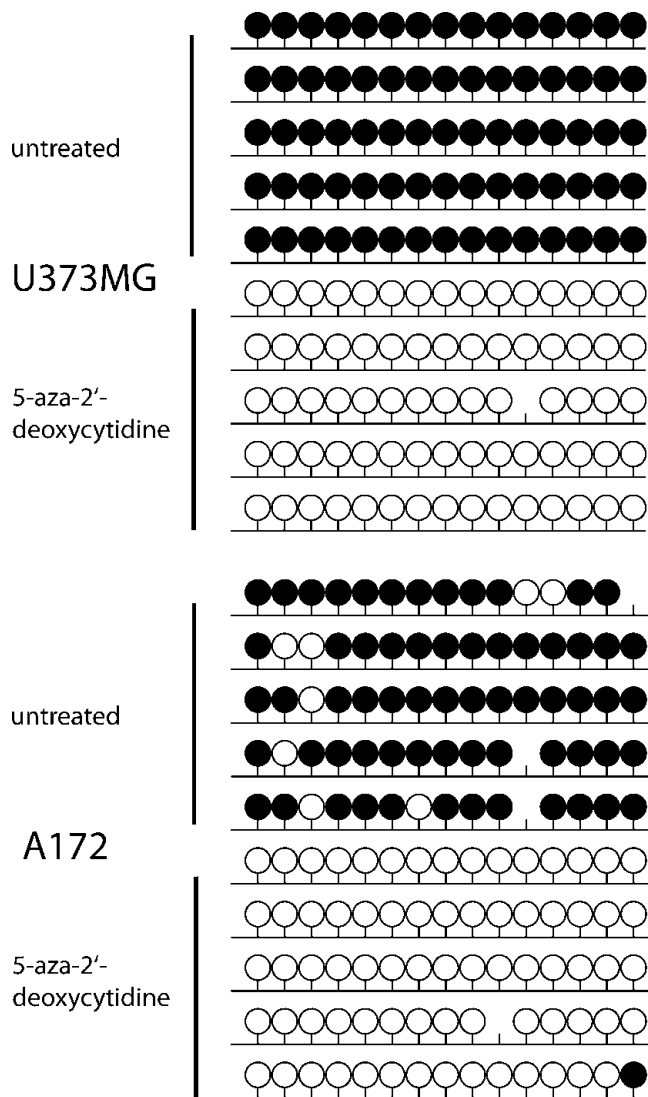


Figure W2. Representative bisulfite sequencing analysis of 5-aza-2'-deoxycytidine-treated and -untreated U373MG and A172 cells showing demethylation within the analyzed region of *RANK/TNFRSF11A*. Black lollipop indicates methylated CpG position; white lollipop, unmethylated CpG position; no circles, uncertain because of the low-quality sequence trace.

Figure W3. Relative transcript levels of *RANK/TNFRSF11A* (*RANK/TNFRSF11A/ARF1*) analyzed by real-time RT-PCR in the glioblastoma cell line U373MG after stable transfection with RANK-pcDNA4/myc-His plasmid (■) or control vector pcDNA4/myc-His (□).

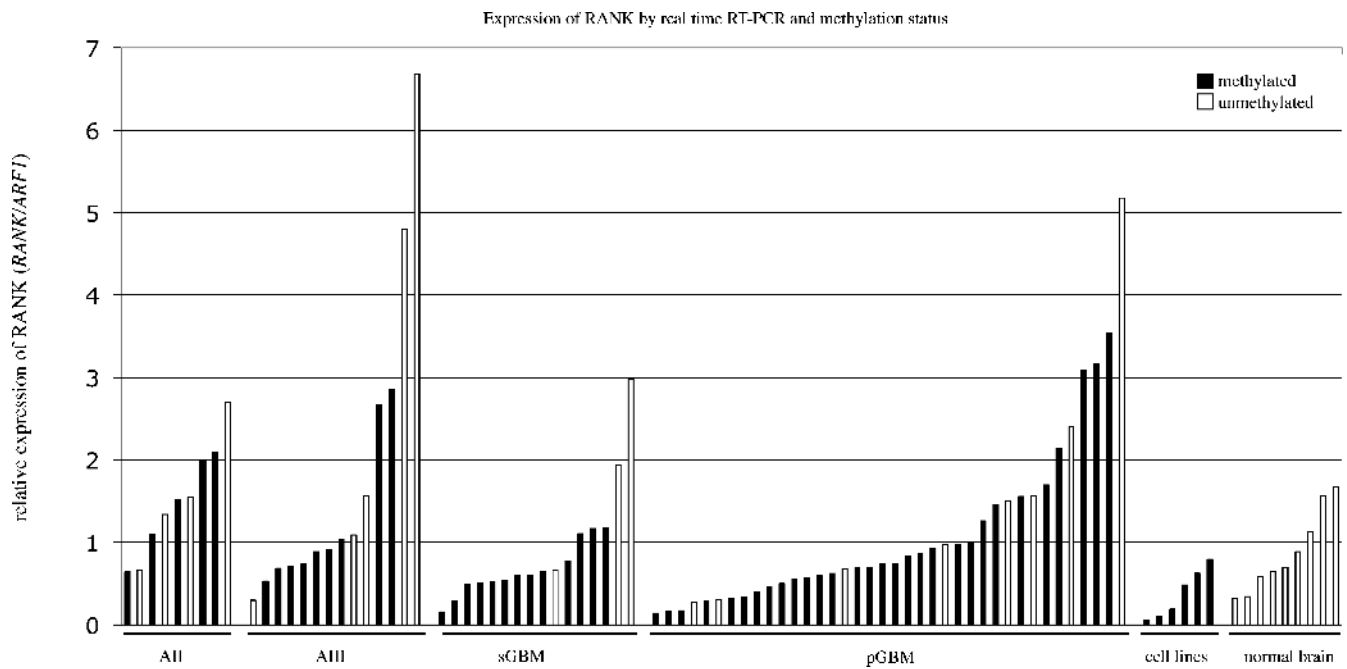


Figure W4. mRNA expression analysis of *RANK/TNFRSF11A* in gliomas, glioblastoma cell lines, and normal brain tissues. This figure shows the relative expression levels of *RANK/TNFRSF11A* (*RANK/TNFRSF11A/ARF1*) obtained by real-time RT-PCR. Results of methylation analysis by pyrosequencing are included in this figure. Black column (■) indicates that the sample is methylated; white column (□), sample is unmethylated. Samples were scored methylated if they exceeded the two-fold SD of white matter control samples (20.3%).