

## Identify the best cut-off value for survival analysis

we identify the cut-off value for distinguishing between high and low expression using R language. Similar to the exhaustive algorithm, we set the proportion of the two groups: more than 30% but less than 70%. The value that could best reflect the discrepancy between the high-expression group and the low-expression group (with the smallest P-value) was identified as the best cut-off value. The detailed R codes are shown as below:

```
R soft version 3.5.1 (https://www.r-project.org/)
```

```
library(survival)
```

```
library(survminer)
```

```
res.cut <- surv_cutpoint(svdata, time = "futime",  
                        event = "fustat",  
                        variables = names(svdata)[3:ncol(svdata)],  
                        minprop = 0.3)
```

```
res.cat <- surv_categorize(res.cut)
```

```
my.surv <- Surv(res.cat$futime, res.cat$fustat)
```

```
pl <- list()
```

```
for (i in colnames(res.cat)[3:ncol(svdata)]) {
```

```
  group <- res.cat[,i]
```

```
  survival_dat <- data.frame(group = group)
```

```
  fit <- survfit(my.surv ~ group)
```

```
  group <- factor(group, levels = c("low", "high"))
```

```
  data.survdif <- survdiff(my.surv ~ group)
```

```
  p.val = 1 - pchisq(data.survdif$chisq, length(data.survdif$n) - 1)
```

```
  HR =
```

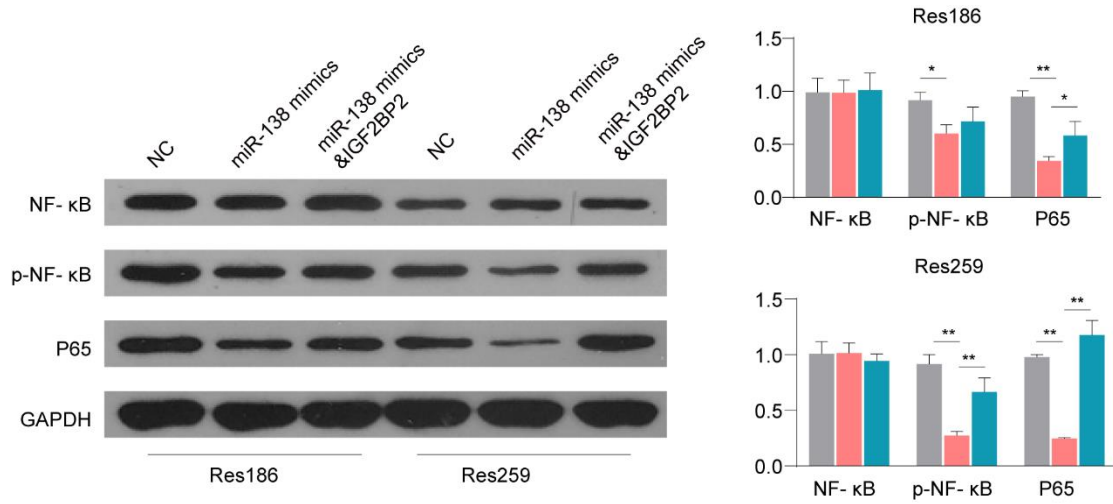
```
(data.survdif$obs[2]/data.survdif$exp[2])/(data.survdif$obs[1]/data.survdif$exp[1])
```

```
  up95 = exp(log(HR) +
```

```
  qnorm(0.975)*sqrt(1/data.survdif$exp[2]+1/data.survdif$exp[1]))
```

```
low95 = exp(log(HR) -  
qnorm(0.975)*sqrt(1/data.survdiff$exp[2]+1/data.survdiff$exp[1]))  
if (p.val>0.05) next  
HR <- paste("Hazard Ratio = ", round(HR,2), sep = "")  
CI <- paste("95% CI: ", paste(round(low95,2), round(up95,2), sep = " - "), sep = "")  
svsort <- svdata[order(svdata[,i]),]
```

Supplementary Figure 1: The expression levels of NF- $\kappa$ B signaling related proteins in Res186 or Res259 cells transfected with miR-138 mimics with or without IGF2BP2 overexpression plasmid were analyzed by western blot.



**Supplementary Table 1. Correlation of clinic-pathological features with miR-138 expression in LGG cohort**

Variables	Clinicopathological features	miR-138 expression		<i>P-value</i>
		High expression (n=40)	Low expression (n=49)	
Age (years)	≤45	20(50.0)	18(36.7)	0.208
	>45	20(50.0)	31(63.3)	
Gender	Male	22(55.0)	28(57.1)	0.890
	Female	18(45.0)	21(42.9)	
WHO grade	I	30(75.0)	22(44.9)	<b>0.004</b>
	II	10(25.0)	27(55.1)	
Metastasis	No	31(78.0)	27(55.1)	<b>0.027</b>
	Yes	9(22.0)	22(44.9)	
Survival status	Dead	9(22.0)	21(47.7)	<b>0.016</b>
	Living	31(78.0)	23(52.3)	

Bold values indicate statistical significance,  $P < 0.05$

**Supplementary Table 2. Univariate and multivariate Cox proportional hazard analyses for overall survival and recurrence-free survival.**

	Univariate analysis			Multivariate analysis		
	HR	95% CI	<i>P</i> value	HR	95% CI	<i>P</i> value
<b>Univariate and multivariate analysis of recurrence-free survival in LGG patients (n=89)</b>						
Age	1.125	0.625–1.720	0.589			
Gender	0.984	0.646-1.219	0.842			
WHO grade	2.341	1.871-2.749	<b>0.015</b>	1.922	1.504-2.495	<b>0.025</b>
Metastasis	1.847	1.421-2.473	<b>0.031</b>	1.711	1.485-2.218	<b>0.032</b>
miR-138 expression	1.618	1.351-1.942	<b>0.044</b>	1.520	1.274-1.822	<b>0.039</b>
<b>Univariate and multivariate analysis of recurrence-free survival in LGG patients (n=89)</b>						
Age	1.126	0.745-1.361	0.884			
Gender	0.853	0.624-1.221	0.647			
WHO grade	2.689	1.989-3.271	<b>0.026</b>	2.552	1.812-2.942	<b>0.022</b>
Metastasis	1.958	1.671-2.704	<b>0.032</b>	1.822	1.509-2.219	<b>0.039</b>
miR-138 expression	2.034	1.817-2.626	<b>0.038</b>	2.114	1.805-3.022	<b>0.019</b>

Bold values indicate statistical significance,  $P < 0.05$