

Table S2: Clinicopathological features of two gene-risk groups in CGGA and TCGA dataset.

Features	Training set CGGA RNA-seq cohort (n=325)			Validation set TCGA RNA-seq cohort (n=667)		
	High-risk	Low-risk	<i>P</i> value	High-risk	Low-risk	<i>P</i> value
	group (n=162)	group (n=163)		group (n=333)	group (n=334)	
Age			<0.001			<0.001
Median	46.5	39		54	39	
Gender			0.148			0.734
Female	54	68		136	146	
Male	108	95		191	192	
TCGA subtype			<0.001			<0.001
Classical	60	14		85	1	
Mesenchymal	68	0		97	0	
Neural	9	72		31	79	
Proneural	25	77		55	182	
WHO Tumor grade			0.002			<0.001
II	13	96		42	206	
III	34	38		131	131	
IV	115	29		155	1	
IDH status			<0.001			<0.001
Mutation	35	132		98	327	
Wildtype	127	31		225	10	
1p/19q status			<0.001			<0.001
Codeletion	7	48		10	158	
Non-codeletion	140	110		311	181	