

Table S1 Primer used in RT-qPCR

Gene	Forward sequence	Reverse sequence
<i>ANGPTL7</i>	TGCCATCTACGACTGCTCTTCC	GCCTGAAGTCTCCATGTCACAG
<i>SLC2A14</i>	CAATCGGCTCTTTCCAGTTTGGC	CAAGGACCAGAGATTCGTGAGC
<i>IFNG</i>	GAGTGTGGAGACCATCAAGGAAG	TGCTTTGCGTTGGACATTCAAGTC
<i>SMPD1</i>	GCTGGCTCTATGAAGCGATGGC	AGAGCCAGAAGTTCTCACGGGA
<i>POR</i>	ACTCTGCTCTCGTCAACCAGCT	TGGGTGCTTCTTGTTGACTCC
<i>VDR</i>	CGCATCATTGCCATACTGCTGG	CCACCATCATTACACGAACTGG
<i>WIPI2</i>	CGACAACCTGCTACTTGGCGTAC	AGTGCCGCTAAAGGACTGTCGT
<i>TFR2</i>	GCACCTCAAAGCCGTAGTGTAC	CCACCTGTTTCATAGAGAGTCTGC
<i>GLUD1</i>	CTCCAGACATGAGCACAGGTGA	CCAGTAGCAGAGATGCGTCCAT
<i>STAT3</i>	CTTTGAGACCGAGGTGTATCACC	GGTCAGCATGTTGTACCACAGG
<i>ALOX15B</i>	CAATGCCGAGTTCTCCTTCCATG	TGATGTGCAGGGTGTATCGGGT
<i>MAP1LC3A</i>	GCTACAAGGGTGAGAAGCAGCT	CTGGTTCACCAGCAGGAAGAAG
<i>CHAC1</i>	GTGGTGACGCTCCTTGAAGATC	GAAGGTGACCTCCTTGGTATCG
<i>PRNP</i>	TTCGGCAGTGACTATGAGGACC	TTGTGGTGACCGTGTGCTGCTT
<i>RGS4</i>	ACATCGGCTAGGTTTCTGCTG	CAGGTTTTCCAGTGATTCAGCCC
<i>GAPDH</i>	GTCTCCTCTGACTTCAACAGCG	ACCACCCTGTTGCTGTAGCCAA

RT-qPCR, real-time polymerase chain reaction.

Table S2 The univariate and multivariate Cox analysis

Clinical features	Univariate Cox analysis			Multivariate Cox analysis		
	HR	95% CI	P value	HR	95% CI	P value
Gender	1.1	0.87–1.39	0.412			
Age, years						
≤46	1 (reference)					
>46	1.15	0.92–1.45	0.214			
Radio						
Treated	1 (reference)			1 (reference)		
Un-treated	1.44	1.10–1.89	0.008	1.16	0.86–1.55	0.327
Chemo						
TMZ	1 (reference)			1 (reference)		
Un-treated	1.98	1.51–2.59	<0.001	2.11	1.58–2.84	<0.001
Histology						
Primary	1 (reference)			1 (reference)		
Recurrent	1.55	1.22–1.97	<0.001	1.85	1.44–2.38	<0.001
Secondary	2.16	1.45–3.23	<0.001	3.2	2.02–5.07	<0.001
IDH						
Mutant	1 (reference)			1 (reference)		
Wildtype	1.34	1.01–1.75	0.038	1.53	1.12–2.10	<0.001
1p/19q						
Codel	1 (reference)			1 (reference)		
Non-codel	2.014	1.16–3.51	0.014	1.82	1.00–3.30	0.049
MGMTp						
Methylated	1 (reference)					
Un-methylated	1.09	0.87–1.37	0.442			
Risk score						
Low	1 (reference)			1 (reference)		
High	5.65	4.22–8.48	<0.001	1.71	1.35–2.16	<0.001

CI, confidence interval; HR, hazard ratio; IDH, isocitrate dehydrogenases; MGMTp, O-6-methylguanine-DNA methyltransferase promoter; TMZ, temozolomide.

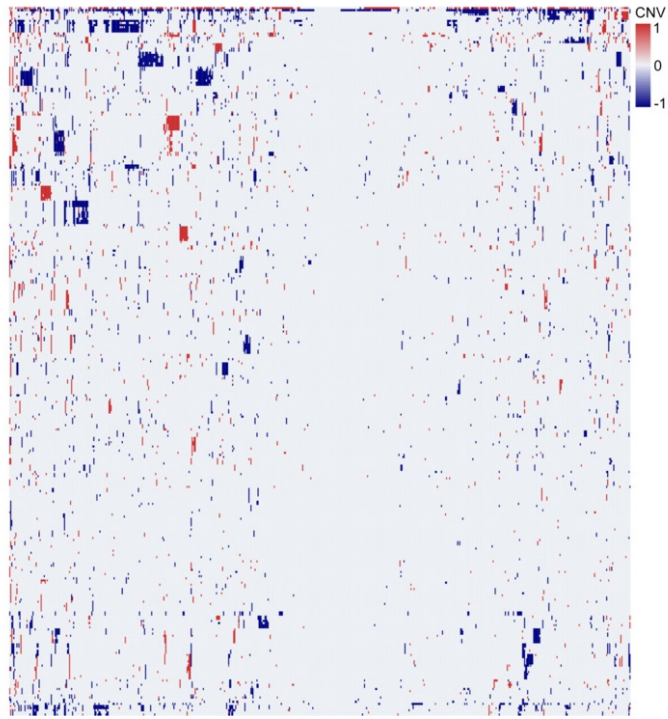


Figure S1 The CNV status of ferroptosis related genes. Heatmap of CNV in 334 ferroptosis related genes. CNV, copy number variation.