Relationship between FMNL1 expression and clinical GBM features

		Total n=217	%	FMNL1 expression				P-value
				High n=109	%	Low n=108	%	
Age(mean±SD)		64.92±15.12		67.7±13.93		62.1±15.87		0.006
Gender								
	Male	122	56.2	66	60.6	56	51.9	0.219
	Female	95	43.8	43	39.4	52	48.1	
Location								
	Dominant side	98	45.2	53	48.6	45	41.7	0.129
	Non-dominant side	89	41.0	37	33.9	52	48.1	
	Bilateral	27	12.4	17	15.6	10	9.30	
	Posterior fossa	3	1.40	2	1.80	1	0.90	
Karnofsky performance status								
	0-70	128	59.0	72	66.1	56	51.9	0.039
	80-100	89	41.0	37	33.9	52	48.1	
Extent of surgical resection								
	Total+subtotal removal	119	54.8	50	45.9	69	63.9	0.010
	Partial removal+biopsy	98	45.2	59	54.1	39	36.1	
Number of surgeries								
	Single	185	85.3	104	95.4	81	75.0	<0.001
	Multiple	32	14.7	5	4.60	27	25.0	

Groups were compared by $\chi 2$ test with $P < 0.05$ considered statistically significant.

Supplementary Table S1

Gene	Forward sequence	Reverse sequence
GAPDH	TGCACCACCAACTGCTTAG	GAGGCAGGGATGATGTTC
FMNL1	GGTCCTCCTGATGCCCTAGGAA	TGTGAAGACAGTGCCGGTGA
CHI3L1	CTCAAGAACAGGAACCCCAA	TCTGGGTGTTGGAGGCTATC
CD44	CTGATCATCTTGGCATCCCT	AGCTTTTCTTCTGCCCACA
VIM	TGCCCTTAAAGGAACCAATG	GCTTCAACGGCAAAGTTCTC
RELB	CAGCCTCGTGGGGAAAGAC	GCCCAGGTTGTTAAAACTGTGC
TRADD	GCTGTTTGAGTTGCATCCTAGC	CCGCACTTCAGATTTCGCA
PDPN	ACCAGTCACTCCACGGAGAAA	GGTCACTGTTGACAAACCATCT

Supplementary Table S2