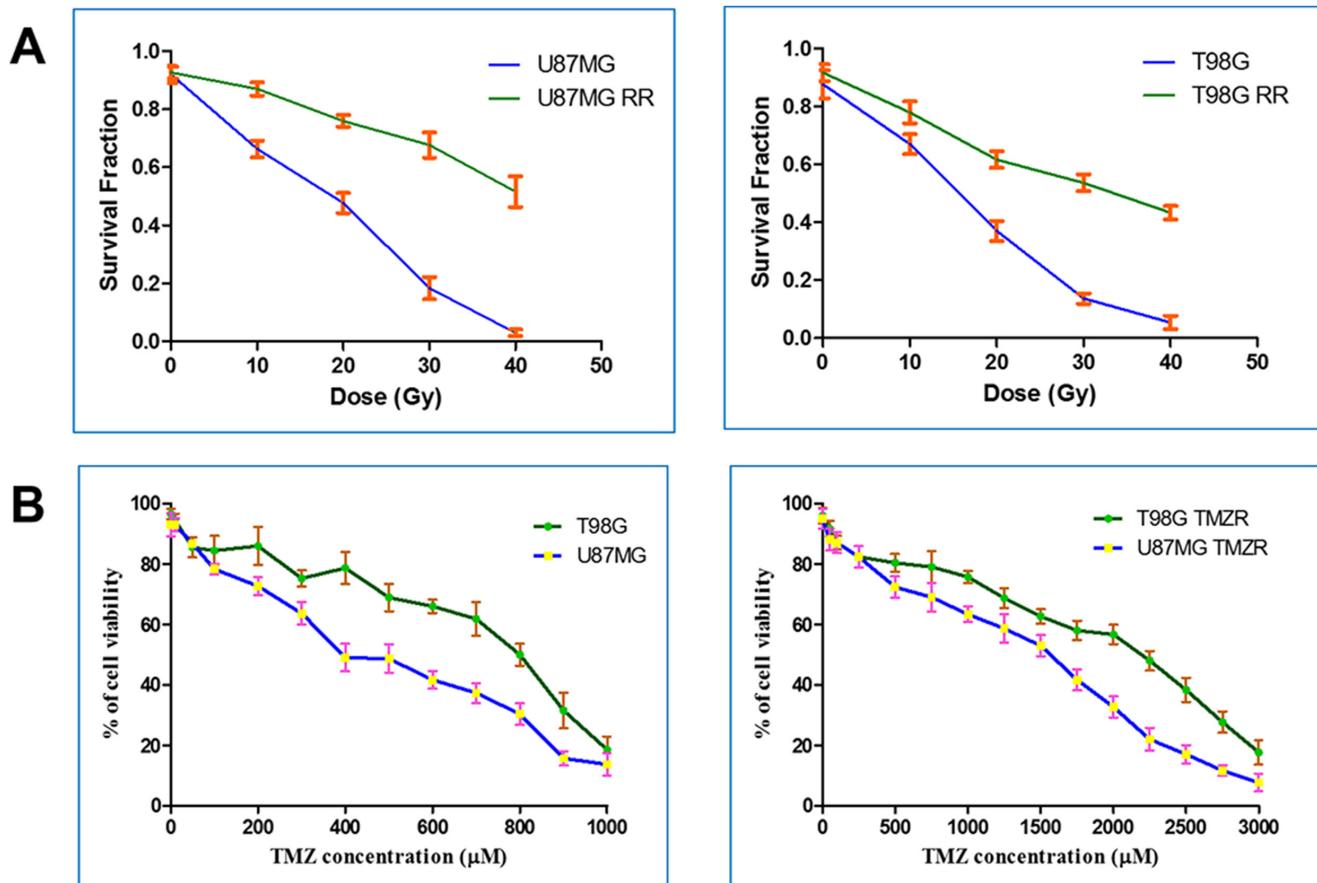


Transcriptional regulation of HSPB1 by Friend leukemia integration-1 factor modulates radiation and temozolomide resistance in glioblastoma

SUPPLEMENTARY MATERIALS



Supplementary Figure 1: (A) Determination of survival fraction in parental U87MG and T98G cells and radio-resistant U87MG RR and T98G RR cells. (B) Determination of IC₅₀ of temozolomide (TMZ) in parental U87MG and T98G cells and TMZ-resistant U87MG TMZR and T98G TMZR cells.

Turquoise Region: Primers (Forward and Reverse)

Yellow Region: Amplified region

Other highlights: Predicted binding regions

Supplementary Figure 2: Sequence of HSPB1 5 kb upstream region for prediction of transcription factor binding sites.

Identifier	Position	Mismatches	Score	Binding Factor	Sequence
<u>AS\$ETS1_10</u>	2219 (+)	0	100.00	<u>c-Ets-1</u>	ACAGGAAGTC
<u>ELK1\$CONS_02</u>	2219 (+)	0	90.91	<u>Elk-1</u>	ACMGGAAAGTNC
<u>AS\$CETS1P54_07</u>	2219 (+)	0	100.00	<u>c-Ets-1 54</u>	ACAGGAAGTC
<u>TCF2ALPHA\$CONS</u>	2220 (+)	0	87.50	<u>TCF-2alpha</u>	SAGGAAGY
<u>FLI1\$CONS_01</u>	2220 (+)	0	93.75	<u>Fli-1</u>	CMGGAAGT
<u>MOUSE\$TIMP1_02</u>	2220 (+)	0	100.00	<u>c-Ets-1</u>	CAGGAAG
<u>AS\$ELK1_13</u>	2220 (-)	0	100.00	<u>Elk-1, SAP-1a,</u> <u>SAP-1b, SRF</u>	TTCCTG
<u>PEA3\$CONS</u>	2221 (+)	0	91.67	<u>c-Ets-1 54,</u> <u>c-Ets-1 68,</u> <u>c-Ets-2 58-64,</u>	AGGAAR

```
seq( 2220.. 2279)      aggaagtccagactaattcaagttgcggatggcgttgcggcagtgttttttt  
Segments:
```

<u>1.1.3.0</u>	2212	2221	p=	
<u>3.1.1.9</u>	2217	2226	=K-2a==	
<u>3.5.2.0</u>	2217	2226	Ets-1 =	
<u>1.6.1.0</u>	2259	2268		=AP-2alph=
<u>1.3.1.2</u>	2260	2269		====USF====
<u>9.9.539</u>	2261	2270		====NF-1==
<u>9.9.428</u>	2270	2279		====ISGF-3=
<u>3.1.1.2</u>	2272	2281		====Antp
<u>1.1.1.5</u>	2273	2282		====GCN

```
seq( 1740.. 1799)      atcccgccacttgggagtctgaggcaggaggatcgcttgaaccaggaggcggaggttg  
Segments:
```

<u>9.9.539</u>	1732	1741	<u>==</u>	
<u>1.1.3.0</u>	1738	1747	<u>/EBpalp=</u>	
<u>1.1.1.1</u>	1758	1767		<u>====c-Jun==</u>
<u>1.1.1.2</u>	1759	1768		<u>====c-Fos==</u>
<u>9.9.29</u>	1760	1769		<u>=====AP-1==</u>
<u>1.2.1.0</u>	1762	1771		<u>=====E1====</u>
<u>1.2.2.0</u>	1762	1771		<u>=====MyoD==</u>
<u>3.5.2.0</u>	1762	1771		<u>=c-Ets-1 =</u>
<u>2.3.1.0</u>	1786	1796		<u>=====Sp1====</u>
<u>2.2.1.1</u>	1797	1806		<u>=====</u>

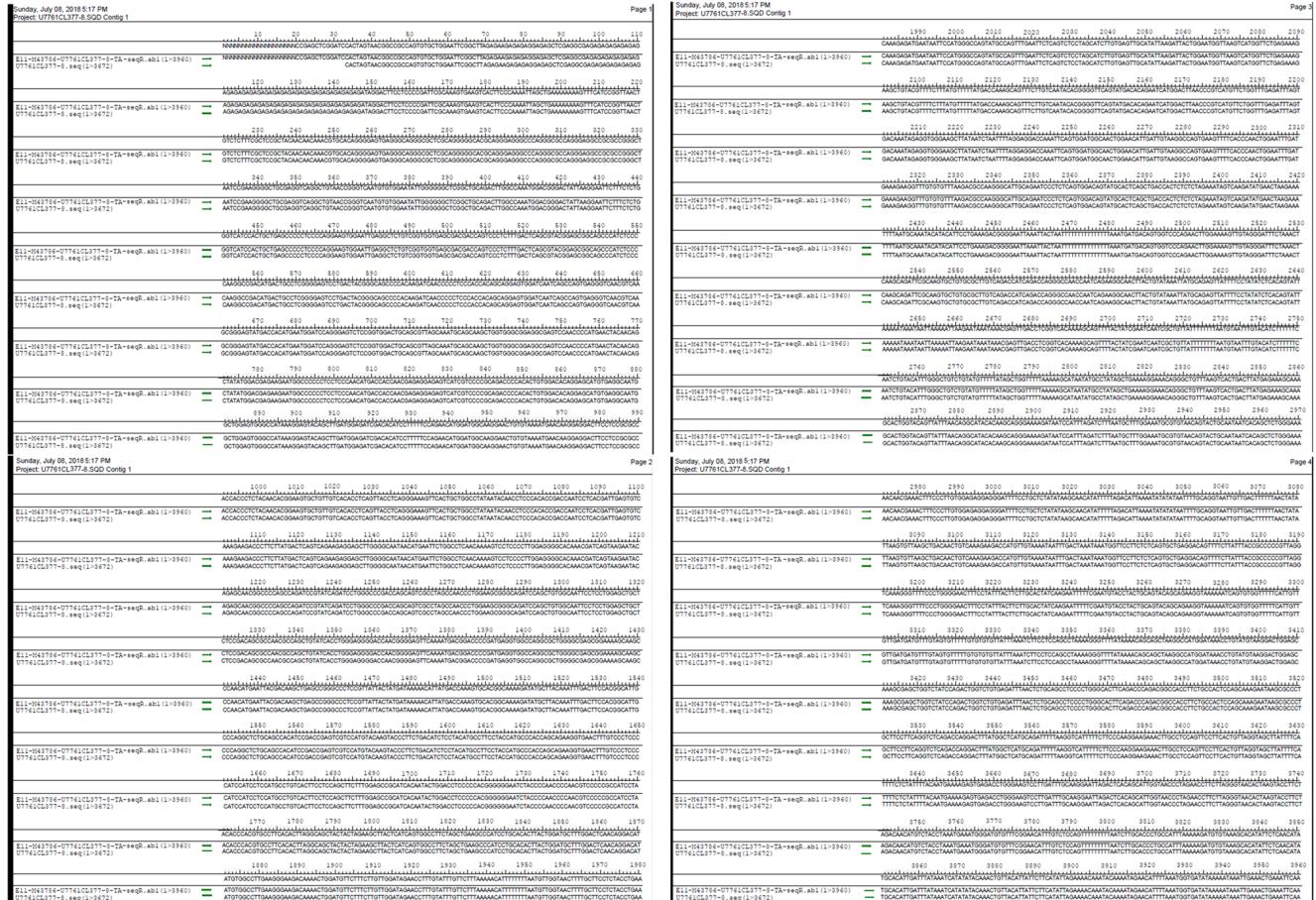
```
seq( 4800.. 4859)      cctgtctggctctgtccctcctaacagaaggacggccctggccacgggccacagccagca  
Segments:
```

Segments:		
<u>2.2.1.1</u>	4817 4826	<u>==GATA-1=</u>
<u>3.5.2.0</u>	4817 4826	<u>==c-Ets-1=</u>
<u>2.3.1.0</u>	4828 4841	<u>=====Sp1=====</u>
<u>2.3.1.0</u>	4835 4848	<u>=====Sp1=====</u>
<u>1.3.1.2</u>	4836 4845	<u>====USF====</u>
<u>1.3.2.1</u>	4836 4845	<u>====c-Myc==</u>
<u>1.3.2.2</u>	4836 4845	<u>====Max1==</u>
<u>1.6.1.0</u>	4836 4845	<u>====AP-2alpha=</u>
<u>9.9.539</u>	4838 4847	<u>====NF-1==</u>
<u>2.3.1.0</u>	4847 4856	<u>=====Sp1====</u>
<u>1.1.1.1</u>	4852 4861	<u>==c-Jun</u>
<u>1.5.1</u>	4852 4861	<u>=====EF-C</u>

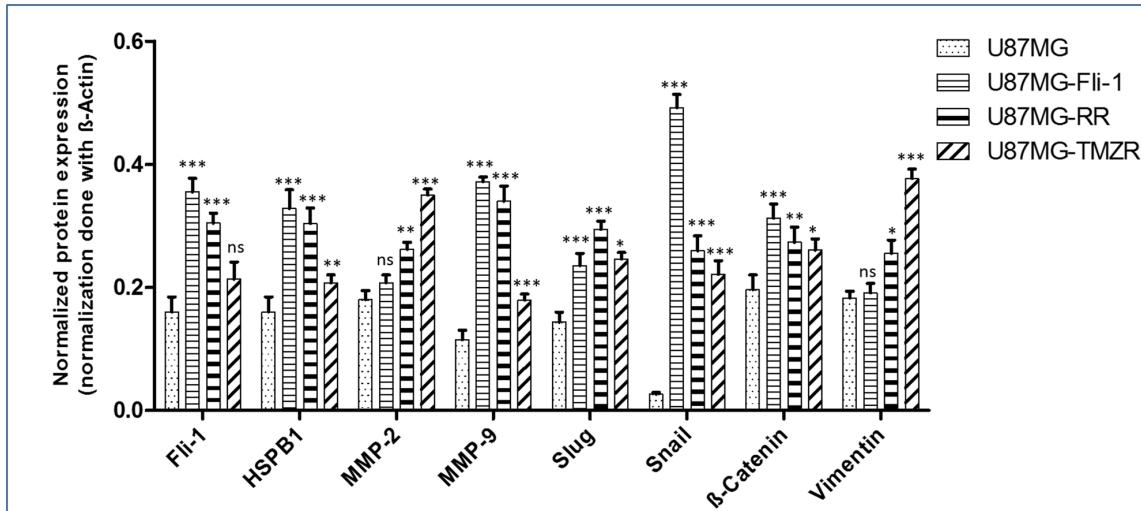
Supplementary Figure 3: Prediction of Fli-1 transcription factor in 5 KB upstream region of HSPB1 using ALIBABA and PATCH detection software.

Binding Site 3:TTAGCCGGGTATGGTGGCACATGCCGTAAATCCCAGCCACTTGGGAGTCT**GAGGAGGAG**GATCGCTTAACCCAGGAGGCGGAGGTTGCAGTGAGCTGAGATTGCCA**Mutation:**TTAGCCGGGTATGGTGGCACATGCCGTAAATCCCAGCCACTTGGGAGTCT**TGAAAGTACA**GATCGCTTAACCCAGGAGGCGGAGGTTGCAGTGAGCTGAGATTGCCA**Binding Site 6:**AGGCTGGAGTCAGTGGCGCATCTAGCTCCCCGCAACCTCTGCCCT**GGAA**TGATCCTCGCCTCAGCTTCCCAGTAGCCGGATTACAGGCACCCATC**Mutation:**AGGCTGGAGTCAGTGGCGCATCTAGCTCCCCGCAACCTCTGCCCT**TACG**TGATCCTCGCCTCAGCTTCCCAGTAGCCGGATTACAGGCACCCATC**Binding Site 7:**TGCTCTTAAG**GA**AGATACATATAGTAGGAGATGTGACAGTAATCTTCTCTGGCCCTCTCAGCAGTGTGAGCTGGGGTTGATCTGGCCAGTGCCTGTTAGGGAAAGGG**GA**AAATGGCCAA**Mutation:**TGCTCTTAAT**ACG**AGATACATATAGTAGGAGATGTGACAGTAATCTTCTCTGGCCCTCTCAGCAGTGTGAGCTGGGGTTGATCTGGCCAGTGCCTGTTAGGGAAAGGG**TACG**ATGGCCAA

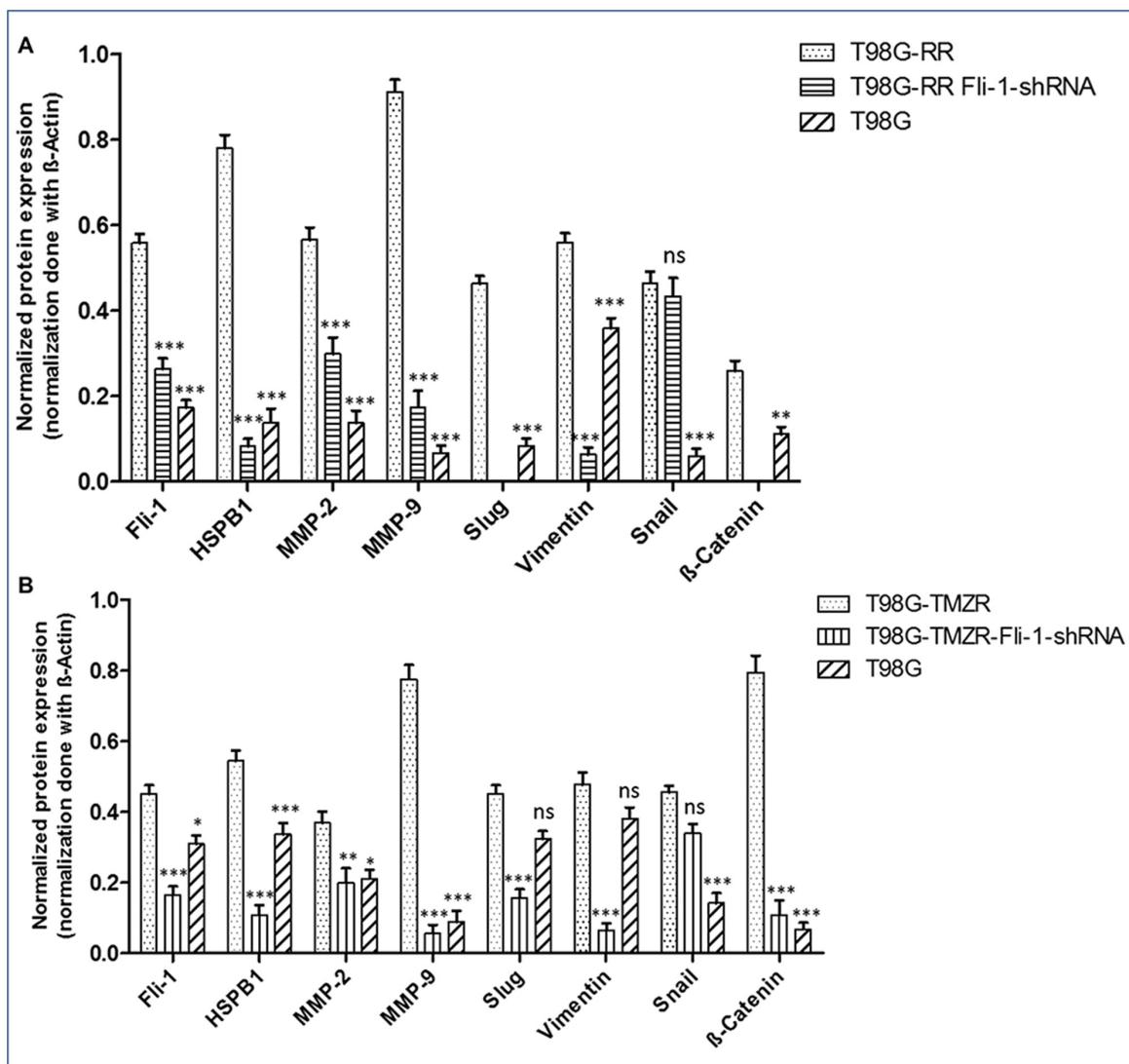
Supplementary Figure 4: Sequence of ~120-bp upstream region of HSPB1 containing the mutated binding sites 3, 6 and 7 and the respective control oligonucleotides without mutations.



Supplementary Figure 5: The sequencing data of the overexpressing Fli-1 plasmid.



Supplementary Figure 6: Densitometry plot of Figure 5C. Western blotting analysis of Fli-1, HSPB1, MMP-2, MMP-9 and EMT proteins in U87MG, U87MG RR, TMZ-resistant U87MG and U87MG Fli-1 cells.



Supplementary Figure 7: (A, B) Densitometry plot of Figure 6E and 6F. Western blotting analysis of Fli-1, HSPB1, MMP-2, MMP-9 and EMT proteins in parental T98G, radio-resistant T98G RR, TMZ-resistant T98G, T98G RR Fli-1 shRNA and T98G TMZR Fli-1 shRNA cells. Each bar represents the average of three independent experiments. The level of significance is indicated by *P < 0.05, **P < 0.01, ***P < 0.001.

Supplementary Table 1: The primer sequences for qRT-PCR

	Primer Sequence (5'-3')
HSPB1	F GAGACTGCCGCCAAGTAAAG R TTTGACAGGTGGTGCTTG
HSP 40	F GGAAGGGACCCATTTCATT R CCACCTCCAAAAGACGGAAA
HSP 70	F CCAGCTGAAGAAGGGTCAAG R CAGGATCTGGATAGGGCAA
HSP 90	F AGACCCAGTCTTGTGGATGG R ACTCCCCTTCCCCCTAAAT
β-Catenin	F TGCAGTTCGCCTTCACTATG R ACTAGTCGTGGAATGGCACC
Slug	F TGTGTGGACTACCGCTGC R TCCGAAAGAGGGAGAGAGG
Snail	F TGCAGGACTCTAACCCAGAGTTACC R GTGGGATGGCTGCCAGC
Vimentin	F TGTCCAATCGATGTGGATGTTTC R TTGTACCATTCTCTGCCTCCTG

Supplementary Table 2: The ChIP primer sequences for Fli-1 binding sites in the 5 kb upstream of HSPB1

Binding Site	Primer Sequence (5'-3')
1	Forward: GTGTCTACAAAGGGCTGGCA Reverse: CTGCTCACCTTGGCCCAG
2	Forward: GGAGAGAGAGAAAGGCATTATGA Reverse: CCACTGAAGTCTTGCCTG
3	Forward: CGAAACCCGTTCTACTAAAA Reverse: CTCACTCTATCACTCAGGCTGG
4	Forward: CAACAACCTAAACAGGGACCTAAGTC Reverse: GGCTCCTATCTCCCAGCTTG
5	Forward: TCTCCCTCTGTGATGTGGG Reverse: GAAACACTGCCAGGAACC
6	Forward: GAGACAGAGTCTCGTTCTGTCAC Reverse: TACAAAAAATTAGCCAGGTGTGAT
7	Forward: AACCAAGTGCTTCTTAAGGAAAGATAC Reverse: CCTGGGATTGAAGAGAGGG
8	Forward: TGCAATGCATGACTGTTACCA Reverse: TAGGCGTGTGGACTTGAA
9	Forward: TCACACCGCGTGTGGT Reverse: TGGAGCCGTGCCACG