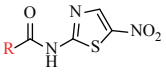
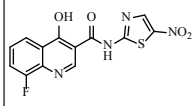
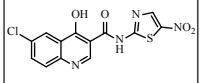
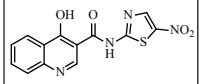
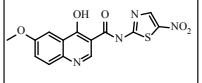
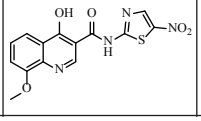
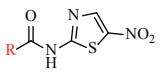
Supplementary Figure 1

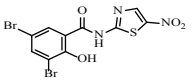
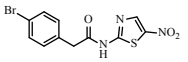
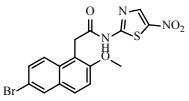
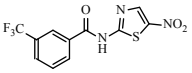
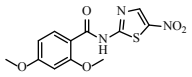
A



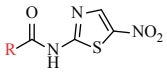
Compound	Structure	IC50（μM） U87MG/ EGFRvIII	IC50 (μM) U87MG
20		1.42	18.94
13		1.55	13.32
11		1.89	17.11
12		2.37	21.14
14		2.61	19.83

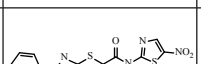
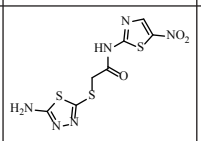
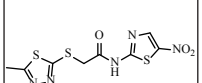
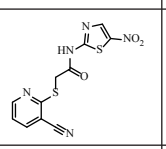
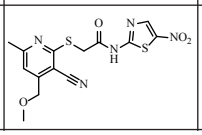
B



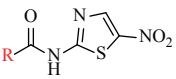
Compound	Structure	IC50(μM) U87MG/ EGFRvIII	IC50 (μM) U87MG
19		3.03	35.41
1		3.59	33.12
2		4.81	36.81
16		4.83	25.12
18		5.03	39.16

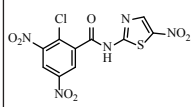
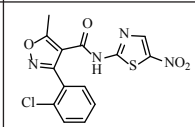
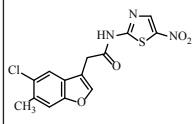
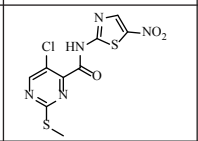
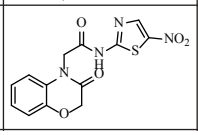
C



Compound	Structure	IC50(μM) U87MG/ EGFRvIII	IC50 (μM) U87MG
7		4.81	25.11
8		5.35	19.98
6		5.79	23.12
10		7.14	26.81
9		7.23	25.17

D

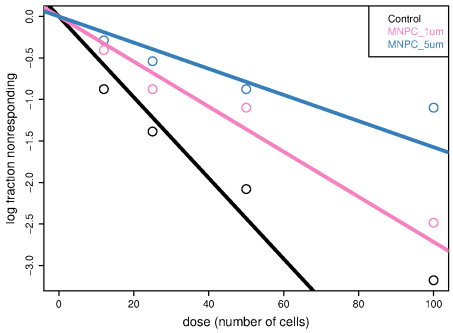


Compound	Structure	IC50(μM) U87MG/ EGFRvIII	IC50 (μM) U87MG
17		3.61	15.33
15		6.22	27.64
3		6.98	31.74
4		7.18	25.31
5		8.11	31.15

Supplementary Figure 2

A

HK296 – EGFRvIII

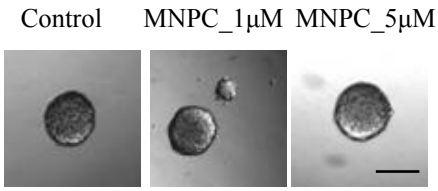


HK296 – EGFRvIII

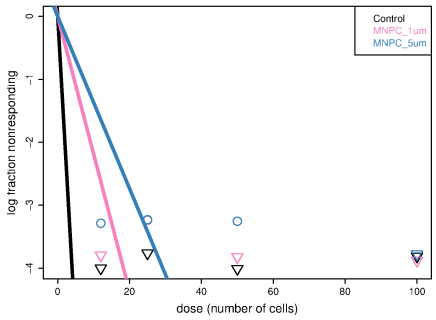
Group	Stem cell frequency	*p*-value vs control
Control	1/21.1	-
MNPC_1μM	1/37.3	0.0045
MNPC_5μM	1/64	6.17 E-08

B

HK408 – no EGFRvIII

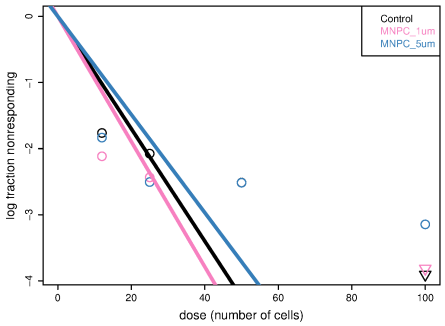


HK408 – no EGFRvIII



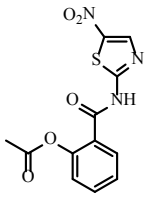
C

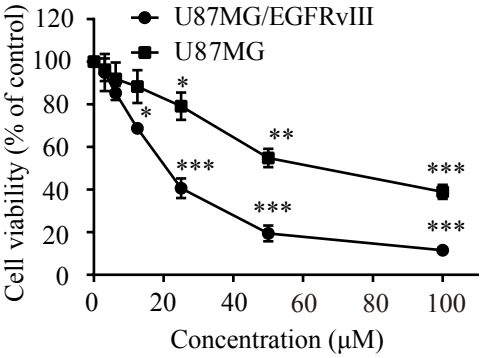
HK157 – no EGFRvIII



D

NTZ



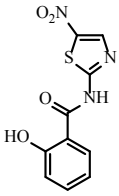


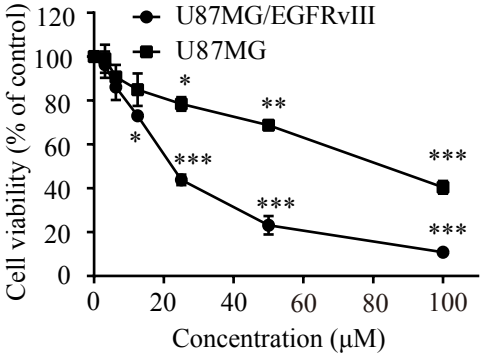
U87MG IC50: 66.7 μM

U87MG/EGFRvIII IC50: 19.4 μM

E

TIZ

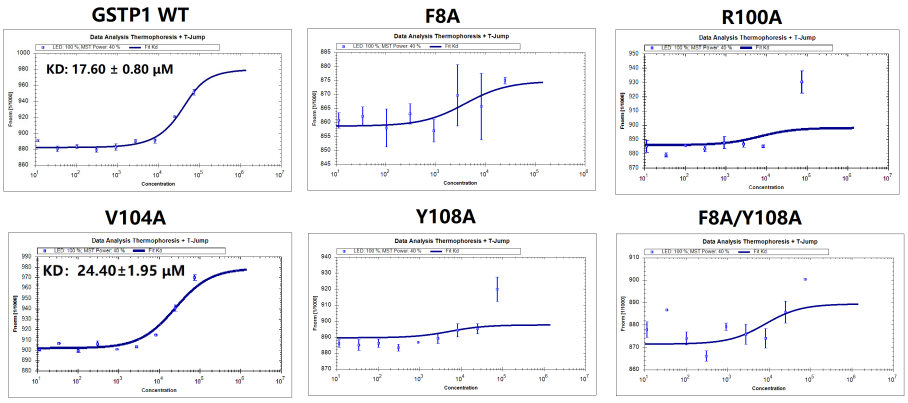




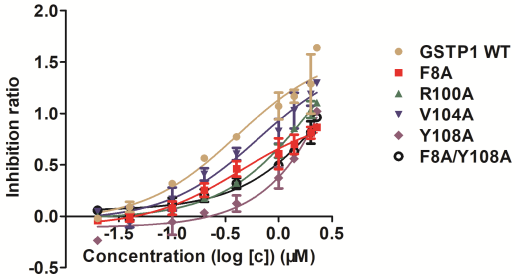
U87MG IC50: 82.9 μM

U87MG/EGFRvIII IC50: 22.4 μM

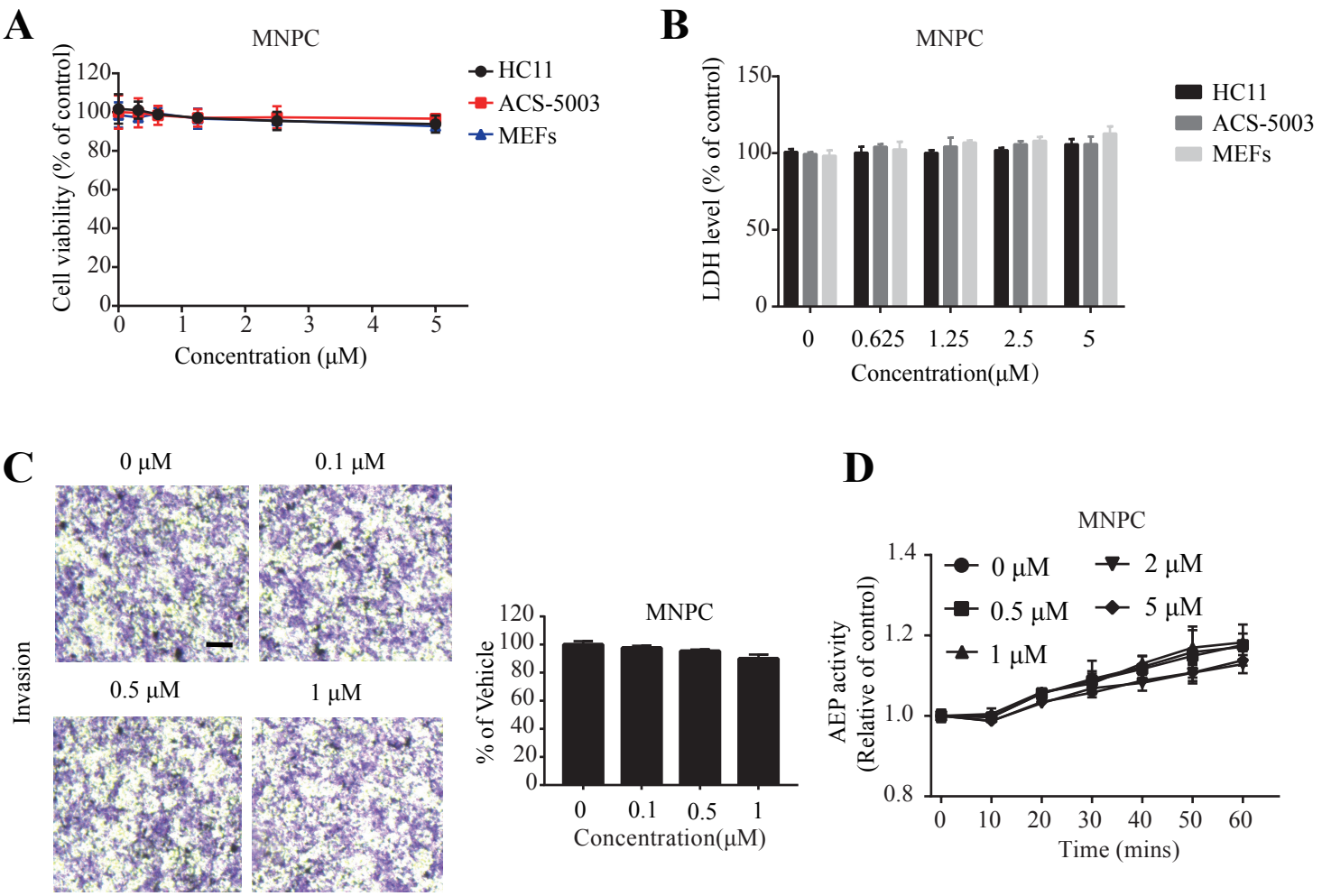
F



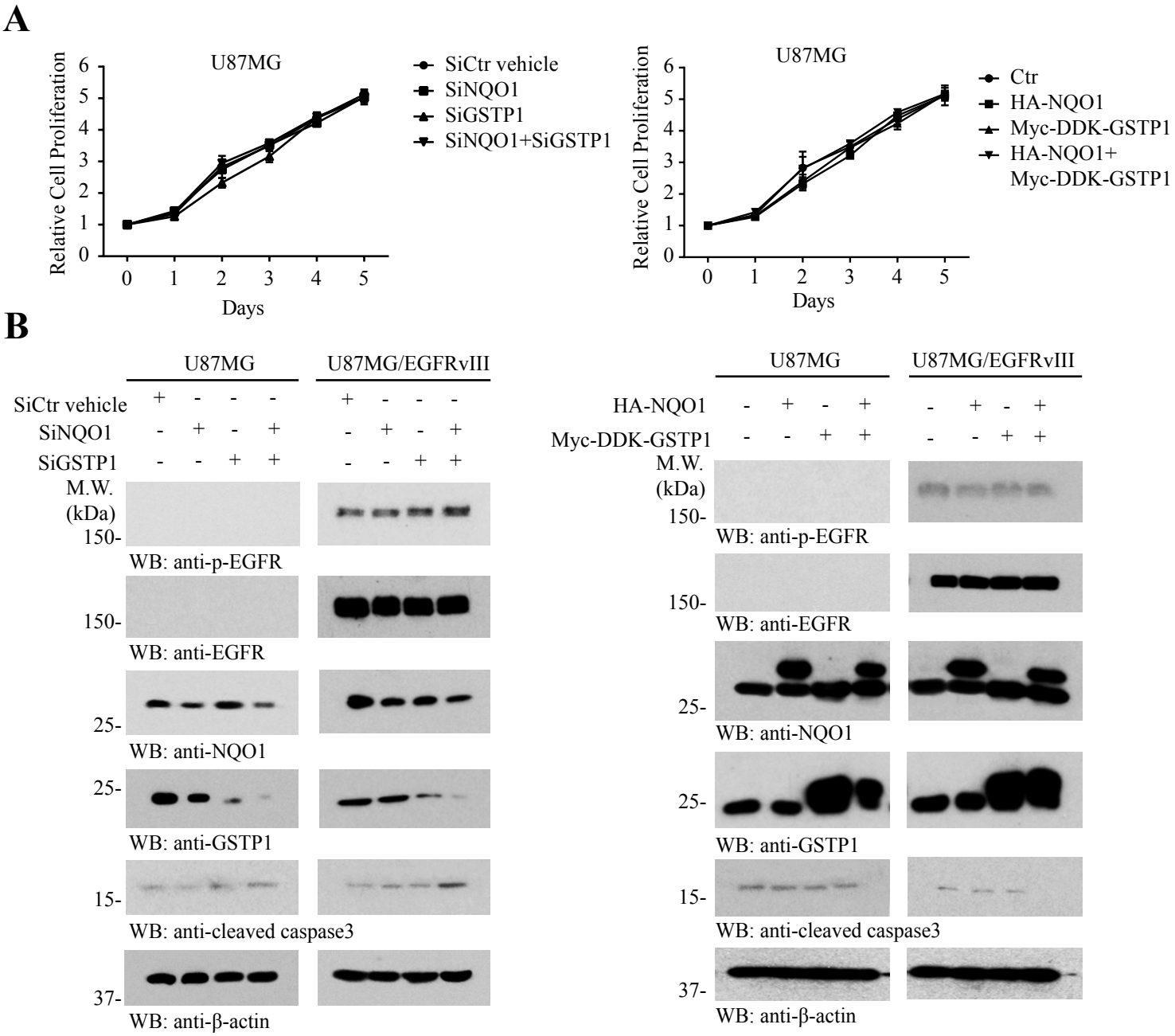
G



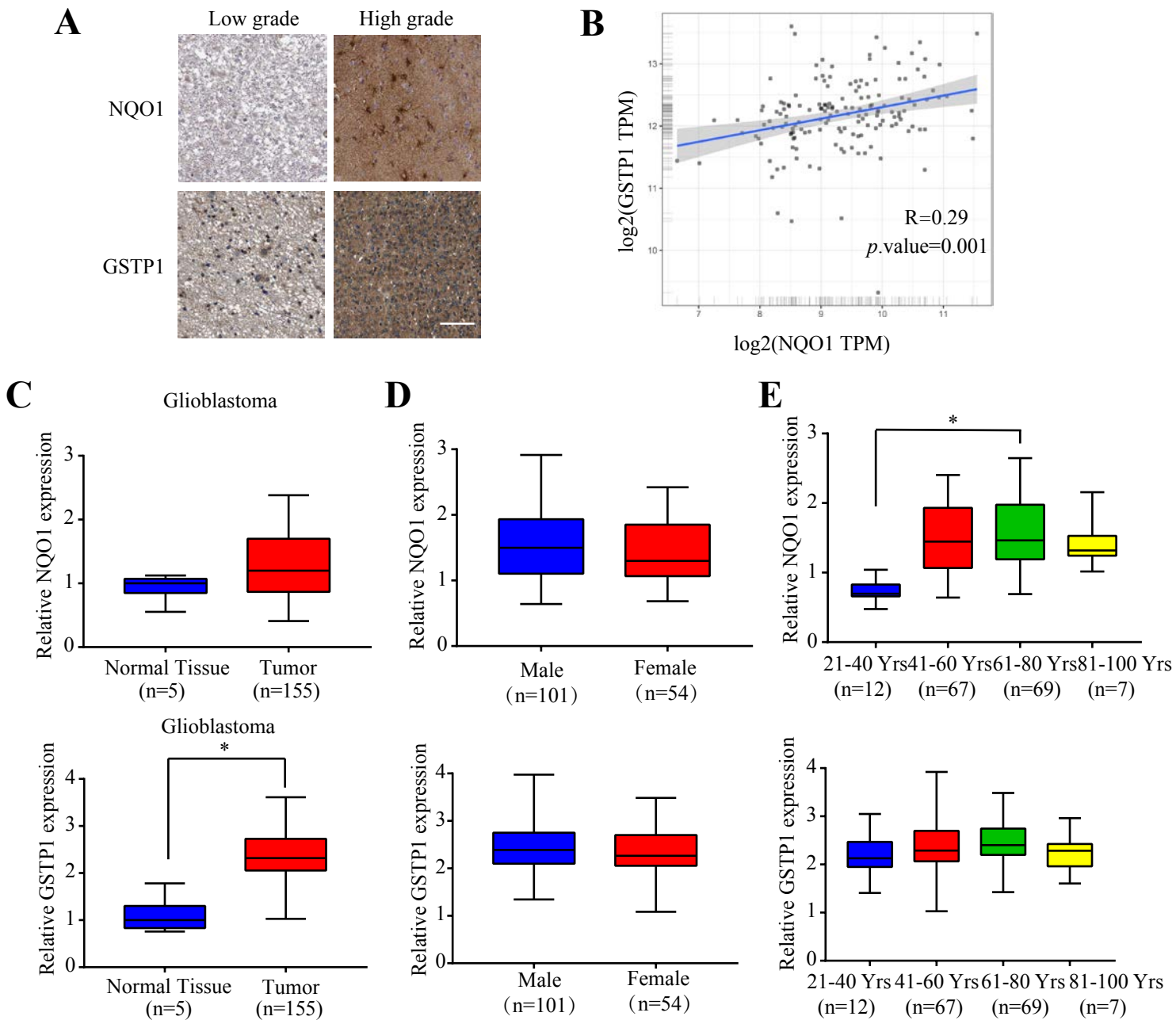
Supplementary Figure 3



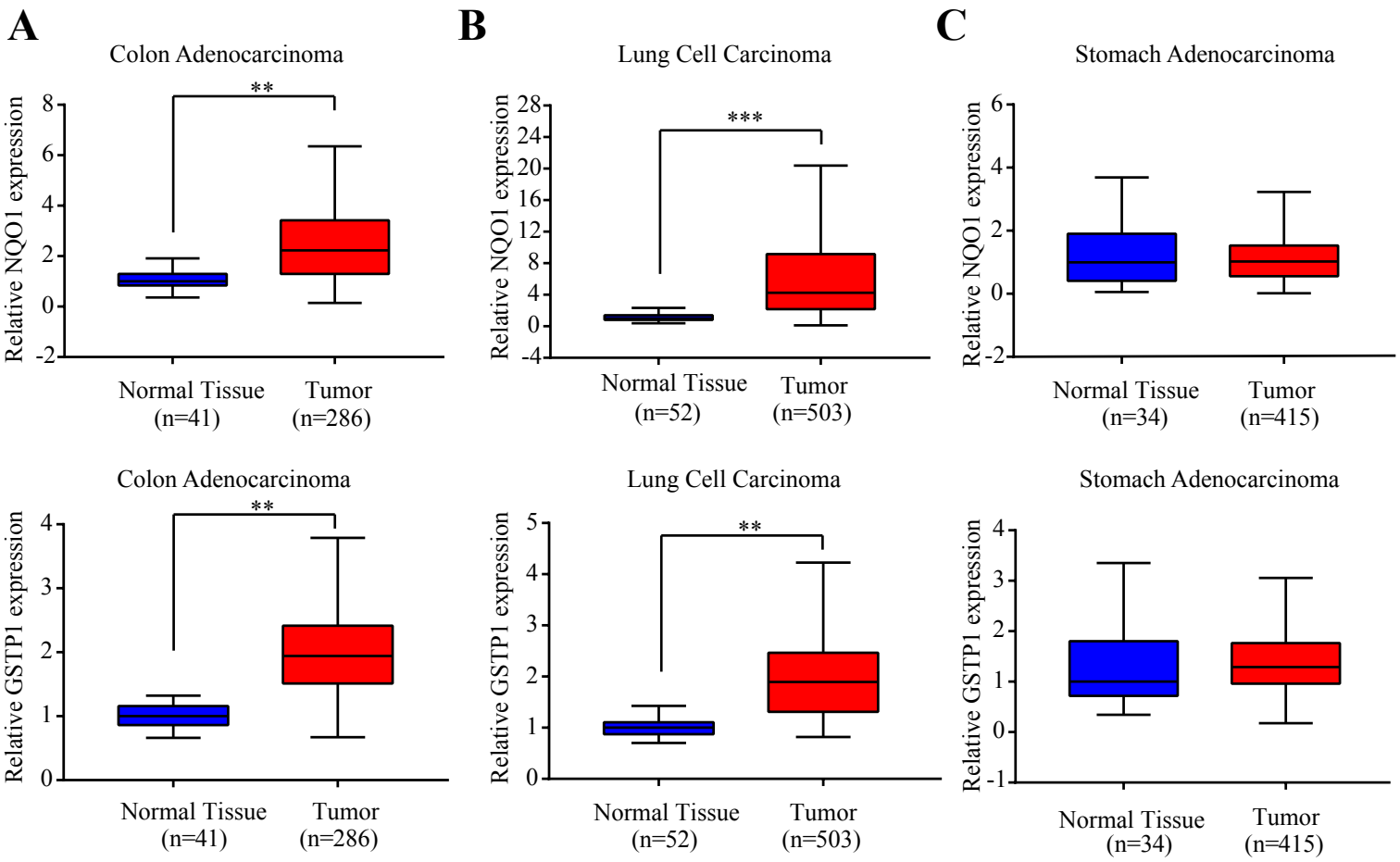
Supplementary Figure 4



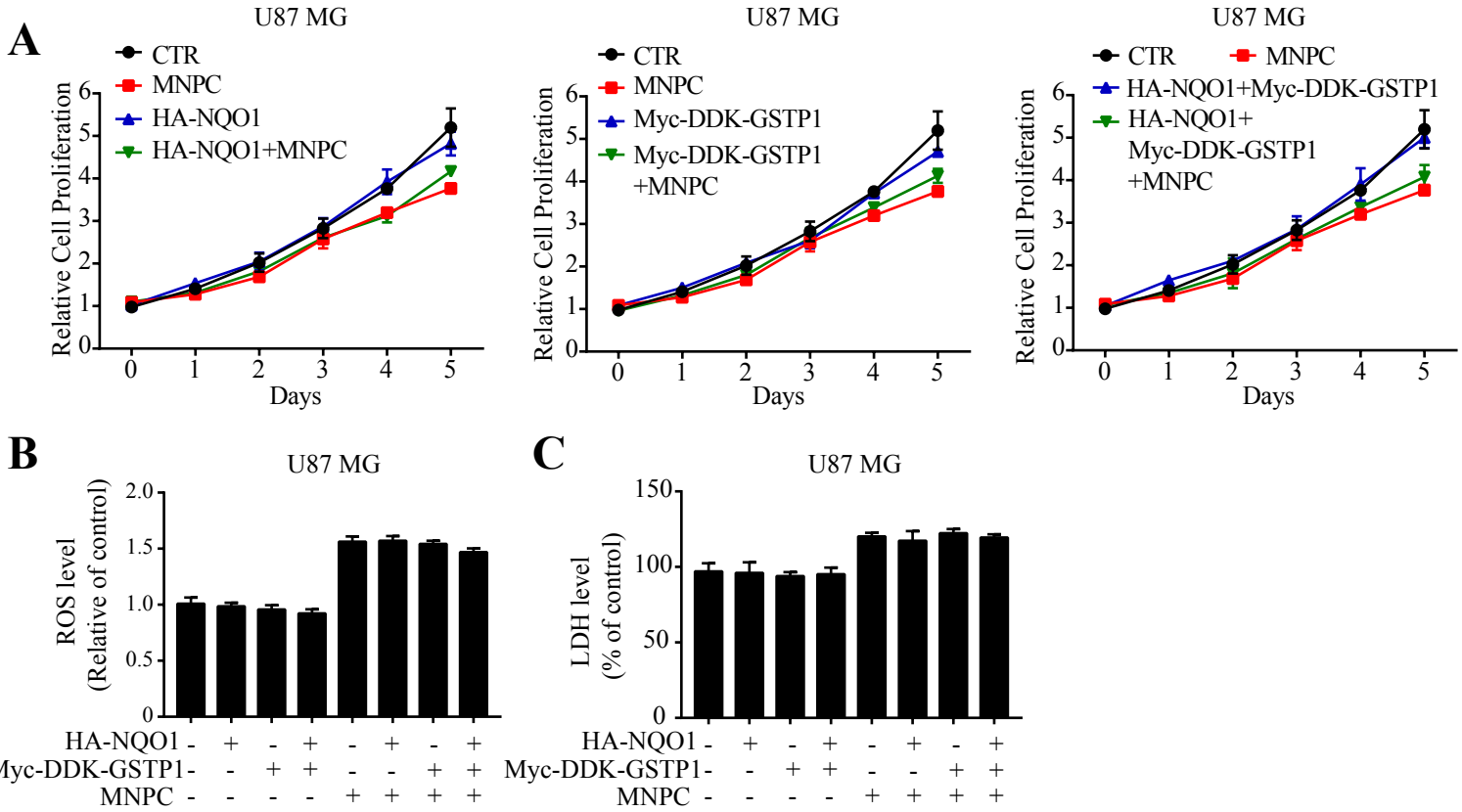
Supplementary Figure 5



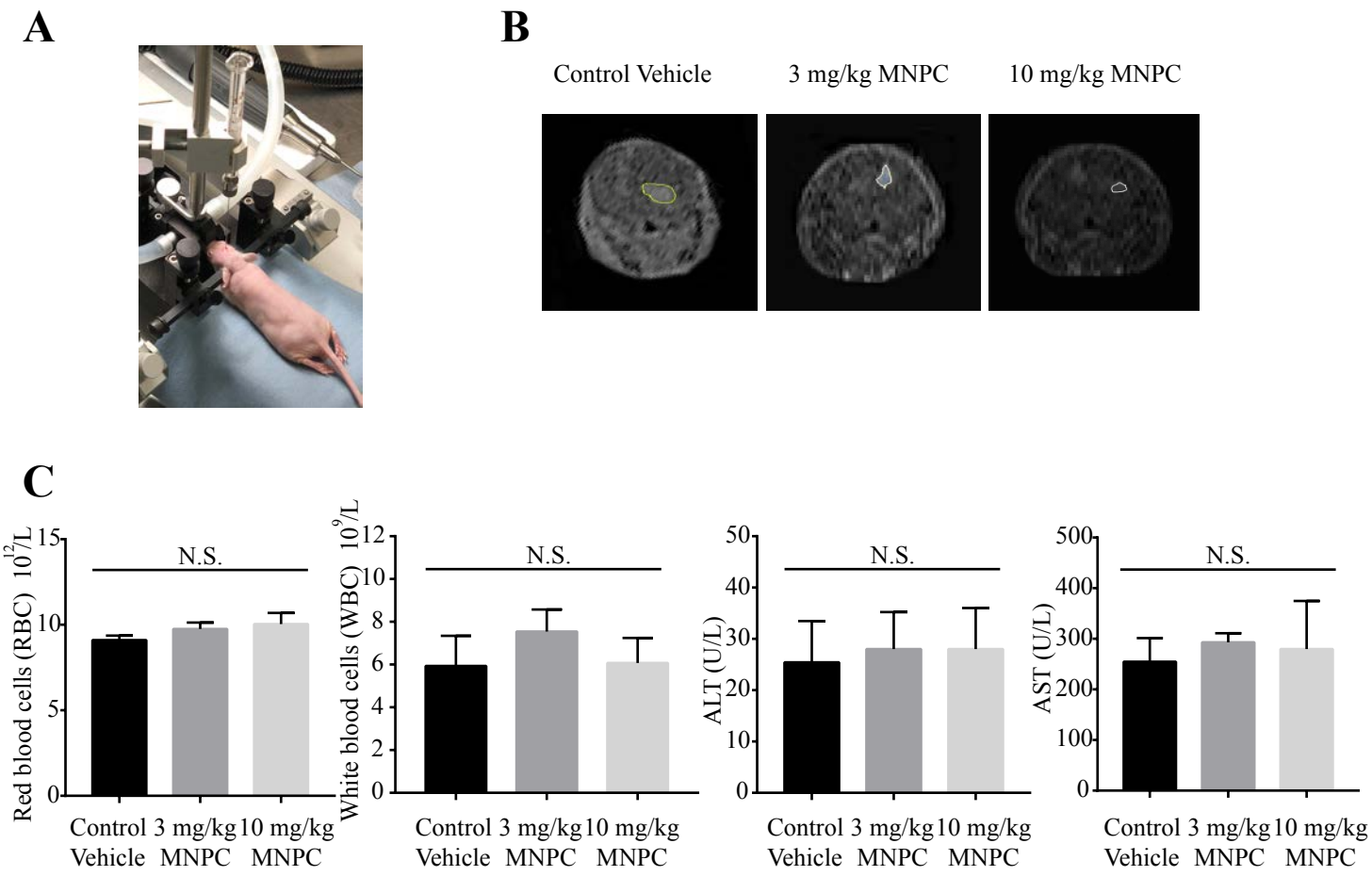
Supplementary Figure 6



Supplementary Figure 7



Supplementary Figure 8



Supplementary Table 1. Binding affinities and inhibitory effects of MNPC with GSTP1 and its mutants.

Protein	Kd (μM) [a]	IC_{50} (μM)
GSTP1 WT	17.60 ± 0.80	0.40 ± 0.39
F8A	n.b.[b]	2.42 ± 0.36
R100A	n.b.	2.37 ± 0.38
V104A	24.40 ± 1.95	0.65 ± 0.19
Y108A	n.b.	25.74 ± 1.41
F8A/Y108A	n.b.	4.01 ± 0.60

Each value was expressed as mean ± SEM(n=3).

[a]The Kd value is automatic calculated by the curve fitting, and presents as means ± SEM for three experiments.

[b]n.b. is no clear binding detected in the MST measurement.

Supplementary Table 2. Crystallographic Data and Refinement Statistics.

Parameters	NQO1/MNPC complex	GSTP1
Data collection		
Space group	P41	P212121
Cell dimensions		
a, b, c (Å)	47.882, 147.882, 209.791	69.655,82.179，89.324
α, β, γ (°)	90, 90, 90	90, 90, 90
Resolution range (Å)	32.66-2.50(2.54-2.50)	24.11-1.58(1.62-1.58)
Rsym (%)	9.6 (60.5)	9.4 (23.8)
Completeness (%)[a]	99.8 (99.8)	99.7 (99.4)
Redundancy	6.8 (6.0)	5.4 (5.2)
$I/\sigma I$[a]	13.9 (1.8)	32.6 (10.9)
Refinement		
Total reflections	154628	70461
R_{work}/R_{free}[c]	0.222,0.264	0.200, 0.223
No. atoms		
Protein	25956	3378
Ligand	853	33
Water	249	426
Average *B*-factor (Å2)	36.3	11.0
Ramachandran Plot (%)		
Favored	94.76	97.14
Allowed	5.14	2.62
Outliers	0.1	0.24
Root mean square deviations		
R.m.s.d. bond lengths (Å)	0.008	0.005
R.m.s.d. bond angle (°)	0.946	0.875

Values in parenthesis are for highest resolution shell. 5 % of the data was used in the Rfree calculation.

Supplementary Table 3. The primers used for mutagenesis.

	Nucleotide sequence
F8A forward	AAGCCAGTATACACTCCGCTATC
F8A reverse	CGAACTGGGGCATAGACCACGGTGTAGGG
F8A forward1	TGGTCTATGCCCCAGTTCGAGGCCGCTGC
F8A reverse1	GATAGCGGAGTGTATACTGGCTT
R100Aforward	AAGCCAGTATACACTCCGCTATC
R100A reverse	AGATGAGGGAGATGTATTTGCAGGCGAGGTCCT
R100A forward1	CTGCAAATACATCTCCCTCATCTACACCAACTA
R100A reverse1	GATAGCGGAGTGTATACTGGCTT
V104A forward	AAGCCAGTATACACTCCGCTATC
V104A reverse	ATGAGGGAGGCGTATTTGCAGCGGAGGTC
V104A forward1	GCAAATACGCCTCCCTCATCTACACCAAC
V104A reverse1	GATAGCGGAGTGTATACTGGCTT
Y108A forward	AAGCCAGTATACACTCCGCTATC
Y108A reverse	CGATGAGGGAGATGTATTTGCAGCGGAGGTCCT
Y108A forward1	CTGCAAATACATCTCCCTCATCGCCACCAACTA
Y108A reverse1	GATAGCGGAGTGTATACTGGCTT
F8A/Y108A forward	AAGCCAGTATACACTCCGCTATC
F8A/Y108A reverse	CGATGAGGGAGATGTATTTGCAGCGGAGGTCCT
F8A/Y108A forward1	CTGCAAATACATCTCCCTCATCGCCACCAACTA
F8A/Y108A reverse1	GATAGCGGAGTGTATACTGGCTT