**Supplemental Informations for Identification and Characterization of a Suite of Tumor Targeting Peptides for Non-Small Cell Lung Cancer**

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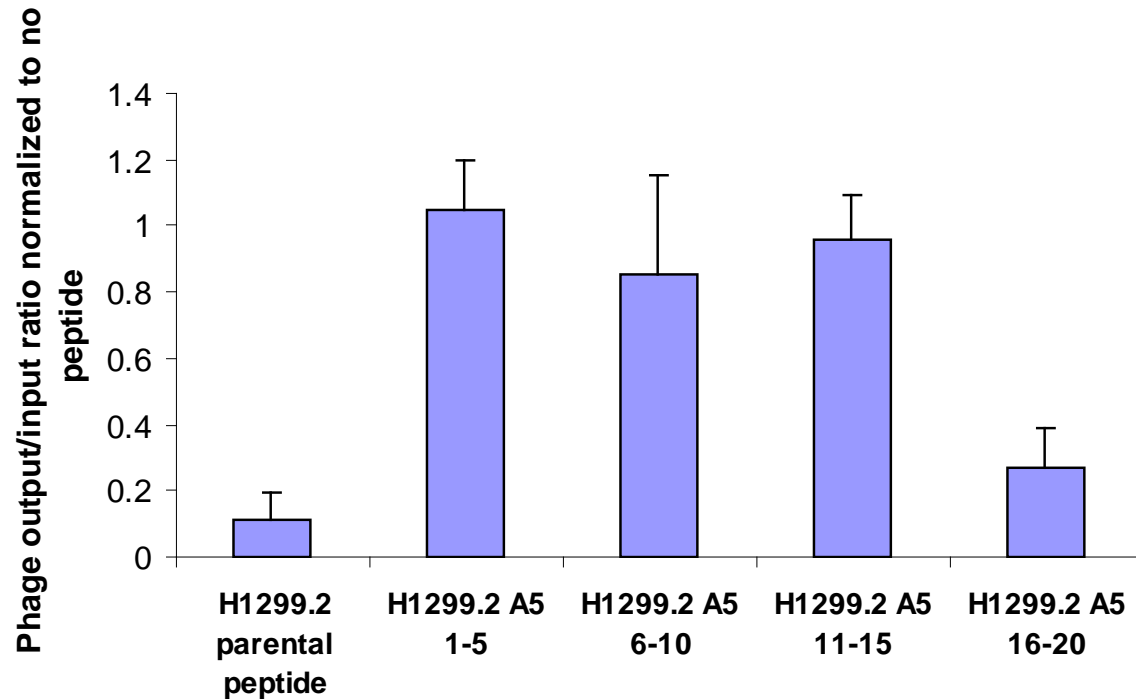
Supplemental Figure S1. The H1299.2 peptide can be truncated to a 15-mer with no loss of binding activity. A. A series of peptides were synthesized in which 5-amino acid blocks were replaced with alanine residues. The ability of the peptides to block uptake of H1299.2 phage as described in the text. Changing the c-terminal 5 amino acids to alanine does not affect the ability of the peptide to compete with phage binding while the other 3 peptides are nonfunctional. The half maximal binding affinity of the 15-mer is the same as the full length parental peptide.

No primary antibody control
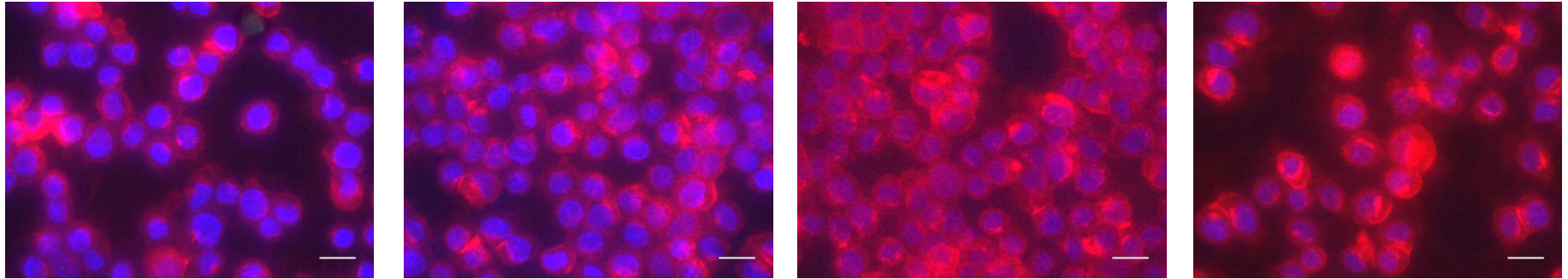
Mouse Anti-phage antibody
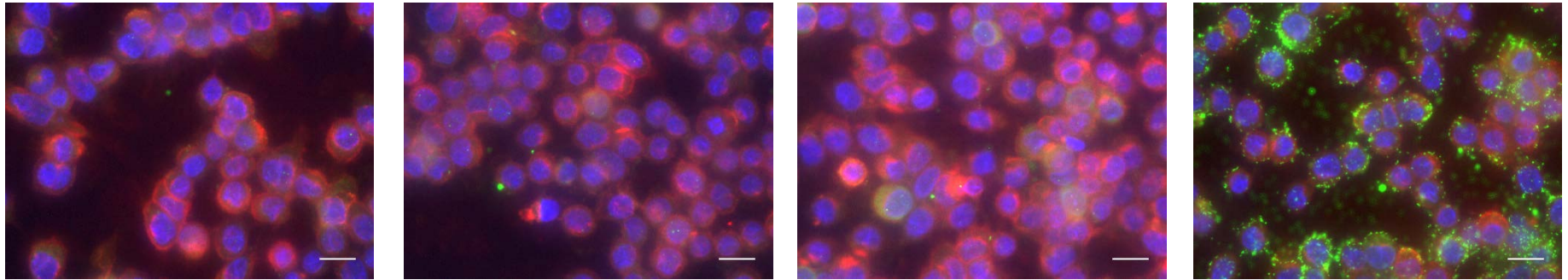
No phage	**Control phage**	**H2009.1 phage**	**H460.1 phage**

**Supplementary Figure S2. The H460.1 phage displays similar binding patterns as the free H460.1 tetrameric peptide.** MCF-7 cells were seeded on 8 well chamber slide and cultured overnight. Cell were incubated for 10 minutes with the indicated phage clone at 1×10^8 cfu/ml or without phage. Unbound phage were removed and cells were washed 4 times with PBS+/0.1%BSA followed by 2 HCl-Glycine rinses. Cells were washed with PBS and fixed in PBS-buffered formalin. Samples were permeabilized and treated with 2% goat serum and 2% BSA in PBS containing 0.1% Triton X-100 (Perm and Block Buffer). After 10 minutes in Perm and Block Buffer, samples were incubated for 30 min as indicated with 1:100 dilution of mouse anti-phage antibody (in-house generated antibody). Samples were washed 3 times with PBS +/0.1% BSA (5 min each) prior to incubation (30 min) with 1:200 dilution of goat ant-mouse IgG-Alexafluor 488 conjugate (Invitrogen) in Perm and Block Buffer. Samples were washed 3 times with PBS+/0.1% BSA followed by 2 PBS only washes. Cells were counterstained with 10µg/ml wheat germ agglutinin-Texas Red conjugate for 10 min followed by 2 PBS rinses. Samples were overlaid with Vectashield + DAPI prior to fluorescence microscopy. Scale bars represent 20 microns.
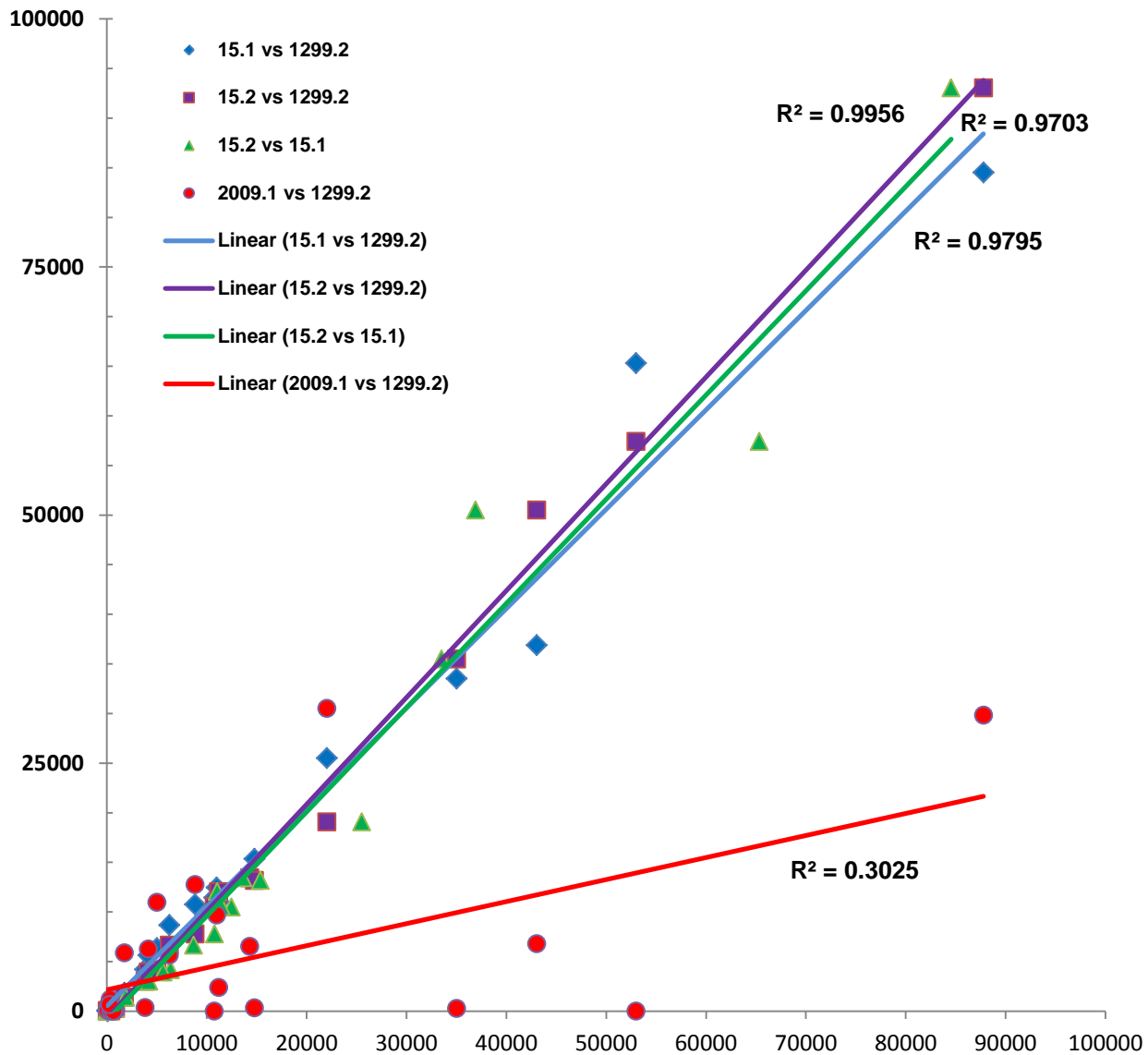
Supplementary Figure S3. There is a linear correlation between of binding scores of the triplet peptide group, H1299.2, HCC15.1, and HCC15.2. Binding scores were generated as described in the manuscript. R^2 values are indicated.
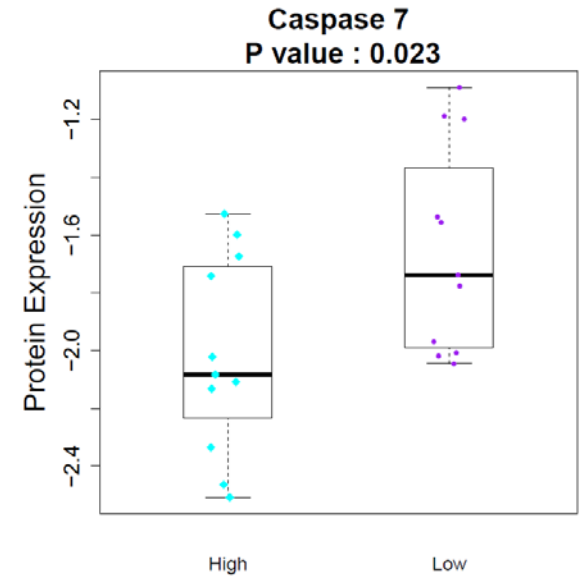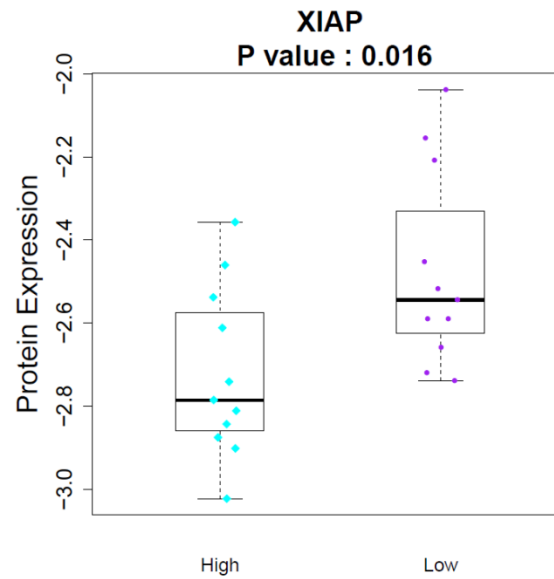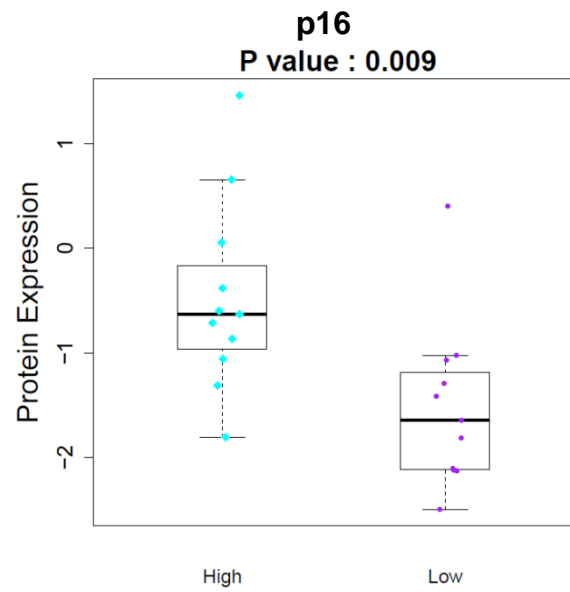
Supplemental Figure S4. Peptide Binding of the triplet cluster correlates to expression levels of three proteins. Cells were dichotomized into high and low binders of H1299.2, HCC15.1, and HCC15.2 using a cell binding score as 5000 as a benchmark and compared to expression levels of 200 proteins analyzed by RPPA (t test analysis)
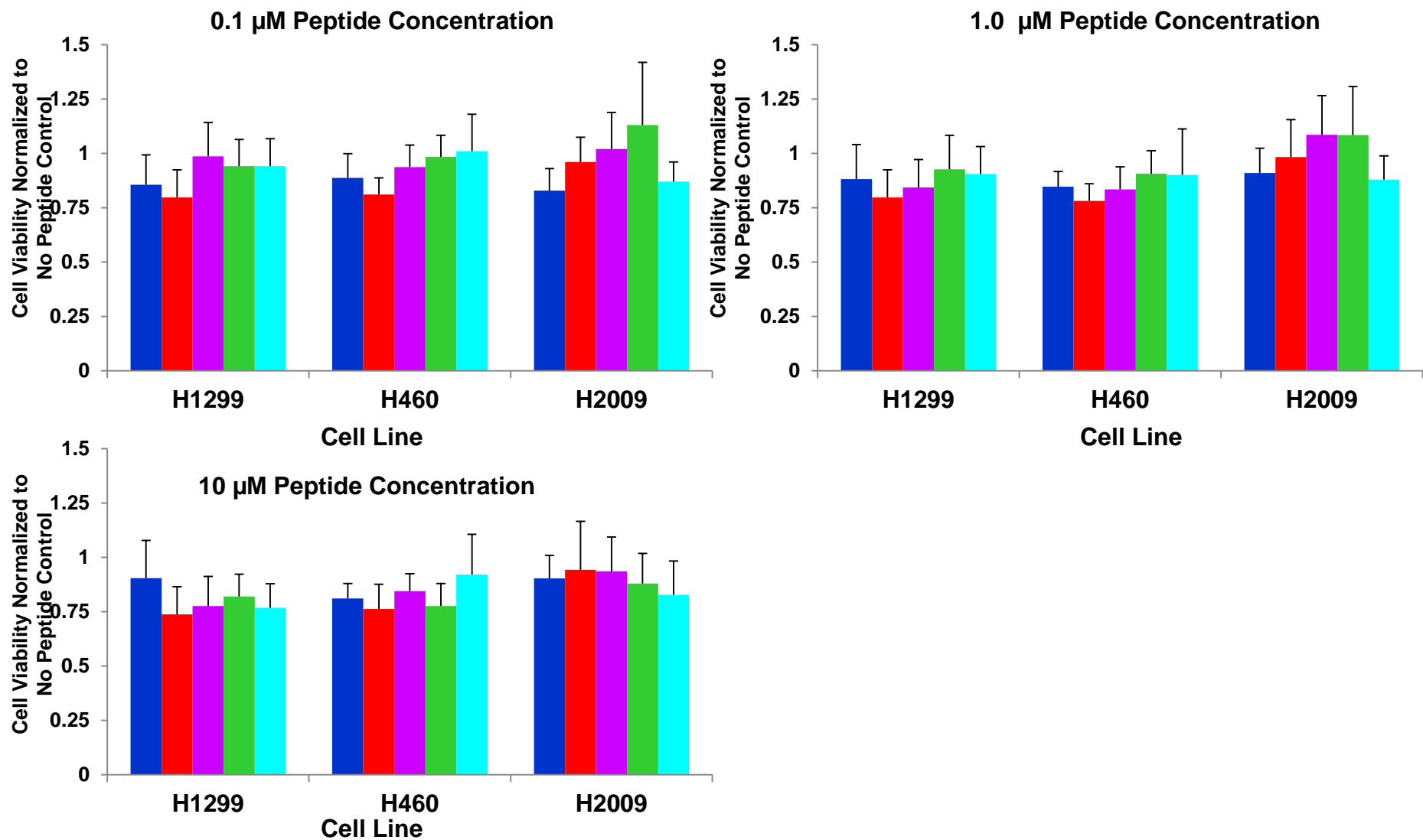
Supplemental Figure S5. The isolated NSCLC-binding peptides do not affect cell growth. Cells were plated in 96 well plates at concentrations of 1,000 cells/well (460 and 1299 cells) or 2,000 cells per well (2009 cells). Peptides were added to the cell media 24 h later at the indicated concentration. Cell viability was determined using the CellTiter-Glo® Luminescent Assay per manufacturer's protocol at 72 hrs.

Table S-I Selectivity of Phage Clones on NSCLC cell lines

	H1299.1	H1299.2	H2009.1	H460.1	A549.1	HCC15.1	HCC15.2	HCC95.1	H1155.1	H1155.2	H661.1
A549 (lung AD)	12 ± 2.8	17 ± 3.9	9.2 ± 1.6	14 ± 1.2	21 ± 2.7	1.1 ± 0.32	33 ± 5.5	1.1 ± 0.32	5 ± 2.7	5.4 ± 3.8	1.9 ± 0.46
Calu-1 (lung mucoepidermoid)	45 ± 17	92 ± 19	0.53 ± 0.14	3.8 ± 1.4	2.8 ± 0.48	1.4 ± 0.39	28 ± 9.4	1.3 ± 0.31	4.2 ± 1.6	1.5 ± 0.66	2.0 ± 0.46
Calu-3 (lung AD)	1.2 ± 0.58	1.6 ± 0.29	34 ± 13	1.0 ± 0.59	1.6 ± 1.1	0.73 ± 0.11	1.4 ± 0.98	2.8 ± 0.8	12 ± 6	3.0 ± 0.62	2.8 ± 2.3
H1155 (lung LC)	3.3 ± 1.7	1.2 ± 0.44	2.6 ± 0.49	6.6 ± 2.2	2.2 ± 1.4	0.56 ± 0.19	1.7 ± 0.61	2.1 ± 1.2	55 ± 21	61 ± 7.9	2.7 ± 2.1
HCC1171 (lung carcinoma)	27 ± 3.1	35 ± 6.9	2.9 ± 1.5	0.38 ± 0.23	0.47 ± 0.27	4.3 ± 1.7	45 ± 2.9	1.0 ± 0.27	1.9 ± 1.0	3.3 ± 1.6	1.0 ± 0.12
H1264 (lung AD)	2.6 ± 0.69	7.3 ± 2.6	1.3 ± 0.8	2.7 ± 2.1	0.36 ± 0.21	3.9 ± 1.9	66 ± 13	0.83 ± 0.24	2.8 ± 1.7	3.2 ± 1.3	1.2 ± 0.36
H1299 (lung LC)	190 ± 20	83 ± 17	4.7 ± 0.23	6.3 ± 2.8	11.3 ± 3.3	170 ± 75	100 ± 37	1.6 ± 0.59	3.1 ± 1.1	5.1 ± 2.6	3.7 ± 1.8
H1355 (lung AD)	6.4 ± 3.9	4.5 ± 3.2	2.9 ± 0.92	2.5 ± 0.66	2.8 ± 1.9	4.3 ± 2.6	25 ± 3.8	2.8 ± 0.8	5.8 ± 2.6	3.8 ± 1.8	0.99 ± 0.21
H1437 (lung AD)	1.8 ± 1.2	3.6 ± 1.3	2.3 ± 0.96	3.3 ± 1.2	3.4 ± 1.2	3.6 ± 1.5	0.95 ± 0.24	2.5 ± 1.2	12 ± 2.6	8.5 ± 3.3	2.1 ± 0.55
H157 (lung SQ)	14 ± 4.6	3.7 ± 0.7	8.7 ± 4.1	2.3 ± 1.3	3.2 ± 2.7	10 ± 5.3	14 ± 9.5	0.71 ± 0.2	1.1 ± 0.62	2.4 ± 0.68	2.6 ± 2.2
H1648 (lung AD, lymph node met)	1.4 ± 0.22	14 ± 2	230 ± 99	6.6 ± 1.2	4.1 ± 2	1.1 ± 0.26	17 ± 5.3	3.3 ± 1.1	3.5 ± 0.47	1.3 ± 0.38	1.2 ± 0.48
H1650 (Lung AD/BAC)	0.55 ± 0.14	2.0 ± 0.3	15 ± 5.5	1.5 ± 0.64	1.4 ± 0.35	0.34 ± 0.071	0.22 ± 0.13	0.87 ± 0.71	4.4 ± 2.8	3 ± 1.3	0.65 ± 0.27
H1666 (lung AD/BAC)	0.84 ± 0.25	0.86 ± 0.15	34 ± 10	7 ± 3.8	9.4 ± 1.2	0.42 ± 0.092	5 ± 2.1	0.41 ± 0.072	2.1 ± 1	1.7 ± 0.18	0.97 ± 0.42
H1819 (lung AD, lymph node met)	0.97 ± 0.53	8.6 ± 4.1	250 ± 30	6.4 ± 1.9	3.1 ± 2.7	0.96 ± 0.098	10 ± 1.7	2.2 ± 1.8	2.9 ± 1.3	1.5 ± 0.75	4.4 ± 2.7
H1975 (lung AD)	0.39 ± 0.16	0.57 ± 0.25	120 ± 17	0.93 ± 0.22	3.4 ± 1.3	0.46 ± 0.14	3.5 ± 0.98	0.55 ± 0.072	3.6 ± 1.4	1.2 ± 0.65	1.0 ± 0.12
H1993 (AD, lymph node met of 1993)	27 ± 6	100 ± 16	37 ± 7.9	3.3 ± 2.2	4 ± 2.3	32 ± 10	1.2 ± 0.2	39 ± 15	2.8 ± 1.4	2.7 ± 1.4	1.2 ± 0.2.0
H2009 (lung AD, lymph node met)	31 ± 14	310 ± 140	300 ± 1.8	6.2 ± 2.4	2.2 ± 0.96	68 ± 21	36 ± 24	0.56 ± 0.26	4 ± 1.6	9.6 ± 6.8	4.3 ± 2.9
H2073 (lung AD)	21 ± 5.5	25 ± 3.6	54 ± 18	2.8 ± 0.99	0.74 ± 0.33	60 ± 20	9.3 ± 2.8	0.87 ± 0.43	1.5 ± 0.81	2.8 ± 1.4	1.2 ± 0.82
H2086 (lung AD)	3.6 ± 1.4	7.8 ± 4	380 ± 120	6.9 ± 2.4	4.1 ± 1	1.3 ± 1.1	14 ± 3.3	0.57 ± 0.32	2.7 ± 0.55	2.7 ± 0.73	0.85 ± 0.18
H2087 (lung AD, lymph node met)	39 ± 13	79 ± 42	2.9 ± 1.4	6.0 ± 3.6	4.2 ± 0.94	1.3 ± 1.1	14 ± 3.3	0.57 ± 0.32	2.7 ± 0.55	2.7 ± 0.73	0.85 ± 0.18
H2122 (lung AD)	1.7 ± 0.39	3.6 ± 1.3	48 ± 6	5.1 ± 1.7	4.8 ± 1.5	0.56 ± 0.14	5.9 ± 1.6	0.53 ± 0.099	3.5 ± 1.9	2.5 ± 1.7	1.2 ± 0.34
H2126 (lung AD)	0.91 ± 0.55	11 ± 5.8	28 ± 10	0.23 ± 0.1	7.1	3.9 ± 0.4	3.2 ± 1.5	0.37 ± 0.035	1.3 ± 0.7	4.7 ± 0.35	0.28 ± 0.15
H2347 (lung AD)	0.79 ± 0.46	0.33 ± 0.12	38 ± 9.2	0.99 ± 0.57	0.67 ± 0.31	2 ± 0.87	7.8 ± 1.8	0.76 ± 0.26	5.5 ± 3.4	3.7 ± 1.8	1.1 ± 0.38
H2882 (lung carcinoma)	1.5 ± 0.36	1.1 ± 0.56	1.4 ± 0.22	0.54 ± 0.17	0.4 ± 0.11	0.91 ± 0.39	1.6 ± 0.89	3.3 ± 2.7	6.0 ± 1.4	5.1 ± 1.0	1.6 ± 0.89
H322(Lung AD/BAC)	6.2 ± 2.5	10 ± 3.8	68 ± 17	1.1 ± 0.33	0.71 ± 0.23	3.8 ± 1.1	17 ± 1.5	2.5 ± 1.5	20 ± 1.7	12 ± 2.1	3.6 ± 1.9
H358 (Lung AD/BAC)	29 ± 6.6	43 ± 13	130 ± 19	2.2 ± 1.1	0.9 ± 0.29	6.7 ± 3.2	13 ± 3.9	3.8 ± 3	1.9 ± 0.89	2.6 ± 1.7	1.4 ± 0.6
H441(lung AD/BAC)	2.4 ± 0.94	1.8 ± 0.73	19 ± 4.4	0.95 ± 0.38	0.8 ± 0.38	1.7 ± 1.4	2.3 ± 0.82	1.1 ± 0.093	4.6 ± 1.4	3.3 ± 1.2	3.8 ± 1.7
H460 (lung LC)	3.2 ± 0.81	1.1 ± 0.33	2 ± 0.45	120 ± 25	150 ± 35	0.83 ± 0.21	0.64 ± 0.49	6.9 ± 4.8	3.2 ± 1.1	1.4 ± 0.91	0.54 ± 0.08
H661 (lung LC)	2.8 ± 1	2.8 ± 2	5.9 ± 1.9	2.4 ± 0.8	2.2 ± 0.5	22 ± 1.5	10 ± 1.7	0.88 ± 0.3	2.5 ± 1.1	6.1 ± 2.4	26 ± 5.8
HCC827 (lung AD)	1.9 ± 0.66	2.2 ± 1.4	180 ± 66	4.1 ± 0.99	6.3 ± 2.5	3.2 ± 1.6	2.2 ± 0.12	0.75 ± 0.39	5.4 ± 1.9	14 ± 2.3	6.8 ± 2.5
HCC1359 (lung SQ)	2.1 ± 1.2	3.1 ± 0.75	5.4 ± 1.3	1.2 ± 0.44	0.72 ± 0.36	0.8 ± 0.2	1.2 ± 0.53	0.8 ± 0.35	2.9 ± 1.1	3.9 ± 1.6	1.0 ± 0.3
HCC15 (lung SQ)	16 ± 2.6	16 ± 1.4	1.0 ± 0.51	7.6 ± 3	14 ± 4.2	44 ± 18	220 ± 32	0.67 ± 0.16	1.3 ± 0.52	5.6 ± 1.5	5.9 ± 1.2
HCC2279 (lung AD)	13 ± 6.9	3.9 ± 1.8	3.1 ± 2	0.64 ± 0.39	1.4 ± 0.6	2.8 ± 0.56	20 ± 3.8	2.5 ± 1.3	1.2 ± 0.18	2.8 ± 1.0	1.4 ± 0.54
HCC2450 (lung SQ)	2.6 ± 0.97	3.5 ± 0.48	3.1 ± 0.92	1.7 ± 0.8	1.5 ± 0.65	0.86 ± 0.52	2.4 ± 1.7	0.46 ± 0.15	1.5 ± 0.21	3.4 ± 1.1	0.68 ± 0.17
HCC366 (lung adenosquamous)	8.5 ± 4	19 ± 12	3.5 ± 1.4	1.8 ± 0.59	1.2 ± 0.49	2.3 ± 1.8	21 ± 2.3	0.72 ± 0.19	1.4 ± 0.72	1.9 ± 1.1	0.61 ± 0.26
HCC461 (lung AD)	1.8 ± 0.64	3.4 ± 2	10 ± 5.8	1.6 ± 0.75	1.9 ± 0.54	4.2 ± 1.7	25 ± 8.6	0.48 ± 0.07	4.2 ± 1.7	5.7 ± 1.6	0.5 ± 0.52
HCC515 (lung AD)	5.3 ± 3.4	1.7 ± 0.29	95 ± 29	0.61 ± 0.18	0.43 ± 0.1	2.2 ± 0.68	13 ± 3.9	1.7 ± 0.42	2.2 ± 0.68	0.86 ± 0.25	1.3 ± 0.4
HCC78 (lung AD)	0.96 ± 0.56	3.8 ± 0.4	95 ± 21	0.51 ± 0.2	0.84 ± 0.39	1.6 ± 0.8	1.8 ± 0.75	0.97 ± 0.18	3.6 ± 0.93	1.5 ± 0.69	1.6 ± 0.35
HCC95 (lung SQ)	1.6 ± 0.55	1.2 ± 0.66	1.8 ± 0.74	1.8 ± 0.3	2.9 ± 1.1	0.66 ± 0.22	1.2 ± 0.34	20 ± 2.7	1.1 ± 0.27	2.5 ± 1.2	1.9 ± 1.0
PC9 (lung AD)	1.9 ± 0.62	5.8 ± 2.2	47 ± 16	0.22 ± 0.05	0.56 ± 0.29	2.5 ± 1.2	32 ± 8.5	0.46 ± 0.19	3.2 ± 0.88	6.3 ± 4.0	1.3 ± 0.52
BEAS-2B (Normal Control)	4.2 ± 0.40	3.1 ± 0.67	4.1 ± 2.0	0.51 ± 0.23	2.7 ± 1.3	1.3 ± 1.2	2.7 ± 0.81	0.29 ± 0.18	1.4 ± 0.79	2.4 ± 1.2	0.29 ± 0.14
Total Number of Cell Lines with Selectivity ≥ 20	8	8	18	1	2	6	13	2	2	1	1

Selectivity ≥ 20 are indicated in red for clarity
Errors are respresented as S.E.M.

Table S-II Selectivity of Phage Clones on Other Cancer Cell Lines

	H1299.1	H1299.2	H2009.1	H460.1	A549.1	HCC15.1	HCC15.2	HCC95.1	H1155.1	H1155.2	H661.1
MCF7(breast)	1.5 ± 1.1	2.6 ± 2.3	15 ± 3.8	530 ± 170	50 ± 15	4.2 ± 3	1.7 ± 0.33	1.1 ± 0.14	2.6 ± 0.55	5.6 ± 2.1	2.9 ± 0.97
T47D (breast)	10 ± 2.2	12 ± 2.3	0.57 ± 0.038	0.82 ± 0.024	1.2 ± 0.19	24 ± 6.0	14 ± 3.1	2.7 ± 1.8	5.1 ± 0.71	4.7 ± 1.3	4.3
MDA-MB-468 (breast)	1.5 ± 0.24	2.6 ± 0.97	25 ± 7.6	1.9 ± 0.22	3.8 ± 1.1	0.59 ± 0.42	0.83 ± 0.54	ND	0.25 ± 0.13	0.78 ± 0.60	ND
MDA-MB-231 (breast)	28 ± 13.3	16 ± 6.1	1 ± 0.23	2.4 ± 1.1	0.94 ± 0.26	170 ± 78	150 ± 38	1.4 ± 0.91	3.3 ± 1.1	8.5 ± 1.9	3.3 ± 1.6
PC3 (prostate)	4.2 ± 1.6	12 ± 2.4	0.8 ± 0.26	1.7 ± 0.56	0.51 ± 0.13	6.6 ± 0.87	5.1 ± 0.8	6.7 ± 4.2	5.1 ± 4	11 ± 4.7	0.71 ± 0.17
LnCap (carcinoma)	1.8 ± 1.1	0.31 ± 0.27	1.3 ± 0.71	0.44 ± 0.17	0.13 ± 0.06	1.9 ± 1.2	4.8 ± 1.3	2.3 ± 1.4	7.8 ± 3.7	23 ± 0.7	0.86 ± 0.51
SCOV3 (ovarian)	2 ± 0.59	6.1 ± 3.4	7.7 ± 4.9	1.9 ± 0.52	0.97 ± 0.37	2.7 ± 1.1	51 ± 17	0.78 ± 0.44	1.1 ± 0.23	2.3 ± 1.1	0.21 ± 0.0088
MiaPaCa (pancreatic)	20 ± 5.3	90 ± 20	1.6 ± 1	0.53 ± 0.29	0.89 ± 0.29	3.7 ± 1.9	35 ± 4.1	0.57 ± 0.16	0.44 ± 0.29	1.2 ± 0.41	1.7 ± 0.97
Panc1 (pancreatic)	19 ± 6.6	44 ± 12	1.4 ± 0.5	0.85 ± 0.28	0.66 ± 0.33	9.0 ± 3.0	15 ± 3.5	0.77 ± 0.23	2.0 ± 0.40	2.2 ± 0.40	1.4 ± 0.51
SW480 (colorectal)	4.5 ± 2.2	9.1 ± 2	6.6 ± 3.3	2.1 ± 0.55	3.5 ± 0.75	61 ± 2.7	120 ± 12	0.82 ± 0.39	2 ± 0.73	14 ± 1.3	0.77 ± 0.38
HUH7 (liver)	200 ± 60	290 ± 65	2.9 ± 1.6	330 ± 95	250 ± 72	210 ± 53	140 ± 40	2.2 ± 0.53	3.3 ± 2.1	2.1 ± 0.86	2.2 ± 0.67
Total Number of Cell Lines with Selectivity ≥ 20	3	3	1	2	2	3	5	0	0	1	0

Selectivity ≥ 20 are indicated in red for clarity

Errors are represented as S.E.M.

H1299.2 Monomer

Normalized Binding

log(inhibitor) vs. normalized response -- Variable slope

Best-fit values	
LogIC50	-7.687
HillSlope	-1.251
IC50	2.057E-08
Std. Error	
LogIC50	0.1235
HillSlope	0.3508
95% Confidence Intervals	
LogIC50	-7.954 to -7.420
HillSlope	-2.009 to -0.4933
IC50	1.113e-008 to 3.801e-008
Goodness of Fit	
Degrees of Freedom	13
R square	0.8755
Absolute Sum of Squares	2506
Sy.x	13.88
Number of points	
Analyzed	15
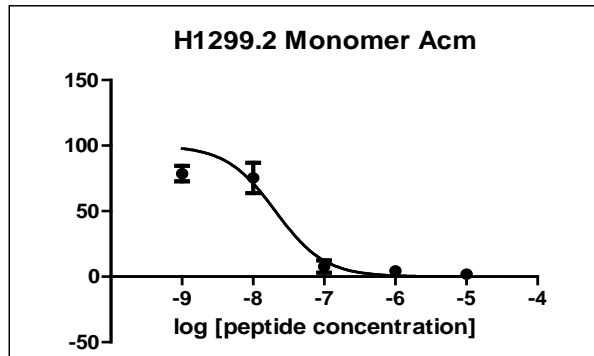
H1299.2 Tetramer

log(inhibitor) vs. normalized response -- Variable slope

Best-fit values	
LogIC50	-9.918
HillSlope	-0.5365
IC50	1.209E-10
Std. Error	
LogIC50	0.2429
HillSlope	0.1706
95% Confidence Intervals	
LogIC50	-10.43 to -9.407
HillSlope	-0.8950 to -0.1780
IC50	3.731e-011 to 3.915e-010
Goodness of Fit	
Degrees of Freedom	18
R square	0.6083
Absolute Sum of Squares	4960
Sy.x	16.6
Number of points	
Analyzed	20
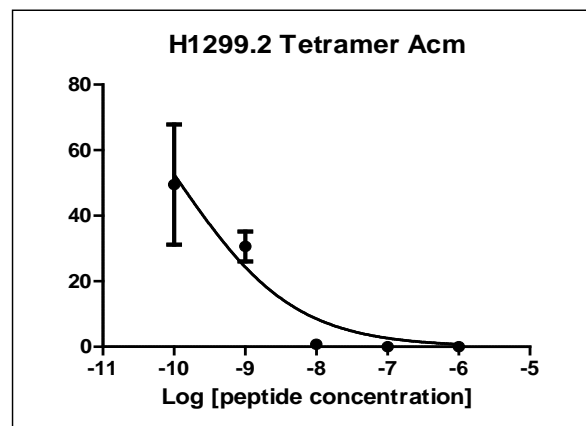
H2009.1 Monomer

log(inhibitor) vs. normalized response -- Variable slope

Best-fit values	
LogIC50	-7.666
HillSlope	-1.234
IC50	2.158E-08
Std. Error	
LogIC50	0.1829
HillSlope	0.4716
95% Confidence Intervals	
LogIC50	-8.044 to -7.288
HillSlope	-2.210 to -0.2585
IC50	9.029e-009 to 5.157e-008
Goodness of Fit	
Degrees of Freedom	23
R square	0.7462
Absolute Sum of Squares	14061
Sy.x	24.73
Number of points	
Analyzed	25
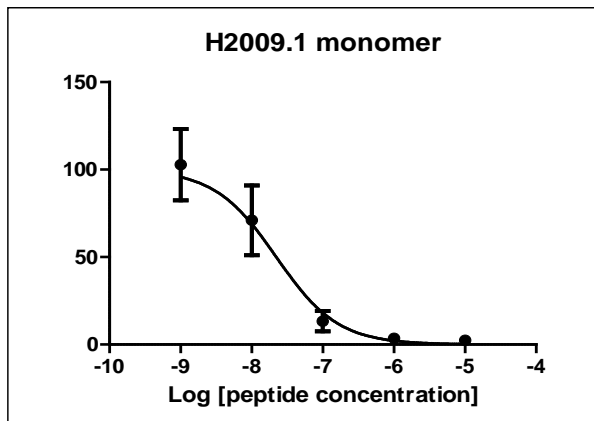
H2009.1 Tetramer

log(inhibitor) vs. normalized response -- Variable slope
Best-fit values
LogIC50	-9.463
HillSlope	-0.7789
IC50	3.441E-10
Std. Error	
LogIC50	0.09652
HillSlope	0.1319
95% Confidence Intervals	
LogIC50	-9.670 to -9.256
HillSlope	-1.062 to -0.4960
IC50	2.136e-010 to 5.543e-010
Goodness of Fit	
Degrees of Freedom	14
R square	0.9018
Absolute Sum of Squares	1248
Sy.x	9.443
Number of points	
Analyzed	16
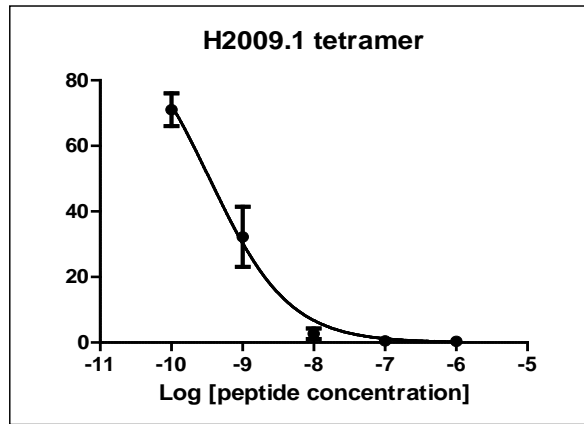
H1299.1 Monomer

log(inhibitor) vs. normalized response -- Variable slope
Best-fit values
LogIC50	-5.716
HillSlope	-0.6501
IC50	0.000001923
Std. Error	
LogIC50	0.1658
HillSlope	0.2073
95% Confidence Intervals	
LogIC50	-6.122 to -5.310
HillSlope	-1.157 to -0.1429
IC50	7.558e-007 to 4.894e-006
Goodness of Fit	
Degrees of Freedom	6
R square	0.7532
Absolute Sum of Squares	1290
Sy.x	14.66
Number of points	
Analyzed	8
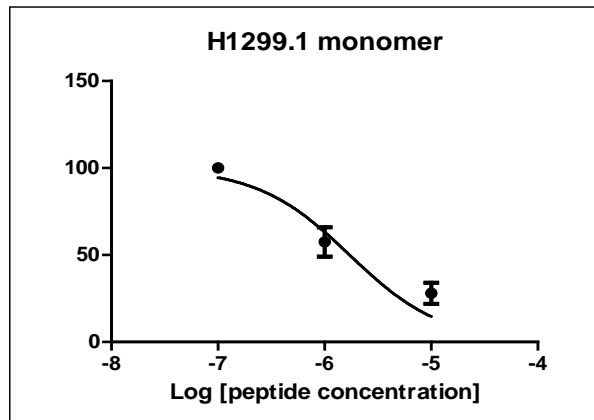
H1299.1 Tetramer

log(inhibitor) vs. normalized response -- Variable slope
Best-fit values
LogIC50	-7.377
HillSlope	-1.198
IC50	4.202E-08
Std. Error	
LogIC50	0.1019
HillSlope	0.2685
95% Confidence Intervals	
LogIC50	-7.604 to -7.149
HillSlope	-1.796 to -0.5995
IC50	2.491e-008 to 7.088e-008
Goodness of Fit	
Degrees of Freedom	10
R square	0.887
Absolute Sum of Squares	1456
Sy.x	12.07
Number of points	
Analyzed	12
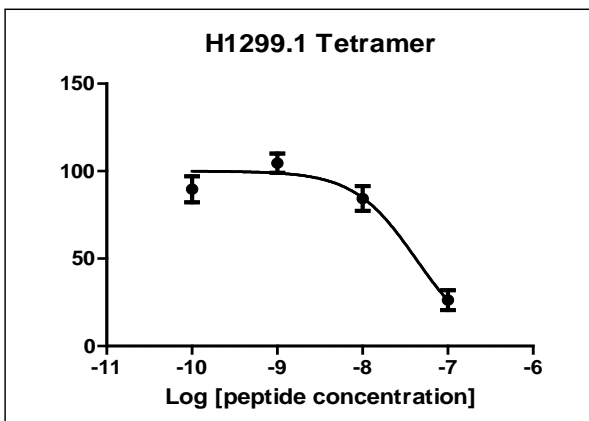
HCC15.1 Monomer

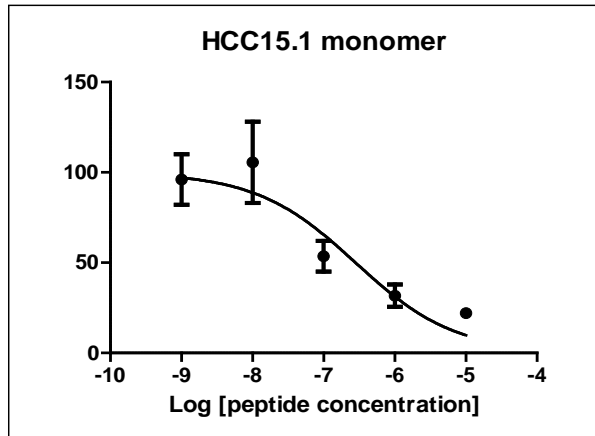log(inhibitor) vs. normalized response
Best-fit values
LogIC50   -6.409
IC50   3.897E-07
Std. Error
LogIC50   0.1337
95% Confidence Intervals
LogIC50   -6.693 to -6.126
IC50   2.028e-007 to 7.485e-007
Goodness of Fit
Degrees of Freedom   16
R square   0.6414
Absolute Sum of Squares   7017
Sy.x   20.94
Number of points
Analyzed   17

HCC15.1 Tetramer

log(inhibitor) vs. normalized response -- Variable slope
Best-fit values
LogIC50   -11.15
HillSlope   -0.3465
IC50   7.086E-12
Std. Error
LogIC50   0.1964
HillSlope   0.06073
95% Confidence Intervals
LogIC50   -11.57 to -10.73
HillSlope   -0.4777 to -0.2153
IC50   2.668e-012 to 1.882e-011
Goodness of Fit
Degrees of Freedom   13
R square   0.8525
Absolute Sum of Squares   1220
Sy.x   9.686
Number of points
Analyzed   15
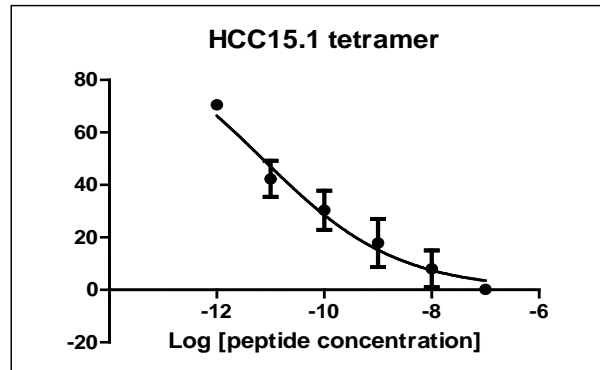
HCC15.2 Monomer

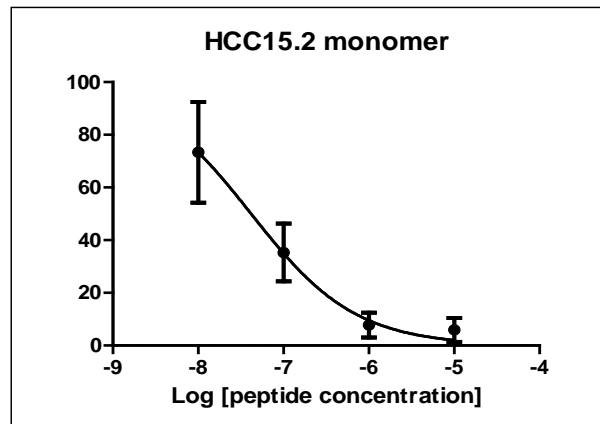   Normalized Binding
log(inhibitor) vs. normalized response
Best-fit values
LogIC50   -7.36
IC50   4.362E-08
Std. Error
LogIC50   0.1714
95% Confidence Intervals
LogIC50   -7.737 to -6.983
IC50   1.830e-008 to 1.040e-007
Goodness of Fit
Degrees of Freedom   11
R square   0.7055
Absolute Sum of Squares   3564
Sy.x   18
Number of points
Analyzed   12

HCC15.2 Tetramer

log(inhibitor) vs. normalized response
Best-fit values
LogIC50   -7.795
IC50   1.603E-08
Std. Error
LogIC50   0.1056
95% Confidence Intervals
LogIC50   -8.014 to -7.576
IC50   9.680e-009 to 2.654e-008
Goodness of Fit
Degrees of Freedom   22
R square   0.8753
Absolute Sum of Squares   3597
Sy.x   12.79
Number of points
Analyzed   23
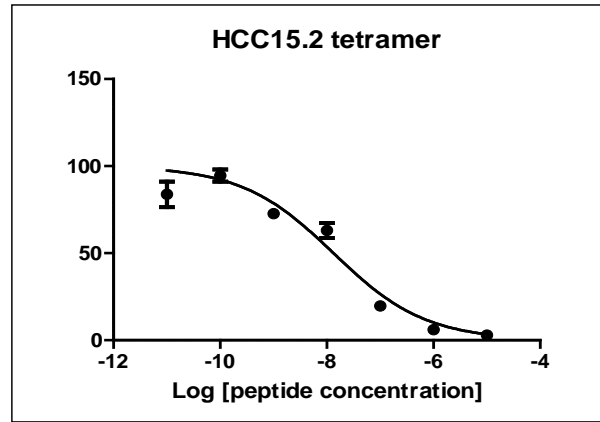
Table S-IV peptide Cross-Blocking Data

		10-Fold Excess Unlabled Peptide		
		15.1	15.2	1299.2
AF488 Labled Peptide	15.1	0.28	0.7	0.56
	15.2	0.12	0.14	0.12
	1299.2	0.15	0.93	0.11

All Data normalized to no competitor peptide

Table S-V Mutational Status of Different Cell Lines

	EGFR	BRAF	KRAS	NRAS	STK11 (LBK1)	CDKN2A	p53	PTEN	PIK3CA	RB1	Cluster	Phenotype
Calu-3 (lung AD)							1				1	E
H1648 (lung AD, lymph node met)						1	1				1	E
H1993 (lung AD)					1		1				1	E
H2009 (lung AD, lymph node met)			1		1		1			1	1	E
H2073 (lung AD)					1		1			1	1	M
PC-9 (lung AD)	1					1	1				1	E
H358 (Lung AD/BAC)			1				1				1	E
OvaCAR433 (ovarian)											1	ND
Calu-1 (lung SQ)			1				1				2	M
H1299 (lung LC)				1							2	M
H1355 (lung AD)			1		1		1				2	M
H157 (lung SQ)			1		1	1	1				2	M
H2087 (lung AD, lymph node met)		1		1			1				2	M
HUH7 (liver)							1				2	ND
MDA-MB-231 (breast)		1	1				1	1	1		2	ND
MiaPaCa (pancreatic)											2	ND
PC3 (prostate)							1	1			2	ND
SW480 (colon)											2	ND
Panc1 (pancreatic)			1			1	1				2	ND
T47D (breast)							1		1		2	ND
H1975 (lung AD)	1					1	1		1		4	E
H1819 (lung AD, lymph node met)							1				4	E
H441(lung AD/BAC)			1				1				4	E
MDA-MB-468 (breast)							1	1	1	1	4	ND
A549 (lung AD)			1		1	1					3	M
H1155 (lung LC)			1				1	1			3	M
H1437 (lung AD)					1	1	1				3	E
H1666 (lung AD/BAC)		1			1	1					3	E
H2126 (lung AD)					1	1	1				3	E
H2882 (lung carcinoma)							1				3	M
H460 (lung Ad)			1		1		1		1		3	M
HCC15 (lung SQ)				1	1	1	1			1	3	M
HCC2450 (lung SQ)									1		3	E
MCF7(breast)							1		1		3	ND
SCOV3 (ovarian)							1	1	1		3	ND

Mutations are noted in red.

	EGFR	BRAF	KRAS	NRAS	STK11	CDKN2A	p53	PTEN	PIK3CA	RB1
Total number of samples with mutation	2	3	11	3	11	14	26	4	7	4
Percentage of samples with the mutation	5.71%	8.57%	31.43%	8.57%	31.43%	40.00%	74.29%	11.43%	20.00%	11.43%

Total Number of Samples: 35

H2009.1 (12)	2	0	3	0	3	6	11	1	3	3
H1299.2 (20)	0	2	7	2	5	5	16	2	1	2
HCC15.1 (20)	0	2	7	2	5	5	16	2	1	2
HCC15.2 (20)	0	2	7	2	5	5	16	2	1	2
No Binders (11)	0	1	3	1	6	9	6	1	4	1
Group 1 (++++)	1	0	2	0	3	2	7	0	0	2
Group 2 (-+++)	0	2	5	2	2	3	9	2	1	0
Group 3 (----)	1	0	1	0	0	1	4	1	2	1

Table S-VI Statistical Analysis of Correlations between Mutational Status and peptide Binding

2X2 Tables and Fisher's Exact Tests

← ← H2009 → →		0	1	p-value
EGFR	WT	23	10	0.1109
	Mutant	0	2	
BRAF	WT	20	12	0.5361
	Mutant	3	0	
KRAS	WT	15	9	0.7091
	Mutant	8	3	
NRAS	WT	20	12	0.5361
	Mutant	3	0	
STK11	WT	15	9	0.7091
	Mutant	8	3	
CDKN2A	WT	15	6	0.4769
	Mutant	8	6	
p53	WT	8	1	0.1211
	Mutant	15	11	
PTEN	WT	20	11	1.0000
	Mutant	3	1	
PIK3CA	WT	18	10	1.0000
	Mutant	5	2	
RB1	WT	22	9	0.1061
	Mutant	1	3	

---- ← H1299.2, HCC15.1, HCC15.2 → ---		triplet 0	1	p-value
EGFR	WT	18	19	1.0000
	Mutant	1	1	
BRAF	WT	18	18	0.6071
	Mutant	1	2	
KRAS	WT	15	13	0.4801
	Mutant	4	7	
NRAS	WT	18	18	0.6071
	Mutant	1	2	
STK11	WT	13	15	0.7311
	Mutant	6	5	
CDKN2A	WT	6	15	**0.0104**
	Mutant	13	5	
p53	WT	5	4	0.1871
	Mutant	14	16	
PTEN	WT	17	18	1.0000
	Mutant	2	2	
PIK3CA	WT	10	19	**0.0033**
	Mutant	9	1	
RB1	WT	17	18	1.0000
	Mutant	2	2	

Cluster 2		cluster 2 0	1	p-value
EGFR	WT	25	12	0.5956
	Mutant	2	0	
BRAF	WT	26	10	0.2191
	Mutant	1	2	
KRAS	WT	21	7	0.2681
	Mutant	6	5	
NRAS	WT	26	10	0.2191
	Mutant	1	2	
STK11	WT	18	10	0.4463
	Mutant	9	2	
CDKN2A	WT	12	9	**0.0959**
	Mutant	15	3	
p53	WT	6	3	1.0000
	Mutant	21	9	
PTEN	WT	25	10	0.5733
	Mutant	2	2	
PIK3CA	WT	20	11	0.3938
	Mutant	7	1	
RB1	WT	23	12	0.2916
	Mutant	4	0	

Cluster 1		group 1 0	1	p-value
EGFR	WT	30	7	0.3725
	Mutant	1	1	
BRAF	WT	28	8	1.0000
	Mutant	3	0	
KRAS	WT	22	6	1.0000
	Mutant	9	2	
NRAS	WT	28	8	1.0000
	Mutant	3	0	
STK11	WT	23	5	0.6632
	Mutant	8	3	
CDKN2A	WT	15	6	0.2472
	Mutant	16	2	
p53	WT	1	1	0.6526
	Mutant	23	7	
PTEN	WT	27	8	0.5628
	Mutant	4	0	
PIK3CA	WT	23	8	0.1683
	Mutant	8	0	
RB1	WT	29	6	0.1803
	Mutant	2	2	

Cluster 3		Null 0	1	p-value
EGFR	WT	25	12	1.0000
	Mutant	2	0	
BRAF	WT	25	11	1.0000
	Mutant	2	1	
KRAS	WT	19	9	1.0000
	Mutant	8	3	
NRAS	WT	25	11	1.0000
	Mutant	2	1	
STK11	WT	22	6	0.0615
	Mutant	5	6	
CDKN2A	WT	18	3	**0.0346**
	Mutant	9	9	
p53	WT	4	5	0.1018
	Mutant	23	7	
PTEN	WT	24	11	1.0000
	Mutant	3	1	
PIK3CA	WT	23	7	**0.1038**
	Mutant	4	5	
RB1	WT	24	11	1.0000
	Mutant	3	1	

Double mutant analyses

		H2009 0	1	p-value
KRAS STK11	otherwise	19	11	0.6399
	2 X Mut	4	1	
KRAS CDKN2	otherwise	18	12	0.1412
	2 X Mut	5	0	
STK11 CDKN2	otherwise	16	12	**0.0695**
	2 X Mut	7	0	

		H1299 0	1	p-value
KRAS STK11	otherwise	13	17	1.0000
	2 X Mut	2	3	
KRAS CDKN2	otherwise	13	17	1.0000
	2 X Mut	2	3	
STK11 CDKN2	otherwise	9	19	**0.0274**
	2 X Mut	6	1	

		Null Group 0	1	p-value
KRAS STK11	otherwise	21	9	0.6399
	2 X Mut	3	2	
KRAS CDKN2	otherwise	21	9	0.6399
	2 X Mut	3	2	
STK11 CDKN2	otherwise	23	5	**0.0017**
	2 X Mut	1	6	

Table S-VII RPPA Correlation Data

H2009.1 Analysis

Marker	ttest p value	FullSerum High.vs.Low.FoldChange	Pearson Correlation	Pearson P value	
pMet_Tyr1234/1235	0.000831888	26.22884228	0.581864805	0.004500447	Markers with p values < 0.05 are included in the table
ATR	0.013944487	8.144478052	0.570587521	0.00555347	p values < 0.01 are highlighted in yellow
E Cadherin	0.001049363	4.03952645	0.583287481	0.004380326	
Met	0.007218458	3.755117416	0.544074815	0.008854727	
STAT5_pY694	0.0003967	3.142244909	0.714167552	0.000189006	
EGFR_pY1173	0.002363457	3.139161137	0.580030013	0.004659411	
pAxl Y779	0.012085971	2.914584473	0.560394064	0.006674249	
STAT6_pY641	0.007460998	2.728949329	0.551371743	0.00781674	
beta-Catenin	0.005461583	2.336955152	0.446872546	0.037066428	
Her2_pY1248	0.001064712	2.208096008	0.606850653	0.002747734	
MACC1	0.005369179	1.894460728	0.462996203	0.030012015	
Src_pY416	0.02574993	1.80260343	0.48998129	0.020621459	
STAT3_pY705-2	0.015883992	1.757080299	0.529403496	0.011286194	
STAT3_pY705-1	0.041953767	1.618057612	0.550791596	0.007895406	
N Cadherin	0.001851895	-1.168381738	-0.658269446	0.000866922	
TAZ.1	0.028214489	-1.180086868	-0.548418902	0.008223966	
Stathamin	0.03220062	-1.424910793	-0.377902069	0.082913829	
RAD50	0.028171093	-1.596260352	-0.470027588	0.027290357	
Thymidylate synthase	0.017338785	-1.644269789	-0.49379446	0.019510745	

H1299.2/HCC15.1/HCC15.2 Analysis

Marker	FullSerum ttestpvalue	FullSerum High.vs.Low.FoldChange	Pearson Correlation	Pearson P value
p16	0.013559309	2.031347507	0.382171631	0.079217822
XIAP	0.020023271	-1.185240268	-0.549366751	0.008091386
VASP	0.004237199	1.429702674	0.415426389	0.054516309
PDK1_pS241	0.047194833	-1.230937203	-0.366630969	0.093288979
Caspase 7	0.013390989	-1.323391571	-0.577621644	0.004875154

H2009.1 — H2009 tumor/ H460

		2009 tumor	460 tumor	liver	lung	spleen	tumor	H2009 tumor/liver	H2009 tumor/lung	H2009 tumor/spleen	H460/liver	H460/lung	H460/spleen
30 µg	Mouse 1	1810	37	7800	75	50.20	49.5	0.2	24.0	36.1	0.005	0.49	0.73
30 µg	Mouse 2	17300	428	10500	2270	Below detection lim	40.4	1.6	7.6		0.041	0.19	
30 µg	Mouse 3	9300	433	7580	48	26.20	21.5	1.2	192.9	355.0	0.057	8.98	16.53
30 µg	Mouse 4	7970	384	5590	177	2.13	20.8	1.4	45.0	3741.8	0.069	2.17	180.28
30 µg	Mouse 5	13600	112	9310	129	18.30	121.4	1.5	105.4	743.2	0.012	0.87	6.12
	average	9996	279	8156	540	24.21	50.7	1.2	75.0	1219.0	0.037	2.54	50.91
	SEM	2626	85	833	433	10	19	0.25	34	853	0.012	1.65	43.25

H1299.2 — H1299 tumor/ H460

		1299 tumor	460 tumor	liver	lung	spleen	tumor	H1299 tumor/liver	H1299 tumor/lung	H2009 tumor/spleen	H460/liver	H460/lung	H460/spleen
53 µg	Mouse 1	8200	4165	41	3050	below detection	2.0	200.2	2.7		101.71	1.37	
53 µg	Mouse 2	2355	618	310.70	4685	84.60	3.8	7.6	0.5	27.8	1.99	0.13	7.30
53 µg	Mouse 3	9710	2070	652	1475	146	4.7	14.9	6.6	66.7	3.18	1.40	14.23
	average	6755	2284	334	3070	115.05	3.5	74.2	3.3	47.3	35.62	0.97	10.76
	SEM	2242.77	1783.42	305.96	926.70	30.45	0.80	63.04	1.78		33.04	0.42	

15.1 — H1299 tumor/ H460

		1299 tumor	460 tumor	liver	lung	spleen	tumor	H 1299 tumor/liver	H1299 tumor/lung	H1299 tumor/spleen	H460/Liver	H460/Lung	H460/spleen
43 µg	Mouse 1	2410	503	6570	432	12.64	4.8	0.4	5.6	190.7	0.08	1.16	39.81
43 µg	Mouse 2	2030	572	4025	270	below detection	3.6	0.5	7.5		0.14	2.12	
63 ug	Mouse 3	1013	688	2435	741	68.20	1.5	0.4	1.4	14.9	0.28	0.93	10.08
	average	1818	587	4343	277.61		3.3	0.4	4.8	102.8	0.17	1.40	24.95
	SEM	417.05	53.85	1204.24	138.28		0.97	0.04	1.82		0.06	0.36	

H460.1 — H460 tumor/ H1299

			460 tumor	liver	lung	spleen	tumor	H460 tumor/liver	H460 tumor/lung	H460 tumor/spleen	H1299/Liver	H1299/lung	H1299/spleen
44 µg	Mouse 1	169	1425	1480	94	16.0	8.4	1.0	15.1	89.3	0.11	1.79	10.60
44 µg	Mouse 2	no tumor	1605	1245	96	64.6		1.3	24.9	24.9			
89 ug	Mouse 3	105	4865	3380	1945	63.9	46.3	1.4	2.5	76.1	0.03	0.05	1.64
	average	137	2632	2035	712	48.1	27.4	1.2	14.2	63.4	0.07	0.92	6.12
	SEM		1117.87	675.91	616.65	16.09		0.14	6.47	19.66			

15.2 — H1299 tumor/ H460

		1299 tumor	460 tumor	liver	lung	spleen	tumor	tumor/liver	tumor/lung	tumor/spleen
33 µg	Mouse 1	1013	688	2435	741	68.20	1.5	0.4	1.4	14.9