Supplementary Table 1: *EZH2* Co-Expression Gene Signature

Top 116 genes co-expressed with *EZH2* across 9 Oncomine studies

Gene Symbol	Description
ALS2CR4	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4
ATIC	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase
ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
AURKA	aurora kinase A
BIRC5	baculoviral IAP repeat-containing 5
BOP1	block of proliferation 1
BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)
BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)
C13orf34	chromosome 13 open reading frame 34
C1orf112	chromosome 1 open reading frame 112
CCNA2	cyclin A2
CCNB1	cyclin B1
CCNB2	cyclin B2
CDC20	cell division cycle 20 homolog (S. cerevisiae)
CDC25A	cell division cycle 25 homolog A (S. pombe)
CDC6	cell division cycle 6 homolog (S. cerevisiae)
CDC7	cell division cycle 7 homolog (S. cerevisiae)
CDCA3	cell division cycle associated 3
CDCA8	cell division cycle associated 8
CDK1	cyclin-dependent kinase 1
CDKN3	cyclin-dependent kinase inhibitor 3
CENPE	centromere protein E, 312kDa
CENPF	centromere protein F, 350/400kDa (mitosin)
CENPM	centromere protein M
CENPW	centromere protein W
CHEK1	CHK1 checkpoint homolog (S. pombe)
CKAP2	cytoskeleton associated protein 2
CKS1B	CDC28 protein kinase regulatory subunit 1B
CKS2	CDC28 protein kinase regulatory subunit 2
CSE1L	CSE1 chromosome segregation 1-like (yeast)
CSTF1	cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kDa
CTPS	CTP synthase
DBF4	DBF4 homolog (S. cerevisiae)
DBN1	drebrin 1
DEPDC1	DEP domain containing 1
DLGAP5	discs, large (Drosophila) homolog-associated protein 5
DTL	denticleless homolog (Drosophila)
ECT2	Epithelial cell transforming sequence 2 oncogene
ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)

ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)
EXO1	exonuclease 1
EZH2	enhancer of zeste homolog 2 (Drosophila)
FANCI	Fanconi anemia, complementation group I
FBXO5	F-box protein 5
FEN1	flap structure-specific endonuclease 1
FOXM1	forkhead box M1
GINS1	GINS complex subunit 1 (Psf1 homolog)
GINS2	GINS complex subunit 2 (Psf2 homolog)
GMNN	geminin, DNA replication inhibitor
GOT1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)
GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)
H2AFX	H2A histone family, member X
H2AFZ	H2A histone family, member Z
HMGA1	high mobility group AT-hook 1
HMGB2	high-mobility group box 2
HMMR	hyaluronan-mediated motility receptor (RHAMM)
HN1	hematological and neurological expressed 1
KIAA0101	KIAA0101
KIF11	kinesin family member 11
KIF14	kinesin family member 14
KIF15	kinesin family member 15
KIF18A	kinesin family member 18A
KIF18B	kinesin family member 18B
KIF20A	kinesin family member 20A
KIF20B	kinesin family member 20B
KIF23	kinesin family member 23
KIF2C	kinesin family member 2C
KIFC1	kinesin family member C1
KNTC1	kinetochore associated 1
KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
LMNB1	lamin B1
LMNB2	lamin B2
MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)
MCM10	minichromosome maintenance complex component 10
MCM7	minichromosome maintenance complex component 7
MKI67	antigen identified by monoclonal antibody Ki-67
MLF1IP	MLF1 interacting protein
MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2,
NCAPG	non-SMC condensin I complex, subunit G
NCAPG2	non-SMC condensin II complex, subunit G2
NCAPH	non-SMC condensin I complex, subunit H
NDC80	NDC80 homolog, kinetochore complex component (S. cerevisiae)
NUP205	nucleoporin 205kDa
OLA1	Obg-like ATPase 1
PAICS	phosphoribosylaminoimidazole carboxylase

PBK	PDZ binding kinase
PCNA	proliferating cell nuclear antigen
PFN2	profilin 2
PLK4	polo-like kinase 4
POLA1	polymerase (DNA directed), alpha 1, catalytic subunit
POLE2	polymerase (DNA directed), epsilon 2 (p59 subunit)
PPAT	Phosphoribosyl pyrophosphate amidotransferase
PRIM1	primase, DNA, polypeptide 1 (49kDa)
PSMD14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
PTTG1	pituitary tumor-transforming 1
RFC4	replication factor C (activator 1) 4, 37kDa
SLC7A5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
SMC2	structural maintenance of chromosomes 2
SMC4	structural maintenance of chromosomes 4
SPAG5	sperm associated antigen 5
SRM	spermidine synthase
STIL	SCL/TAL1 interrupting locus
STMN1	stathmin 1
TACC3	transforming, acidic coiled-coil containing protein 3
TFRC	Transferrin receptor (p90, CD71)
TMEM106C	transmembrane protein 106C
TOP2A	Topoisomerase (DNA) II alpha 170kDa
TOPBP1	topoisomerase (DNA) II binding protein 1
TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)
TRIP13	thyroid hormone receptor interactor 13
TROAP	trophinin associated protein (tastin)
TYMS	thymidylate synthetase
UBE2C	ubiquitin-conjugating enzyme E2C
UBE2S	ubiquitin-conjugating enzyme E2S
UNG	uracil-DNA glycosylase
WDR12	WD repeat domain 12

Supplementary Table 2: Gene function enrichment analysis of *EZH2* co-expressed gene signature

C1: number of genes in a cluster or list that have this annotation term
C2: number of annotated genes in this cluster or list
C3: number of all genes on array that have this annotation term
C4: number of all annotated genes on array
P-value: binomial approximated p-value for hypergeometric distribution

*****Gene Ontology*****

C1	C2	C3	C4	P-value	Term Name
81	112	5956	12364	0	protein binding
73	112	3967	12364	0	nucleus
58	112	3873	12364	0.000005	cytoplasm
49	112	439	12364	0	cell cycle
38	112	243	12364	0	cell division
36	112	186	12364	0	mitosis
36	112	1621	12364	0	nucleotide binding
35	112	1250	12364	0	ATP binding
30	112	436	12364	0	nucleoplasm
24	112	667	12364	0	cytoskeleton
20	112	144	12364	0	DNA replication
18	112	294	12364	0	cell proliferation
18	112	103	12364	0	spindle
16	112	203	12364	0	microtubule
15	112	224	12364	0	DNA repair
14	112	155	12364	0	chromosome
12	112	46	12364	0	phosphoinositide-mediated signaling
11	112	53	12364	0	condensed chromosome kinetochore
11	112	71	12364	0	kinetochore
11	112	54	12364	0	microtubule motor activity
11	112	65	12364	0	microtubule-based movement
11	112	109	12364	0	motor activity
10	112	236	12364	0.000062	response to DNA damage stimulus
10	112	47	12364	0	spindle pole
8	112	59	12364	0	anaphase-promoting complex-dependent proteasomal degradation
8	112	41	12364	0	chromosome segregation
7	112	47	12364	0	chromosome, centromeric region
7	112	135	12364	0.000247	microtubule organizing center
7	112	14	12364	0	spindle organization
6	112	12	12364	0	chromosome condensation

6	112	58	12364	0.000017	negative regulation of mitotic ubiquitin-protein ligase
6	112	61	12364	0.000022	positive regulation of mitotic ubiquitin-protein ligase
6	112	38	12364	0.000002	regulation of cyclin-dependent protein kinase activity
5	112	49	12364	0.000092	microtubule cytoskeleton
5	112	14	12364	0	mitotic sister chromatid segregation
5	112	25	12364	0.000004	spindle microtubule
4	112	19	12364	0.00003	chromosome organization
4	112	23	12364	0.000063	condensed chromosome
4	112	5	12364	0	condensin complex
4	112	36	12364	0.000347	DNA metabolic process
4	112	44	12364	0.000734	G1/S transition of mitotic cell cycle
4	112	8	12364	0.000001	M phase of mitotic cell cycle
4	112	19	12364	0.00003	midbody
4	112	12	12364	0.000005	mitotic cell cycle checkpoint
4	112	11	12364	0.000004	mitotic cell cycle spindle assembly checkpoint
4	112	12	12364	0.000005	mitotic chromosome condensation
4	112	26	12364	0.000101	nuclear chromosome
3	112	6	12364	0.000025	'de novo' IMP biosynthetic process
3	112	20	12364	0.000846	anaphase-promoting complex
3	112	14	12364	0.000302	DNA unwinding involved in replication
3	112	20	12364	0.000846	G2/M transition of mitotic cell cycle
3	112	13	12364	0.000243	kinesin complex
3	112	15	12364	0.000369	male germ cell nucleus
3	112	10	12364	0.000113	mitotic cell cycle
3	112	15	12364	0.000369	mitotic spindle organization
3	112	17	12364	0.00053	nucleotide-excision repair, DNA gap filling
3	112	13	12364	0.000243	oocyte maturation
3	112	8	12364	0.000059	outer kinetochore of condensed chromosome
3	112	15	12364	0.000369	purine nucleotide biosynthetic process
3	112	15	12364	0.000369	regulation of mitosis
3	112	11	12364	0.000149	replication fork
2	112	5	12364	0.000987	lamin filament
2	112	5	12364	0.000987	purine base biosynthetic process
2	112	3	12364	0.00036	regulation of chromosome segregation
64 reported significant, 0 expected false positive (209 terms assessed for enrichment at p-value threshold 0.001)					

Supplementary Table 3: Chou Talalay Combination Index Analysis

H23 DZNep + Etoposide
CI Simulations

Fa	CI	Est. s.d.	Etop (μM)	DZNep (μM)
0.02	1E+12	6E+14	0.002	0.002
0.05	2E+08	2E+10	0.006	0.006
0.1	3.2E+05	6.2E+06	0.020	0.020
0.15	5586	40440	0.040	0.040
0.2	260.4	908.6	0.067	0.067
0.25	20.85	38.69	0.104	0.104
0.3	2.449	2.339	0.152	0.152
0.35	0.512	0.190	0.215	0.215
0.4	0.280	0.058	0.297	0.297
0.45	0.268	0.050	0.405	0.405
0.5	0.291	0.050	0.549	0.549
0.55	0.323	0.052	0.744	0.744
0.6	0.360	0.054	1.014	1.014
0.65	0.404	0.059	1.400	1.400
0.7	0.456	0.065	1.978	1.978
0.75	0.521	0.077	2.893	2.893
0.8	0.608	0.096	4.470	4.470
0.85	0.732	0.131	7.571	7.571
0.9	0.937	0.202	15.24	15.24
0.95	1.396	0.400	47.20	47.20
0.99	3.370	1.587	573.2	573.2

SW1573 DZNep + Etoposide
CI Simulations

Fa	CI	Est. s.d.	Etop (μM)	DZNep (μM)
0.02	103.7	187.1	0.003	0.003
0.05	11.34	11.85	0.012	0.012
0.1	3.154	2.540	0.036	0.036
0.15	1.996	1.617	0.069	0.069
0.2	1.607	1.244	0.114	0.114
0.25	1.412	1.012	0.171	0.171
0.3	1.287	0.845	0.244	0.244
0.35	1.196	0.717	0.337	0.337
0.4	1.122	0.614	0.456	0.456
0.45	1.058	0.530	0.610	0.610
0.5	1.001	0.461	0.810	0.810
0.55	0.948	0.405	1.077	1.077
0.6	0.898	0.360	1.439	1.439
0.65	0.849	0.326	1.948	1.948
0.7	0.799	0.304	2.693	2.693
0.75	0.748	0.294	3.845	3.845
0.8	0.694	0.296	5.781	5.781
0.85	0.634	0.311	9.471	9.471
0.9	0.562	0.339	18.24	18.24
0.95	0.463	0.384	52.62	52.62
0.99	0.301	0.450	546.2	546.2

H460 DZNep + Etoposide
CI Simulations

Fa	CI	Est. s.d.	Etop (μM)	DZNep (μM)
0.02	19.85	45.27	0.001	0.001
0.05	10.29	17.48	0.004	0.004
0.1	6.175	8.073	0.014	0.014
0.15	4.510	4.924	0.030	0.030
0.2	3.562	3.355	0.055	0.055
0.25	2.932	2.422	0.090	0.090
0.3	2.474	1.807	0.139	0.139
0.35	2.121	1.376	0.206	0.206
0.4	1.837	1.061	0.297	0.297
0.45	1.600	0.824	0.422	0.422
0.5	1.398	0.643	0.596	0.596
0.55	1.221	0.504	0.842	0.842
0.6	1.064	0.400	1.197	1.197
0.65	0.921	0.326	1.728	1.728
0.7	0.790	0.276	2.559	2.559
0.75	0.667	0.246	3.943	3.943
0.8	0.550	0.230	6.467	6.467
0.85	0.435	0.221	11.77	11.77
0.9	0.319	0.209	26.08	26.08
0.95	0.193	0.181	94.31	94.31
0.99	0.064	0.112	1612	1612

H23 GSK126 + Etoposide
CI Simulations

Fa	CI	Est. s.d.	Etop (μM)	GSK126 (μM)
0.02	0.743	0.307	0.024	0.024
0.05	0.813	0.254	0.073	0.073
0.1	0.895	0.217	0.175	0.175
0.15	0.958	0.197	0.302	0.302
0.2	1.011	0.187	0.456	0.456
0.25	1.060	0.183	0.640	0.640
0.3	1.105	0.185	0.861	0.861
0.35	1.149	0.192	1.126	1.126
0.4	1.193	0.204	1.449	1.449
0.45	1.237	0.219	1.844	1.844
0.5	1.282	0.240	2.337	2.337
0.55	1.329	0.265	2.960	2.960
0.6	1.380	0.295	3.768	3.768
0.65	1.435	0.331	4.847	4.847
0.7	1.498	0.375	6.343	6.343
0.75	1.570	0.430	8.530	8.530
0.8	1.658	0.502	11.97	11.97
0.85	1.772	0.602	18.05	18.05
0.9	1.937	0.758	31.14	31.14
0.95	2.240	1.076	75.14	75.14
0.99	3.101	2.159	525.8	525.8

SW1573 GSK126 + Etoposide
CI Simulations

Fa	CI	Est. s.d.	Etop (μM)	GSK126 (μM)
0.02	55.27	406.2	0.006	0.006
0.05	21.45	103.9	0.020	0.020
0.1	10.73	35.36	0.048	0.048
0.15	7.059	18.05	0.084	0.084
0.2	5.164	10.83	0.128	0.128
0.25	3.993	7.080	0.180	0.180
0.3	3.192	4.861	0.244	0.244
0.35	2.605	3.439	0.320	0.320
0.4	2.154	2.477	0.414	0.414
0.45	1.796	1.799	0.529	0.529
0.5	1.503	1.308	0.674	0.674
0.55	1.258	0.947	0.857	0.857
0.6	1.049	0.680	1.096	1.096
0.65	0.868	0.483	1.416	1.416
0.7	0.709	0.343	1.863	1.863
0.75	0.567	0.252	2.519	2.519
0.8	0.440	0.201	3.559	3.559
0.85	0.323	0.179	5.407	5.407
0.9	0.214	0.165	9.423	9.423
0.95	0.110	0.142	23.11	23.11
0.99	0.026	0.087	167.7	167.7

H460 GSK126 + Etoposide
CI Simulations

Fa	CI	Est. s.d.	Etop (μM)	GSK126 (μM)
0.02	76.45	168.7	0.003	0.003
0.05	30.72	49.90	0.011	0.011
0.1	14.97	18.65	0.033	0.033
0.15	9.593	9.982	0.065	0.065
0.2	6.861	6.168	0.107	0.107
0.25	5.202	4.109	0.161	0.161
0.3	4.085	2.862	0.230	0.230
0.35	3.280	2.049	0.319	0.319
0.4	2.671	1.492	0.433	0.433
0.45	2.193	1.099	0.580	0.580
0.5	1.808	0.815	0.773	0.773
0.55	1.491	0.608	1.029	1.029
0.6	1.224	0.459	1.379	1.379
0.65	0.997	0.353	1.872	1.872
0.7	0.801	0.281	2.593	2.593
0.75	0.629	0.231	3.714	3.714
0.8	0.477	0.197	5.603	5.603
0.85	0.342	0.170	9.217	9.217
0.9	0.219	0.142	17.85	17.85
0.95	0.107	0.116	51.94	51.94
0.99	0.023	0.223	549.5	549.5

Supplementary Table 3 Continued

HCC15 DZNep + Etoposide
CI Simulations

Fa	CI	Est. s.d.	Etop (µM)	DZNep (µM)
0.02	164.6	156.3	0.002	0.002
0.05	14.29	9.971	0.009	0.009
0.1	2.199	1.132	0.029	0.029
0.15	0.781	0.324	0.062	0.062
0.2	0.423	0.152	0.111	0.111
0.25	0.298	0.099	0.177	0.177
0.3	0.248	0.077	0.268	0.268
0.35	0.227	0.067	0.389	0.389
0.4	0.218	0.061	0.553	0.553
0.45	0.216	0.059	0.773	0.773
0.5	0.217	0.059	1.074	1.074
0.55	0.220	0.060	1.493	1.493
0.6	0.225	0.064	2.089	2.089
0.65	0.231	0.070	2.966	2.966
0.7	0.238	0.079	4.313	4.313
0.75	0.246	0.090	6.514	6.514
0.8	0.257	0.106	10.44	10.44
0.85	0.270	0.128	18.49	18.49
0.9	0.288	0.164	39.49	39.49
0.95	0.321	0.235	134.5	134.5
0.99	0.406	0.469	2017	2017

A549 DZNep + Etoposide
CI Simulations

Fa	CI	Est. s.d.	Etop (µM)	DZNep (µM)
0.02	159.85	561.11	8E-05	8E-05
0.05	8.957	16.333	0.001	0.001
0.1	1.085	1.005	0.005	0.005
0.15	0.428	0.240	0.014	0.014
0.2	0.303	0.142	0.031	0.031
0.25	0.274	0.117	0.062	0.062
0.3	0.271	0.103	0.111	0.111
0.35	0.277	0.093	0.191	0.191
0.4	0.287	0.086	0.316	0.316
0.45	0.298	0.080	0.513	0.513
0.5	0.311	0.078	0.823	0.823
0.55	0.324	0.079	1.321	1.321
0.6	0.339	0.084	2.142	2.142
0.65	0.355	0.096	3.546	3.546
0.7	0.373	0.114	6.077	6.077
0.75	0.394	0.140	11.00	11.00
0.8	0.420	0.176	21.68	21.68
0.85	0.454	0.231	49.32	49.32
0.9	0.502	0.320	147.0	147.0
0.95	0.592	0.512	857.0	857.0
0.99	0.851	1.245	42135	42135

H157 DZNep + Etoposide
CI Simulations

Fa	CI	Est. s.d.	Etop (µM)	DZNep (µM)
0.02	4.250	4.229	0.047	0.047
0.05	1.211	0.617	0.116	0.116
0.1	0.642	0.200	0.240	0.240
0.15	0.523	0.144	0.375	0.375
0.2	0.483	0.124	0.525	0.525
0.25	0.467	0.112	0.694	0.694
0.3	0.461	0.104	0.885	0.885
0.35	0.460	0.098	1.104	1.104
0.4	0.461	0.094	1.357	1.357
0.45	0.465	0.091	1.655	1.655
0.5	0.469	0.090	2.009	2.009
0.55	0.474	0.089	2.440	2.440
0.6	0.480	0.091	2.974	2.974
0.65	0.487	0.094	3.657	3.657
0.7	0.494	0.099	4.560	4.560
0.75	0.503	0.107	5.816	5.816
0.8	0.514	0.119	7.682	7.682
0.85	0.527	0.136	10.76	10.76
0.9	0.546	0.163	16.83	16.83
0.95	0.578	0.215	34.69	34.69
0.99	0.655	0.367	171.3	171.3

HCC15 GSK + Etoposide
CI Simulations

Fa	CI	Est. s.d.	Etop (µM)	GSK126 (µM)
0.02	401.6	1637	0.012	0.012
0.05	3.539	3.885	0.044	0.044
0.1	0.698	0.428	0.122	0.122
0.15	0.606	0.319	0.229	0.229
0.2	0.573	0.264	0.367	0.367
0.25	0.549	0.228	0.542	0.542
0.3	0.530	0.202	0.763	0.763
0.35	0.513	0.185	1.039	1.039
0.4	0.498	0.174	1.388	1.388
0.45	0.484	0.168	1.833	1.833
0.5	0.471	0.166	2.406	2.406
0.55	0.458	0.167	3.159	3.159
0.6	0.445	0.172	4.170	4.170
0.65	0.431	0.179	5.571	5.571
0.7	0.418	0.188	7.592	7.592
0.75	0.403	0.200	10.68	10.68
0.8	0.387	0.215	15.77	15.77
0.85	0.369	0.234	25.29	25.29
0.9	0.346	0.259	47.37	47.37
0.95	0.311	0.297	130.5	130.5
0.99	0.247	0.369	1224	1224

A549 GSK126 + Etoposide
CI Simulations

Fa	CI	Est. s.d.	Etop (µM)	GSK126 (µM)
0.02	1.072	1.193	0.001	0.001
0.05	0.902	0.747	0.004	0.004
0.1	0.787	0.495	0.019	0.019
0.15	0.724	0.372	0.047	0.047
0.2	0.679	0.295	0.093	0.093
0.25	0.645	0.240	0.163	0.163
0.3	0.616	0.198	0.266	0.266
0.35	0.591	0.166	0.417	0.417
0.4	0.568	0.141	0.633	0.633
0.45	0.548	0.123	0.945	0.945
0.5	0.528	0.111	1.399	1.399
0.55	0.509	0.105	2.072	2.072
0.6	0.491	0.105	3.094	3.094
0.65	0.472	0.110	4.699	4.699
0.7	0.453	0.119	7.345	7.345
0.75	0.433	0.132	12.01	12.01
0.8	0.412	0.149	21.09	21.09
0.85	0.387	0.168	41.71	41.71
0.9	0.356	0.193	103.1	103.1
0.95	0.313	0.228	445.2	445.2
0.99	0.238	0.286	11262	11262

H157 GSK126 + Etoposide
CI Simulations

Fa	CI	Est. s.d.	Etop (µM)	GSK126 (µM)
0.02	3.010	1.435	0.354	0.354
0.05	2.040	0.806	0.565	0.565
0.1	1.502	0.505	0.816	0.816
0.15	1.243	0.377	1.026	1.026
0.2	1.078	0.304	1.219	1.219
0.25	0.959	0.255	1.405	1.405
0.3	0.865	0.219	1.590	1.590
0.35	0.788	0.193	1.780	1.780
0.4	0.723	0.172	1.978	1.978
0.45	0.665	0.155	2.189	2.189
0.5	0.613	0.141	2.417	2.417
0.55	0.565	0.129	2.668	2.668
0.6	0.519	0.119	2.952	2.952
0.65	0.476	0.110	3.281	3.281
0.7	0.434	0.103	3.672	3.672
0.75	0.392	0.096	4.158	4.158
0.8	0.349	0.090	4.792	4.792
0.85	0.303	0.084	5.692	5.692
0.9	0.251	0.077	7.153	7.153
0.95	0.185	0.068	10.35	10.35
0.99	0.095	0.049	23.38	23.38

Supplementary Table 3 Continued

PC9 DZNep + Etoposide CI Simulations

Fa	CI	Est. s.d.	Etop (μM)	DZNep (μM)
0.02	28.21	24.02	0.040	0.040
0.05	3.420	2.107	0.087	0.087
0.1	0.715	0.328	0.161	0.161
0.15	0.325	0.129	0.237	0.237
0.2	0.219	0.083	0.316	0.316
0.25	0.182	0.069	0.401	0.401
0.3	0.171	0.066	0.495	0.495
0.35	0.170	0.066	0.598	0.598
0.4	0.175	0.068	0.714	0.714
0.45	0.183	0.071	0.846	0.846
0.5	0.192	0.075	0.999	0.999
0.55	0.204	0.079	1.180	1.180
0.6	0.217	0.085	1.399	1.399
0.65	0.233	0.092	1.670	1.670
0.7	0.251	0.101	2.019	2.019
0.75	0.273	0.112	2.487	2.487
0.8	0.301	0.128	3.158	3.158
0.85	0.338	0.150	4.217	4.217
0.9	0.396	0.189	6.190	6.190
0.95	0.510	0.277	11.51	11.51
0.99	0.892	0.649	45.30	45.302

PC9 GSK126 + Etoposide CI Simulations

Fa	CI	Est. s.d.	Etop (μM)	GSK126 (μM)
0.02	38.43	44.77	0.035	0.035
0.05	5.103	3.771	0.093	0.093
0.1	1.124	0.534	0.202	0.202
0.15	0.519	0.194	0.327	0.327
0.2	0.352	0.123	0.470	0.470
0.25	0.300	0.106	0.633	0.633
0.3	0.290	0.104	0.822	0.822
0.35	0.300	0.110	1.043	1.043
0.4	0.320	0.119	1.302	1.302
0.45	0.348	0.131	1.610	1.610
0.5	0.382	0.146	1.984	1.984
0.55	0.422	0.164	2.444	2.444
0.6	0.470	0.187	3.024	3.024
0.65	0.526	0.215	3.775	3.775
0.7	0.595	0.252	4.786	4.786
0.75	0.682	0.302	6.214	6.214
0.8	0.798	0.373	8.380	8.380
0.85	0.966	0.485	12.04	12.04
0.9	1.244	0.691	19.47	19.47
0.95	1.874	1.222	42.32	42.32
0.99	4.632	4.204	235.3	235.3

Supplementary Table 4: Mutational Data of NSCLC Cell Lines Used in this Study

Cell Line	Gender	Age	Ethnicity	Subtype	Stage	Smoke (pack/yr)	Biopsy	PIK3CA	Kras	Nras	p53	SMARCA4	EGFR	CDKN2A	LKB1
H1975	F	N/A	N/A	AdC	N/A	non-smoker	primary	G118D	WT	WT	R273H	WT	T790M, L858R	E69*	Q37* het
H2030	M	N/A	N/A	AdC	N/A	unknown	metastasis	WT	G12C	WT	G262V	deletion	WT	WT	E317*
HCC4006	M	N/A	Caucasian	AdC	N/A	non-smoker	N/A	WT	WT	WT	N/A	N/A	L747_E749del	N/A	WT
A549	M	58	Caucasian	AdC	N/A	unknown	primary	WT	G12S	WT	WT	Q729*	WT	deletion	Q37*
HCC2450	M	52	Caucasian	SCC	IIIB	unknown	primary	H1047R	N/A	N/A	deletion	N/A	N/A	N/A	N/A
PC9	M	45	East Asian	AdC	N/A	unknown	N/A	WT	WT	WT	N/A	N/A	E746_A750del	G67V	WT
Calu1	M	47	Caucasian	EpiC	III	unknown	pleura	WT	G12C	WT	WT	WT	WT	WT	WT
H1650	M	27	Caucasian	AdC (BAC)	IIIB	10	pleura	WT	WT	WT	deletion	WT	E746X	deletion	WT
H522	M	60	Caucasian	AdC	II	60	primary	WT	WT	WT	P191*	P270*	WT	WT	WT
H2126	M	65	Caucasian	LC	IIIB	non-smoker	pleura	WT	WT	WT	E62*	W764R	WT	deletion	deletion
H157	M	59	Caucasian	SCC	IIIB	50	metastasis	WT	G12R	WT	E298*	T58*	WT	E69*	deletion
H1299	M	43	Caucasian	LC	IIIA	50	lymph node	WT	WT	Q61K	deletion	Y560*	WT	hypermeth	WT
HCC15	M	47	Afr-American	SCC	N/A	unknown	primary	WT	WT	mut	mut	M272*	WT	mut/hyperm	deletion
HCC827	F	39	Caucasian	AdC	N/A	4	N/A	WT	WT	WT	V218del	WT	E746_A750del	N/A	WT
H322	M	52	Caucasian	AdC (BAC)	IV	60	lymph node	WT	WT	WT	N/A	N/A	WT	deletion	WT
H2009	F	68	Caucasian	AdC	IV	30	lymph node	E711D	G12A	WT	R273L	WT	WT	WT	WT
Sw1573	F	44	Caucasian	AdC	N/A	unknown	primary	K111E	G12C	WT	WT	WT	WT	deletion	WT
Calu6	F	61	Caucasian	AdC (Ana)	N/A	unknown	primary	N/A	Q61K	WT	R196*	WT	WT	WT	WT
H441	M	33	N/A	AdC (pap)	IIIA	non-smoker	pleura	WT	G12V	WT	R158L	WT	WT	hypermeth	WT
HCC95	M	64	Caucasian	SCC	IV	unknown	pleura	Amplified	WT	WT	WT	WT	WT	mut/hyperm	WT
H520	M	N/A	N/A	SCC	N/A	non-smoker	primary	WT	WT	WT	W146*	WT	WT	G45*	WT
H460	M	N/A	N/A	LC	N/A	non-smoker	primary	E545K	Q61H	WT	mut	WT	WT	deletion	Q37*
Calu3	M	25	Caucasian	AdC	N/A	unknown	pleura	Amplified	WT	WT	M237I	WT	WT	hypermeth	WT
H2122	F	46	Caucasian	AdC	IV	30	pleura	WT	G12C	WT	Q16L, C176F	WT	WT	deletion	P281*
H23	M	51	Afr-American	AdC	N/A	40	primary	WT	G12C	WT	M246I	K1533N	WT	hypermeth	W322*
H3255	F	47	Caucasian	AdC	IIIB	non-smoker	N/A	Amplified	G12C	WT	N/A	N/A	L858R	N/A	N/A
Cell Line	Gender	Age	Ethnicity	Subtype	Stage	Smoke (pack/yr)	Biopsy	PIK3CA	Kras	Nras	p53	SMARCA4	EGFR	CDKN2A	LKB1

Supplementary Table 5: Shared differentially expressed genes in *EGFR* and *BRG1* mutant NSCLC cell lines

Probe	Symbol	Description	p-value	log2 fold change for Brg1mut - WT	log2 fold change for EGFRmut - WT
201983_s_at	**EGFR**	epidermal growth factor receptor	0.014	2.178	2.232
210986_s_at	**TPM1**	tropomyosin 1 (alpha)	0.007	1.525	1.743
218368_s_at	**TNFRSF12A**	tumor necrosis factor receptor, 12A	0.004	1.172	1.173
205130_at	**MOK**	MOK protein kinase	0.013	0.928	0.891
217785_s_at	**YKT6**	YKT6 v-SNARE homolog (S. cerevisiae)	0.01	0.913	1.196
219088_s_at	**ZNF576**	zinc finger protein 576	7E-04	0.907	1.008
202408_s_at	**PRPF31**	PRP31 pre-mRNA processing factor 31	0.001	0.755	0.974
218261_at	**AP1M2**	adaptor-related protein complex 1, mu	0.013	0.748	0.937
202578_s_at	**DDX19A**	DEAD (Asp-Glu-Ala-Asp) box 19A	0.002	0.716	0.531
201144_s_at	**EIF2S1**	eukaryotic translation initiation factor 2	0.012	0.69	0.79
216299_s_at	**XRCC3**	X-ray repair complementing defective	0.003	0.574	0.572
217784_at	**YKT6**	YKT6 v-SNARE homolog (S. cerevisiae)	0.002	0.531	0.81
1773_at	**FNTB**	farnesyltransferase, CAAX box, beta	0.003	0.514	0.408
218408_at	**TIMM10**	membrane 10 homolog (yeast)	0.004	0.475	0.727
221769_at	**SPSB3**	SOCS box containing 3	0.008	0.471	0.614
202927_at	**PIN1**	peptidylprolyl cis/ NIMA-interacting 1	0.007	0.456	0.451
211289_x_at	**CDK11**	cyclin dependent kinase 11	0.006	0.438	0.373
218206_x_at	**SCAND1**	SCAN domain containing 1	0.005	0.396	0.543
214244_s_at	**ATP6V0E1**	ATPase V0 subunit e1	0.005	0.384	0.481
221907_at	**TRMT61A**	tRNA methyltransferase	0.006	0.378	0.522
221650_s_at	**MED18**	mediator complex subunit 18	0.008	0.251	0.29