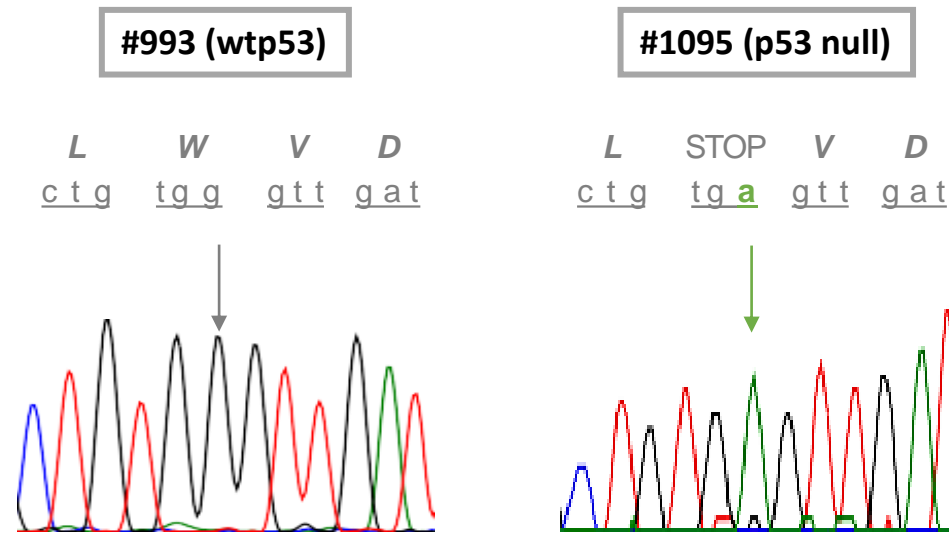


a



b

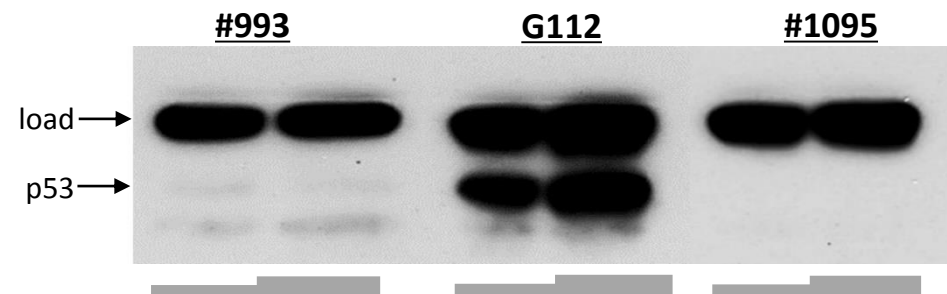
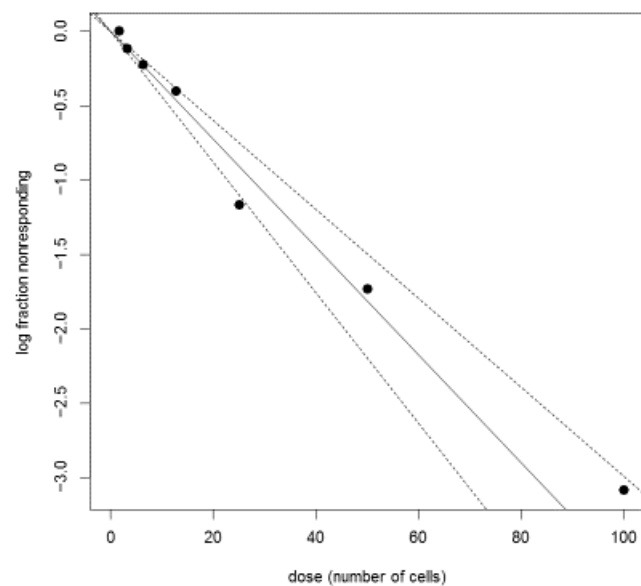


Figure S1

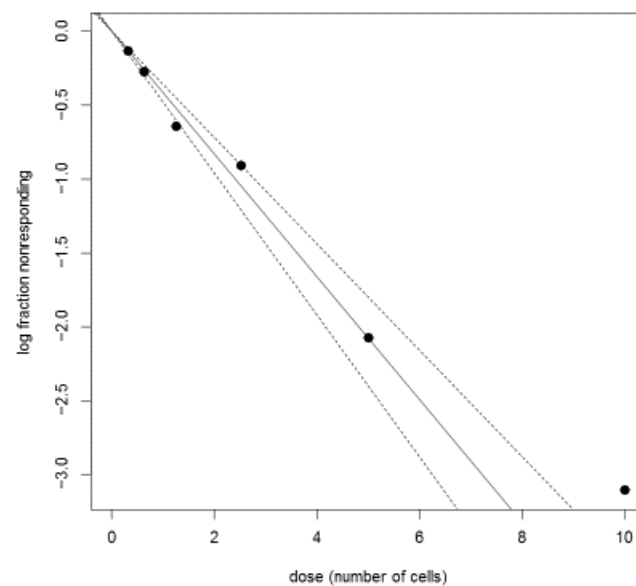
C

#993 (wtp53)



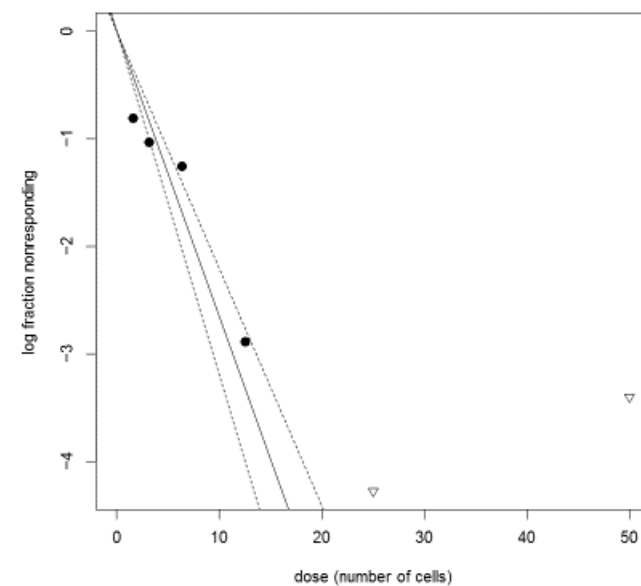
Group	Lower	Estimate	Upper
#993	33.4	27.6	22.8

G112 (R273H-p53)



Group	Lower	Estimate	Upper
G112SP	2.78	2.41	2.08

#1095 (p53 null)

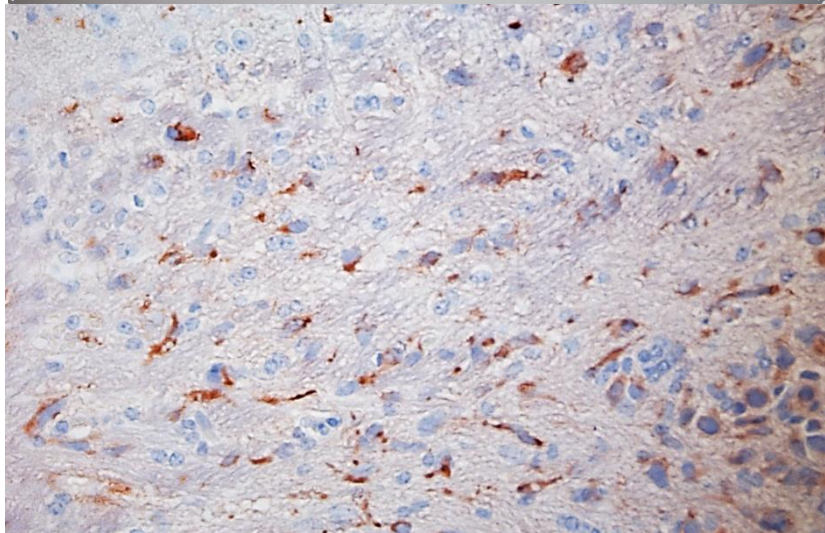
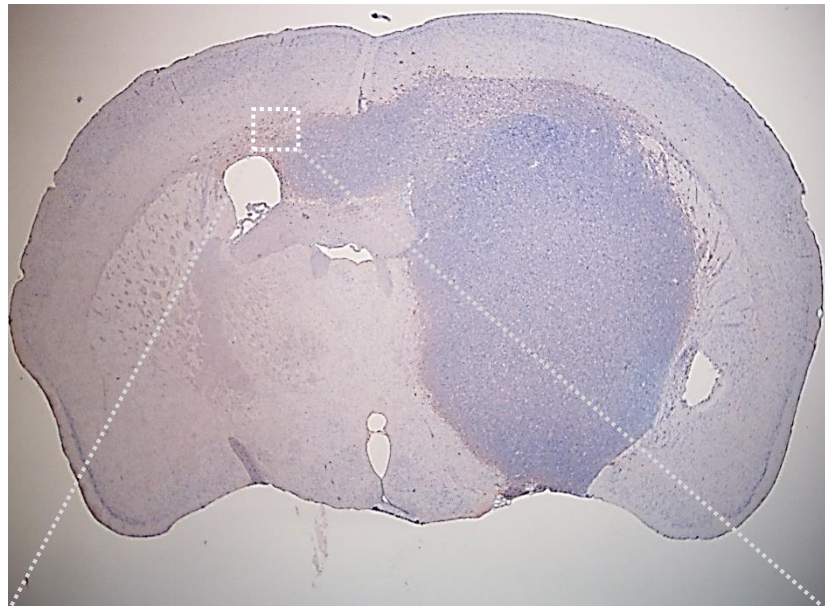


Group	Lower	Estimate	Upper
#1095	4.53	3.77	3.13

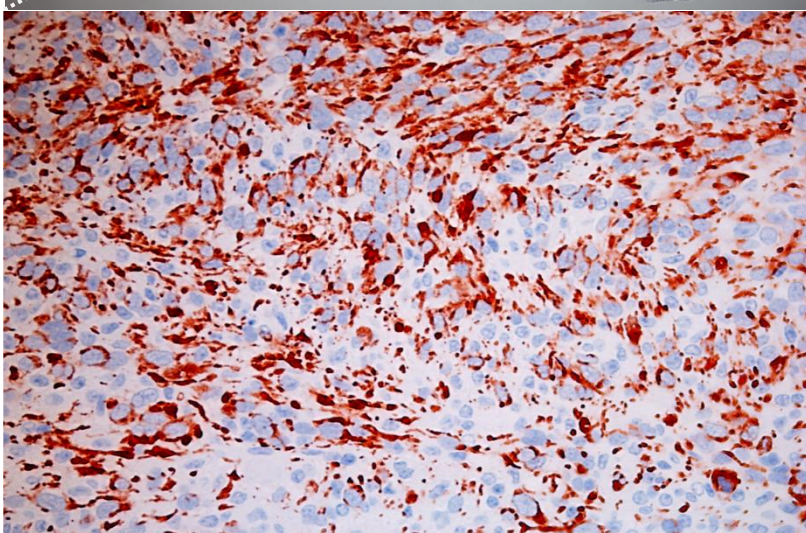
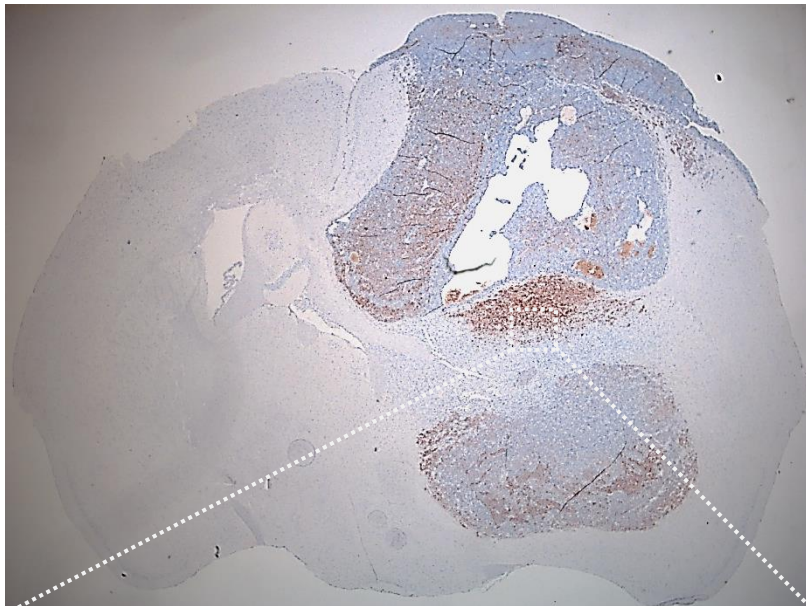
Figure S1

d

#993 (wtp53)



G112 (R273H-p53)



#1095 (p53 null)

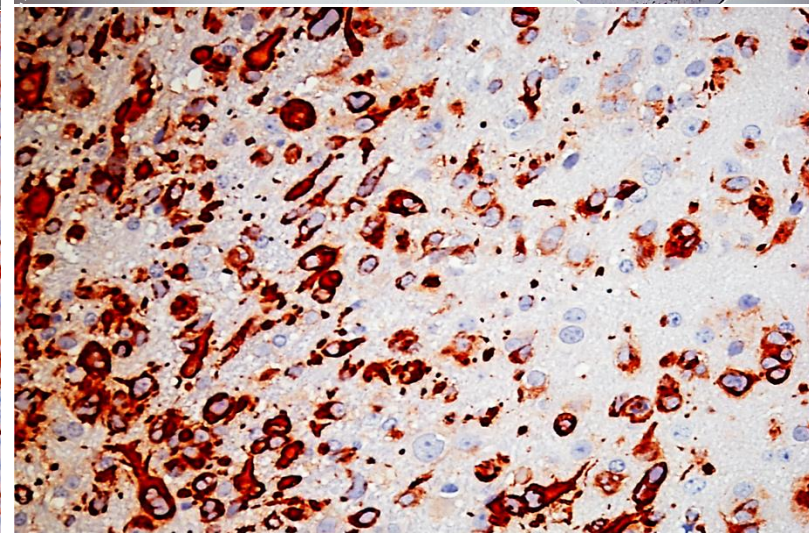
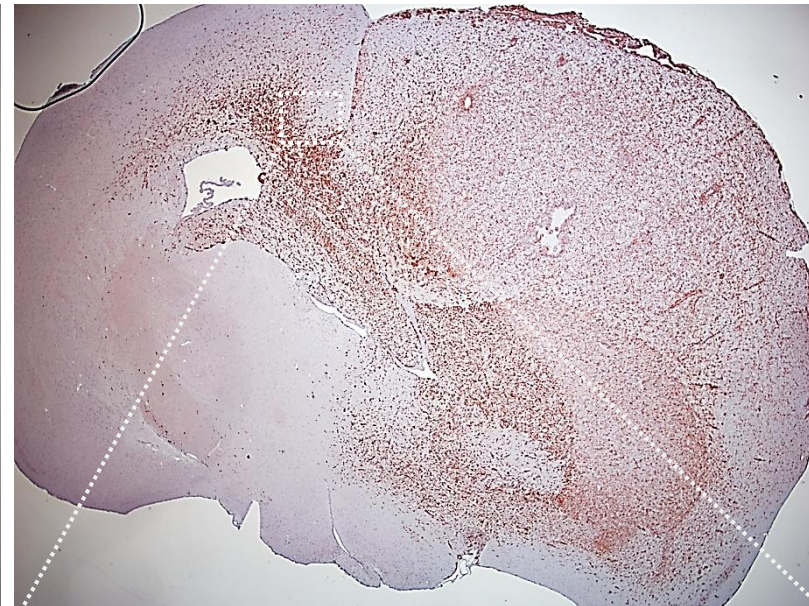


Figure S1

a)

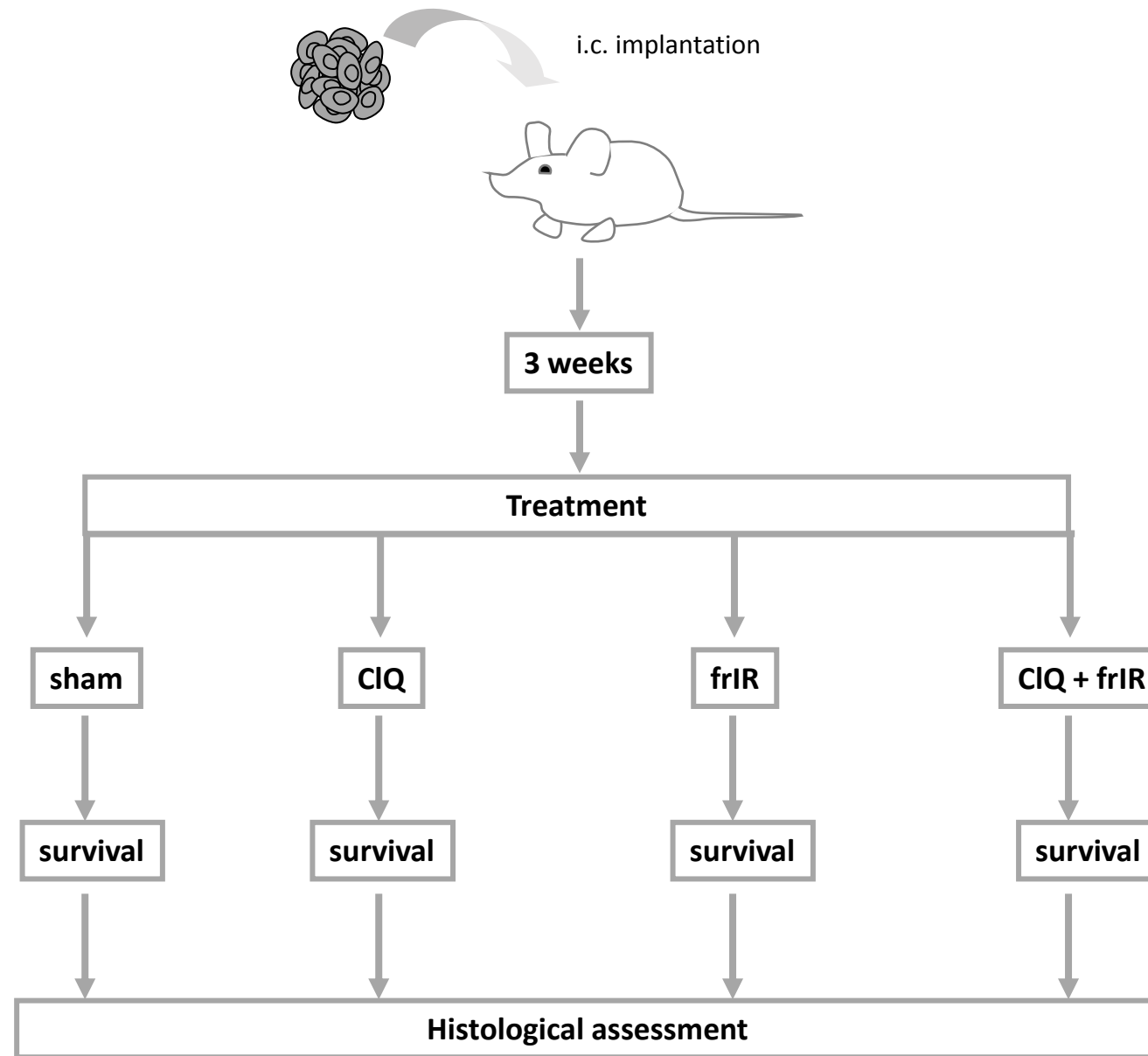


Figure S2

b)

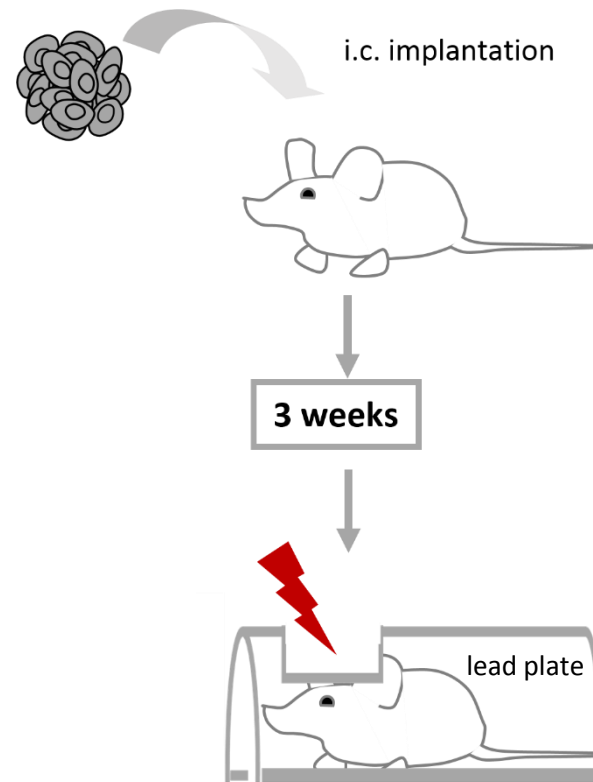


Figure S2

a

#993 (wt p53)

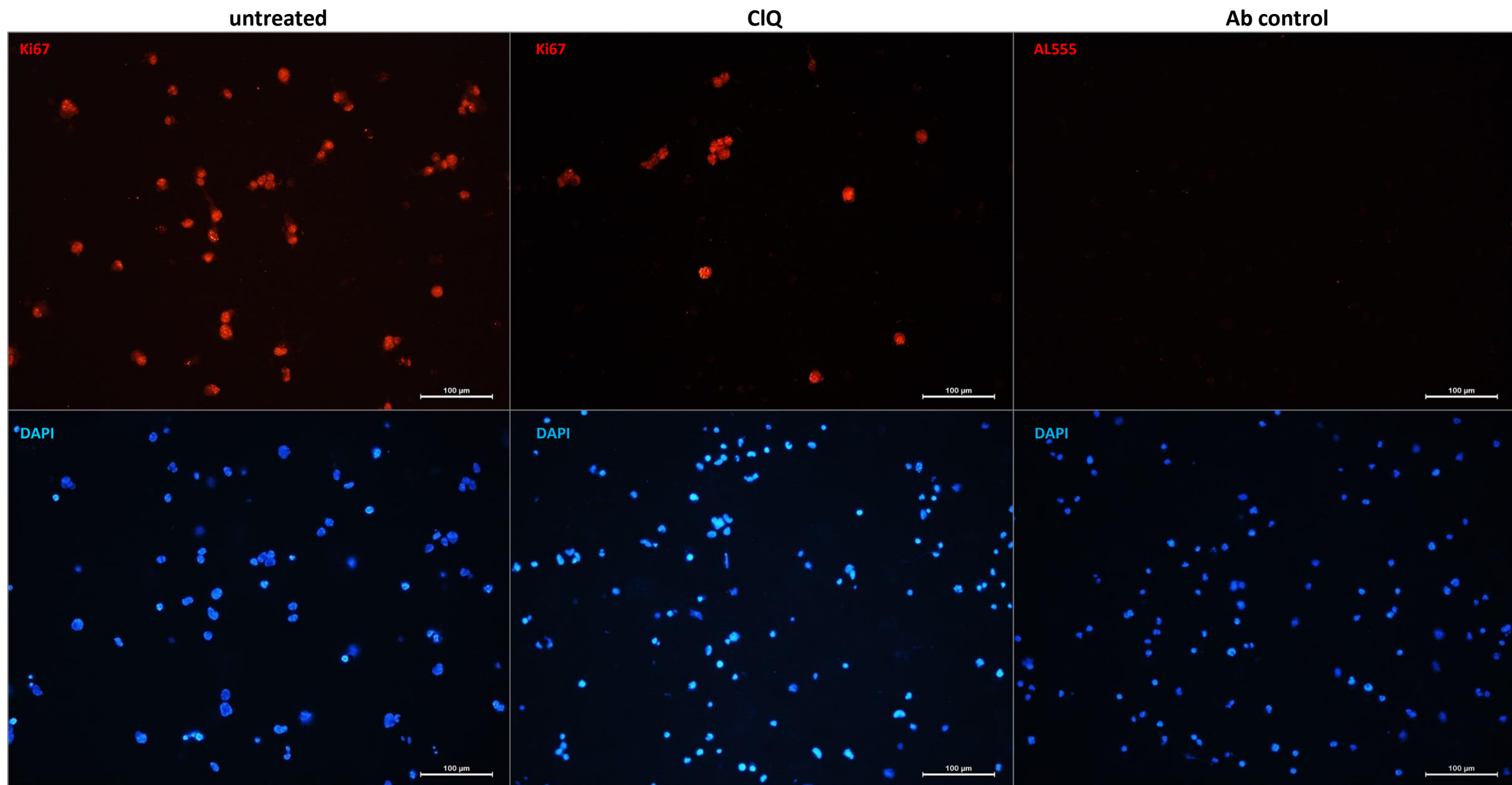


Figure S3

b

G112 (R273H-p53)

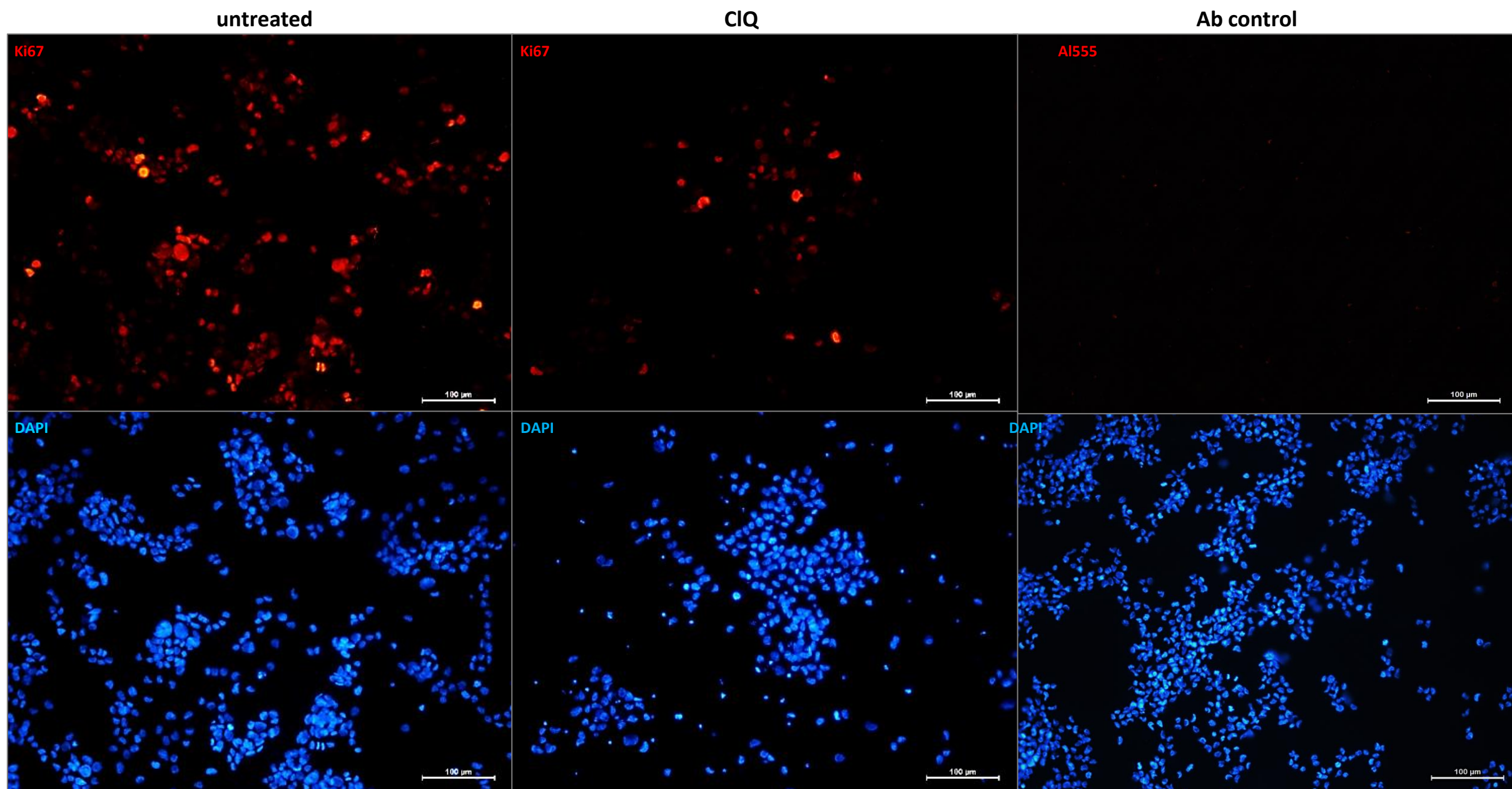


Figure S3

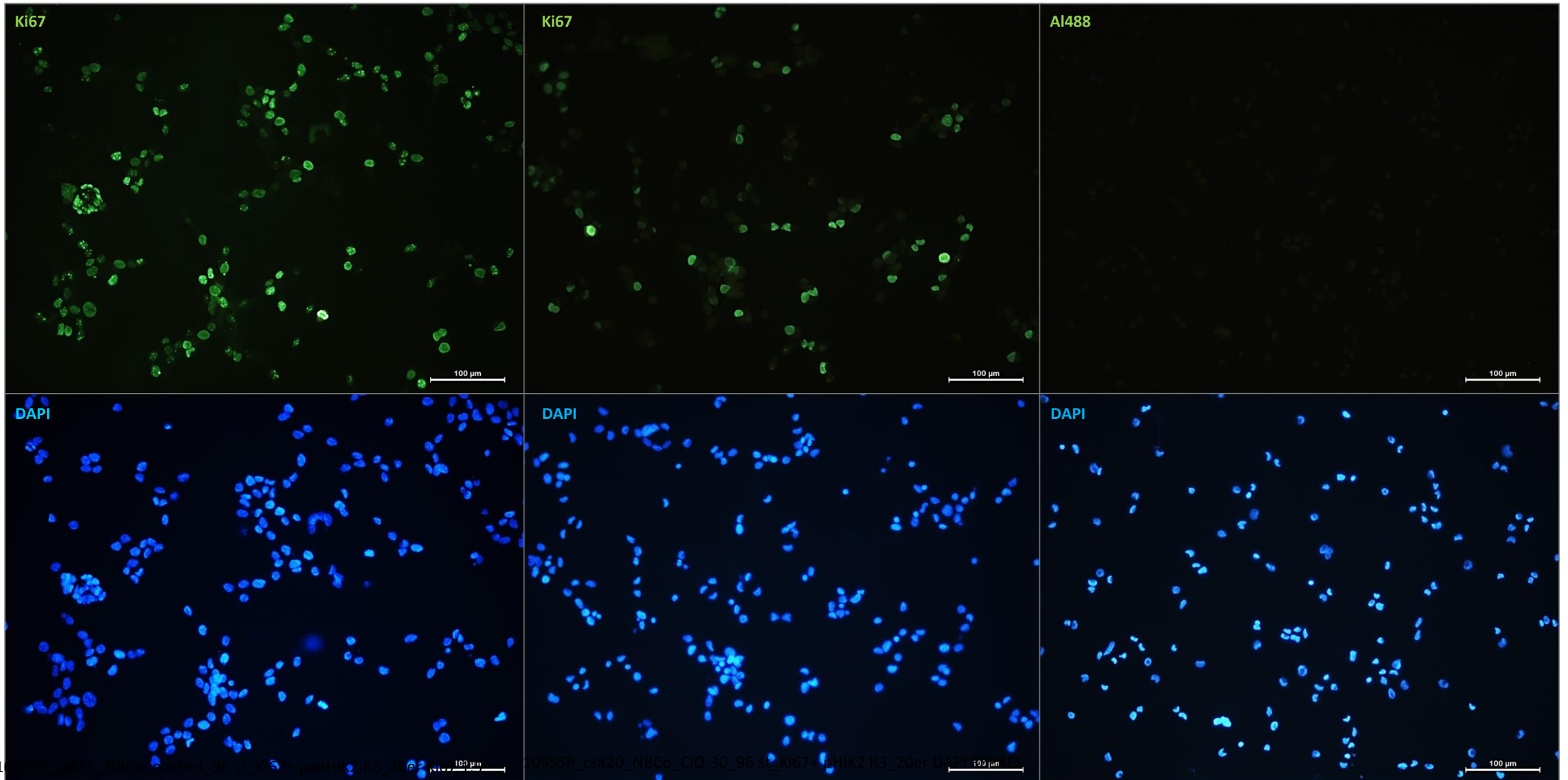
#1095 (p53 null)

C

untreated

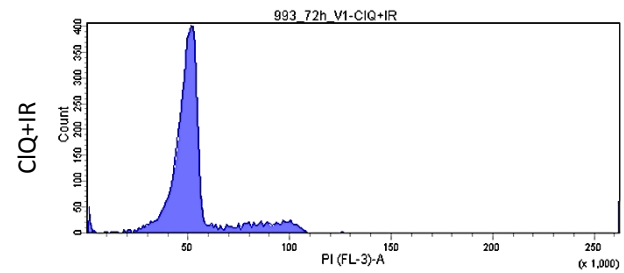
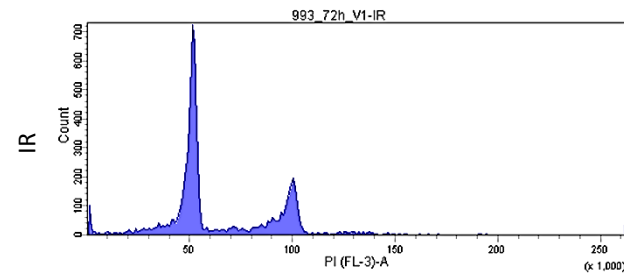
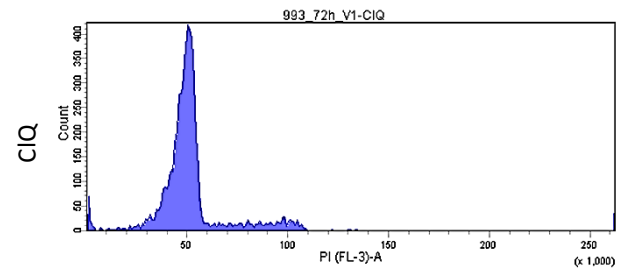
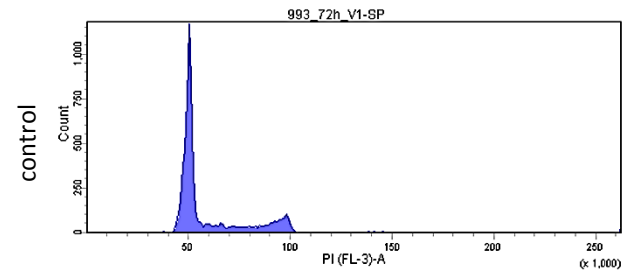
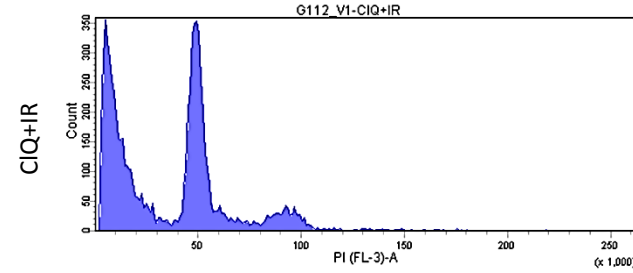
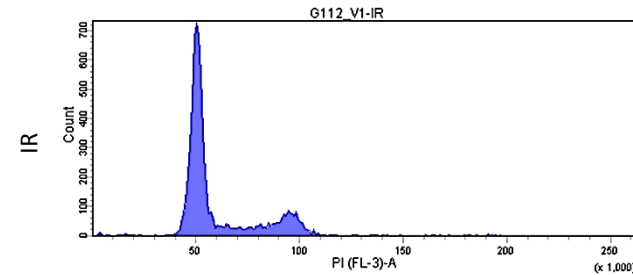
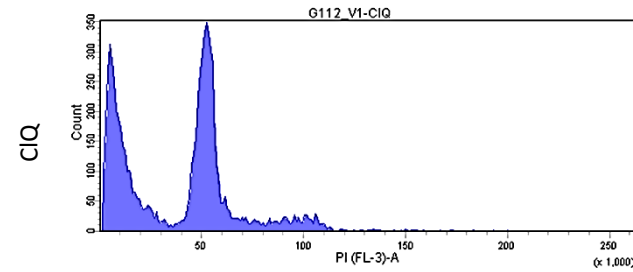
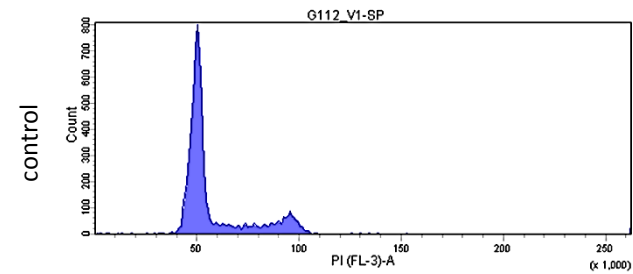
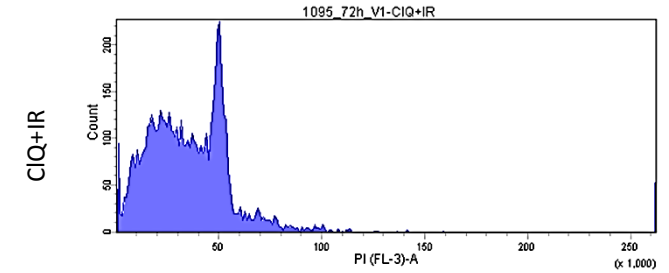
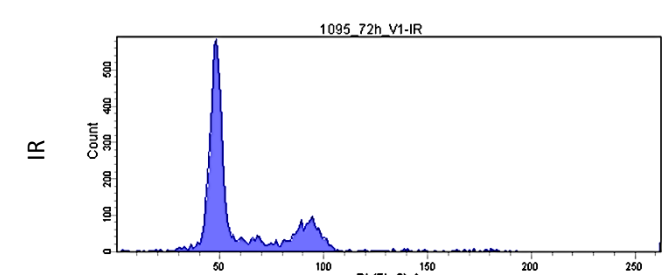
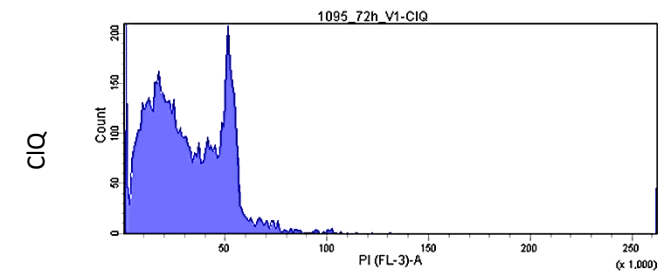
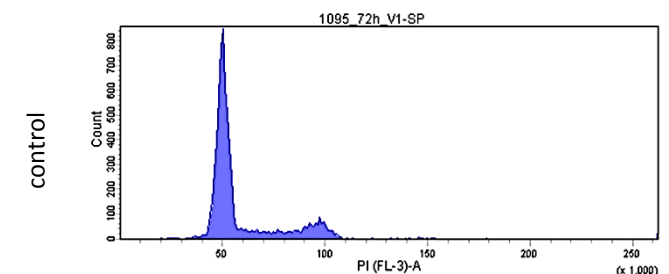
CIQ

Ab control



sec

Figure S3

#993 (wt p53)**G112 (R273H-p53)****#1095 (p53 null)****Figure S4**

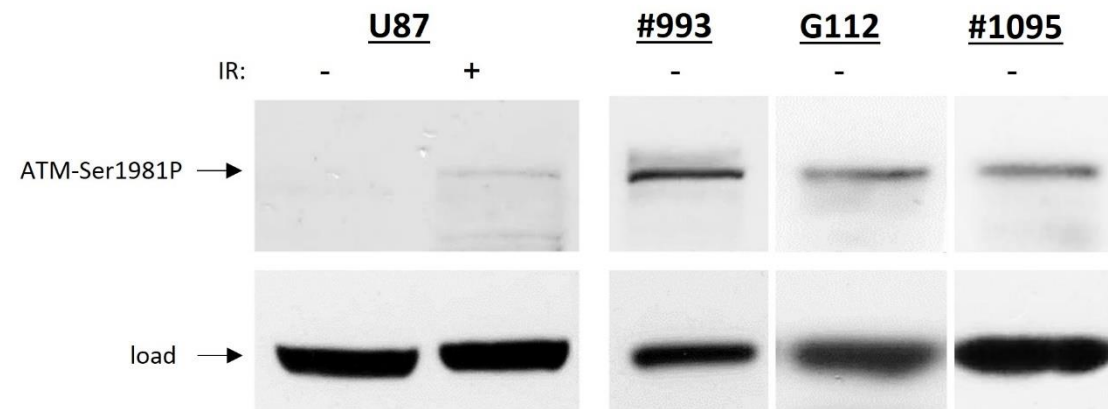


Figure S5

a

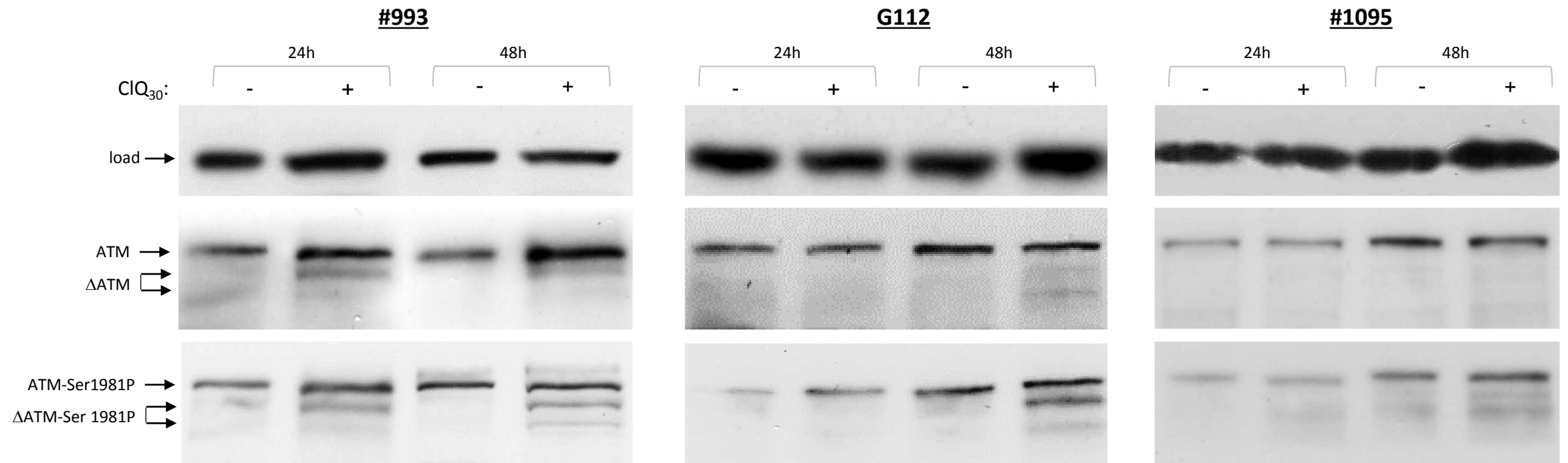


Figure S6

b

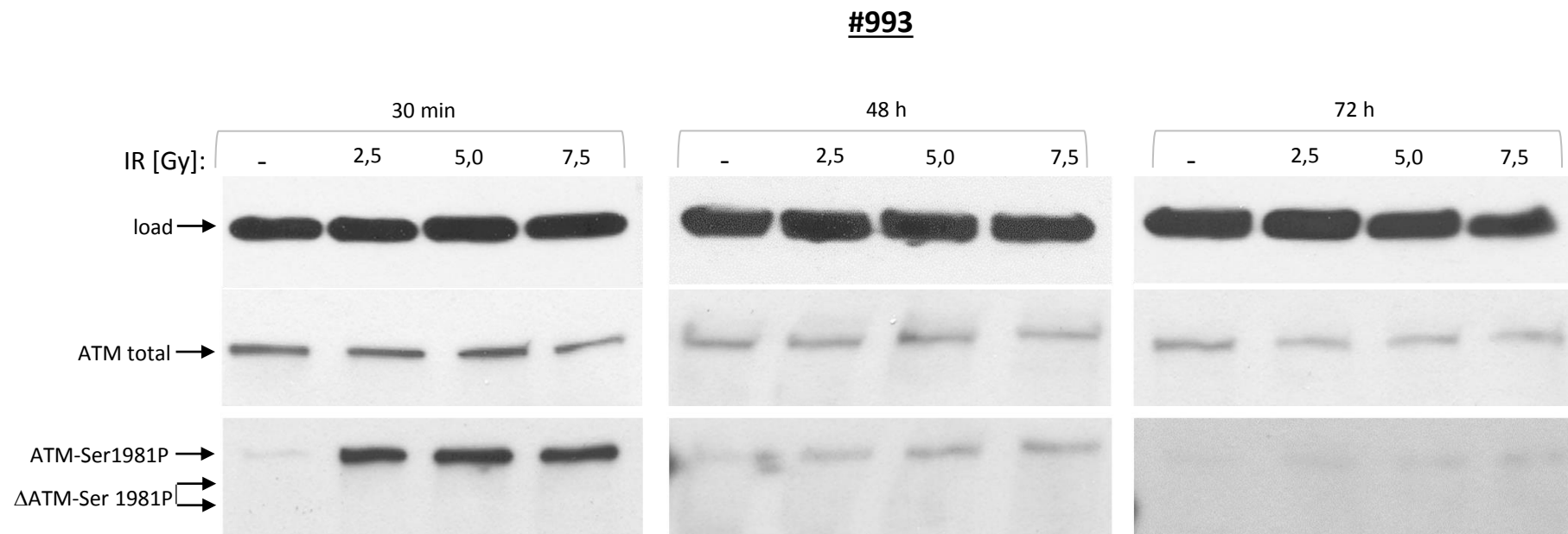


Figure S6

a

CIQ_DEGs_#993 (wtp53)

Probe	Symbol	Description	logFC #993 CIQ vs untreated	P.Value #993 CIQ vs untreated	FDR #993 CIQ vs untreated
10024_at	TROAP	trophinin associated protein (tas)	-1,089224694	1,12E-008	3,41E-006
10112_at	KIF20A	kinesin family member 20A	-1,51878522	2,22E-010	2,59E-007
1033_at	CDKN3	cyclin-dependent kinase inhibitor	-1,10629628	1,04E-008	3,25E-006
10371_at	SEMA3A	sema domain, immunoglobulin d	-1,371386841	2,95E-008	6,64E-006
10403_at	NDC80	NDC80 homolog, kinetochore co	-1,479461246	3,28E-009	1,48E-006
10615_at	SPAG5	sperm associated antigen 5	-1,125836192	1,09E-009	7,98E-007
1062_at	CENPE	centromere protein E, 312kDa	-1,426468934	4,65E-008	9,31E-006
10635_at	RAD51AP1	RAD51 associated protein 1	-1,327058656	6,99E-008	1,34E-005
10682_at	EBP	emopamil binding protein (sterol	1,25911264	8,17E-010	6,74E-007
10721_at	POLQ	polymerase (DNA directed), thet	-1,266294243	2,04E-007	3,14E-005
10733_at	PLK4	polo-like kinase 4 (Drosophila)	-1,250013612	4,05E-008	8,62E-006
11004_at	KIF2C	kinesin family member 2C	-1,34467197	3,60E-009	1,53E-006
11065_at	UBE2C	ubiquitin-conjugating enzyme E2	-1,077519291	3,40E-009	1,50E-006
11113_at	CIT	citron (rho-interacting, serine/thr	-1,058557873	2,25E-007	3,38E-005
11161_at	C14orf1	chromosome 14 open reading fra	1,119682631	5,08E-008	1,00E-005
113115_at	FAM54A	family with sequence similarity 5	-1,043804999	1,83E-007	2,87E-005
1410_at	CRYAB	crystallin, alpha B	1,026350939	7,61E-009	2,69E-006
146956_at	EME1	essential meiotic endonuclease	-1,145995374	1,12E-007	1,94E-005
150221_at	RIMBP3C	RIMS binding protein 3C	-1,42153587	0,000947503	0,035251727
150468_at	CKAP2L	cytoskeleton associated protein	-1,450643508	8,81E-011	1,59E-007
151246_at	SGOL2	shugoshin-like 2 (S. pombe)	-1,538298644	3,75E-010	4,12E-007
151648_at	SGOL1	shugoshin-like 1 (S. pombe)	-1,302146493	1,51E-008	4,20E-006
157313_at	CDCA2	cell division cycle associated 2	-1,295357771	4,49E-008	9,16E-006
157570_at	ESCO2	establishment of cohesion 1 hom	-1,598861831	2,75E-008	6,39E-006
158471_at	PRUNE2	prune homolog 2 (Drosophila)	1,207525049	8,07E-009	2,75E-006
1717_at	DHCR7	7-dehydrocholesterol reductase	1,347347924	2,24E-011	6,32E-008
1718_at	DHCR24	24-dehydrocholesterol reductase	1,001865609	5,26E-008	1,03E-005
1763_at	DNA2	DNA replication helicase 2 homc	-1,02678217	2,87E-006	0,000290317

Figure S7

b

Probe	Symbol	Description	logFC #993 CIQ vs untreated	P.Value #993 CIQ vs untreated	FDR #993 CIQ vs untreated
2170_at	FABP3	fatty acid binding protein 3, mus	2,005550665	2,42E-009	1,24E-006
2177_at	FANCD2	Fanconi anemia, complementatio	-1,160062695	8,79E-008	1,55E-005
2187_at	FANCB	Fanconi anemia, complementatio	-1,319742454	7,34E-007	9,50E-005
2194_at	FASN	fatty acid synthase	1,199029246	2,02E-008	5,23E-006
219790_at	RTKN2	rhotekin 2	-1,58672524	6,94E-008	1,34E-005
220042_at	C11orf82	chromosome 11 open reading fra	-1,059750794	1,49E-006	0,000176055
220134_at	C18orf24	chromosome 18 open reading fra	-1,159800013	1,21E-008	3,54E-006
221150_at	C13orf3	chromosome 13 open reading fra	-1,304631264	8,56E-009	2,82E-006
2222_at	FDFT1	farnesyl-diphosphate farnesyltra	1,055670855	8,54E-010	6,76E-007
2224_at	FDPS	farnesyl diphosphate synthase (f	1,339085985	3,54E-012	2,33E-008
22974_at	TPX2	TPX2, microtubule-associated, h	-1,208617691	5,11E-010	4,92E-007
22995_at	CEP152	centrosomal protein 152kDa	-1,224930239	6,91E-007	9,11E-005
23175_at	LPIN1	lipin 1	1,154855364	1,15E-008	3,45E-006
23397_at	NCAPH	non-SMC condensin I complex, s	-1,124297825	2,44E-008	5,90E-006
24137_at	KIF4A	kinesin family member 4A	-1,364296701	2,92E-008	6,64E-006
2494_at	NR5A2	nuclear receptor subfamily 5, gro	-1,074243736	5,32E-007	7,17E-005
255394_at	TCP11L2	t-complex 11 (mouse)-like 2	1,207017902	2,79E-008	6,41E-006
259266_at	ASPM	asp (abnormal spindle) homolog,	-1,374532969	7,55E-009	2,69E-006
283431_at	GAS2L3	growth arrest-specific 2 like 3	-1,362695449	1,56E-009	9,66E-007
2846_at	LPAR4	lysophosphatidic acid receptor 4	-1,117705621	2,58E-005	0,00198455
284992_at	CCDC150	coiled-coil domain containing 150	-1,377118834	2,37E-009	1,24E-006
286151_at	FBXO43	F-box protein 43	-1,181930841	2,04E-008	5,23E-006
29127_at	RACGAP1	Rac GTPase activating protein 1	-1,072090453	1,72E-008	4,73E-006
3161_at	HMMR	hyaluronan-mediated motility rec	-1,124591612	1,43E-007	2,36E-005
343099_at	CCDC18	coiled-coil domain containing 18	-1,103023973	1,30E-007	2,21E-005
347240_at	KIF24	kinesin family member 24	-1,001927841	1,91E-007	2,98E-005
347731_at	LRRTM3	leucine rich repeat transmembra	-1,054923233	4,63E-008	9,31E-006
3638_at	INSIG1	insulin induced gene 1	1,444487764	1,39E-011	4,75E-008
375444_at	C5orf34	chromosome 5 open reading fran	-1,088822218	5,72E-007	7,60E-005
3832_at	KIF11	kinesin family member 11	-1,156423099	7,04E-007	9,17E-005
39_at	ACAT2	acetyl-Coenzyme A acetyltransf	1,274906128	1,93E-010	2,38E-007

Figure S7

C

Probe	Symbol	Description	logFC #993 CIQ vs untreated	P.Value #993 CIQ vs untreated	FDR #993 CIQ vs untreated
4047_at	LSS	lanosterol synthase (2,3-oxidosc	1,122695118	3,54E-008	7,61E-006
4085_at	MAD2L1	MAD2 mitotic arrest deficient-like	-1,45495862	1,75E-008	4,76E-006
4288_at	MKI67	antigen identified by monoclonal	-1,122972876	7,75E-008	1,43E-005
4597_at	MVD	mevalonate (diphospho) decarbo	1,132866547	7,88E-010	6,74E-007
4603_at	MYBL1	v-myb myeloblastosis viral onco	-1,160321916	3,89E-007	5,61E-005
4751_at	NEK2	NIMA (never in mitosis gene a)-r	-1,260741692	2,44E-009	1,24E-006
50814_at	NSDHL	NAD(P) dependent steroid dehyd	1,253678078	3,94E-011	9,74E-008
51203_at	NUSAP1	nucleolar and spindle associated	-1,269184356	7,87E-009	2,73E-006
51478_at	HSD17B7	hydroxysteroid (17-beta) dehydro	1,222537624	0,00013483	0,00760309
51512_at	GTSE1	G-2 and S-phase expressed 1	-1,143496205	1,21E-008	3,54E-006
53353_at	LRP1B	low density lipoprotein-related pr	1,022647953	4,71E-007	6,66E-005
5347_at	PLK1	polo-like kinase 1 (Drosophila)	-1,24526622	1,34E-009	8,55E-007
54443_at	ANLN	anillin, actin binding protein	-1,388659462	1,06E-009	7,98E-007
54478_at	FAM64A	family with sequence similarity 6	-1,228741633	8,95E-008	1,57E-005
54821_at	ERCC6L	excision repair cross-complemen	-1,615998378	2,03E-008	5,23E-006
54873_at	PALMD	palmdelphin	-1,026847857	4,90E-007	6,83E-005
54892_at	NCAPG2	non-SMC condensin II complex,	-1,055511832	5,54E-009	2,07E-006
55010_at	C12orf48	chromosome 12 open reading fra	-1,378058059	8,46E-008	1,51E-005
55143_at	CDCA8	cell division cycle associated 8	-1,201909605	1,19E-006	0,000147179
55215_at	FANCI	Fanconi anemia, complementatio	-1,0866537	5,07E-007	6,97E-005
55247_at	NEIL3	nei endonuclease VIII-like 3 (E. c	-1,474875965	2,26E-009	1,24E-006
55320_at	C14orf106	chromosome 14 open reading fra	-1,181587058	8,28E-008	1,50E-005
55329_at	MNS1	meiosis-specific nuclear structur	-1,351894559	1,28E-007	2,19E-005
55345_at	C4orf21	chromosome 4 open reading fran	-1,055603862	1,27E-006	0,000154107
55355_at	HJURP	Holliday junction recognition prot	-1,190856709	7,39E-009	2,69E-006
55388_at	MCM10	minichromosome maintenance c	-1,034739786	2,76E-006	0,000282633
55635_at	DEPDC1	DEP domain containing 1	-1,203446411	1,39E-007	2,32E-005
55771_at	PRR11	proline rich 11	-1,202912243	3,88E-009	1,54E-006
55789_at	DEPDC1B	DEP domain containing 1B	-1,244595019	9,81E-009	3,13E-006
55872_at	PBK	PDZ binding kinase	-1,601857891	3,90E-009	1,54E-006

Figure S7

d

Probe	Symbol	Description	logFC #993 CIQ vs untreated	P.Value #993 CIQ vs untreated	FDR #993 CIQ vs untreated
55902_at	ACSS2	acyl-CoA synthetase short-chain	1,270824058	1,24E-010	1,98E-007
56992_at	KIF15	kinesin family member 15	-1,473551451	3,04E-008	6,75E-006
57082_at	CASC5	cancer susceptibility candidate 5	-1,493793006	2,72E-008	6,39E-006
57405_at	SPC25	SPC25, NDC80 kinetochore component	-1,472807972	5,28E-012	2,61E-008
57650_at	KIAA1524	KIAA1524	-1,209168964	4,33E-008	8,95E-006
5983_at	RFC3	replication factor C (activator 1) 3	-1,054531028	2,69E-008	6,39E-006
6241_at	RRM2	ribonucleotide reductase M2 polypeptide	-1,138488224	1,05E-008	3,25E-006
6307_at	SC4MOL	sterol-C4-methyl oxidase-like	1,17905442	1,80E-008	4,81E-006
6319_at	SCD	stearoyl-CoA desaturase (delta-9)	1,275894886	2,80E-014	5,53E-010
64105_at	CENPK	centromere protein K	-1,08765816	2,33E-008	5,69E-006
64151_at	NCAPG	non-SMC condensin I complex, subunit G	-1,274424255	2,08E-009	1,20E-006
6491_at	STIL	SCL/TAL1 interrupting locus	-1,14454901	1,38E-008	3,95E-006
6565_at	SLC15A2	solute carrier family 15 (H ⁺ /peptide)	-1,047785742	1,00E-005	0,000872656
675_at	BRCA2	breast cancer 2, early onset	-1,013227035	1,22E-006	0,000150047
677807_at	SNORA22	small nucleolar RNA, H/ACA box	1,071728985	0,001066584	0,038037664
6790_at	AURKA	aurora kinase A	-1,125210189	8,51E-009	2,82E-006
699_at	BUB1	budding uninhibited by benzimidazole	-1,408561792	1,29E-009	8,48E-007
7018_at	TF	transferrin	1,623492994	4,35E-009	1,69E-006
701_at	BUB1B	budding uninhibited by benzimidazole	-1,433215512	6,59E-011	1,30E-007
7108_at	TM7SF2	transmembrane 7 superfamily member	1,339665049	5,01E-010	4,92E-007
7143_at	TNR	tenascin R (restrictin, janusin)	-1,140439309	1,69E-005	0,001392452
7153_at	TOP2A	topoisomerase (DNA) II alpha 17	-1,222894022	2,11E-009	1,20E-006
7272_at	TTK	TTK protein kinase	-1,707133652	1,59E-010	2,10E-007
7516_at	XRCC2	X-ray repair complementing defective	-1,011422703	7,40E-007	9,51E-005
79071_at	ELOVL6	ELOVL family member 6, elongation	1,003205781	3,96E-007	5,68E-005
79733_at	E2F8	E2F transcription factor 8	-1,302816466	1,98E-009	1,19E-006
79801_at	SHCBP1	SHC SH2-domain binding protein	-1,219004921	3,64E-009	1,53E-006
7984_at	ARHGEF5	Rho guanine nucleotide exchange	1,590642658	0,000468802	0,02071204
79866_at	C13orf34	chromosome 13 open reading frame	-1,486829361	6,54E-011	1,30E-007
81624_at	DIAPH3	diaphanous homolog 3 (Drosophila)	-1,173999252	2,26E-007	3,38E-005
81930_at	KIF18A	kinesin family member 18A	-1,540900917	3,36E-008	7,30E-006

Figure S7

e

Probe	Symbol	Description	logFC #993 CIQ vs untreated	P.Value #993 CIQ vs untreated	FDR #993 CIQ vs untreated
8342_at	HIST1H2BM	histone cluster 1, H2bm	-1,053868785	2,55E-005	0,001967854
83461_at	CDCA3	cell division cycle associated 3	-1,433633318	2,68E-012	2,33E-008
83540_at	NUF2	NUF2, NDC80 kinetochore comp	-1,310186527	2,53E-009	1,25E-006
83990_at	BRIP1	BRCA1 interacting protein C-terr	-1,034453779	2,19E-006	0,000240308
84824_at	FCRLA	Fc receptor-like A	1,158022788	1,40E-010	1,98E-007
890_at	CCNA2	cyclin A2	-1,254531232	2,72E-009	1,28E-006
891_at	CCNB1	cyclin B1	-1,503325343	1,44E-011	4,75E-008
89839_at	ARHGAP11E	Rho GTPase activating protein 1	-1,489673573	8,84E-009	2,87E-006
9055_at	PRC1	protein regulator of cytokinesis 1	-1,235860321	2,73E-009	1,28E-006
9133_at	CCNB2	cyclin B2	-1,239027552	4,34E-008	8,95E-006
9134_at	CCNE2	cyclin E2	-1,042230477	1,25E-006	0,000152591
9156_at	EXO1	exonuclease 1	-1,254033153	3,58E-007	5,21E-005
92211_at	PCDH21	protocadherin 21	1,146903181	1,16E-009	8,23E-007
9232_at	PTTG1	pituitary tumor-transforming 1	-1,110943355	7,05E-008	1,34E-005
9415_at	FADS2	fatty acid desaturase 2	1,055782386	2,79E-009	1,29E-006
9493_at	KIF23	kinesin family member 23	-1,427337386	1,38E-010	1,98E-007
9585_at	KIF20B	kinesin family member 20B	-1,270617743	2,68E-007	3,96E-005
9768_at	KIAA0101	KIAA0101	-1,144136781	4,81E-007	6,75E-005
9787_at	DLGAP5	discs, large (Drosophila) homolo	-1,520557272	1,22E-009	8,32E-007
9824_at	ARHGAP11A	Rho GTPase activating protein 1	-1,181800944	5,43E-007	7,26E-005
9833_at	MELK	maternal embryonic leucine zipp	-1,076852765	4,30E-008	8,95E-006
983_at	CDC2	cell division cycle 2, G1 to S and	-1,563353634	7,09E-010	6,38E-007
9928_at	KIF14	kinesin family member 14	-1,401389389	3,81E-009	1,54E-006
995_at	CDC25C	cell division cycle 25 homolog C	-1,261221854	1,49E-008	4,20E-006

Figure S7

a

CIQ_DEGs_G112 (R273H)

Probe	Symbol	Description	logFC G112 CIQ vs untr	P.Value G112 CIQ vs untr	FDR G112 CIQ vs untr
100033805_at	SNORD115-31	small nucleolar RNA, C/D box 115-31	-0,711657548	1,96E-006	6,54E-005
10007_at	GNPDA1	glucosamine-6-phosphate deaminase 1	0,772892	5,71E-012	1,53E-009
100129196_at	LOC100129196	similar to hCG2033298	-0,616059764	7,91E-005	0,001399894
100129762_at	LOC100129762	similar to KIAA0367	1,103630612	5,42E-015	4,13E-012
100133188_at	LOC100133364	hypothetical LOC100133364	0,91738411	3,21E-014	1,99E-011
10085_at	EDIL3	EGF-like repeats and discoidin I-like domains 3	-1,069723465	4,65E-015	3,68E-012
10112_at	KIF20A	kinesin family member 20A	-0,704770275	3,55E-011	6,75E-009
10253_at	SPRY2	sprouty homolog 2 (Drosophila)	-0,946604911	2,78E-014	1,83E-011
10371_at	SEMA3A	sema domain, immunoglobulin domain (Ig), short b	-0,734522097	8,19E-012	2,11E-009
10437_at	IFI30	interferon, gamma-inducible protein 30	1,079246586	1,21E-013	5,30E-011
10457_at	GPNUMB	glycoprotein (transmembrane) numb	2,311213114	6,03E-023	1,19E-018
10493_at	VAT1	vesicle amine transport protein 1 homolog (T. califc	0,663255905	2,21E-010	3,24E-008
10577_at	NPC2	Niemann-Pick disease, type C2	1,004417609	1,18E-013	5,30E-011
10769_at	PLK2	polo-like kinase 2 (Drosophila)	-0,585759398	1,31E-009	1,40E-007
10891_at	PPARGC1A	peroxisome proliferator-activated receptor gamma,	0,698675129	2,52E-012	7,67E-010
11010_at	GLIPR1	GLI pathogenesis-related 1	-0,860821051	5,12E-014	2,60E-011
1116_at	CHI3L1	chitinase 3-like 1 (cartilage glycoprotein-39)	-0,646882965	3,46E-011	6,75E-009
112770_at	C1orf85	chromosome 1 open reading frame 85	0,585853019	1,38E-010	2,17E-008
113146_at	AHNAK2	AHNAK nucleoprotein 2	0,596022265	5,59E-009	4,81E-007
114907_at	FBXO32	F-box protein 32	1,153858498	9,41E-016	1,02E-012
116496_at	FAM129A	family with sequence similarity 129, member A	0,776804015	1,54E-012	4,83E-010
1183_at	CLCN4	chloride channel 4	0,592528217	3,04E-010	4,23E-008
1186_at	CLCN7	chloride channel 7	0,758483866	4,17E-011	7,72E-009
1193_at	CLIC2	chloride intracellular channel 2	0,762183175	5,06E-012	1,39E-009
1200_at	TPP1	tripeptidyl peptidase I	1,190330849	9,33E-017	2,05E-013
1244_at	ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	0,630896828	1,07E-012	3,60E-010
128344_at	C1orf88	chromosome 1 open reading frame 88	0,653802258	9,36E-010	1,06E-007
128637_at	TBC1D20	TBC1 domain family, member 20	0,638969224	2,47E-013	1,00E-010
134429_at	STARD4	StAR-related lipid transfer (START) domain contain	0,872170769	5,87E-013	2,08E-010

Figure S8

b

Probe	Symbol	Description	logFC G112 CIQ vs untr	P.Value G112 CIQ vs untr	FDR G112 CIQ vs untr
138639_at	PTPDC1	protein tyrosine phosphatase domain containing 1	0,893940432	1,88E-015	1,77E-012
1435_at	CSF1	colony stimulating factor 1 (macrophage)	0,807308891	8,32E-014	4,02E-011
1491_at	CTH	cystathionase (cystathionine gamma-lyase)	0,699884596	2,55E-011	5,43E-009
1497_at	CTNS	cystinosis, nephropathic	0,612474241	2,51E-009	2,42E-007
1509_at	CTSD	cathepsin D	0,62345171	4,59E-011	8,33E-009
153222_at	C5orf41	chromosome 5 open reading frame 41	0,610044575	7,25E-009	6,01E-007
158471_at	PRUNE2	prune homolog 2 (Drosophila)	1,095021586	2,23E-016	4,02E-013
162394_at	SLFN5	schlafen family member 5	1,087347333	2,90E-016	4,42E-013
1649_at	DDIT3	DNA-damage-inducible transcript 3	1,608247203	2,40E-019	1,19E-015
1717_at	DHCR7	7-dehydrocholesterol reductase	0,800342565	1,02E-014	7,18E-012
1848_at	DUSP6	dual specificity phosphatase 6	-1,439855174	7,01E-018	2,31E-014
1958_at	EGR1	early growth response 1	-1,025198827	9,76E-016	1,02E-012
202374_at	STK32A	serine/threonine kinase 32A	0,737348076	3,94E-010	5,28E-008
2035_at	EPB41	erythrocyte membrane protein band 4.1 (elliptocyte)	0,7715115	1,00E-012	3,43E-010
2113_at	ETS1	vets erythroblastosis virus E26 oncogene homolog 1	0,611114762	1,90E-012	5,86E-010
2118_at	ETV4	ets variant gene 4 (E1A enhancer binding protein, ets-1)	-1,106373552	8,68E-017	2,05E-013
2119_at	ETV5	ets variant gene 5 (ets-related molecule)	-0,850582169	1,13E-013	5,30E-011
2180_at	ACSL1	acyl-CoA synthetase long-chain family member 1	0,871186309	4,42E-012	1,25E-009
218_at	ALDH3A1	aldehyde dehydrogenase 3 family, member A1	-0,688470108	3,21E-011	6,49E-009
2194_at	FASN	fatty acid synthase	1,073975374	2,15E-014	1,46E-011
2196_at	FAT2	FAT tumor suppressor homolog 2 (Drosophila)	-1,169895931	9,20E-016	1,02E-012
2222_at	FDFT1	farnesyl-diphosphate farnesyltransferase 1	0,672728934	4,43E-012	1,25E-009
222484_at	LNK2	ligand of numb-protein X 2	0,595088032	5,21E-010	6,69E-008
2224_at	FDPS	farnesyl diphosphate synthase (farnesyl pyrophosphatase)	0,764947299	1,37E-011	3,15E-009
2239_at	GPC4	glypican 4	-0,722340733	1,15E-009	1,25E-007
22822_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	-0,662269737	8,84E-012	2,24E-009
22885_at	ABLIM3	actin binding LIM protein family, member 3	0,90697846	4,36E-014	2,33E-011
23007_at	PLCH1	phospholipase C, eta 1	-0,810270617	9,92E-011	1,61E-008
23175_at	LPIN1	lipin 1	1,230766508	1,20E-018	4,74E-015
2353_at	FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog 1	-0,660050583	6,52E-010	7,96E-008

Figure S8

C

Probe	Symbol	Description	logFC G112 CIQ vs untr	P.Value G112 CIQ vs untr	FDR G112 CIQ vs untr
23645_at	PPP1R15A	protein phosphatase 1, regulatory (inhibitor) subun	0,667043088	1,01E-009	1,12E-007
24137_at	KIF4A	kinesin family member 4A	-0,585464805	2,48E-007	1,14E-005
2512_at	FTL	ferritin, light polypeptide	0,950172466	2,30E-008	1,57E-006
254958_at	REXO1L1	REX1, RNA exonuclease 1 homolog (S. cerevisiae)	-0,824506223	0,001323898	0,012665015
255394_at	TCP11L2	t-complex 11 (mouse)-like 2	0,749514758	7,26E-011	1,23E-008
255743_at	NPNT	nephronectin	-0,608863384	3,75E-011	7,00E-009
255928_at	SYT14	synaptotagmin XIV	0,610114951	7,89E-010	9,30E-008
256987_at	SERINC5	serine incorporator 5	0,848234005	2,83E-012	8,50E-010
25925_at	ZNF521	zinc finger protein 521	-0,70464454	5,68E-011	1,01E-008
25928_at	SOSTDC1	sclerostin domain containing 1	1,11510801	1,20E-013	5,30E-011
26278_at	SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	-0,627395584	6,21E-010	7,68E-008
2669_at	GEM	GTP binding protein overexpressed in skeletal mus	1,007800216	7,45E-015	5,46E-012
2673_at	GFPT1	glutamine-fructose-6-phosphate transaminase 1	0,608666162	1,57E-011	3,49E-009
27303_at	RBMS3	RNA binding motif, single stranded interacting prot	-0,635668305	4,44E-010	5,86E-008
2799_at	GNS	glucosamine (N-acetyl)-6-sulfatase	0,675557754	8,49E-010	9,83E-008
2805_at	GOT1	glutamic-oxaloacetic transaminase 1, soluble (asp	0,790836376	1,65E-010	2,55E-008
2835_at	GPR12	G protein-coupled receptor 12	-0,595811745	4,65E-006	0,000137228
28526_at	TRDC	T cell receptor delta constant	-1,100143064	3,49E-014	2,03E-011
285605_at	DTWD2	DTW domain containing 2	0,978515203	8,66E-013	3,01E-010
285888_at	CNPY1	canopy 1 homolog (zebrafish)	-0,630820844	5,96E-011	1,03E-008
287_at	ANK2	ankyrin 2, neuronal	0,663831171	8,75E-010	1,01E-007
28951_at	TRIB2	tribbles homolog 2 (Drosophila)	-0,741080095	9,76E-011	1,61E-008
2896_at	GRN	granulin	0,762058638	3,64E-011	6,87E-009
3037_at	HAS2	hyaluronan synthase 2	-0,6196211	2,55E-010	3,66E-008
3073_at	HEXA	hexosaminidase A (alpha polypeptide)	0,812087917	1,85E-013	7,80E-011
3156_at	HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	0,694954585	2,04E-010	3,08E-008
3157_at	HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase	0,779985102	1,34E-013	5,78E-011
3162_at	HMOX1	heme oxygenase (decycling) 1	0,8145864	2,90E-011	6,00E-009
3304_at	HSPA1B	heat shock 70kDa protein 1B	0,665467775	2,39E-008	1,61E-006
3371_at	TNC	tenascin C	0,727636826	4,70E-014	2,45E-011
340529_at	PABPC1L2A	poly(A) binding protein, cytoplasmic 1-like 2A	-0,753450827	9,70E-005	0,001650875

Figure S8

d

Probe	Symbol	Description	logFC G112 CIQ vs untr	P.Value G112 CIQ vs untr	FDR G112 CIQ vs untr
3417_at	IDH1	isocitrate dehydrogenase 1 (NADP), soluble	0,839432429	5,34E-012	1,45E-009
347735_at	SERINC2	serine incorporator 2	0,714313465	1,74E-011	3,79E-009
3638_at	INSIG1	insulin induced gene 1	0,906294292	3,61E-014	2,04E-011
3782_at	KCNN3	potassium intermediate/small conductance calciur	-0,589982612	8,47E-009	6,87E-007
387758_at	FIBIN	fin bud initiation factor	0,594456774	3,15E-007	1,40E-005
3934_at	LCN2	lipocalin 2	0,714444612	2,29E-009	2,24E-007
3955_at	LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosamir	-0,760487235	1,14E-011	2,75E-009
401190_at	RGS7BP	regulator of G-protein signaling 7 binding protein	0,613849867	1,03E-007	5,55E-006
4047_at	LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol	1,047239054	1,74E-016	3,44E-013
4071_at	TM4SF1	transmembrane 4 L six family member 1	-0,705102317	4,70E-013	1,72E-010
4074_at	M6PR	mannose-6-phosphate receptor (cation dependent)	0,594166277	1,01E-009	1,12E-007
4323_at	MMP14	matrix metalloproteinase 14 (membrane-inserted)	0,740108868	1,17E-012	3,85E-010
440015_at	LOC440015	similar to double homeobox, 4	-0,614689558	4,56E-005	0,000901033
467_at	ATF3	activating transcription factor 3	0,596587984	6,17E-011	1,05E-008
4688_at	NCF2	neutrophil cytosolic factor 2	0,704383173	2,71E-011	5,70E-009
4758_at	NEU1	sialidase 1 (lysosomal sialidase)	1,251878833	2,81E-016	4,42E-013
4779_at	NFE2L1	nuclear factor (erythroid-derived 2)-like 1	0,749653515	1,93E-011	4,16E-009
482_at	ATP1B2	ATPase, Na ⁺ /K ⁺ transporting, beta 2 polypeptide	-0,64060874	9,19E-012	2,27E-009
4856_at	NOV	nephroblastoma overexpressed gene	1,720341681	3,97E-020	2,62E-016
4919_at	ROR1	receptor tyrosine kinase-like orphan receptor 1	1,02787474	7,56E-017	2,05E-013
50650_at	ARHGEF3	Rho guanine nucleotide exchange factor (GEF) 3	0,589473809	2,72E-009	2,61E-007
5184_at	PEPD	peptidase D	0,652830475	3,31E-011	6,63E-009
5208_at	PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphata	0,840089563	1,18E-011	2,77E-009
5327_at	PLAT	plasminogen activator, tissue	-1,878928756	1,55E-022	1,53E-018
5337_at	PLD1	phospholipase D1, phosphatidylcholine-specific	-0,629838907	1,16E-011	2,76E-009
54020_at	SLC37A1	solute carrier family 37 (glycerol-3-phosphate trans	0,62960635	2,35E-009	2,29E-007
54557_at	SGTB	small glutamine-rich tetratricopeptide repeat (TPR)	0,891727925	1,30E-011	3,02E-009
5476_at	CTSA	cathepsin A	0,656097847	4,25E-013	1,62E-010
54800_at	KLHL24	kelch-like 24 (Drosophila)	1,055183409	7,40E-016	9,28E-013

Figure S8

e

Probe	Symbol	Description	logFC G112 CIQ vs untr	P.Value G112 CIQ vs untr	FDR G112 CIQ vs untr
54873_at	PALMD	palmdelphin	-0,678661644	2,58E-010	3,68E-008
54978_at	C2orf18	chromosome 2 open reading frame 18	0,608072073	4,62E-010	6,03E-008
55062_at	WIP1	WD repeat domain, phosphoinositide interacting 1	0,937312732	2,51E-015	2,26E-012
55117_at	SLC6A15	solute carrier family 6, member 15	0,995405311	1,69E-015	1,68E-012
55238_at	SLC38A7	solute carrier family 38, member 7	0,588952318	1,38E-009	1,46E-007
55247_at	NEIL3	nei endonuclease VIII-like 3 (E. coli)	-0,676557924	1,34E-010	2,13E-008
55283_at	MCOLN3	mucolipin 3	0,733836575	3,44E-011	6,75E-009
55314_at	TMEM144	transmembrane protein 144	0,923322253	3,17E-013	1,26E-010
55331_at	PHCA	phytoceramidase, alkaline	-0,959334375	2,95E-014	1,89E-011
55740_at	ENAH	enabled homolog (Drosophila)	-0,616169272	6,03E-011	1,04E-008
55902_at	ACSS2	acyl-CoA synthetase short-chain family member 2	0,60113002	1,88E-010	2,89E-008
56180_at	MOSPD1	motile sperm domain containing 1	0,610333374	8,59E-007	3,22E-005
5660_at	PSAP	prosaposin	0,70985959	7,52E-014	3,72E-011
56907_at	SPIRE1	spire homolog 1 (Drosophila)	0,899698274	5,00E-012	1,39E-009
57016_at	AKR1B10	aldo-keto reductase family 1, member B10 (aldose	-0,61216227	0,000299178	0,00407079
57381_at	RHOJ	ras homolog gene family, member J	-0,814788552	2,03E-013	8,38E-011
5803_at	PTPRZ1	protein tyrosine phosphatase, receptor-type, Z poly	-1,005565617	3,42E-014	2,03E-011
58527_at	C6orf115	chromosome 6 open reading frame 115	0,695093156	2,54E-008	1,68E-006
58528_at	RRAGD	Ras-related GTP binding D	1,018370424	4,00E-013	1,55E-010
619190_at	FDPSL2A	MGC44478	0,633450062	0,001407313	0,013270582
6307_at	SC4MOL	sterol-C4-methyl oxidase-like	1,021882824	3,20E-012	9,45E-010
6319_at	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	0,783108932	1,69E-011	3,72E-009
6400_at	SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	0,59677613	2,91E-011	6,00E-009
64121_at	RRAGC	Ras-related GTP binding C	0,913394009	4,49E-015	3,68E-012
643246_at	MAP1LC3B2	microtubule-associated protein 1 light chain 3 beta	0,771138821	3,70E-008	2,30E-006
643428_at	LOC643428	hypothetical LOC643428	-0,837154249	2,37E-009	2,30E-007
6713_at	SQLE	squalene epoxidase	0,600081966	3,55E-011	6,75E-009
677798_at	SNORA9	small nucleolar RNA, H/ACA box 9	-0,629362387	3,73E-007	1,61E-005
6809_at	STX3	syntaxin 3	0,746918644	2,82E-010	3,98E-008
7042_at	TGFB2	transforming growth factor, beta 2	-0,912082592	9,73E-012	2,38E-009

Figure S8

Probe	Symbol	Description	logFC G112 CIQ vs untr	P.Value G112 CIQ vs untr	FDR G112 CIQ vs untr
7048_at	TGFBR2	transforming growth factor, beta receptor II (70/80k	-0,585236778	1,34E-008	1,01E-006
7153_at	TOP2A	topoisomerase (DNA) II alpha 170kDa	-0,684794439	5,65E-011	1,01E-008
7316_at	UBC	ubiquitin C	0,671691587	2,02E-007	9,57E-006
7447_at	VSNL1	visinin-like 1	-0,586901243	1,03E-008	8,19E-007
7453_at	WARS	tryptophanyl-tRNA synthetase	0,859124567	4,05E-014	2,23E-011
79993_at	ELOVL7	ELOVL family member 7, elongation of long chain	0,666645437	5,81E-010	7,32E-008
80727_at	TTYH3	tweety homolog 3 (Drosophila)	-0,753878291	1,25E-012	4,04E-010
80818_at	ZNF436	zinc finger protein 436	-0,585473329	3,08E-010	4,27E-008
8165_at	AKAP1	A kinase (PRKA) anchor protein 1	0,708730661	5,92E-011	1,03E-008
81848_at	SPRY4	sprouty homolog 4 (Drosophila)	-0,832261845	1,31E-012	4,19E-010
8404_at	SPARCL1	SPARC-like 1 (hevin)	-0,680409093	4,33E-012	1,25E-009
84418_at	C5orf32	chromosome 5 open reading frame 32	0,669768449	1,55E-011	3,49E-009
84707_at	BEX2	brain expressed X-linked 2	0,628822422	1,65E-008	1,19E-006
8507_at	ENC1	ectodermal-neural cortex (with BTB-like domain)	-0,690003395	9,62E-009	7,71E-007
8553_at	BHLHB2	basic helix-loop-helix domain containing, class B,	0,689247115	3,50E-011	6,75E-009
8878_at	SQSTM1	sequestosome 1	0,788821893	5,42E-013	1,95E-010
891_at	CCNB1	cyclin B1	-0,595714279	1,81E-008	1,28E-006
8934_at	RAB7L1	RAB7, member RAS oncogene family-like 1	0,620423852	5,95E-010	7,45E-008
8974_at	P4HA2	procollagen-proline, 2-oxoglutarate 4-dioxygenase	0,604547489	2,17E-010	3,24E-008
90293_at	KLHL13	kelch-like 13 (Drosophila)	-0,906506831	4,91E-016	6,94E-013
91373_at	UAP1L1	UDP-N-acteylglucosamine pyrophosphorylase 1-li	0,683352585	9,01E-012	2,26E-009
91445_at	RNF185	ring finger protein 185	0,669045048	1,88E-008	1,33E-006
9156_at	EXO1	exonuclease 1	-0,60152734	7,03E-012	1,85E-009
9388_at	LIPG	lipase, endothelial	0,962640368	4,51E-013	1,69E-010
9493_at	KIF23	kinesin family member 23	-0,599425603	1,11E-009	1,21E-007
9518_at	GDF15	growth differentiation factor 15	0,893113226	1,50E-011	3,41E-009
953_at	ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	0,690533221	1,08E-010	1,74E-008
96459_at	FNIP1	folliculin interacting protein 1	0,917727705	4,46E-015	3,68E-012
9709_at	HERPUD1	homocysteine-inducible, endoplasmic reticulum st	0,715931664	7,09E-012	1,85E-009
9787_at	DLGAP5	discs, large (Drosophila) homolog-associated prote	-0,627158451	2,95E-010	4,13E-008
9890_at	LPPR4	plasticity related gene 1	0,987214069	7,50E-016	9,28E-013

Figure S8

CIQ_DEGs_#1095 (p53 null)

Probe	Symbol	Description	logFC #1095_CIQ vs untreated	P-Value #1095_CIQ vs untreated	FDR #1095_CIQ vs untreated
10457_at	GPNMB	glycoprotein	3,34	2,10E-16	0,00%
3488_at	IGFBP5	insulin-like	-2,34	2,37E-14	0,00%
2170_at	FABP3	fatty acid b	2,19	1,84E-13	0,00%
8869_at	ST3GAL5	ST3 beta-g	1,92	1,30E-14	0,00%
5046_at	PCSK6	proprotein	1,55	5,60E-12	0,00%
3397_at	ID1	inhibitor of	-1,53	2,31E-10	0,00%
51050_at	PI15	peptidase	1,44	3,01E-09	0,00%
115265_at	DDIT4L	DNA-dama	1,32	1,33E-10	0,00%
9518_at	GDF15	growth diffe	1,30	1,73E-12	0,00%
79365_at	BHLHE41	basic helix	1,29	7,11E-13	0,00%
1410_at	CRYAB	crystallin, c	1,28	2,27E-12	0,00%
9411_at	ARHGAP2	Rho GTPase	-1,27	7,12E-11	0,00%
5208_at	PFKFB2	6-phospho	1,27	6,31E-11	0,00%
256987_at	SERINC5	serine inco	1,26	2,97E-12	0,00%
344148_at	NCKAP5	NCK-asso	1,22	1,50E-07	0,00%
7128_at	TNFAIP3	tumor necr	-1,19	1,80E-11	0,00%
23305_at	ACSL6	acyl-CoA s	1,17	1,07E-09	0,00%
64122_at	FN3K	fructosami	1,16	8,78E-09	0,00%
119548_at	PNLIPRP3	pancreatic	1,12	8,40E-08	0,00%
28526_at	TRDC	T cell rece	-1,11	1,12E-08	0,00%
3399_at	ID3	inhibitor of	-1,06	2,02E-10	0,00%
127495_at	LRRRC39	leucine ric	1,03	8,81E-09	0,00%
3675_at	ITGA3	integrin, al	-1,02	5,90E-11	0,00%
9388_at	LIPG	lipase, enc	1,01	7,90E-09	0,00%

Figure S9

AAH-APOCIG-1 ARRAY

Each antibody is spotted in duplicate vertically		A	B	C	D	E	F	G	H
	1	POS	POS	NEG	Akt (P-Ser473)	ATM (P-Ser1981)	BAD (P-Ser112)	Caspase-3 (Cleaved Asp175)	Caspase-7 (Cleaved Asp198)
	2								
	3	CHK1 (P-Ser296)	CHK2 (P-Thr68)	eIF-2a (P-Ser51)	ERK1 (P-T202/Y204)	HSP27 (P-Ser82)	IKBa (P-Ser32)	JNK (P-Thr183/Tyr185)	NFKBP65 (P-Ser536)
	4				ERK2 (P-Y185/Y187)				
	5	PARP1 (Cleaved Asp214/Gly215)	p27 (P-Thr198)	P38 (P-Thr180/Tyr182)	P53 (P-Ser15)	SMAD2 (P-Ser245/250/255)	TAK1 (P-Ser412)	NEG	POS
	6								

Figure S10

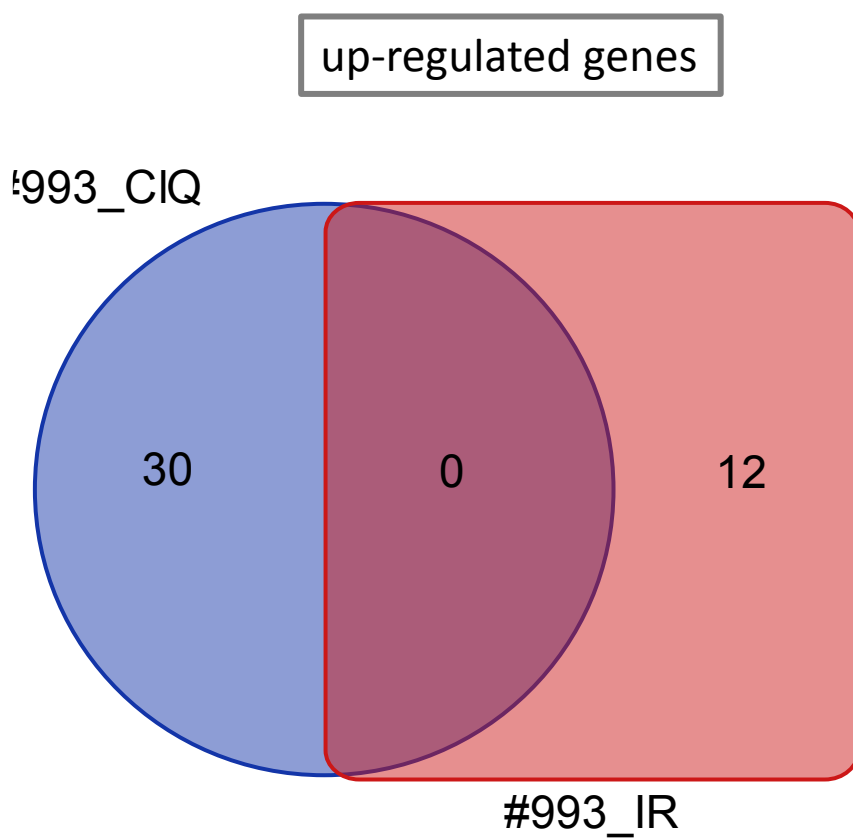
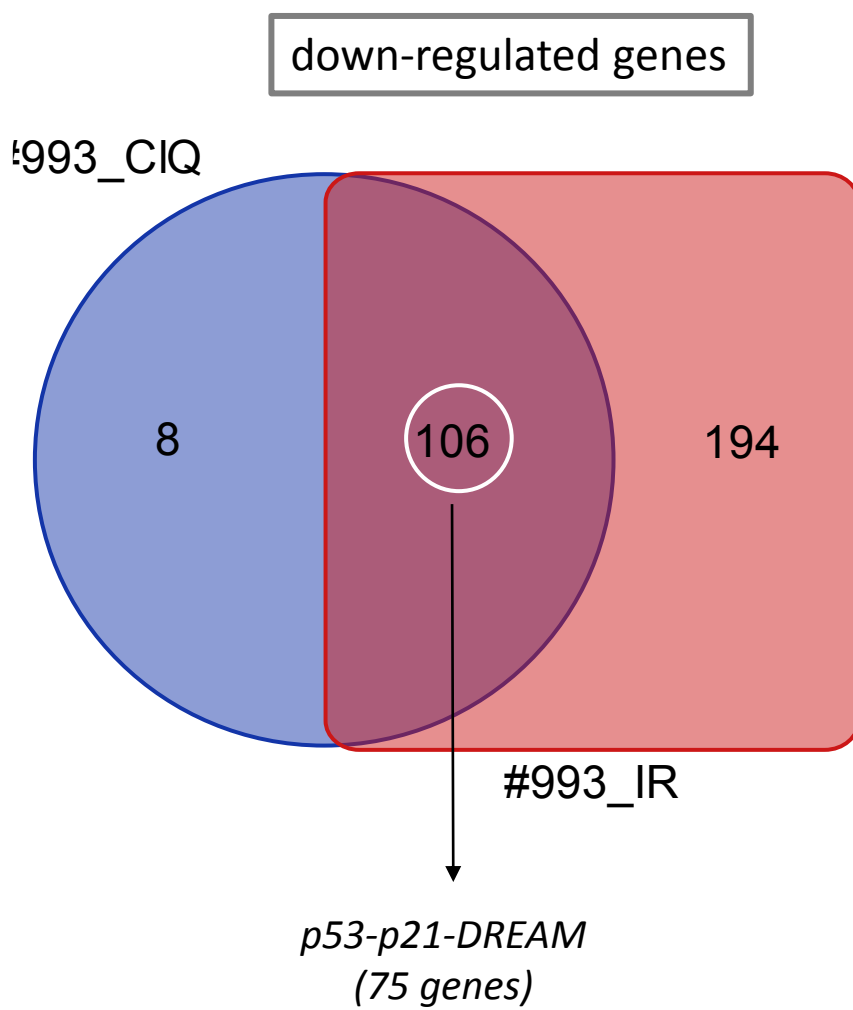


Figure S11

Figure 12 rev

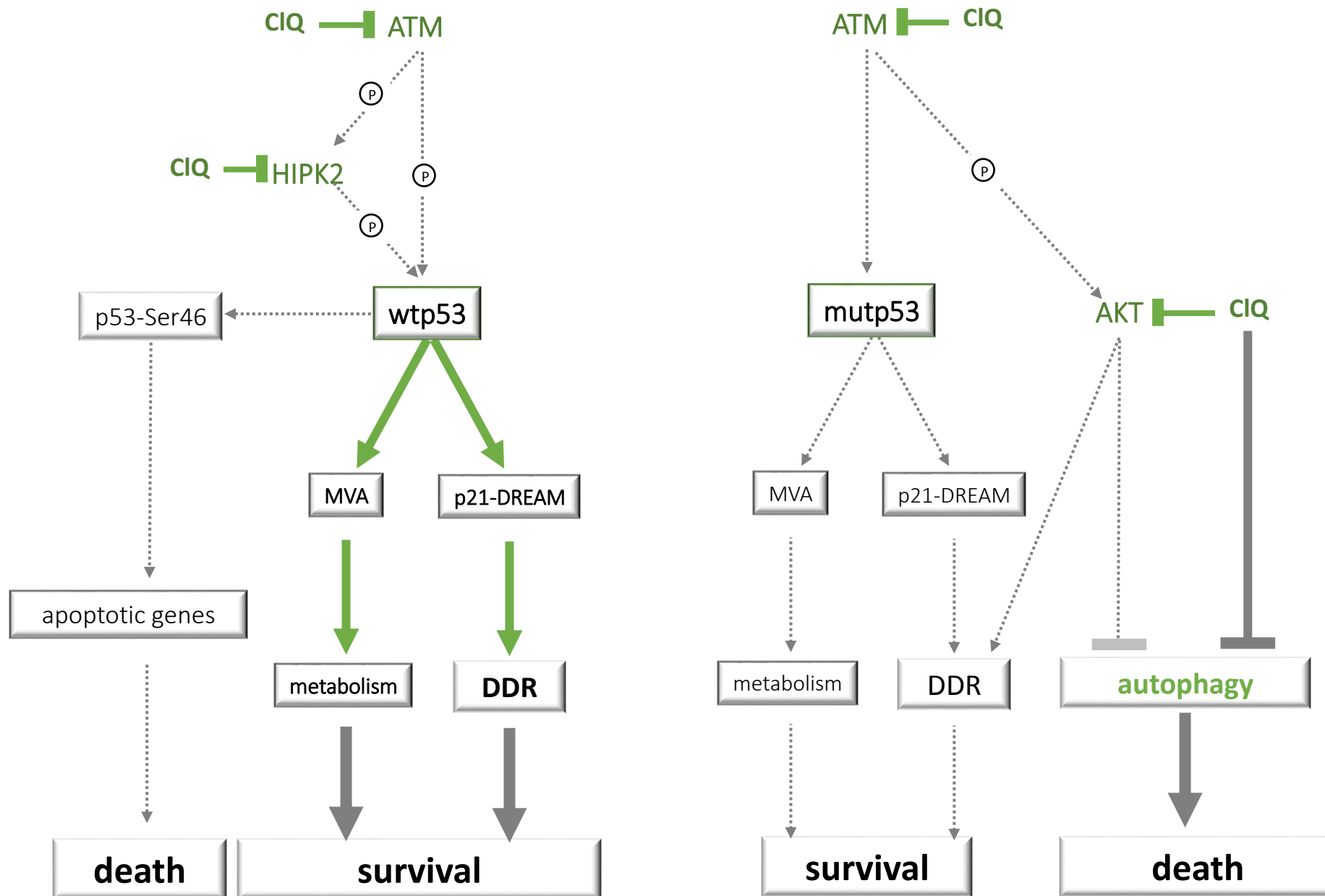


Table S1**a)**

up-regulated CIQ_DEGs		
Gene	Function in GB	Reference
<i>acsl6</i>	associated with therapy resistance	Zhuo et al. (89)
<i>cryab</i>	associated with therapy resistance	Goplen et al. (90)
<i>ddit4l</i>	associated with therapy resistance	Foltyn et al. (91)
<i>fabp3</i>	associated with stemness	Lewis et al. (92)
<i>gdf15</i>	associated with poor prognosis	Guo et al. (93)
<i>gpnmb</i>	associated with stemness	Feng et al. (94)
<i>nckap5</i>	associated with poor prognosis	Akçay et al. (95)
<i>pcsk6</i>	associated with invasion	Delic et al. (96)
<i>pfkfb2</i>	associated with invasion	He et al. (97)
<i>st3gal5</i>	associated with stemness	Putthisen et al. (98)

b)

down-regulated CIQ_DEGs		
Gene	Function in GB	Reference
<i>arhgap29</i>	associated with invasion	Mariani et al. (99)
<i>id1</i>	associated with chemoresistance	Sachdeva et al. (100)
<i>id3</i>	promotes stemness	Nair et al. (101)
<i>Igfbp5</i>	promotes invasion but inhibits proliferation	Dong et al. (102)
<i>Itga3</i>	promotes radioresistance	Serafim et al. (103)
<i>tnfaip3</i>	promotes GSCs survival and tumorigenicity	Hjelmeland et al. (104)

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