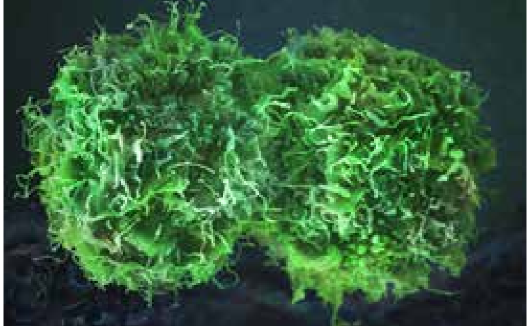

THE ESSENTIALS OF
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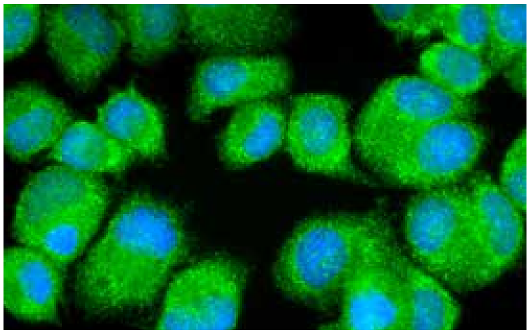
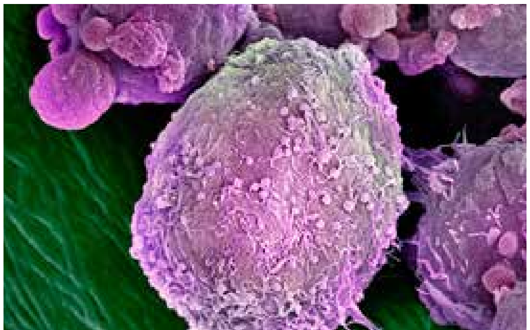
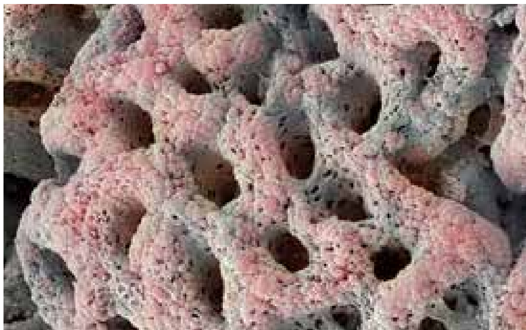
p53 Hotspot Mutation Cell Panels







p53 is a tumor suppressor protein encoded by the TP53 gene in humans. It controls the cellular response to DNA damage through the induction of cell-cycle arrest, apoptosis and cellular senescence, and by regulating key stages of metabolism, tumor metastasis and invasion. As a result, p53 has been described as "the guardian of the genome".[1] About half of human tumors contain mutations or deletions of p53,2 the remainder have mutations in genes that partially block the p53 pathway. Approximately, 95% of p53 mutations lie in the core DNA-binding domain and 40% of these mutations occur in one of six "hotspots;" all of which are known to severely restrict p53 function.[2] ATCC p53 mutation cell line panels are composed of the most commonly used human cancer cell lines from breast, lung, colon, pancreatic, hematopoietic and lymphoid tissues. Moreover, they cover p53 hotpost mutations at codon 175, 245, 248, 273, and 282. These panels are useful tools for the study of p53 function, wild-type p53 function reactivation, cancer biology, and anti-cancer drug discovery.

Table of Contents

[1] Read, A., Strachan, T.(Wiley, New York, 1999).

[2] Hollstein, M, Sidransky, D, Vogelstein, B & Harris, CC. p53 mutations in human cancers. Science 253, 49-53 (1991).

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ATCC distributes to more than 165 countries on 6 continents and has a growing international network of 12 distribution partners. Our infrastructure and experience in biological materials logistics enables us to work effectively with researchers no matter where they are located.

BREAST CANCER p53 HOTSPOT MUTATION CELL PANEL

The Breast Cancer p53 Hotspot Mutation Cell Panel (ATCC® TCP-2010™) is composed of eight select cell lines derived from breast cancer. This panel combines wild-type p53 cell lines with mutant p53 cell lines that carry hotspot mutations in one of the following codons: 175, 248, 249, or 273. The p53 status of each line was sequenced and validated by ATCC. The panel is useful for anti-cancer drug targeting or reactivation of mutant p53, as well as studies related to p53 molecular mechanisms.

ATCC® No.	Name	Histology	Tumor Source	TP53 status	Zygosity	Gene Mutation†	Protein Sequence†
HTB-25™	MDA-MB-175-VII	ductal carcinoma	metastasis (pleural effusion)	WT			
HTB-27™	MDA-MB-361	adenocarcinoma	metastasis (brain)	WT			
CRL-2351™	AU565	adenocarcinoma	metastasis (pleural effusion)	MUT	homozygous	c.524G>A	p.R175H
HTB-30™	SK-BR-3	adenocarcinoma	metastasis (pleural effusion)	MUT	homozygous	c.524G>A	p.R175H
CRL-2315™	HCC70	ductal carcinoma	primary	MUT	homozygous	c.743G>A	p.R248Q
HTB-122™	BT-549	ductal carcinoma	primary	MUT	homozygous	c.747G>C	p.R249S
CRL-2314™	HCC38	ductal carcinoma	primary	MUT	homozygous	c.818G>T	p.R273L
HTB-132™	MDA-MB-468	adenocarcinoma	metastasis (pleural effusion)	MUT	homozygous	c.818G>A	p.R273H

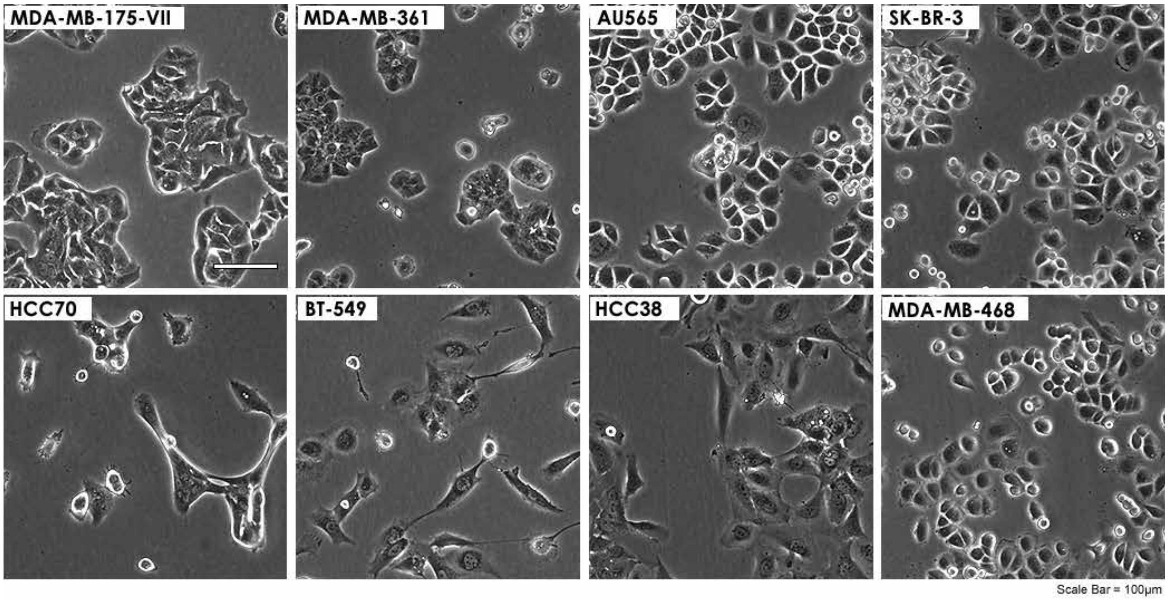

Figure 1. Cell morphology of eight cell lines in the Breast Cancer p53 Hotspot Mutation Cell Panel. Two p53 wild-type breast cancer cell lines, MDA-MB-175-VII and MDA-MB-361, and six p53 hotspot mutation breast cancer cell lines, AU565, SK-BR-3, HCC70, BT-549, HCC38 and MDA-MB-468, were maintained in ATCC recommended culture conditions. Each cell line was grown using ATCC recommended culture conditions. Cell morphology was observed under Nikon™ microscopy, and images of the indicated cell lines were captured by Olympus® digital camera.

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†For a description of the sequence variation nomenclature please refer to: *den Dunnen JT and Antonarakes SE (2000), Hum. Mutat. 15:7-12.*

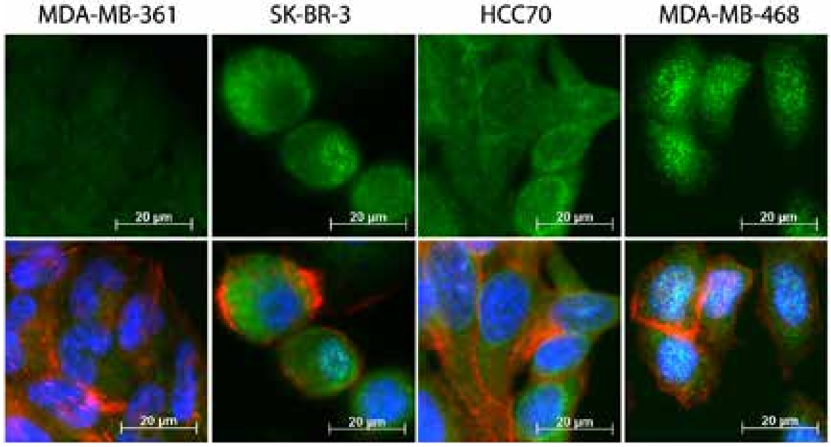


Figure 2. Immunofluorescence staining of p53. The indicated p53 wild-type and p53 mutation cells were grow on collagen-coated coverslips. Cells were fixed with 4% paraformaldehyde. p53 was stained with p53 primary antibody and Alexa Fluor 488 secondary antibody (green). F-actin was visualized with phalloidin Alexa Fluor 594 (red). Nuclei of the cells were visualized with Hoechst 33342 (blue). Single florescence channel images of p53 staining are shown in the upper row, and multichannel merged images are shown in the bottom row.

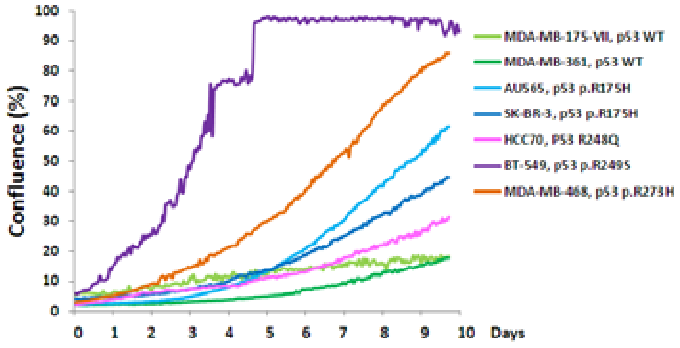


Figure 3. Cell growth kinetics. The indicated p53 wild-type and p53 mutation cells were cultured in ATCC recommended media, and plated at 3000 cells/well in 96-well plates. Cell growth kinetics were constantly monitored for 10 days using a label-free automated IncuCyte™ live-cell imaging system (Essen Bioscience).

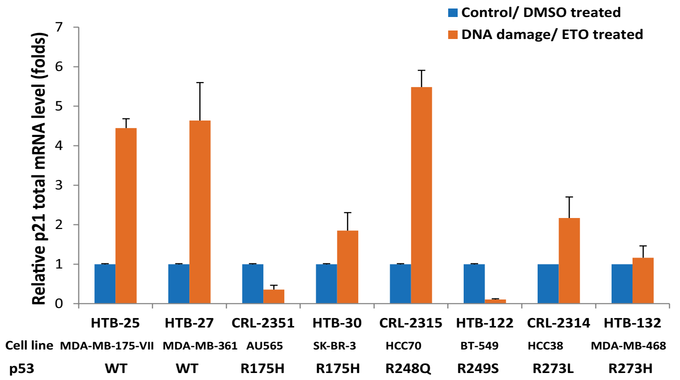


Figure 4. Real time PCR analysis of total mRNA levels of p21, a downstream target of p53, in the indicated p53 wild-type and p53 mutation cell lines. Cells were treated with 20 µM etoposide (ETO) for 6 hours to induce DNA damage, or treated with DMSO as a control. Total mRNA levels of p21 and the housekeeping gene 36B4 were determined by real time quantitative PCR. Relative p21 total mRNA changes were normalized to 36B4.

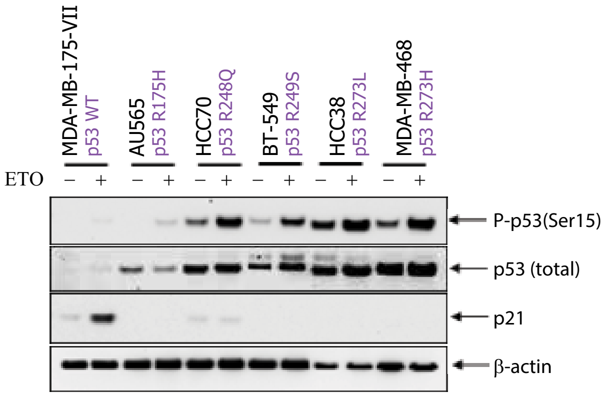
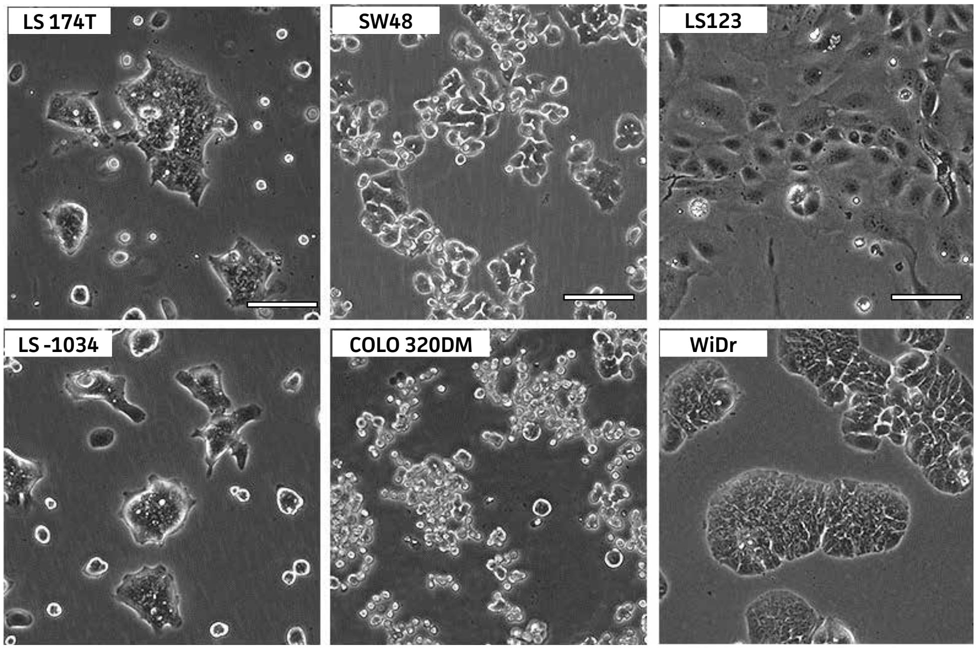


Figure 5. The indicated p53 wild-type and p53 mutation cells were treated with 20 µM etoposide (ETO) for 8 hours to induce DNA damage, or treated with DMSO as a control. Western blotting assay was used to examine phosphorylation of p53 at Serine 15, total protein expression of p53, and expression of p21, a downstream target of p53. β-actin protein was also examined as a control.

COLON CANCER p53 HOTSPOT MUTATION CELL PANEL

The Colon Cancer p53 Hotspot Mutation Cell Panel (ATCC® No. TCP-2020™) is composed of six select cell lines derived from colon cancer. This panel combines wild-type p53 cell lines with mutant p53 cell lines that carry hotspot mutations in one of the following codons: 175, 245, 248, or 273. The p53 status of each line was sequenced and validated by ATCC. The panel is useful for novel anti-cancer drug targeting or reactivation of mutant p53, as well as studies related to p53 molecular mechanisms.

ATCC® No.	Name	Tissue	Histology	Tumor Source	TP53 status	Zygosity	Gene Mutation[†]	Protein Sequence[†]
CL-188™	LS174T	colon	adenocarcinoma	primary	WT	-	-	-
CCL-231™	SW48	colon	adenocarcinoma	primary	WT	-	-	-
CCL-255™	LS123	colon	adenocarcinoma	primary	MUT	homozygous	c.524G>A	p.R175H
CRL-2158™	LS1034	colon	adenocarcinoma	primary	MUT	homozygous	c.733G>A	p.G245S
CCL-220™	COLO 320DM	colon	adenocarcinoma	primary	MUT	homozygous	c.742C>T	p.R248W
CCL-218™	WiDr	colon	adenocarcinoma	primary	MUT	homozygous	c.818G>A	p.R273H



Scale Bar = 100μm

Figure 1. Cell morphology of the six cell lines in the Colon Cancer p53 Hotspot Mutation Cell Panel. Two p53 wild-type colon cancer cell lines, LS174T and SW48, and four p53 hotspot mutation colon cancer cell lines, LS123, LS1034, COLO 320DM, and WiDr, were maintained in ATCC recommended culture conditions. Each cell line was grown using ATCC recommended culture conditions. Cell morphology was observed under Nikon™ microscopy, and images of the indicated cell lines were captured by Olympus® digital camera.

[†] For a description of the sequence variation nomenclature please refer to: *den Dunnen JT and Antonarakes SE (2000), Hum. Mutat. 15:7-12.*

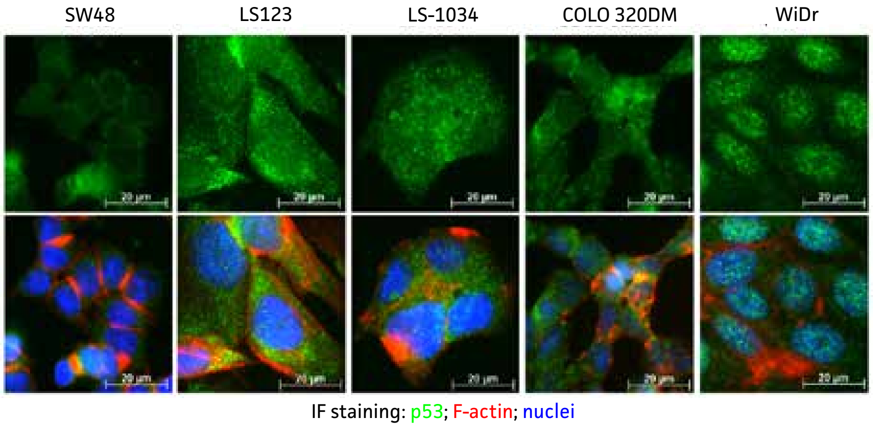


Figure 2. Cellular localization of p53. The indicated p53 wild-type and p53 mutation cells were grow on collagen-coated coverslips. Cells were fixed with 4% paraformaldehyde. p53 was stained with p53 primary antibody and Alexa Fluor 488 secondary antibody (green). F-actin was visualized with phalloidin Alexa Fluor 594 (red). Nuclei of the cells were visualized with Hoechst 33342 (blue). Single florescence channel images of p53 staining are shown in the upper row, and multichannel merged images are shown in the bottom row.

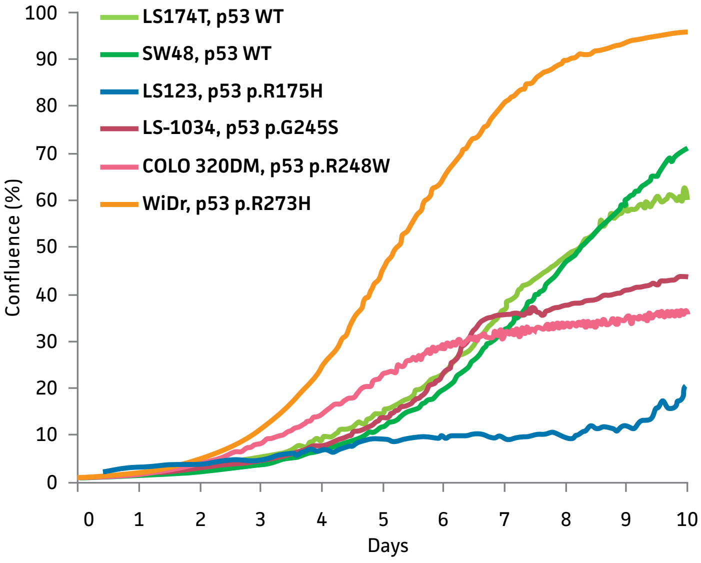


Figure 3. Cell growth kinetics. The indicated p53 wild-type and p53 mutation cells were cultured in ATCC recommended media, and plated at 3000 cells/well in 96-well plate. The cell growth kinetics were constantly monitored for 10 days using a label-free automated IncuCyte® live-cell imaging system (Essen Bioscience).

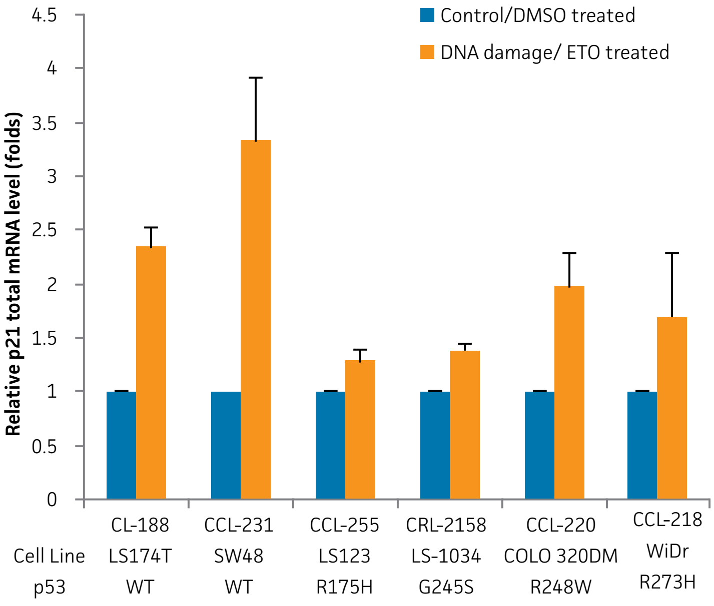


Figure 4. p53-target gene expression changes in response to DNA damage. The indicated cell lines were treated with 20 µM etoposide (ETO) for 6 hours to induce DNA damage, or treated with DMSO as a control. Total mRNA level of p21 and 36B4 were determined by real time quantitative PCR. Relative p21 total mRNA changes were normalized to the housekeeping gene 36B4.

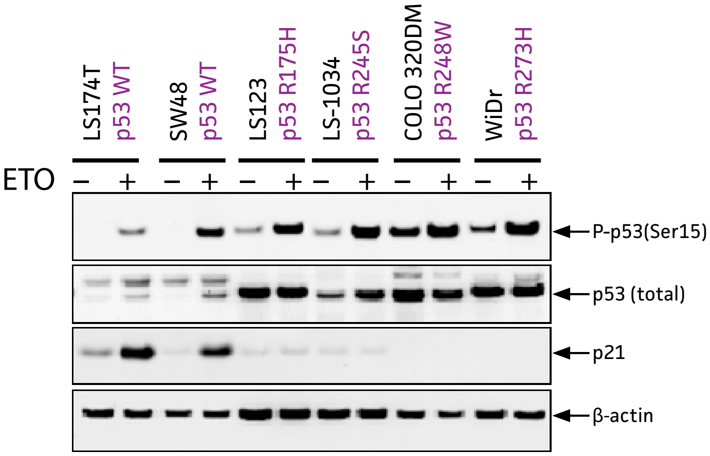


Figure 5. p53 phosphorylation in response to DNA damage. The indicated p53 wild-type and p53 mutation cells were treated with 20 µM etoposide (ETO) for 8 hours to induce DNA damage, or treated with DMSO as a control. Western blotting assay was used to examine phosphorylation of p53 at Serine 15, total protein expression of p53, and expression of p21, a downstream target of p53. β-actin protein was also examined as a control.

LEUKEMIA p53 HOTSPOT MUTATION CELL PANEL

The Leukemia p53 Hotspot Mutation Cell Panel (ATCC® No. TCP-2070™) is composed of six select suspension cell lines derived from individuals with leukemia. This panel combines wild-type p53 cell lines with mutant p53 cell lines that carry hotspot mutations in one of the following codons: 175, 248 and 273. The p53 status of each line was sequenced and validated by ATCC. The panel is useful for anti-cancer drug targeting or reactivation of mutant p53, as well as studies related to p53 molecular mechanisms.

ATCC® No.	Name	Primary Site, Tissue	Histology	TP53 status	Zygosity	Gene mutation†	Protein Sequence†
TIB-190™	CESS	blood	acute myeloid leukemia (AML)	WT	-	-	-
CCL-240™	HL-60	blood	acute promyelocytic leukemia (APL)	NULL	homozygous	c.(del)	-
CCL-119™	CCRF-CEM	blood	acute lymphoblastic leukemia (ALL)	MUT	heterozygous	c.524G>A; c.743G>A	p.R175H; p.R248Q
CRL-2265™	CEM/C1	blood	acute lymphoblastic leukemia (ALL)	MUT	heterozygous	c.524G>A	p.R175H
CRL-2724™	KASUMI-1	blood	acute myeloid leukemia (AML)	MUT	homozygous	c.743G>A	p.R248Q
CRL-1621™	ARH-77	blood	plasma cell leukemia, carry EBV	MUT	homozygous	c.818G>A	p.R273H

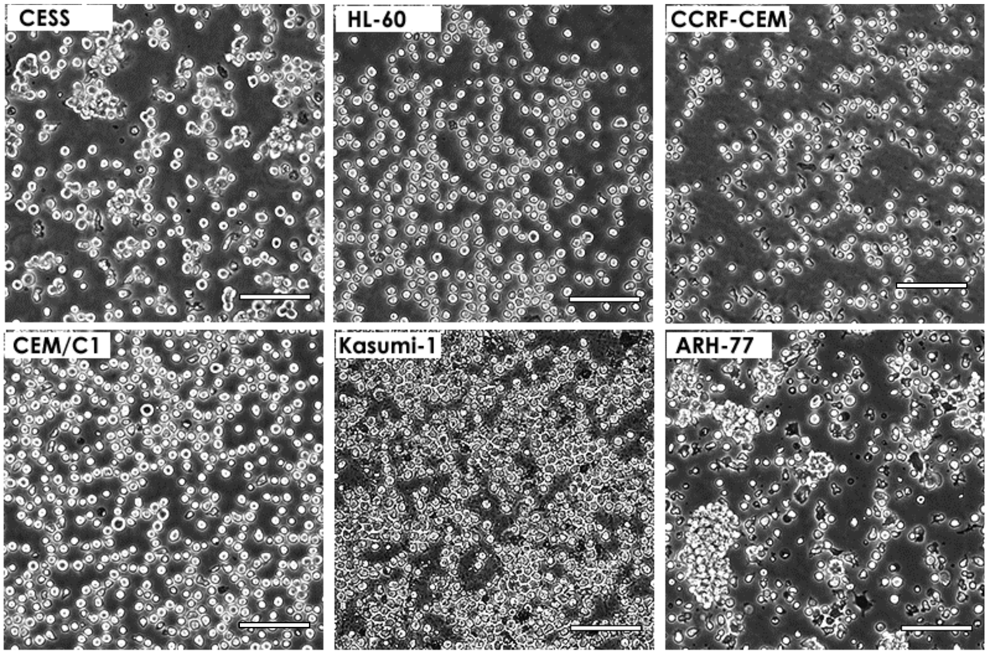


Figure 1. Cell morphology of the six cell lines in the Leukemia p53 Hotspot Mutation Cell Panel. Each cell line was grown using the ATCC recommended culture conditions. Cell morphology was observed under Nikon™ microscopy, and images of the indicated cell lines were captured by Olympus® digital camera.

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†For a description of the sequence variation nomenclature please refer to: *den Dunnen JT and Antonarakes SE (2000), Hum. Mutat. 15:7-12.*

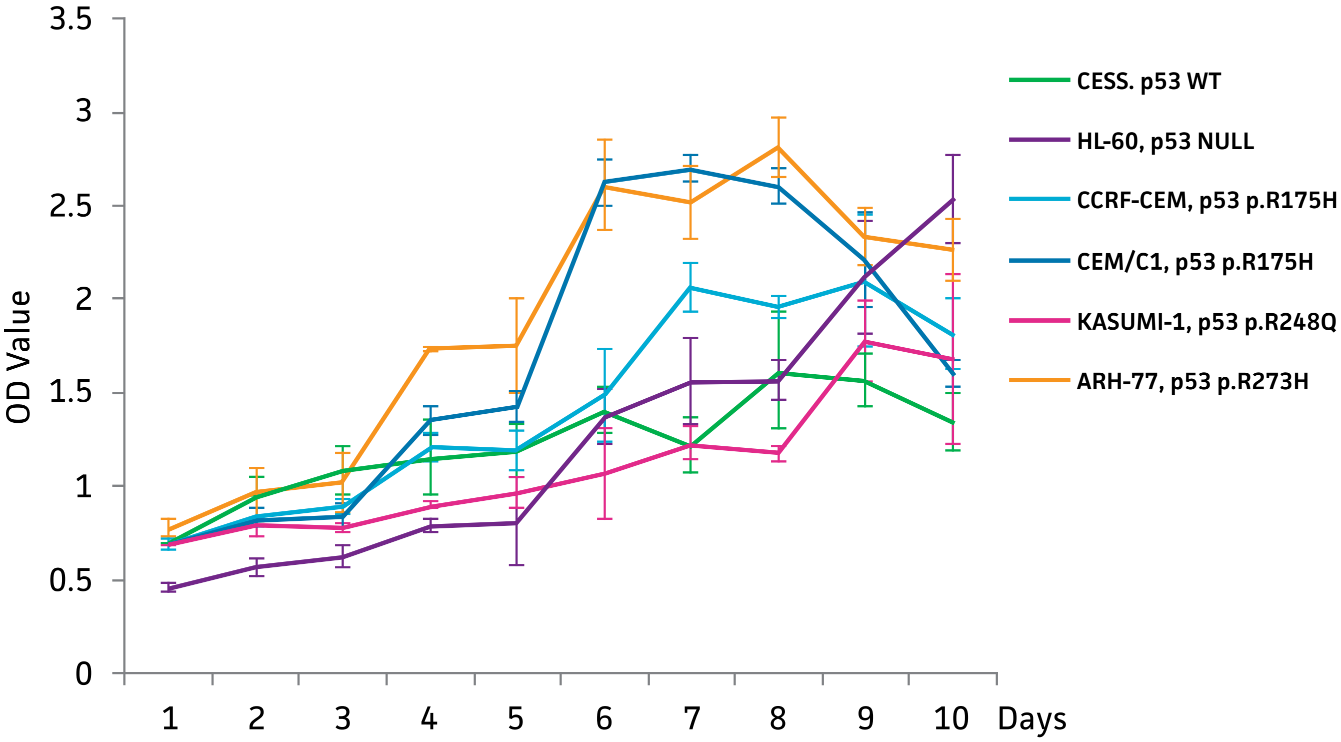


Figure 2. Cell growth kinetics. The indicated p53 wild-type and p53 mutation cells were cultured in ATCC recommended media, and plated at 3000 cells/well in 96-well plates. The cell growth kinetics were monitored for 10 days by CellTiter 96® AQueous One Solution Cell Proliferation Assay (Promega).

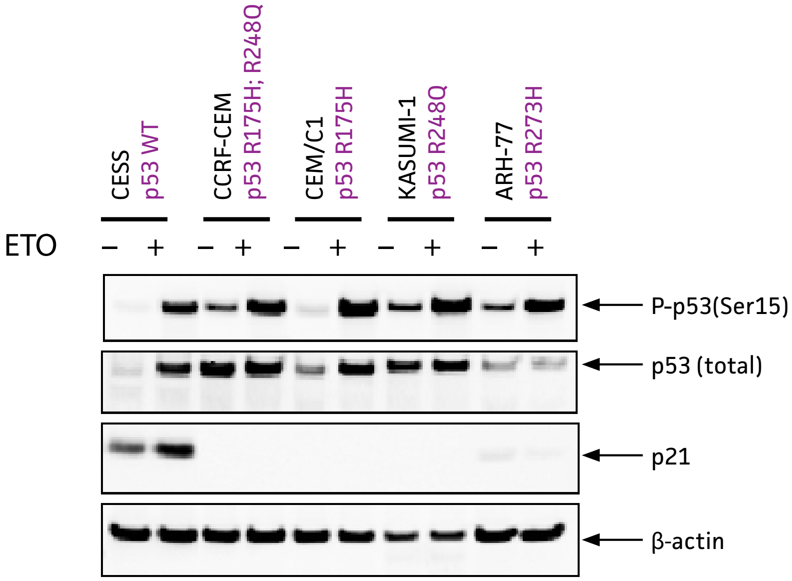
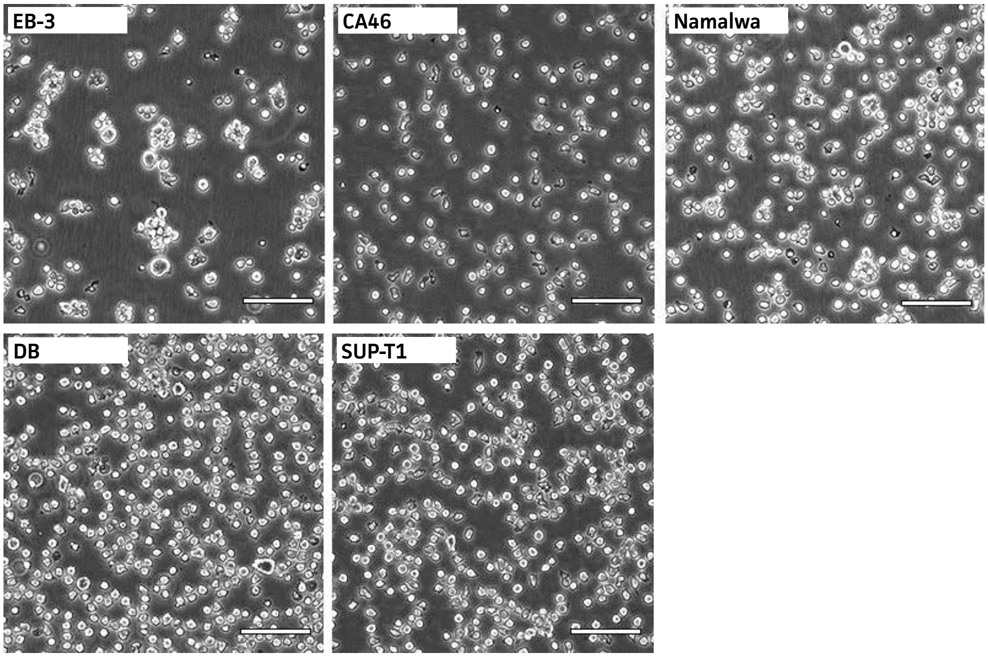


Figure 3. The indicated p53 wild-type and p53 mutation cells were treated with 20 μM etoposide (ETO) for 8 hours to induce DNA damage, or treated with DMSO as a control. Western blotting was used to examine phosphorylation of p53 at Serine 15, total protein expression of p53, and expression of p21, a downstream target of p53. β-actin protein was also examined as a control.

LYMPHOMA p53 HOTSPOT MUTATION CELL PANEL

The Lymphoma p53 Hotspot Mutation Cell Panel (ATCC® No. TCP-2050™) is composed of five select suspension cell lines derived from lymphomas. This panel combines wild-type p53 cell lines with mutant p53 cell lines that carry hotspot mutations in one of the following codons: 248 and 273. The p53 status of each line was sequenced and validated by ATCC. The panel is useful for anti-cancer drug targeting or reactivation of mutant p53, as well as studies related to p53 molecular mechanisms.

ATCC® No.	Name	Tissue	Histology	TP53 status	Zygosity	Gene mutation†	Protein Sequence†
CCL-85™	EB-3	lymph node	Burkitt lymphoma	WT	-	-	-
CRL-1648™	CA46	lymph node	Burkitt lymphoma	MUT	homozygous	c.743G>A	p.R248Q
CRL-1432™	Namalwa	lymph node	Burkitt lymphoma, carry EBV	MUT	homozygous	c.743G>A	p.R248Q
CRL-2289™	DB	lymph node	large B-cell lymphoma	MUT	heterozygous	c.743G>A	p.R248Q
CRL-1942™	SUP-T1	lymph node	T cell lymphoblastic lymphoma	MUT	heterozygous	c.818G>A	p.R273H



Scale Bar = 100µm

Figure 1. Cell morphology of five cell lines in the Lymphoma p53 Hotspot Mutation Cell Panel. Each cell line was grown using the ATCC recommended culture conditions. Cell morphology was observed under Nikon™ microscopy, and images of the indicated cell lines were captured by Olympus® digital camera.

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† For a description of the sequence variation nomenclature please refer to: *den Dunnen JT and Antonarakes SE (2000), Hum. Mutat. 15:7-12.*

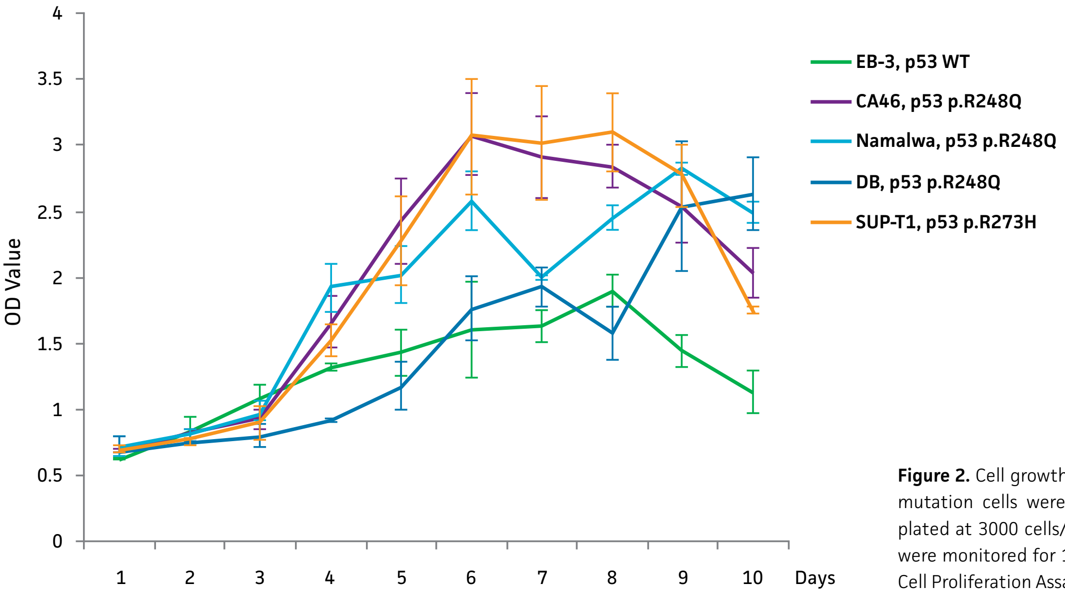


Figure 2. Cell growth kinetics. The indicated p53 wild-type and p53 mutation cells were cultured in ATCC recommended media, and plated at 3000 cells/well in 96-well plates. The cell growth kinetics were monitored for 10 days by CellTiter 96® AQueous One Solution Cell Proliferation Assay (Promega).

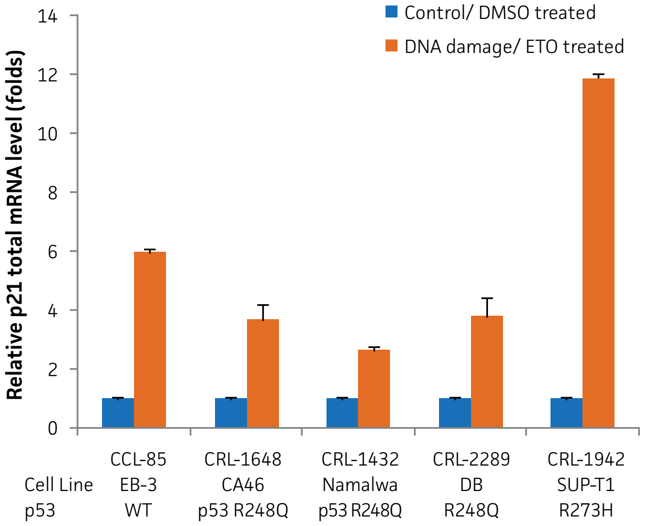


Figure 3. Real time PCR analysis of total mRNA levels of p21, a downstream target of p53, in the indicated p53 wild-type and p53 mutation cell lines. Cells were treated with 20μM etoposide (ETO) for 6 hours to induce DNA damage, or treated with DMSO as a control. Total mRNA level of p21 and 36B4 were determined by real time quantitative PCR. Relative p21 total mRNA changes were normalized to the housekeeping gene 36B4.

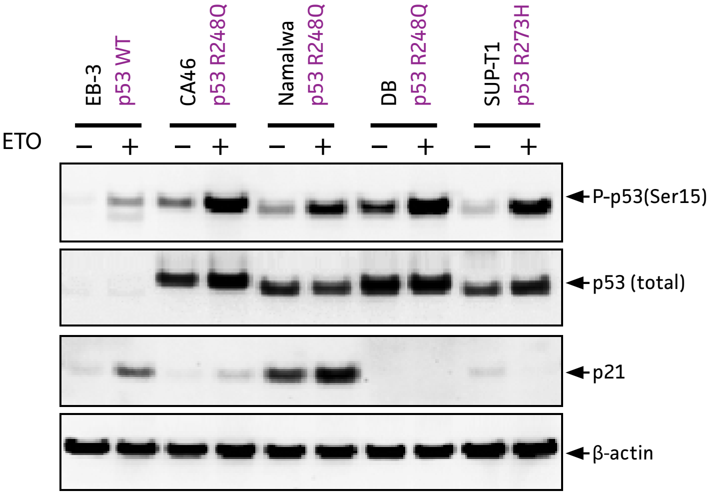
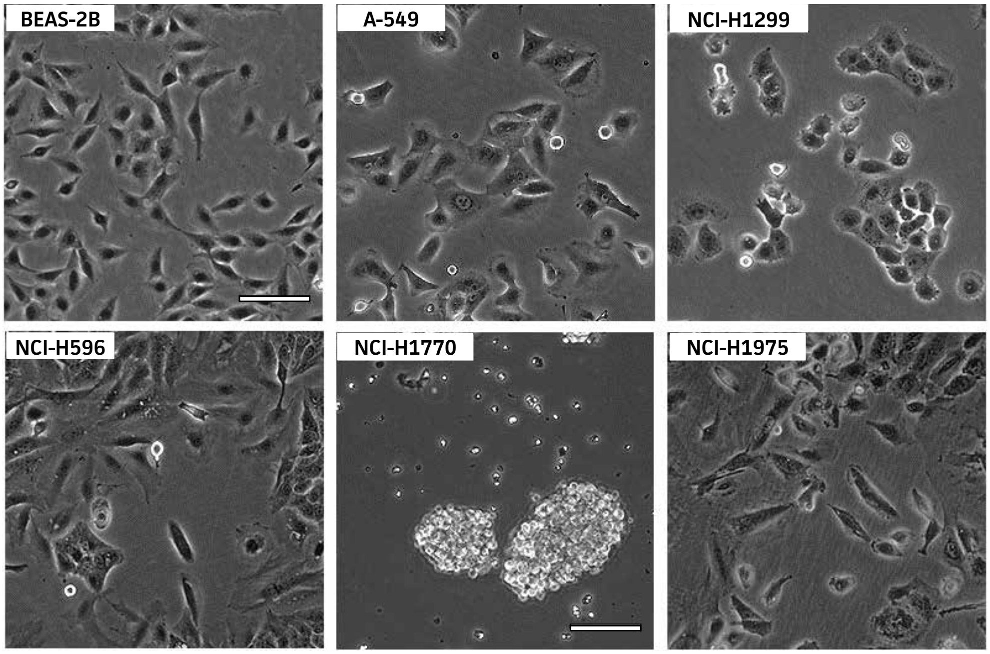


Figure 4. The indicated p53 wild-type and p53 mutation cells were treated with 20 μM etoposide (ETO) for 8 hours to induce DNA damage, or treated with DMSO as a control. Western blotting assay was used to examine phosphorylation of p53 at Serine 15, total protein expression of p53, and expression of p21, a downstream target of p53. β-actin

NON-SMALL CELL LUNG CANCER p53 HOTSPOT MUTATION CELL PANEL

Non-Small Cell Lung Cancer p53 Hotspot Mutation Cell Panel (ATCC® No. TCP-2030™) is composed of six select cell lines derived from lung tumors. This panel combines wild-type p53 cell lines with mutant p53 cell lines that carry hotspot mutations in one of the following codons: 245, 248, or 273. The p53 status of each line was sequenced and validated by ATCC. The panel is useful for anti-cancer drug targeting or reactivation of mutant p53, as well as studies related to p53 molecular mechanisms.

ATCC® No.	Name	Tissue	Histology	Tumor Source	TP53 status	Zygosity	Gene mutation†	Protein Sequence†
CRL-9609™	BEAS-2B	lung	normal tissue,S V-40 immortalized	NA	WT	-	-	-
CCL-185™	A549	lung	non-small cell lung carcinoma	primary	WT	-	-	-
CRL-5803™	NCI-H1299	lung	non-small cell lung carcinoma	metastasis (lymph node)	NULL	homozygous	c.(del)	-
HTB-178™	NCI-H596	lung	adenosquamous carcinoma	primary	MUT	homozygous	c.733G>T	p.G245C
CRL-5893™	NCI-H1770	lung	non-small cell lung carcinoma	metastasis (lymph node)	MUT	homozygous	c.741 742CC>TT	p.R248W
CRL-5908™	NCI-H1975	lung	adenocarcinoma	primary	MUT	homozygous	c.818G>A	p.R273H



Scale Bar = 100μm

Figure 1. Cell morphology of the six cell lines in the Non-Small Cell Lung Cancer p53 Hotspot Mutation Cell Panel. The two p53 wild-type lung cell lines, BEAS-2B and A549, one p53 null cell line, NCI-H1299, and three p53 hotspot mutation lung cancer cell lines, NCI-H594, NCI-H1770, and NCI-H1975, were maintained in ATCC recommended culture conditions. Cell morphology was observed under Nikon™ microscopy, and images of the indicated cell lines were captured by Olympus® digital camera.

†For a description of the sequence variation nomenclature please refer to: *den Dunnen JT and Antonarakes SE (2000), Hum. Mutat. 15:7-12.*

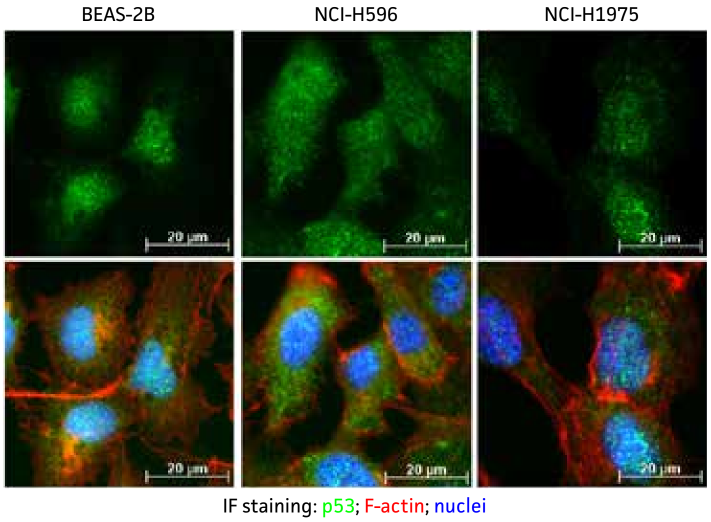


Figure 2. Cellular localization of p53. The indicated p53 wild-type and p53 mutation cells were grow on collagen-coated coverslips. Cells were fixed with 4% paraformaldehyde. p53 was stained with p53 primary antibody and Alexa Fluor 488 secondary antibody (green). F-actin was visualized with phalloidin Alexa Fluor 594 (red). Nuclei of the cells were visualized with Hoechst 33342 (blue). Single florescence channel images of p53 staining are shown in the upper row, and multichannel merged images are shown in the bottom row.

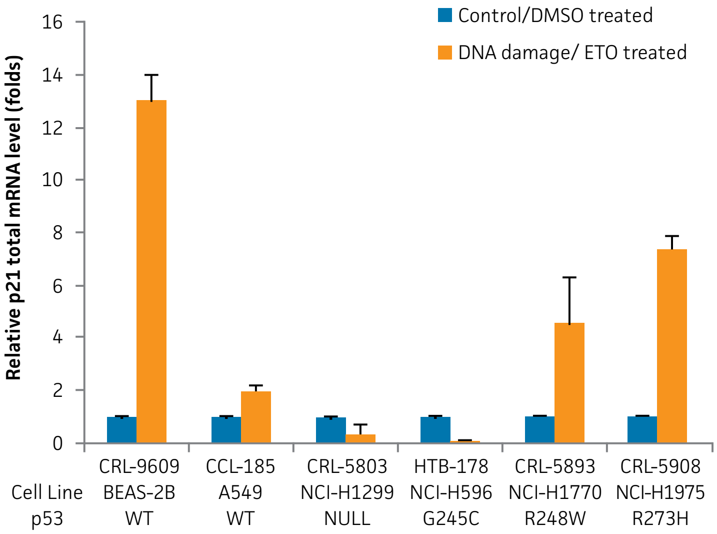


Figure 4. p53-target gene expression changes in response to DNA damage. The indicated cell lines were treated with 20 µM etoposide (ETO) for 6 hours to induce DNA damage, or treated with DMSO as a control. Total mRNA level of p21 and 36B4 were determined by real time quantitative PCR. Relative p21 total mRNA changes were normalized to the housekeeping gene 36B4.

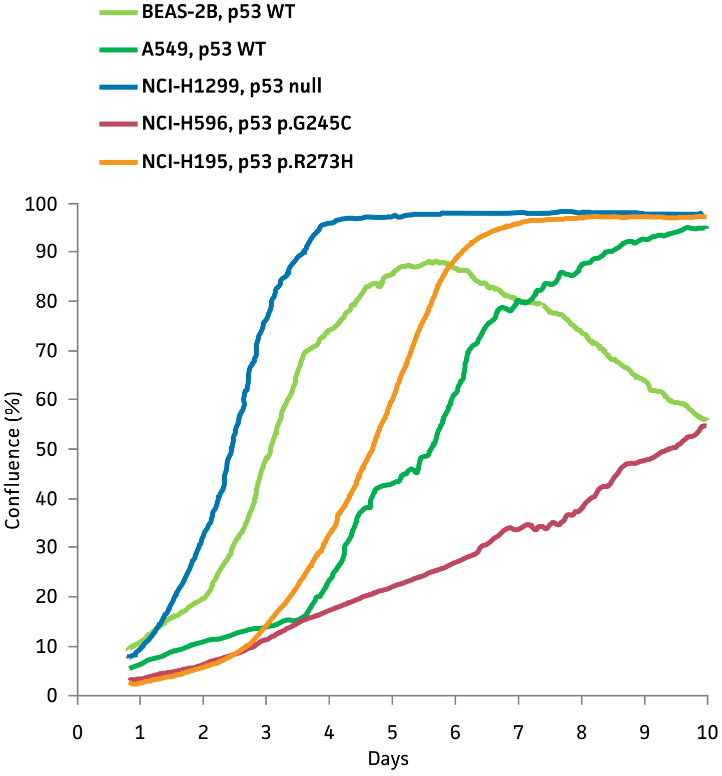


Figure 3. Cell growth kinetics. The indicated p53 wild-type and p53 mutation cells were cultured in ATCC recommended media, and plated at 3000 cells/well in 96-well plates. The cell growth kinetics were constantly monitored for 10 days using a label-free automated IncuCyte® live-cell imaging system (Essen Bioscience).

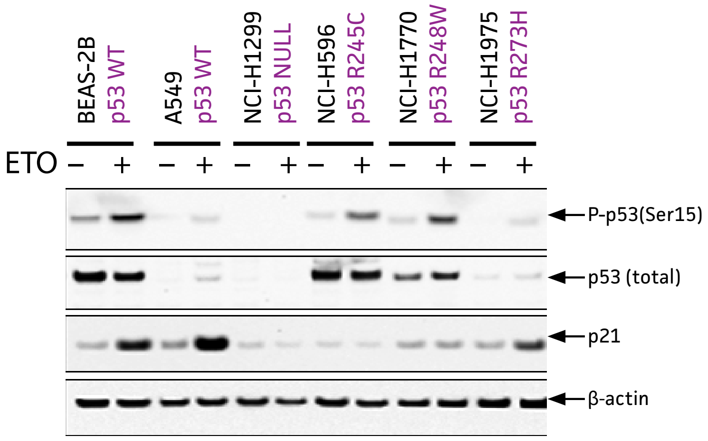


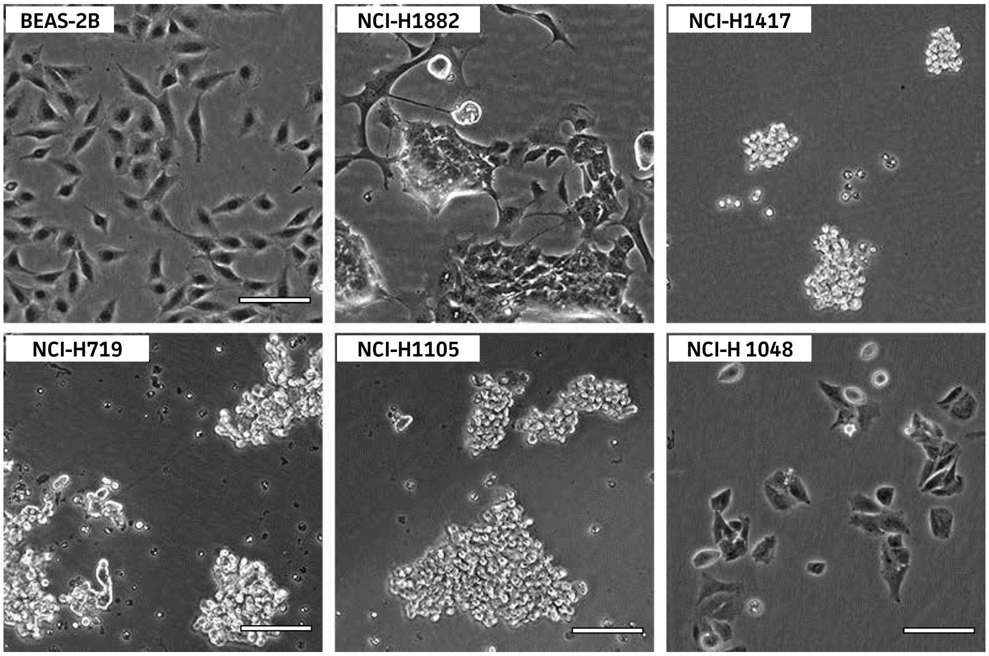
Figure 5. p53 phosphorylation in response to DNA damage. The indicated p53 wild-type and p53 mutation cells were treated with 20 µM etoposide (ETO) for 8 hours to induce DNA damage, or treated with DMSO as a control. Western blotting assay was used to examine phosphorylation of p53 at Serine 15, total protein expression of p53, and expression of p21, a downstream target of p53. β-actin protein was also examined as a control.

Testing performed for each ATCC cell line was completed on current (2012) distribution material. ATCC provides these data in good faith, but makes no warranty, express or implied, nor assumes any legal liability or responsibility for any purpose for which the data are used.

SMALL CELL LUNG CANCER p53 HOTSPOT MUTATION CELL PANEL

The Small Cell Lung Cancer p53 Hotspot Mutation Cell Panel (ATCC® No. TCP-2040™) is composed of six select cell lines derived from the lung. This panel combines wild-type p53 cell lines with mutant p53 cell lines that carry hotspot mutations in one of the following codons: 175, 248, 249, or 273. The p53 status of each line was sequenced and validated by ATCC. The panel is useful for anti-cancer drug targeting or reactivation of mutant p53, as well as studies related to p53 molecular mechanisms.

ATCC® No.	Name	Tissue	Histology	Tumor Source	TP53 Status	Zygosity	Gene Mutation†	Protein Sequence†
CRL-9609™	BEAS-2B	lung	normal tissue,SV-40 immortalized	NA	WT	-	-	-
CRL-5903™	NCI-H1882	lung	small cell lung carcinoma	metastasis (bone marrow)	WT	-	-	-
CRL-5869™	NCI-H1417	lung	small cell lung carcinoma	primary	MUT	homozygous	c.524G>T	p.R175L
CRL-5837™	NCI-H719	lung	small cell lung carcinoma	metastasis (bone marrow)	MUT	homozygous	c.743G>A	p.R248Q
CRL-5856™	NCI-H1105	lung	small cell lung carcinoma	metastasis (lymph node)	MUT	homozygous	c.747G>T	p.R249S
CRL-5853™	NCI-H1048	lung	small cell lung carcinoma	metastasis (pleural effusion)	MUT	heterozygous	c.817C>T	p.R273C



Scale Bar = 100µm

Figure 1. Cell morphology of six cell lines in the Small Cell Lung Cancer p53 Hotspot Mutation Cell Panel. Each cell line was grown using the ATCC recommended culture conditions. Cell morphology was observed under Nikon™ microscopy, and images of the indicated cell lines were captured by Olympus® digital camera.

†For a description of the sequence variation nomenclature please refer to: *den Dunnen JT and Antonarakes SE (2000), Hum. Mutat. 15:7-12.*

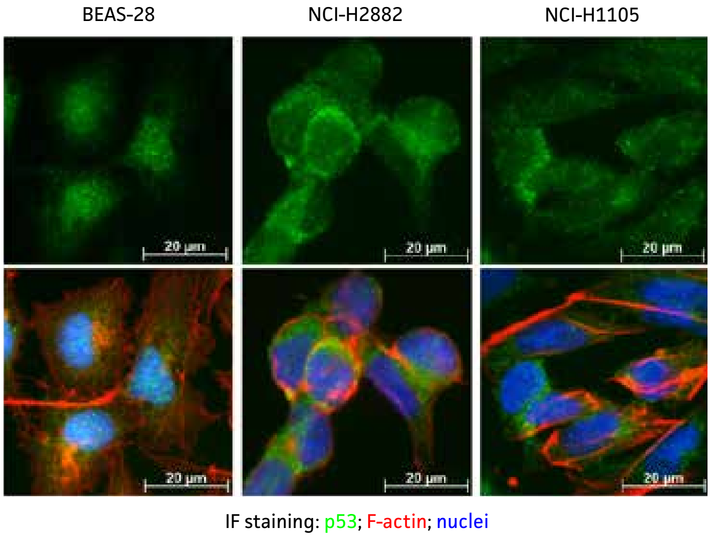


Figure 2. Cellular localization of p53. The indicated p53 wild-type and p53 mutation cells were grow on collagen-coated coverslips. Cells were fixed with 4% paraformaldehyde. p53 was stained with p53 primary antibody and Alexa Fluor 488 secondary antibody (green). F-actin was visualized with phalloidin Alexa Fluor 594 (red). Nuclei of the cells were visualized with Hoechst 33342 (blue). Single florescence channel images of p53 staining are shown in the upper row, and multichannel merged images are shown in the bottom row.

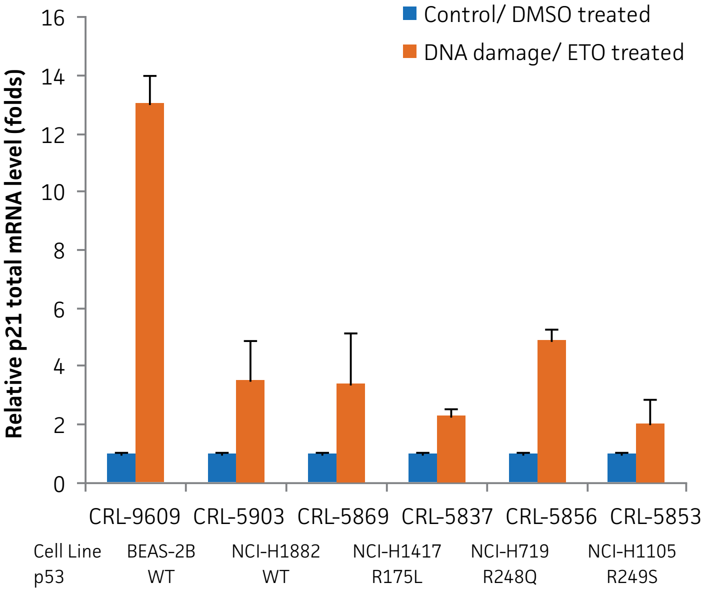


Figure 4. Real time PCR analysis of total mRNA levels of p21, a downstream target of p53, in the indicated p53 wild-type and p53 mutation cell lines. Cells were treated with 20 µM etoposide (ETO) for 6 hours to induce DNA damage, or treated with DMSO as a control. Total mRNA level of p21 and 36B4 were determined by real time quantitative PCR. Relative p21 total mRNA changes were normalized to the housekeeping gene 36B4.

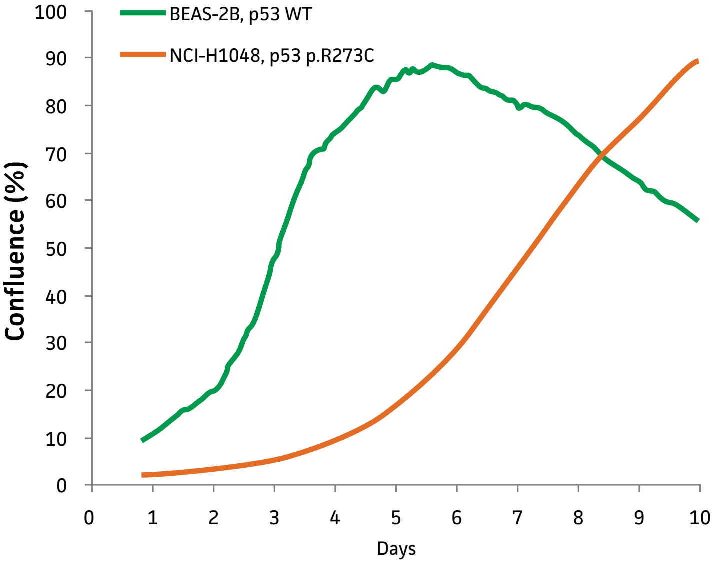


Figure 3. Cell growth kinetics. The indicated p53 wild-type and p53 mutation cells were cultured in ATCC recommended media, and plated at 3000 cells/well in 96-well plates. The cell growth kinetics were constantly monitored for 10 days using a label-free automated IncuCyte® live-cell imaging system (Essen Bioscience).

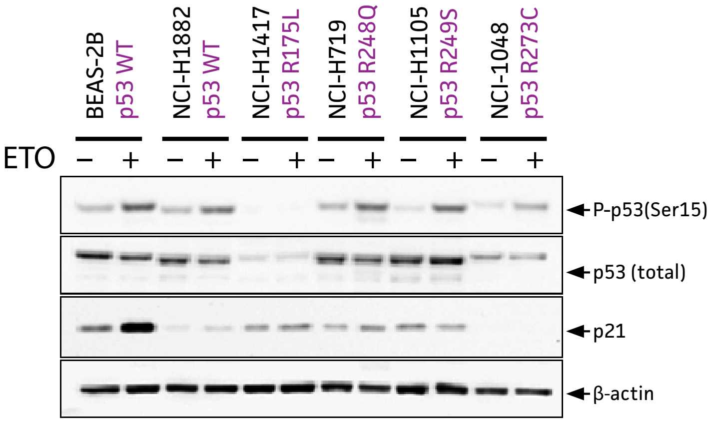


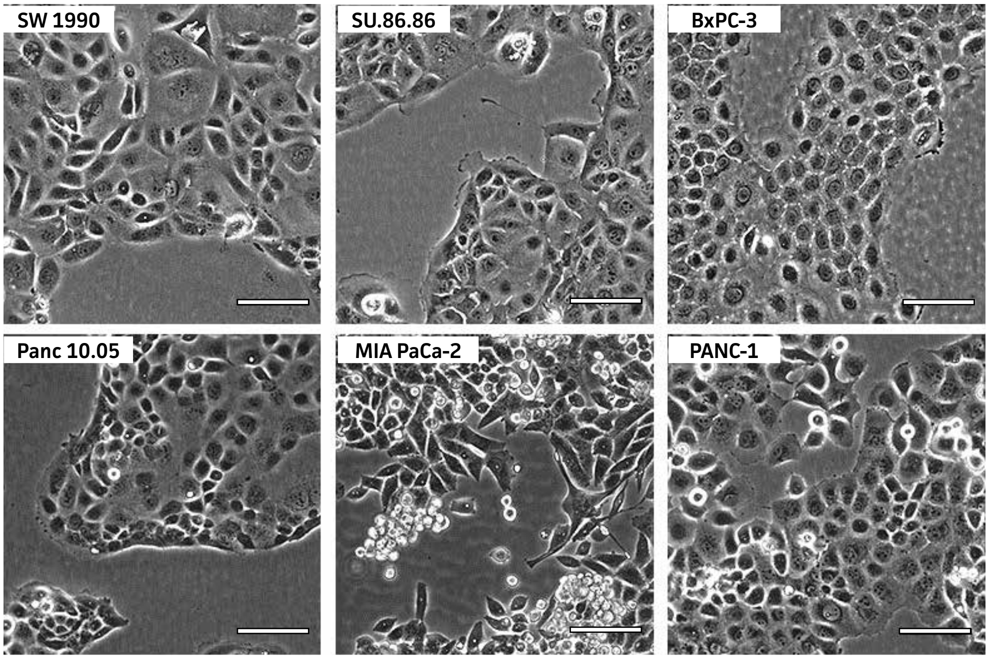
Figure 5. The indicated p53 wild-type and p53 mutation cells were treated with 20 µM etoposide (ETO) for 8 hours to induce DNA damage, or treated with DMSO as a control. Western blotting assay was used to examine phosphorylation of p53 at Serine 15, total protein expression of p53, and expression of p21, a downstream target of p53. µ-actin protein was also examined as a control.

Testing performed for each ATCC cell line was completed on current (2012) distribution material. ATCC provides these data in good faith, but makes no warranty, express or implied, nor assumes any legal liability or responsibility for any purpose for which the data are used.

PANCREATIC CANCER p53 HOTSPOT MUTATION CELL PANEL

The Pancreatic Cancer p53 Hotspot Mutation Cell Panel (ATCC® No. TCP-2060™) is composed of six select adhesion cell lines derived from individuals with pancreatic cancers. This panel combines wild-type p53 cell lines with mutant p53 cell lines that carry hotspot mutations in one of the following codons: 220, 245, 248, 255 and 273. The p53 status of each line was sequenced and validated by ATCC. The panel is useful for anti-cancer drug targeting or reactivation of mutant p53, as well as studies related to p53 molecular mechanisms.

ATCC® No.	Name	Primary Site, Tissue	Histology	TP53 status	Zygosity	Gene mutation†	Protein Sequence†
CRL-2172™	SW1990	pancreas	adenocarcinoma	WT	-	-	-
CRL-1837™	SU.86.86	pancreas	adenocarcinoma	MUT	homozygous	c.733G>A	p.G245S
CRL-1687™	BXPC-3	pancreas	adenocarcinoma	MUT	homozygous	c.659A>G	p.Y220C
CRL-2547™	Panc 10.05	pancreas	adenocarcinoma	MUT	heterozygous	c.764T>A	p.I255N
CRL-1420™	MIA-PaCa-2	pancreas	carcinoma	MUT	homozygous	c.742C>T	p.R248W
CRL-1469™	PANC-1	pancreas	carcinoma	MUT	homozygous	c.818G>A	p.R273H



Scale Bar = 100μm

Figure 1. Cell morphology of the six cell lines in the Pancreatic cancer p53 Hotspot Mutation Cell Panel. One p53 wild-type pancreatic cancer cell line and five p53 hotspot mutation pancreatic cancer cell lines were maintained in ATCC recommended culture conditions. Cell morphology was observed under Nikon™ microscopy, and images of the indicated cell lines were captured by Olympus® digital camera.

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†For a description of the sequence variation nomenclature please refer to: *den Dunnen JT and Antonarakes SE (2000), Hum. Mutat. 15:7-12.*

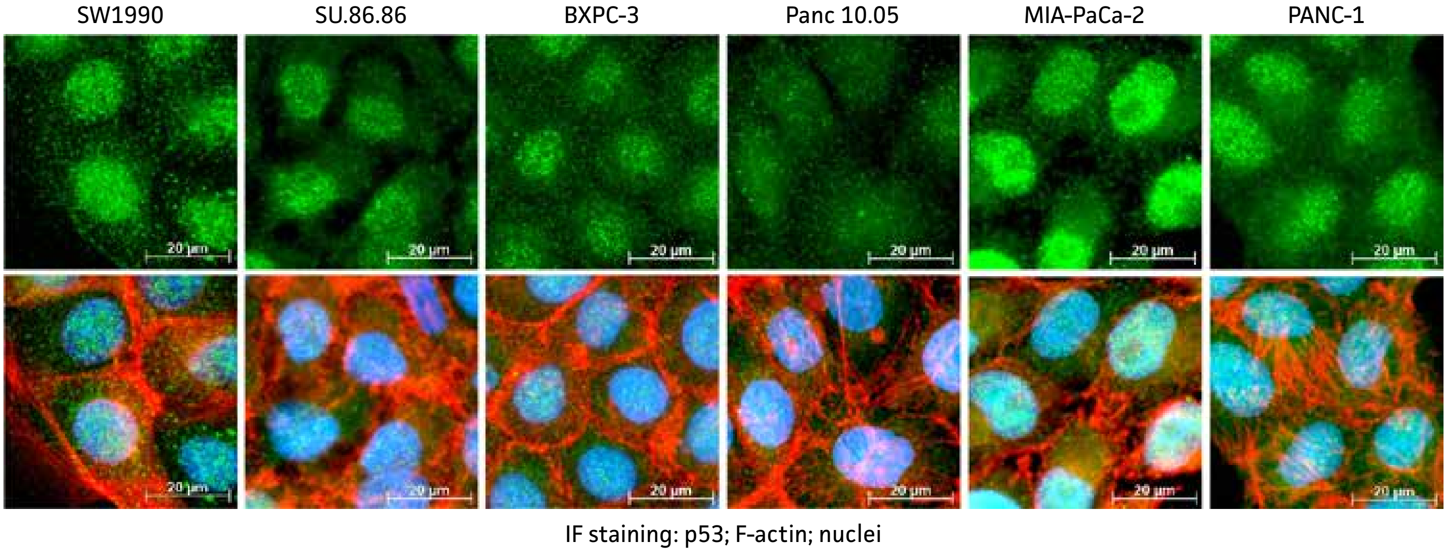
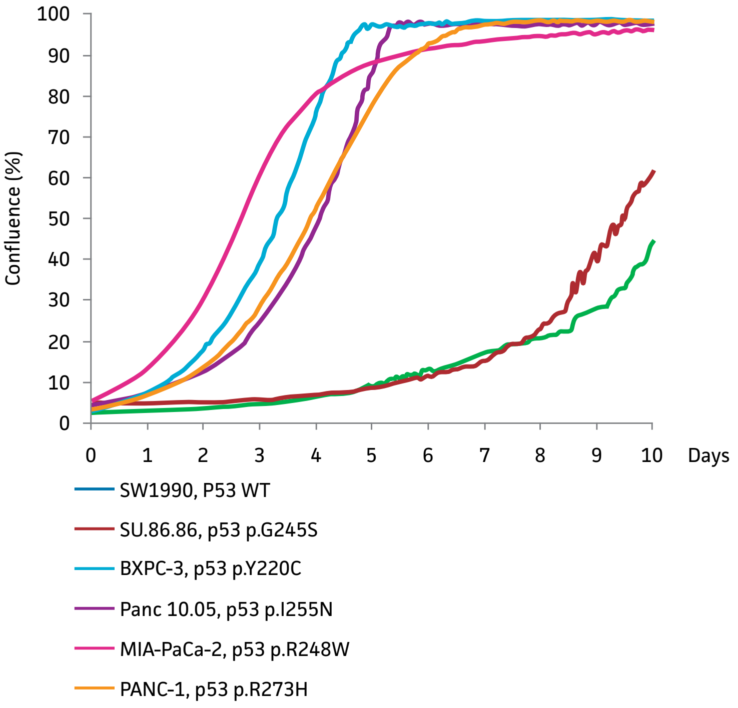


Figure 2. Immunofluorescence staining of p53. The indicated p53 wild-type and p53 mutation cells were grow on collagen-coated coverslips. Cells were fixed with 4% paraformaldehyde. p53 was stained with p53 primary antibody and Alexa Fluor 488 secondary antibody (green). F-actin was visualized with phalloidin Alexa Fluor 594 (red). Nuclei of the cells were visualized with Hoechst 33342 (blue). Single florescence channel images of p53 staining are shown in the upper row, and multichannel merged images are shown in the bottom row.



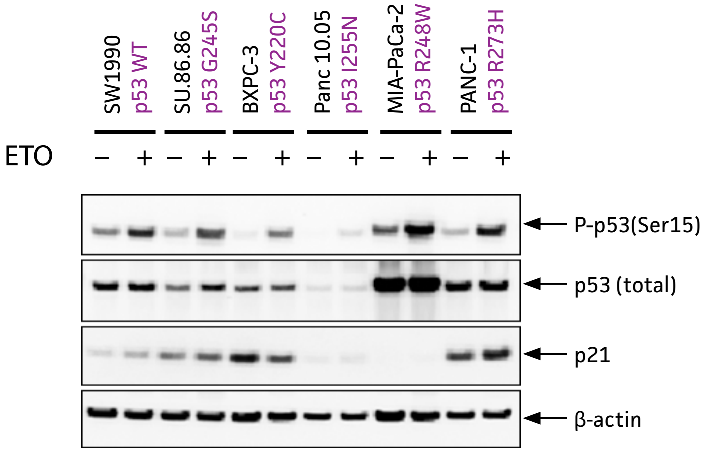
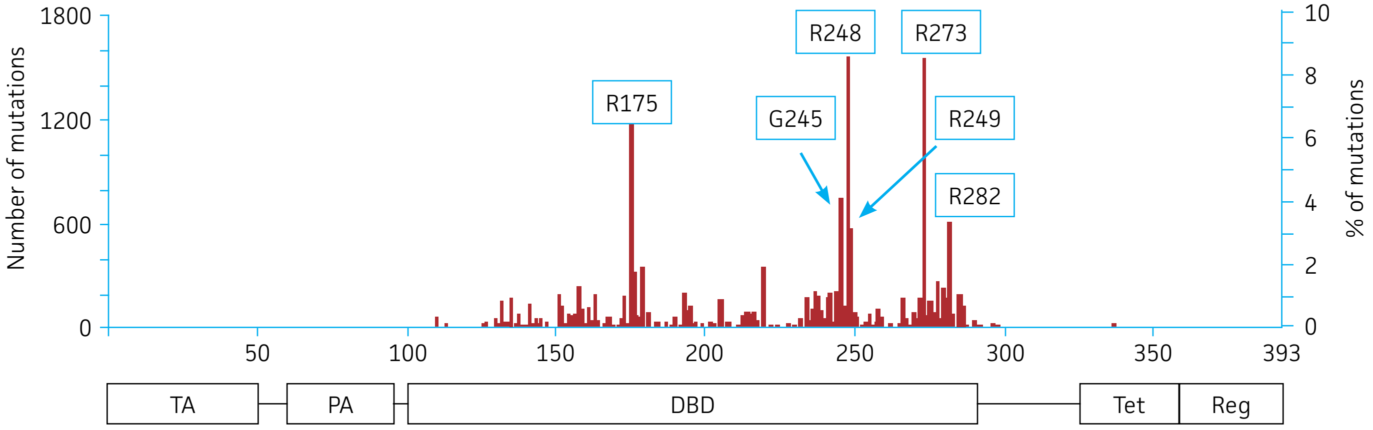


Figure 3. Cell growth kinetics. The indicated p53 wild-type and p53 mutation cells were cultured in ATCC recommended media, and plated at 3000 cells/well in 96-well plate. The cell growth kinetics were constantly monitored for 10 days using a label-free automated IncuCyte® live-cell imaging system (Essen Bioscience).

Figure 4. The indicated p53 wild-type and p53 mutation cells were treated with 20 μM etoposide (ETO) for 8 hours to induce DNA damage, or treated with DMSO as a control. Western blotting was used to examine phosphorylation of p53 at Serine 15, total protein expression of p53, and expression of p21, a downstream target of p53. β-actin protein was also examined as a control.

VALIDATED p53 HOTSPOT MUTATION CELL LINE LIST



Christopher J. Brown et. al., *Trends in Pharmacological Sciences*, 2011

This list includes cell lines that contain mutations in one of the three most commonly mutated p53 codons (i.e. 175, 248, and 273). Cell lines that are either wild-type or null for p53 expression and can be used as controls to facilitate your research. The mutational status of the lines listed below was validated at ATCC.

p53 Wild Type Cell Line

ATCC® No.	**Designation**	**Tissue**	**Disease**	**TP53 status**
HTB-96™	U-2 OS	bone	osteosarcoma	WT
HTB-25™	MDA-MB-175-VII	breast	duct carcinoma	WT
HTB-27™	MDA-MB-361	breast	adenocarcinoma	WT
CL-188™	LS174T	colon	adenocarcinoma	WT
CCL-231™	SW48	colon	adenocarcinoma	WT
TIB-190™	CESS	blood	acute myeloid leukemia (AML)	WT
CRL-9609™	BEAS-2B	lung	normal tissue,SV-40 immortalized	WT
CRL-5903™	NCI-H1882	lung	small cell lung carcinoma (SCLC)	WT
CCL-185™	A549	lung	non-small cell lung carcinoma (NSCLC)	WT
CCL-85™	EB-3	lymph node	Burkitt lymphoma, NOS	WT
CRL-2172™	SW1990	pancreas	adenocarcinoma	WT
CRL-1739™	AGS	stomach	adenocarcinoma	WT

p53 Null Cell Line

ATCC® No.	**Designation**	**Tissue**	**Disease**	**TP53 status**
HTB-85™	Saos-2	bone	osteosarcoma	NULL
CCL-240™	HL-60	blood	acute promyelocytic leukemia	NULL
CRL-5803™	NCI-H1299	lung	non-small cell lung carcinoma (NSCLC)	NULL
HTB-103™	KATO-III	stomach	carcinoma	NULL

p53 Hotspot Codon 175 Mutation Cell Line

ATCC® No.	Designation	Tissue	Disease	TP53 status	Zygosity	Gene sequence[†]	Protein Sequence[†]
CRL-2351™	AU565	breast	adenocarcinoma	MUT	homozygous	c.524G>A	p.R175H
HTB-30™	SK-BR-3	breast	adenocarcinoma	MUT	homozygous	c.524G>A	p.R175H
CCL-255™	LS123	colon	adenocarcinoma	MUT	heterozygous	c.524G>A	p.R175H
CCL-119™	CCRF-CEM	blood	acute lymphoblastic leukemia (ALL)	MUT	heterozygous	c.524G>A	p.R175H
CRL-2265™	CEM/C1	blood	acute lymphoblastic leukemia (ALL), camptothecin (CPT) resistant	MUT	heterozygous	c.524G>A	p.R175H
CRL-5869™	NCI-H1417	lung	small cell lung carcinoma (SCLC)	MUT	homozygous	c.524G>T	p.R175L

p53 Hotspot Codon 248 Mutation Cell Line

ATCC® No.	Designation	Tissue	Disease	TP53 status	Zygosity	Gene sequence[†]	Protein Sequence[†]
CRL-2315™	HCC70	breast	duct carcinoma	MUT	homozygous	c.743G>A	p.R248Q
CCL-220™	COLO 320DM	colon	adenocarcinoma	MUT	homozygous	c.742C>T	p.R248W
CRL-2724™	KASUMI-1	blood	acute myeloid leukemia (AML)	MUT	homozygous	c.743G>A	p.R248Q
CCL-119™	CCRF-CEM	blood	acute lymphoblastic leukemia (ALL)	MUT	heterozygous	c.524G>A	p.R175H
CRL-5893™	NCI-H1770	lung	non-small cell lung carcinoma (NSCLC)	MUT	homozygous	c.741-742CC>TT	p.R248W
CRL-5837™	NCI-H719	lung	small cell lung carcinoma (SCLC)	MUT	homozygous	c.743G>A	p.R248Q
CRL-1648™	CA46	lymph node	Burkitt lymphoma	MUT	homozygous	c.743G>A	p.R248Q
CRL-1432™	Namalwa	lymph node	Burkitt lymphoma, carry EBV	MUT	homozygous	c.743G>A	p.R248Q
CRL-2289™	DB	lymph node	large B-cell lymphoma	MUT	heterozygous	c.743G>A	p.R248Q
CRL-1420™	MIA-PaCa-2	pancreas	carcinoma	MUT	homozygous	c.742C>T	p.R248W

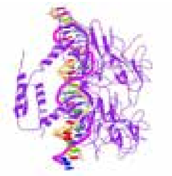
p53 Hotspot Codon 273 Mutation Cell Line

ATCC® No.	Designation	Tissue	Disease	TP53 status	Zygosity	Gene sequence[†]	Protein Sequence[†]
HTB-132™	MDA-MB-468	breast	adenocarcinoma	MUT	homozygous	c.818G>A	p.R273H
CRL-2314™	HCC38	breast	ductal carcinoma	MUT	homozygous	c.818G>T	p.R273L
CCL-218™	WiDr	colon	adenocarcinoma	MUT	homozygous	c.818G>A	p.R273H
CRL-1621™	ARH-77	blood	plasma cell leukemia, carry EBV	MUT	homozygous	c.818G>A	p.R273H
CRL-5853™	NCI-H1048	lung	small cell lung carcinoma (SCLC)	MUT	heterozygous	c.140delC	p.P47FS*76
CRL-5908™	NCI-H1975	lung	non-small cell lung carcinoma (NSCLC)	MUT	homozygous	c.818G>A	p.R273H
CRL-1942™	SUP-T1	lymph node	T cell lymphoblastic lymphoma	MUT	heterozygous	c.743G>A	p.R248Q
CRL-1469™	PANC-1	pancreas/duct	carcinoma	MUT	homozygous	c.818G>A	p.R273H

Other p53 hotspot mutation cell lines

ATCC® No.	Designation	Tissue	Disease	TP53 status	Gene sequence[†]	Protein Sequence[†]
CRL-1687™	BXPC-3	pancreas	adenocarcinoma	MUT	c.659A>G	p.Y220C
CRL-1837™	SU.86.86	pancreas	adenocarcinoma	MUT	c.733G>A	p.G245S
CRL-2158™	LS-1034	colon	adenocarcinoma	MUT	c.733G>A	p.G245S
HTB-178™	NCI-H596	lung	non-small cell lung carcinoma (NSCLC)	MUT	c.733G>T	p.G245C
CRL-5856™	NCI-H1105	lung	small cell lung carcinoma (SCLC)	MUT	c.747G>T	p.R249S
HTB-122™	BT-549	breast	duct carcinoma	MUT	c.747G>C	p.R249S
CRL-2547™	Panc 10.05	pancreas	adenocarcinoma	MUT	c.764T>A	p.I255N

[†] For a description of the sequence variation nomenclature please refer to: *den Dunnen JT and Antonarakes SE (2000), Hum. Mutat. 15:7-12.*



p53 MUTATION CELL LINES IN COSMIC DATABASE

Tumor source	Histology	Zygosity	Gene Sequence[†]	Protein Sequence[†]	Name	ATCC® No.
ADRENAL GLAND, CORTEX						
primary	Carcinoma, primary small cell	homozygous	c.577C>T	p.H193Y	SW-13	CCL-105™
BONE						
primary	Osteosarcoma	homozygous	c.1_1182del1182	p.0?	Saos-2	HTB-85™
primary	Osteosarcoma	homozygous	c.467G>C	p.R156P	HOS	CRL-1543™
BONE MARROW						
primary	Leukemia, acute myelogenous	homozygous	c.672+1G>A	p.?	KG-1	CCL-246™
primary	Leukemia, chronic myelogenous	homozygous	c.697_699delCAC	p.H233del	MEG-01	CRL-2021™
metastasis, pleural effusion	Leukemia, chronic myelogenous	homozygous	c.406_407insC	p.Q136fs*13	K-562	CCL-243™
BRAIN						
primary	Glioblastoma, astrocytoma	homozygous	c.638G>A	p.R213Q	U-118 MG	HTB-15™
primary	Glioblastoma, multiforme	homozygous	c.711G>A	p.M237I	T98G	CRL-1690™
primary	Astrocytoma	homozygous	c.817C>T	p.R273C	SW 1088	HTB-12™
primary	Astrocytoma	heterozygous	c.817C>T	p.R273C	SW 1783	HTB-13™
primary	Astrocytoma	heterozygous	c.818G>A	p.R273H	SW 1783	HTB-13™
metastasis, bone marrow	Neuroblastoma, embryonal	homozygous	c.329G>T	p.R110L	SK-N-DZ	CRL-2149™
metastasis, bone marrow	Neuroblastoma, embryonal	homozygous	c.737T>G	p.M246R	SK-N-FI	CRL-2142™
BREAST						
primary	Carcinoma, primary ductal	homozygous	c.1024C>T	p.R342*	UACC-893	CRL-1902™
primary	Carcinoma, primary ductal	homozygous	c.220_226delGCCCCTG	p.A74fs*47	HCC1419	CRL-2326™
primary	Carcinoma, primary ductal	homozygous	c.322_324delGGT	p.G108del	HCC1187	CRL-2322™
primary	Carcinoma	homozygous	c.394A>C	p.K132Q	BT-20	HTB-19™
primary	Carcinoma, ductal	homozygous	c.488A>G	p.Y163C	HCC1954	CRL-2338™
primary	Carcinoma, primary ductal	homozygous	c.524G>A	p.R175H	HCC1395	CRL-2324™
primary	Carcinoma, primary ductal	homozygous	c.659A>G	p.Y220C	HCC1419	CRL-2326™
primary	Carcinoma, primary ductal	homozygous	c.673-2A>T	p.?	HCC1599	CRL-2331™
primary	Carcinoma, primary ductal	homozygous	c.742C>T	p.R248W	HCC2157	CRL-2340™
primary	Carcinoma, primary ductal	homozygous	c.743G>A	p.R248Q	HCC70	CRL-2315™
primary	Carcinoma, primary ductal	homozygous	c.743G>A	p.R248Q	HCC1143	CRL-2321™

Tumor source	Histology	Zygosity	Gene Sequence[†]	Protein Sequence[†]	Name	ATCC® No.
primary	Carcinoma, ductal, papillary	homozygous	c.747G>C	p.R249S	BT-549	HTB-122™
primary	Carcinoma, primary acantholytic squamous cell	homozygous	c.766_767insAA	p.T256fs*90	HCC1806	CRL-2335™
primary	Carcinoma, primary ductal	homozygous	c.818G>T	p.R273L	HCC38	CRL-2314™
primary	Carcinoma, primary ductal	homozygous	c.847C>T	p.R283C	HCC2218	CRL-2343™
primary	Carcinoma, ductal	homozygous	c.853G>A	p.E285K	BT-474	HTB-20™
primary	Carcinoma, primary metaplastic	heterozygous	c.880G>T	p.E294*	HCC1569	CRL-2330™
primary	Carcinoma, primary ductal	homozygous	c.916C>T	p.R306*	HCC1937	CRL-2336™
metastasis, pleural effusion	Carcinoma, medulallary	homozygous	c.261_286delAGCCCCCTCCTGGCCCCTGTCATCTT	p.A88fs*52	MDA-MB-157	HTB-24™
metastasis, pleural effusion	Adenocarcinoma	homozygous	c.524G>A	p.R175H	AU565	CRL-2351™
metastasis, pleural effusion	Carcinoma, ductal	homozygous	c.580C>T	p.L194F	T-47D	HTB-133™
metastasis, pleural effusion	Adenocarcinoma	homozygous	c.707A>G	p.Y236C	MDA-MB-415	HTB-128™
metastasis, pleural effusion	Adenocarcinoma	homozygous	c.818G>A	p.R273H	MDA-MB-468	HTB-132™
metastasis, pleural effusion	Adenocarcinoma	homozygous	c.839G>A	p.R280K	MDA-MB-231	HTB-26™
metastasis, pleural effusion	Adenocarcinoma	homozygous	c.839G>C	p.R280T	CAMA-1	HTB-21™
CAECUM						
primary	Carcinoma	heterozygous	c.378C>A	p.Y126*	LS411N	CRL-2159™
primary	Carcinoma	homozygous	c.733G>A	p.G245S	LS1034	CRL-2158™
primary	Carcinoma	heterozygous	c.817C>T	p.R273C	SNU-C2B	CCL-250™
primary	Carcinoma	heterozygous	c.818G>A	p.R273H	SNU-C2B	CCL-250™
metastasis, abdominal wall	Adenocarcinoma	homozygous	c.818G>A	p.R273H	NCI-H508	CCL-253™
metastasis, ascites	Adenocarcinoma	homozygous	c.672G>T	p.E224D	NCI-H716	CCL-251™
metastasis, common duct node	Adenocarcinoma	homozygous	c.473G>T	p.R158L	NCI-H747	CCL-252™
CEREBELLUM						
primary	Medulloblastoma, desmoplastic	homozygous	c.725G>T	p.C242F	Daoy	HTB-186™
primary	Neuroectoderm, primitive, malignant	homozygous	c.823T>G	p.C275G	PFSK-1	CRL-2060™
CERVIX						
primary	Carcinoma	homozygous	c.817C>T	p.R273C	C-33 A	HTB-31™
metastasis, lymph node	Carcinoma	homozygous	c.734G>T	p.G245V	HT-3	HTB-32™
COLON						
primary	Adenocarcinoma	heterozygous	c.1101-2A>C	p.?	HCT-15	CCL-225™
primary	Adenocarcinoma	homozygous	c.476C>A	p.A159D	SW1116	CCL-233™
primary	Adenocarcinoma	heterozygous	c.524G>A	p.R175H	LS123	CCL-255™
primary	Adenocarcinoma	homozygous	c.610G>T	p.E204*	C2BBe1	CRL-2102™
primary	Adenocarcinoma	homozygous	c.712_725delTGTAACAGTTCCTG	p.C238fs*21	SW1417	CCL-238™
primary	Adenocarcinoma	heterozygous	c.722C>T	p.S241F	HCT-15	CCL-225™

Tumor source	Histology	Zygosity	Gene Sequence†	Protein Sequence†	Name	ATCC® No.
primary	Adenocarcinoma	homozygous	c.742C>T	p.R248W	COLO 320HSR	CCL-220.1™
primary	Adenocarcinoma	homozygous	c.818G>A	p.R273H	HT-29	HTB-38™
metastasis, ascites	Adenocarcinoma	homozygous	c.308_333>TA	p.Y103_L111>L	COLO 205	CCL-222™
metastasis, lung	Carcinoma	homozygous	c.376-1G>T	p.?	T84	CCL-248™
metastasis, lymph node	Adenocarcinoma	homozygous	c.818G>A	p.R273H	SW620	CCL-227™
metastasis, lymph node	Adenocarcinoma	homozygous	c.925C>T	p.P309S	SW620	CCL-227™
metastasis, ovary	Adenocarcinoma	homozygous	c.785G>T	p.G262V	SW 626	HTB-78™
metastasis, peritoneum	Adenocarcinoma	homozygous	c.497C>A	p.S166*	SNU-C1	CRL-5972™

CONNECTIVE TISSUE

primary	Fibrosarcoma	homozygous	c.637C>T	p.R213*	SW 684	HTB-91™
primary	Liposarcoma	homozygous	c.752T>A	p.I251N	SW 872	HTB-92™

EYE, RETINA

primary	Retinoblastoma	heterozygous	c.292C>T	p.P98S	WERI-Rb-1	HTB-169™

KIDNEY

primary	Adenocarcinoma, renal cell	heterozygous	c.560-2A>G	p.?	786-O	CRL-1932™
primary	Adenocarcinoma, renal cell	heterozygous	c.832C>G	p.P278A	786-O	CRL-1932™
metastasis, pleural effusion	Tumor, Wilms'	homozygous	c.733G>A	p.G245S	SK-NEP-1	HTB-48™

LIVER

primary	Carcinoma, hepatocellular	homozygous	c.481G>A	p.A161T	SNU-449	CRL-2234™
primary	Carcinoma, hepatocellular, pleomorphic	homozygous	c.490A>T	p.K164*	SNU-387	CRL-2237™
primary	Carcinoma, hepatocellular	heterozygous	c.715A>G	p.N239D	SNU-475	CRL-2236™
primary	Carcinoma, hepatocellular	homozygous	c.747G>T	p.R249S	PLC/PRF/5	CRL-8024™
primary	Carcinoma, hepatocellular	heterozygous	c.785G>A	p.G262D	SNU-475	CRL-2236™

LUNG

primary	Adenocarcinoma, large cell	heterozygous	c.430C>T	p.Q144*	NCI-H1581	CRL-5878™
primary	Carcinoma, squamous cell	homozygous	c.438G>A	p.W146*	NCI-H520	HTB-182™
primary	Carcinoma, small cell	homozygous	c.440T>A	p.V147D	NCI-H1963	CRL-5982™
primary	Carcinoma, squamous cell	homozygous	c.472C>G	p.R158G	NCI-H2170	CRL-5928™
primary	Carcinoma, squamous cell	homozygous	c.499C>T	p.Q167*	SW 900	HTB-59™
primary	Carcinoma, small cell	homozygous	c.524G>T	p.R175L	NCI-H1417	CRL-5869™
primary	Adenocarcinoma, non-small cell	homozygous	c.527G>A	p.C176Y	NCI-H1651	CRL-5884™
primary	Carcinoid, atypical	homozygous	c.528C>G	p.C176W	NCI-H720	CRL-5838™
primary	Carcinoma, small cell	homozygous	c.528C>G	p.C176W	SHP-77	CRL-2195™
primary	Adenocarcinoma, non-small cell	homozygous	c.572delC	p.P191fs*56	NCI-H522	CRL-5810™
primary	Adenocarcinoma	heterozygous	c.578A>G	p.H193R	SK-LU-1	HTB-57™
primary	Carcinoma, anaplastic	homozygous	c.586C>T	p.R196*	Calu-6	HTB-56™

Tumor source	Histology	Zygosity	Gene Sequence†	Protein Sequence†	Name	ATCC® No.
primary	Adenocarcinoma, non-small cell	heterozygous	c.625A>T	p.R209*	NCI-H1793	CRL-5896™
primary	Adenocarcinoma, non-small cell	homozygous	c.659A>G	p.Y220C	NCI-H2342	CRL-5941™
primary	Carcinoid	homozygous	c.681_681delT	p.D228fs*19	UMC-11	CRL-5975™
primary	Carcinoma, small cell lung cancer	heterozygous	c.722C>T	p.S241F	DMS 53	CRL-2062™
primary	Carcinoma, adenosquamous	homozygous	c.733G>T	p.G245C	NCI-H596	HTB-178™
primary	Adenocarcinoma, non-small cell	homozygous	c.738G>C	p.M246I	NCI-H23	CRL-5800™
primary	Carcinoma, small cell	homozygous	c.783-2A>C	p.?	NCI-H2227	CRL-5934™
primary	Adenocarcinoma, non-small cell	heterozygous	c.818G>A	p.R273H	NCI-H1793	CRL-5896™
primary	Adenocarcinoma, non-small cell	homozygous	c.818G>A	p.R273H	NCI-H1975	CRL-5908™
primary	Adenocarcinoma, non-small cell	homozygous	c.818G>T	p.R273L	NCI-H1734	CRL-5891™
primary	Adenocarcinoma, non-small cell	homozygous	c.818G>T	p.R273L	NCI-H1838	CRL-5899™
primary	Carcinoma, non-small cell	homozygous	c.879_880GG>CT	p.E294>*	NCI-H810	CRL-5816™
primary	Adenocarcinoma, squamous cell	homozygous	c.919+1G>T	p.?	NCI-H1703	CRL-5889™
primary	Adenocarcinoma, non-small cell	homozygous	c.991C>T	p.Q331*	NCI-H2228	CRL-5935™
metastasis, adrenal gland	Carcinoma, small cell	homozygous	c.844C>G	p.R282G	NCI-H510A	HTB-184™
metastasis, ascites	Carcinoma, small cell	homozygous	c.783-1G>T	p.?	NCI-H1694	CRL-5888™
metastasis, ascites	Adenocarcinoma, non-small cell	homozygous	c.818G>A	p.R273H	NCI-H2405	CRL-5944™
metastasis, bone marrow	Carcinoma, small cell	homozygous	c.469G>T	p.V157F	NCI-H2196	CRL-5932™
metastasis, bone marrow	Carcinoma, small cell	homozygous	c.673-2A>C	p.?	NCI-H1092	CRL-5855™
metastasis, bone marrow	Carcinoma, small cell	homozygous	c.673-2A>T	p.?	NCI-H209	HTB-172™
metastasis, bone marrow	Carcinoma, small cell	homozygous	c.707A>G	p.Y236C	NCI-H345	HTB-180™
metastasis, bone marrow	Carcinoma, small cell	homozygous	c.743G>A	p.R248Q	NCI-H719	CRL-5837™
metastasis, bone marrow	Carcinoma, small cell	homozygous	c.743G>T	p.R248L	NCI-H1618	CRL-5879™
metastasis, bone marrow	Carcinoma, small cell	homozygous	c.953_971del19	p.P318fs*21	NCI-H146	HTB-173™
metastasis, bone marrow	Carcinoma, small cell	homozygous	c.97-1G>C	p.?	NCI-H711	CRL-5836™
metastasis, bone marrow	Carcinoma, small cell variant	homozygous	c.97-1G>C	p.?	NCI-H526	CRL-5811™
metastasis, brain	Carcinoma, small cell	homozygous	c.830G>T	p.C277F	NCI-H250	CRL-5828™
metastasis, liver	Carcinoma, small cell	homozygous	c.463A>C	p.T155P	DMS 153	CRL-2064™
metastasis, liver	Adenocarcinoma, non-small cell	homozygous	c.725G>T	p.C242F	NCI-H1755	CRL-5892™
metastasis, lymph node	Carcinoma, small cell	homozygous	c.1001G>T	p.G334V	NCI-H1184	CRL-5858™
metastasis, lymph node	Adenocarcinoma	homozygous	c.104_105insT	p.L35fs*8	NCI-H1648	CRL-5882™
metastasis, lymph node	Adenocarcinoma, non-small cell	homozygous	c.184G>T	p.E62*	NCI-H838	CRL-5844™

Tumor source	Histology	Zygosity	Gene Sequence[†]	Protein Sequence[†]	Name	ATCC® No.
metastasis, lymph node	Carcinoma, small cell	homozygous	c.193A>T	p.R65*	NCI-H2330	CRL-5940™
metastasis, lymph node	Adenocarcinoma, non-small cell	homozygous	c.461G>T	p.G154V	NCI-H2291	CRL-5939™
metastasis, lymph node	Carcinoma, small cell variant	homozygous	c.464C>A	p.T155N	NCI-H524	CRL-5831™
metastasis, lymph node	Adenocarcinoma, non-small cell	homozygous	c.469G>T	p.V157F	NCI-H2087	CRL-5922™
metastasis, lymph node	Carcinoma,large cell	homozygous	c.473G>T	p.R158L	NCI-H661	HTB-183™
metastasis, lymph node	Carcinoma, non-small cell	homozygous	c.492G>T	p.K164N	NCI-H650	CRL-5835™
metastasis, lymph node	Carcinoma, small cell	homozygous	c.537T>G	p.H179Q	NCI-H1436	CRL-5871™
metastasis, lymph node	Carcinoma, small cell	homozygous	c.625A>T	p.R209*	NCI-H2141	CRL-5927™
metastasis, lymph node	Carcinoma,large cell	heterozygous	c.644G>T	p.S215I	NCI-H661	HTB-183™
metastasis, lymph node	Carcinoma, small cell	homozygous	c.658T>G	p.Y220D	NCI-H2029	CRL-5913™
metastasis, lymph node	Carcinoma, small cell	homozygous	c.659A>G	p.Y220C	NCI-H748	CRL-5841™
metastasis, lymph node	Carcinoma, small cell	homozygous	c.725G>C	p.C242S	NCI-H889	CRL-5817™
metastasis, lymph node	Adenocarcinoma, non-small cell	homozygous	c.726C>G	p.C242W	NCI-H1993	CRL-5909™
metastasis, lymph node	Carcinoma, small cell	homozygous	c.733G>C	p.G245R	NCI-H1930	CRL-5906
metastasis, lymph node	Carcinoma, non-small cell, neuroendocrine	homozygous	c.741_742CC>TT	p.R248W	NCI-H1770	CRL-5893™
metastasis, lymph node	Carcinoma, small cell	homozygous	c.747G>T	p.R249S	NCI-H1105	CRL-5856™
metastasis, lymph node	Adenocarcinoma, non-small cell	homozygous	c.785G>T	p.G262V	NCI-H2030	CRL-5914™
metastasis, lymph node	Carcinoma,large cell	homozygous	c.818G>A	p.R273H	NCI-H1155	CRL-5818™
metastasis, lymph node	Adenocarcinoma	homozygous	c.818G>T	p.R273L	NCI-H2009	CRL-5911™
metastasis, lymph node	Adenocarcinoma, non-small cell	homozygous	c.818G>T	p.R273L	NCI-H1623	CRL-5881™
metastasis, lymph node	Carcinoma, small cell	homozygous	c.848G>C	p.R283P	NCI-H64	CRL-5976™
metastasis, lymph node	Adenocarcinoma, non-small cell	homozygous	c.993+1G>T	p.?	NCI-H1693	CRL-5887™
metastasis, mediastinal	Carcinoma, small cell	homozygous	c.637C>T	p.R213*	DMS 114	CRL-2066™
metastasis, pericardial fluid	Adenocarcinoma, papillary	homozygous	c.473G>T	p.R158L	NCI-H441	HTB-174™
metastasis, pleural effusion	Carcinoma, small cell	heterozygous	c.140delC	p.P47fs*76	NCI-H1048	CRL-5853™
metastasis, pleural effusion	Carcinoma, non-small cell	homozygous	c.184G>T	p.E62*	NCI-H2126	CCL-256™
metastasis, pleural effusion	Carcinoma, small cell	homozygous	c.202G>T	p.E68*	NCI-H1522	CRL-5874™
metastasis, pleural effusion	Carcinoma, small cell	homozygous	c.430C>T	p.Q144*	NCI-H2171	CRL-5929™
metastasis, pleural effusion	Carcinoma, small cell	homozygous	c.461G>T	p.G154V	NCI-H446	HTB-171™
metastasis, pleural effusion	Adenocarcinoma, non-small cell	heterozygous	c.47A>T	p.Q16L	NCI-H2122	CRL-5985™

Tumor source	Histology	Zygosity	Gene Sequence[†]	Protein Sequence[†]	Name	ATCC® No.
metastasis, pleural effusion	Carcinoma, small cell	homozygous	c.488A>G	p.Y163C	NCI-H378	CRL-5808™
metastasis, pleural effusion	Carcinoma, small cell	homozygous	c.511G>T	p.E171*	NCI-H69	HTB-119™
metastasis, pleural effusion	Adenocarcinoma, non-small cell	heterozygous	c.527G>T	p.C176F	NCI-H2122	CRL-5985™
metastasis, pleural effusion	Adenocarcinoma	homozygous	c.672+1G>A	p.?	NCI-H1792	CRL-5895™
metastasis, pleural effusion	Adenocarcinoma	homozygous	c.673-2A>G	p.?	NCI-H1650	CRL-5883™
metastasis, pleural effusion	Adenocarcinoma	homozygous	c.711G>T	p.M237I	Calu-3	HTB-55™
metastasis, pleural effusion	Carcinoma, small cell	homozygous	c.722C>G	p.S241C	NCI-H187	CRL-5804™
metastasis, pleural effusion	Adenocarcinoma, non-small cell	homozygous	c.800G>C	p.R267P	NCI-H1437	CRL-5872™
metastasis, pleural effusion	Carcinoma, small cell	heterozygous	c.817C>T	p.R273C	NCI-H1048	CRL-5853™
metastasis, pleural effusion	Carcinoma, small cell lung cancer	homozygous	c.834_835TG>A	p.R280fs*65	DMS 79	CRL-2049™
metastasis, pleural effusion	Adenocarcinoma	homozygous	c.853G>A	p.E285K	NCI-H1355	CRL-5865™
metastasis, pleural effusion	Carcinoma, squamous cell	homozygous	c.892G>T	p.E298*	SK-MES-1	HTB-58™
metastasis, soft tissue	Carcinoma, small cell	homozygous	c.1024C>T	p.R342*	NCI-H774	CRL-5842™
metastasis, soft tissue	Adenocarcinoma	homozygous	c.743G>T	p.R248L	NCI-H1573	CRL-5877™
LUNG, BRONCHUS						
primary	Carcinoid	homozygous	c.496_497ins9	p.Q165_S166insYKQ	NCI-H727	CRL-5815™
primary	Carcinoma	heterozygous	c.824G>T	p.C275F	ChaGo-K-1	HTB-168™
primary	Carcinoma	homozygous	c.97-1G>C	p.?	ChaGo-K-1	HTB-168™
LYMPH NODE						
metastasis, ovary	Lymphoma, Burkitt's	homozygous	c.731G>A	p.G244D	EB2	HTB-61™
LYMPHOID						
primary	Leukemia, acute lymphocytic	heterozygous	c.541C>T	p.R181C	Reh	CRL-8286™
primary	Lymphoma, cutaneous	homozygous	c.586C>T	p.R196*	H9	HTB-176™
primary	Lymphoma, Burkitt's	homozygous	c.638G>A	p.R213Q	Raji	CCL-86™
primary	Lymphoma, Burkitt's	heterozygous	c.700T>C	p.Y234H	Raji	CCL-86™
primary	Lymphoma, Burkitt's	homozygous	c.743G>A	p.R248Q	CA46	CRL-1648™
primary	Lymphoma, Burkitt's	homozygous	c.760_761AT>GA	p.I254D	Ramos.2G6.4C10	CRL-1923™
primary	Leukemia, acute lymphoblastic	heterozygous	c.916C>T	p.R306*	MOLT-4	CRL-1582™
metastasis, ascites	Lymphoma, Burkitt's	homozygous	c.394A>C	p.K132Q	Jiyoye	CCL-87™
metastasis, ascites	Lymphoma, non-Hodgkin's	homozygous	c.412G>C	p.A138P	RL	CRL-2261™
metastasis, ascites	Lymphoma, Burkitt's	heterozygous	c.473G>A	p.R158H	ST486	CRL-1647™
metastasis, ascites	Lymphoma, diffuse mixed	heterozygous	c.646G>A	p.V216M	HT	CRL-2260™
metastasis, ascites	Lymphoma, undifferentiated	homozygous	c.713G>A	p.C238Y	MC116	CRL-1649™
metastasis, ascites	Lymphoma, Burkitt's	heterozygous	c.715A>G	p.N239D	ST486	CRL-1647™

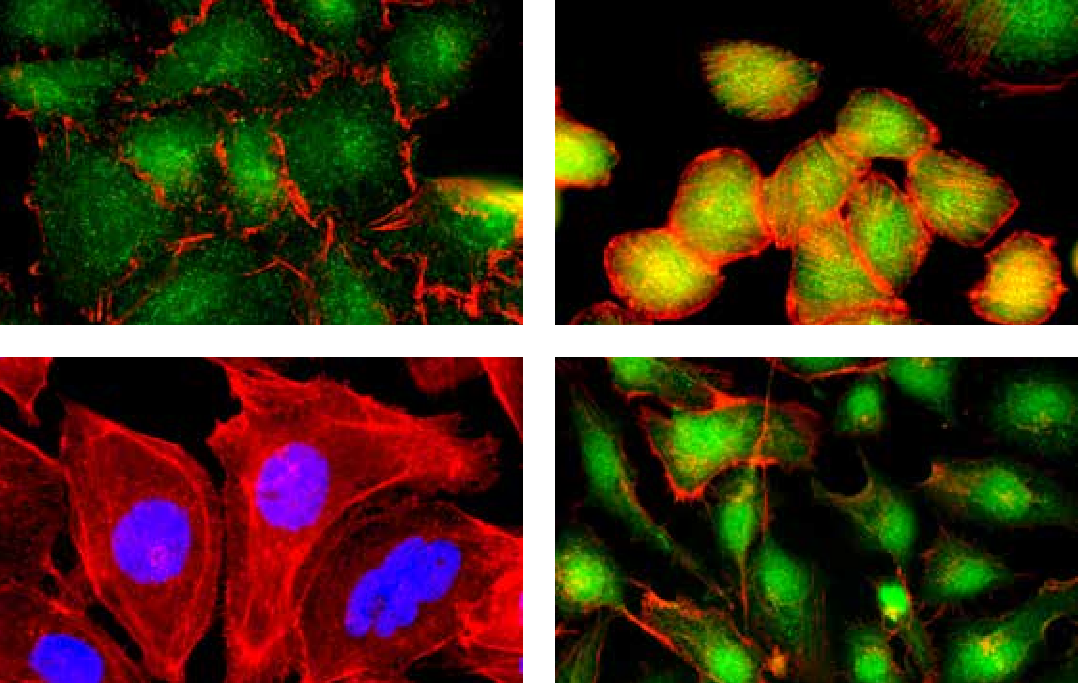
Tumor source	Histology	Zygosity	Gene Sequence†	Protein Sequence†	Name	ATCC® No.
metastasis, ascites	Lymphoma, large B cell	heterozygous	c.743G>A	p.R248Q	DB	CRL-2289™
metastasis, ascites	Lymphoma, diffuse mixed	heterozygous	c.818G>A	p.R273H	HT	CRL-2260™
metastasis, pleural effusion	Lymphoma, histiocytic	homozygous	c.559+1G>A	p.?	TUR	CRL-2367™
metastasis, pleural effusion	Lymphoma, T-cell lymphoblastic	heterozygous	c.743G>A	p.R248Q	SUP-T1	CRL-1942™
metastasis, pleural effusion	Lymphoma, T-cell lymphoblastic	heterozygous	c.800G>T	p.R267L	SUP-T1	CRL-1942™
metastasis, pleural effusion	Lymphoma, T-cell lymphoblastic	heterozygous	c.818G>A	p.R273H	SUP-T1	CRL-1942™
MUSCLE						
primary	Rhabdomyosarcoma	homozygous	c.354_355insCA	p.A119fs*5	A-673	CRL-1598™
primary	Rhabdomyosarcoma	homozygous	c.742C>T	p.R248W	RD	CCL-136™
OVARY						
primary	Adenocarcinoma	homozygous	c.406C>T	p.Q136*	Caov-3	HTB-75™
metastasis, ascites	Adenocarcinoma	homozygous	c.267delC	p.S90fs*33	SK-OV-3	HTB-77™
metastasis, fallopian tube	Adenocarcinoma	homozygous	c.440T>A	p.V147D	Caov-4	HTB-76™
PANCREAS						
primary	Adenocarcinoma	homozygous	c.376-1G>T	p.?	Panc 03.27	CRL-2549™
primary	Adenocarcinoma	homozygous	c.659A>G	p.Y220C	BxPC-3	CRL-1687™
primary	Carcinoma	homozygous	c.742C>T	p.R248W	MIA PaCa-2	CRL-1420™
primary	Adenocarcinoma	heterozygous	c.764T>A	p.I255N	Panc 10.05	CRL-2547™
metastasis, ascites	Adenocarcinoma	homozygous	c.403delT	p.C135fs*35	AsPC-1	CRL-1682™
metastasis, ascites	Adenocarcinoma	homozygous	c.451C>T	p.P151S	HPAF-II	CRL-1997™
metastasis, liver	Adenocarcinoma, ductal	homozygous	c.724T>C	p.C242R	CFPAC-1	CRL-1918™
PERIPHERAL BLOOD						
primary	Leukemia, acute promyelocytic	homozygous	c.1_1182del1182	p.0?	HL-60	CCL-240™
primary	Leukemia, acute T cell	heterozygous	c.1083delG	p.G361fs*8	J.RT3-T3.5	TIB-153™
primary	Lymphoma, cutaneous T cell	homozygous	c.376-1G>A	p.?	HH	CRL-2105™
primary	Lymphoma, Burkitt's	heterozygous	c.455C>T	p.P152L	GA-10 (Clone 4)	CRL-2393™
primary	Leukemia, acute monocytic	homozygous	c.520_545del26	p.R174fs*3	THP-1	TIB-202™
primary	Leukemia, acute lymphoblastic	heterozygous	c.524G>A	p.R175H	CCRF-CEM	CCL-119™
primary	Leukemia, acute T cell	heterozygous	c.586C>T	p.R196*	J.RT3-T3.5	TIB-153™
primary	Lymphoma, Burkitt's	heterozygous	c.695T>A	p.I232N	GA-10 (Clone 4)	CRL-2393™
primary	Leukemia, acute lymphoblastic	heterozygous	c.743G>A	p.R248Q	CCRF-CEM	CCL-119™
primary	Leukemia, acute myeloblastic	homozygous	c.743G>A	p.R248Q	Kasumi-1	CRL-2724™
primary	Lymphoma, Burkitt's	heterozygous	c.797G>A	p.G266E	Daudi	CCL-213™
primary	Leukemia, acute lymphoblastic	homozygous	c.814G>A	p.V272M	Loucy	CRL-2629™
primary	Leukemia, plasma cell	homozygous	c.818G>A	p.R273H	ARH-77	CRL-1621™
primary	Plasmacytoma, myeloma	homozygous	c.853G>A	p.E285K	RPMI 8226	CCL-155™
primary	Leukemia, acute monocytic	homozygous	c.993+2T>G	p.?	AML-193	CRL-9589™

Tumor source	Histology	Zygosity	Gene Sequence[†]	Protein Sequence[†]	Name	ATCC® No.
PHARYNX						
primary	Carcinoma, squamous cell	heterozygous	c.376-1G>A	p.?	FaDu	HTB-43™
primary	Carcinoma, squamous cell	heterozygous	c.743G>T	p.R248L	FaDu	HTB-43™
metastasis, pleural effusion	Carcinoma	homozygous	c.524G>A	p.R175H	Detroit 562	CCL-138™
PROSTATE						
primary	Carcinoma	heterozygous	c.992A>G	p.Q331R	22Rv1	CRL-2505™
metastasis, brain	Carcinoma	heterozygous	c.668C>T	p.P223L	DU 145	HTB-81™
metastasis, brain	Carcinoma	heterozygous	c.820G>T	p.V274F	DU 145	HTB-81™
metastasis, bone	Adenocarcinoma	homozygous	c.414delC	p.K139fs*31	PC-3	CRL-1435™
RECTUM						
primary	Adenocarcinoma	homozygous	c.742C>T	p.R248W	SW837	CCL-235™
primary	Adenocarcinoma	homozygous	c.743G>A	p.R248Q	SW1463	CCL-234™
RETROPERITONEAL						
primary	Primitive neuroectodermal, malignant	homozygous	c.527G>T	p.C176F	SK-PN-DW	CRL-2139™
SALIVARY GLAND						
primary	Carcinoma, epidermoid	homozygous	c.539delA	p.E180fs*67	A-253	HTB-41™
SKIN						
primary	Melanoma, malignant	homozygous	c.434_435TG>GT	p.L145R	SK-MEL-28	HTB-72™
primary	Melanoma	homozygous	c.578A>G	p.H193R	CHL-1	CRL-9446™
primary	Carcinoma, epidermoid	homozygous	c.818G>A	p.R273H	A-431	CRL-1555™
metastasis, lymph node	Melanoma, malignant	homozygous	c.497C>A	p.S166*	RPMI-7951	HTB-66™
metastasis, lymph node	Melanoma, malignant	heterozygous	c.772G>A	p.E258K	MeWo	HTB-65™
metastasis, lymph node	Melanoma, malignant	homozygous	c.799C>T	p.R267W	SK-MEL-3	HTB-69™
metastasis, lymph node	Melanoma, malignant	homozygous	c.820G>T	p.V274F	A2058	CRL-11147™
metastasis, lymph node	Melanoma, malignant	heterozygous	c.949C>T	p.Q317*	MeWo	HTB-65™
metastasis, pleural effusion	Melanoma, amelanotic	heterozygous	c.797G>A	p.G266E	MDA-MB-435S	HTB-129™
metastasis, skin	Melanoma, malignant	heterozygous	c.733G>A	p.G245S	SK-MEL-2	HTB-68™
STOMACH						
metastasis, ascites	Carcinoma	homozygous	c.614A>T	p.Y205F	SNU-16	CRL-5974™
metastasis, ascites	Carcinoma	homozygous	c.783-2A>C	p.?	SNU-5	CRL-5973™
metastasis, liver	Carcinoma	homozygous	c.743G>A	p.R248Q	NCI-N87	CRL-5822™
metastasis, pleural effusion	Carcinoma	homozygous	c.1_1182del1182	p.0?	KATO III	HTB-103™
TESTIS						
primary	Teratocarcinoma	homozygous	c.814delG	p.V272fs*73	NCCIT	CRL-2073™
TONGUE						
primary	Carcinoma, squamous cell	homozygous	c.451C>T	p.P151S	SCC-4	CRL-1624™
primary	Carcinoma, squamous cell	homozygous	c.578A>T	p.H193L	CAL 27	CRL-2095™

Tumor source	Histology	Zygosity	Gene Sequence[†]	Protein Sequence[†]	Name	ATCC® No.
primary	Carcinoma, squamous cell	homozygous	c.625_626delAG	p.R209fs*6	SCC-25	CRL-1628™
primary	Carcinoma, squamous cell	homozygous	c.672+1G>T	p.?	SCC-15	CRL-1623™
primary	Carcinoma, squamous cell	homozygous	c.822_853del32	p.C275fs*20	SCC-9	CRL-1629™
UNKNOWN						
metastasis, lung	Histiocytoma, fibrous	heterozygous	c.741_742CC>TT	p.R248W	GCT	TIB-223™
metastasis, lung	Histiocytoma, fibrous	heterozygous	c.948_949CC>TT	p.Q317*	GCT	TIB-223™
metastasis, lymph node	Carcinoma, epidermoid	heterozygous	c.404G>T	p.C135F	A388	CRL-7905™
URINARY BLADDER						
primary	Carcinoma, transitional cell	homozygous	c.1045G>T	p.E349*	TCCSUP	HTB-5™
primary	Carcinoma, transitional cell	homozygous	c.338T>G	p.F113C	UM-UC-3	CRL-1749™
primary	Carcinoma, transitional cell	homozygous	c.378C>G	p.Y126*	T24	HTB-4™
primary	Carcinoma	homozygous	c.749C>T	p.P250L	HT-1376	CRL-1472™
primary	Carcinoma, transitional cell	heterozygous	c.783_919del137	p.?	J82	HTB-1™
primary	Carcinoma	homozygous	c.839G>C	p.R280T	5637	HTB-9™
primary	Carcinoma, transitional cell	homozygous	c.960G>C	p.K320N	J82	HTB-1™
UTERUS						
primary	Leiomyosarcoma	heterozygous	c.524G>A	p.R175H	SK-UT-1	HTB-114™
primary	Leiomyosarcoma	heterozygous	c.743G>A	p.R248Q	SK-UT-1	HTB-114™
UTERUS, ENDOMETRIUM						
primary	Carcinoma	heterozygous	c.216delC	p.V73fs*50	RL95-2	CRL-1671™
primary	Adenocarcinoma	homozygous	c.524G>A	p.R175H	KLE	CRL-1622™
primary	Carcinoma	heterozygous	c.652_654delGTG	p.V218del	RL95-2	CRL-1671™
metastasis, lymph node	Adenocarcinoma	heterozygous	c.1165G>T	p.G389W	AN3 CA	HTB-111™
metastasis, lymph node	Adenocarcinoma	heterozygous	c.267delC	p.S90fs*33	AN3 CA	HTB-111™
metastasis, lymph node	Adenocarcinoma	heterozygous	c.638G>A	p.R213Q	AN3 CA	HTB-111™
VULVA						
primary	Carcinoma, squamous cell	homozygous	c.473G>A	p.R158H	SW 954	HTB-117™
primary	Leiomyosarcoma	heterozygous	c.733G>A	p.G245S	SK-LMS-1	HTB-88™
metastasis, lymph node	Carcinoma	heterozygous	c.797G>T	p.G266V	SW 962	HTB-118™

[†] For a description of the sequence variation nomenclature please refer to: *den Dunnen JT and Antonarakes SE (2000), Hum. Mutat. 15:7-12.*

The mutation data was obtained from the Sanger Institute Catalogue Of Somatic Mutations In Cancer web site, http://www.sanger.ac.uk/cosmic Bamford et al (2004) The COSMIC (Catalogue of Somatic Mutations in Cancer) database and website. Br J Cancer, 91,355-358. ATCC and The Sanger Institute provide these data in good faith, but make no warranty, express or implied, nor assumes any legal liability or responsibility for any purpose for which the data are used.



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