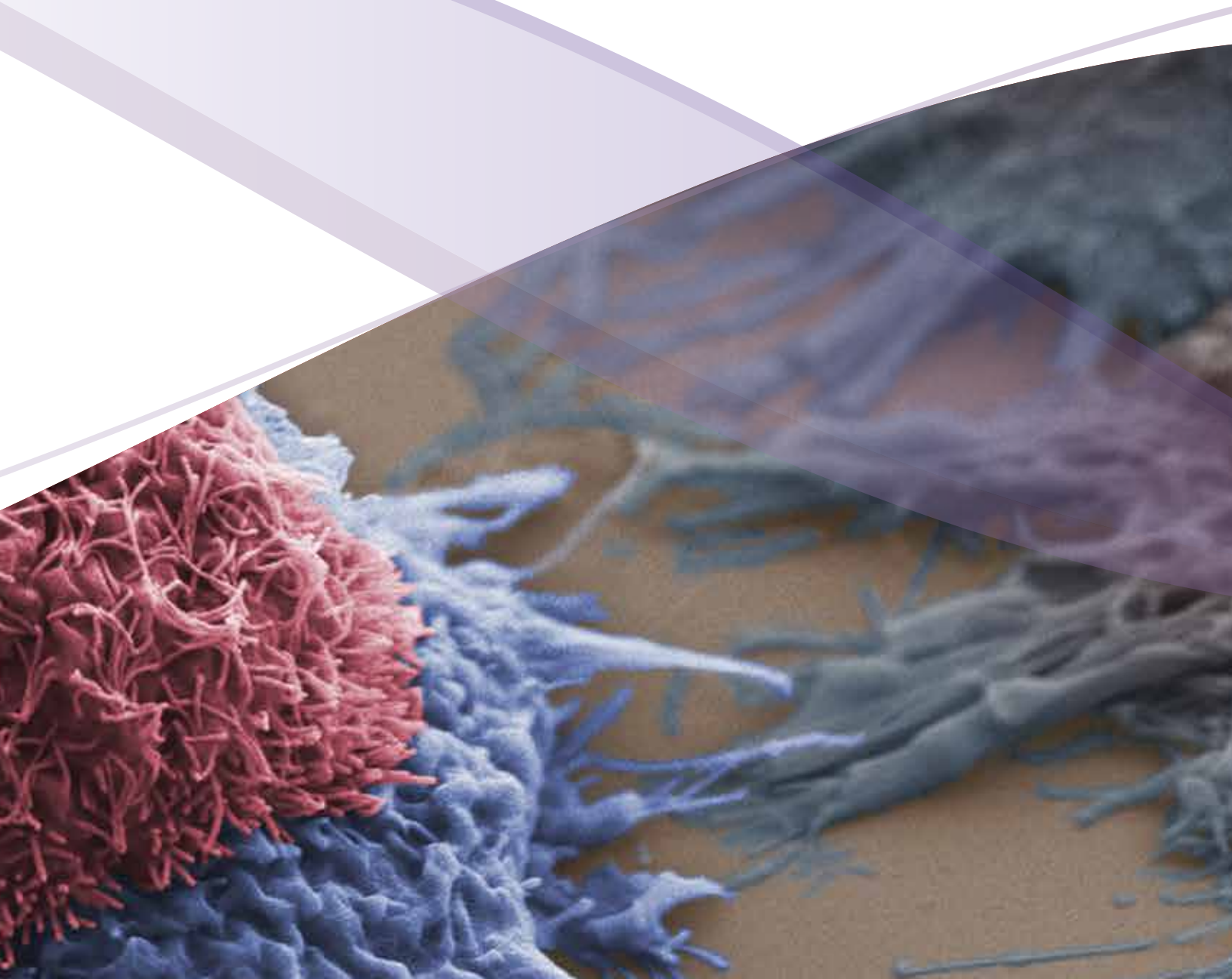
ATCC®

Tumor Cell Panels by Gene Mutations and Tissue Origins



TISSUE-SPECIFIC TUMOR CELL PANELS

The value of tumor cell lines, as research models and drug discovery tools, is greatly enhanced when there is an understanding of the underlying genetic abnor*mali*ties that drive their phenotype. ATCC has taken the first step for your research by annotating our tumor cell lines with gene mutation data from the Sanger Institute COSMIC database,[1] and additional in-house testing.

ATCC Tumor Cell Panels are powerful tools to accelerate your discoveries in cancer research, compound screening, biomarker selection, pathway analysis, and targeted therapeutic development. Each panel consists of cell lines that are:

- Easy to grow using "classic" media formulations
- Grouped by tissue of tumor origin
- Annotated with published data relevant to your research, such as known mutations in select oncogenes or receptors1

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[1]The mutation data was obtained from the Sanger Institute Catalogue of Somatic Mutations In Cancer website, 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.

BLADDER CANCER

BLADDER CANCER CELL PANEL (ATCC® TCP-1020™)

The Bladder Cancer Cell Panel is composed of eight bladder tumor cell lines with varying degrees of genetic complexity. Each culture contains genomic mutations in one or more of the following genes according to the Sanger COSMIC database: PIK3CA, RB1, RAS, TSC1, CDKN2A, PTEN, and TP53. The table below provides more information for the cell lines included in this panel.

ATCC® No.	Name	Primary Site, Tissue	Tumor Source	Histology	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
HTB-9™	5637	urinary bladder	primary	carcinoma	TP53 RB1 TP53	heterozygous homozygous homozygous	c.733G>A c.975T>A c.839G>C	p.G245S p.Y325* p.R280T
CRL-1473™	HT-1197	urinary bladder	primary	carcinoma	NRAS PIK3CA	heterozygous heterozygous	c.182A>G c.1633G>A	p.Q61R p.E545K
CRL-1472™	HT-1376	urinary bladder	primary	carcinoma	RB1 TP53	homozygous homozygous	c.2104C>T c.749C>T	p.Q702* p.P250L
HTB-2™	RT4	urinary bladder	primary	carcinoma	CDKN2A TSC1	homozygous homozygous	c.1_471del471 c.1669delC	p.0? p.L557fs*72
CRL-2169™	SW780	urinary bladder	primary	carcinoma	CDKN2A	homozygous	c.1_471del471	p.0?
HTB-4™	T-24	urinary bladder	primary	carcinoma	HRAS TP53	homozygous homozygous	c.35G>T c.378C>G	p.G12V p.Y126*
HTB-5™	TCCSUP	urinary bladder	primary	carcinoma	PIK3CA RB1 TP53	heterozygous homozygous homozygous	c.1633G>A c.1696_2787del1092 c.1045G>T	p.E545K p.? p.E349*
CRL-1749™	UM-UC-3	urinary bladder	primary	carcinoma	CDKN2A KRAS PTEN TP53	homozygous homozygous homozygous homozygous	c.1_471del471 c.34G>T c.1_1212del1212 c.338T>G	p.0? p.G12C p.0? p.F113C

CULTURE MEDIUM

While most cell lines can replicate in more than one culture medium, their characteristics may alter when the medium is changed. For this reason, starting cell cultures in the same medium used by ATCC is recommended for the best results (see the Appendix for the medium recommendations for each of the cell lines listed in this brochure). For details on adapting a cell line to a new medium, see page 14 of the *ATCC Animal Cell Culture Guide*.

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

BONE CANCER

BONE CANCER CELL PANEL (ATCC® TCP-1009™)

The Bone Cancer Cell Panel is composed of five bone cancer cell lines with varying degrees of genetic complexity. Four lines contain genomic mutations in one or more of the following genes according to the Sanger COSMIC database: CDKN2A, BRAF, TP53, RB1, and PTEN. One cell line without coding mutations serves as a control. The table below provides more information for the cell lines included in this panel.

ATCC® No.	Name	Primary Site, Tissue	Tumor Source	Histology	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
CRL-1598™	A673	bone	primary	Ewing's sarcoma	BRAF CDKN2A TP53	heterozygous homozygous homozygous	c.1799T>A c.1_471del471 c.354_355insCA	p.V600E p.0? p.A119fs*5
CRL-1543™	HOS	bone	primary	osteosarcoma	CDKN2A TP53	homozygous homozygous	c.1_471del471 c.467G>C	p.0? p.R156P
HTB-85™	Saos-2	bone	primary	osteosarcoma	RB1 TP53	homozygous homozygous	c.2212_2787del576 c.1_1182del1182	p.? p.0?
CRL-2139™	SK-PN-DW	bone	primary primary primary	Ewing's sarcoma	PTEN RB1 TP53	homozygous homozygous homozygous	c.1_79del79 c.234G>A c.527G>T	p.? p.W78* p.C176F
HTB-96™	U-2 OS	bone	primary	osteosarcoma	There are no coding mutations in CDKN2A, TP53, RB1, PTEN, and BRAF. Also, according to the Sanger COSMIC database, mutations have not been detected for this cell line in another 59 genes.			

GROWTH CURVES

Cells grow at different rates in each of the different phases of the growth cycle and the calculated doubling time may be a composite of growth during more than one of these phases. Growth during exponential growth or log phase is fairly constant and reproducible for a given set of growth conditions.

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

BRAIN CANCER

BRAIN CANCER CELL PANEL (ATCC® TCP-1017™)

The Brain Cancer Cell Panel is composed of four brain cancer cell lines with varying degrees of genetic complexity. Each culture contains genomic mutations in one or more of the following genes according to the Sanger COSMIC database: TP53, CDKN2A, PTEN, and NF1. The table below provides more information for the cell lines included in this panel.

ATCC® No.	Name	Primary Site, Tissue	Tumor Source	Histology	Tumorigenic	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
CRL-2060™	PFSK-1	brain	primary	primitive neuroectodermal tumor (PNET)	yes	TP53	homozygous	c.823T>G	p.C275G
CRL-1620™	A172	brain	primary	glioma	no	CDKN2A PTEN	homozygous homozygous	c.1_471del471 c.165_1212del1048	p.0? p.R55fs*1
HTB-12™	SW1088	brain	primary	glioma	yes	CDKN2A PTEN TP53	homozygous homozygous homozygous	c.1_471del471 c.165_1212del1048 c.817C>T	p.0? p.R55fs*1 p.R273C
HTB-186™	Daoy	brain	primary	medulloblastoma	yes	CDKN2A NF1 TP53	homozygous homozygous homozygous	c.1_471del471 c.61_4835del4775 c.725G>T	p.0? p.? p.C242F

GLIOMA CELL PANEL (ATCC® TCP-1018™)

The Glioma Cell Panel is composed of five glioma cell lines with varying degrees of genetic complexity. Each culture contains genomic mutations in one or more of the following genes according to the Sanger COSMIC database: CDKN2A, PTEN, and TP53. The table below provides more information for the cell lines included in this panel.

ATCC® No.	Name	Primary Site, Tissue	Tumor Source	Histology	Tumorigenic	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
CRL-1620™	A172	brain	primary	glioma	no	CDKN2A PTEN	homozygous homozygous	c.1_471del471 c.165_1212del1048	p.0? p.R55fs*1
HTB-12™	SW1088	brain	primary	glioma	yes	CDKN2A PTEN TP53	homozygous homozygous homozygous	c.1_471del471 c.165_1212del1048 c.817C>T	p.0? p.R55fs*1 p.R273C
HTB-148™	H4	brain	primary	glioma	no	CDKN2A PTEN	homozygous homozygous	c.1_471del471 c.1_1212del1212	p.0? p.0?
HTB-15™	U-118-MG	brain	primary	glioma	yes	CDKN2A PTEN TP53	homozygous homozygous homozygous	c.1_471del471 c.1026+1G>T c.638G>A	p.0? p.? p.R213Q
HTB-14™	U-87-MG	brain	primary	glioma	yes	CDKN2A PTEN CDKN2C	homozygous homozygous homozygous	c.1_471del471 c.209+1G>T c.1_507del507	p.0? p.? p.0?

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

BREAST CANCER

BREAST CANCER CELL PANEL (ATCC® 30-4500K)

The ATCC Breast Cancer Cell Panel reflects important genomic abnor*mali*ties found in primary breast tumors and could reveal how they contribute to breast cancer pathologies. Each panel of 45 cell lines has undergone standard ATCC authentication and quality control procedures. Through the use of this panel, breast cancer investigators across diverse fields of expertise and different research locations can generate consistent, reproducible results with confidence.

Features:

- Comprehensive — The panel represents the most diverse collection of breast cell lines available.
- Consistent — Each panel has components derived from the same seed stock, keeping passage numbers constant from lot to lot.
- Convenient — A compact-disc containing signed certificate of analysis and product sheet for each component cell line is shipped with each panel.
- Value — The warranty of the panel has been extended to 60 days.
- Savings — Researchers can save hundreds of dollars compared to purchasing each cell line individually.

Visit the ATCC website www.atcc.org for a full listing of the 45 cell lines.

BREAST CANCER P53 HOTSPOT MUTATION CELL PANEL (ATCC® TCP-2010™)

p53 is a tumor suppressor protein encoded by the TP53 gene that responds to DNA damage by regulating cell-cycle arrest, apoptosis and senescence. The Breast Cancer p53 Hotspot Mutation Cell Panel is composed of eight select cell lines derived from breast cancer that have been sequenced and validated by ATCC. This panel includes WT p53 cell lines as well as cultures with p53 hotspot mutations at codons 175, 248, 249, or 273. 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	Tumor Source	Histology	TP53 status	Zygosity	Gene Sequence*	Protein Sequence*
HTB-25™	MDA-MB-175-VII	breast	metastasis (pleural effusion)	ductal carcinoma	WT	-	-	-
HTB-27™	MDA-MB-361	breast	metastasis (brain)	adenocarcinoma	WT	-	-	-
CRL-2351™	AU565	breast	metastasis (pleural effusion)	adenocarcinoma	MUT	homozygous	c.524G>A	p.R175H
HTB-30™	SK-BR-3	breast	metastasis (pleural effusion)	adenocarcinoma	MUT	homozygous	c.524G>A	p.R175H
CRL-2315™	HCC70	breast	primary	ductal carcinoma	MUT	homozygous	c.743G>A	p.R248Q
HTB-122™	BT-549	breast	primary	ductal carcinoma	MUT	homozygous	c.747G>C	p.R249S
CRL-2314™	HCC38	breast	primary	ductal carcinoma	MUT	homozygous	c.818G>T	p.R273L
HTB-132™	MDA-MB-468	breast	metastasis (pleural effusion)	adenocarcinoma	MUT	homozygous	c.818G>A	p.R273H

TRIPLE NEGATIVE BREAST CANCER CELL PANELS

ATCC has developed three Triple Negative Breast Cancer Cell Panels based on how cell lines are classified into one of six subtypes. Triple Negative Breast Cancer Panel 1, Basal-like Morphology (ATCC® TCP-1001™) is composed of nine triple negative breast tumor cell lines that share a basal-like morphology. Triple Negative Breast Cancer Panel 2, Mesenchymal & Luminal Morphology (ATCC® TCP-1002™) is composed of six triple negative breast tumor cell lines that share a mesenchymal-like morphology or LAR subtype. Triple Negative Breast Cancer Panel 3 (ATCC® TCP-1003™) contains all the items in ATCC® TCP-1001™ and ATCC® TCP-1002™ plus two triple negative breast cancer cell lines with an unclassified morphology.

TRIPLE NEGATIVE BREAST CANCER CELL PANEL 1 (ATCC® TCP-1001™) BASAL-LIKE MORPHOLOGY

ATCC® No.	Name	Subtype[1]	Primary Site, Tissue	Tumor Source	Histology	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
CRL-2331™	HCC1599	BL1	breast	primary	primary ductal carcinoma	BRCA2 TP53	homozygous homozygous	c.4550_4559del10 c.673-2A>T	p.K1517fs*23 p.?
CRL-2336™	HCC1937	BL1	breast	primary	primary ductal carcinoma	BRCA1 TP53	homozygous homozygous	c.5266_5267insC c.916C>T	p.Q1756fs*74 p.R306*
CRL-2321™	HCC1143	BL1	breast	primary	primary ductal carcinoma	TP53	homozygous	c.743G>A	p.R248Q
HTB-132™	MDA-MB-468	BL1	breast	metastasis, pleural effusion	adenocarcinoma	PTEN RB1 SMAD4 TP53	homozygous homozygous homozygous homozygous	c.253+1G>T c.265_2787del2523 c.1_1659del1659 c.818G>A	p.? p.? p.0? p.R273H
CRL-2314™	HCC38	BL1	breast	primary	primary ductal carcinoma	CDKN2A TP53	homozygous homozygous	c.1_471del471 c.818G>T	p.0? p.R273L
CRL-2315™	HCC70	BL2	breast	primary	primary ductal carcinoma	PTEN TP53	homozygous homozygous	c.270delT c.743G>A	p.F90fs*9 p.R248Q
CRL-2335™	HCC1806	IM	breast	primary	primary acantholytic squamous cell carcinoma	CDKN2A KDM6A STK11 TP53	homozygous homozygous homozygous homozygous	c.1_471del471 c.444_564del121 c.1109_1302del194 c.766_767insAA	p.0? p.0 p.? p.T256fs*90
CRL-2322™	HCC1187	IM	breast	primary	primary ductal carcinoma	TP53	homozygous	c.322_324delGGT	p.G108del
HTB-123™	DU4475	IM	breast	metastasis, skin	carcinoma	APC BRAF MAP2K4 RB1	homozygous heterozygous homozygous homozygous	c.4729G>T c.1799T>A c.1_1200del1200 c.1_2787del2787	p.E1577* p.V600E p.0? p.0?

TRIPLE NEGATIVE BREAST CANCER CELL PANEL 2 (ATCC® TCP-1002™) MESENCHYMAL-LIKE MORPHOLOGY

ATCC® No.	Name	Subtype[1]	Primary Site, Tissue	Tumor Source	Histology	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
HTB-122™	BT-549	M	breast	ductal carcinoma	ductal carcinoma	PTEN RB1 TP53	homozygous homozygous homozygous	c.823delG c.265_607del343 c.747G>C	p.V275fs*1 p.? p.R249S
HTB-126™	Hs 578T	MSL	breast	carcinoma	carcinoma	CDKN2A HRAS PIK3R1 TP53	homozygous heterozygous homozygous homozygous	c.1_471del471 c.35G>A c.1358_1359insTAA c.469G>T	p.0? p.G12D p.N453_T454insN p.V157F
HTB-26™	MDA-MB-231	MSL	breast	adenocarcinoma	adenocarcinoma	BRAF CDKN2A KRAS NF2 TP53	heterozygous homozygous heterozygous homozygous homozygous	c.1391G>T c.1_471del471 c.38G>A c.691G>T c.839G>A	p.G464V p.0? p.G13D p.E231* p.R280K
HTB-130™	MDA-MB-436	MSL	breast	adenocarcinoma	adenocarcinoma	BRCA1 RB1	homozygous homozygous	c.5277+1G>A c.607_608ins227	p.? p.G203fs*9
HTB-24™	MDA-MB-157	MSL	breast	medullary carcinoma	medullary carcinoma	NF1 TP53	homozygous homozygous	c.8253_8268del16 c.261_286delAGCCCCCTCCTGGCCCCTGTCATCTT	p.S2751fs*27 p.A88fs*52
HTB-131™	MDA-MB-453	LAR	breast	carcinoma	carcinoma	CDH1 PIK3CA	homozygous heterozygous	c.1913G>A c.3140A>G	p.W638* p.H1047R

CONTAINED IN ATCC® TCP-1003™, DESCRIBED BELOW. UNCLASSIFIED MORPHOLOGY

ATCC® No.	Name	Subtype[1]	Primary Site, Tissue	Tumor Source	Histology	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
HTB-19™	BT-20	-	breast	carcinoma	carcinoma	CDKN2A PIK3CA PIK3CA TP53	homozygous heterozygous heterozygous homozygous	c.1_471del471 c.1616C>G c.3140A>G c.394A>C	p.0? p.p539R p.H1047R p.K132Q
CRL-2324™	HCC1395	-	breast	primary ductal carcinoma	primary ductal carcinoma	BRCA1 CDKN2A PTEN TP53	homozygous homozygous homozygous homozygous	c.5251C>T c.1_471del471 c.635_1212del578 c.524G>A	p.R1751* p.0? p.N212fs*1 p.R175H

[1]These subtypes are classified as: (1) Basal-like, including subtypes BL1 (basal-like 1), BL2 (basal-like 2) and IM (immunomodulatory); (2) Mesenchymal-like, including subtypes M (mesenchymal) and MSL (mesenchymal stem-like); and, (3) LAR (luminal androgen receptor) with an LAR subtype.

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

COLON CANCER

Colon Cancer Cell Panel 1, KRAS is composed of eight colon cancer cell lines. Seven of the 8 cell lines carry a KRAS mutation as well as other mutations with varying degrees of genetic complexity.

COLON CANCER CELL PANEL 1, KRAS (ATCC® TCP-1006™)

ATCC® No.	Name	Primary Site, Tissue	Tumor Source	Histology	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
CRL-5972™	SNU-C1	colon	metastasis, peritoneum	adenocarcinoma	TP53	homozygous	c.497C>A	p.S166*
HTB-39™	SK-CO-1	colon	metastasis, ascites	adenocarcinoma	APC APC KRAS	heterozygous heterozygous heterozygous	c.3266delT c.4328delC c.35G>T	p.F1089fs*37 p.P1443fs*30 p.G12V
CCL-233™	SW1116	colon	primary	adenocarcinoma	APC APC KRAS TP53	heterozygous heterozygous heterozygous homozygous	c.4287_4296delAAC-CATGCCA c.790C>T c.35G>C c.476C>A	p.Q1429fs*41 p.Q264* p.G12A p.A159D
CCL-237™	SW948	colon	primary	adenocarcinoma	APC APC KRAS PIK3CA	heterozygous heterozygous heterozygous heterozygous	c.3340C>T c.4285C>T c.182A>T c.1624G>A	p.R1114* p.Q1429* p.Q61L p.E542K
CCL-248™	T84	colon	metastasis, lung	carcinoma	APC KRAS PIK3CA TP53	homozygous heterozygous heterozygous homozygous	c.4464delA c.38G>A c.1624G>A c.376-1G>T	p.L1488fs*19 p.G13D p.E542K p.?
CCL-255™	LS123	colon	primary	adenocarcinoma	APC APC KRAS SMAD4 TP53	heterozygous heterozygous heterozygous homozygous heterozygous	c.1873C>T c.4348C>T c.34G>A c.988G>T c.524G>A	p.Q625* p.R1450* p.G12S p.E330* p.R175H
CCL-229™	LoVo	colon	metastasis, lymph node	adenocarcinoma	APC APC FBXW7 KRAS MSH2	heterozygous heterozygous heterozygous heterozygous homozygous	c.3340C>T c.4290delC c.1513C>T c.38G>A c.1077_1386del310	p.R1114* p.M1431fs*42 p.R505C p.G13D p.?
CCL-235™	SW837	rectum	primary	adenocarcinoma	APC APC FAM123B FBXW7 KRAS TP53	heterozygous heterozygous homozygous homozygous heterozygous homozygous	c.4348C>T c.637C>T c.1489C>T c.1205_1206insT c.34G>T c.742C>T	p.R1450* p.R213* p.R497* p.L403fs*34 p.G12C p.R248W

COLON CANCER CELL PANEL 2, BRAF (ATCC® TCP-1007™)

Colon Cancer Cell Panel 2, BRAF is composed of eight colon cancer cell lines. Six of the eight cell lines carry a BRAF mutation in addition to mutations in other genes. The table below provides more information for the cell lines included in each panel.

ATCC® No.	Name	Primary Site, Tissue	Tumor Source	Histology	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
CRL-5972™	SNU-C1	colon	metastasis, peritoneum	adenocarcinoma	TP53	homozygous	c.497C>A	p.S166*
CCL-231™	SW48	colon	primary	adenocarcinoma	CTNNB1 EGFR FBXW7	heterozygous heterozygous heterozygous	c.98C>A c.2155G>A c.2001delG	p.S33Y p.G719S p.S668fs*39
CRL-2577™	RKO	colon	primary	carcinoma	BRAF NF1 NF1 PIK3CA	heterozygous heterozygous heterozygous heterozygous	c.1799T>A c.1882delT c.7022delA c.3140A>G	p.V600E p.Y628fs*3 p.N2341fs*5 p.H1047R
CCL-222™	COLO 205	colorectal, colon	metastasis, ascites	adenocarcinoma	APC BRAF SMAD4 TP53	homozygous heterozygous homozygous homozygous	c.4666_4667insA c.1799T>A c.1_667del667 c.308_333>TA	p.T1556fs*3 p.V600E p.? p.Y103_L111>L

ATCC® No.	Name	Primary Site, Tissue	Tumor Source	Histology	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
CCL-238™	SW1417	colon	primary	adenocarcinoma	APC BRAF PIK3R1 TP53	homozygous heterozygous homozygous homozygous	c.4348C>T c.1799T>A c.1_2175del2175 c.712_725delTGTA-ACAGTTCCTG	p.R1450* p.V600E p.0? p.C238fs*21
CRL-2159™	LS411N	colorectal, cecum	primary	carcinoma	APC APC BRAF FBXW7 TP53	heterozygous heterozygous homozygous heterozygous heterozygous	c.2365C>T c.4666_4667insA c.1799T>A c.1514G>A c.378C>A	p.Q789* p.T1556fs*3 p.V600E p.R505H p.Y126*
CCL-253™	NCI-H508	cecum	metastasis, abdominal wall	adenocarcinoma	BRAF PIK3CA TP53	heterozygous heterozygous homozygous	c.1786G>C c.1633G>A c.818G>A	p.G596R p.E545K p.R273H
HTB-38™	HT-29	colorectal, colon	primary	carcinoma	APC APC BRAF PIK3CA SMAD4 TP53	heterozygous heterozygous heterozygous heterozygous homozygous homozygous	c.2557G>T c.4666_4667insA c.1799T>A c.1345C>A c.931C>T c.818G>A	p.E853* p.T1556fs*3 p.V600E p.P449T p.Q311* p.R273H

COLON CANCER P53 HOTSPOT MUTATION CELL PANEL (ATCC® TCP-2020™)

p53 is a tumor suppressor protein encoded by the TP53 gene that responds to DNA damage by regulating cell-cycle arrest, apoptosis and senescence. The Colon Cancer p53 Hotspot Mutation Cell Panel is composed of six select cell lines derived from colon cancer that have been sequenced and validated by ATCC. The panel includes both WT p53 cell lines as well as cultures with p53 hotspot mutations at codons 175, 245, 248, or 273. 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	Primary Site, Tissue	Tumor Source	Histology	TP53 status	Zygosity	Gene Sequence*	Protein Sequence*
CL-188™	LS174T	colon	primary	adenocarcinoma	WT	-	-	-
CCL-231™	SW48	colon	primary	adenocarcinoma	WT	-	-	-
CCL-255™	LS123	colon	primary	adenocarcinoma	MUT	homozygous	c.524G>A	p.R175H
CRL-2158™	LS1034	colon	primary	adenocarcinoma	MUT	homozygous	c.733G>A	p.G245S
CCL-220™	COLO 320DM	colon	primary	adenocarcinoma	MUT	homozygous	c.742C>T	p.R248W
CCL-218™	WiDr	colon	primary	adenocarcinoma	MUT	homozygous	c.818G>A	p.R273H

ATCC CELL AUTHENTICATION TESTING SERVICE FOR STR PROFILE ANALYSIS

Short Tandem Repeat (STR) profiling, is a rapid, reproducible and standardized PCR-based method used to unambiguously identify or authenticate human cell lines at individual donor resolution. Given that misidentified cell lines continue to plague research, authentication of human cell lines via STR profile analysis is becoming a requirement of many journals and funding agencies.

Take advantage of our decades of experience with STR profiling and our unmatched expertise in interpreting data from over a thousand cancer cell lines. Send your human cell lines to the ATCC Cell Authentication Testing Service for STR profile analysis.

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

GYNECOLOGICAL CANCER

CERVICAL CANCER CELL PANEL (ATCC® TCP-1022™)

The Cervical Cancer Cell Panel is composed of four cervical tumor cell lines with varying degrees of genetic complexity. Each culture contains genomic mutations in one or more of the following genes according to the Sanger COSMIC database: PIK3CA, BRCA2, STK11, FBXW7, MSH2, PTEN, RB1, and TP53. The table below provides more information for the cell lines included in this panel.

ATCC® No.	Name	Primary Site, Tissue	Tumor Source	Histology	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
CRL-1550™	Ca-Ski	cervix	metastasis	squamous cell carcinoma	PIK3CA	heterozygous	c.1633G>A	p.E545K
CRL-7920™	DoTc2-4510	cervix	primary	carcinoma	BRCA2	homozygous	c.9382C>T	p.R3128*
HTB-35™	SiHa	cervix	primary	squamous cell carcinoma	STK11	homozygous	c.1_1302del1302	p.0?
HTB-31™	C-33-A	cervix	primary	carcinoma	FBXW7 MSH2 MSH2 PIK3CA PTEN PTEN RB1 TP53	heterozygous heterozygous heterozygous heterozygous heterozygous heterozygous homozygous homozygous	c.1394G>A c.2304delA c.2579C>A c.263G>A c.388C>T c.697C>T c.1961-1G>A c.817C>T	p.R465H p.E768fs*44 p.S860* p.R88Q p.R130* p.R233* p.? p.R273C

OVARIAN CANCER CELL PANEL (ATCC® TCP-1021™)

Ovarian Cancer Cell Panel is composed of four ovarian cancer cell lines. They have genomic mutations in one or more of the following genes according to the Sanger COSMIC database: APC, CDKN2A, FAM123B, KRAS, MLH1, NRAS, PIK3CA, STK11, and TP53. The table below provides more information for the cell lines included in this panel.

ATCC® No.	Name	Primary Site, Tissue	Tumor source	Histology	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
CRL-1572™	PA-1	ovary	metastasis, ascites	teratocarcinoma	NRAS	heterozygous	c.35G>A	p.G12D
HTB-75™	Caov-3	ovary	primary	adenocarcinoma	FAM123B STK11 TP53	homozygous homozygous homozygous	c.1_2415del2415 c.1_1302del1302 c.406C>T	p.0? p.0? p.Q136*
HTB-78™	SW626	ovary	primary	adenocarcinoma	APC KRAS TP53	homozygous heterozygous homozygous	c.2926_2927insA c.35G>T c.785G>T	p.R976fs*9 p.G12V p.G262V
HTB-77™	SK-OV-3	ovary	metastasis, ascites	adenocarcinoma	CDKN2A MLH1 PIK3CA TP53	homozygous homozygous heterozygous homozygous	c.1_457del457 c.1_2271del2271 c.3140A>G c.267delC	p.? p.0? p.H1047R p.S90fs*33

GYNECOLOGICAL CANCER CELL PANEL (ATCC® TCP-1024™)

The Gynecological Cancer Cell Panel is composed of nine tumor cell lines representing an array of gynecological cancers with varying degrees of genetic complexity. Each culture contains genomic mutations in one or more of the following genes according to the Sanger COSMIC database: PIK3CA, FAM123B, APC, KRAS, CDKN2A, PTEN, RB1, FBXW7, MAP2K4, and TP53. The table below provides more information for the cell lines included in this panel.

ATCC® No.	Name	Primary Site, Tissue	Tumor Source	Histology	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
HTB-88™	SK-LMS-1	vulva	primary	leiomyosarcoma	TP53	heterozygous	c.733G>A	p.G245S
HTB-32™	HT-3	cervix	primary	carcinoma	TP53	homozygous	c.734G>T	p.G245V
HTB-33™	ME-180	cervix	metastasis	carcinoma	PIK3CA	heterozygous	c.1633G>A	p.E545K
HTB-75™	Caov-3	ovarian	primary	adenocarcinoma	FAM123B STK11 TP53	homozygous homozygous homozygous	c.1_2415del2415 c.1_1302del1302 c.406C>T	p.0? p.0? p.Q136*

ATCC® No.	Name	Primary Site, Tissue	Tumor Source	Histology	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
HTB-78™	SW626	ovarian	primary	adenocarcinoma	APC KRAS TP53	homozygous heterozygous homozygous	c.2926_2927insA c.35G>T c.785G>T	p.R976fs*9 p.G12V p.G262V
CRL-1976™	MES-SA	uterus	primary	uterine sarcoma	CDKN2A	homozygous	c.1_471del471	p.0?
HTB-114™	SK-UT-1	uterus	primary	leiomyosarcoma	APC APC PIK3CA PTEN PTEN RB1 TP53 TP53	heterozygous heterozygous heterozygous heterozygous heterozygous homozygous heterozygous heterozygous	c.3286C>T c.4666delA c.263G>A c.955_958delACTT c.968_969insA c.1959delA c.524G>A c.743G>A	p.Q1096* p.T1556fs*9 p.R88Q p.T319fs*1 p.N323fs*2 p.V654fs*4 p.R175H p.R248Q
CRL-1622™	KLE	endometrium	primary	adenocarcinoma	FBXW7 MAP2K4 TP53	heterozygous homozygous homozygous	c.1436G>A c.1_218del218 c.524G>A	p.R479Q p.? p.R175H
HTB-111™	AN3-CA	endometrium	metastasis	adenocarcinoma	FBXW7 PIK3R1 PTEN TP53 TP53 TP53	heterozygous heterozygous homozygous heterozygous heterozygous heterozygous	c.1321C>T c.1670_1681del-GAGAAATTGACA c.389delG c.1165G>T c.267delC c.638G>A	p.R441W p.R557_K561>Q p.R130fs*4 p.G389W p.S90fs*33 p.R213Q

UTERINE CANCER CELL PANEL (ATCC® TCP-1023™)

The Uterine Cancer Cell Panel is composed of five uterine tumor cell lines with varying degrees of genetic complexity. They have genomic mutations in one or more of the following genes according to the Sanger COSMIC database: CDKN2A, APC, PIK3, PTEN, RB1, FBXW7, MAP2K4, BRCA, HRAS, NF2, and TP53. The table below provides more information for the cell lines included in this panel.

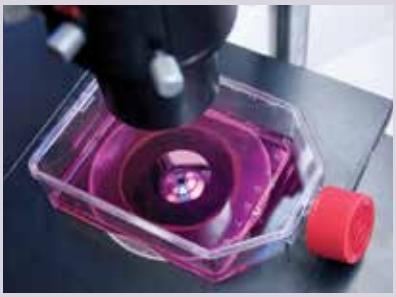
ATCC® No.	Name	Primary Site, Tissue	Tumor Source	Histology	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
CRL-1976™	MES-SA	uterus	primary	uterine sarcoma	CDKN2A	homozygous	c.1_471del471	p.0?
HTB-114™	SK-UT-1	uterus	primary	leiomyosarcoma	APC APC PIK3CA PTEN PTEN RB1 TP53 TP53	heterozygous heterozygous heterozygous heterozygous heterozygous homozygous heterozygous heterozygous	c.3286C>T c.4666delA c.263G>A c.955_958delACTT c.968_969insA c.1959delA c.524G>A c.743G>A	p.Q1096* p.T1556fs*9 p.R88Q p.T319fs*1 p.N323fs*2 p.V654fs*4 p.R175H p.R248Q
CRL-1622™	KLE	endome-trium	primary	adenocarcinoma	FBXW7 MAP2K4 TP53	heterozygous homozygous homozygous	c.1436G>A c.1_218del218 c.524G>A	p.R479Q p.? p.R175H
HTB-111™	AN3-CA	endome-trium	metasta-sis	adenocarcinoma	FBXW7 PIK3R1 PTEN TP53 TP53 TP53	heterozygous heterozygous homozygous heterozygous heterozygous heterozygous	c.1321C>T c.1670_1681del-GAGAAATTGACA c.389delG c.1165G>T c.267delC c.638G>A	p.R441W p.R557_K561>Q p.R130fs*4 p.G389W p.S90fs*33 p.R213Q
CRL-1671™	RL95-2	endome-trium	primary	carcinoma	BRCA2 BRCA2 HRAS NF2 NF2 PTEN PTEN TP53 TP53	heterozygous heterozygous heterozygous heterozygous heterozygous heterozygous heterozygous heterozygous heterozygous	c.4285_4286insT c.5465_5466insA c.183G>T c.1084C>T c.514delA c.968_969insA c.968delA c.216delC c.652_654delGTG	p.Q1429fs*9 p.N1822fs*2 p.Q61H p.Q362* p.R172fs*2 p.N323fs*2 p.N323fs*21 p.V73fs*50 p.V218del

HEAD AND NECK CANCER

HEAD AND NECK CANCER CELL PANEL (ATCC® TCP-1012™)

The Head and Neck Cancer Cell Panel is composed of six cell lines from salivary gland, tongue, hypopharynx and pharynx. Each culture contains genomic mutations in one or more of the following genes according to the Sanger COSMIC database: CDKN2A, TP53, SMAD4, PIK3CA and KDM5C. The table below provides more information for the cell lines included in this panel.

ATCC® No.	Name	Primary Site, Tissue	Tumor Source	Histology	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
HTB-41™	A-253	salivary gland	primary	carcinoma	CDKN2A	homozygous	c.49_61del13	p.A17fs*5
					KDM5C	homozygous	c.3354G>A	p.W1118*
					TP53	homozygous	c.539delA	p.E180fs*67
CRL-1623™	SCC-15	tongue	primary	carcinoma	TP53	homozygous	c.672+1G>T	p.?
CRL-1628™	SCC-25	tongue	primary	carcinoma	CDKN2A	homozygous	c.1_471del471	p.0?
					TP53	homozygous	c.625_626delAG	p.R209fs*6
CRL-1629™	SCC-9	tongue	primary	carcinoma	CDKN2A	homozygous	c.1_150del150	p.?
					TP53	homozygous	c.822_853del32	p.C275fs*20
HTB-43™	FaDu	hypopharynx	primary	carcinoma	CDKN2A	homozygous	c.151-1G>T	p.?
					SMAD4	homozygous	c.1_1659del1659	p.0?
					TP53	heterozygous	c.376-1G>A	p.?
					TP53	heterozygous	c.743G>T	p.R248L
CCL-138™	Detroit 562	pharynx	metastasis	carcinoma	CDKN2A	homozygous	c.1_457del457	p.?
					PIK3CA	heterozygous	c.3140A>G	p.H1047R
					TP53	homozygous	c.524G>A	p.R175H



DISSOCIATION REAGENTS, ATCC® 30-2200™

Q: What can I do if my cells are difficult to remove from the plate after trypsin digestion?

A: There are several factors that can reduce the efficiency of the trypsin. For example, there may be inhibitors in the medium that are inactivating the dissociating enzyme. Make sure to rinse the cell monolayer thoroughly before adding the dissociating solution with a reagent, such as Dulbecco's Phosphate Buffered Saline (D-PBS), 1X (ATCC® 30-2200™).

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

LEUKEMIA

LEUKEMIA CELL PANEL (ATCC® TCP-1010™)

The Leukemia Cell Panel is composed of seven leukemia cell lines representing Acute Myeloid Leukemia (AML), Acute Monocytic Leukemia (AMoL), Chronic Myeloid Leukemia (CML), and Acute Lymphoblastic Leukemia (ALL). Each culture contains genomic mutations in one or more of the following genes according to the Sanger COSMIC database: CDKN2A, KDM6A, TP53, NRAS, NOTCH1, PTEN, FBXW7, FLT3, KRAS, MLH1, and PIK3R1. The table below provides more information for the cell lines included in this panel.

ATCC® No.	Name	Tumor Source	Disease	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
CRL-2724™	KASUMI-1	primary	acute myeloid leukemia (AML)	TP53	homozygous	c.743G>A	p.R248Q
CCL-240™	HL-60	primary	acute myeloid leukemia (AML)	CDKN2A	homozygous	c.238C>T	p.R80*
				NRAS	heterozygous	c.182A>T	p.Q61L
				TP53	homozygous	c.1_1182del1182	p.0?
TIB-202™	THP-1	primary	acute monocytic leukemia (AMoL)	CDKN2A	homozygous	c.1_471del471	p.0?
				KDM6A	homozygous	c.1_1923del1923	p.0
				NRAS	heterozygous	c.35G>A	p.G12D
CCL-243™	K-562	primary	chronic myeloid leukemia (CML)	CDKN2A	homozygous	c.1_471del471	p.0?
				TP53	homozygous	c.406_407insC	p.Q136fs*13
CRL-1873™	RS4;11	metastasis	acute lympho-blastic leukemia (ALL)	CDKN2A	homozygous	c.1_471del471	p.0?
CRL-1582™	MOLT-4	primary	acute lympho-blastic leukemia (ALL)	CDKN2A	homozygous	c.1_471del471	p.0?
				NOTCH1	heterozygous	c.7544_7545delCT	p.P2515fs*4
				NRAS	heterozygous	c.34G>T	p.G12C
				PIK3R1	heterozygous	c.1355_1363>CTG-GAGGGAGTAGGATTA	p.Y452_Q455>SGGSRIK
				PTEN	homozygous	c.800delA	p.K267fs*9
				TP53	heterozygous	c.916C>T	p.R306*
CCL-119™	CCRF-CEM	primary	acute lympho-blastic leukemia (ALL)	CDKN2A	homozygous	c.1_471del471	p.0?
				FBXW7	heterozygous	c.1393C>T	p.R465C
				FLT3	heterozygous	c.1879G>A	p.A627T
				KRAS	heterozygous	c.35G>A	p.G12D
				MLH1	heterozygous	c.298C>T	p.R100*
				MLH1	heterozygous	c.790+1G>A	p.?
				NOTCH1	heterozygous	c.4783_4784ins36	p.R1595>PRLPHNSSFH-FLR
				PTEN	homozygous	c.80_492del413	p.?
				TP53	heterozygous	c.524G>A	p.R175H
				TP53	heterozygous	c.743G>A	p.R248Q

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

LIVER CANCER

LIVER CANCER CELL PANEL (ATCC® TCP-1011™)

The Liver Cancer Cell Panel is composed of seven liver cancer cell lines with varying degrees of genetic complexity. They have genomic mutations in one or more of the following genes according to the Sanger COSMIC database: BRAF, CDKN2A, CTNNB1, NRAS, STK11, and TP53. The table below provides more information for the cell lines included in this panel.

ATCC® No.	Name	Primary Site, Tissue	Histology	Tumor Source	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
CRL-2236™	SNU-475	liver	hepatocellular carcinoma	primary	TP53	heterozygous	c.715A>G	p.N239D
					TP53	heterozygous	c.785G>A	p.G262D
CRL-10741™	C3A	liver	hepatocellular carcinoma	primary	CTNNB1	homozygous	c.14_241del228	p.A5_A80del
					NRAS	heterozygous	c.182A>T	p.Q61L
CRL-2234™	SNU-449	liver	hepatocellular carcinoma	primary	CDKN2A	homozygous	c.1_471del471	p.0?
					TP53	homozygous	c.481G>A	p.A161T
CRL-8024™	PLC/PRF/5	liver	hepatocellular carcinoma	primary	CDKN2A	homozygous	c.334C>G	p.R112G
					STK11	homozygous	c.580G>A	p.D194N
					TP53	homozygous	c.747G>T	p.R249S
CRL-2237™	SNU-387	liver	pleomorphic hepatocellular carcinoma	primary	CDKN2A	homozygous	c.1_471del471	p.0?
					NRAS	heterozygous	c.181C>A	p.Q61K
					TP53	homozygous	c.490A>T	p.K164*
HTB-52™	SK-HEP-1	liver	adenocarcinoma	metastasis, ascites	BRAF	heterozygous	c.1799T>A	p.V600E
					CDKN2A	homozygous	c.1_471del471	p.0?
CRL-2238™	SNU-423	liver	pleomorphic hepatocellular carcinoma	primary	Not determined			

UNIVERSAL *MYCOPLASMA* DETECTION KIT, ATCC® 30-1012K™

The Universal *Mycoplasma* Detection Kit offers a quick and sensitive PCR-based test to detect mycoplasma contaminants in cell culture. All components required for the PCR reaction are provided and have been optimized for amplification. High specificity is obtained through the utilization of a proprietary mix of buffers, dNTPs and thermostable polymerase, combined with universal primers that are specific to the 16S rRNA coding region in the mycoplasma genome. DNA originating from other sources, such as tissue samples or other bacteria, are not amplified. A touchdown PCR regimen increases sensitivity of the assay, along with enhancing specificity.

The kit detects over 60 species of *Mycoplasma*, *Acholeplasma*, Spiroplasma and *Ureaplasma* including the eight species most likely to afflict cell cultures: *M. arginini, M. fermentans, M. hominis, M.hyorhinis, M. orale, M. pirum, M. salivarium, and A. laidlawii*. Samples that are positive for mycoplasma are easily recognized by a distinct PCR product ranging in size from 434 to 468 bp on an agarose gel. Find the Universal *Mycoplasma* Detection Kit product page at **www.atcc.org**.

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

LUNG CANCER

LUNG CANCER CELL PANEL (ATCC® TCP-1016™)

Lung Cancer Cell Panel is composed of seven lung cancer cell lines. They have genomic mutations in one or more of the following genes according to the Sanger COSMIC database: CDKN2A, EGFR, KRAS, NRAS, PIK3CA, PIK3R1, SMARCA4, STK11, and TP53.The table below provides more information for the cell lines included in this panel.

ATCC® No.	Name	Primary Site, Tissue	Tumor Source	Histology	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
CRL-5803™	NCI-H1299	lung	metastasis, lymph node	large cell carcinoma	NRAS	heterozygous	c.181C>A	p.Q61K
CRL-5875™	NCI-H1563	lung	primary	non-small-cell lung carcinoma (NSCLC)	CDKN2A	homozygous	c.1_471del471	p.0?
CRL-5872™	NCI-H1437	lung	metastasis, pleural effusion	non-small-cell lung carcinoma (NSCLC)	CDKN2A	homozygous	c.1_471del471	p.0?
					TP53	homozygous	c.800G>C	p.R267P
HTB-183™	NCI-H661	lung	metastasis, lymph node	large cell carcinoma	CDKN2A	homozygous	c.457+1G>T	p.?
					SMARCA4	homozygous	c.3480delG	p.L1161fs*3
					TP53	homozygous	c.473G>T	p.R158L
					TP53	heterozygous	c.644G>T	p.S215I
CCL-256™	NCI-H2126	lung	metastasis, pleural effusion	non-small-cell lung carcinoma (NSCLC)	CDKN2A	homozygous	c.1_471del471	p.0?
					STK11	homozygous	c.465_862del398	p.?
					TP53	homozygous	c.184G>T	p.E62*
CRL-5877™	NCI-H1573	lung	metastasis, soft tissue	adenocarcinoma	KRAS	heterozygous	c.35G>C	p.G12A
					PIK3R1	heterozygous	c.211G>T	p.G71*
					SMARCA4	homozygous	c.4195G>T	p.E1399*
					TP53	homozygous	c.743G>T	p.R248L
CRL-5908™	NCI-H1975	lung	primary	non-small-cell lung carcinoma (NSCLC)	CDKN2A	homozygous	c.205G>T	p.E69*
					EGFR	heterozygous	c.2369C>T	p.T790M
					EGFR	heterozygous	c.2573T>G	p.L858R
					PIK3CA	heterozygous	c.353G>A	p.G118D
					TP53	homozygous	c.818G>A	p.R273H

NON-SMALL CELL LUNG CANCER P53 HOTSPOT MUTATION CELL PANEL (ATCC® TCP-2030™)

p53 is a tumor suppressor protein encoded by the TP53 gene that responds to DNA damage by regulating cell-cycle arrest, apoptosis and senescence. Non-Small Cell Lung Cancer p53 Hotspot Mutation Cell Panel is composed of six select cell lines derived from the lung that have been sequenced and validated by ATCC. The panel includes WT p53 or null p53 cell lines as well as cultures with p53 hotspot mutations at codons 245, 248, or 273. 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	Tumor Source	Histology	TP53 status	Zygosity	Gene Sequence*	Protein Sequence*
CRL-9609™	BEAS-2B	lung	NA	normal tissue,SV-40 immortalized	WT	-	-	-
CCL-185™	A549	lung	primary	non-small cell lung carcinoma	WT	-	-	-
CRL-5803™	NCI-H1299	lung	metastasis (lymph node)	non-small cell lung carcinoma	NULL	homozygous	c.(del)	-
HTB-178™	NCI-H596	lung	primary	adenosquamous carcinoma	MUT	homozygous	c.733G>T	p.G245C
CRL-5893™	NCI-H1770	lung	metastasis (lymph node)	non-small cell lung carcinoma	MUT	homozygous	c.741 742CC>TT	p.R248W
CRL-5908™	NCI-H1975	lung	primary	adenocarcinoma	MUT	homozygous	c.818G>A	p.R273H

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

SMALL CELL LUNG CANCER P53 HOTSPOT MUTATION CELL PANEL (ATCC® TCP-2040™)

p53 is a tumor suppressor protein encoded by the TP53 gene that responds to DNA damage by regulating cell-cycle arrest, apoptosis and senescence. The Small Cell Lung Cancer p53 Hotspot Mutation Cell Panel is composed of six select cell lines derived from the lung that have been sequenced and validated by ATCC. This panel includes p53 WT cell lines as well as cultures with p53 hotspot mutations at codons 175, 248, 249, or 273. 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	Tumor Source	Histology	TP53 status	Zygosity	Gene Sequence*	Protein Sequence*
CRL-9609™	BEAS-2B	lung	NA	normal tissue,SV-40 immortalized	WT	-	-	-
CRL-5903™	NCI-H1882	lung	metastasis (bone marrow)	small cell lung carcinoma	WT	-	-	-
CRL-5869™	NCI-H1417	lung	primary	small cell lung carcinoma	MUT	homozygous	c.524G>T	p.R175L
CRL-5837™	NCI-H719	lung	metastasis (bone marrow)	small cell lung carcinoma	MUT	homozygous	c.743G>A	p.R248Q
CRL-5856™	NCI-H1105	lung	metastasis (lymph node)	small cell lung carcinoma	MUT	homozygous	c.747G>T	p.R249S
CRL-5853™	NCI-H1048	lung	metastasis (pleural effusion)	small cell lung carcinoma	MUT	heterozygous	c.817C>T	p.R273C

ATCC CELL CULTURE MEDIA

Cells are highly sensitive to their media environment, and may behave differently when their media is changed or when they are thawed into a media different from the one in which they were frozen. ATCC media will keep your cells behaving as expected. Our media is formulated with carefully adjusted buffers, glucose, vitamins and amino acids. The collection includes the "classic" media formulations, and media specially formulated to optimize growth of hybridoma, primary, or stem cells in culture. For more information go to **www.atcc.org**.

LYMPHOMA

LYMPHOMA CELL LINE PANEL (ATCC® TCP-1015™)

The Lymphoma Cell Panel is composed of nine lymphoma cell lines representing a variety of tumor sources and histologies, annotated with gene mutation data from the Sanger COSMIC database. This panel is useful for understanding the relationships of gene mutations among different lymphomas. Complement your ATCC Lymphoma Cell Panel data set with either the Lymphoma p53 Hotspot Mutation Cell Panel (ATCC® TCP-2050™) or the Non-Hodgkin's Lymphoma Cell Panel (ATCC® TCP-1025™).

ATCC® No.	Name	Tumor Source	Histology	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
CRL-2289™	DB	ascites	diffuse large B cell lymphoma	EZH2 TP53	heterozygous heterozygous	c.1936T>A c.743G>A	p.Y646N p.R248Q
CRL-2260™	HT	ascites	B cell lymphoma	PTEN TP53 TP53	homozygous heterozygous heterozygous	c.802-2A>T c.646G>A c.818G>A	p.? p.V216M p.R273H
CRL-2277™	BC-3	pleural effusion	primary effusion lymphoma	CDKN2A PTEN RB1	homozygous homozygous homozygous	c.1_457del457 c.743_744delCT c.649C>T	p.? p.P248fs*4 p.Q217*
CRL-1648™	CA46	lymphoid tissue	Burkitt's lymphoma	TP53	homozygous	c.743G>A	p.R248Q
CCL-86™	Raji	maxilla	Burkitt's lymphoma	TP53 TP53	heterozygous homozygous	c.700T>C c.638G>A	p.Y234H p.R213Q
CCL-213™	Daudi	peripheral blood	Burkitt's lymphoma	CTNNB1 TP53	homozygous heterozygous	c.14_241del228 c.797G>A	p.A5_A80del p.G266E
CRL-2393™	GA-10-Clone-4	peripheral blood	Burkitt's lymphoma	NRAS TP53 TP53	heterozygous heterozygous heterozygous	c.35G>T c.455C>T c.695T>A	p.G12V p.P152L p.I232N
CRL-2105™	HH	peripheral blood	cutaneous T cell lymphoma	TP53	homozygous	c.376-1G>A	p.?
HTB-176™	H9	skin	cutaneous T cell lymphoma	CDKN2A NRAS RB1 SOCS1 TP53	homozygous heterozygous homozygous homozygous homozygous	c.1_471del471 c.181C>A c.138_264del127 c.1_636del636 c.586C>T	p.0? p.Q61K p.? p.0? p.R196*

LYMPHOMA P53 HOTSPOT MUTATION CELL PANEL (ATCC® TCP-2050™)

p53 is a tumor suppressor protein encoded by the TP53 gene that responds to DNA damage by regulating cell-cycle arrest, apoptosis and senescence. The Lymphoma p53 Hotspot Mutation Cell Panel is composed of five select suspension cell lines derived from the lymphoma that have been sequenced and validated by ATCC. This panel includes cell lines of p53 WT as well as with p53 hotspot mutations at codons 248 and 273. 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	TP53 status	Zygosity	Gene Sequence†	Protein Sequence†
CCL-85™	EB-3	Burkitt lymphoma	WT	-	-	-
CRL-1648™	CA46	Burkitt lymphoma	MUT	homozygous	c.743G>A	p.R248Q
CRL-1432™	Namalwa	Burkitt lymphoma, carry EBV	MUT	homozygous	c.743G>A	p.R248Q
CRL-2289™	DB	large B-cell lymphoma	MUT	heterozygous	c.743G>A	p.R248Q
CRL-1942™	SUP-T1	T cell lymphoblastic lymphoma	MUT	heterozygous	c.818G>A	p.R273H

NON-HODGKIN'S LYMPHOMA CELL PANEL (ATCC® TCP-1025™)

The Non-Hodgkin's Lymphoma Cell Panel is composed of nine diffuse histiocytic and one diffuse undifferentiated lymphoma cell lines annotated with published source, diagnosis, and biomarker data (where available). This panel is useful for anti-cancer drug targeting and the development of rapid, accurate molecular-based assays used to detect Non-Hodgkin's lymphoma. All cultures in the panel are EBV negative.

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

ATCC® No.	Name	Source[1,4]	Diagnosis[2,4]	Sex[1,4]	Age[1,4]	CD79 Cell Surface[3]	p53 Mutation[3]	Immunoglobulin[2,4]	Acid Phosphatase[2]
CRL-2955™	SU-DHL-1	pleural effusion	DLNC	Male	10	-	NA	-	+
CRL-2956™	SU-DHL-2	pleural effusion	histiocytic lymphoma	Female	73	NA	NA	-	+
CRL-2957™	SU-DHL-4	peritoneal effusion	DLC	Male	38	+	+	IgG/kappa	+
CRL-2958™	SU-DHL-5	lymph node	DLNC	Female	17	+	-	IgM/lambda	+
CRL-2959™	SU-DHL-6	peritoneal effusion	histiocytic lymphoma	Male	43	+	-	IgM/kappa	+
CRL-2961™	SU-DHL-8	pleural effusion	DLNC	Male	59	-	+	-/lambda (cytoplasm only)2	+
CRL-2963™	SU-DHL-10	pleural effusion	large cell lymphoma	Male	25	+	+	IgG	NA
CRL-2964™	SU-DHL-16	NA	large B-cell lymphoma	NA	NA	+	-	NA	NA
CRL-2969™	NU-DUL-1	cerebral spinal fluid	null large cell lymphoma	Male	43	+	+	-	NA

SU, Stanford University; NU, Northwestern Universtiy; DUL, diffuse undifferentiated lymphoma; DHL, diffuse histiocytic lymphoma; DLNC, diffuse large cell lymphoma, noncleaved cell type; DLC, diffuse large cell lymphoma, cleaved cell type; WT, wild type; NA, not available

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2 Winter JN, et al. Blood. (1984) 63:140-146.

3 Dornan D, et al. Blood. Prepublished online July 24, 2009; doi:10.1182/blood-2009-02-205500.

4 Depositor-supplied information

PANCREATIC CANCER

PANCREATIC CANCER CELL PANEL (ATCC® TCP-1026™)

The Pancreatic Cancer Cell Panel is composed of seven pancreatic cancer cell lines. They have genomic mutations in one or more of the following genes according to the Sanger COSMIC database: CDKN2A, FBXW7, KRAS, MAP2K4, SMAD4, and TP53. The table below provides more information for the cell lines included in this panel.

ATCC® No.	Name	Primary Site, Tissue	Tumor Source	Histology	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
HTB-80™	Capan-2	pancreas	primary	adenocarcinoma	KRAS	heterozygous	c.35G>T	p.G12V
CRL-2547™	Panc 10.05	pancreas	primary	adenocarcinoma	KRAS TP53	heterozygous heterozygous	c.35G>A c.764T>A	p.G12D p.I255N
CRL-1918™	CFPAC-1	pancreas	metastasis, liver	ductal adenocarcinoma	KRAS SMAD4 TP53	heterozygous homozygous homozygous	c.35G>T c.1_1659del1659 c.724T>C	p.G12V p.0? p.C242R
CRL-1997™	HPAF-II	pancreas	metastasis, ascites	adenocarcinoma	CDKN2A KRAS TP53	homozygous heterozygous homozygous	c.85_101del17 c.35G>A c.451C>T	p.R29fs*9 p.G12D p.P151S
CRL-2172™	SW 1990	pancreas	metastasis, spleen	adenocarcinoma	CDKN2A KRAS	homozygous homozygous	c.1_471del471 c.35G>A	p.0? p.G12D
CRL-1687™	BxPC-3	pancreas	primary	adenocarcinoma	CDKN2A MAP2K4 SMAD4 TP53	homozygous homozygous homozygous homozygous	c.1_471del471 c.1041_1200del160 c.1_1659del1659 c.659A>G	p.0? p.? p.0? p.Y220C
CRL-1682™	AsPC-1	pancreas	metastasis, ascites	adenocarcinoma	CDKN2A FBXW7 KRAS MAP2K4 TP53	homozygous heterozygous homozygous homozygous homozygous	c.233_234delTC c.1393C>T c.35G>A c.1-?_393+?del c.403delT	p.L78fs*41 p.R465C p.G12D p.? p.C135fs*35

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

SKIN CANCER

MELANOMA CELL PANEL (ATCC® TCP-1013™)

The Melanoma Cell Panel is composed of three melanoma cancer cell lines with varying degrees of genetic complexity. Each culture contains genomic mutations in one or more of the following genes according to the Sanger COSMIC database: BRAF, CTNNB1, CDKN2A, and STK11. The table below provides more information for the cell lines included in this panel.

ATCC® No.	Name	Primary Site, Tissue	Tumor Source	Histology	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
HTB-67™	SK-MEL-1	skin	primary	*mali*gnant melanoma	BRAF CTNNB1	heterozygous heterozygous	c.1799T>A c.98C>G	p.V600E p.S33C
CRL-1619™	A375	skin	primary	*mali*gnant melanoma	BRAF CDKN2A CDKN2A	homozygous homozygous homozygous	c.1799T>A c.181G>T c.205G>T	p.V600E p.E61* p.E69*
CRL-1424™	G-361	skin	primary	*mali*gnant melanoma	BRAF CDKN2A STK11	heterozygous homozygous homozygous	c.1799T>A c.1_471del471 c.842delC	p.V600E p.0? p.P281fs*6

METASTATIC MELANOMA CELL PANEL (ATCC® TCP-1014™)

The Metastatic Melanoma Cell Panel is composed of four cell lines with varying degrees of genetic complexity. Each culture contains genomic mutations in one or more of the following genes according to the Sanger COSMIC database: BRAF, TP53, CDKN2A and PTEN. The table below provides more information for the cell lines included in this panel.

ATCC® No.	Name	Primary Site, Tissue	Tumor Source	Histology	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
HTB-69™	SK-MEL-3	skin	metastasis	*mali*gnant melanoma	BRAF TP53	heterozygous homozygous	c.1799T>A c.799C>T	p.V600E p.R267W
CRL-7724™	SH-4	skin	metastasis	*mali*gnant melanoma	BRAF CDKN2A	homozygous homozygous	c.1799T>A c.1_471del471	p.V600E p.0?
HTB-71™	SK-MEL-24	skin	metastasis	*mali*gnant melanoma	BRAF CDKN2A PTEN	heterozygous homozygous homozygous	c.1799T>A c.1_471del471 c.80_164del85	p.V600E p.0? p.?
HTB-66™	RPMI-7951	skin	metastasis	*mali*gnant melanoma	BRAF CDKN2A PTEN TP53	heterozygous homozygous homozygous homozygous	c.1799T>A c.47T>G c.1_79del79 c.497C>A	p.V600E p.L16R p.? p.S166*

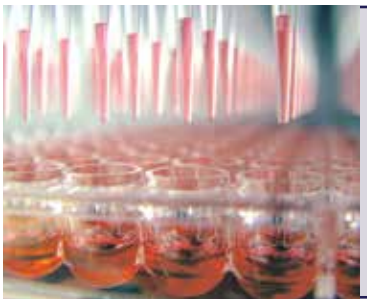
*For a description of the sequence variation nomenclature please refer to: den Dunnen JT and Antonarakes SE (2000), Hum. Mutat. 15:7-12.

SOFT-TISSUE CANCER

SOFT-TISSUE SARCOMA CELL PANEL (ATCC® TCP-1019™)

The Soft-tissue Sarcoma Cell Panel is composed of six soft-tissue tumor cell lines with varying degrees of genetic complexity. Each culture contains genomic mutations in one or more of the following genes according to the Sanger COSMIC database: CDKN2A, IDH1, NRAS, BRAF, PTEN, and TP53. The table below provides more information for the cell lines included in this panel.

ATCC® No.	Name	Primary Site, Tissue	Tumor Source	Histology	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence*
HTB-91™	SW684	connective tissue	primary	fibrosarcoma	TP53	homozygous	c.637C>T	p.R213*
CCL-121™	HT-1080	connective tissue	primary	fibrosarcoma	CDKN2A IDH1 NRAS	homozygous heterozygous heterozygous	c.1_471del471 c.394C>T c.181C>A	p.0? p.R132C p.Q61K
HTB-93™	SW982	synovium	primary	synovial sarcoma	BRAF CDKN2A	heterozygous homozygous	c.1799T>A c.1_471del471	p.V600E p.0?
CCL-136™	RD	striated muscle	primary	rhabdomyosarcoma	NRAS TP53	homozygous homozygous	c.183A>T c.742C>T	p.Q61H p.R248W
TIB-223™	GCT	fibrous tissue	metastasis	*mali*gnant fibrous histiocytoma	BRAF CDKN2A TP53 TP53	heterozygous homozygous heterozygous heterozygous	c.1799T>A c.95_96TG>GT c.741_742CC>TT c.948_949CC>TT	p.V600E p.L32R p.R248W p.Q317*
HTB-92™	SW872	fat	primary	liposarcoma	BRAF CDKN2A PTEN TP53	heterozygous homozygous homozygous homozygous	c.1799T>A c.237_238CC>TT c.1_1212del1212 c.752T>A	p.V600E p.R80* p.0? p.I251N



MTT CELL PROLIFERATION ASSAY, ATCC® 30-1010K™

Q: Can an MTT Cell Proliferation Assay directly replace [3H]-thymidine incorporation assays?

A: Yes, the addition of the dye solution can be substituted at the point in the assay when radioactive thymidine is added. Additionally, because the MTT Cell Proliferation Assay requires less cell manipulation than [3H]-thymidine the possibility of error is reduced and the standard deviation values are lower. In fact, comparisons between [3H]-thymidine incorporation and MTT assays have demonstrated less than 5% difference for determination of growth factor response.

STOMACH CANCER

STOMACH (GASTRIC) CANCER CELL PANEL (ATCC® TCP-1008™)

The Stomach (Gastric) Cancer Cell Panel is composed of six stomach cancer cell lines isolated from both primary and metastatic sites. Each culture contains genomic mutations in one or more of the following genes according to the Sanger COSMIC database: CDKN2A, TP53, SMAD4, CDH1, CTNNB1, KRAS, MLH1 and PIK3CA.The table below provides more information for the cell lines included in this panel.

ATCC® No.	Name	Primary Site, Tissue	Tumor Source	Histology	Mutant Gene	Zygosity	Gene Sequence*	Protein Sequence
HTB-103™	KATOIII	stomach	metastasis	carcinoma	TP53	homozygous	c.1_1182del1182	p.0?
CRL-5822™	NCI-N87	stomach stomach	metastasis metastasis	carcinoma carcinoma	SMAD4 TP53	homozygous homozygous	c.1_955del955 c.743G>A	p.? p.R248Q
CRL-5974™	SNU-16	stomach stomach stomach	metastasis metastasis metastasis	carcinoma carcinoma carcinoma	CDKN2A CDKN2a(p14) TP53	homozygous homozygous homozygous	c.1_471del471 c.1_522del522 c.614A>T	p.0? p.0? p.Y205F
CRL-5973™	SNU-5	stomach stomach stomach	metastasis metastasis metastasis	carcinoma carcinoma carcinoma	CDH1 CDKN2A TP53	heterozygous homozygous homozygous	c.687+1G>C c.238C>T c.783-2A>C	p.? p.R80* p.?
CRL-1739™	AGS	stomach stomach stomach stomach	primary primary primary primary	carcinoma carcinoma carcinoma carcinoma	CDH1 CTNNB1 KRAS PIK3CA	homozygous heterozygous heterozygous heterozygous	c.1733_1734insC c.101G>A c.35G>A c.1357G>A	p.G579fs*9 p.G34E p.G12D p.E453K
CRL-5971™	SNU-1	stomach stomach	primary primary	carcinoma carcinoma	KRAS MLH1	heterozygous homozygous	c.35G>A c.676C>T	p.G12D p.R226*

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

APPENDIX

ADDITIONAL TOOLS FOR CANCER RESEARCH

HTERT IMMORTALIZED CELL LINES

ATCC® human telomerase reverse transcriptase (hTERT) immortalized cell lines represent a breakthrough in cell biology research that combines the in vivo nature of primary cells and the ability to survive continuously in culture of traditional cell lines.

In addition to standard ATCC authentication, all hTERT immortalized cell lines are tested for:

- Extended proliferative capacity
- Selected phenotypic markers from the tissue of interest
- Stable genotype
- Continuous expression of hTERT

ATCC® No.	Description
Barrett's Esophageal Epithelial Cell Lines	
CRL-4027™	CP-A (KR-42421), human Barrett's esophageal epithelium
CRL-4028™	CP-B (CP-52731), human Barrett's esophageal epithelium
CRL-4029™	CP-C (CP-94251), human Barrett's esophageal epithelium
CRL-4030™	CP-D (CP-18821), human Barrett's esophageal epithelium
Bronchial Epithelial Cell Lines	
CRL-4011™	NuLi-1, human bronchial epithelium
CRL-4013™	CuFi-1, human bronchial epithelium
CRL-4015™	CuFi-4, human bronchial epithelium
CRL-4016™	CuFi-5, human bronchial epithelium
CRL-4017™	CuFi-6, human bronchial epithelium
Chondrocyte Fibroblast Cell Lines	
CRL-2846™	CHON-001, human bone cartilage fibroblast
CRL-2847™	CHON-002, human bone cartilage fibroblast
Dermal Microvascular Endothelial Cell Lines	
CRL-4025™	TIME, human dermal microvascular endothelium
Endometrial Fibroblast Cell Lines	
CRL-4003™	T HESCs, human endometrium fibroblast
Foreskin Fibroblasts Cell Lines	
CRL-4001™	BJ-5ta, human foreskin fibroblast
Mammary Epithelial Cell Lines	
CRL-4010™	hTERT-HME1 (ME16C), human mammary epithelium
Pancreas Duct Epithelial Cell Lines	
CRL-4023™	hTERT-HPNE, human pancreas duct epithelium
Renal Epithelial Cell Lines	
CRL-4004™	UMB1949 [UMBSVtel], human renal epithelium
CRL-4008™	SV7tert PDGFtu1, human renal epithelium
CRL-4031™	RPTEC/TERT1, human renal proximal tubules epithelium
Retinal Pigmented Epithelial Cell Lines	
CRL-4000™	hTERT RPE-1, human retinal pigmented epithelium

These materials are subject to claims under U.S. Patent Nos. 6,261,836 and 6,337,200, other pending patent applications, and foreign counterparts thereof. They are provided under the ATCC Material Transfer Agreement and the terms of the Addendum for Commercial and For-Profit Organizations or the Addendum for Noncommercial and Academic Organizations.

The TERT-containing plasmid is not available to commercial and for-profit organizations or for work to be conducted under funding from a commercial organization unless a commercial license is obtained. For information please e-mail ATCC's Office of IP, Licensing and Services.

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

Research Area	Tumor Panel Name	ATCC® No.	Description	Speci
Bladder Cancer	Bladder Cancer Cell Panel	TCP-1020™	A panel of 8 bladder tumor cell lines with varying degrees of genetic complexity. Each cell line has mutations in one or more of the following genes according to the Sanger COSMIC database: PIK3CA, RB1, RAS, TSC1, CDKN2A, PTEN, and TP53.	Huma
Bone Cancer	Bone Cancer Cell Panel	TCP-1009™	A panel of 5 bone cancer cell lines with varying degrees of genetic complexity. Four lines contain mutations in one or more of the following genes according to the Sanger COSMIC database: CDKN2A, BRAF, TP53, RB1, and PTEN. One line without a coding mutation serves as control.	Huma
Brain Cancer	Brain Cancer Cell Panel	TCP-1017™	A panel of 4 brain cancer cell lines with varying degrees of genetic complexity. Each cell line has mutations in one or more of the following genes according to the Sanger COSMIC database: TP53, CDKN2A, PTEN, and NF1.	Huma
	Glioma Cell Panel	TCP-1018™	A panel of 5 glioma tumor cell lines with varying degrees of genetic complexity. Each cell line has mutations in one or more of the following genes according to the Sanger COSMIC database: CDKN2A, PTEN, and TP53.	Huma
Breast Cancer	ATCC Breast Cancer Cell Panel	30-4500K™	A comprehensive set of 45 breast cancer cell lines. Each cell line is derived from the same ATCC master seed stock to eliminate variability. Provides consistency of research and results across disciplines, time and geographic regions including passage number. Each Cell Panel features a compact disc containing signed certificates of analysis and product sheets for each individual cell line.	Huma
	Breast Cancer p53 Hotspot Mutation Cell Panel	TCP-2010™	The Breast Cancer p53 Hotspot Mutation Cell Panel is comprised of 8 select cell lines derived from breast cancer that have been sequenced and validated by ATCC . This panel includes both WT p53 cell lines as well as cell lines with p53 hotspot mutations at codons 175, 248, 249, or 273.	Huma
	Triple-Negative Breast Cancer Cell Panel 1; Basal-Like Morphology	TCP-1001™	A panel of 9 triple-negative breast tumor cell lines sharing a basal-like morphology. See J Clinical Inv (2011) 121(7):2750-2767 for more information.	Huma
	Triple-Negative Breast Cancer Cell Panel 2; Mesenchymal & Luminal Morphology	TCP-1002™	A panel of 6 triple-negative breast tumor cell lines sharing a mesenchymal-like or luminal morphology. See J Clinical Inv (2011) 121(7):2750-2767 for more information.	Huma
	Triple-Negative Breast Cancer Cell Panel 3	TCP-1003™	A panel of 17 triple-negative breast tumor cell lines sharing a mesenchymal-like or luminal morphology. See J Clinical Inv (2011) 121(7):2750-2767 for more information.	Huma
Colon Cancer	Colon Cancer Cell Panel 1, KRAS	TCP-1006™	A panel of 8 colon cancer cell lines with varying degrees of genetic complexity. Each cell line has mutations in one or more of the following genes according to the Sanger COSMIC database: KRAS, APC, FAM123B, FBXW7, MSH2, PIK3CA, SMAD4, and TP53.	Huma
	Colon Cancer Cell Panel 2, BRAF	TCP-1007™	A panel of 8 colon cancer cell lines with varying degrees of genetic complexity. Each cell line has mutations in one or more of the following genes according to the Sanger COSMIC database: BRAF, APC, CTNNB1, EGFR, FBXW7, NF1, PIK3CA, PIK3R1, SMAD4, and TP53.	Huma
	Colon Cancer p53 Hotspot Mutation Cell Panel	TCP-2020™	The Colon Cancer p53 Hotspot Mutation Cell Panel is comprised of 6 select cell lines derived from colon cancer that have been sequenced and validated by ATCC . This panel includes both WT p53 cell lines as well as cell lines with p53 hotspot mutations at codons 175, 245, 248, or 273.	Huma
Gynecological Cancer	Cervical Cancer Cell Panel	TCP-1022™	A panel of 4 cervical tumor cell lines with varying degrees of genetic complexity. Each cell line has mutations in one or more of the following genes according to the Sanger COSMIC database: PIK3CA, BRCA2, STK11, FBXW7, MSH2, PTEN, RB1, and TP53.	Huma
	Gynecological Cancer Cell Panel	TCP-1024™	A panel of 9 tumor cell lines representing an array of gynecological cancers with varying degrees of genetic complexity. Each cell line has mutations in one or more of the following genes according to the Sanger COSMIC database: PIK3CA, FAM123B, APC, KRAS, CDKN2A, PTEN, RB1, FBXW7, MAP2K4, and TP53.	Huma
	Ovarian Cancer Cell Panel	TCP-1021™	A panel of 4 ovarian cancer cell lines with varying degrees of genetic complexity. Each cell line has mutations in one or more of the following genes according to the Sanger COSMIC database: APC, CDKN2A, FAM123B, KRAS, MLH1, NRAS, PIK3CA, STK11, and TP53.	Huma
	Uterine Cancer Cell Panel	TCP-1023™	A panel of 5 uterine tumor cell lines with varying degrees of genetic complexity. Each cell line has mutations in one or more of the following genes according to the Sanger COSMIC database: CDKN2A, APC, PIK3, PTEN, RB1, FBXW7, MAP2K4, BRCA, HRAS, NF2, and TP53	Huma
Head and Neck Cancer	Head and Neck Cancer Cell Panel	TCP-1012™	A panel of 6 cell lines from salivary gland, tongue, hypopharynx and pharynx. Each cell line has mutations in one or more of the following genes according to the Sanger COSMIC database: CDKN2A, TP53, SMAD4, PIK3CA and KDM5C.	Huma

* Please note that individual cell lines may require additional supplements be added to their growth medium. This information and can be found o

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

es	No. of cell lines	Mutant Genes Included	ATCC- Formulated Media and Sera*
an	8	PIK3CA, RB1, RAS, TSC1, CDKN2A, PTEN, TP53	Media: RPMI-1640 Medium (ATCC 30-2001), Eagle's Minimal Essential Medium (ATCC 30-2003), McCoy's 5a Medium Modified, (ATCC 30-2007), Leibovitz's L-15 Medium, (ATCC 30-2008), Serum: Fetal Bovine Serum (ATCC 30-2020)
an	5	CDKN2A, BRAF, TP53, RB1, PTEN	Media: Dulbecco's Modified Eagle's Medium, (ATCC 30-2002), Eagle's Minimal Essential Medium (ATCC 30-2003), McCoy's 5a Medium Modified , (ATCC 30-2007) Serum: Fetal Bovine Serum (ATCC 30-2020)
an	4	TP53, CDKN2A, PTEN, NF1	Media: RPMI-1640 Media (ATCC 30-2001), Dulbecco's Modified Eagle's Medium, (ATCC 30-2002), Leibovitz's L-15 Medium, (ATCC 30-2008), Eagle's Minimal Essential Medium (ATCC 30-2003) Serum: Fetal Bovine Serum (ATCC 30-2020)
an	5	CDKN2A, PTEN, TP53	Media: Dulbecco's Modified Eagle's Medium, (ATCC 30-2002), Leibovitz's L-15 Medium, (ATCC 30-2008), Eagle's Minimum Essential (ATCC 30-2003) Serum: Fetal Bovine Serum (ATCC 30-2020)
an	45	Cell line mutation descriptions for 30-4500K™ can be found on the ATCC website (atcc.org)	Cell line media requirements for 30-4500K™ can be found on the ATCC website (atcc.org)
an	8	TP53 Mutations (codon/AA): 524G>A/ R175H, 524 G>A/ R175H, 743G>A/ R248Q, 747G>C/ R249S, 818G>T/ R273L, 818G>A/ R273H	Media: McCoy's 5a Medium Modified, (ATCC 30-2007), RPMI-1640 Media (ATCC 30-2001), Leibovitz's L-15 Medium, (ATCC 30-2008) Serum: Fetal Bovine Serum (ATCC 30-2020)
an	9	TP53, CDKN2A, KDM6A, PTEN, SMAD4, RB1, BRCA1, BRCA2, CDKN2A, KDM6A, PTEN, SMAD4, RB1, STK11, BRAF, APC, MAP2K4, PIK3R1, NF2	Media: DMEM: F12 Medium (ATCC 30-2006), RPMI-1640 Media (ATCC 30-2001), Leibovitz's L-15 Medium, (ATCC 30-2008), Serum: Fetal Bovine Serum (ATCC 30-2020)
an	6	TP53, CDKN2A, KDM6A, PTEN, HRAS, PIK3R1, NF2, BRCA1, RB1, PIK3CA, CDH1	Media: RPMI-1640 Media (ATCC 30-2001), ATCC-formulated Dulbecco's Modified Eagle's Medium, (ATCC 30-2002), ATCC-formulated Leibovitz's L-15 Medium, (ATCC 30-2008), Serum: Fetal Bovine Serum (ATCC 30-2020),
an	17	TP53, CDKN2A, PIK3CA, PTEN, BRCA1	Media: DMEM: F12 Medium (ATCC-30-2006), RPMI-1640 Media (ATCC 30-2001), Leibovitz's L-15 Medium, (ATCC 30-2008), Eagle's Minimal Essential Medium (ATCC 30-2003). Serum: Fetal Bovine Serum (ATCC 30-2020)
an	8	KRAS, APC, FAM123B, FBXW7, MSH2, PIK3CA, SMAD4, TP53	Media: RPMI-1640 Media (ATCC 30-2001), Eagle's Minimal Essential Medium (ATCC 30-2003), Leibovitz's L-15 Medium (ATCC 30-2008), DMEM: F12 Medium (ATCC-30-2006), F-12K Medium (ATCC 30-2004); Serum: Fetal Bovine Serum (ATCC 30-2020)
an	8	BRAF, APC, CTNNB1, EGFR, FBXW7, NF1, PIK3CA, PIK3R1, SMAD4, TP53	Media: RPMI-1640 Media (ATCC 30-2001), Eagle's Minimal Essential Medium (ATCC 30-2003), Leibovitz's L-15 Medium (ATCC 30-2008), McCoy's 5a Medium Modified, Catalog (ATCC 30-2007). Serum: Fetal Bovine Serum (ATCC 30-2020),
an	6	TP53 Mutations (codon/AA): 524G>A/ R175H, 733G>A/ G245S, 742C>T/ R248W, 818G>A/ R273H	Media: RPMI-1640 Media (ATCC 30-2001), Eagle's Minimum Essential Medium (ATCC 30-2003), Leibovitz's L-15 Medium, (ATCC 30-2008) Serum: Fetal Bovine Serum (ATCC 30-2020)
an	4	PIK3CA, BRCA2, STK11, FBXW7, MSH2, PTEN, RB1, TP53	Media: RPMI-1640 Media (ATCC 30-2001), Dulbecco's Modified Eagle's Medium (ATCC 30-2002), Eagle's Minimal Essential Medium (ATCC 30-2003) Serum: Fetal Bovine Serum (ATCC 30-2020)
an	9	PIK3CA, FAM123B, APC, KRAS, CDKN2A, PTEN, RB1, FBXW7, MAP2K4, TP53	Media: Dulbecco's Modified Eagle's Medium (ATCC 30-2002), Eagle's Minimum Essential Medium (ATCC 30-2003), DMEM:F12 Medium (ATCC 30-2006), McCoy's 5a Medium Modified, Catalog (ATCC 30-2007), Leibovitz's L-15 Medium, (ATCC 30-2008) Serum: Fetal Bovine Serum (ATCC 30-2020)
an	4	APC, CDKN2A, FAM123B, KRAS, MLH1, NRAS, PIK3CA, STK11, TP53	Media: Dulbecco's Modified Eagle's Medium (ATCC 30-2002), Eagle's Minimum Essential Medium (ATCC 30-2003), McCoy's 5a Medium Modified (ATCC 30-2007), Leibovitz's L-15 Medium, (ATCC 30-2008). Serum: Fetal Bovine Serum (ATCC 30-2020),
an	5	CDKN2A, APC, PIK3, PTEN, RB1, FBXW7, MAP2K4, BRCA, HRAS, NF2, TP53	Media: Eagle's Minimal Essential Medium (ATCC 30-2003), DMEM:F12 Medium (ATCC 30-2006), McCoy's 5a Medium Modified, Catalog (ATCC 30-2007) Serum: Fetal Bovine Serum (ATCC 30-2020)
an	6	CDKN2A, TP53, SMAD4, PIK3CA, KDM5C	Media: Eagle's Minimal Essential Medium (ATCC 30-2003), DMEM:F12 Medium (ATCC 30-2006), McCoy's 5a Medium Modified, Catalog (ATCC 30-2007) Serum: Fetal Bovine Serum (ATCC 30-2020)

on our website (www.atcc.org)

Research Area	Tumor Panel Name	ATCC® No.	Description	Speci
Leukemia	Leukemia Cell Panel	TCP-1010™	A panel of 7 leukemia cell lines representing Acute Myeloid Leukemia (AML), Acute Monocytic Leukemia (AMoL), Chronic Myeloid Leukemia (CML), and Acute Lymphoblastic Leukemia (ALL). Each cell line has mutations in one or more of the following genes according to the Sanger COSMIC database: CDKN2A, KDM6A, TP53, NRAS, NOTCH1, PTEN, FBXW7, FLT3, KRAS, MLH1, and PIK3R1.	Huma
Liver Cancer	Liver Cancer Cell Panel	TCP-1011™	A panel of 7 liver cancer cell lines with varying degrees of genetic complexity. Each cell line has mutations in one or more of the following genes according to the Sanger COSMIC database: BRAF, CDKN2A, CTNNB1, NRAS, STK11, and TP53.	Huma
Lung Cancer	Lung Cancer Cell Panel	TCP-1016™	A panel of 7 lung cancer cell lines with varying degrees of genetic complexity. Each cell line has mutations in one or more of the following genes according to the Sanger COSMIC database: CDKN2A, EGFR, KRAS, NRAS, PIK3CA, PIK3R1, SMARCA4, STK11, and TP53.	Huma
	Non-Small Cell Lung Cancer p53 Hotspot Mutation Cell Panel	TCP-2030™	A panel of 6 select cell lines derived from the lung that have been sequenced and validated by ATCC . The Non-Small Cell Lung Cancer p53 Hotspot Mutation Cell Panel includes both WT p53 cell lines as well as cell lines with p53 hotspot mutations at codons 245, 248, or 273.	Huma
	Small Cell Lung Cancer p53 Hotspot Mutation Cell Panel	TCP-2040™	A panel of 6 select cell lines derived from the lung that have been sequenced and validated by ATCC . The Small Cell Lung Cancer p53 Hotspot Mutation Cell Panel includes both WT p53 cell lines as well as cell lines with p53 hotspot mutations at codons 175, 248, 249, or 273.	Huma
Lymphoma	Lymphoma Cell Panel	TCP-1015™	A panel of 9 lymphoma cell lines. Each cell line has mutations in one or more of the following genes according to the Sanger COSMIC database: EZH2, TP53, PTEN, CDKN2A, RB1, CTNNB1, NRAS, and SOCS1.	Huma
	Lymphoma p53 Hotspot Mutation Cell Panel	TCP-2050™	A panel of 5 lymphoma cell lines that have been sequenced and validated by ATCC for p53 hotspot mutations and protein expression. This Cell Panel includes a WT p53 cell line as well as 4 cell lines with p53 hotspot mutations at codons 743 and 818.	Huma
	Non-Hodgkin's Lymphoma Cell Panel	TCP-1025™	A panel of 9 diffuse histiocytic and one diffuse undifferentiated Non-Hodgkin's lymphoma cell lines annotated with published source, diagnosis, and biomarker data (where available). All cell lines in this panel are EBV negative.	Huma
Pancreatic Cancer	Pancreatic Cancer Cell Panel	TCP-1026™	A panel of 7 pancreatic cancer cell lines with varying degrees of genetic complexity. Each cell line has mutations in one or more of the following genes according to the Sanger COSMIC database: CDKN2A, FBXW7, KRAS, MAP2K4, SMAD4, and TP53.	Huma
Skin Cancer	Melanoma Cancer Cell Panel	TCP-1013™	A panel of 3 melanoma cancer cell lines with varying degrees of genetic complexity. Each cell line has mutations in one or more of the following genes according to the Sanger COSMIC database: BRAF, CTNNB1, CDKN2A, and STK11.	Huma
	Metastatic Melanoma Cell Panel	TCP-1014™	A panel of 4 metastatic melanoma cancer cell lines with varying degrees of genetic complexity. Each cell line has mutations in one or more of the following genes according to the Sanger COSMIC database: BRAF, TP53, CDKN2A and PTEN.	Huma
Soft Tissue Cancer	Soft-Tissue Sarcoma Cell Panel	TCP-1019™	A panel of 6 soft-tissue tumor cell lines with varying degrees of genetic complexity. Each cell line has mutations in one or more of the following genes according to the Sanger COSMIC database: CDKN2A, IDH1, NRAS, BRAF, PTEN, and TP53.	Huma
Stomach Cancer	Stomach (Gastric) Cancer Cell Panel	TCP-1008™	A panel of 6 stomach cancer cell lines isolated from both primary and metastatic sites. Each cell line has mutations in one or more of the following genes according to the Sanger COSMIC database: CDKN2A, TP53, SMAD4, CDH1, CTNNB1, KRAS, MLH1 and PIK3CA.	Huma

* Please note that individual cell lines may require additional supplements be added to their growth medium. This information and can be found o

es	No. of cell lines	Mutant Genes Included	ATCC- Formulated Media and Sera*
n	7	CDKN2A, KDM6A, TP53, NRAS, NOTCH1, PTEN, FBXW7, FLT3, KRAS, MLH1, PIK3R1	Media: RPMI-1640 Media (ATCC 30-2001), Iscove's Modified Dulbecco's Medium, (ATCC 30-2005). Serum: Fetal Bovine Serum (ATCC 30-2020)
n	7	BRAF, CDKN2A, CTNNB1, NRAS, STK11, TP53	Media: RPMI-1640 Media (ATCC 30-2001), Eagle's Minimum Essential Medium (ATCC 30-2003) Serum: Fetal Bovine Serum (ATCC 30-2020)
n	7	CDNK2A, EGFR, KRAS, NRAS PIK3CA, PIK3R1, SMARCA4, STK11, TP53	Media: DMEM: F12 Medium (ATCC 30-2006), RPMI-1640 Media (ATCC 30-2001) Serum: Fetal Bovine Serum (ATCC 30-2020)
n	6	TP53 Mutations (codon/AA): 733G>T/ G245C, 741 742CC>TT/ R248W, 818G>A/R273H	Media: RPMI-1640 Media (ATCC 30-2001), F-12K Medium (ATCC 30-2004), DMEM: F12 Medium (ATCC 30-2006), Lonza/Clonetics Corporation BEGM, Kit Catalog No. CC-3170 Serum: Fetal Bovine Serum (ATCC 30-2020)
n	6	TP53 Mutations (codon/AA): 524G>T/ R175L, 743G>A/R248Q, 747G>T/R249S, 817C>T/R273C	Media: RPMI-1640 Media (ATCC 30-2001), DMEM: F12 Medium (ATCC 30-2006), Lonza/ Clonetics Corporation BEGM, Kit Catalog No. CC-3170 Serum: Fetal Bovine Serum (ATCC 30-2020)
n	9	EZH2, TP53, PTEN, CDKN2A, RB1, CTNNB1, NRAS, SOCS1	Media: RPMI-1640 Media (ATCC 30-2001), Serum: Fetal Bovine Serum (ATCC 30-2020)
n	5	TP53 Mutations (codon/AA): 743G>A//R248Q, 743G>A//R248Q, 743G>A//R248Q, 818G>A/ R273H	Media: RPMI-1640 Media (ATCC 30-2001), Iscove's Modified Dulbecco's Medium, (ATCC 30-2005). Serum: Fetal Bovine Serum (ATCC 30-2020)
n	9	CD79, TP53, Immunoglobulin	Media: RPMI-1640 Media (ATCC 30-2001), Serum: Fetal Bovine Serum (ATCC 30-2020)
n	7	CDKN2A, FBXW7, KRAS, MAP2K4, SMAD4, TP53	Media: Eagle's Minimal Essential Medium (ATCC 30-2003), McCoy's 5a Medium Modified, Catalog (ATCC 30-2007), RPMI-1640 Media (ATCC 30-2001), Iscove's Modified Dulbecco's Medium, (ATCC 30-2005), Leibovitz's L-15 Medium, (ATCC 30-2008), Serum: Fetal Bovine Serum (ATCC 30-2020)
n	4	BRAF, CTNNB1, CDKN2A, STK11	Media: Dulbecco's Modified Eagle's Medium (ATCC 30-2002), Eagle's Minimum Essential Medium (ATCC 30-2003), McCoy's 5a Medium Modified, Catalog (ATCC 30-2007) Serum: Fetal Bovine Serum (ATCC 30-2020)
n	4	BRAF, TP53, CDKN2A , PTEN	Media: Eagle's Minimum Essential Medium (ATCC 30-2003), McCoy's 5a Medium Modified, Catalog (ATCC 30-2007) Serum: Fetal Bovine Serum (ATCC 30-2020)
n	6	CDKN2A, IDH1, NRAS, BRAF, PTEN, TP53	Media: Dulbecco's Modified Eagle's Medium (ATCC 30-2002), Eagle's Minimum Essential Medium (ATCC 30-2003), McCoy's 5a Medium Modified, (ATCC 30-2007), Leibovitz's L-15 Medium, (ATCC 30-2008), Serum: Fetal Bovine Serum (ATCC 30-2020)
n	6	CDKN2A, TP53, SMAD4, CDH1, CTNNB1, KRAS, MLH1, PIK3CA	Media: RPMI-1640 Media (ATCC 30-2001), F-12K Medium (ATCC 30-2004), Iscove's Modified Dulbecco's Medium, (ATCC 30-2005) Serum: Fetal Bovine Serum (ATCC 30-2020)

on our website (www.atcc.org)

10801 University Boulevard
Manassas, Virginia 20110-2209

703.365.2700

703.365.2701

sales@atcc.org

www.atcc.org

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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.