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## Abstract

Introduction: Large-scale cancer genome programs have generated a rich data set comprising genetic abnormalities observed in thousands of clinical patient tumors, which provides a major opportunity for the molecular detection of cancer. However, the lack of controls for molecular tests has been a challenge. Because of the reproducible nature of the cell lines, genomic DNAs of fully characterized and authenticated cell lines provide a solution.

Methods: Genomic DNAs were extracted from over 70 commonly used human cancer cell lines derived from the breast, lung, colon, and pancreas, as well as hematopoietic and lymphoid tissue. Cancer gene mutations were identified by next-generation sequencing. Gene copy number changes were analyzed using the qBiomarker Copy Number PCR Assays kit (QIAGEN). Moreover, the selected cell lines were analyzed by quantitative polymerase chain reaction (qPCR), Western blot, and immunofluorescence (IF) staining to verify gene and protein expression mutation.

**Results:** Here, we present over 70 genomic DNAs isolated from authenticated cancer cell lines that contain desired biomarkers for oncological assay development. In addition to driver mutations such as BRAF V600, KRAS G12, PI3K E545 and EGFR T790, the gene copy number amplifications of AKT, FGFR, MET, and ERBB2, and the deletion of PTEN are presented in the cell lines from which the genomic DNAs were extracted. Our analysis shows the systematic molecular characterization and clustering of those human tumor cell lines, which represent the most common human cancer types found in the clinic, such as lung, breast, colon, pancreatic, and skin cancer. These cell lines were fully analyzed by next-generation sequencing to capture the driver gene mutations and allelic frequency. Gene DNA copy number variations were determined as well. Moreover, the gene expression, protein expression, and relevant cell signaling pathway activations have also been profiled. To be paired with mutations, a set of wild type controls derived from normal tissues were characterized in parallel.

**Conclusions:** Overall, genomic DNA from authenticated and well characterized cell lines provide suitable control materials to develop assays for genetic testing.

## Introduction

### ATCC tumor cell panels and related genomic DNAs



ATCC 10801 University Boulevard, Manassas, Virginia 20110-2209 phone: 800.638.6597

# Cell Line Genomic DNAs for the Molecular Diagnosis of Cancer

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## **American Type Culture Collection, Manassas, VA 20110**

## Results

Human	cancer	Cell I	ines cor	itain di	omark	kers – n	nutati	ions	ATCC <sup>®</sup> No.	Cell line name	Gene	Amino acid Change	cDNA Change	NGS Coverage	% Zygosity	Tumor source
	py num							C	CCL-231™	SW48	EGFR	p.G719S	c.2155G>A	35993	G = 69.4, A = 30.3	Colon
	Coll line		AKT1 copy	Measured	AKT2 co	opy Measu	ired		CRL-5908™	NCI-H1975	EGFR	p.T790M	c.2369C>T	11704	C = 33.0, T = 66.9	Lung
ATCC <sup>®</sup> No.	name	Gene	number	CNV of	numbe	er CNV	of so	ource				p.L858R	c.2573T>G	9441	T = 33.7, G = 66.2	
CRI -2321™	HCC1143	AKT1	Amplification	6.21			Z Br	reast				EGFR copy		ERBB2	2 copy Measured	<b>-</b>
CRL-1469™	PANC-1	AKT2	–	-	Amplifica	ition 25.4	6 Par	ncreas	ATCC <sup>®</sup> No.	Cell line name	Gene	number	EGFR	of num	ber CNV of	source
CRL-1622™	KLE	AKT2	-	-	Amplifica	ition 12.5	1 Endo	metrium	CRL-2868™	HCC827	EGFR	Amplification	63.01	varia		Luna
HTB-161™	NIH:OVCAR-	3 AKT2	-	-	Amplifica	ition 9.78	в О	ovary H	HTB-132™	MDA-MB-468	EGFR	Amplification	25.02	-	· _	Breast
HTB-183™	NCI-H661	AKT2	_	-	Slight	t 5.56	6 L	ung	HTB-19™	BT-20	EGFR	Amplification	15.73	-	- –	Breast
					amplifica	tion		ŀ	HTB-178™	NCI-H596	EGFR	Amplification	0.06	-	· _	Lung
			FGFR1 copy	Measured	FGFR2 c	opy Measu	ired _	H	HTB-177™	NCI-H460	EGFR	-	-	-	· _	Lung
ATCC <sup>®</sup> No.	Cell line name	Gene	number	CNV of	numbe	er CNV	of so	umor ( ource	CRL-5928™	NCI-H2170	ERBB2	-	-	Amplifi	cation 128.89	Lung
			variation	FGFR1	variatio	on FGFF	R2 00		-11B-20™ 	BI-4/4	ERBB2	_	-	Amplifi	cation 29.7	Breast
HTB-23™	MDA-MB- 134-VI	FGFR1	Amplification	14.22	-	-	Br	reast			LNDDZ	_	_	Ampin		Diedsi
CRL-2066™	DMS 114	FGFR1	Amplification	7.17	-	-	L	ung		Cell line		Amino acid		NGS	0/ 🕇	Tumor
CCI -235™	SW837	FGFR1	Slight	39	_	_	C	Colon	AICC° NO.	name	Gene	Change		Coverage	% Zygosity	source
002 200	011001		amplification	0.0			Ũ	(	CRL-2177™	SW 1271	NRAS	p.Q61R	c.182A>G	26732	G = 99.8%	Lung
CCL-246™	KG-1	FGFR1	amplification	3.87	-	-	Leu	ikemia (	CRL-2273™	CHP-212	NRAS	p.Q61K	c.181C>A	49859	C = 50.7, A = 49.1	Brain
CRL-5974™	SNU-16	FGFR2	_	-	Amplifica	ition 451.1	16 Sto	omach	CRL-7585™	Hs 852.T	NRAS	p.G12V	c.35G>T	66411	G = 38.0, T = 61.8	Skin
HTB-103™	KATO III	FGFR2	-	-	Amplifica	ition 138.6	52 Sto	omach	CRL-9068™ TIR 202™	NCI-H929 тнр 1	NRAS	p.G13D	c.38G>A	21896	A = 53.9, G = 45.9 A = 70.1, C = 20.9	Nyeloma
									CRL-2547™	Panc 10.05	KRAS	p.G12D	c.35G>A	42708	G = 52.7. A = 47.3	Pancreas
ATCC <sup>®</sup> No.	Cell line	Gene	MYC cop	y number	Measure	d CNV of	Tumor so	ource (	CRL-2549™	Panc 03.27	KRAS	p.G12V	c.35G>T	58913	G = 47.0, T = 52.9	Pancreas
	name		varia	ation	M	YC		H	HTB-174™	NCI-H441	KRAS	p.G12V	c.35G>T	87521	G = 52.8, T = 47.1	Lung
CRL-5974™	SNU-16	MYC	Amplif	ication	50	.48	Stoma	ch (	CL-187™	LS 180	KRAS	p.G12D	c.35G>A	91234	G = 51.3, A = 48.6	Colon
CRL-2081™	MSTO-211H	MYC	Amplif	ication	38	.92	Mesotheli	lioma (	CCL-225™	HCT-15	KRAS	p.G13D	c.38G>A	49764	G = 52.1, A = 47.8	Colon
HIB-175™	NCI-H82	MYC	Amplif	ication	35	.63	Lung	]				A mine e sial				<b>T</b>
ПТБ-1/Т <sup>™</sup> ССГ-240™		MYC	Slight am	nlification	19	.00 43	Lung	) nia	ATCC <sup>®</sup> No.	name	Gene	Amino acid Change	DNA Change	NGS Coverage	% Zygosity	source
			olight diff	pinioation	0.	-10	Leaken	H	HTB-19™	BT-20	PIK3CA	p H1047R	c 3140A>G	7062	A = 64 3 G = 35 6	Breast
	Cell line	-	MET co	ov number	Measure	d CNV of	_	ŀ	HTB-131™	MDA-MB-453	PIK3CA	p.H1047R	c.3140A>G	10415	A = 35.6, G = 64.2	Breast
ATCC <sup>⊮</sup> No.	name	Gene	var	iation	M	ET	Tumor so	burce	HTB-112™	HEC-1-A	PIK3CA	p.G1049R	c.3145G>C	6981	G = 38.8, C = 61.0	Endometriu
CRL-5973™	SNU-5	MET	Amp	ification	71	.88	Stoma	ch H	HTB-178™	NCI-H596	PIK3CA	p.E545K	c.1633G>A	2669	G = 68.5, A = 31.4	Lung
HTB-135™	Hs 746T	MET	Amp	ification	23	.96	Stoma	ich C	CRL-1739™	AGS	PIK3CA	p.E545A	c.1634A>C	9377	A = 23.6, C = 76.3	Stomach
CRL-2351™	AU565	MET	Slight a	nplification	1.	99	Breas	st	CCL-237™	SW948	PIK3CA	p.E542K	c.1624G>A	13713	G = 52.7, A = 47.2	Colon
								F	HIB-121™	B1-483	PIK3CA	p.E542K	c.1633G>A	11779	A = 49.8, C = 50.0	Breast
	Cell line	Cono A	mino acid	A Change	NGS	9/ <b>7</b>	. Ti	umor <sup>+</sup>	HTB-27™	MDA-MB-361	PIK3CA	p.⊏545K	c 1700A>G	916	G = 79.7, A = 20.1 A = 64.2 G = 35.8	Breast
AICC NO.	name	Gene	Change	A Change	Coverage		y so	ource				p		0.0	, , , , , , , , , , , , , , , , , , , ,	
• <b>-</b> · · · <b>·</b> ·	1	MAPK3	p.R96R c	.288C>T	3346 (	C = 36.5, T = 4	40.5		ATCC <sup>®</sup> No.	Cell line	Gene	Amino acid	DNA Change	NGS	% Zvaositv	Tumor
CRL-2577 ™	RKO F	PIK3CA   BDAE	p.H1047R c.	3140A>G	1359 A	A = 45.5, G = 5	54.4 C	Colon		name		Change		Coverage		source
HTR_Q™	5637		p.voue c.	236G>A	67777 (	r = 29.0, A = 0 r = 56.1 A = 4	09.0 43.8 RI	ladder	HTB-66™	RPMI-7951	BRAF	p.V600E	c.1799T>A	1599	T = 62.5, A = 37.1	Skin
			n P246S	736C>T	0476 (	$\Sigma = A 1 A T = B$	58.6 G		CCL-238™	SW1417	BRAF	p.V600E	c.1799T>A	3697	T = 58.6, A = 41.2	Colon
			p.r 2403 C	CO245C	0404	C = 00.0	JU.U		CL 224™		BRAF		c.17991>A	5043 1122	T = 43.8, A = 55.8 T = 22.0, A = 77.8	Skin
			p.1228V C	.082A>G	9124	G = 99.8							c.1799 1800TG	4122	T = 37.7, A = 62.1,	
HIB-2™	RI4 I	MAPK3	p.A109A c	32/G>A	14152 (	j = 62.6, A = (	37.2 BI	ladder (	CRL-1676™	WM-266-4	BRAF	p.V600D	-AT	6776	G = 37,4, T = 62.5	Skin
	Coll lino	•	mino acid		NGS		т	umor								
ATCC <sup>®</sup> No.	name	Gene	Change DN	A Change	Coverage	% Zygosity	y so	burce A	ATCC <sup>®</sup> No.	Cell line name	Gene	Amino acid Change	DNA Change	NGS Coverage	% Zygosity	Tumor source
HTB-31™	C-33-A	PTEN	p.R233* c	.697C>T	65522 (	C = 51.9, T = 4	48.0 C	ervix				p.Y27S	c.80A>C	50463	A = 9.6. C = 89.9	
HTB-111™	AN3 CA	PTEN	p.R130fs c.38	9_389delG	14373	Deletion = 99	9.3 Endo	ometrium	HTB-62™	P3HR-1	MYC	p.E54D	c.162G>A	66485	G = 10.8, A = 82.6	Burkitt's
CRL-1718™	CCF-	PTEN	p.L112R c	.335T>G	20249	G = 99.6	В	Brain	110 02		in r o	p.P72S	c.214C>T	68482 68305	C = 17.6, T = 81.2	lymphoma
	51161											p.Q1131 p.V201	c.58G>A	22792	G = 12.1, A = 86.5	
												p.P72S	c.214C>T	30456	C = 13.8, T = 85.3	Burkitt's
Real tin	ne PCR	analv	sis of m	RNA le	vels			(	גנ-1048™	UA40		р. <b>Р75Н</b> р.L193V	c.224C>A c.577C>G	∠9467 21112	C = 17.2, A = 80.3 C = 54.9, G = 44.7	lymphom
												p.Q321H	c.963G>C	30065	G = 50.1, C = 49.5	
	SNP +	F	EGFR									p.Q51L n P72T	c.152A>T	50033 49383	A = 8.1, T = 87.8 C = 21.0 A = 77.7	Rurkitt's
	Amp	amp	olification		<b>-</b> <sup>90</sup>	WT Cell Lines	S	C	CRL-1647™	ST486	MYC	p.T110P	c.328A>C	50765	A = 7.2, C = 92.2	lymphom
<mark>ري</mark> <sub>60</sub>					<u>s</u>											

Human and cou	cancer	cell	lines co ariations	ntain b	iomar	kers	– mu	tations	ATCC <sup>®</sup> No.	Cell line name	Gene	Amino acid Change	cDNA Change	NGS Coverage	% Zygosity	Tumor source
	y nunn								CCL-231™	SW48	EGFR	p.G719S	c.2155G>A	35993	G = 69.4, A = 30.3	Colon
			AKT1 copy	Measured	AKT2	сору 🛛	leasured	Turner	CRL-5908™	NCI-H1975	EGFR	p.T790M	c.2369C>T	11704	C = 33.0, T = 66.9	Lung
ATCC <sup>®</sup> No.	name	Gene	number	CNV of	num	ber	CNV of	source				p.L858R	c.2573T>G	9441	T = 33.7, G = 66.2	0
CRL-2321™	HCC1143	AKT1	Amplification	6.21	-		-	Breast		Cell line		EGFR copy	Measured CNV	of ERBB2	2 copy Measured	Tumor
CRL-1469™	PANC-1	AKT2	-	-	Amplifi	cation	25.46	Pancreas	ATCC <sup>®</sup> No.	name	Gene	number variation	EGFR	num varia	ber CNV of ERBB2	source
CRL-1622™	KLE	AKT2	-	-	Amplific	cation	12.51	Endometrium	CRL-2868™	HCC827	EGFR	Amplification	63.01	-		Lung
HTB-161™	NIH:OVCAR-	-3 AKT2	-	-	Amplific	cation	9.78	Ovary	HTB-132™	MDA-MB-468	EGFR	Amplification	25.02	-	· –	Breast
HTB-183™	NCI-H661	AKT2	-	-	Slig	ht	5.56	Lung	HTB-19™	BT-20	EGFR	Amplification	15.73	-	· –	Breast
					ampinio	alion			HTB-178™	NCI-H596	EGFR	Amplification	0.06	-	· –	Lung
	Coll line		FGFR1 copy	/ Measured	FGFR2	сору М	leasured	Tumor	HTB-177™	NCI-H460	EGFR	-	-	-		Lung
ATCC <sup>®</sup> No.	name	Gene	number	CNV of	num	ber	CNV of	source		NCI-H2170	ERBB2	_	-	Amplifi	cation 128.89	Lung
			variation	FGFR1	varia	lion	FGFR2		HTB-20™ HTB-27™	BT-474	ERBB2	-	-	Amplili Amplifi	cation 16.85	Breast
HTB-23™	134-VI	FGFR <sup>2</sup>	Amplification	14.22	-		-	Breast	1110-21					Апріп		Dicast
CRL-2066™	DMS 114	FGFR <sup>2</sup>	Amplification	7.17	-		-	Lung		Cell line	Gana	Amino acid		NGS	$\frac{9}{7}$	Tumor
CCL-235™	SW837	FGFR <sup>2</sup>	Slight	3.9	_		_	Colon	AICC NO.	name	Gene	Change		Coverage	% Zygosity	source
			amplification						CRL-2177™	SW 1271	NRAS	p.Q61R	c.182A>G	26732	G = 99.8%	Lung
CCL-246™	KG-1	FGFR'	amplification	3.87	-		-	Leukemia	CRL-2273™	CHP-212	NRAS	p.Q61K	c.181C>A	49859	C = 50.7, A = 49.1	Brain
CRL-5974™	SNU-16	FGFR	2 –	-	Amplific	cation	451.16	Stomach	CRL-7585™	Hs 852.T	NRAS	p.G12V	c.35G>T	66411	G = 38.0, T = 61.8	Skin
HTB-103™	KATO III	FGFR	2 –	-	Amplific	cation	138.62	Stomach	CRL-9068 ™ TIB-202™		NRAS	p.G13D	C.38G>A	21896 60288	A = 53.9, G = 45.9 A = 70.1 G = 29.9	Iviyeioma
									CRL-2547™	Panc 10.05	KRAS	p.G12D	c.35G>A	42708	G = 52.7. A = 47.3	Pancreas
ATCC <sup>®</sup> No.	Cell line	Gene	MYC co	by number	Measu	red CNV	of Tur	nor source	CRL-2549™	Panc 03.27	KRAS	p.G12V	c.35G>T	58913	G = 47.0, T = 52.9	Pancreas
	name		var	iation		МҮС			HTB-174™	NCI-H441	KRAS	p.G12V	c.35G>T	87521	G = 52.8, T = 47.1	Lung
CRL-5974™	SNU-16	MYC	Ampl	ification	5	50.48	S	Stomach	CL-187™	LS 180	KRAS	p.G12D	c.35G>A	91234	G = 51.3, A = 48.6	Colon
CRL-2081™	MSTO-211H	MYC	Ampl	ification	3	8.92	Mes	sothelioma	CCL-225™	HCT-15	KRAS	p.G13D	c.38G>A	49764	G = 52.1, A = 47.8	Colon
HIB-175™	NCI-H82	MYC	Ampli	ification		35.63 0.06		Lung						NOO		<b>-</b>
ПТВ-17Т™ ССГ-240™		MYC	Ampi Slight an	nolification		9.00		Lung	ATCC <sup>®</sup> No.	name	Gene	Amino acid Change	DNA Change	NGS Coverage	% Zygosity	source
		WIT C	Olight di	npinioation		0.40		catchila	HTB-19™	BT-20	PIK3CA	n H1047R	c 3140A>G	7062	A = 64.3 G = 35.6	Breast
	Cell line	-	MET co	oov number	Measu	red CNV	of		HTB-131™	MDA-MB-453	PIK3CA	p.H1047R	c.3140A>G	10415	A = 35.6, G = 64.2	Breast
ATCC <sup>⊮</sup> No.	name	Gen	e va	riation	modod	MET	Tun	nor source	HTB-112™	HEC-1-A	PIK3CA	p.G1049R	c.3145G>C	6981	G = 38.8, C = 61.0	Endometriu
CRI -5973™	SNU-5	ME	C Amr	olification		71 88	ç	Stomach	HTB-178™	NCI-H596	PIK3CA	p.E545K	c.1633G>A	2669	G = 68.5, A = 31.4	Lung
HTB-135™	Hs 746T	ME	r Amr	olification	2	23.96	ç	Stomach	CRL-1739™	AGS	PIK3CA	p.E545A	c.1634A>C	9377	A = 23.6, C = 76.3	Stomach
CRL-2351™	AU565	ME	Slight a	amplification		1.99		Breast	CCL-237™	SW948	PIK3CA	p.E542K	c.1624G>A	13713	G = 52.7, A = 47.2	Colon
			C						H1B-121™	B1-483	PIK3CA	p.E542K	c.1634A>C	11779	A = 49.8, C = 50.0	Breast
	Cell line	Cono	Amino acid		NGS	0/ 7.		Tumor	HTB-27™	MDA-MB-361	PIK3CA	p.E545K	c 1700A>G	916	A = 64.2 $G = 35.8$	Breast
AICC'NO.	name	Gene	Change	va change	Coverage	% <b>∠y</b>	gosity	source				pinteerry	0.110011 0	010		
<b></b>		MAPK3	p.R96R	c.288C>T	3346	C = 36.5	5, T = 40.5		ATCC <sup>®</sup> No.	Cell line	Gene	Amino acid	DNA Change	NGS	% Zvaositv	Tumor
CRL-2577™	RKO		p.H1047R c	.3140A>G	1359	A = 45.5	6, G = 54.4 6 A = 60.6	Colon		name		Change		Coverage		source
HTR_Q™	5637		p.v000E C	236G>∆	67777	G = 56.1	0, A = 09.0 1 $A = 43.8$	Bladder	HTB-66™	RPMI-7951	BRAF	p.V600E	c.1799T>A	1599	T = 62.5, A = 37.1	Skin
			p.P.246S	- 736C>T	0476	C = 41.4	1,77 10.0 1 T - 58 6	Skin	CCL-238™	SW1417	BRAF	p.V600E	c.1799T>A	3697	T = 58.6, A = 41.2	Colon
			p.r 2403		0404	0 - 41.4	+, 1 – 30.0 - 00 0	Skin			BRAF	p.V600E	c.17991>A	5643	I = 43.8, A = 55.8 T = 22.0 A = 77.8	Skin
			p.1228V (	C.08ZA>G	9124	G =	99.8	SKIN					c.1799 1800TG	4122	T = 37.7, A = 62.1,	
HIB-2™	RI4	MAPK3	p.A109A 0	c.327G>A	14152	G = 62.6	5, A = 37.2	Bladder	CRL-1676™	WM-266-4	BRAF	p.V600D	>AT	6776	G = 37,4, T = 62.5	Skin
	Cell line		Amino acid		NGS	o/ <b>-</b>	•7	Tumor		Cell line		Amino acid		NGS		Tumor
AICC° NO.	name	Gene	Change	NA Change	Coverage	% ∠y	gosity	source	ATCC <sup>®</sup> No.	name	Gene	Change	DNA Change	Coverage	% Zygosity	source
HTB-31™	C-33-A	PTEN	p.R233*	c.697C>T	65522	C = 51.9	9, T = 48.0	Cervix				p.Y27S	c.80A>C	50463	A = 9.6, C = 89.9	
HTB-111™	AN3 CA	PTEN	p.R130fs c.3	89_389delG	14373	Deletio	on = 99.3	Endometrium	HTB-62™	P3HR-1	MYC	p.E54D	c.162G>A	66485	G = 10.8, A = 82.6	Burkitt's
CRL-1718™	CCF-	PTEN	p.L112R	c.335T>G	20249	G =	99.6	Brain				p.P725 p.Q113H	c.214C>1 c.339G>C	68482 68395	C = 17.6, T = 81.2 G = 9.6, C = 89.2	iymphoma
	01101											p.V20I	c.58G>A	22792	G = 12.1, A = 86.5	
									CRI -1648™	CA46	MYC	p.P72S n P75H	c.214C>T c.224C>∆	30456 29467	C = 13.8, T = 85.3 $C = 17.2 \Delta = 80.3$	Burkitt's
Real tir	ne PCR	analy	/sis of m	RNA le	vels							p.L193V	c.577C>G	21112	C = 54.9, G = 44.7	lymphoma
		-										p.Q321H	c.963G>C	30065	G = 50.1, C = 49.5	
	SNP +		EGFR							OT400		p.QoTL p.P72T	c.214C>A	49383	A = 0.1, T = 87.8 C = 21.0, A = 77.7	Burkitt's
<b>(sp</b> )	Amp	am	plification		<b>(9</b> 0	W			UKL-1647™	51480	WYC	p.T110P	c.328A>C	50765	A = 7.2, C = 92.2	lymphoma
<b>60</b> 80 <b>60 6 6 6 6 6 6 6 6 6 6</b>					<b>60</b> 80 - 80 - 70 - 70 - 70 - 70 - 70 - 70 -		VV I					p.A198V	c.593C>T	31630	C = 5.7, T = 93.0	
70 60					70 - 60 -											

Human and cor	cancer	cell	lines cor ariations	ntain bi	omar	kers –	· mu	tations	ATCC <sup>®</sup> No.	Cell line name	Gene	Amino acid Change	cDNA Change	NGS Coverage	% Zygosity	Tumor source
	Sy num								CCL-231™	SW48	EGFR	p.G719S	c.2155G>A	35993	G = 69.4, A = 30.3	Colon
			AKT1 copy	Measured	AKT2 c	opy Mea	asured	<b>-</b>	CRL-5908™	NCI-H1975	EGFR	p.T790M	c.2369C>T	11704	C = 33.0, T = 66.9	Lung
ATCC <sup>®</sup> No.	Cell line name	Gene	number	CNV of	numb	er C	NV of	lumor source				p.L858R	c.2573T>G	9441	T = 33.7, G = 66.2	9
CRL-2321™	HCC1143	AKT1	Amplification	6.21	-		_	Breast		Cell line		EGFR copy	Measured CNV	of ERBB2	2 copy Measured	Tumor
CRL-1469™	PANC-1	AKT2	-	-	Amplific	ation 2	5.46	Pancreas	ATCC <sup>®</sup> No.	name	Gene	number variation	EGFR	num varia	ber CNV of ERBB2	source
CRL-1622™	KLE	AKT2	-	-	Amplific	ation 1	2.51	Endometrium	CRL-2868™	HCC827	EGFR	Amplification	63.01	-	- –	Lung
HTB-161™	NIH:OVCAR-	3 AKT2	-	-	Amplific	ation	9.78	Ovary	HTB-132™	MDA-MB-468	EGFR	Amplification	25.02	-	· –	Breast
HTB-183™	NCI-H661	AKT2	-	-	Sligh	nt .	5.56	Lung	HTB-19™	BT-20	EGFR	Amplification	15.73	-		Breast
					amplific	ation		C .	HTB-178™	NCI-H596	EGFR	Amplification	0.06	-	· –	Lung
			FGFR1 copy	Measured	FGFR2	copy Mea	asured		HTB-177™	NCI-H460	EGFR	-	-	-		Lung
ATCC <sup>®</sup> No.	Cell line	Gene	number	CNV of	numb	er Cl	NV of	Tumor	CRL-5928™	NCI-H2170	ERBB2	-	-	Amplifi	cation 128.89	Lung
			variation	FGFR1	variat	ion F	GFR2		HTB-20™	BI-474	ERBB2	-	-	Amplifi	cation 29.7	Breast
HTB-23™	мDА-МВ- 134-VI	FGFR1	Amplification	14.22	_		-	Breast	HIB-27 ***	MDA-MB-301	ERDDZ	-	_	Ampiiii	Callon 10.85	Breast
CRL-2066™	DMS 114	FGFR1	Amplification	7.17	-		-	Lung	ATCC <sup>®</sup> No.	Cell line	Gene	Amino acid	DNA Change	NGS	% Zvgositv	Tumor
CCL-235™	SW837	FGFR1	Slight	3.9	-		-	Colon		name		Change		Coverage	// _JgoonJ	source
			Slight	2.07					CRL-2177™	SW 1271	NRAS	p.Q61R	c.182A>G	26732	G = 99.8%	Lung
CCL-246™	KG-1	FGFR1	amplification	3.87	-		-	Leukemia	CRL-2273™	CHP-212	NRAS	p.Q61K	c.181C>A	49859	C = 50.7, A = 49.1	Brain
CRL-5974™	SNU-16	FGFR2	2 –	-	Amplific	ation 4	51.16	Stomach	CRL-7565		NRAS NRAS	p.G12V	C.35G>1	21896	G = 38.0, T = 61.8 $\Delta = 53.9, G = 45.9$	SKIII Myeloma
HTB-103™	KATO III	FGFR2	-	-	Amplific	ation 13	38.62	Stomach	TIB-202™	THP-1	NRAS	p.G12D	c.35G>A	60288	A = 70.1. G = 29.9	Leukemia
									CRL-2547™	Panc 10.05	KRAS	p.G12D	c.35G>A	42708	G = 52.7, A = 47.3	Pancreas
ATCC <sup>®</sup> No.	Cell line	Gene	MYC cop	y number	Measur	ed CNV of	Tum	or source	CRL-2549™	Panc 03.27	KRAS	p.G12V	c.35G>T	58913	G = 47.0, T = 52.9	Pancreas
	name		Varia	ation					HTB-174™	NCI-H441	KRAS	p.G12V	c.35G>T	87521	G = 52.8, T = 47.1	Lung
CRL-5974™	SNU-16	MYC	Amplif	ication	5	0.48	S	tomach	CL-187™	LS 180	KRAS	p.G12D	c.35G>A	91234	G = 51.3, A = 48.6	Colon
	MSTO-211H	MYC	Amplif	ication	38	8.92	Mes	othelioma	CCL-225™	HCT-15	KRAS	p.G13D	c.38G>A	49764	G = 52.1, A = 47.8	Colon
			Amplif		3	0.03 0.06		Lung		Coll line		Amino ooid		NCS		Tumor
CCL-240™	HI -60	MYC	Slight am	nlification	C	9.00	le	eukemia	ATCC <sup>®</sup> No.	name	Gene	Change	DNA Change	Coverage	% Zygosity	source
		in to		pinioation	Ū		L		HTB-19™	BT-20	PIK3CA	p H1047R	c 3140A>G	7062	A = 64 3 G = 35 6	Breast
	Cell line	-	MET co	nv number	Measur	ed CNV of			HTB-131™	MDA-MB-453	PIK3CA	p.H1047R	c.3140A>G	10415	A = 35.6, G = 64.2	Breast
ATCC <sup>®</sup> No.	name	Gen	e var	iation	Noucui	NET	Tum	or source	HTB-112™	HEC-1-A	PIK3CA	p.G1049R	c.3145G>C	6981	G = 38.8, C = 61.0	Endometriu
CRI -5973™	SNU-5	MET	- Amol	ification	7	1 88	S	tomach	HTB-178™	NCI-H596	PIK3CA	p.E545K	c.1633G>A	2669	G = 68.5, A = 31.4	Lung
HTB-135™	Hs 746T	MET	- Ampl	lification	2	3.96	S	tomach	CRL-1739™	AGS	PIK3CA	p.E545A	c.1634A>C	9377	A = 23.6, C = 76.3	Stomach
CRI -2351™	AU565	MET	- Slight ar	molification	1	99		Breast	CCL-237™	SW948	PIK3CA	p.E542K	c.1624G>A	13713	G = 52.7, A = 47.2	Colon
	10000		onginta	npinioadion				Diodot	HTB-121™	BT-483	PIK3CA	p.E542K	c.1634A>C	11779	A = 49.8, C = 50.0	Breast
	Cell line		mino acid		NGS			Tumor	HTB-27™	MDA-MB-361	PIK3CA	p.E545K	c.1633G>A	4681	G = 79.7, A = 20.1	Breast
ATCC <sup>®</sup> No.	name	Gene	Change DN	A Change	Coverage	% Zygc	osity	source				p.Koo/K	C.1700A>G	910	A = 04.2, G = 35.8	
		MAPK3	p.R96R c	.288C>T	3346	C = 36.5, 1	r = 40.5			Cell line	Cono	Amino acid		NGS		Tumor
CRL-2577™	RKO F	PIK3CA	p.H1047R c.3	3140A>G	1359	A = 45.5, C	6 = 54.4	Colon	AICC <sup>®</sup> NO.	name	Gene	Change		Coverage		source
	5007	BRAF	p.V600E c.	1799T>A	257	T = 29.6, A	A = 69.6		HTB-66™	RPMI-7951	BRAF	p.V600E	c.1799T>A	1599	T = 62.5, A = 37.1	Skin
HIB-9 <sup>™</sup>	5637	MAPK1	р.к/9к с	.236G>A	6////	G = 56.1, F	4 = 43.8	Bladder	CCL-238™	SW1417	BRAF	p.V600E	c.1799T>A	3697	T = 58.6, A = 41.2	Colon
HTB-65™	MeWo	MAPK3	p.P246S c	.736C>T	9476	C = 41.4, 1	58.6	Skin	CRL-7898™	A101D	BRAF	p.V600E	c.1799T>A	5643	T = 43.8, A = 55.8	Skin
CRL-9446™	CHL-1 I	MAPK3	p.I228V c	.682A>G	9124	G = 99	9.8	Skin	CCL-224™	COLO 201	BRAF	p.V600E	c.1799T>A	4122	T = 22.0, A = 77.8	Colon
HTB-2™	RT4 I	MAPK3	p.A109A c	.327G>A	14152	G = 62.6, A	A = 37.2	Bladder	CRL-1676™	WM-266-4	BRAF	p.V600D	c.1799_18001G >AT	6776	G = 37.7, A = 62.1, G = 37,4, T = 62.5	Skin
	Coll lino		mino acid		NGS			Tumor								
ATCC <sup>®</sup> No.	name	Gene	Change DN	A Change	Coverage	% Zygo	sity	source	ATCC <sup>®</sup> No.	Cell line name	Gene	Amino acid Change	DNA Change	NGS Coverage	% Zygosity	Tumor source
HTB-31™	C-33-A	PTEN	p.R233* c	.697C>T	65522	C = 51.9, T	= 48.0	Cervix				p.Y27S	c.80A>C	50463	A = 9.6. C = 89.9	
HTB-111™	AN3 CA	PTEN	p.R130fs c.38	39_389delG	14373	Deletion :	= 99.3	Endometrium	HTB-62™	P3HR-1	MYC	р.Е54D	c.162G>A	66485	G = 10.8, A = 82.6	Burkitt's
CRL-1718™	CCF-	PTEN	p.L112R c	.335T>G	20249	G = 99	9.6	Brain	1110 02		in r c	p.P72S	c.214C>T	68482 68205	C = 17.6, T = 81.2	lymphoma
	SHG1						-					p.V20I	c.58G>A	22792	G = 9.0, C = 89.2 G = 12.1, A = 86.5	
										0.4.40		p.P72S	c.214C>T	30456	C = 13.8, T = 85.3	Burkitt's
Real tin	ne PCR	analy	sis of m	RNA le	vels				CRL-1648™	CA46	MYC	p.P75H	c.224C>A	29467 21112	C = 17.2, A = 80.3 C = 54.9, G = 44.7	lymphoma
		~··· <b>~·</b> )										p.Q321H	c.963G>C	30065	G = 50.1, C = 49.5	
(												p.Q51L	c.152A>T	50033	A = 8.1, T = 87.8	
00	Amp	am	EGFR			WT Ce	ll Lines		CRL-1647™	ST486	MYC	p.P72T	c.214C>A	49383 50765	C = 21.0, A = 77.7 A = 7.2, C = 02.2	Burkitt's
<b>olds)</b>		am			<b>(folds)</b>		WT					p.110P p.A198V	c.593C>T	31630	C = 5.7, T = 93.0	
£ °0																

Human	cancer	Cell I Per va	ines cor riations	itain di	omark	kers – n	nutations	ATCC <sup>®</sup> No.	Cell line name	Gene	Amino acid Change	cDNA Change	NGS Coverage	% Zygosity	Tumor source
	y nank							CCL-231™	SW48	EGFR	p.G719S	c.2155G>A	35993	G = 69.4, A = 30.3	Colon
	Coll line		AKT1 copy	Measured	AKT2 co	opy Measu	red <sub>Tumor</sub>	CRL-5908™	NCI-H1975	EGFR	p.T790M	c.2369C>T	11704	C = 33.0, T = 66.9	Lung
ATCC <sup>®</sup> No.	name	Gene	number	CNV of	numbe	er CNV	of source				p.L858R	c.25/31>G	9441	I = 33.7, G = 66.2	
CRI -2321™	HCC1143	AKT1	Amplification	6 21			Breast				EGFR copy		ERBB	2 copy Measured	<b>-</b>
CRL-1469™	PANC-1	AKT2	-	-	Amplifica	ition 25.46	6 Pancreas	ATCC <sup>®</sup> No.	Cell line name	Gene	number	Measured CNV	of num	ber CNV of	source
CRL-1622™	KLE	AKT2	_	-	Amplifica	ition 12.5	1 Endometrium	 CRI -2868™	HCC827	FGFR	Amplification	63.01	Varia		Lung
HTB-161™	NIH:OVCAR-	3 AKT2	-	-	Amplifica	ition 9.78	Ovary	HTB-132™	MDA-MB-468	EGFR	Amplification	25.02	-		Breast
HTB-183™	NCI-H661	AKT2	_	_	Slight	t 5 56	Lung	HTB-19™	BT-20	EGFR	Amplification	15.73	-		Breast
					amplifica	tion	Lang	HTB-178™	NCI-H596	EGFR	Amplification	0.06	-	- –	Lung
			FGER1 conv	Measured	FGFR2 c	onv Measu	red	HTB-177™	NCI-H460	EGFR	-	-	-		Lung
ATCC <sup>®</sup> No.	Cell line	Gene	number	CNV of	numbe	er CNV (	of Tumor	CRL-5928™	NCI-H2170	ERBB2	-	-	Amplif	ication 128.89	Lung
			variation	FGFR1	variatio	on FGFR		HTB-20™	BT-474	ERBB2	-	-	Amplif	ication 29.7	Breast
HTB-23™	MDA-MB- 134-\/I	FGFR1	Amplification	14.22	-	-	Breast	HTB-27 <sup>™</sup>	MDA-MB-361	ERBB2	-	-	Amplif	ication 16.85	Breast
CRL-2066™	DMS 114	FGFR1	Amplification	7.17	_	_	Luna		Coll ling		Amino acid		NGS		Tumor
	014/027		Slight	2.0			Calar	ATCC <sup>®</sup> No.	name	Gene	Change	DNA Change	Coverage	% Zygosity	source
UUL-235 ""	50037	FGFRI	amplification	3.9	-	-	Colon	CRL-2177™	SW 1271	NRAS	p.Q61R	c.182A>G	26732	G = 99.8%	Lung
CCL-246™	KG-1	FGFR1	Slight	3.87	-	-	Leukemia	CRL-2273™	CHP-212	NRAS	p.Q61K	c.181C>A	49859	C = 50.7, A = 49.1	Brain
CRL-5974™	SNU-16	FGFR2	-	-	Amplifica	ition 451.1	6 Stomach	CRL-7585™	Hs 852.T	NRAS	p.G12V	c.35G>T	66411	G = 38.0, T = 61.8	Skin
HTB-103™	KATO III	FGFR2	_	-	Amplifica	ition 138.6	2 Stomach	CRL-9068™	NCI-H929	NRAS	p.G13D	c.38G>A	21896	A = 53.9, G = 45.9	Myeloma
								TIB-202™	THP-1	NRAS	p.G12D	c.35G>A	60288	A = 70.1, G = 29.9	Leukemia
	Cell line	Cono	MYC cop	y number	Measure	d CNV of		CRL-2547 ™	Panc 10.05	KRAS	p.G12D	c.35G>A	42708	G = 52.7, A = 47.3 G = 47.0 T = 52.9	Pancreas
AICC <sup>°</sup> NO.	name	Gene	vari	ation	M	YC	iumor source	HTB-174 <sup>™</sup>	NCI-H441	KRAS	p.G12V	c.35G>T	87521	G = 52.8. T = 47.1	Lung
CRL-5974™	SNU-16	MYC	Ampli	fication	50	.48	Stomach	CL-187™	LS 180	KRAS	p.G12D	c.35G>A	91234	G = 51.3, A = 48.6	Colon
CRL-2081™	MSTO-211H	MYC	Ampli	fication	38	.92	Mesothelioma	CCL-225™	HCT-15	KRAS	p.G13D	c.38G>A	49764	G = 52.1, A = 47.8	Colon
HTB-175™	NCI-H82	MYC	Ampli	fication	35	.63	Lung								
HTB-171™	NCI-H446	MYC	Ampli	fication	19	.06	Lung	ATCC <sup>®</sup> No.	Cell line	Gene	Amino acid	DNA Change	NGS	% Zygosity	Tumor
CCL-240™	HL-60	MYC	Slight an	plification	9.	43	Leukemia						Topo		Desest
	<b>•</b> • • •							HIB-19™ ⊔TD 131™	BI-20		p.H1047R	c.3140A>G	10415	A = 64.3, G = 35.6	Breast
ATCC <sup>®</sup> No.	name	Gene		py number riation	measure M	ET	Tumor source	HTB-112™	HEC-1-A	PIK3CA	p.G1049R	c.3145G>C	6981	G = 38.8, $C = 61.0$	Endometri
			A man	lification	74	00	Stomach	HTB-178™	NCI-H596	PIK3CA	p.E545K	c.1633G>A	2669	G = 68.5, A = 31.4	Lung
			Атр	lification	11	.00	Stomach	CRL-1739™	AGS	PIK3CA	p.E545A	c.1634A>C	9377	A = 23.6, C = 76.3	Stomach
			Slight a	molification	23	00	Breast	CCL-237™	SW948	PIK3CA	p.E542K	c.1624G>A	13713	G = 52.7, A = 47.2	Colon
GIL-2001	A0000		Signa	mpinication	1.	33	Diedol	HTB-121™	BT-483	PIK3CA	p.E542K	c.1634A>C	11779	A = 49.8, C = 50.0	Breast
	Cell line	Δ	mino acid		NGS		Tumor	HTB-27™	MDA-MB-361	PIK3CA	p.E545K	c.1633G>A	4681	G = 79.7, A = 20.1	Breast
ATCC <sup>®</sup> No.	name	Gene	Change DN	IA Change	Coverage	% Zygosity	source				p.K567R	c.1/00A>G	916	A = 64.2, G = 35.8	
		MAPK3	p.R96R c	:.288C>T	3346 0	C = 36.5, T = 4	10.5		Cell line		Amino acid		NGS		Tumor
CRL-2577™	RKO F	PIK3CA p	.H1047R c.	3140A>G	1359 A	A = 45.5, G = 8	54.4 Colon	ATCC <sup>∞</sup> No.	name	Gene	Change	DNA Change	Coverage	% Zygosity	source
		BRAF	p.V600E c	.1799T>A	257	Γ = 29.6, Α = 6	9.6	HTB-66™	RPMI-7951	BRAF	p.V600E	c.1799T>A	1599	T = 62.5, A = 37.1	Skin
HTB-9™	5637 I	MAPK1	p.R79K c	.236G>A	67777 C	G = 56.1, A = 4	13.8 Bladder	CCL-238™	SW1417	BRAF	p.V600E	c.1799T>A	3697	T = 58.6, A = 41.2	Colon
HTB-65™	MeWo I	MAPK3	p.P246S c	:.736C>T	9476 0	C = 41.4, T = 5	58.6 Skin	CRL-7898™	A101D	BRAF	p.V600E	c.1799T>A	5643	T = 43.8, A = 55.8	Skin
CRL-9446™	CHL-1 I	MAPK3	p.I228V c	.682A>G	9124	G = 99.8	Skin	CCL-224™	COLO 201	BRAF	p.V600E	c.1799T>A	4122	T = 22.0, A = 77.8	Colon
HTB-2™	RT4 I	MAPK3	p.A109A c	.327G>A	14152 (	G = 62.6, A = 3	Biadder	CRL-1676™	WM-266-4	BRAF	p.V600D	c.1799_18001G >AT	6776	f = 37.7, A = 62.1, G = 37,4, T = 62.5	Skin
	Cell line	Cono A	mino acid		NGS		Tumor		Cell line		Amino acid		NGS		Tumor
AICC' NO.	name	Gene	Change Dr		Coverage		source	ATCC <sup>®</sup> No.	name	Gene	Change	DNA Change	Coverage	% Zygosity	source
HTB-31™	C-33-A	PTEN	p.R233* c	c.697C>T	65522 (	C = 51.9, T = 4	8.0 Cervix				p.Y27S	c.80A>C	50463	A = 9.6, C = 89.9	
HTB-111™	AN3 CA	PTEN	p.R130fs c.3	39_389delG	14373	Deletion = 99	.3 Endometrium	HTB-62™	P3HR-1	MYC	p.E54D	c.162G>A	66485	G = 10.8, A = 82.6	Burkitt's
CRL-1718™	CCF- STTG1	PTEN	p.L112R c	:.335T>G	20249	G = 99.6	Brain				p.Q113H	c.339G>C	68395	G = 9.6, C = 89.2	lymphom
	01101										p.V20I	c.58G>A	22792	G = 12.1, A = 86.5	
								CRI -1648™	CA46	MYC	p.P72S p P75H	c.214C>T c.224C>A	30456 29467	C = 13.8, T = 85.3 C = 17.2 A = 80.3	Burkitt's
Real tin	ne PCR	analy	sis of m	RNA le	vels						p.L193V	c.577C>G	21112	C = 54.9, G = 44.7	lymphom
											p.Q321H	c.963G>C	30065	G = 50.1, C = 49.5	
	SNP +	E	GFR			MIT OF US			ST406		p.Q5TL p.P72T	c.214C>A	49383	C = 21.0, A = 77.7	Burkitt's
<u>ت</u> 90	Amp	amp	lification		्र १९	w i Cell Lines		UKL-1647™	51480	WIYC	p.T110P	c.328A>C	50765	A = 7.2, C = 92.2	lymphoma
0															

Human	cancer	<sup>r</sup> cell   ber va	lines co riations	ntain bi	omar	kers -	– mu	tations	ATCC <sup>®</sup> No.	Cell line name	Gene	Amino acid Change	cDNA Change	NGS Coverage	Second Strain St	Tumor source
	Sy num			•					CCL-231™	SW48	EGFR	p.G719S	c.2155G>A	35993	G = 69.4, A = 30.3	Colon
	Coll line		AKT1 copy	Measured	AKT2 d	сору М	easured	Tumor	CRL-5908™	NCI-H1975	EGFR	p.T790M	c.2369C>T	11704	C = 33.0, T = 66.9	Lung
ATCC <sup>®</sup> No.	name	Gene	number	CNV of	num	per (	CNV of	source				p.L858R	c.2573T>G	9441	T = 33.7, G = 66.2	C .
			Amplification	AK I 1	variat	ion	AK12	Broast				EGER copy		FRBB	2 copy Measured	
CRL-2321			Amplineation	- 0.21	- Amplific	ation	-	Dieasi	ATCC <sup>®</sup> No.	Cell line	Gene	number	Measured CNV	of num	nber CNV of	Tumor
CRL-1409™	KI F	AKT2	_	_	Amplific		12 51	Endometrium			ECED	variation		varia	ation ERBB2	
HTR-161™		-3 AKT2	_	_	Amplific		9.78	Ovary	CRL-2868 ™		EGFR	Amplification	63.01	-		Lung
					Slig	nt	5.70	e vary	HTB-19™	RT-20	EGFR	Amplification	15 73	-		Breast
HIB-183 <sup>IIII</sup>	NCI-H661	AK12	-	-	amplific	ation	5.50	Lung	HTB-178™	NCI-H596	EGFR	Amplification	0.06	-		Luna
									HTB-177™	NCI-H460	EGFR		-	-		Lung
ATCC <sup>®</sup> No.	Cell line	Gene	FGFR1 cop	y Measured CNV of	FGFR2	copy M per (	easured CNV of	Tumor	CRL-5928™	NCI-H2170	ERBB2	-	-	Amplif	ication 128.89	Lung
	name		variation	FGFR1	variat	ion I	FGFR2	source	HTB-20™	BT-474	ERBB2	-	_	Amplif	ication 29.7	Breast
HTB-23™	MDA-MB-	FGFR1	Amplificatior	า 14.22	_		_	Breast	HTB-27™	MDA-MB-361	ERBB2	-	-	Amplif	ication 16.85	Breast
CRI -2066™	DMS 114	FGER1	Amplification	n 717	_		_	Lung		Coll line		Amino ooid		NCS		Tumor
			Slight					Lung	ATCC <sup>®</sup> No.	name	Gene	Change	DNA Change	NGS Coverage	% Zygosity	source
CCL-235™	SW837	FGFR1	amplification	า <u>3.9</u>	-		-	Colon	CRL-2177™	SW 1271	NRAS	p.Q61R	c.182A>G	26732	G = 99.8%	Lung
CCL-246™	KG-1	FGFR1	Slight	3.87	-		-	Leukemia	CRL-2273™	CHP-212	NRAS	p.Q61K	c.181C>A	49859	C = 50.7, A = 49.1	Brain
CRI -5974™	SNU-16	FGFR2		_	Amplific	ation	451 16	Stomach	CRL-7585™	Hs 852.T	NRAS	p.G12V	c.35G>T	66411	G = 38.0, T = 61.8	Skin
HTB-103™	KATO III	FGFR2	_	_	Amplific	ation	138 62	Stomach	CRL-9068™	NCI-H929	NRAS	p.G13D	c.38G>A	21896	A = 53.9, G = 45.9	Myeloma
					, inpine		100.02	Clonicoli	TIB-202™	THP-1	NRAS	p.G12D	c.35G>A	60288	A = 70.1, G = 29.9	Leukemia
	Cell line		MYC co	pv number	Measur	ed CNV o	of _		CRL-2547™	Panc 10.05	KRAS	p.G12D	c.35G>A	42708	G = 52.7, A = 47.3	Pancreas
ATCC <sup>®</sup> No.	name	Gene	var	iation	N	AYC	Tun	nor source	CRL-2549™		KRAS	p.G12V	c.35G>1	58913 97524	G = 47.0, T = 52.9	Pancreas
CRL-5974™	SNU-16	MYC	Amp	lification	5	0.48	S	Stomach	CI -187™	IS 180	KRAS	p.G12V	c.35G>A	91234	G = 52.0, T = 47.1 G = 51.3, A = 48.6	Colon
CRL-2081™	MSTO-211H	MYC	Ampl	lification	3	8.92	Me	sothelioma	CCL-225™	HCT-15	KRAS	p.G12D	c.38G>A	49764	G = 52.1, A = 47.8	Colon
HTB-175™	NCI-H82	MYC	Ampl	lification	3	5.63		Lung							,	
HTB-171™	NCI-H446	MYC	Ampl	lification	1	9.06		Lung	ATCC <sup>®</sup> No	Cell line	Gene	Amino acid	DNA Change	NGS	% Zvaosity	Tumor
CCL-240™	HL-60	MYC	Slight ar	mplification	ę	9.43	L	eukemia		name		Change	BRAChange	Coverage		source
									HTB-19™	BT-20	PIK3CA	p.H1047R	c.3140A>G	7062	A = 64.3, G = 35.6	Breast
ATCC <sup>®</sup> No.	Cell line	Gene	MET co	opy number	Measur	ed CNV o	of Tun	nor source	HTB-131™	MDA-MB-453	PIK3CA	p.H1047R	c.3140A>G	10415	A = 35.6, G = 64.2	Breast
	name		Va	ariation	<u>Г</u>	NEI			HTB-112™	HEC-1-A	PIK3CA	p.G1049R	c.3145G>C	6981	G = 38.8, C = 61.0	Endometriu
CRL-5973™	SNU-5	MET	Am	plification	7	1.88	S	Stomach		NCI-H596	PIK3CA	p.E545K	C.1633G>A	2009	G = 68.5, A = 31.4	Lung
HTB-135™	Hs 746T	MET	Am	plification	2	3.96	ę	Stomach	CCL-237™	AG3 SW948	PIK3CA	p.E543A	c 1624G>A	13713	A = 23.0, C = 70.3 G = 52.7 A = 47.2	Colon
CRL-2351™	AU565	MET	Slight a	amplification		1.99		Breast	HTB-121™	BT-483	PIK3CA	p.E542K	c.1634A>C	11779	A = 49.8, C = 50.0	Breast
												p.E545K	c.1633G>A	4681	G = 79.7, A = 20.1	Propot
ATCC <sup>®</sup> No.	Cell line	Gene	mino acid	NA Change	NGS	% Zyc	osity	Tumor			FINJUA	p.K567R	c.1700A>G	916	A = 64.2, G = 35.8	DiedSl
	name		Change		Soverage			source								
CRI -2577™	<b>RKO</b>		p.R96R	C.288C>1	3346	C = 36.5, $\Delta = 45.5$	I = 40.5	Colon	ATCC <sup>®</sup> No.	Cell line	Gene	Amino acid	DNA Change	NGS	% Zygosity	Tumor
		BRAF	p.1110471C ( p.V600E (	c.1799T>A	257	T = 29.6.	A = 69.6	COON						Coverage	T 00 5 A 07 4	Source
HTB-9™	5637	MAPK1	, p.R79К	c.236G>A	67777	G = 56.1,	A = 43.8	Bladder		RPMI-7951	BRAF	p.V600E	c.17991>A	1599	I = 62.5, A = 37.1 T = 58.6 A = 41.2	Skin
HTB-65™	MeWo	MAPK3	p.P246S	c.736C>T	9476	C = 41.4.	T = 58.6	Skin	CRI -7898™	A101D	BRAF	p.v600E	c 1799T>A	5643	T = 43.8  A = 55.8	Skin
CRI -9446™	CHI -1	MAPK3	n 1228\/	c 682A>G	9124	G =	99.8	Skin	CCL-224™	COLO 201	BRAF	p.V600E	c.1799T>A	4122	T = 22.0, $A = 77.8$	Colon
			p.1220 V	c 327G>A	1/152	G = 62.6	$\Delta = 37.2$	Bladder	CPI -1676™	WM-266-4	BRAF		c.1799_1800TG	6776	T = 37.7, A = 62.1,	Skin
1110-2	1114		p.A103A	0.0210-A	14152	G = 02.0,	A = 31.2	Diaduei		VVIVI-200- <del>4</del>	DIVAI	p.v000D	>AT	0770	G = 37,4, T = 62.5	OKIII
	Cell line		mino acid		NGS			Tumor		Coll line		Amino acid		NGS		Tumor
ATCC <sup>∞</sup> No.	name	Gene	Change D	NA Change	Coverage	% Zyç	josity	source	ATCC <sup>®</sup> No.	name	Gene	Change	DNA Change	Coverage	% Zygosity	source
HTB-31™	C-33-A	PTEN	p.R233*	c.697C>T	65522	C = 51.9,	T = 48.0	Cervix				p.Y27S	c.80A>C	50463	A = 9.6, C = 89.9	
HTB-111™	AN3 CA	PTEN	p.R130fs c.3	389_389delG	14373	Deletior	n = 99.3	Endometrium	HTB-62™	P3HR-1	MYC	p.E54D	c.162G>A	66485	G = 10.8, A = 82.6	Burkitt's
CRL-1718™	CCF-	PTEN	p.L112R	c.335T>G	20249	G = 9	99.6	Brain				p.P72S	c.214C>T	68482 68395	C = 17.6, T = 81.2 G = 9.6, C = 89.2	lymphom
	51161											p.V20I	c.58G>A	22792	G = 12.1, A = 86.5	
										CA 40		p.P72S	c.214C>T	30456	C = 13.8, T = 85.3	Burkitt's
<b>Real tin</b>	ne PCR	analv	sis of m	<b>RNA</b> le	vels				UKL-1648™	UH40	WIYC	р.Р75Н p.L193V	c.224U>A c.577C>G	29467 21112	C = 17.2, A = 80.3 C = 54.9, G = 44.7	lymphom
• • • •	1	<b>J</b>										p.Q321H	c.963G>C	30065	G = 50.1, C = 49.5	
	SND +		EGEP									p.Q51L	c.152A>T	50033	A = 8.1, T = 87.8	Devel 344
<b>—</b> 90	Amp	amr	Dification		90 -	WT	Cell Lines		CRL-1647™	ST486	MYC	p.P721 p.T110P	C.214C>A C.328A>C	49383 50765	C = 21.0, A = 77.7 A = 7.2, C = 92.2	Burkitt's
80 80					80 - 80 -		WT					p.A198V	c.593C>T	31630	C = 5.7, T = 93.0	, p
70			_		<b>66</b>											

																source
									CCL-231™	SW48	EGFR	p.G719S	c.2155G>A	35993	G = 69.4, A = 30.3	Colon
	Coll line		AKT1 copy	Measured	AKT2 c	opy Meas	ured	Tumor	CRL-5908™	NCI-H1975	EGFR	p.T790M	c.2369C>T	11704	C = 33.0, T = 66.9	Lung
ATCC <sup>®</sup> No.	name	Gene	number	CNV of	numb	er CN	/ of	source				p.L858R	c.2573T>G	9441	T = 33.7, G = 66.2	
CRL-2321™	HCC1143	ΔΚΤ1	Amplification	AKT1 6.21	variati	on An	-	Breast				EGFR copy		, ERBB	2 copy Measured	
CRI -1469™	PANC-1	AKT2	-	-	Amplifica	ation 25	46	Pancreas	ATCC <sup>®</sup> No.	Cell line name	Gene	number	Measured CNV	of nun	nber CNV of	Tumor source
CRI -1622™	KIE	AKT2	_	_	Amplifica	ation $12$	51	Endometrium			ECER		63.01	varia	ation ERBB2	Lung
HTB-161™	NIH:OVCAR-	-3 AKT2	_	_	Amplifica	ation 9.7	78	Ovarv	URL-2000 ····· HTB-132™		EGFR		25.02	-		Breast
					Sligh	t EV	EC	Lung	HTB-19™	BT-20	EGFR	Amplification	15.73	-		Breast
ПIВ-103''''		ANIZ	_	-	amplifica	ation 5.0	00	Lung	HTB-178™	NCI-H596	EGFR	Amplification	0.06	-		Lung
									HTB-177™	NCI-H460	EGFR	-	-			Lung
ATCC <sup>®</sup> No.	Cell line	Gene	number	CNV of		copy meas er CN\	vrea v of	Tumor	CRL-5928™	NCI-H2170	ERBB2	-	-	Amplif	fication 128.89	Lung
	name		variation	FGFR1	variati	on FGF	-R2	source	HTB-20™	BT-474	ERBB2	-	-	Amplif	fication 29.7	Breast
HTB-23™	MDA-MB- 134-VI	FGFR1	Amplification	14.22	-	-	-	Breast	HTB-27™	MDA-MB-361	ERBB2	-	-	Amplif	fication 16.85	Breast
CRL-2066™	DMS 114	FGFR1	Amplification	7.17	-	-	-	Lung		Cell line	0.000	Amino acid		NGS		Tumor
CCI -235™	SW837	FGFR1	Slight	39	_	_	_	Colon	AICC <sup>°</sup> NO.	name	Gene	Change		Coverage	% Zygosity	source
002 200			amplification	0.0				Colori	CRL-2177™	SW 1271	NRAS	p.Q61R	c.182A>G	26732	G = 99.8%	Lung
CCL-246™	KG-1	FGFR1	amplification	3.87	-	-	-	Leukemia	CRL-2273™	CHP-212	NRAS	p.Q61K	c.181C>A	49859	C = 50.7, A = 49.1	Brain
CRL-5974™	SNU-16	FGFR2	_	-	Amplifica	ation 451	.16	Stomach	CRL-7585™	Hs 852.T	NRAS	p.G12V	c.35G>T	66411	G = 38.0, T = 61.8	Skin
HTB-103™	KATO III	FGFR2	-	-	Amplifica	ation 138	6.62	Stomach	CRL-9068 ™	NCI-H929	NRAS	p.G13D	c.38G>A	21896	A = 53.9, G = 45.9	Myeloma
									TIB-202 <sup>™</sup>	Panc 10.05	KRAS	p.G12D	C.35G>A	42708	A = 70.1, G = 29.9 G = 52.7 A = 47.3	Pancreas
ATCC <sup>®</sup> No	Cell line	Gene	МҮС сору	number	Measure	d CNV of	Tum	or source	CRL-2549™	Panc 03.27	KRAS	p.G12D	c.35G>T	58913	G = 47.0. T = 52.9	Pancreas
	name		varia	tion	M	YC	Turr		HTB-174™	NCI-H441	KRAS	p.G12V	c.35G>T	87521	G = 52.8, T = 47.1	Lung
CRL-5974™	SNU-16	MYC	Amplifi	cation	50	.48	S	Stomach	CL-187™	LS 180	KRAS	p.G12D	c.35G>A	91234	G = 51.3, A = 48.6	Colon
CRL-2081™	MSTO-211H	MYC	Amplifi	cation	38	8.92	Mes	sothelioma	CCL-225™	HCT-15	KRAS	p.G13D	c.38G>A	49764	G = 52.1, A = 47.8	Colon
HTB-175™	NCI-H82	MYC	Amplifi	cation	35	5.63		Lung								
HTB-171™	NCI-H446	MYC	Amplifi		19	0.06		Lung	ATCC <sup>®</sup> No.	Cell line	Gene	Amino acid	DNA Change	NGS	% Zygosity	Tumor
CCL-240™	HL-60	MYC	Slight amp	olification	9	.43	L	eukemia						coverage		Source
				_					HIB-19 <sup>™</sup>		PIK3CA	p.H1047R	c.3140A>G	7062	A = 64.3, G = 35.6	Breast
ATCC <sup>®</sup> No.	Cell line	Gene	MET cop vari	y number ation	Measure M	ed CNV of	Tum	nor source				p.m1047R	c 3145G>C	6081	A = 35.0, G = 64.2	Endometri
			Vari						HTB-178™	NCI-H596	PIK3CA	p.G1049K	c 1633G>A	2669	G = 68.5 $A = 31.4$	
CRL-5973™	SNU-5	MET	Ampli	fication	71	.88	S	Stomach	CRL-1739™	AGS	PIK3CA	p.E545A	c.1634A>C	9377	A = 23.6, C = 76.3	Stomach
HIB-135™	Hs 7461	MEI	Ampli	fication	23	3.96	S	Stomach	CCL-237™	SW948	PIK3CA	р.Е542К	c.1624G>A	13713	G = 52.7, A = 47.2	Colon
CRL-2351™	AU565	MEI	Slight an	plification	1	.99		Breast	HTB-121™	BT-483	PIK3CA	p.E542K	c.1634A>C	11779	A = 49.8, C = 50.0	Breast
									HTB-27™	MDA-MB-361	PIK3CA	p.E545K	c.1633G>A	4681	G = 79.7, A = 20.1	Breast
ATCC <sup>®</sup> No.	Cell line name	Gene	mino acid Change DNA	A Change	NGS Soverage	% Zygos	ity	Tumor source				p.K567R	c.1700A>G	916	A = 64.2, G = 35.8	
		MAPK3	p.R96R c.2	288C>T	3346	C = 36.5, T =	= 40.5			Cell line	0	Amino acid		NGS		Tumor
CRL-2577™	RKO	PIK3CA	p.H1047R c.3	140A>G	1359	A = 45.5, G =	= 54.4	Colon	AICC <sup>°</sup> NO.	name	Gene	Change		Coverage	% Zygosity	source
		BRAF	p.V600E c.1	799T>A	257	T = 29.6, A =	= 69.6		HTB-66™	RPMI-7951	BRAF	p.V600E	c.1799T>A	1599	T = 62.5, A = 37.1	Skin
HIB-9™	5637	MAPK1	p.R79K c.2	236G>A	67777 (	G = 56.1, A =	= 43.8	Bladder	CCL-238™	SW1417	BRAF	p.V600E	c.1799T>A	3697	T = 58.6, A = 41.2	Colon
HTB-65™	MeWo	MAPK3	p.P246S c.	736C>T	9476	C = 41.4, T =	= 58.6	Skin	CRL-7898™	A101D	BRAF	p.V600E	c.1799T>A	5643	T = 43.8, A = 55.8	Skin
CRL-9446™	CHL-1	MAPK3	p.I228V c.6	682A>G	9124	G = 99.8	8	Skin	CCL-224™	COLO 201	BRAF	p.V600E	c.1799T>A	4122	T = 22.0, A = 77.8	Colon
HTB-2™	RT4	MAPK3	p.A109A c.3	327G>A	14152 (	G = 62.6, A =	= 37.2	Bladder	CRL-1676™	WM-266-4	BRAF	p.V600D	c.1799_18001G >AT	6776	I = 37.7, A = 62.1, G = 37,4, T = 62.5	Skin
ATCC <sup>®</sup> No	Cell line	Gene	mino acid	Change	NGS	% 7//005	itv	Tumor		Cell line		Amino acid		NGS		Tumor
	name	Cene	Change Change		Coverage	/0 <b>Zyg</b> 03	l y	source	AICC <sup>°</sup> NO.	name	Gene	Change	DNA Change	Coverage	% Zygosity	source
HTB-31™	C-33-A	PTEN	p.R233* c.	697C>T	65522 (	C = 51.9, T =	= 48.0	Cervix				p.Y27S	c.80A>C	50463	A = 9.6, C = 89.9	
HTB-111™	AN3 CA	PTEN	p.R130fs c.38	9_389delG	14373	Deletion = 9	99.3	Endometrium	HTB-62™	P3HR-1	MYC	p.E54D	c.162G>A	66485 68482	G = 10.8, A = 82.6	Burkitt's
CRL-1718™	CCF- STTG1	PTEN	p.L112R c.3	335T>G	20249	G = 99.6	6	Brain				p.P723	c.339G>C	68395	G = 9.6, C = 89.2	Tymphom
	01101											p.V20I	c.58G>A	22792	G = 12.1, A = 86.5	
									C.RI _16//Ջ™	CA46	MYC	p.P72S n P754	c.214C>T	30456 20467	C = 13.8, T = 85.3 C = 17.2 = 0.2	Burkitt's
<b>Real tin</b>	ne PCR	analy	sis of mF	RNA lev	vels				UINE-1040***			p.r.75n p.L193V	c.577C>G	23407	C = 17.2, R = 60.3 C = 54.9, G = 44.7	lymphom
												p.Q321H	c.963G>C	30065	G = 50.1, C = 49.5	
	SNP +		GFR									p.Q51L	c.152A>T	50033 40383	A = 8.1, T = 87.8 C = 21.0 A = 77.7	Rurkitt's
L. L										07400		$p = 1 \ge 1$	0.21407A	49000	O = 21.0. A = 11.1	DUIKIUS
90 a	Amp	amp	lification		<del>•</del> <sup>90</sup>	WT Cell Li	nes		CRL-1647™	51486	MYC	p.T110P	c.328A>C	50765	A = 7.2, C = 92.2	lymphom



Summary

Over 70 genomic DNAs isolated from authenticated human cancer lines contain the desired biomarkers for oncological analysis and assay development, which are useful tools in the nucleic acid-based detection for cancer.

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