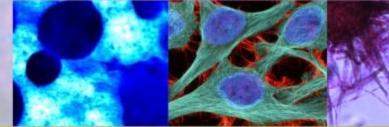
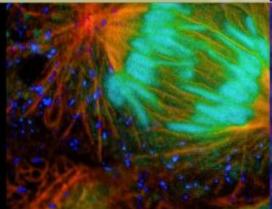
THE IMPORTANCE OF STANDARDS IN MOLECULAR-BASED ASSAYS

Liz Kerrigan Director, Standards May 8, 2014







THE ESSENTIALS OF LIFE SCIENCE RESEARCH GLOBALLY DELIVERED "

ATCC

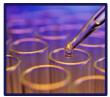
- Founded in 1925, ATCC is a non-profit organization with headquarters in Manassas, VA
- ATCC serves and supports the scientific community with industry-standard products and innovative solutions
- World's leading biological resource center and provider of biological standards
- Broad range of biological materials
 - Cell lines
 - Microorganisms
 - Native & synthetic nucleic acids
 - Reagents







Overview



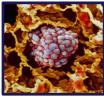
Principles of assay development



- Assay design
- Assay sensitivity
- Analytical specificity & microbial interference
- · Controls for nucleic acid based assays



Microbial standards & tools for assay development



Challenging assay design with cancer cell lines & nucleic acids



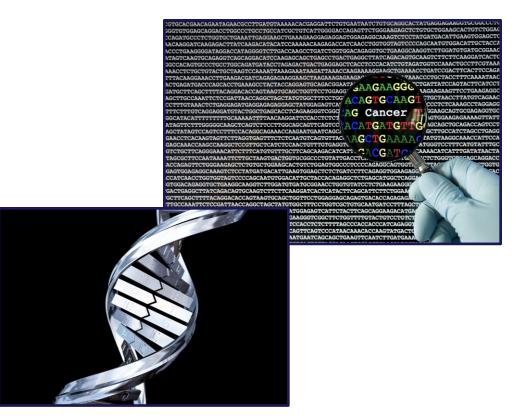
ATCC

Using Biological Standards in Proficiency Testing programs

Standards for Next-Gen sequencing

Utility for molecular testing

- Improved sensitivity
- Improved specificity
- Time to results
- Ability to multiplex





Assay development

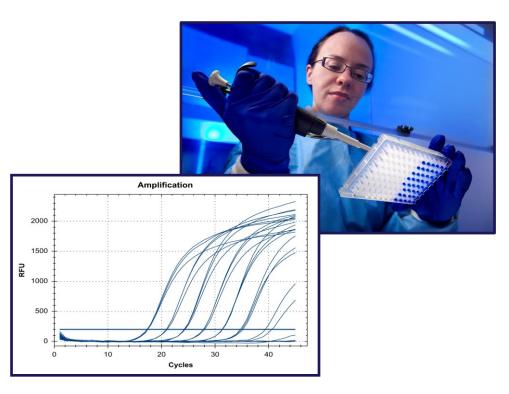
- Assay design
 - Design goals
 - Qualitative or quantitative assay
 - Target genes
 - Relevant strains and variants
 - Updates

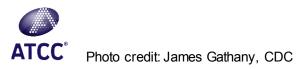




Analytical sensitivity, specificity & interference

- Analytical sensitivity
 - Limit of Detection (LoD)
 - Reactivity
- Analytical specificity
 - Cross reactivity
- Interference
 - Clinical specimens





Controls for nucleic acid based assays

- Used for verification of assay performance in your analytical and clinical studies:
 - **Negative Control:** to rule out contamination
 - Positive Control: to verify PCR reagents & instrument are running properly
 - Internal Control: to verify that a sample result is not caused by PCR inhibitors
 - External Control: to verify that lysis & extraction processes are functioning properly



The changing landscape of microbial genomics

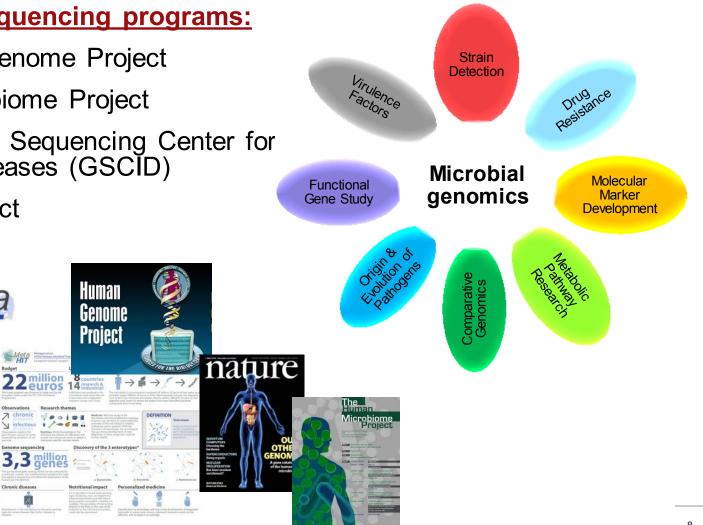
Large scale sequencing programs:

- The Human Genome Project
- Human Microbiome Project

Meta

- JCVI Genomic Sequencing Center for Infectious Diseases (GSCID)
- MetaHIT Project

ATCC



Highly characterized microbial strains for assay development

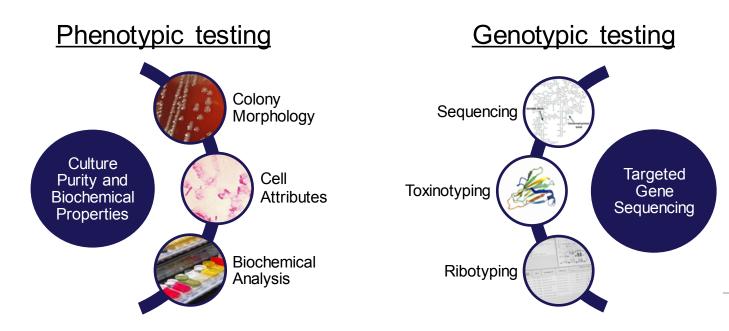


ATCC

ATCC utilizes both classical and modern techniques

- Phenotypic analysis
- Genotypic analysis
- Functional analysis

No single method of identification is sufficient



40 Clostridium difficile strains

ATCC [®] No.	Strain	Toxinotype	Binary Toxin	EIA*	Ribotype	Isolation Source
BAA-1804™		0	ND	+	053	Clinical isolate, USA
BAA-1870™	4118	IIIb	Y	+	027	Clinical isolate, USA ME
BAA-1803™		IIIc	Y	+	027	Clinical isolate, USA
BAA-1801™	3232	tcdA-, tcdB-	ND	-	010	Human feces, Belgium
BAA-1875™	5325	V	Y	+	078	Clinical isolate, USA GA
43598™	1470	VIII	ND	+	017	Human feces, Belgium
BAA-1812™		XII	ND	+	024	Clinical isolate, USA
BAA-1814™		XXII	Y	+	251	Clinical isolate, USA

*Enzyme Immuno Assay (EIA) performed with the Wampole™ C. DIFF QUIK CHEK COMPLETE® kit or the equivalent ND= Not Detected

Native DNA is available from six different strains

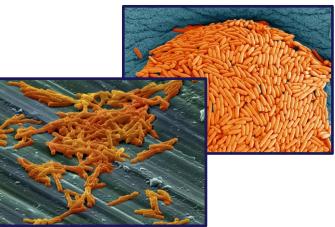




Photo credit: Annie Cavanagh, David Goulding, Wellcome Trust Sanger Institute

Quantitated, frozen, Clostridium difficile strains

Tools for Assay Development

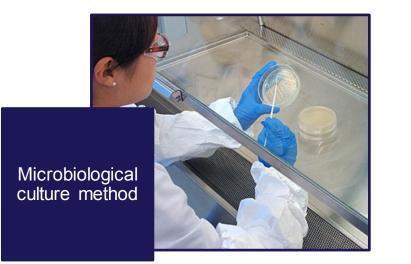
ATCC [®] No.	Strain	Toxinotype	Ribotype	Titer (CFU/vial)	ddPCR™ (Bacteria/vial)	Isolation source
BAA-1382- FZ™	630	0	012	4.9 x 10 ⁶	9.6 x 10 ⁸	Genome sequenced, clinical isolate, Switzerland
17858-FZ™	1253	0	054	1.0 x 10 ⁸	5.9 x 10 ⁸	Unknown
9689-FZ™	90556-M6S	0	001	2.2 x 10 ⁷	3.97 x 10 ⁸	Type strain
43255-FZ™	VPI 10463	0	087	1.2 x 10 ⁸	9.2 x 10 ⁸	Abdominal wound
43593-FZ™	1351	tcdA-, tcdB-	060	1.5 x 10 ⁸	5.4 x 10 ⁸	Human feces, Belgium
43596-FZ™	545	0	012	1.1 x 10 ⁸	2.62 x 10 ⁸	Human feces, Belgium
43599-FZ™	2022	0	001	4.5 x 10⁵	7.38 x 10 ⁸	Human feces, Belgium
43601-FZ™	7322	tcdA-, tcdB-	031	4.0 x 10 ⁷	3.86 x 10 ⁸	Human feces, Belgium
51695-FZ™	BDMS 18 AN	0	001	3.3 x 10 ⁶	3.98 x 10 ⁸	
700792- FZ™	14797-2	0	005	4.6 x 10 ⁷	1.5 x 10 ⁹	Human feces, Michigan, 1977

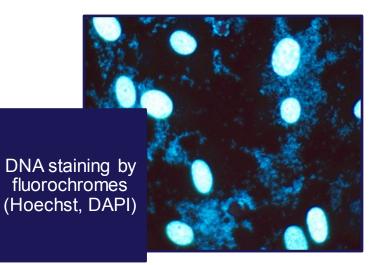
*Post preservation material is checked for total bacterial cell count (per vial) using ddPCR™



Bio-Rad[®], CFX96[™], Droplet Digital[™] PCR, Real-Time PCR Detection System, and CFX Manager[™] 3.0 Software are registered trademarks or trademarks of Bio-Rad Laboratories, Inc.

Detecting mycoplasma







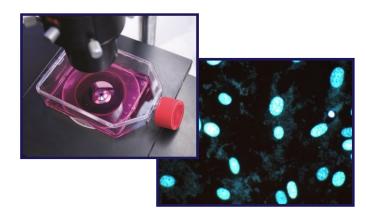


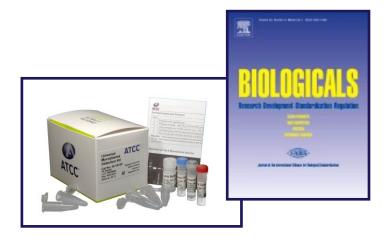


Tools for mycoplasma assay development

<u>Titered Mycoplasma Reference Strains Panel (ATCC[®] MP-7[™]):</u>

- A panel of 10 titered mycoplasma reference strains with calculated genome copy numbers
- Highly viable and dispersed
- Useful for assay development
- Useful for comparing culture- and molecular-based detection assays*







*Dabrazhynetskaya A, et al. *Biologicals* 41(6): 377-383, 2013. PubMed: 23910092

Titered Mycoplasma Reference Strains Panel (ATCC[®] MP-7[™])

ATCC [®] No.	Species	Post Preservation Titer	GenBank (Strain Specific)
15531-TTR [™]	Mycoplasma pneumoniae	1.0 x 10 ⁸ cfu/mL	CP002077.1
17981-TTR [™]	Mycoplasma hyorhinis	6.6 x 10 ⁷ cfu/mL	AF258792.1
19610-TTR [™]	Mycoplasma gallisepticum	2.17 x 10 ⁸ cfu/mL	JN935873.1
19989-TTR [™]	Mycoplasma fermentans	1.0 x 10 ⁹ cfu/mL	AP009608.1
23064-TTR [™]	Mycoplasma salivarium	1.67 x 10 ⁹ cfu/mL	AB680625.1
23206-TTR [™]	Acholeplasma laidlawii	7.10 x 10 ⁸ cfu/mL	CP000896.1
23714-TTR [™]	Mycoplasma orale	3.08 x 10 ⁸ cfu/mL	NR_043199.1
23838-TTR [™]	Mycoplasma arginini	3.7 x 10 ⁹ cfu/mL	NR_041743.1
25204-TTR [™]	Mycoplasma synoviae	1.0 x 10 ⁹ cfu/mL	NR_044811.1
27545-TTR [™]	Mycoplasma hominis	1.3 x 10 ⁸ cfu/mL	JN935871.1

Each strain is prepared with a low genome copy (GC) to colony forming unit (CFU) ratio, which is ideal for use in the development and validation of PCR-based methods of detection.



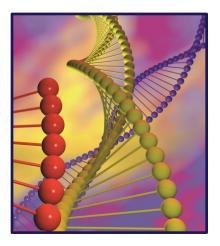
CRM quantitated mycoplasma genomic DNA

Key Features:

- Certified Reference Material
- Quantitated Genome copy number is based on the quantification of the 16S rRNA gene from nine averaged samples using <u>ddPCR</u>[™]. (1.0x10⁶-1.0x10⁷ genome copies/µL)
- Extracted from the titered mycoplasma reference strains (MP-7[™])

Use as a quantitative external control for:

- Inclusivity/exclusivity testing
- Establishing limits of detection (LoD)
- Verification or comparison of test methods
- Other molecular applications



CRM quantitated mycoplasma genomic DNA

Certified Reference Materials

- Produced under an ISO Guide 34 accredited process
- Established chain of custody

Extracted from ATCC Genuine Cultures®

- Agarose gel electrophoresis to ensure integrity
- Spectrophotometry to evaluate purity
- QX100 Droplet Digital[™] PCR to calculate quantity
- PCR to confirm functional activity
- Sequence analysis of 16S rRNA to confirm species identity







CRM quantitated mycoplasma genomic DNA

ATCC [®] No.	Species	Genome Size (bp)	16S RNA Copy Number	GenBank
qCRM-15531D	Mycoplasma pneumoniae	811088	1	CP002077.1
qCRM-17981D	Mycoplasma hyorhinis	806507	1	GCA_000383515.1
qCRM-19610D	Mycoplasma gallisepticum	920684	1	GCA_000428645.1
qCRM-19989D	Mycoplasma fermentans	1004014	2	AP009608
qCRM-23064D	Mycoplasma salivarium	твр	1	GCA_000485555.1
qCRM-23206D	Acholeplasma laidlawii	1496992	2	CP000896.1
qCRM-23714D	Mycoplasma orale	710549	1	GCA_000420105.1
qCRM-23838D	Mycoplasma arginini	758854	2	GCA_000428625.1
qCRM-25204D	Mycoplasma synoviae	736709	2	GCA_000385095.1
qCRM-27545D	Mycoplasma hominis	684158	2	GCA_000385075.1



ATCC[®] Genuine Nucleics



PicoGreen® and RiboGreen® are registered trademarks of Molecular Probes, Inc.

ATCC[®]

ATCC native nucleic acids

Whole genome preparations extracted from ATCC Genuine Cultures®

- More than 750 catalog items
- Agarose gel electrophoresis to ensure integrity
- Spectrophotometry to evaluate purity
- PicoGreen[®] or RiboGreen[®] to calculate concentration
- PCR to confirm functional activity
- Sequence analysis of conserved genomic regions to confirm species identity
- Custom preparations available
- DNA from bacteria, fungi, protists, and viral strains
- RNA from viral strains

PicoGreen® and RiboGreen® are registered trademarks of Molecular Probes, Inc.

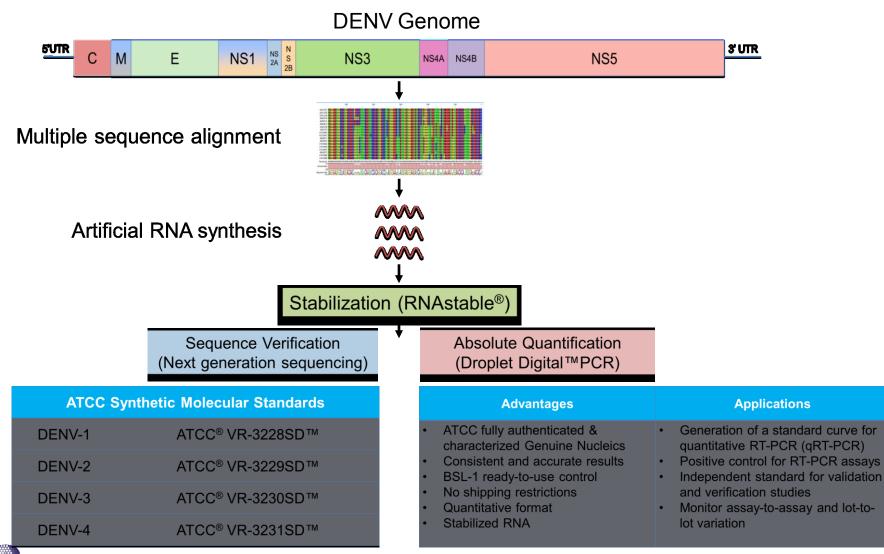
ATCC synthetic nucleic acids

- Synthetically created nucleic acids to serve as a genetic surrogate for microorganisms that are:
 - Difficult to culture
 - Can not be cultured in vitro
 - Select agents and/or BSL 3.





Synthetic molecular standards for Dengue virus





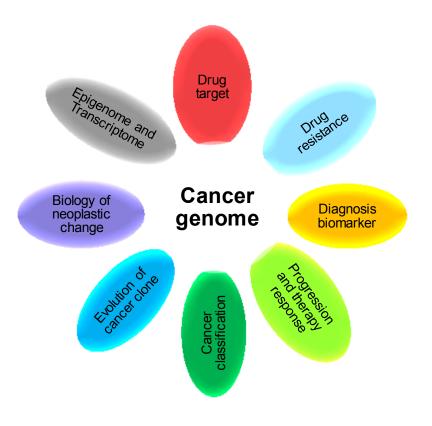
Bio-Rad[®], CFX96[™], Droplet Digital[™] PCR, Real-Time PCR Detection System, and CFX Manager[™] 3.0 Software are registered trademarks or trademarks of Bio-Rad Laboratories, Inc. RNAstable[®] is registered trademark of Biomātrica, Inc.

The changing landscape of the cancer genome

Large scale sequencing programs:

- The Cancer Genome Atlas (TCGA)
- International Cancer Genome Consortium (ICGC)
- Catalogue of Somatic Mutations in Cancer (COSMIC)

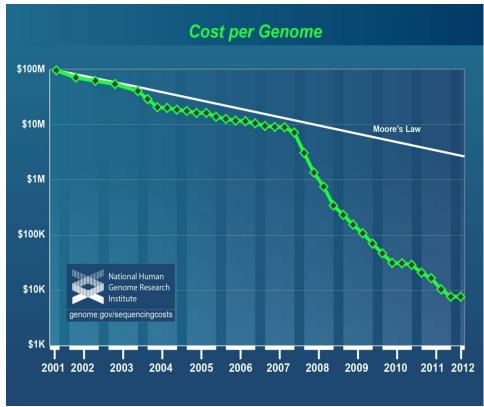


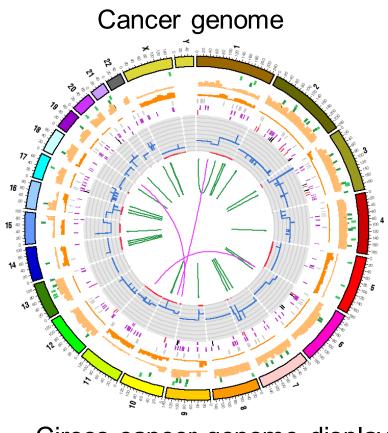




NGS leads to genomic age

Next generation sequencing





Circos cancer genome display



Challenges in molecular testing

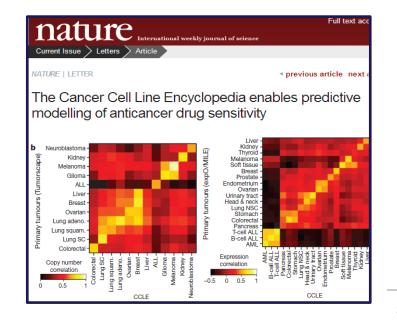
- Omics data storage
- Data analysis
- Quality standards for each step from sample to answer
- Appropriate and reliable controls

Although over 1900 genetic tests are available, the majority of tests still need characterized references or QC materials



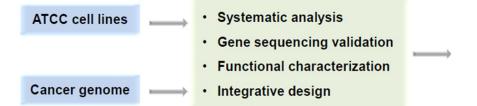
Using authenticated cell lines as controls

- Fully authenticated
- COI and STR testing to avoid inter-species and intra-species contamination or misidentification
- Characterized tumor genetic alterations
- Stable molecular profiles
- Control FFPE process
- Control IF or IHC staining process





ATCC Molecular Signature Cell Panels



Molecular Signature Cell Panels

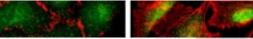
- Driver gene focused
- Signaling pathway focused
- Integrative design

PANELS BY MOLECULAR SIGNATURE

Each panel in the molecular signature collection is composed of cell lines that have been sequenced and validated for mutations in specific genes, such as p53. These panels harness the combined forces of genomic data and highly reliable, authenticated ATCC tumor cell lines to provide solid experimental platforms for cancer research and drug discovery.

p53 hotspot mutation panels

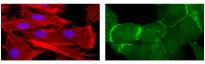
THE ESSENTIALS OF

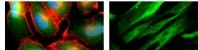


NON-SMALL CELL LUNG CANCER P53 HOTSPOT MUTATION CELL PANEL

Genetic Alteration Cell Panels

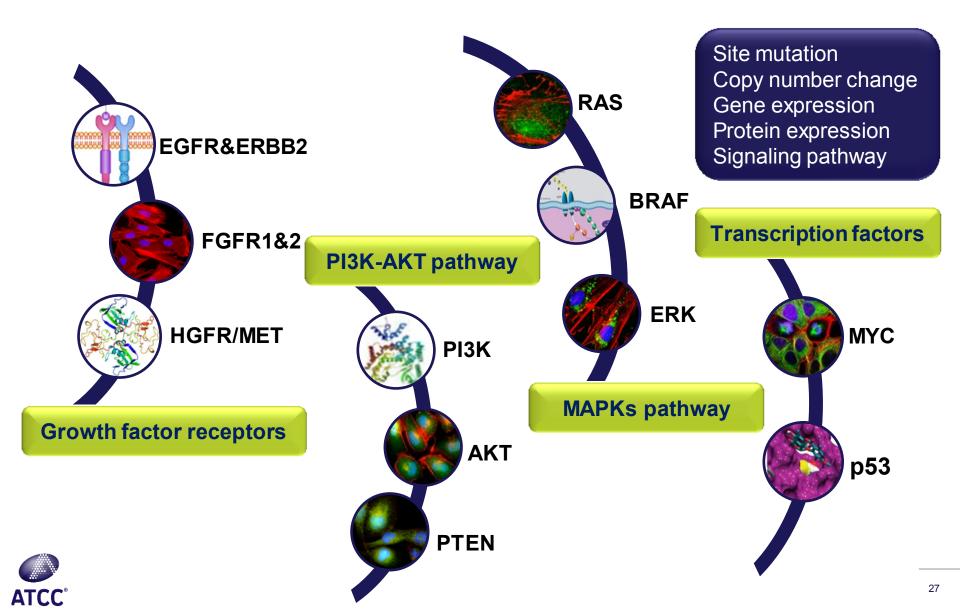
Genetic Alteration Panels







Molecular Signature Cell Panels



EGFR cell panel characteristics

EGFR Genetic Alteration Cell Panel (ATCC[®] TCP-1027[™])

ATCC [®] number	Cell line name	Gene	cDNA Change	Zygosity	Amino acid Change	EGFR copy number variation	ERBB2 copy number variation	Tumor source
CRL-2868™	HCC827	EGFR	c.2236_2250delGAA TTAAGAGAAGCA	Heterozygous	p.ELREA746del	amplification	-	lung
CRL-2871™	HCC4006	EGFR	c.2236_2244delGAA TTAAGA	Heterozygous	p.ELR746del	-	-	lung
CCL-231™	SW48	EGFR	c.2155G>A	Heterozygous	p.G719S	-	-	colon
	NCI-H1975	EGFR	c.2369C>T	Heterozygous	p.T790M	-	-	lung
CRL-5908™	NOI-111970		c.2573T>G	Heterozygous	p.L858R		-	
HTB-132™	MDA-MB-468	EGFR	-	-	-	amplification	-	breast
HTB-19™	BT-20	EGFR	-	-	-	amplification	-	breast
HTB-178™	NCI-H596	EGFR	-	-	-	amplification	-	lung
HTB-177™	NCI-H460	EGFR	-	-	-	-	-	lung
CRL-5928™	NCI-H2170	ERBB2	-	-	-	-	amplification	lung
HTB-20™	BT-474	ERBB2	-	-	-	-	amplification	breast
HTB-27™	MDA-MB-361	ERBB2	-	-	-	-	amplification	breast



ATCC Certified Reference Material (CRM)

Reference materials are:

- Stable with respect to one or more specified property.
- Possess a stated level of confidence for Traceability and Values of Uncertainty, where applicable.

The intended uses of ATCC Certified Reference Materials are:

- To challenge assay performance.
- Validate or compare test methods.
- Establish sensitivity, linearity, and specificity during assay validation or implementation.
- To benchmark critical assay performance during development/validation for regulatory submissions and production lot release.
- For use in testing and calibration in ISO 17025 accredited laboratories.





Certified Reference Materials from ATCC are accompanied by a Certificate of Analysis.

KRAS mutation **CRM** cell lines and **DNAs**

KRAS mutation analysis is currently used as a predictive marker of therapeutic response

ATCC [®] No.	Cell line name	AA change	DNA change
CRM-TIB-161™	HuT 78	WT	WT
CRM-CCL-119™	CCRF-CEM	p.G12D	c.35G>A
CRM-CCL-185™	A549	p.G12S	c.34G>A
CRM-CRL-1420 ™	MIA PaCa-2	p.G12C	c.34G>T
CRM-HTB-174™	NCI-H441	p.G12V	c.35G>A
CRM-CRL-3211™	PSN1	p.G12R	c.34G>C
CRM-CCL-155™	RPMI 8226	p.G12A	c.35G>C
CRM-HTB-26™	MDA-MB-231	p.G13D	c.38G>A

CRM DNAs are now available



Need for Biological Standards in Proficiency Testing

Key issues in Molecular testing

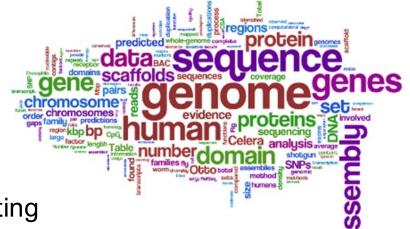
Rapidly moving field

- Test relevant, actionable targets
 - Need high quality, challenging, well characterized PT materials
 - Consistent, traceable
 - Representatives of contemporary strains
 - Genetic variations/mutations
 - New emerging strain variants
- New Technology Developments
 - -NGS
 - Maldi-Tof
 - Multiplex assays

Reference material for Next-Gen Sequencing

Characterize platforms & methods:

- DNA sequencing
- NGS technologies and platforms
- Research applications
- Clinical diagnostic applications
 - Assay validation
- Facilitate tool development for evaluating performance
 - Somatic calls for:
 - Single nucleotide variants (SNVs)
 - Indels
 - Structural variants
 - Copy number variation
 - RNA fusion detection

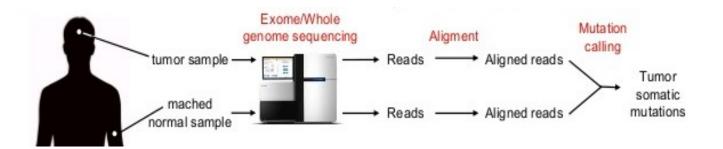




Advantages of tumor/normal pairs

ATCC [®] No.	Name	Cancer Type	Tissue Source	ATCC [®] No.	Name	Tissue Source
CRL-1974™	COLO 829	Melanoma, malignant	Skin	CRL-1980™	COLO 829BL	B lymphoblast

- First comprehensive catalog of somatic mutations from an individual cancer
- Both cell lines sequenced in 2009
- Somatic calls published in 2010*





Tumor/normal cell line and DNA pair

COLO 829 / COLO 829BL

- Whole genome sequencing of COLO 829 and COLO 829BL at a depth of 90x is being generated by Illumina and TGen to build a set of consensus calls
- HiSeq 90x WGS at Illumina & TGen
- SNVs, Indels, Copy NVs, SVs
 - Confirmed by PCR & sequencing
- Complete genomic WGS
- Multiple dilution series analyzed

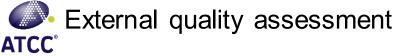




Conclusions

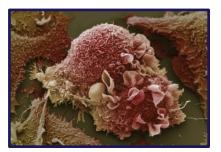
Why are Standards needed?

- To establish sensitivity, linearity, and specificity during assay validation or implementation
- To benchmark critical assay performance during development/ validation for regulatory submissions and production lot release
- Move from growth based methods to molecular methods, establish method equivalence
- Evaluation of assay variability & assay comparison
- Validate or compare test methods
- For use in inter-laboratory studies and comparisons
- For use in testing and calibration in ISO 17025 accredited laboratories
- Production of laboratory reference materials
- Development of standard protocols
- Method maintenance



Thank you!

Register for more webinars in the ATCC "*Excellence in Research*" webinar series at <u>www.atcc.org/webinars</u>.



June 5, 2014 10:00 am or 3:00 pm (ET)

Dr. Doug Storts and Dr. Yvonne Reid will discuss the recent advances in STR profiling technologies and how the Standard STR protocol is transforming scientific practices.

Thank you for joining today! Please send additional questions to <u>tech@atcc.org</u>

