

PURIFIED AND QUANTITATIVE GENOMIC CELL LINE DNA

Precision approaches to disease diagnostics and treatment as well as innovations in nucleic acid quantitation have enabled the creation of better tools for assay development. Accordingly, ATCC has developed purified and quantitative cell line genomic DNA (qDNA) with known mutation allelic frequency and gene copy number, which can provide a reliable and more sustainable alternative to patient tissue-derived controls for oncology molecular diagnostic assays. These whole genome preparations save you the time and cost associated with culturing the cells as well as extracting and quantitating the nucleic acids yourself.

ATCC qDNA are extracted from patient samples or cell lines that contain biomarkers that have been quantified by validated methods for each product lot. Because qDNA are fully quantified by NGS and droplet digital PCR (ddPCR™; BioRad), they are compatible with several lab-developed and commercially available assays as BSL-1, ready-to-use controls for your assays. They can be used for the generation of a standard curve, as positive controls for molecular-based assay development, as independent standards for validation and verification, and for monitoring assay-to-assay and lot-to-lot variation.

Specification and characteristics for each lot of gDNA includes:

- ddPCR™ quantitated for high-precision analysis
- Next-generation sequenced
- Well-characterized genetic alterations
- Absolute mutation/amplification copy number

- Agarose gel electrophoresis to ensure integrity
- Spectrophotometry to evaluate purity
- PCR to confirm functional activity
- STR profiling to ensure identity

Further, each of our products is manufactured under ISO 9001 certified and ISO/IEC 17025 accredited processes, so you can trust your results and reproduce your data – every time.

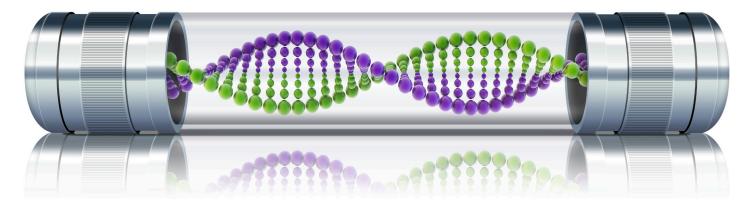


Table 1: Purified and quantified genomic DNA

CRL-1648DQ™CA46Burkitt's lymphomaTP53 R248Q $\sqrt{}$ $\sqrt{}$ $\sqrt{}$ HTB-30DQ™SK-BR-3Breast adenocarcinomaTP53 p.R175H $\sqrt{}$ $\sqrt{}$ HTB-122DQ™BT-549Breast ductal carcinomaTP53 p.R249S $\sqrt{}$ $\sqrt{}$ HTB-131DQ™MDA-MB-453Breast carcinomaPIK3CA p.H1047R $\sqrt{}$ $\sqrt{}$ CCL-225DQ™HCT-15Colon adenocarcinomaKRAS p.G13D $\sqrt{}$ $\sqrt{}$ CCL-227DQ™SW620Colon adenocarcinomaKRAS p.G12V $\sqrt{}$ $\sqrt{}$ TP53 p.R273H $\sqrt{}$ $\sqrt{}$ $\sqrt{}$	
HTB-122DQ™ BT-549 Breast ductal carcinoma HTB-131DQ™ MDA-MB-453 Breast carcinoma PIK3CA p.H1047R √ √ √ CCL-225DQ™ HCT-15 Colon adenocarcinoma KRAS p.G13D √ √ √ CCL-227DO™ SW620 Colon adenocarcinoma	
Carcinoma HTB-131DQ™ MDA-MB-453 Breast carcinoma PIK3CA p.H1047R √ √ √ CCL-225DQ™ HCT-15 Colon adenocarcinoma KRAS p.G13D √ √ √ CCL-227DO™ SW620 Colon adenocarcinoma KRAS p.G12V √ √	
CCL-225DQ™ HCT-15 Colon adenocarcinoma KRAS p.G13D √ √ √ √ CCL-227DQ™ SW620 Colon adenocarcinoma KRAS p.G12V √ √ √	
CCL-227DO™ SW620 Colon adenocarcinoma KRAS p.G12V √ √ √	
CCL-227DO™ SW620 Colon adenocarcinoma	
TP53 p.R273H $\sqrt{}$	
v v	
<u>CCL-231DQ</u> [™] SW48 Colon adenocarcinoma EGFR p.G719S $$	
<u>CL-187DQ</u> [™] LS180 Colon adenocarcinoma KRAS p.G12D $$	
<u>CRL-2158DQ</u> [™] LS1034 Colon carcinoma TP53 p.G245S $$	
$\frac{\text{CRL-5974DQ}^{\text{\tiny{TM}}}}{\text{SNU-16}}$ Stomach undifferenti- MYC amplification − $$ $$ ated adenocarcinoma	
HTB-111DQ [™] AN3 CA Endometrium PTEN p.R130fs $$ $$ $$ adenocarcinoma	
EGFR pELREA746del √ √	$\sqrt{}$
CRL-2868DQ™ HCC827 Lung adenocarcinoma EGFR amplification –	
<u>CRL-5908DQ</u> [™] NCI-H1975 Lung non-small cell EGFR p.T790M; $$ $$ $$ $$ carcinoma EGFR p.L858R	
$\frac{\text{CRL-2177DQ}^{\text{\tiny{TM}}}}{\text{SW 1271}}$ SW 1271 Lung small cell NRAS p.Q61R $$ $$ $$ carcinoma	
$\frac{\text{CRL-5928DQ}^{\text{TM}}}{\text{NCI-H2170}}$ NCI-H2170 Lung squamous cell HER 2 amplification − $$ $$ carcinoma	
CRL-7898DQ [™] A101D Skin malignant BRAF p.V600E $$ $$ $$ melanoma	

^{*}CoA report mutation allelic frequency result – NGS (Coverage > 10,000X)

Table 2: Tumor and normal reference cell line genomic DNA for detecting somatic mutations

Cancer type	Tissue source	Name	ATCC® No.	Tissue source	Name	ATCC® No.
Primary site of dis	sease		Normal pairing			
Primary Ductal Carcinoma	Mammary gland; breast	HCC1395	SC-CRL-2324_D™	Peripheral Blood	HCC1395 BL	SC-CRL-2325_D™











QGDN-032022-v07

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NGS result uncertainty is equal or smaller than $\pm 5\%$. The reported uncertainty represents uncertainty expressed at approximately the 99% confidence level using a coverage factor of k=3.

^{**}CoA report gene copy number result – ddPCR™ (Average of nine data points)
ddPCR™ uncertainty is equal or smaller than ± 30%. The reported uncertainty represents uncertainty expressed at approximately the 99% confidence level using a coverage factor of k=3.