

AmplideX[®]

mPCR *FMR1* Kit



A streamlined PCR approach for the detection and quantification of methylation status in the *FMR1* gene

Sensitive, allele-specific methylation quantification is rapidly delivered in this easy-to-use assay. The innovative design improves turnaround time by fivefold compared to Southern blot (<8 hours vs. 1 week). This assay was designed to complement the AmplideX PCR/CE *FMR1* Reagents*.

REDUCED COMPLEXITY

- Eliminates the need for Southern blot
- Easily quantify allele-specific methylation with digestion, PCR, and CE
- Includes spike-in digestion and amplification controls to ensure high performance with every sample

OPTIMIZED WORKFLOW

- PCR and CE design empowers simple implementation
- Results in under a day
- Flexible use on widely installed CE equipment

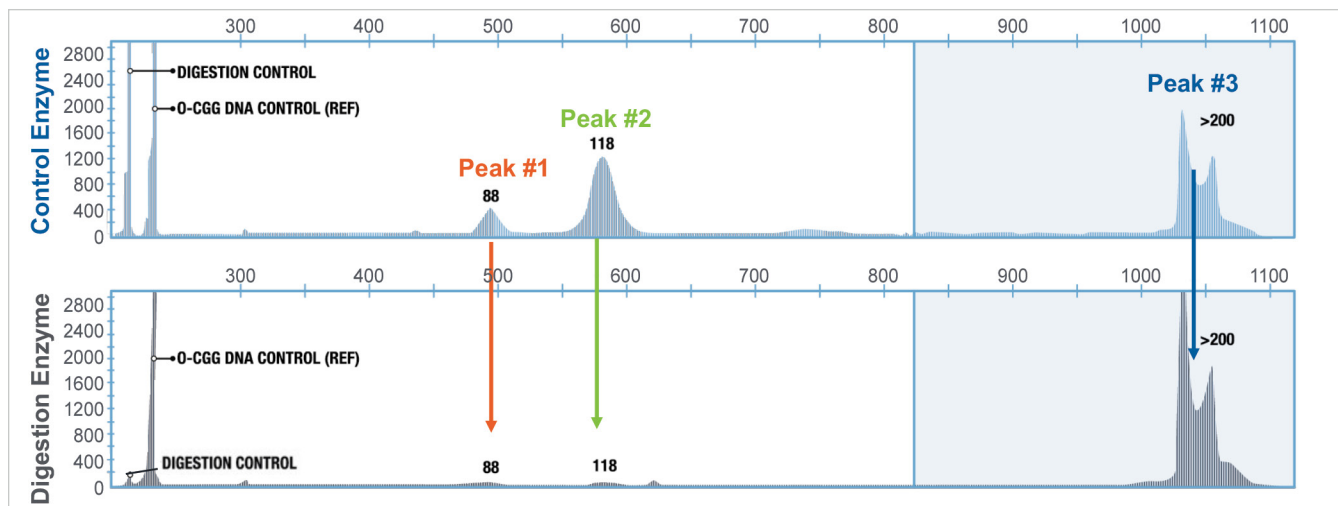
QUALITY RESULTS

- Provides allele-specific methylation quantification consistent with Southern blot analysis
- Detects lower abundance methylation and size mosaics
- High quality controls available from a single vendor ensure sensitive, reliable testing

AmplideX mPCR *FMR1* * Workflow – <1 day from DNA to data



SIMPLER ALLELE-SPECIFIC METHYLATION QUANTIFICATION



Digestion control confirms complete digestion of unmethylated alleles

| | Calculated Methylation | | |
|--------------|------------------------|---------|------------|
| | Peak #1 | Peak #2 | Peak #3 |
| CGG repeats | 88 | 118 | >200, >200 |
| % Methylated | 1% | 0% | 100%, 100% |

- Control and methylation-sensitive digestions allow comparison of peak heights to determine percent methylation
- Methylation protects from digestion, ensuring simple detection of unmethylated peaks

KIT RESULTS CORRELATE WELL WITH OBSERVED PHENOTYPE

Phenotype[†]

- Male in his 50s with normal cognitive function and severe anxiety. Self-referred because brother and sister have FXS. Daughter has a premutation.

Outcomes: Methylation mosaicism

- Lack of severe intellectual disability (here, normal intelligence) was consistent with methylation mosaicism, which included an unmethylated full mutation as the primary allele.

| | Methylation Results | | |
|--------------|---------------------|---------|---------|
| | Peak #1 | Peak #2 | Peak #3 |
| CGG repeats | 53 | 153 | >200 |
| % Methylated | 3% | 96% | 4% |

ORDERING INFORMATION

| Part Number | Product Description | Number of Reactions |
|-------------|--------------------------------------|---------------------|
| 49442 | AmplideX mPCR <i>FMR1</i> Kit* | 24 reactions |
| 49513 | AmplideX PCR/CE <i>FMR1</i> Control* | 24 ul |
| 49514 | AmplideX mPCR <i>FMR1</i> Control* | 24 ul |

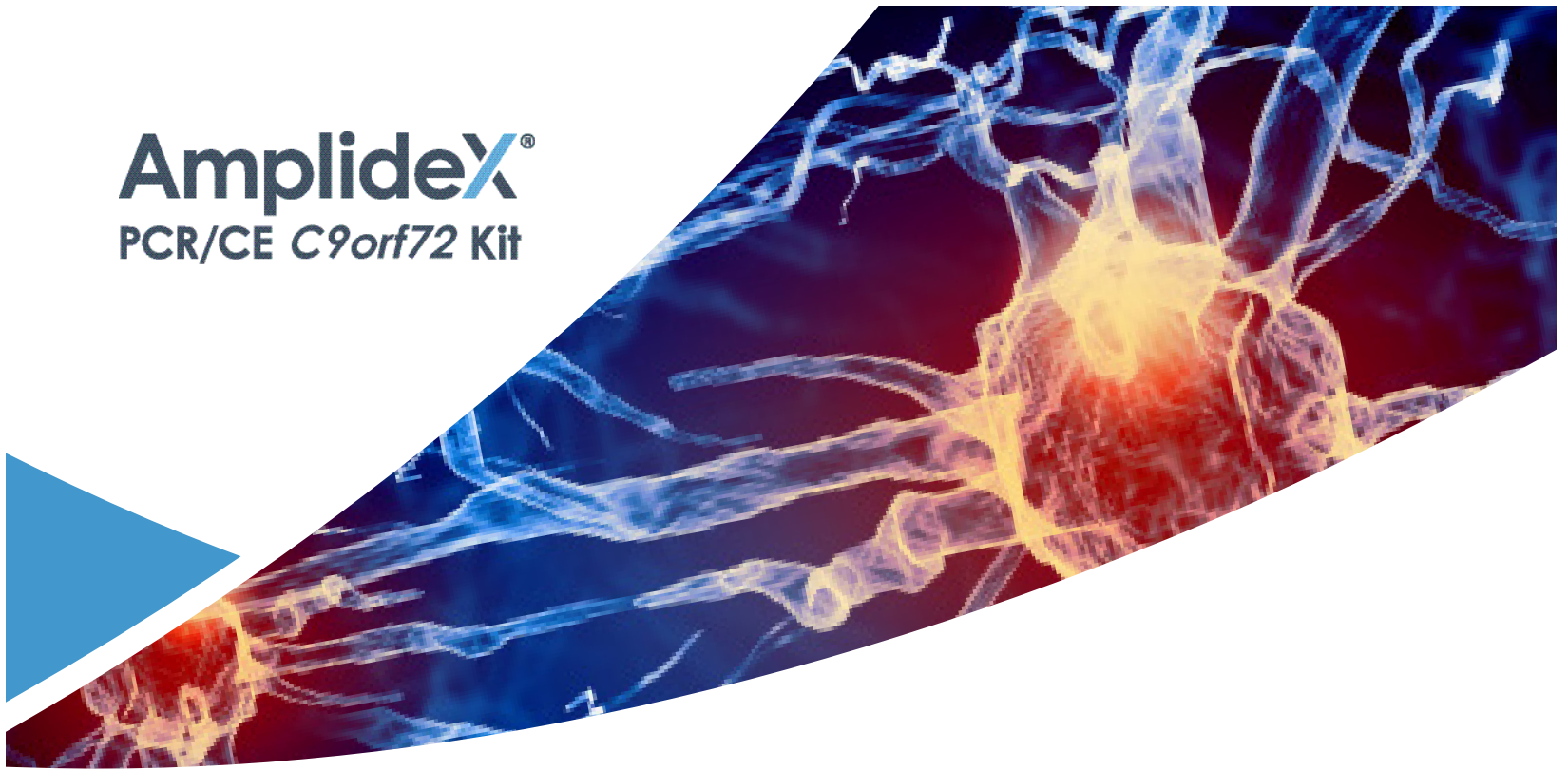
For more information, please contact asuragen.com

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[†]Case courtesy of Rush University Medical Center

AmplideX[®]

PCR/CE *C9orf72* Kit



A better understanding of hexanucleotide repeat expansions in the *C9orf72* gene requires a robust PCR amplification assay. The AmplideX[®] PCR/CE *C9orf72* Kit is a research tool for the reliable amplification of pathogenic hexanucleotide repeats (GGGGCC) in the *C9orf72* gene that are associated with amyotrophic lateral sclerosis (ALS) and frontotemporal dementia (FTD). Using our proprietary GC-rich PCR chemistry and building on the success of our AmplideX *FMR1* product, this kit provides a simple, single-tube PCR workflow to profile *C9orf72* repeat sequences.



Figure 1: AmplideX PCR/CE *C9orf72* Kit components

SIMPLE WORKFLOW

- Single PCR reaction for both sizing and screening
- A single sourced kit consisting of all PCR reagents needed for *C9orf72* repeat amplification
- Streamlined workflow with minimal hands-on time
- Decreased need for Southern blot analysis

IMPROVED PERFORMANCE

- Five-fold improvement in length of alleles sized: accurate sizing up to 145 repeats
- Detection of alleles greater than 145 repeats
- Reveal low-level mosaicism and minor alleles
- Identifies sequence variability near the repeat region

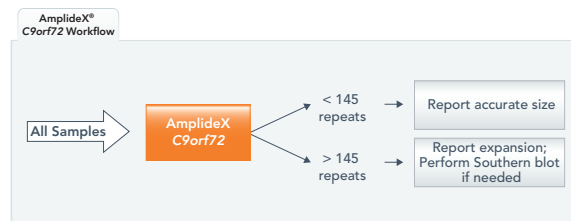


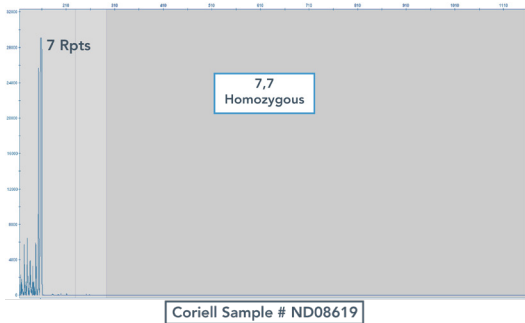
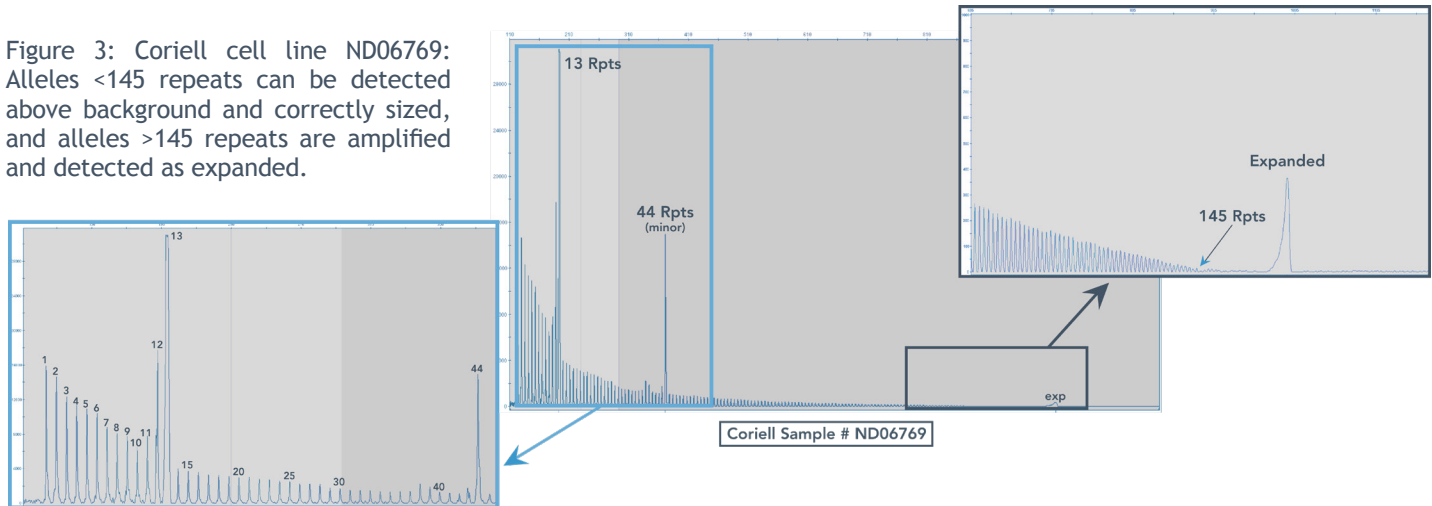
Figure 2: AmplideX PCR/CE *C9orf72* Kit workflow

AmplideX[®]

PCR/CE *C9orf72* Kit

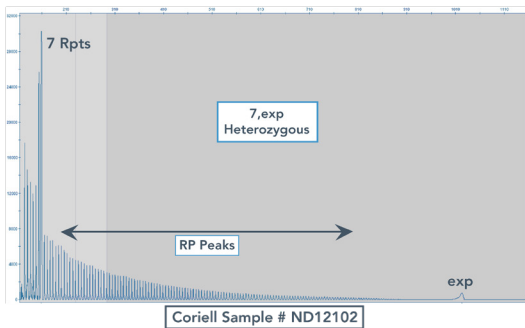
ACCURATELY SIZE UP TO 145 REPEATS AND DETECT ALLELES GREATER THAN 145 REPEATS

Figure 3: Coriell cell line ND06769: Alleles <145 repeats can be detected above background and correctly sized, and alleles >145 repeats are amplified and detected as expanded.



CLEAR ZYGOSITY RESOLUTION THROUGH DISTINCT REPEAT-PRIMED PATTERN

Figure 4: Side by side comparison of 2 Coriell cell lines: ND08619 (7,7 homozygous) and ND12102 (7,expanded heterozygous): Extension of the repeat-primed peak pattern beyond the shorter allele clearly differentiates the heterozygous sample from homozygous sample.



KIT ORDERING INFORMATION

AmplideX PCR/CE *C9orf72* Kit*

[P/N 49581] 50 REACTIONS

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Asuragen, Inc.
2150 Woodward Street, Suite 100
Austin TX 78744
asuragen.com
2500-624 Rev A 2017



AmplideX[®]

PCR/CE *CFTR* Kit*



Providing the broadest coverage of the U.S. population[†] of any commercially available, targeted *CFTR* testing kit

The AmplideX[®] PCR/CE *CFTR* Kit* brings the simplicity and scalability of AmplideX technology to *CFTR* variant detection. Offering the streamlined detection of 67 pathogenic variants, and covering approximately 93%[†] of the U.S. population, the assay provides the broadest coverage of any commercially available, targeted testing kit. The assay is optimized for use on widely established laboratory equipment and delivers genotype results from DNA in under five hours.

REDUCED COMPLEXITY

- Broad coverage[†] provided using only PCR/CE workflow
- Similar testing process to AmplideX PCR/CE *FMR1** and *SMN1/2 Plus** kits eases implementation
- Streamlined data analysis via AmplideX Reporter software

OPTIMIZED WORKFLOW

- Easy-to-use workflow with fewer hands on steps than most competitor assays
- Flexible use on widely installed CE equipment
- <5 hrs from DNA to data

QUALITY RESULTS

- Built on the latest prevalence data to provide the best coverage[†] for all U.S. ethnicities
- Detects complex yet key *CFTR* mutations (CNVs, STRs, SNPs, INDELs) and resolves zygosity
- Excellent concordance with other methods



Figure 1. AmplideX PCR/CE *CFTR* Kit* workflow.

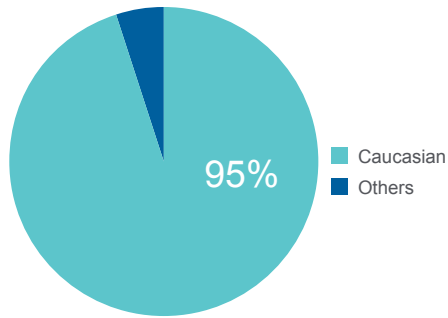


Figure 2A. Ethnic diversity of 89K patients in CFTR2 database.

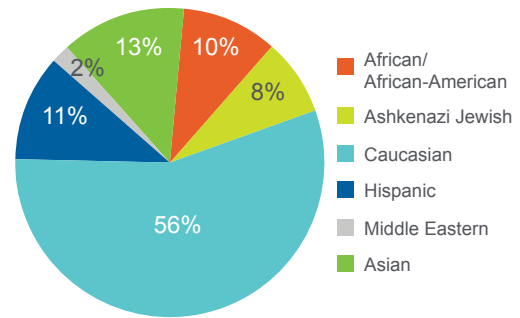


Figure 2B. Ethnic diversity of 115K subjects in U.S. study.[†]

| Commercial Kit Manufacturer/Panel | Full Product Name | # of Variants Detected | % Coverage, CFTR2 | % Coverage, U.S. | % Coverage Difference, U.S. |
|-----------------------------------|---|------------------------|-------------------|------------------|-----------------------------|
| Asuragen | AmplideX PCR/CE CFTR Kit | 67 | 92.1% | 93.0% | - |
| Luminex 97 | xTAG Cystic Fibrosis (CFTR) 97 kit (Custom) | 97 | 92.2% | 88.2% | 4.8% |
| Illumina | MiSeqDx Cystic Fibrosis 139 Variant Assay | 139 | 94.3% | 87.7% | 5.3% |
| Agena | iPLEXPro CFTR Panel | 74 | 91.5% | 86.9% | 6.1% |
| Elucigene | CF-EU2v1 | 50 | 90.5% | 86.2% | 6.8% |
| Luminex 60 | xTAG Cystic Fibrosis (CFTR) 60 kit v2 | 60 | 91.2% | 86.1% | 6.9% |
| Luminex 39 | xTAG Cystic Fibrosis (CFTR) 39 kit v2 | 39 | 89.1% | 80.7% | 12.3% |

Table 1. Percent coverage of variants detected by commercially available kits based on frequencies observed in the CFTR2 database** and the U.S. population.

| 76 Cell Lines from Coriell Repository | | | | | |
|---------------------------------------|---------|-------------------|---------|--------|--------------------------|
| Sample Agreement with Reference Assay | | Sanger Sequencing | | | Overall Sample Agreement |
| | | WT/WT | MUT/MUT | MUT/WT | |
| CFTR PCR/CE Assay | WT/WT | 22 | 0 | 0 | 22/22 (100%) |
| | MUT/MUT | 0 | 24 | 0 | 24/24 (100%) |
| | MUT/WT | 0 | 0 | 27 | 27/27 (100%) |

Table 2A. Mutations in Cell Lines Detected by Prototype PCR/CE CFTR Kit and Sanger Sequencing.

| 102 Clinical Samples Across 3 Sites | | | | | |
|---------------------------------------|---------|---|---------|--------|--------------------------|
| Sample Agreement with Reference Assay | | xTAG® Cystic Fibrosis (CFTR) 60 kit v2 or Sanger Sequencing | | | Overall Sample Agreement |
| | | WT/WT | MUT/MUT | MUT/WT | |
| CFTR PCR/CE Assay | WT/WT | 34 | 0 | 0 | 34/34 (100%) |
| | MUT/MUT | 0 | 19 | 0 | 19/19 (100%) |
| | MUT/WT | 0 | 0 | 49 | 49/49 (100%) |

Table 2B. Mutations in Clinical Samples Detected by Prototype PCR/CE CFTR Kit and Either xTAG® Cystic Fibrosis (CFTR) 60 Kit v2 or Sanger Sequencing.

ORDERING INFORMATION

| Part Number | Product Description | Number of Reactions |
|-------------|--------------------------|---------------------|
| A00076 | AmplideX PCR/CE CFTR Kit | 50 |
| A00077 | AmplideX PCR/CE CFTR Kit | 100 |

For more information please contact asuragen.com

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**The Clinical and Functional Translation of CFTR (CFTR2); available at <http://cftr2.org>

[†]Beauchamp, et al. Genet Med. 2019 Nov;21(11):2569-2576.

AmplideX[®]

PCR/CE *DMPK* Kit*

Simply and Reliably Size *DMPK* Repeat Expansions within a Single Day

The AmplideX[®] PCR/CE *DMPK* Kit* introduces a groundbreaking alternative for the detection and sizing of CTG repeats within the *DMPK* gene. Challenged by very large trinucleotide expansions, *DMPK* analysis has required the use of Southern blot technology, thereby limiting many laboratories' ability to resolve these repeat sequences. By introducing a simple, streamlined, PCR-only workflow, the AmplideX PCR/CE *DMPK* Kit* can replace Southern blot and put *DMPK* analysis within the reach of laboratories everywhere.

REDUCED COMPLEXITY

- Proprietary PCR solutions for GC-rich amplification and detection
- May eliminate need for Southern blot
- Resolves zygosity and detects mosaicism

OPTIMIZED WORKFLOW

- Direct injection of PCR products into CE instruments
- Fully kitted, end-to-end solutions that significantly reduce hands-on-time
- Sample-to-result possible within a single shift

QUALITY PERFORMANCE

- Accurate sizing of alleles ≤ 200 CTG repeats and detection of all alleles > 200 repeats using CE
- Optional AGE protocol allows sizing of alleles up to 1000 repeats
- Analysis tool converts raw base pair data into repeat number



Figure 1. AmplideX PCR/CE *DMPK* Workflow, including optional AGE workflow for larger expansions.

AmplideX[®]

PCR/CE *DMPK* Kit*

| Sample Name | External Lab <i>PCR + Southern</i> | Asuragen <i>PCR/CE</i> | Asuragen <i>PCR/AGE (allele 2)</i> |
|-------------|---------------------------------------|---------------------------|---------------------------------------|
| S1 | 10, 300-500 | 11, >200 | Smear, High Mosaic 300-500 |
| S2 | 4, 1200-1350 | 5, >200 | ~1100 |
| S3 | 4, 1100-1500 | 5, >200 | Smear, High Mosaic >500 |
| S4 | 11, 200-300 | 12, >200 | ~260-350 |
| S5 | 4, 800-900 | 5, >200 | ~650-700 |
| S6 | 25, 1050 | 26, >200 | ~1000 |
| S7 | 12, 100-150 | 13, 71, 129 | 70, 130 |
| S8 | 11, 1900-2220 | 12, >200 | 700, 1900 |
| S9 | 21, 300 | 22, >200 | Mosaic, 261 |
| S10 | 4, 50-250 | 5, >200 | 150, Smear >200 |

*AmplideX detects mosaicism down to 5%

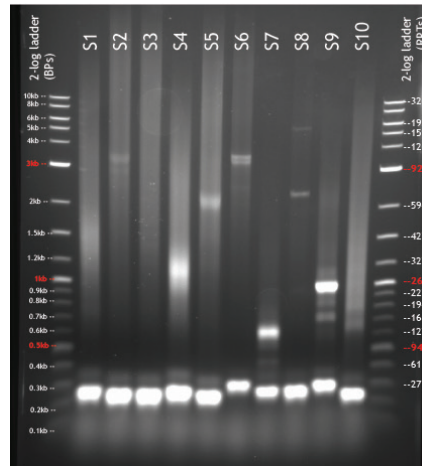


Figure 2. Comparison of residual clinical sample results between Asuragen (AmplideX Kit) and partner lab (PCR + Southern blot).

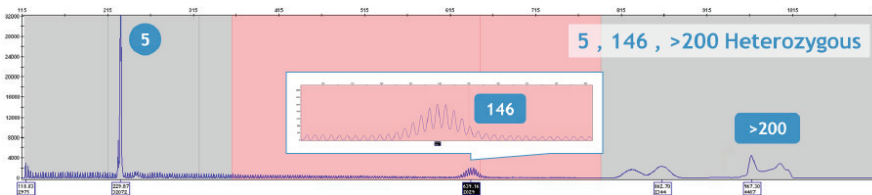


Figure 3. Sensitive and accurate sizing of *DMPK* expansions up to 200 repeats.

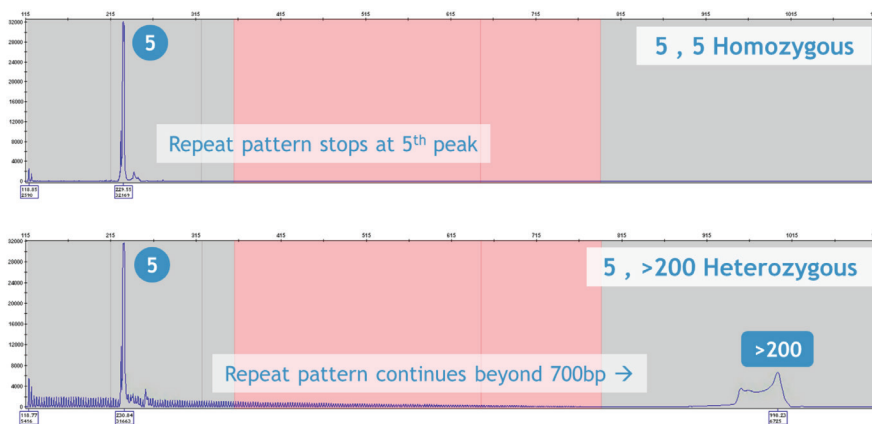


Figure 4. Clear resolution of zygosity.

KIT ORDERING INFORMATION

AmplideX PCR/CE *DMPK* Kit*

[P/N: 49655] 32 REACTIONS

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2150 Woodward Street, Suite 100
Austin TX 78744
asuragen.com

2000-027 Rev B 08/2018

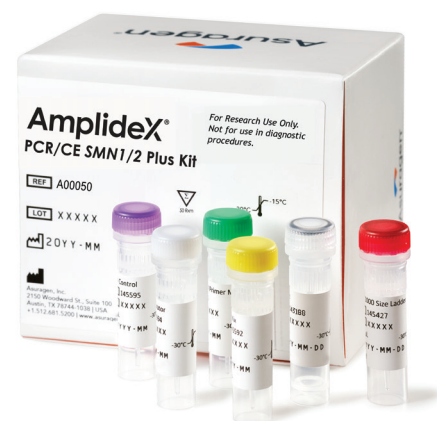
AmplideX[®]

PCR/CE SMN1/2 Plus Kit*

SMN1 and SMN2 Copy Number, Silent Carrier, and Disease Modifier Genotyping—in Less Than Four Hours

Copy number variations in *SMN1* and *SMN2* are, respectively, associated with the onset and severity of spinal muscular atrophy (SMA), a debilitating and life-threatening illness of the central nervous system. Recent studies have demonstrated that transmission risk and disease severity may be impacted by the presence of additional variants, such as *SMN1* gene duplication events and disease modifier in *SMN2*.

The AmplideX[®] PCR/CE *SMN1/2* Plus Kit* revolutionizes the analysis of these two genes by delivering comprehensive results in less than four hours. Powered by AmplideX technology, the assay accurately quantifies *SMN1* and *SMN2* exon 7 copy number and also detects *SMN1* gene duplication and *SMN2* disease modifier variants - all from a single reaction. The assay shares a common workflow with other assays in the AmplideX product portfolio and is optimized for use on widely established laboratory equipment.



REDUCED COMPLEXITY

- Similar workflow to AmplideX PCR/CE *FMR1*⁺ kit eases implementation and training
- Multiplexed, scalable design allows analysis of single-nucleotide variants, small indels, and copy-number changes from a single PCR reaction
- Assay-specific software automates variant calls and streamlines data analysis

OPTIMIZED WORKFLOW

- DNA-to-data in less than four hours with only 60 minutes of hands-on-time
- Optimized for use on commonly installed CE equipment
- Fully-kitted solution sourced from a single vendor

QUALITY PERFORMANCE

- Ability to differentiate between 0, 1, 2, 3 and ≥4 copies for both *SMN1* and *SMN2*
- Automated variant and copy-number genotyping
- Accuracy demonstrated through comparisons with multiple orthogonal methods



Figure 1. Assay workflow for AmplideX PCR/CE *SMN1/2* Plus Kit*

AmplideX[®]

PCR/CE SMN1/2 Plus Kit *

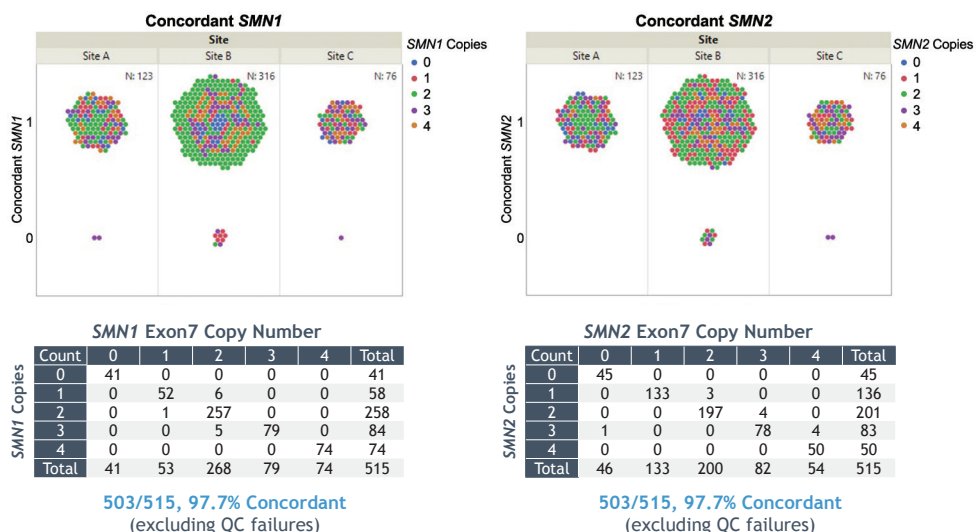


Figure 2. Excellent concordance of SMN1 and SMN2 copy number across sites for 500+ measurements using the AmplideX PCR/CE SMN1/2 Plus Kit*

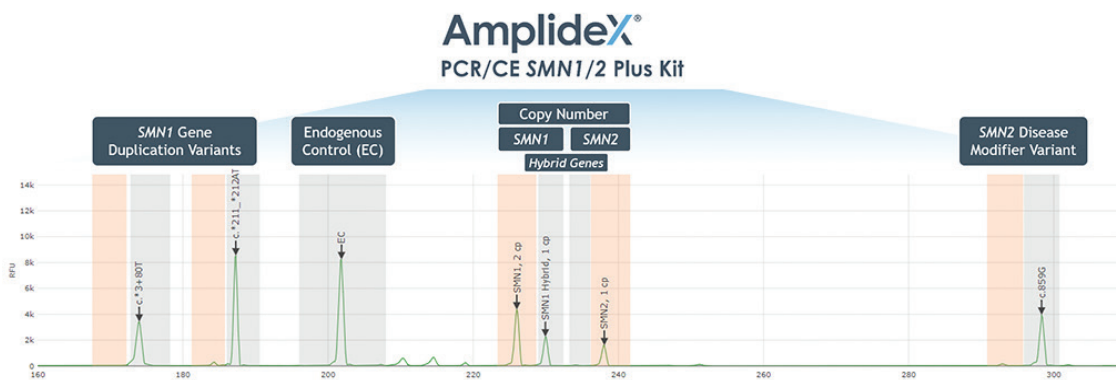


Figure 3. Example Electropherogram Output - One reaction provides information on SMN1 and SMN2 copy number, disease modifier variant and gene duplication variants

| Product Name | Number of Reactions | Catalog Number |
|--|---------------------|----------------|
| AmplideX [®] PCR/CE SMN1/2 Plus Kit (RUO) | 50 | A00050 |
| AmplideX [®] PCR/CE SMN1/2 Plus Kit (RUO) | 100 | A00054 |



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2150 Woodward Street, Suite 100
Austin TX 78744
asuragen.com
2000-098 rev. B

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† CE-IVD for US Export Only.

AmplideX[®]

PCR/CE *HTT**

Sensitive and Accurate Sizing of CAG Repeats in the *HTT* Gene

The AmplideX[®] PCR/CE *HTT* Kit makes the detection and sizing of CAG trinucleotide repeats in the *HTT* gene easier than ever. Accurate sizing of the CAG expansions in *HTT* is challenged by the presence of adjacent SNPs and variable CCG repeats, which can complicate primer binding and cause allele dropouts. With its unique, two-primer design, the AmplideX PCR/CE *HTT* Kit overcomes these challenges to accurately and reliably report the number of repeats in one day, from as little as 10ng gDNA.

REDUCED COMPLEXITY

- Proprietary PCR solutions for GC-rich amplification and detection
- Eliminates need for multiple PCRs - one result, straightforward analysis
- Resolves zygosity and detects large expansions

OPTIMIZED WORKFLOW

- Fully kitted, end-to-end solutions that significantly reduce hands-on-time
- Sample-to-result possible within a single shift
- Identical PCR and CE conditions as the AmplideX[®] PCR/CE *DMPK* Kit

QUALITY PERFORMANCE

- Reliable, unambiguous results and a robust stutter peak pattern
- Accurate sizing across the entire CAG repeat range
- Software converts raw base pair data into number of repeats



Figure 1. AmplideX PCR/CE *HTT* Kit Workflow.

AmplideX[®]

PCR/CE *HTT**

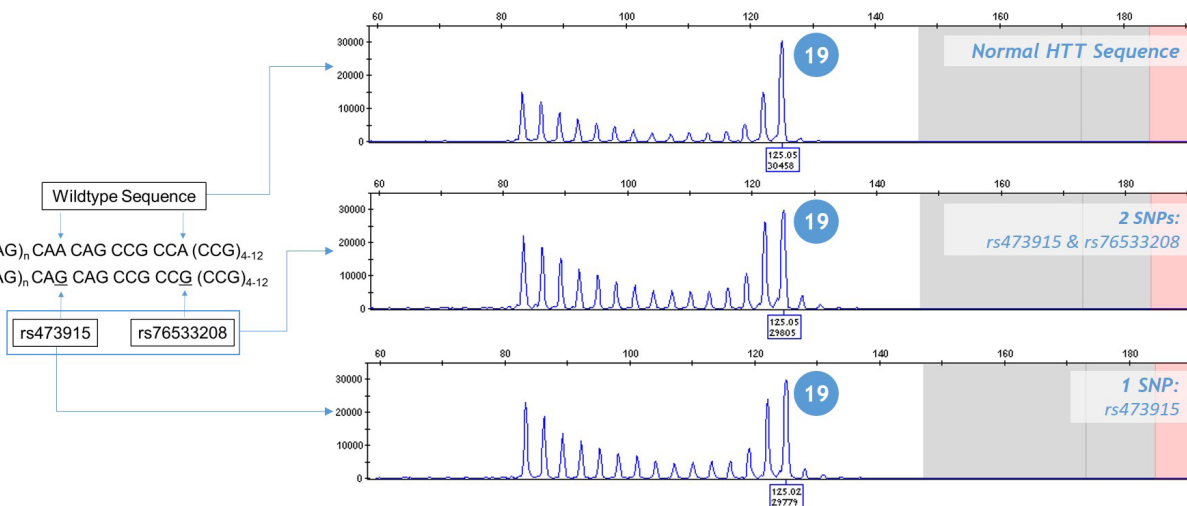


Figure 2. Repeat profile is conserved across known SNPs

| Sample ID Number | Reported Genotype | Reported Alleles | Observed Alleles |
|------------------|--------------------|------------------|------------------|
| NA20206 | NORMAL | 17, 18 | 18, 18 |
| NA20207 | NORMAL | 19, 21 | 19, 21 |
| NA20208 | EXPANDED | 35, 45 | 35, 45 |
| NA20209 | EXPANDED | 45, 47 | 45, 47 |
| NA20210 | EXPANDED | 17, 74 or 75 | 17, 75 |
| NA20245 | NORMAL | 15, 15 | 15, 15 |
| NA20246 | NORMAL | 15, 24 | 15, 24 |
| NA20247 | INTERMEDIATE | 15, 29 | 15, 29 |
| NA20248 | REDUCED PENETRANCE | 17, 36 | 17, 36 |
| NA20249 | REDUCED PENETRANCE | 22, 39 | 22, 39 |
| NA20250 | EXPANDED | 15, 40 | 15, 40 |
| NA20251 | EXPANDED | 39, 50 | 39, 50 |
| NA20252 | EXPANDED | 22, 65 or 66 | 22, 63', 66 |
| NA20253 | EXPANDED | 22, 101 | 22, 100, 128' |
| SRM 2393 A | INTERMEDIATE | 15, 29 | 15, 29 |
| SRM 2393 B | REDUCED PENETRANCE | 17, 36 | 17, 36 |
| SRM 2393 C | EXPANDED | 15, 40 | 15, 40 |
| SRM 2393 D | EXPANDED | 35, 45 | 35, 45 |
| SRM 2393 E | EXPANDED | 39, 50 | 39, 50 |
| SRM 2393 F | EXPANDED | 17, 75 | 17, 75 |

*Additional minor peak consistently identified with Asuragen assay

Figure 3. 100% Concordance (± 1 repeat) observed with previously characterized samples, as reported by Kalman et al. (2007)

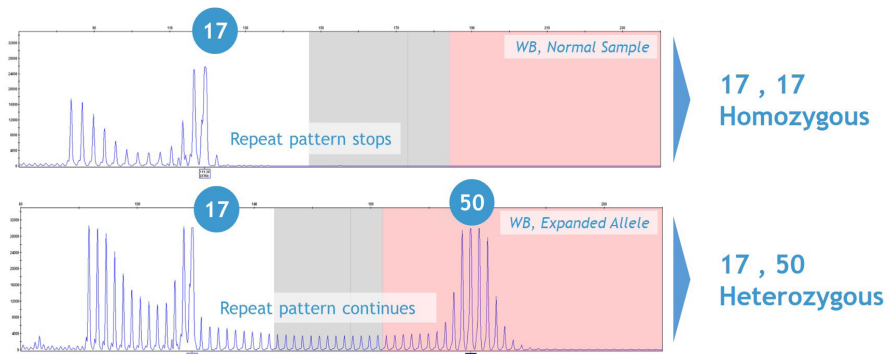


Figure 4. Clear resolution of zygosity.

KIT ORDERING INFORMATION

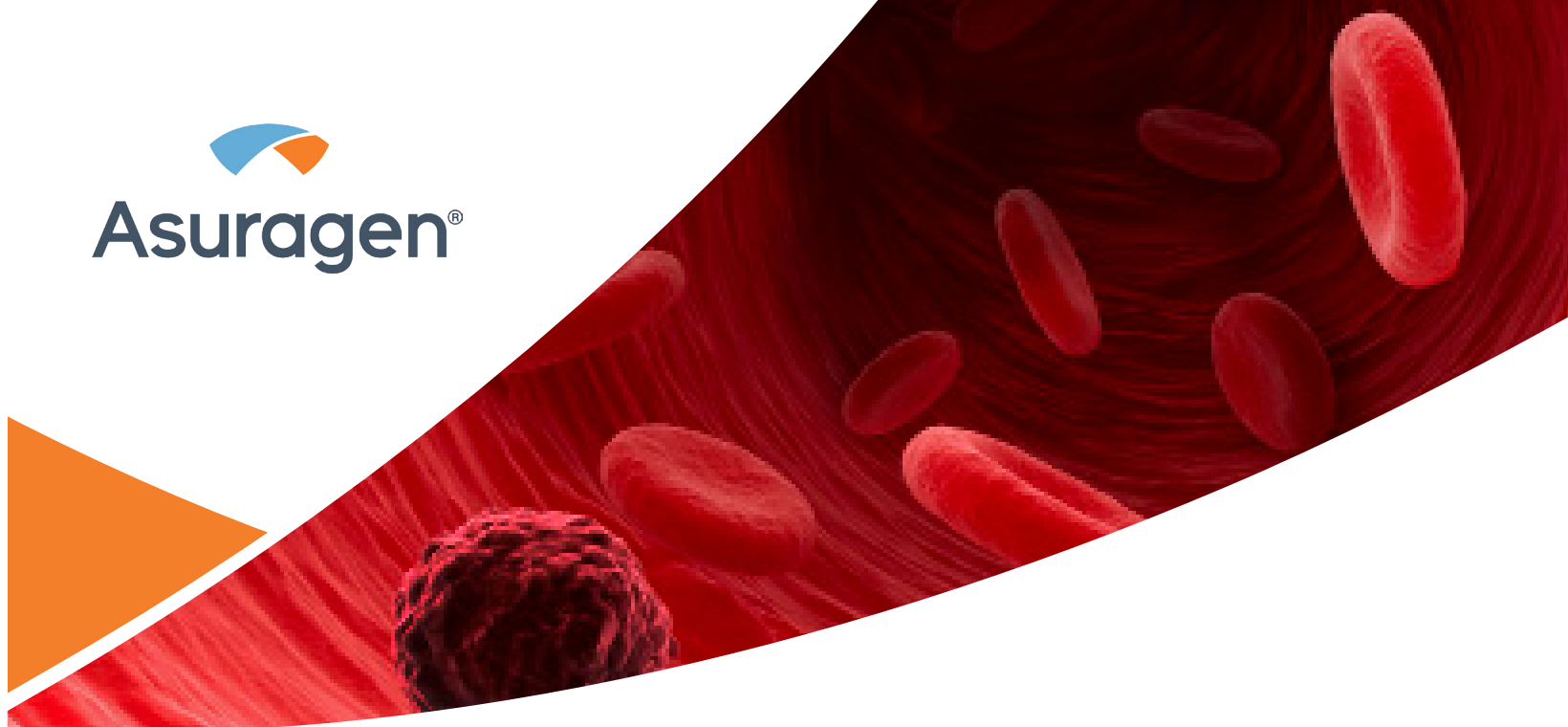
AmplideX PCR/CE *HTT* Kit*

[P/N: 49657] 32 REACTIONS

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2150 Woodward Street, Suite 100
Austin TX 78744
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2000-064 Rev A 12/2018



| Product Name | Number of Reactions | Catalog Number |
|--|---------------------|----------------|
| QuantideX [®] qPCR BCR-ABL IS Kit [†] | 60 | 86003 |
| QuantideX [®] qPCR BCR-ABL minor Kit [†] | 60 | 49640 |

[†] CE-marked for US export only.

QuantideX[®]

qPCR BCR-ABL IS Kit & qPCR BCR-ABL minor Kit[†]

Complete solution for ultra-sensitive quantitation of *BCR-ABL1* fusions for molecular response monitoring in Chronic Myeloid Leukemia



Sensitive | Reliable | Simple



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 asuragen.com

3000-001

[†] CE-marked for US export only.

QuantideX[®]

qPCR BCR-ABL IS Kit & qPCR BCR-ABL minor Kit[†]

Advances in TKI therapy have driven 5-year survival rates in CML patients to nearly 90%¹ and are helping to make treatment-free remission a reality for a significant number of patients². However, to accurately assess response to treatment and determine eligibility for treatment cessation, a rapid, accurate and highly sensitive assay for measurement of disease burden is required.

The QuantideX[®] BCR-ABL Portfolio offers simple, reliable, ultra-sensitive quantitation of both the Major and minor breakpoints, allowing any molecular laboratory to assess the deepest molecular response with unprecedented ease and deliver the results physicians and patients rely on.

Reduced Complexity

- **Direct reporting on the International Scale (IS)*:**
Multi-point standard curve reduces variability and removes need for costly, complex sample exchange
- **Single method, comprehensive reporting:**
QuantideX[®] Reporter Software[†] provides automated calculation of %IS*, *BCR-ABL1/ABL1* %ratio and *ABL1* copy number**

Streamlined: Multiplexed design yields workflow and cost efficiencies

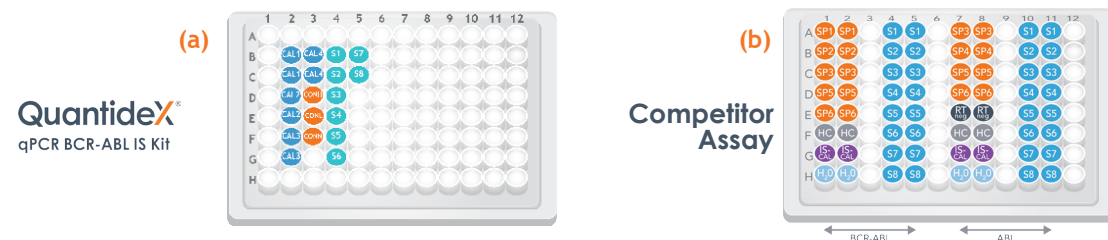


Figure 1: Comparison of plate layout for an 8 sample run between the (a) Asuragen assay, which features a multiplexed design and samples run in singlicate, resulting in only 19 reactions; and (b) a competitor assay, which features a singleplex design and samples run in duplicate, resulting in 60-64 reactions.

Optimized Workflow

- **Reduced hands-on time:**
Multiplexed design amplifies and detects both fusion and control genes in the same reaction
- **Simplified inventory & quality management:**
All necessary RT and qPCR reagents and controls in a single, vendor-sourced kit to reduce QC burden
- **Common workflows:**
Major & minor kits share common workflows to streamline testing and reduce risk of error

Simple: Two Kits. One Workflow.

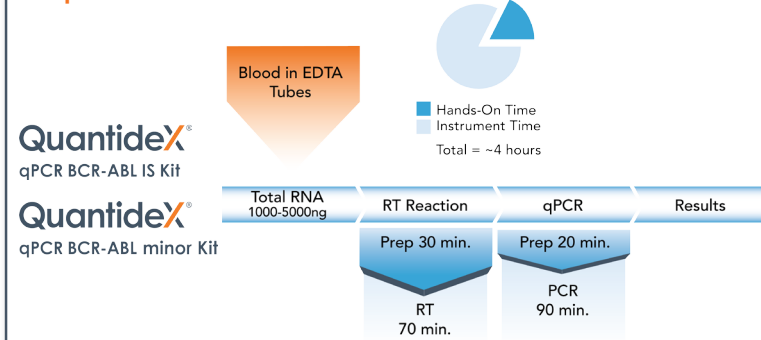


Figure 2: Both kits share a common workflow with limited hands-on-time, maximizing laboratory efficiency and sample throughput.

Quality Performance

- **Performance established using human RNA:**
Limits of Detection (LOD) of MR4.7 (0.002% IS) and LR4.61 (0.0025% ratio) confirmed in human RNA, not cell lines
- **Multi-point Armored RNA[®]-based standards:**
Provide reproducible, traceable RNA quantitation values
- **Increased analytical sensitivity without compromising analytical specificity:**
Unique Limit of Blank (LOB) approach used to minimize miscalling of non-leukemic low positives

Reproducible: Proven sensitivity based on rigorous testing criterion

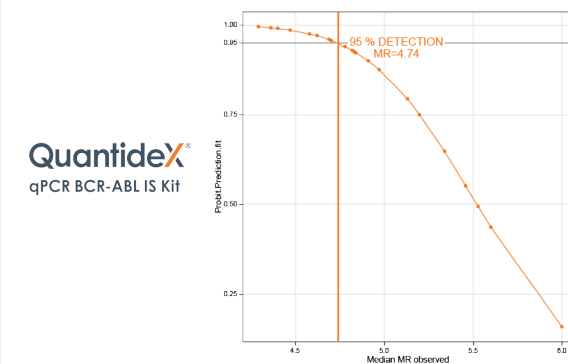


Figure 3: LOD of the QuantideX qPCR BCR-ABL IS Kit as determined by CLSI EP17-A2 guidelines by testing Human RNA dilutions ranging from MR4.4 to MR6: 60 replicates of each dilution for a total of 1680 data points.

| | Replicates tested | Log Reduction | Median LOD (%ratio) |
|---|-------------------|---------------|---------------------|
| QuantideX [®] qPCR BCR-ABL IS Kit Human RNA | 90 | LR4.61 | 0.0025% |
| QuantideX [®] qPCR BCR-ABL minor Kit Cell Lines | 80 | LR5.31 | 0.0005% |

Table 1: LOD of the QuantideX[®] qPCR BCR-ABL minor Kit as determined by CLSI EP17-A2 guidelines by testing Human RNA and cell line dilutions spanning multiple lots, batch runs, days, operators, and instruments.

Precise: Minimal variability across the entire dynamic range

| Target MR | Mean MR | Std Dev | Limits of Agreement (95%) |
|-----------|---------|---------|---------------------------|
| 1 | 0.697 | 0.092 | 1.53 |
| 2 | 1.634 | 0.069 | 1.37 |
| 3 | 2.658 | 0.053 | 1.28 |
| 3.5 | 3.185 | 0.077 | 1.43 |
| 4 | 3.675 | 0.092 | 1.53 |

Table 2: Precision evaluated using 5 different levels of positive specimens, tested by 3 operators over 20 runs each. Each level was tested 90 times for a total of 450 data points.

| Target LR | Mean LR | Std Dev |
|-----------|---------|---------|
| 1 | 0.98 | 0.12 |
| 2 | 1.95 | 0.17 |
| 3 | 2.96 | 0.12 |
| 4 | 3.98 | 0.17 |

Table 3: Assay precision determined by testing 4 different log reduction (LR) levels in human RNA, using 2 operators, and 8 runs for a total of 192 data points.

[†] CE-marked for US export only. *QuantideX[®] qPCR BCR-ABL IS Kit only. **QuantideX[®] qPCR BCR-ABL minor Kit only.

¹ American Cancer Society ² Saußele S, et al. Leukemia (2016) 30, 1638–1647.

[†] CE-marked for US export only.