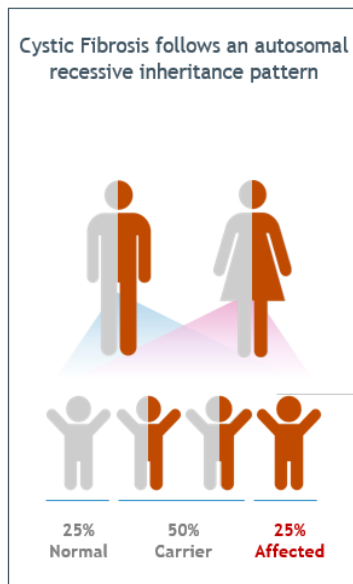


AmplideX PCR/CE *CFTR* Prototype Assay has Broad Coverage for Diverse Populations

- Cystic Fibrosis is an autosomal recessive condition caused by mutations in the *CFTR* gene.
- More than 2000 *CFTR* variants have been identified. Disease varies by severity of the mutations, genetic modifiers, and environmental factors. The mutation profiles varies greatly with different population groups.
- Reliable detection of *CFTR* mutations is crucial to inform disease diagnosis, therapy decisions, carrier screening and pre-natal testing.
- AmplideX PCR/CE *CFTR* Prototype addresses both European (ECFS guidelines) & US recommendations (ACMG/ACOG guidelines) for *CFTR* mutation detection.

Asuragen's kit is designed to detect more at-risk couples³ than any other commercial Kit



| | % COVERAGE ¹ | At-Risk Couple Detection Rate ² | For every 20 ARCs ³ detected by Asuragen, # missed by others |
|-----------------|-------------------------|--|---|
| Asuragen® | 93.0% | 86.5% | -- |
| Illumina | 87.8% | 77.0% | -2 |
| Luminex* | 87.0% | 75.7% | 2-3 |
| Agena | 86.9%* | 75.5%* | 2-3 |
| Elucigen | 86.2% | 74.3% | 2-3 |
| GenMark ACMG 23 | 78.9% | 62.3% | 5 |

*Luminex xTAG® Cystic Fibrosis (CFTR) 71 kit v2

This product is under development. Performance specifications have not been finalized

¹ Based on US population demographics
² % coverage squared for carrier alleles in both parents
³ Predicted at-risk couples (ARC) is calculated from *CFTR* mutation coverage assuming fully pathogenic alleles

Contemporary View of *CFTR* Variants Emphasizes Quality Over Quantity

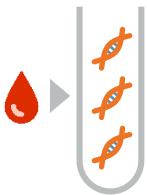
“...the number of variants should not be used as a comparator; instead, the focus should always be on sensitivity and specificity (either analytical or clinical) of known pathogenic variants.”

Beauchamp et al. (2019)

For additional information about this poster and others from Asuragen, visit <https://asuragen.com/eshg-20/>

This product is under development. Performance specifications have not been finalized

AmplideX PCR/CE CFTR Prototype System includes all necessary Reagents and Software to go from Sample to Results in ~ 5 hours



Agnostic DNA isolation approach with conservative sample input requirements



Kit include necessary reagents for both PCR and CE steps and assay is compatible with widely-established instruments



Automated interpretation of results is enabled through push-button analytics modules

DNA to Data Within One Day

Software Report

Data Visualization

Tube A: Asuragen_Sample3-A_A03_2020-03-09-12-37-16-01.fea



Tube B: Asuragen_Sample3-B_B03_2020-03-09-12-39-52-01.fea



RUO: For Research Use Only Not for use in diagnostic procedures

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Sample: Sample 3

Batch Details

Project: Demo Project
Batch: CFTR Batch1
Operator: admin
Date Analyzed: 3/9/2020 2:55:30 PM

Assay: Tube A, Tube B
Instrument: 35XX
Sample QC: PASS
Marked for Review: False

Analysis Results

| Sample | Well | Assay | Mutations | Variants | Poly T/TG |
|---------|----------|--------|-----------|--------------------------|-----------|
| Sample3 | A3 B3 | A B | 2 2 | PROBdet/WT, 265T>35aa/WT | - |

Comments

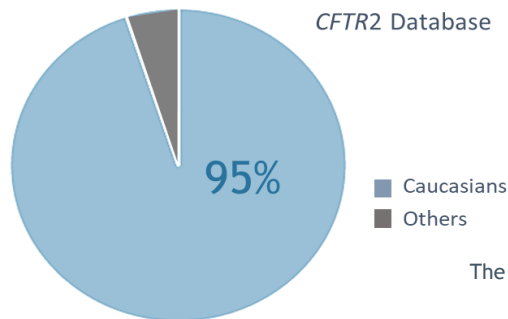
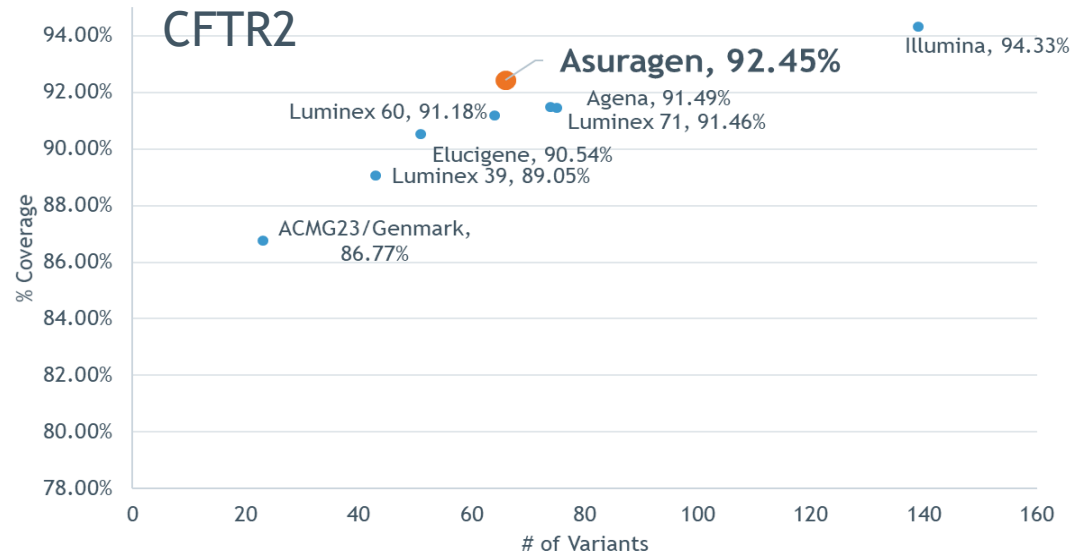
No comments.

RUO: For Research Use Only Not for use in diagnostic procedures

Page 1 of 2

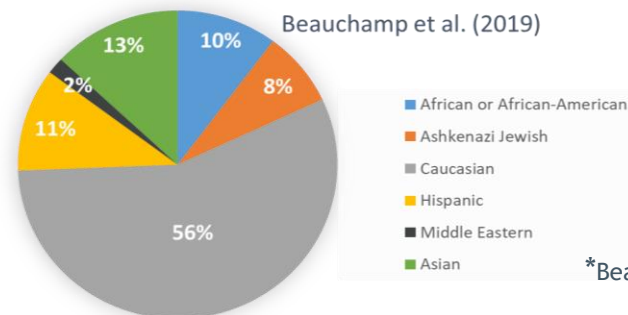
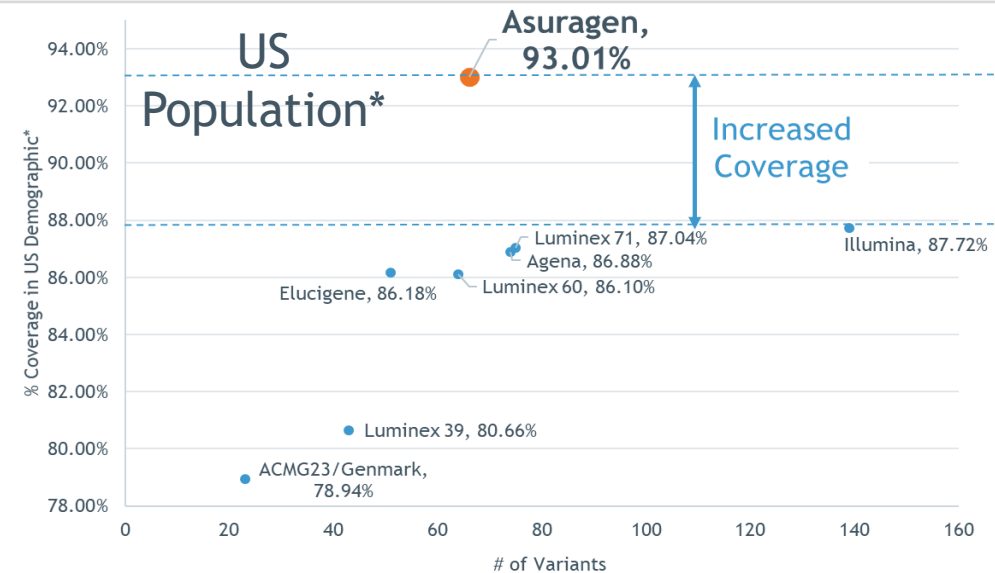
A Rapid Prototype Multiplex PCR/CE Assay and Software System has Broad Coverage of Pathogenic *CFTR* Mutations for Diverse Populations

- The AmplideX PCR/CE *CFTR* Prototype assay genotypes 66 pathogenic variants that address >92% mutant prevalence in an ethnically diverse US demographic and [CFTR2.org](http://cftr2.org)
- The Prototype addresses both European and US recommendations for *CFTR* mutation detection
 - Targets at least one pathogenic mutation in >96% of CF patients as per ECFS guidelines.
 - Includes all 23 ACMG/ACOG minimum list recommended *CFTR* mutations.



CFTR2 database lacks ethnic diversity

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



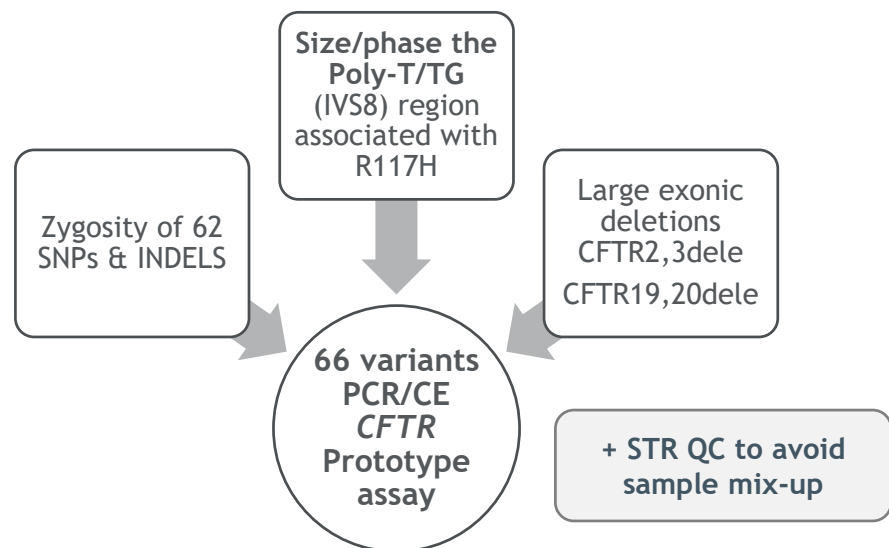
More actionable information for the diverse US population

*Beauchamp K. et al. (2019) Genet in Med 21:1948-1957

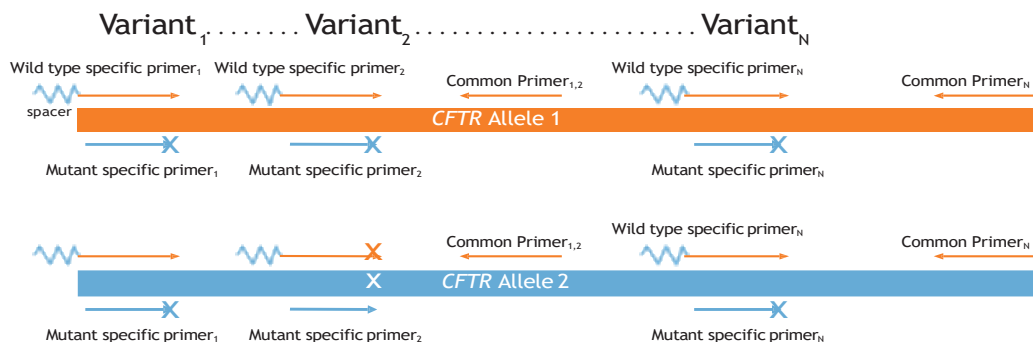
This product is under development. Performance specifications have not been finalized

A Two-Tube PCR/CE Assay was Designed to Detect Multiple Classes of Variants using a Streamlined Workflow, and Evaluated across 508 Samples

Detects SNPs, INDELs, CNVs and IVS8 poly-T/TG modifier

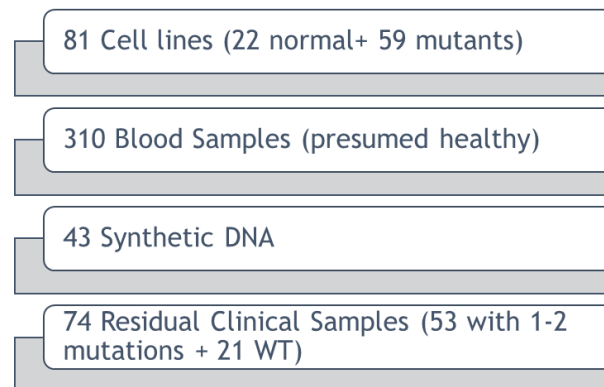


Allele-specific primers amplify wild-type or mutant allele variants with a set of common primers



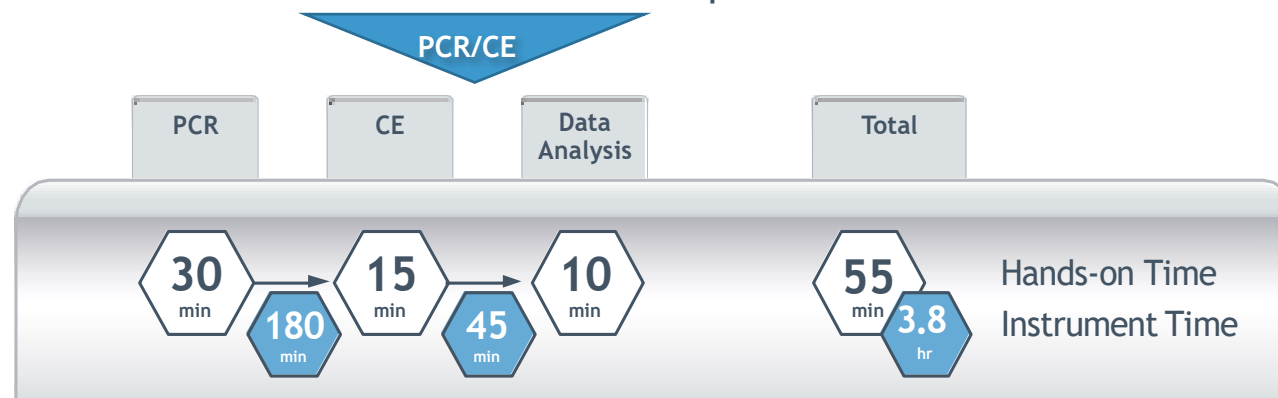
This product is under development. Performance specifications have not been finalized

Cell line, synthetic, presumed normal blood and residual Clinical samples were evaluated

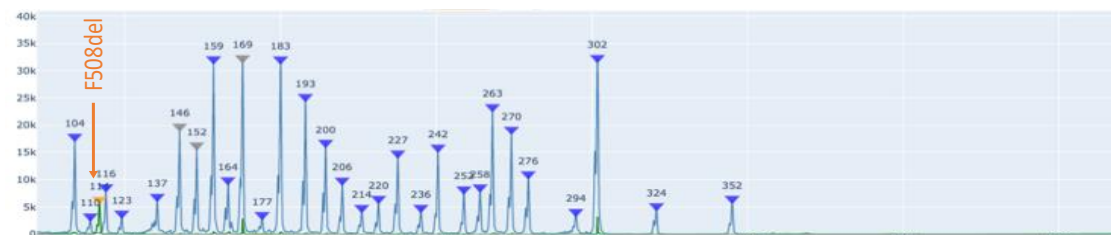


DNA Samples Evaluated in this Study

Streamlined Workflow ~ 5 hours from Sample to Results

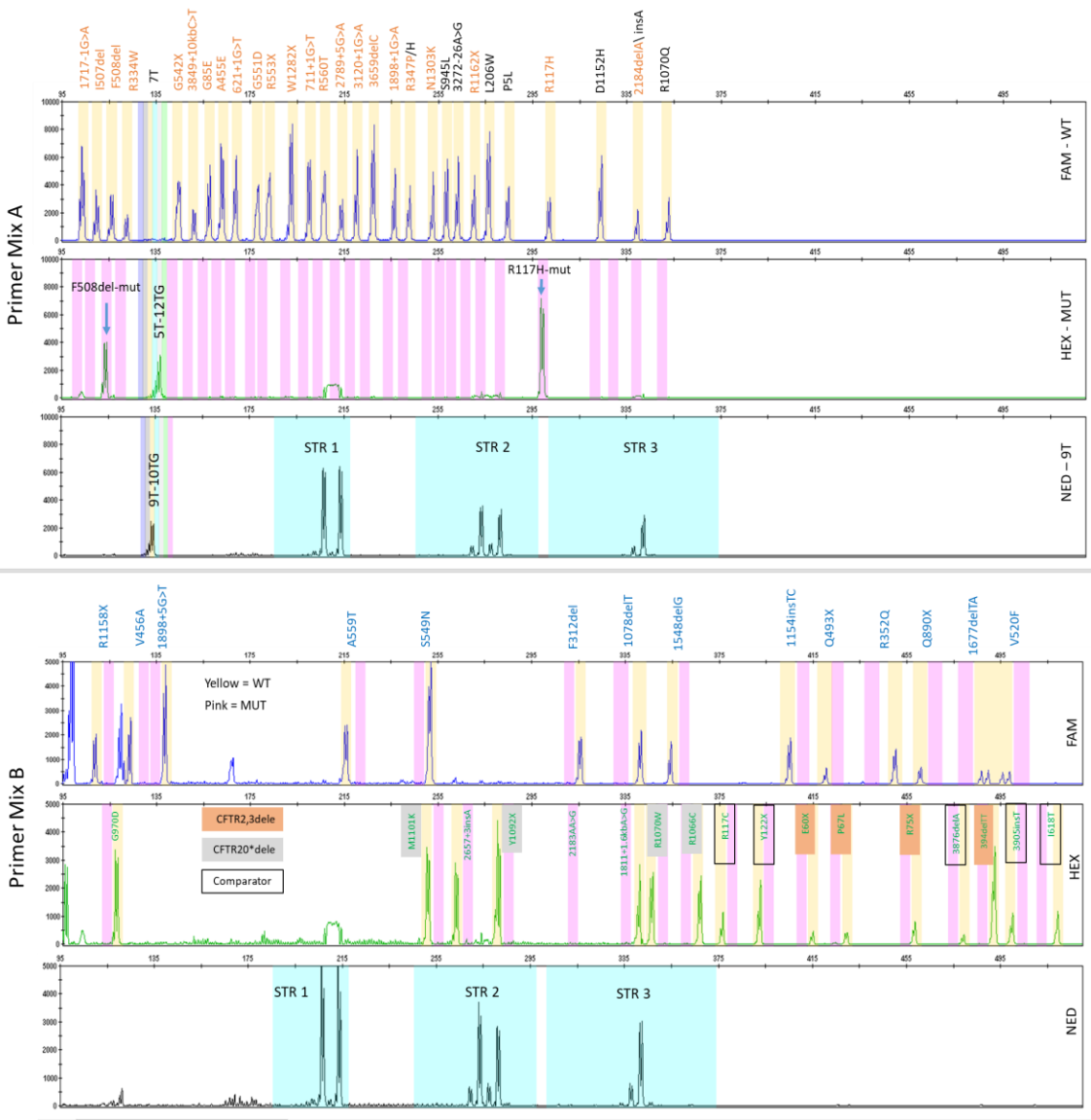


OUTPUT



The Prototype Accurately Determined Zygosity for 81 cell lines and >10,500 alleles with 100% Agreement to Reference Results

Prototype PCR/CE *CFTR* Assay Profile for Two-Tube PCR (Primer Mix A,B) with NA13591, a Compound Heterozygote Mutant F508del & R117H with 5T allele

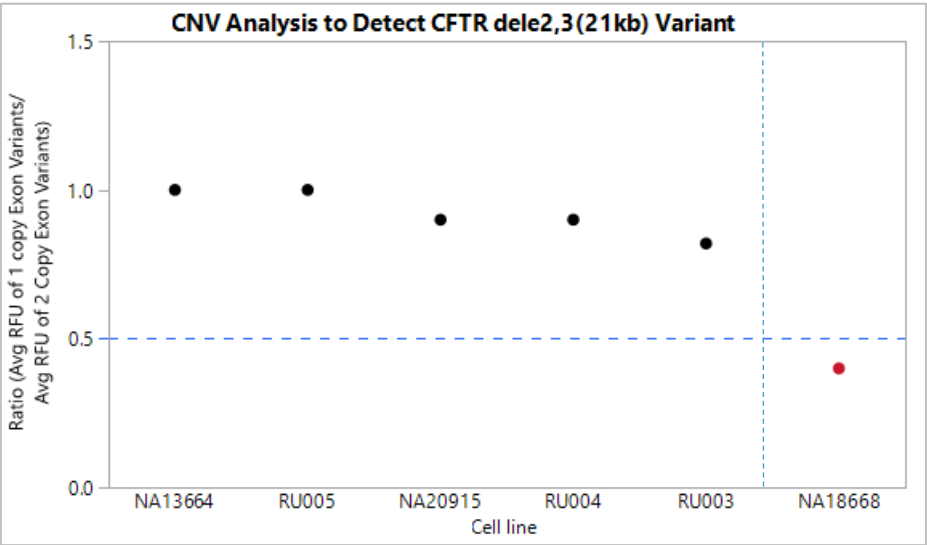


100% Agreement of Prototype Assay with the Comparator Method for Zygosity and IVS8 Sizing-Phasing

| IVS8 Size Distribution and Agreement | 10 TG | 11 TG | 12 TG | Totals | Agreement with comparator assay for observed allele peak | Sanger Sequencing | | | Variant Agreement |
|--------------------------------------|--------------|--------------|--------------|----------------|--|-------------------|---------|--|-------------------|
| | | | | | | Homozygous | | Heterozygous | |
| | | | | | | wt/wt | mut/mut | wt/mut | |
| 5T | - | 2 | 2 | 4/4 (100%) | Prototype PCR/CE <i>CFTR</i> Assay | wt/wt | 5114 | - | 5114/5114 (100%) |
| 7T | 39 | 72 | 10 | 121/121 (100%) | | mut/mut | - | 5 4 var. - Tube A 1 var. - Tube B | 5/5 (100%) |
| 9T | 35 | 2 | - | 37/37 (100%) | | wt/mut | - | 65 45 var. - Tube A 20 var. - Tube B | 65/65 (100%) |
| | 74/74 (100%) | 76/76 (100%) | 12/12 (100%) | 162/162 (100%) | | | | | |

Variants R347H/R347P are detected by the same allele specific primers and cannot be differentiated.
2184delA, 2184insA and 2183AA>G are detected by the same allele specific wild type primer but with different mutant primers.

CNV analysis accurately determined *CFTR*dele2,3 HET variant in cell line NA18668



Ratio of Exon 3 variants (averaged) to Exon 04, 14, 23 variants (averaged) was ~0.4 in this cell line vs 0.8-1 in other wt cell lines shown here.

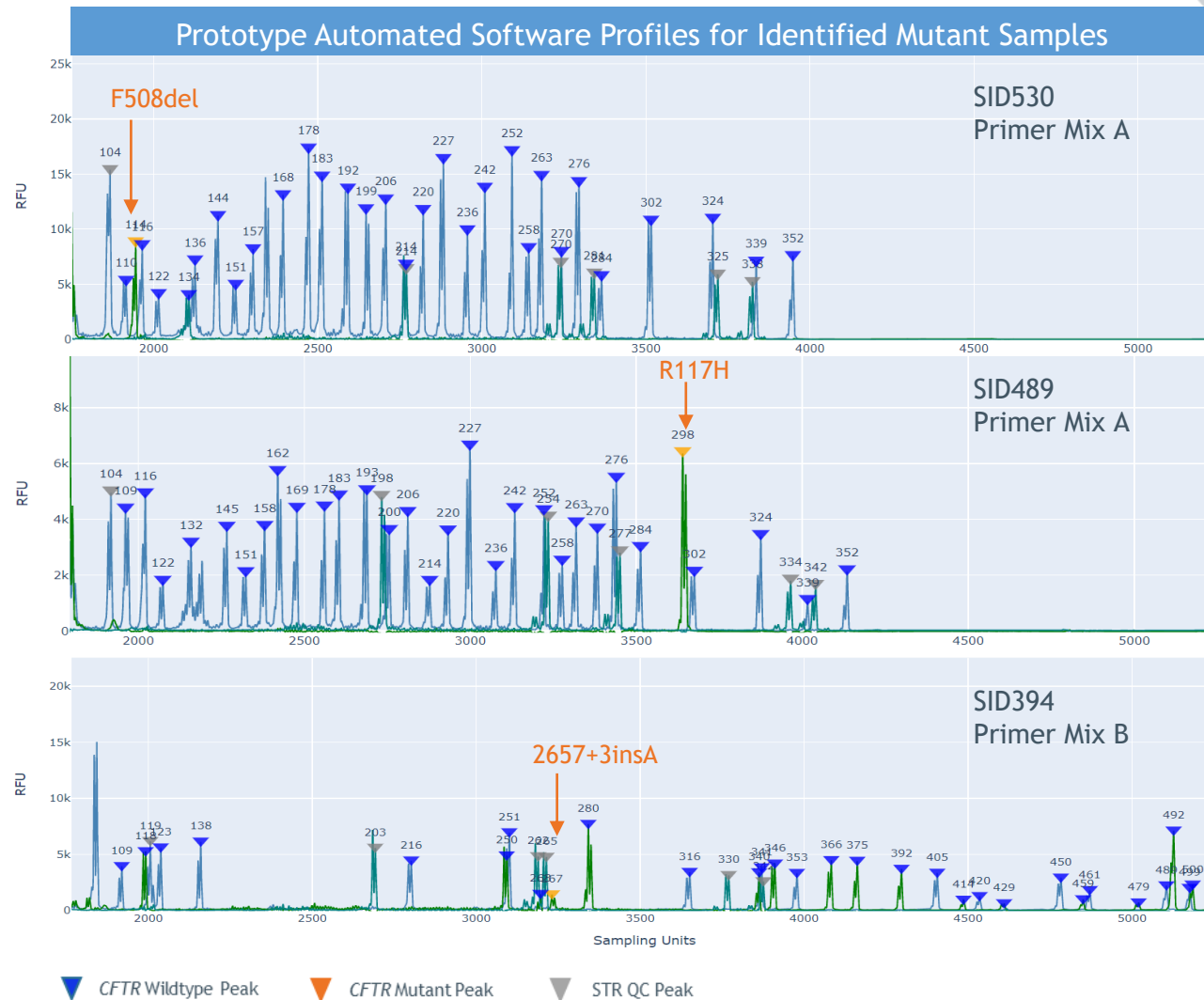
The Prototype PCR/CE *CFTR* assay Identified 12 *CFTR* Carriers from 310 Presumed Normal WB Donors

- The Prototype assay showed 100% agreement of all 12 mutant alleles and IVS8 sizing/phasing with Comparator (Sanger Sequencing).
- Prototype Automated Software accurately identified all 12 mutant variants that were called manually on GeneMapper® software.

| Sample ID | Mutant Allele & Zygosity | Allele 1 (T-TG) | Allele 2 (T-TG) | Sanger Sequencing Agreement |
|-----------|--------------------------|-----------------|-----------------|-----------------------------|
| SID530 | F508del Het | 7T-12TG | 9T-10TG | ✓ |
| SID637 | F508del Het | 7T-10TG | 9T-10TG | ✓ |
| SID278 | F508del Het | 9T-10TG | 9T-10TG | ✓ |
| SID388 | F508del Het | 7T-11TG | 9T-10TG | ✓ |
| SID396 | F508del Het | 7T-11TG | 9T-10TG | ✓ |
| SID481 | F508del Het | 7T-10TG | 9T-10TG | ✓ |
| SID562 | F508del Het | 7T-11TG | 9T-10TG | ✓ |
| SID569 | F508del Het | 7T-11TG | 9T-10TG | ✓ |
| SID489 | R117H Het | 7T-10TG | 7T-12TG | ✓ |
| SID302 | D1152H Het | 7T-11TG | 7T-11TG | ✓ |
| SID301 | D1152H Het | 7T-11TG | 7T-11TG | ✓ |
| SID394 | 2657+3insA Het | 7T-10TG | 7T-10TG | ✓ |

Observed carrier frequency across reactions was similar to the recently published[†] carrier rate observed in the US population (1 in 26)

| | Estimated | Actual |
|--------------|--------------------------------|----------------|
| Primer Mix A | $1/26 * 86\% = 3.3\%$, 10-11 | 11/310 (3.54%) |
| Primer Mix B | $1/26 * 7.01\% = 0.27\%$, 0-1 | 1/310 (0.32%) |



[†]Westemeyer M et al. Genet Med. 2020, PMID: 32366966

The Prototype PCR/CE *CFTR* assay Accurately Determined Zygosity for 74 Residual Clinical Samples with 100% Agreement to an Orthogonal Assay

| Sample Agreement with Reference Assay | | | xTAG® Cystic Fibrosis (CFTR) 60 Kit v2 | | | Overall Sample Agreement |
|---------------------------------------|----------------------------|---------|--|---------|--------------|--------------------------|
| | | | Homozygous or Compound Heterozygous | | Heterozygous | |
| | | | WT/WT | MUT/MUT | MUT/WT | |
| Prototype <i>CFTR</i> PCR/CE Assay | Homozygous or Compound Het | WT/WT | 21 | 0 | 0 | 21/21 (100%) |
| | | MUT/MUT | 0 | 18 | 0 | 18/18 (100%) |
| | Heterozygous | MUT/WT | 0 | 0 | 35 | 35/35 (100%) |

- A total of 21 distinct variants were represented in 53 mutated Clinical samples
- All mutations and their zygosity agreed with the reference assay calls

| Variants Identified | No. of Samples |
|---------------------|----------------|
| F508del | 24 |
| D1152H | 5 |
| R117H | 5 |
| G542X | 4 |
| G551D | 4 |
| 621+1G>T | 3 |
| 1717-1G>A | 2 |
| 2789+5G>A | 2 |
| 3120+1G>A | 2 |
| 3659delC | 2 |
| 711+1G>T | 2 |
| R1162X | 2 |
| W1282X | 2 |
| 1898+1G>A | 1 |
| 3849+10kbC>T | 1 |
| 394delTT | 1 |
| E60X | 1 |
| G85E | 1 |
| L206W | 1 |
| M1101K | 1 |
| R347H or P | 1 |

Note: 13 samples were compound heterozygotes with > 1 mutation