



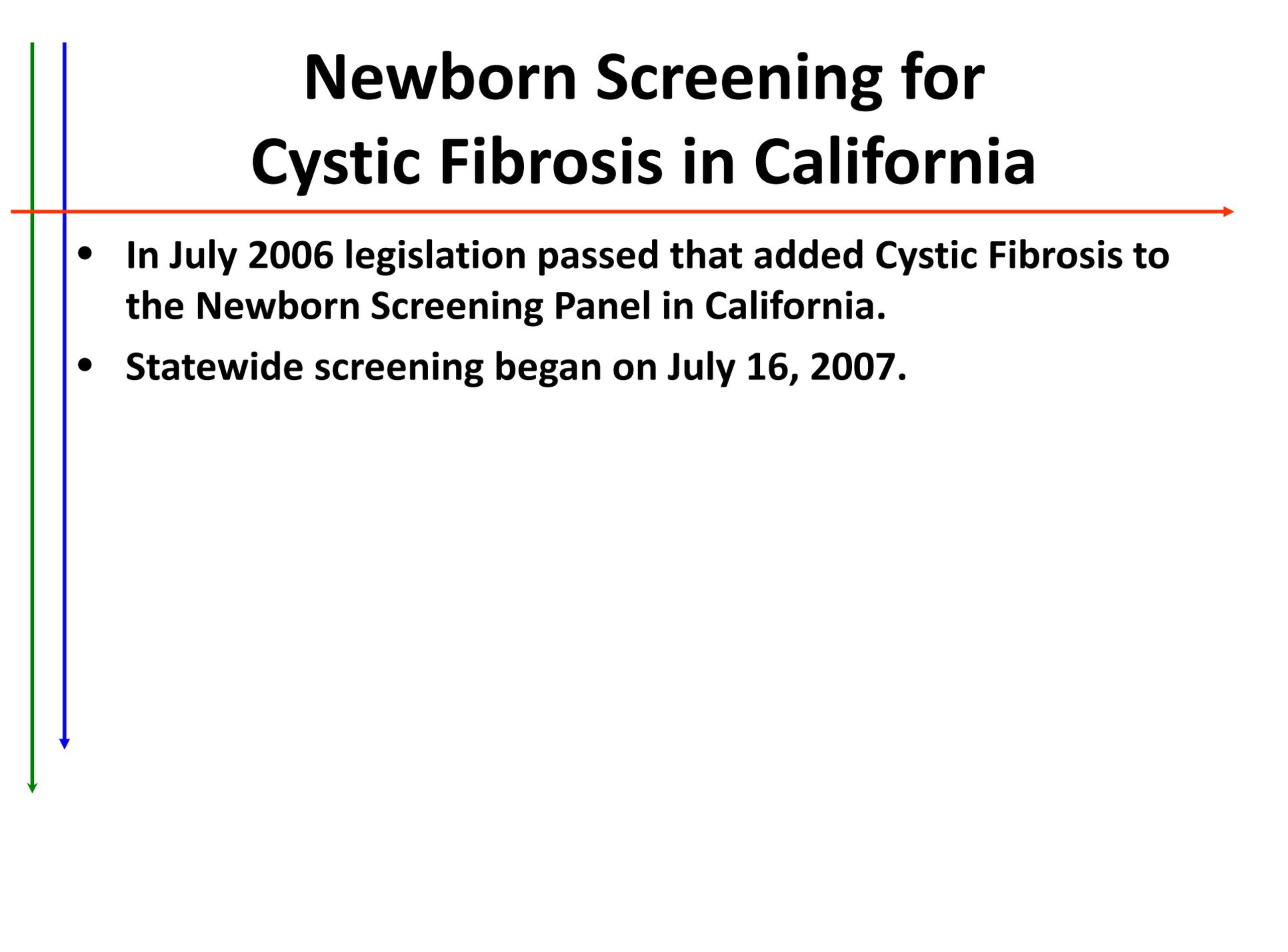
Overview of the First Eight Years Of Newborn Screening For Cystic Fibrosis: The California Experience.

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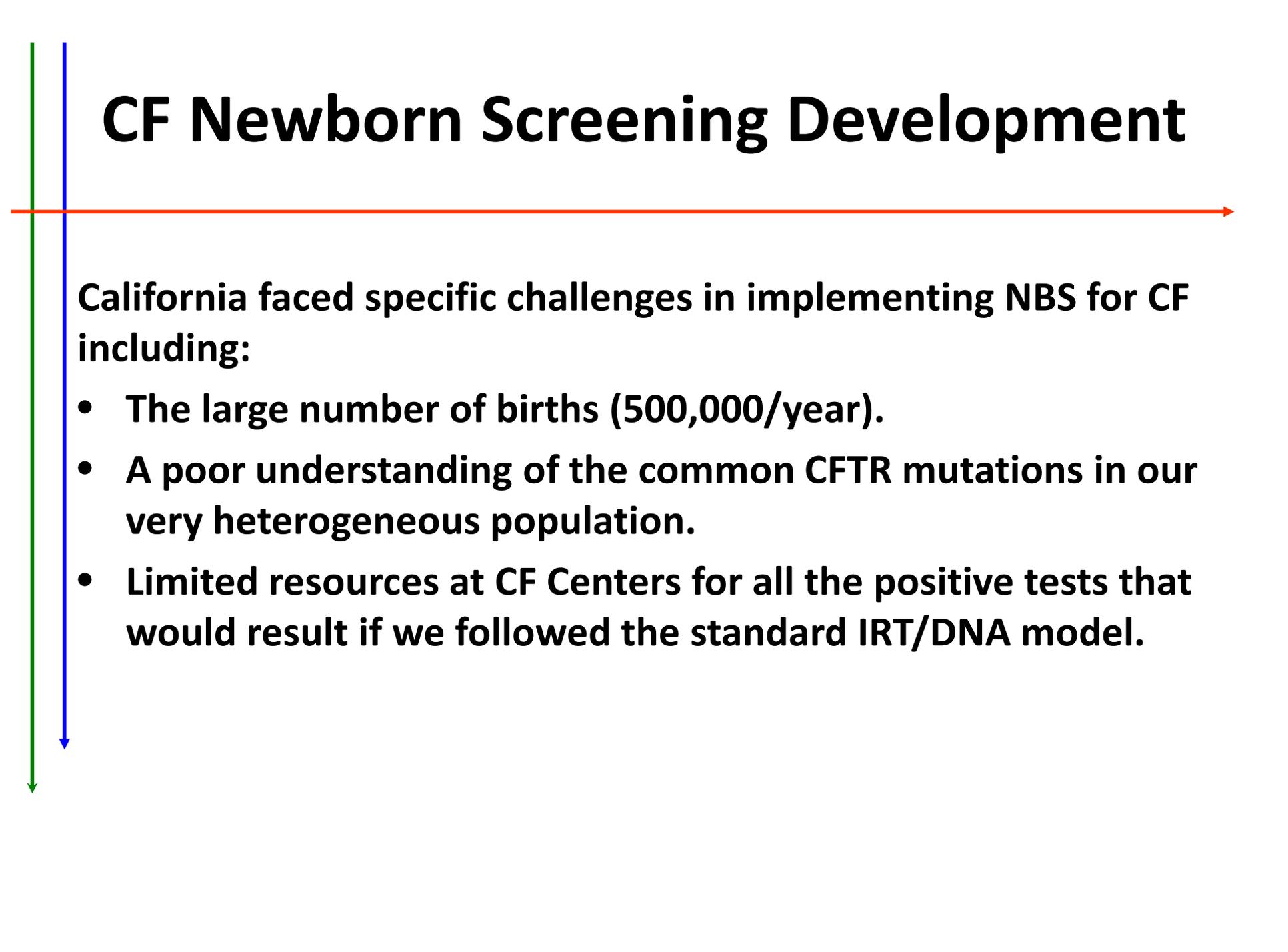
California Newborn Screening Program



Newborn Screening for Cystic Fibrosis in California

- **In July 2006 legislation passed that added Cystic Fibrosis to the Newborn Screening Panel in California.**
- **Statewide screening began on July 16, 2007.**

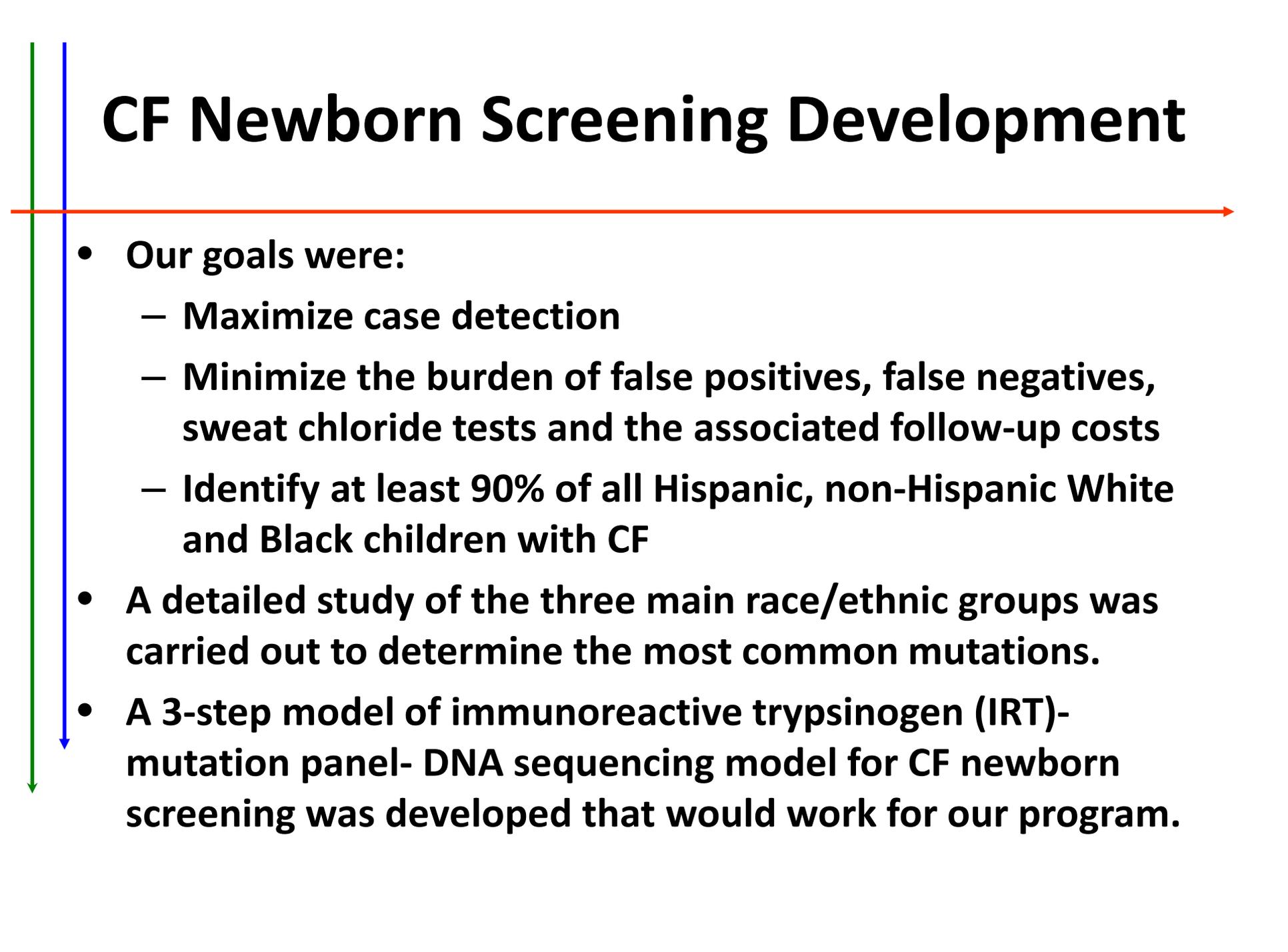
CF Newborn Screening Development



California faced specific challenges in implementing NBS for CF including:

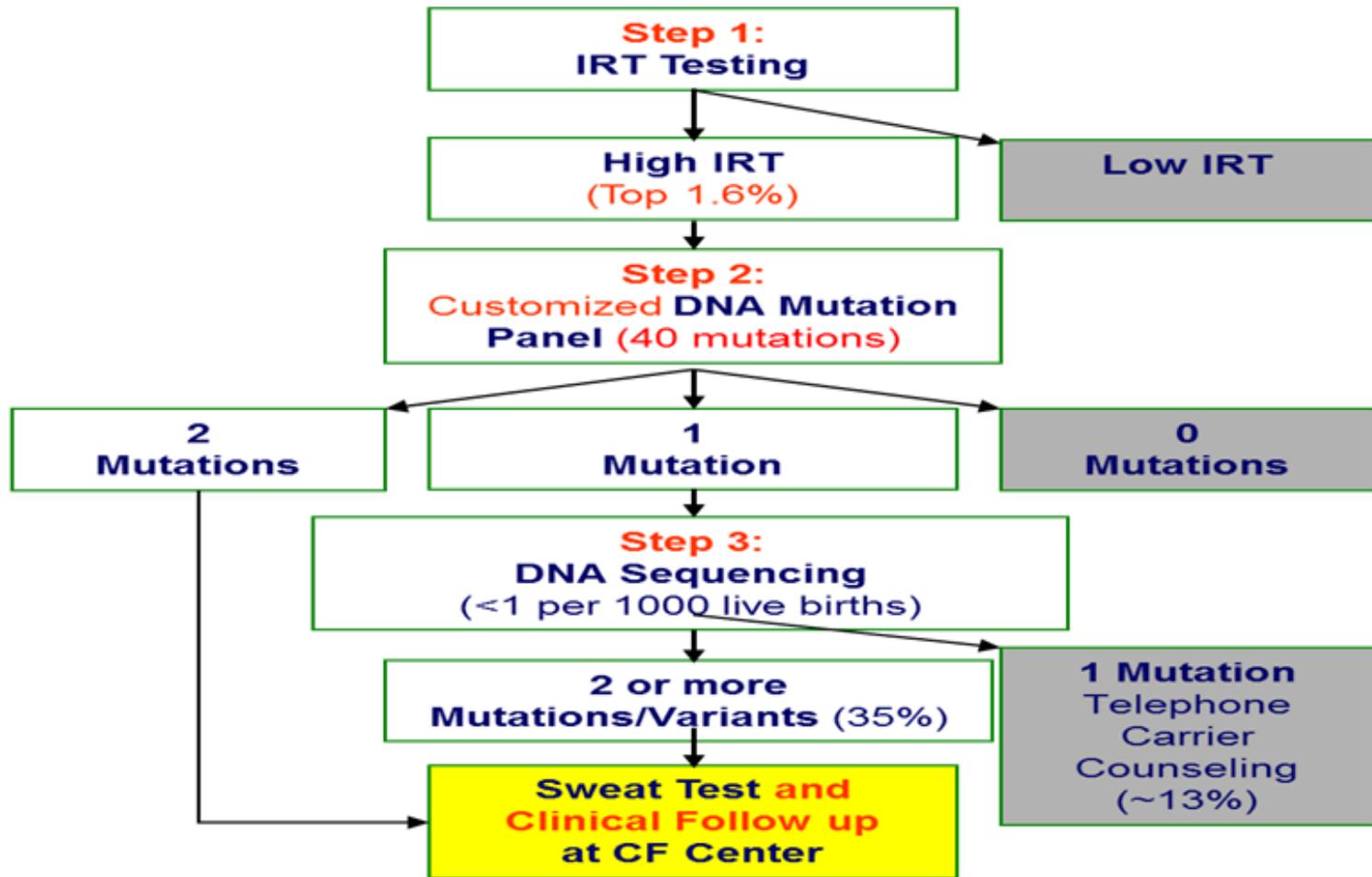
- **The large number of births (500,000/year).**
- **A poor understanding of the common CFTR mutations in our very heterogeneous population.**
- **Limited resources at CF Centers for all the positive tests that would result if we followed the standard IRT/DNA model.**

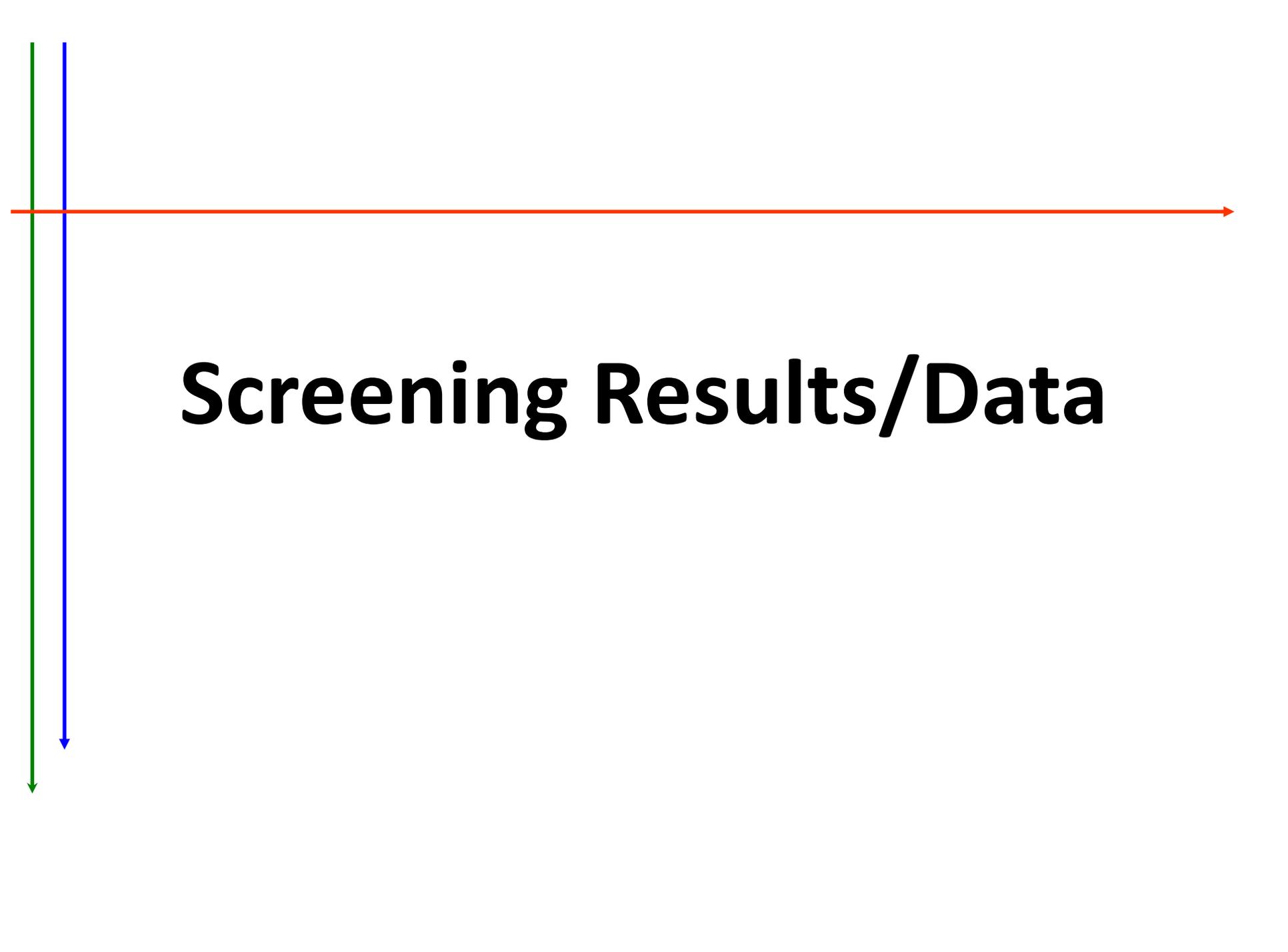
CF Newborn Screening Development



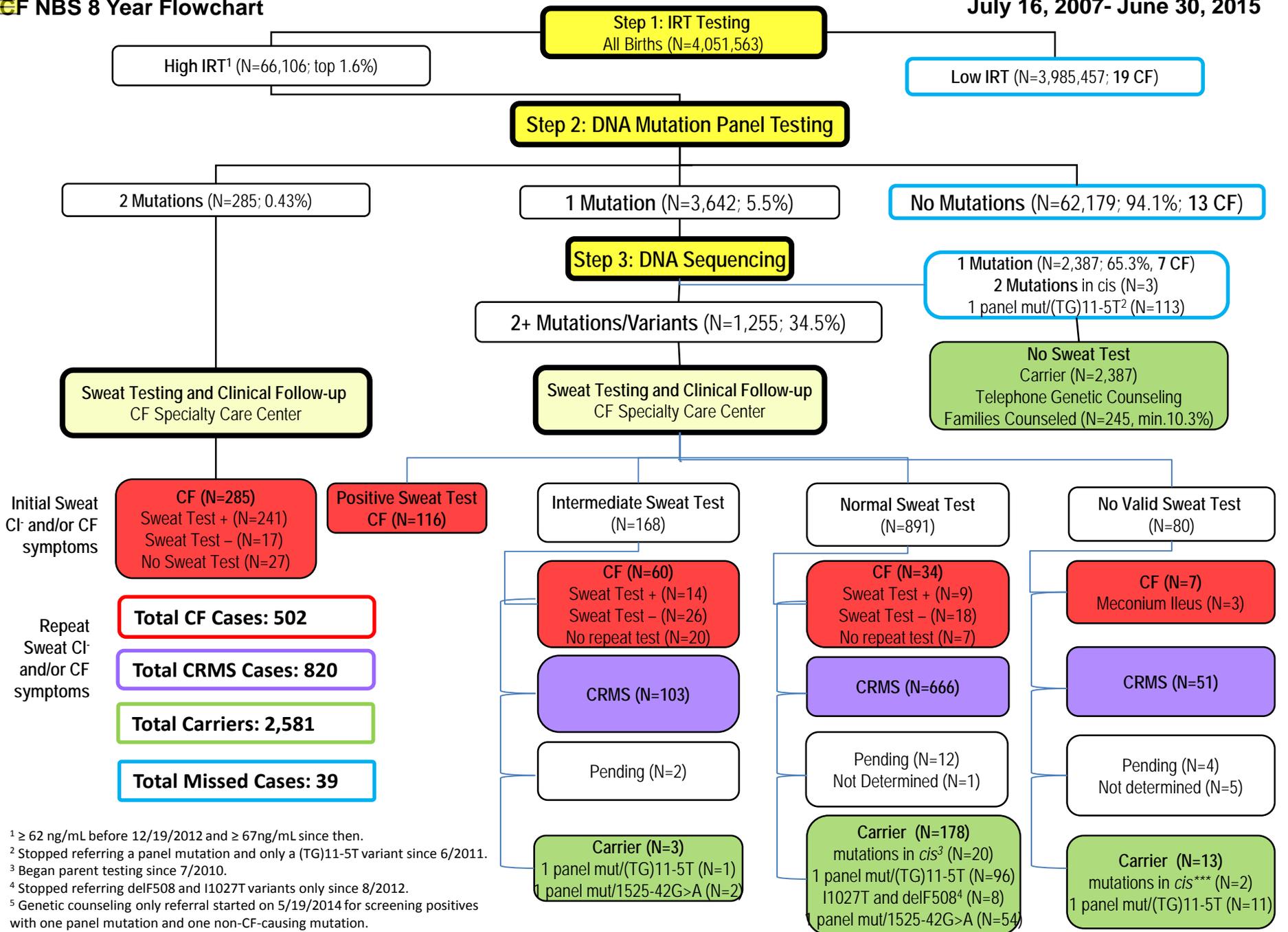
- **Our goals were:**
 - **Maximize case detection**
 - **Minimize the burden of false positives, false negatives, sweat chloride tests and the associated follow-up costs**
 - **Identify at least 90% of all Hispanic, non-Hispanic White and Black children with CF**
- **A detailed study of the three main race/ethnic groups was carried out to determine the most common mutations.**
- **A 3-step model of immunoreactive trypsinogen (IRT)-mutation panel- DNA sequencing model for CF newborn screening was developed that would work for our program.**

California 3 Step CF NBS Model



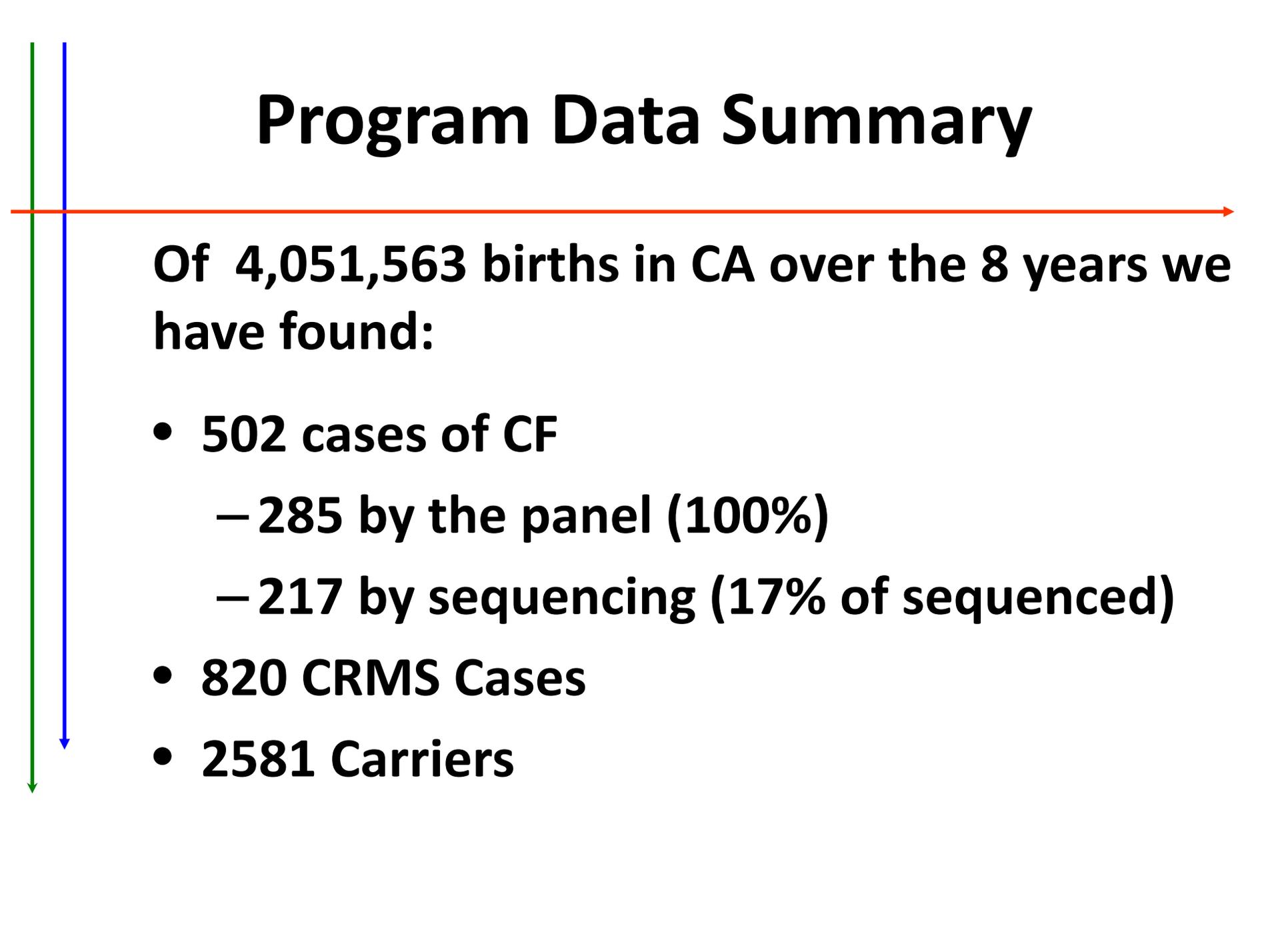


Screening Results/Data



¹ ≥ 62 ng/mL before 12/19/2012 and ≥ 67ng/mL since then.
² Stopped referring a panel mutation and only a (TG)11-5T variant since 6/2011.
³ Began parent testing since 7/2010.
⁴ Stopped referring delF508 and I1027T variants only since 8/2012.
⁵ Genetic counseling only referral started on 5/19/2014 for screening positives with one panel mutation and one non-CF-causing mutation.
⁶ Stopped testing benign 1525-42G>A variant since 7/2015.

Program Data Summary



Of 4,051,563 births in CA over the 8 years we have found:

- **502 cases of CF**
 - **285 by the panel (100%)**
 - **217 by sequencing (17% of sequenced)**
- **820 CRMS Cases**
- **2581 Carriers**

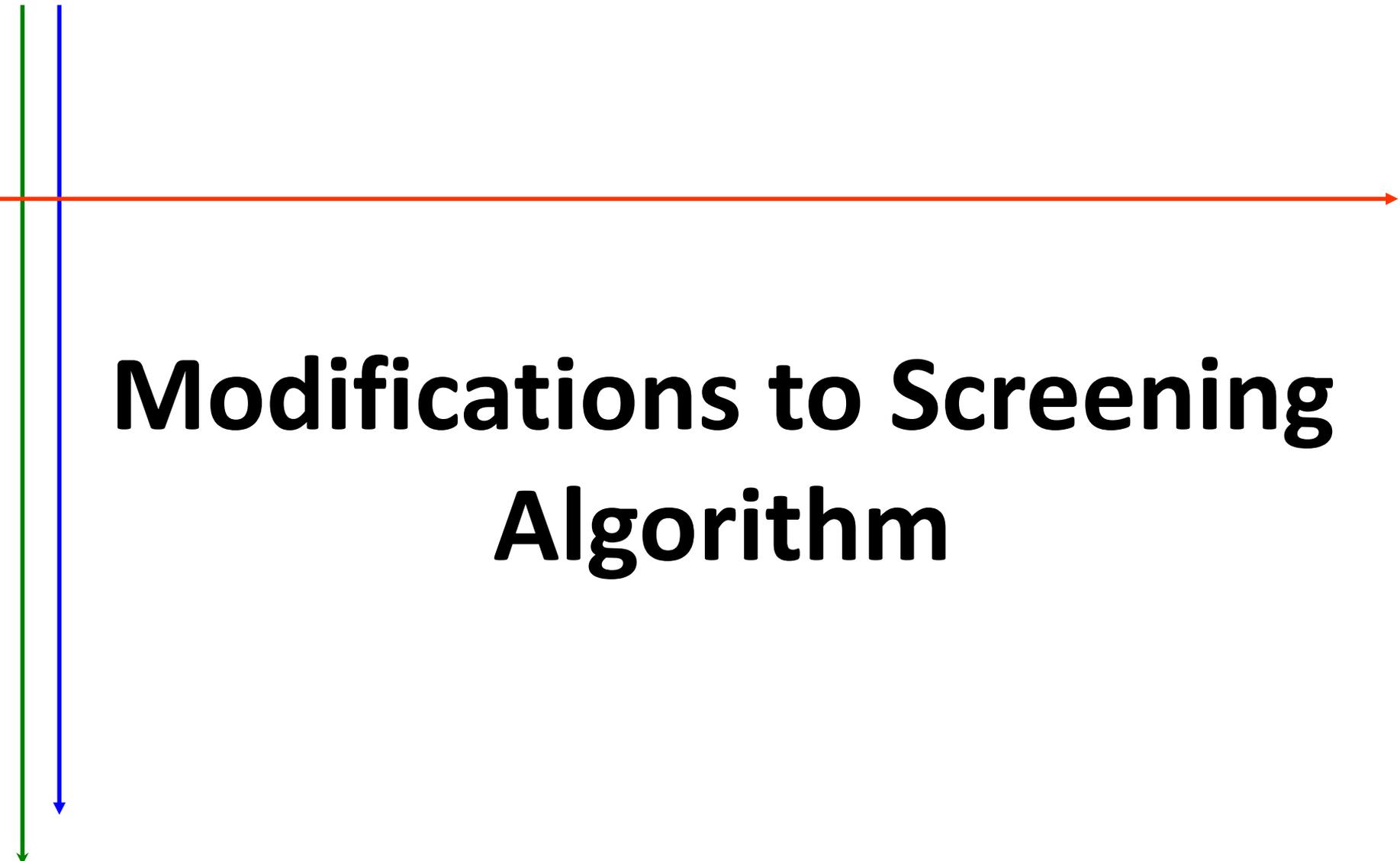
Program Data Summary



- **368 unique mutations/variants were found in newborns with positive DNA sequencing results, including 38 panel mutations.**
 - **200 mutations/variants were seen only once and 111 were novel.**
 - **Of the 111 newborns with novel mutations detected, 23 (21%) were diagnosed with CF**
 - **Of cases diagnosed with CF by DNA sequencing, only about half have an initial positive sweat test.**
 - **The most common mutations associated with this 'progression' from CRMS to CF were IVS8 (TG)13-5T, R117H-7T and D1152H**
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Estimated CF Prevalence by Race/Ethnicity

Client Race/Ethnicity	Live births screened	Screen positive	Diagnosed CF	Missed CF	Prevalence 1/X
Hispanic/Latino	1,664,800	510	153	14	9,969
Non-Hispanic White	1,035,354	632	231	9	4,314
Non-Hispanic Asian	383,058	23	4	3	54,723
Non-Hispanic Black	211,199	97	18	1	11,116
Other /Multiple	757,152	278	96	12	7,011
Total	4,051,563	1,540	502	39	7,489

A decorative graphic consisting of three lines and arrows. A vertical green line and a vertical blue line are on the left side. A horizontal red arrow points to the right, crossing both vertical lines. The blue line has a downward-pointing arrowhead at the bottom, and the green line also has a downward-pointing arrowhead at the bottom.

Modifications to Screening Algorithm



IVS8 Poly 5T/TG

- **At the start of the program we initially called out all IVS8 Poly 5T with an 11, 12 or 13 TG tract**
- **After approximately 3 years we had a large number of 11TG-5T (over 100) and follow-up data indicated that they nearly all had negative sweat tests and no symptoms.**
- **Additional literature was published that confirmed these findings and reported the primary possible concern is congenital bilateral absence of the vas deferens (CBAVD) .**
- **On June 1, 2011 we discontinued calling 11TG-5T as positive. They are now considered 'carriers' but there is a small chance of CBAVD in males with 11TG-5T.**

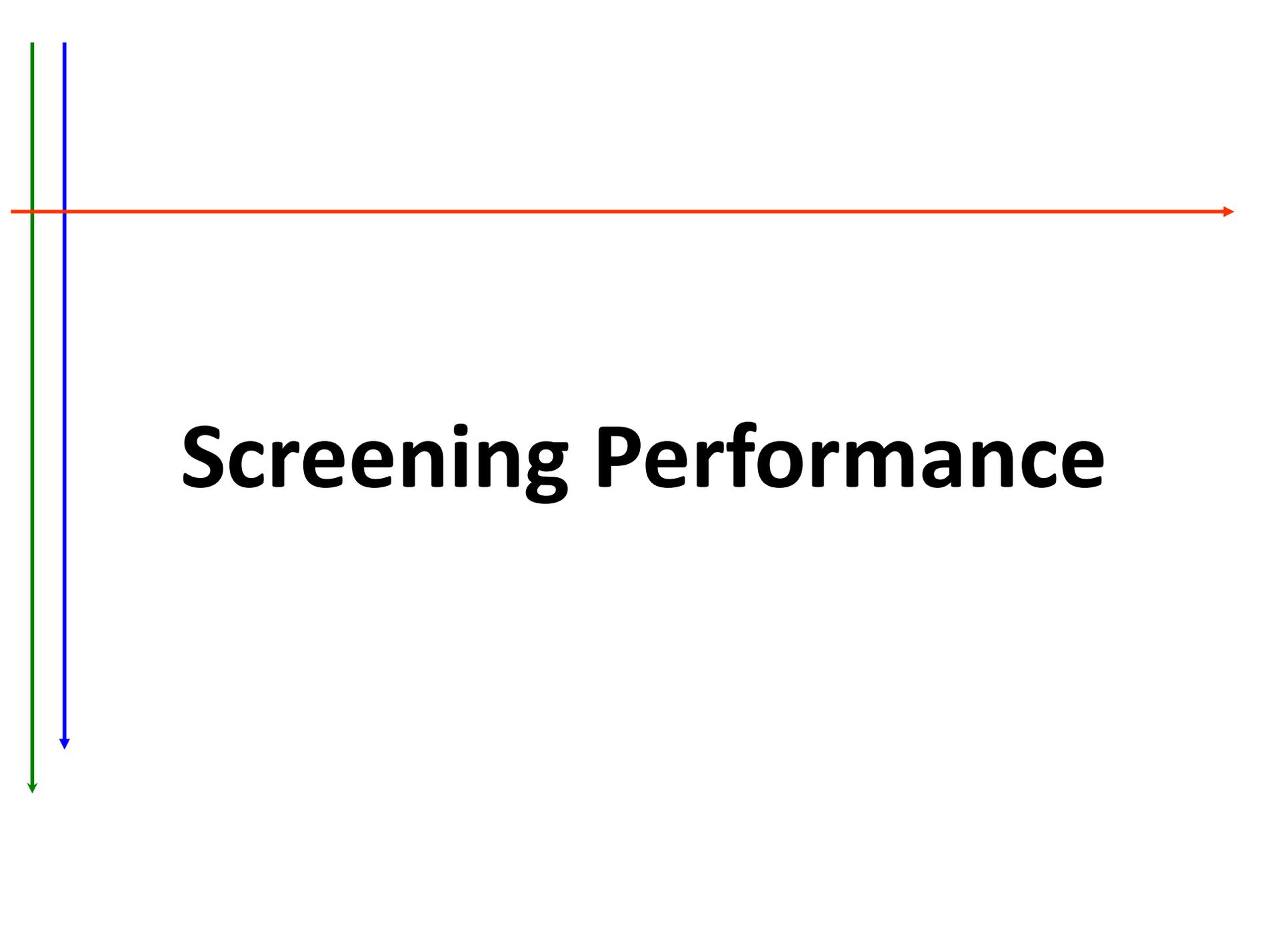


CFTR2 'Non-CF Causing Mutations'

- Based on John Hopkins-based CFTR2, there is a group of mutations called out by the California program that CFTR2 describes as 'non CF causing'.
- The mutations that CFTR2 updated are: R668C, G576A, G576A + R668C, L997F, R31C, R1162L, V754M, S1235R.
- On May 2014: continue to refer these children to the CF centers as CF screen positive, but recommend genetic counseling as the minimum follow-up.

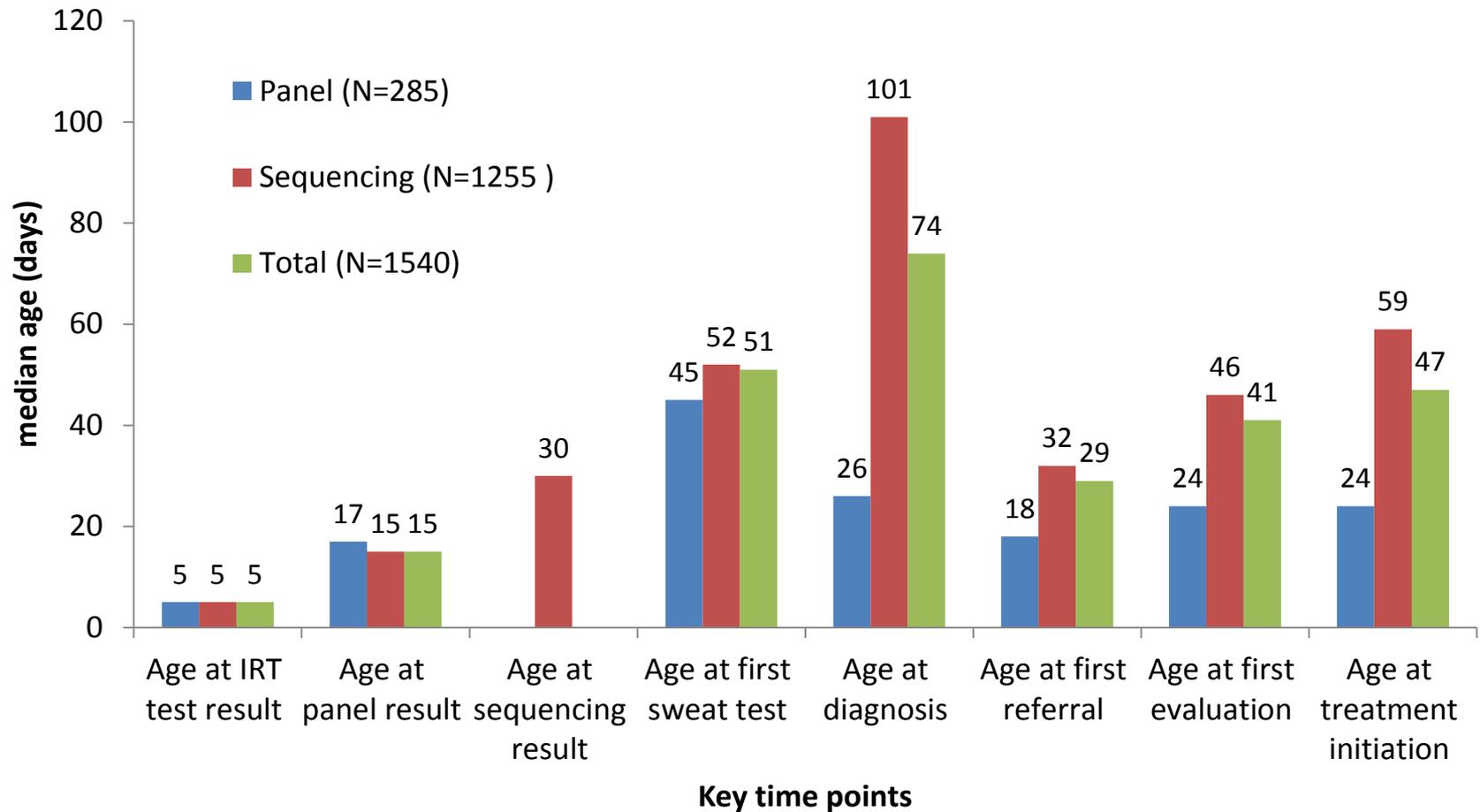
1525-42G>A

- In Spring 2015 we stopped reporting out 1525-42G>A as a mutation through sequencing because newborns/infants with this mutation have had negative sweat tests and done well.
- This mutation is very common in Hispanics and is now classified as a benign polymorphism.
 - was detected in 4.3% of Hispanics in a study by Shrijver et al 2015.
 - Consistent with our findings of a frequency of 1.88% in the CA population as a whole and 4.94% in the Hispanic population.



Screening Performance

Median Age at Key Screening Points for Screen Positive Cases: July 16, 2007–June 30, 2015





Screening Performance - Detection

- The ratio of screen positives to cases detected is **3.1 to 1**.
(1,540 screen positives / 502 cases detected)
- Case detection rate = **92.8%**
 - 502 cases detected by screening / 541 total CF cases
- Missed cases: **39** CF cases with negative screening results were reported
 - 19 by low IRT
 - 13 by negative panel
 - 7 had negative sequencing



Lessons Learned

- Including sequencing increases the time for result reporting.
 - DNA Testing leads to a group who are found to have at least two CFTR mutations or variations but display no symptoms. In California we call this group CRMS.
 - Even with sequencing, there are gross deletions or duplications that are not picked up as well as possible lab errors.
 - It is very important that physicians know to make referrals if there are signs and symptoms consistent with CF – even with a negative screen.
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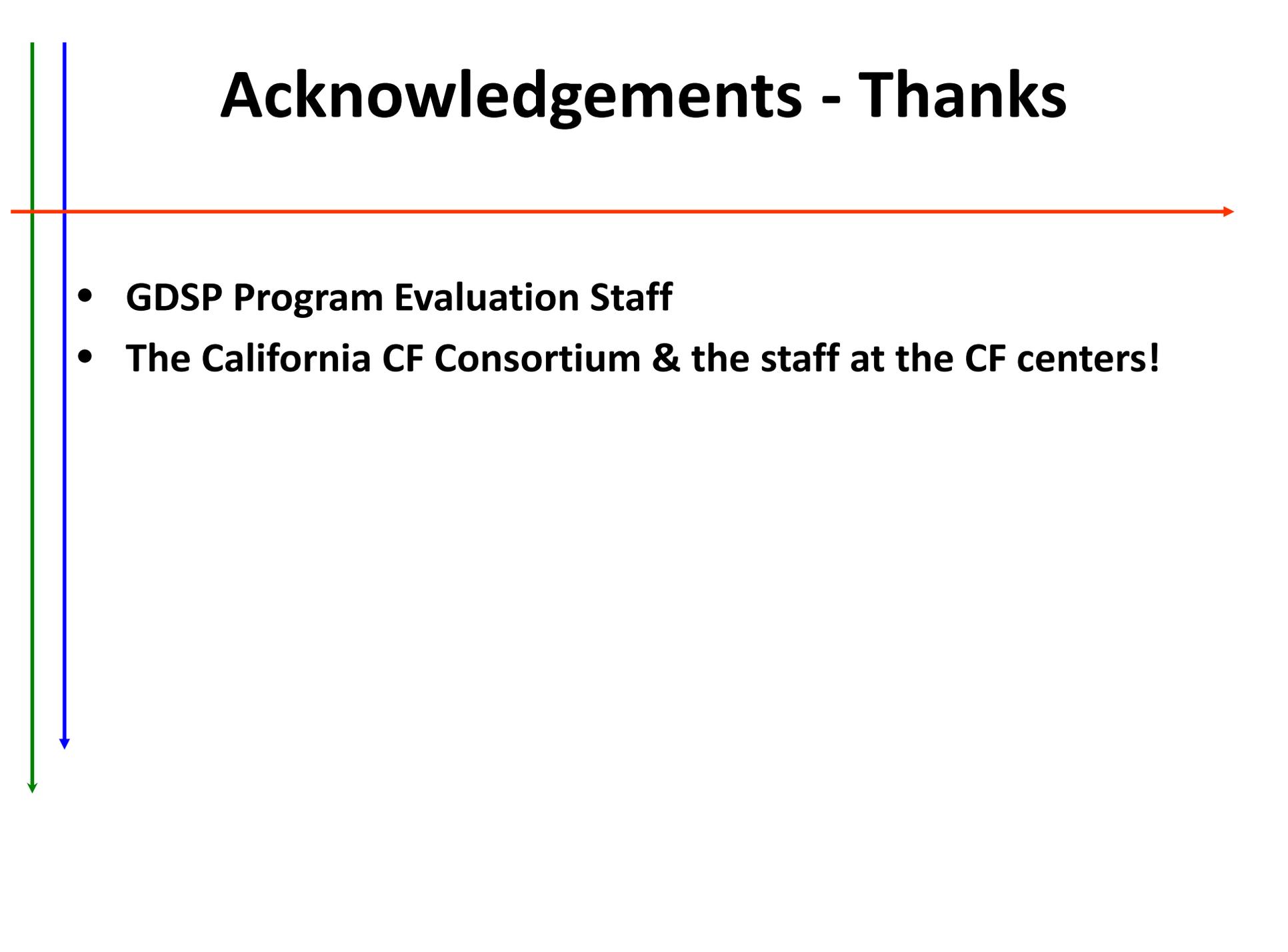


In Summary



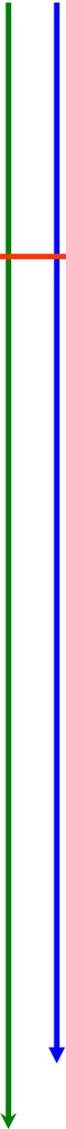
- Including sequencing greatly reduces the false positive rate.
- Sequencing provides more information for the medical team for those who are referred to a CF center.
- We have evidence that a single initial sweat chloride test may not be the best diagnostic ‘gold standard’
 - 43% of diagnosed cases by sequencing did not have an initial positive sweat test (>60 mmol/L).

Acknowledgements - Thanks



- **GDSP Program Evaluation Staff**
- **The California CF Consortium & the staff at the CF centers!**

Questions



CA CF 40 Mutation Panel

#	Mutation	#	Mutation
1	1288insTA	21*	delI507
2*	1717-1G>A	22	G330X
3	1812-1G>A	23*	G542X
4	2055del9>A	24*	G551D
5	2105-2117del13insAGAAA	25*	G85E
6	2307insA	26	H199Y
7*	3120+1G>A	27*	N1303K
8	3272-26A>G	28	P205S
9	3791delC	29	Q98R
10*	3849+10kbC>T	30	R1066C
11	3876delA	31*	R1162X
12	406-1G>A	32*	R334W
13*	621+1G>T	33*	R553X
14	663delT	34	R75X
15*	711+1G>T	35	S492F
16	935delA	36	S549N
17	A559T	37	W1089X
18	CFTRdele2,3(21kb)	38	W1204X (3743G>A)
19	delF311	39	W1204X (3744G>A)
20*	delF508	40*	W1282X

* Mutation included on ACMG 23 Panel