

Figure 3: Multiplexing Capabilities of the MiSeqDx Cystic Fibrosis 139-Variant Assay. A highly multiplexed method simultaneously sequences up to 48 samples in a single sequencing run.

Widely Adopted NGS Platform

Illumina sequencing by synthesis (SBS) technology is widely adopted in the sequencing community. Through massively parallel sequencing using a proprietary reversible terminator-based method, SBS enables detection of single bases as they are incorporated into growing DNA strands. A fluorescently labeled terminator is imaged as each dNTPs (dATP, dCTP, dGTP, or dTTP) are added and then cleaved to allow incorporation of the next base. Because all four reversible terminator-bound dNTPs are present during each sequencing cycle, natural competition minimizes incorporation bias. The result is base-by-base sequencing for highly accurate data even in difficult regions, such as homopolymers.

Easy Results Interpretation

Results from the MiSeqDx Cystic Fibrosis 139-Variant Assay are presented in an easy-to-read fashion that a board-certified molecular geneticist or equivalent can readily interpret. The report includes assay name, sample ID, dbSNP ID, and the call rate for each sample (Figure 4). Call rates must be $\geq 99\%$ to be considered valid.

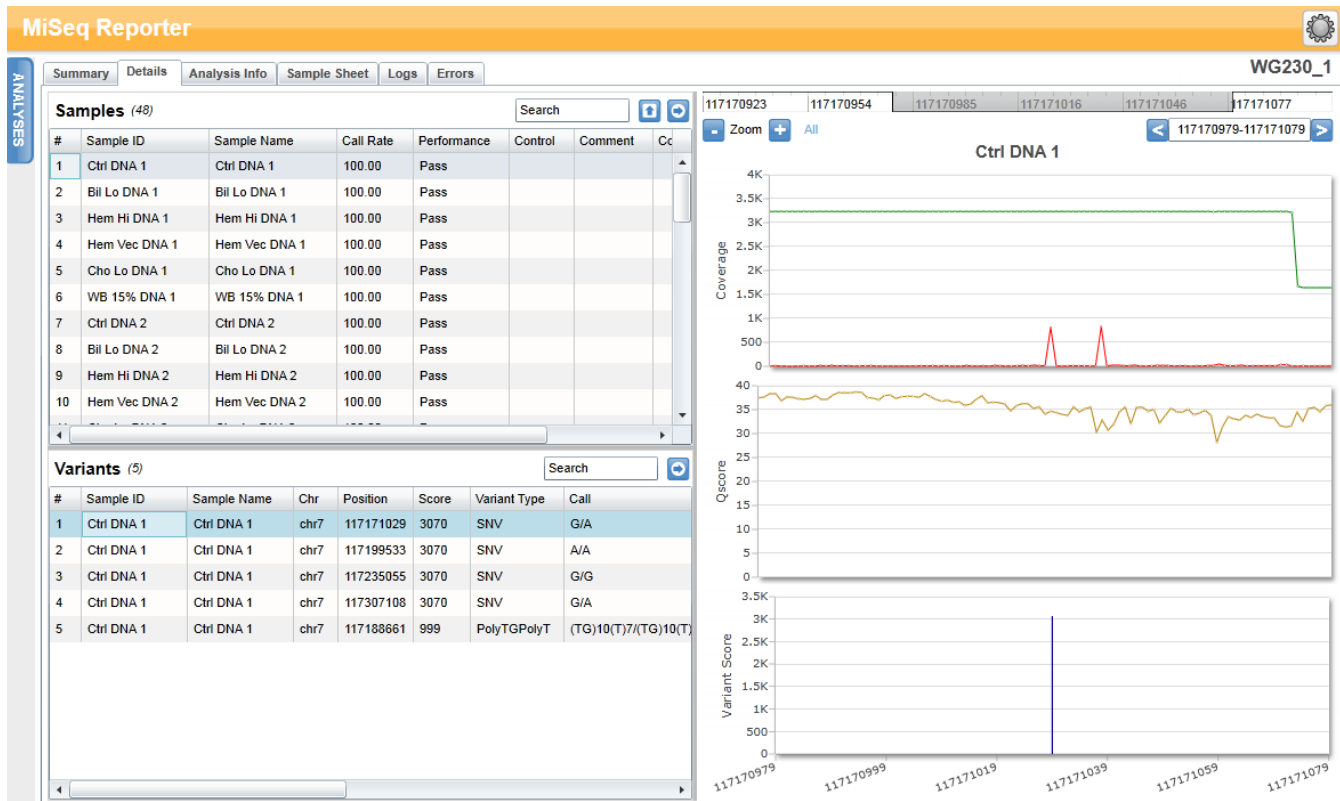


Figure 4: Easy Visualization Using the MiSeq Reporter Software.

Table 3: The MiSeqDx Cystic Fibrosis 139-Variant Assay Offers the Largest Panel of Clinically Relevant *CFTR* Variants

General Population ^a				
M1V	1213delT	1898+3A>G	2347delG	M1101K
CFTRdele2,3	1248+1G>A	1717-8G>A	R764X	E1104X
Q39X	1259insA	1717-1G>A	2585delT	3659delC
G85E	W401X(c.1202G>A)	G542X	2622+1G>A	3849+10kbC>T
E92X	W401X(c.1203G>A)	S549R(c.1645A>C)	E831X	W1282X
Q98X	1341+1G>A	S549R(c.1647T>G)	R851X	Q1313X
R117H	1461ins4	S549N	2789+5G>A	4209TGTT>AA
621+1G>T	A455E	G551D	L927P	CFTRdele22,23
711+3A>G	L467P	R553X	3007delG	4382delA
R334W	S489X	R560K	G970R	<i>I506V</i>
S341P	I507del	R709X	3120G>A	<i>I507V</i>
R347H	F508del	2184delA	3120+1G>A	<i>F508C</i>
R347P	Q525X ^b	L732X	3121-1G>A	
Regional European ^a				
E60X	G178R	1525-1G>A	2184insA	W1089X
P67L	711+1G>T	Q493X	E822X	Y1092X(C>A)
R75X	712-1G>T	1677delTA	W846X	Y1092X(C>G)
394delTT	Q220X	V520F	2711delT	R1158X
405+1G>A	852del22	Q552X	Q890X	S1196X
E92K	1078delT	R560T	S945L	G1244E
457TAT>G	I336K	E585X	3272-26A>G	S1251N
D110H	T338I	1898+1G>A	L1065P	3905insT
R117C	1154insTC	2143delT	R1066C	4005+1G>A
Y122X	R352Q	K710X	R1066H	N1303K
574delA	<i>PolyTG/PolyT</i>	2183AA>G	L1077P	4016insT
Middle Eastern ^a	US Hispanic ^a	Hispanic ^a	African American ^a	Native American ^a
S466X(C>A)	406-1G>A	663delT	G330X	R1162X
S466X(C>G)	711+5G>A	H199Y	A559T	
1548delG ^b	1812-1G>A	P205S	2307insA	
	S492F	L206W	3791delC	
	W1204X (c.3611G>A)	1811+1.6kb A>G		
	W1204X (c.3612G>A)	3876delA		

Listed within each demographic by genomic coordinate order. **Bold** indicates that these mutations are part of the ACMG-23 list recommended for CF screening. *Italics* indicates that these mutations are conditionally reported.

^a Demographic data source: Castellani C, Cuppens H, Macek Jr M, Cassiman JJ, Kerem E, et al. (2008) Consensus on the use and interpretation of cystic fibrosis mutation analysis in clinical practice. *J Cyst Fibros* 7: 179-196.

^b Mutation is classified in the CFTR2 database (www.cfr2.org) as a CF-causing variant while Sosnay et al. (Sosnay PR, Siklosi KR, Van Goor F, Kaniecki K, Yu H, et al. (2013) Defining the disease liability of variants in the cystic fibrosis transmembrane conductance regulator gene. *Nat Genet.* 45: 1160-1167.) classifies the variant as a mutation of unknown significance. The database classification is more current and reflects the completed functional testing, which was not available at the time of the Sosnay publication.

