

Cardiomyopathy and Arrhythmia Panels

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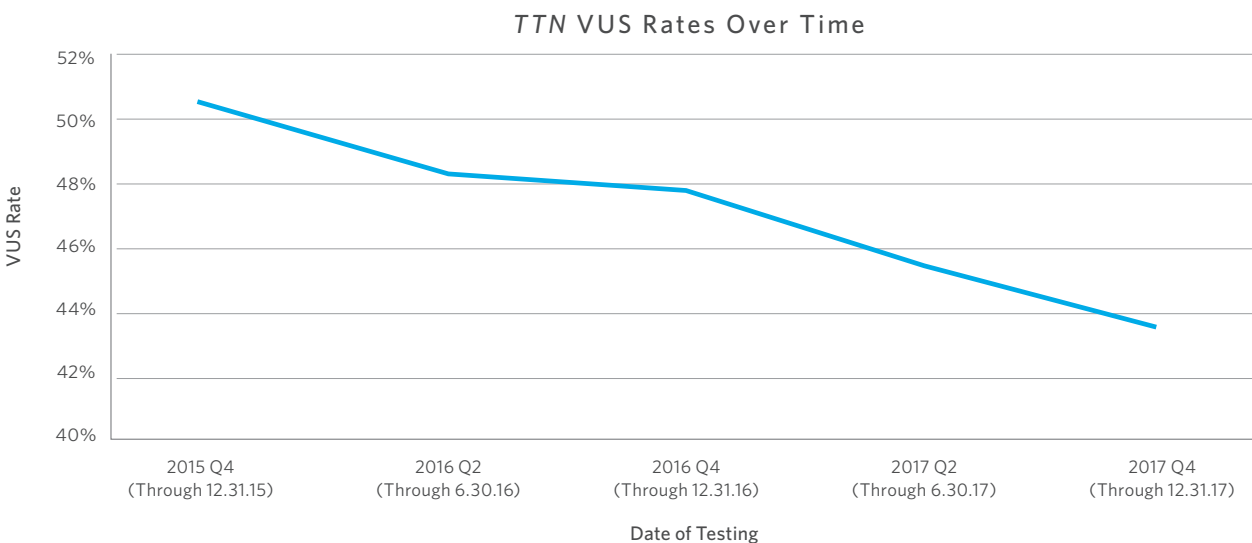
With more patients undergoing cardiovascular genetic testing, the genetic causes of inherited cardiomyopathies and arrhythmias are becoming clearer. Many variants of unknown significance (VUS) are being resolved, rendering them clinically useful and allowing for family-based decision making.

We retrospectively analyzed results from 1,421 cardiomyopathy and arrhythmia panels performed at our laboratory since January 2015. Of these panels, 354 returned pathogenic or likely pathogenic results, giving a total diagnostic yield of 25%. From late 2015 to late 2017, the overall VUS rate for cardiomyopathies and arrhythmias decreased from 38% to 35%. As more patients are tested according to current clinical guidelines^{1,2}, the evidence will increase, and the interpretation of results will continue to improve.

OVERALL RESULT CLASSIFICATION			
Test Name	Positive	VUS	Negative
CardioNext (including TTN)	16%	69%	15%
CMNext (including TTN)	29%	57%	14%
HCMNext	31%	27%	42%
DCMNext	30%	40%	30%
RhythmNext	24%	34%	42%
CPVTNext	31%	38%	31%
ARVCNext	21%	18%	61%

Clarifying *TTN* Results

Defects in *TTN* cause several forms of cardiomyopathy, with dilated cardiomyopathy (DCM) being the most prominent^{3,4}. However, due to the size of the gene and the many isoforms of *TTN*, genetic analysis is complicated, with laboratory expertise being critical for interpretation. With accumulating laboratory data and experience at Ambry, our VUS rate for *TTN* has decreased significantly, as shown in the figure below. Overall, including *TTN* on our CMNext panel has improved the detection rate by 21%.



1. Ackerman MJ, Priori SG, Willems S *et al.* Heart Rhythm Society/European Heart Rhythm Association expert consensus statement on the state of genetic testing for the channelopathies and cardiomyopathies. *Heart Rhythm*. 2011 Aug;8(8):1308-39.
2. Hershberger RD, Givertz M, Ho CY *et al.* Genetic Evaluation of Cardiomyopathy – a Heart Failure Society of America Practice Guideline. *Journal of Cardiac Failure*. 2018.
3. Roberts AM, Ware JS, Herman DS, *et al.* Integrated allelic, transcriptional, and phenomic dissection of the cardiac effects of titin truncations in health and disease. *Science translational medicine*. 2015;7(270):270ra6.
4. Norton N, Li D, Rampersaud E, *et al.* Exome Sequencing and Genome-Wide Linkage Analysis in 17 Families Illustrates the Complex Contribution of *TTN* Truncating Variants to Dilated Cardiomyopathy. *Circulation Cardiovascular genetics*. 2013;6(2)