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There's nothing more personal than genomics.

Identify inherited cardiac conditions with one comprehensive research tool.

TruSight® Cardio is a comprehensive, cost-effective solution for identifying causal variants associated with inherited cardiac conditions (ICCs). Covering 174 genes, this assay uses a single next-generation sequencing (NGS) panel to analyze variants associated with 17 ICCs, including variants linked to most cardiomyopathies and arrhythmias. The single workflow reduces the cost of managing multiple assays.

Sudden Cardiac Arrest (SCA) is one of the leading causes of non-traumatic mortality in the US[1,2]

25%

25% of SCA is related to **inherited cardiac conditions (ICCs)**[1,2]

50%

In people **under 35 years of age, 50%** of SCA is related to ICCs[1,2]

100,000

In the US alone, **roughly 100,000 people per year die** of SCA–approximately the same amount of people who die from Alzheimer's disease[1,2]

70%

Diagnostic yield of genetic testing for causal variants in **genes related to ICCs is as high as 70%**[3]

1. Zipes DP, Wellens HJ. Sudden cardiac death. Circulation. 1998;98(21):2334-2351.
2. Deo R, Albert CM. Epidemiology and genetics of sudden cardiac death. Circulation. 2012;125(4):620-637.
3. Ackerman MJ, Priori SG, Willems S, Berul C, Brugada R, et al. HRS/EHRA expert consensus statement on the state of genetic testing for the channelopathies and cardiomyopathies. Europace. 2001;13(8):1077-1109.

Streamline and manage your workflow with a single solution.

TruSight® Cardio is a comprehensive and affordable targeted sequencing panel for profiling ICCs.

174 Genes

99% > 20x coverage

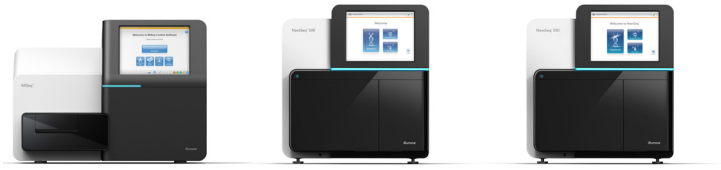
250× Average coverage

Get enhanced targeted coverage with consistent uniformity.

Obtain outstanding accuracy with an average mean coverage of 300x, and over 99% of coding regions covered at a depth of 20x or greater (Table 1).

TruSight® Cardio delivers 99.9% accuracy or greater at a depth of 20x or greater for core genes associated with ICCs (Table 2).

Work across your existing Illumina sequencing systems.



MiSeq® NextSeq® 500 NextSeq® 550

To learn more about the comprehensive solution for researching inherited cardiac conditions, contact your Illumina Sales representative or visit www.Illumina.com/trusightcardio

Table 1: Coverage Summary

Sample	Mean Region Coverage Depth	Target Coverage at 20×
1	370.4×	99.9%
2	327.6×	99.9%
3	348.2×	99.9%
4	369.5×	99.9%
5	295.1×	99.9%
6	290.8×	99.8%
7	317.2×	99.8%
8	221.7×	99.7%
9	275.7×	99.7%
10	241.1×	99.5%
11	275.0×	99.7%
12	272.6×	99.7%

Table 2: Performance

Gene	% bases covered at ≥20×	% targets covered > 20× avg. min coverage
ACTA2	98.1	100.0
CACNA2D1	100.0	100.0
DSC2	100.0	100.0
DSG2	100.0	100.0
DSP	100.0	100.0
ELN	100.0	100.0
FBN1	99.5	100.0
GJA5	100.0	100.0
KCNE1	100.0	100.0
KCNE2	100.0	100.0
KCNH2	98.2	100.0
KCNJ2	100.0	100.0
KCNQ1	92.6	100.0
KRAS	100.0	100.0
LDLR	100.0	100.0
LMNA	99.7	100.0
MYBPC3	99.6	100.0
MYH6	100.0	100.0
MYH7	100.0	100.0
NOTCH1	98.8	100.0
PKP2	100.0	100.0
PTPN11	100.0	100.0
RAF1	100.0	100.0
RYR2	100.0	100.0
SCN5A	99.3	100.0
SOS1	100.0	100.0
TGFBR1	93.9	100.0
TGFBR2	100.0	100.0
TNNI3	100.0	100.0
TNNT2	99.3	100.0
TTN	99.9	99.9

Twelve samples were sequenced using the TruSight Cardio Sequencing Kit run on the MiSeq System. PCR duplicates and highest and lowest performers were removed from analysis. Performance was calculated from average counts per base (bases covered) and counts per regions (regions covered) across the remaining 10 samples. Full Illumina data available upon request.)

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