SeqCap EZ Cardiology Panels
Analyze genetic mutations associated with hereditary cardiac disorders

SeqCap EZ Cardiology Panels are optimized hybridization-based panels for NGS that target genes associated with hereditary cardiac disorders. Each panel was developed using guidance from published literature, scientific collaborators, and Roche Sequencing Solutions’ scientific experts.

- **Greater than 99.0% of bases covered** at 20X and 50X when each panel is sequenced to an average depth of 250X
- **Excellent coverage uniformity** for all 3 panels (Fold 80 base penalty <1.5)
- **The HyperCap Workflow with SeqCap EZ Cardiology Panels** streamlines the production of target-enriched libraries and ensures integrated support and one-source purchasing from a single trusted vendor

### Three specialized, cardiology-focused panels

<table>
<thead>
<tr>
<th>SeqCap Design Share Cardiology Panels</th>
<th>Size</th>
<th># of genes covered</th>
</tr>
</thead>
<tbody>
<tr>
<td>SeqCap EZ Cardiomyopathy Panel</td>
<td>372 kb</td>
<td>76</td>
</tr>
<tr>
<td>SeqCap EZ Channelopathy and Arrhythmias Panel</td>
<td>203 kb</td>
<td>54</td>
</tr>
<tr>
<td>SeqCap EZ Sudden Cardiac Death Panel</td>
<td>610 kb</td>
<td>140</td>
</tr>
</tbody>
</table>
**SeqCap EZ Cardiomyopathy Panel**

- Achieve comprehensive, uniform coverage of 76 genes from the CCDS and ClinVar databases
- Attain 100% coverage at 20X and >99.9% coverage at 50X with an average sequencing depth of 250X

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**Figure 1. Performance metrics for the SeqCap EZ Cardiomyopathy Panel.** Target-enriched libraries were prepared using HapMap gDNA as input into the HyperCap Workflow v2.0 using the KAPA HyperPrep Library Preparation Kit. Different DNA samples were used to generate 8 individual libraries which were then 8-plexed prior to capture with the SeqCap EZ Cardiomyopathy Panel using 125 ng of each library. Captures were performed in duplicate; bars represent average values within each capture. Sequencing was performed on an Illumina® MiSeq® instrument (MiSeq Reagent Kit v2; 2 x 101 bp). For analysis, reads were subsampled to an average coverage depth of 250X.

**A) Capture efficiency.** Percent of mapped non-duplicate reads on-target is the percent of mapped, de-duplicated reads overlapping the target region by at least 1 bp, with no padding or buffer. The percent of bases in padded targets is the percent of bases that fall within 250 bp of the primary target regions of the panel.

**B) Uniformity.** Fold 80 base penalty is a measure of sequencing uniformity; lower numbers are better, with the best theoretical value equal to 1. Zero coverage regions are excluded.

**C) Variant coverage.** Bars indicate % coverage indicated depths (20X or 50X).

**D) Coverage depth vs sequencing reads.**

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**SeqCap EZ Cardiomyopathy Panel**

Panel size: 76 genes; 372 kb

This research panel covers genes associated with the following disorders: Hypertrophic Cardiomyopathy, Arrhythmogenic Right Ventricular Cardiomyopathy, Dilated Cardiomyopathy, Left Ventricular Non-Compaction Cardiomyopathy, and Restrictive Cardiomyopathy.
**SeqCap EZ Channelopathy and Arrhythmias Panel**

- Achieve comprehensive, uniform coverage of 54 genes from the CCDS and ClinVar databases
- Attain 100% coverage at 20X and 50X with an average sequencing depth of 250X

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**A) Capture efficiency.** Percent of mapped non-duplicate reads on-target is the percent of mapped, de-duplicated reads overlapping the target region by at least 1 bp, with no padding or buffer. The percent of bases in padded targets is the percent of bases that fall within 250 bp of the primary target regions of the panel.

**B) Uniformity.** Fold 80 base penalty is a measure of sequencing uniformity; lower numbers are better, with the best theoretical value equal to 1. Zero coverage regions are excluded.

**C) Variant coverage.** Bars indicate % coverage indicated depths (20X or 50X).

**D) Coverage depth vs sequencing reads.**

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**SeqCap EZ Channelopathy and Arrhythmias Panel**

<table>
<thead>
<tr>
<th>Panel size</th>
<th>54 genes; 203 kb</th>
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<tbody>
<tr>
<td>This research panel covers genes associated with the following disorders:</td>
<td>Long QT 1-7, Cathexolaminergic Polymorphic Ventricular Tachycardia, Idiopathic VT (regional), Brugada Syndrome, Arrhythmogenic Right Ventricular Cardiomyopathy, Sick Sinus Syndrome/Atrial Standstill, Short QT Syndrome, and Familial Atrial Fibrillation</td>
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</tbody>
</table>
**SeqCap EZ Sudden Cardiac Death Panel**

- Achieve comprehensive, uniform coverage of 140 genes from the CCDS and ClinVar databases
- Attain 100% coverage at 20X and >99.9% coverage at 50X with an average sequencing depth of 250X

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**Figure 3. Performance metrics for the SeqCap EZ Sudden Cardiac Death Panel.** Target-enriched libraries were prepared using HapMap gDNA as input into the HyperCap Workflow v2.0 using the KAPA HyperPrep Library Preparation Kit. Different DNA samples were used to generate 8 individual libraries which were then 8-plexed prior to capture with the SeqCap EZ Sudden Cardiac Death Panel using 125 ng of each library. Captures were performed in duplicate; bars represent average values within each capture. Sequencing was performed on an Illumina® MiSeq® instrument (MiSeq Reagent Kit v2; 2 x 101 bp). For analysis, reads were subsampled to an average coverage depth of 250X.

A) Capture efficiency. Percent of mapped non-duplicate reads on-target is the percent of mapped, de-duplicated reads overlapping the target region by at least 1 bp, with no padding or buffer. The percent of bases in padded targets is the percent of bases that fall within 250 bp of the primary target regions of the panel.

B) Uniformity. Fold 80 base penalty is a measure of sequencing uniformity; lower numbers are better, with the best theoretical value equal to 1. Zero coverage regions are excluded.

C) Variant coverage. Bars indicate % coverage indicated depths (20X or 50X).

D) Coverage depth vs sequencing reads.

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**SeqCap EZ Sudden Cardiac Death Panel**

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<td>This research panel covers genes associated with the following disorders:</td>
<td>All disorders covered by the Cardiomyopathy Panel and the Channelopathy and Arrhythmias Panel, plus other thoracic aortic aneurysms and dissections, Marfan's Syndrome, and Loeys-Dietz Syndrome</td>
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Data on file.
For Research Use Only. Not for use in diagnostic procedures.
SeqCap EZ Design Share: Cardiology Panels

SeqCap EZ Cardiology Panels are part of Roche Sequencing Solutions’ Design Share Portfolio. Design Share makes it easy to access pre-designed NGS panels that are developed by Roche Sequencing Solutions or in collaboration with researchers around the world. Review the full portfolio at sequencing.roche.com/designshare.

Learn about HyperCap Workflow—an integrated, <2-day sample preparation workflow for target-enriched NGS that combines KAPA library preparation and SeqCap target enrichment probes—at sequencing.roche.com/hypercap.

Ordering Information

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Request an evaluation:

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