**SeqCap EZ Neurology Panels**
Expert-driven panels for variant detection in neurology research applications

SeqCap EZ Neurology Panels enable researchers to detect variants in genes that are most commonly associated with the research of Central Nervous System (CNS) disorders. Developed using guidance from publications, literature, and Roche Sequencing Solutions’ scientific experts, SeqCap EZ Neurology Panels are optimized for use with the HyperCap Workflow, which integrates KAPA library preparation and SeqCap EZ target enrichment products in a single streamlined workflow.

**Panels Description**
- **SeqCap EZ Epilepsy:** 530 Kb panel targeting 168 genes for epilepsy research
- **SeqCap EZ Movement Disorders:** 647 Kb panel targeting 209 genes for movement disorders research
- **SeqCap EZ Neurodegeneration:** 289 Kb panel targeting 98 genes for neurodegeneration research
- **SeqCap EZ Neurodevelopment:** 663 Kb panel targeting 181 genes for neurodevelopment research
- **SeqCap EZ Neuromuscular:** 669 Kb panel targeting 144 genes for neuromuscular disorders research
- **SeqCap EZ Neuropathy:** 309 Kb panel targeting 93 genes for neuropathy research

**Features and Benefits**
- **Panel breadth:** Six research-focused neurology panels provide flexibility to match the right content to your research goal
- **Sequencing efficiency:** Compact panels that are carefully re-balanced and pre-optimized to deliver more uniform target coverage and allow increased result confidence for more samples per run
- **Expert-driven content:** Sequence what matters for each neurology research area by using panels that are designed by experts and allow comprehensive gene coverage and relevant variant detection
- **Single vendor service and support:** Compatible with the HyperCap Workflow, convenient one-stop shop for ordering, service, and support for a complete sample prep solution

For Research Use Only. Not for use in diagnostic procedures.
Confident variant detection, increased sequencing efficiency

**SeqCap EZ Epilepsy Panel**

- Comprehensive coverage of 168 genes from CCDS and ClinVar databases
- Achieve uniform sequencing depth with a low (1.40) Fold 80 base penalty*
- 98.8% coverage at 20X and 97.6% at 50X*

---

**SeqCap EZ Epilepsy Panel**

<table>
<thead>
<tr>
<th>Panel Size</th>
<th>168 genes; 530 kb (capture target)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Product Type</td>
<td>SeqCap EZ Share Prime Choice</td>
</tr>
<tr>
<td>Internal Reference #</td>
<td>4000035570</td>
</tr>
<tr>
<td>Design Name</td>
<td>180116_HG38_Epilepsy_EZ_HX3</td>
</tr>
</tbody>
</table>

*Average across eight HapMap samples

---

Figure 1. Single capture, 8-plexed per SeqCap EZ Epilepsy Panel. Eight different HapMap samples were prepared using KAPA HyperPrep Library Preparation Kit following the Hypercap Workflow User’s Guide v2.1. Captures were 8-plexed (using 125 ng of each sample library). Each capture was sequenced using an Illumina® MiSeq® Instrument (MiSeq Reagent Kit v2; 2 x 100 bp). Data was subsampled to an average coverage depth of 269X.
**SeqCap EZ Movement Disorders Panel**

- Comprehensive coverage of 209 genes from CCDS and ClinVar databases
- Achieve uniform sequencing depth with a low (1.56) Fold 80 base penalty*
- 99.5% coverage at 20X and 98.4% at 50X*

---

**Figure 2. Single capture, 8-plexed per SeqCap EZ Movement Disorders Panel.**

Eight different HapMap samples were prepared using KAPA HyperPrep Library Preparation Kit following the Hypercap Workflow User’s Guide v2.1. Captures were 8-plexed (using 125 ng of each sample library). Each capture was sequenced using an Illumina® MiSeq® Instrument (MiSeq Reagent Kit v2; 2 x 100 bp). Data was subsampled to an average coverage depth of 259X.

---

**Mean coverage vs. reads**

---

**SeqCap EZ Movement Disorders Panel**

| **Panel Size** | 209 genes; 647 kb (capture target) |
| **Product Type** | SeqCap EZ Share Prime Choice |
| **Internal Reference #** | 4000035580 |
| **Design Name** | 180116_HG38_MoveDis_EZ_HX3 |

*Average across eight HapMap samples*
**SeqCap EZ Neurodegeneration Panel**

- Comprehensive coverage of 98 genes from CCDS and ClinVar databases
- Achieve uniform sequencing depth with a low (1.49) Fold 80 base penalty*
- 99.7% coverage at 20X and 98.9% at 50X*

![Graphs showing sequencing efficiency and uniformity, percent of bases covered at 20X and 50X, and mean coverage vs. reads.](image)

*Average across eight HapMap samples*
SeqCap EZ Neurodevelopment Panel

- Comprehensive coverage of 181 genes from CCDS and ClinVar databases
- Achieve uniform sequencing depth with a low (1.54) Fold 80 base penalty*
- 99.0% coverage at 20X and 97.8% at 50X*

**Figure 4. Single capture, 8-plexed per SeqCap EZ Neurodevelopment Panel.**

Eight different HapMap samples were prepared using KAPA HyperPrep Library Preparation Kit following the Hypercap Workflow User’s Guide v2.1. Captures were 8-plexed (using 125 ng of each sample library). Each capture was sequenced using an Illumina® MiSeq® Instrument (MiSeq Reagent Kit v2; 2 x 100 bp). Data was subsampled to an average coverage depth of 264X.

**SeqCap EZ Neurodevelopment Panel**

<table>
<thead>
<tr>
<th>Panel Size</th>
</tr>
</thead>
<tbody>
<tr>
<td>181 genes; 663 kb (capture target)</td>
</tr>
<tr>
<td>Product Type</td>
</tr>
<tr>
<td>SeqCap EZ Share Prime Choice</td>
</tr>
<tr>
<td>Internal Reference #</td>
</tr>
<tr>
<td>4000035600</td>
</tr>
<tr>
<td>Design Name</td>
</tr>
<tr>
<td>180116_HG38_NeuDev_EZ_HX3</td>
</tr>
</tbody>
</table>

*Average across eight HapMap samples
**SeqCap EZ Neuromuscular Panel**

- Comprehensive coverage of 144 genes from CCDS and ClinVar databases
- Achieve uniform sequencing depth with a low (1.58) Fold 80 base penalty*
- 98.7% coverage at 20X and 97.8% at 50X*

---

**Figure 5. Single capture, 8-plexed per SeqCap EZ Neuromuscular Panel.**

Eight different HapMap samples were prepared using KAPA HyperPrep Library Preparation Kit following the Hypercap Workflow User’s Guide v2.1. Captures were 8-plexed (using 125 ng of each sample library). Each capture was sequenced using an Illumina® MiSeq® Instrument (MiSeq Reagent Kit v2; 2 x 100 bp). Data was subsampled to an average coverage depth of 258X.

---

**SeqCap EZ Neuromuscular Panel**

<table>
<thead>
<tr>
<th>Panel Size</th>
<th>144 genes; 669 kb (capture target)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Product Type</td>
<td>SeqCap EZ Share Prime Choice</td>
</tr>
<tr>
<td>Internal Reference</td>
<td>4000035610</td>
</tr>
<tr>
<td>Design Name</td>
<td>180116_HG38_NeuMusc_EZ_HX3</td>
</tr>
</tbody>
</table>

*Average across eight HapMap samples
**SeqCap EZ Neuropathy Panel**

- Comprehensive coverage of 93 genes from CCDS and ClinVar databases
- Achieve uniform sequencing depth with a low (1.40) Fold 80 base penalty*
- 99.2% coverage at 20X and 98.8% at 50X*

**Figure 6. Single capture, 8-plexed per SeqCap EZ Neuropathy Panel.**
Eight different HapMap samples were prepared using KAPA HyperPrep Library Preparation Kit following the Hypercap Workflow User’s Guide v2.1. Captures were 8-plexed (using 125 ng of each sample library). Each capture was sequenced using an Illumina® MiSeq® Instrument (MiSeq Reagent Kit v2; 2 x 100 bp). Data was subsampled to an average coverage depth of 273X.

**SeqCap EZ Neuropathy Panel**

| Panel Size | 93 genes; 309 kb (capture target) |
| Product Type | SeqCap EZ Share Prime Choice |
| Internal Reference # | 4000035620 |
| Design Name | 180116_HG38_NeuPath_EZ_HX3 |

*Average across eight HapMap samples*
Design Share Portfolio

SeqCap EZ Neurology Panels are now available as 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. Our newest panels include:

- SeqCap EZ Prime Exome: CCDS focused exome with a 37 Mb capture target, optimized for uniformity and sequencing efficiency
- SeqCap EZ Cardiology Panels: Three different cardiology research panels covering Cardiomyopathy, Channelopathy and Arrhythmias, and Sudden Cardiac Death

To access the full portfolio, design files and gene lists, please visit: sequencing.roche.com/designshare.

Contact us!
Please contact us for demo data.

Published by:
Roche Sequencing Solutions, Inc.
4300 Hacienda Drive
Pleasanton, CA 94588

sequencing.roche.com

Data on file.
For Research Use Only. Not for use in diagnostic procedures.
HYPERCAP KAPA and SEQCAP are trademarks of Roche. All other product names and trademarks are the property of their respective owners.
© 2018 Roche Sequencing Solutions, Inc. All rights reserved.