The SeqCap EZ Inherited Disease Panel is an optimized NGS hybridization-based assay that targets the exonic regions of over 4,100 medically relevant genes comprising 11.8 Mb of capture target. It delivers highly uniform sequencing coverage for genes classified as pathogenic from OMIM and content from scientific collaborators. This single panel comprehensively targets many commonly run NGS disease panels and PCR-based single-gene assays.

Features

- >98% of base pairs covered at a minimum of 20x depth with 18M reads
- Fast, easy and integrated 1.5 day workflow (HyperCap workflow v1.0)
- Enzymatic DNA fragmentation available

Benefits

- Single vendor support for library prep, target enrichment and associated reagents
- Increase lab efficiency and decrease sequencing costs with uniform panel coverage
- Evaluate specific hereditary disease states from a single panel by creating subsets of gene panels from the same design during data analysis.

For Research Use Only. Not for use in diagnostic procedures.
Meets the needs for efficient sequencing requirements

- At 11.8 Mb of capture design, the optimized SeqCap EZ Inherited Disease Panel was developed by our scientific collaborators and shown to have high performance
- At DNA input amounts as low as 100 ng, the panel delivers greater than 98% coverage of the target bases at a depth of ≥ 20x with 8M 2x100 reads. The efficient sequencing performance makes the SeqCap EZ Inherited Disease Panel an ideal fit for benchtop and high-throughput sequencers alike

Design Share Portfolio

The SeqCap EZ Inherited Disease Panel (Design Name: 150803_HG38_IDP2_REZ_HX3) is now part of Roche Sequencing Solutions Design Share Portfolio. Design Share makes it easy to access pre-designed NGS panels that are developed by Roche or in collaboration with researchers around the world. Please access the full portfolio at sequencing.roche.com/designshare

Low duplication rates with high on-target reads. With 18M reads, the SeqCap EZ Inherited Disease Panel exhibited low duplication rates, high on-target rates and excellent coverage depth. The experiment was conducted using 100 ng of gDNA with the KAPA Library Prep Kit and by hybridizing overnight. (SeqCap EZ Library SR Users Guide v5.0). This design is also compatible with the new streamlined HyperCap workflow v1.0.