Clinical Research Exome V2

Frequently Asked Questions

What differentiates CRE V2 from V1?

Based on analysis from Emory University and the Children's Hospital of Philadelphia, the CRE V2 is comprised of the SureSelect Human All Exon V6, as well as enhanced coverage of an additional 1,099 disease-associated genes; in excess of 75,000 splice sites of non-coding exons; more than 12,000 previously reported deep intronic variants; over 800 previously reported variants in promoter regions, and non-coding RNAs. 71 breakpoint spanning probes have also been included for common deletions. The 65.7 Mb CRE V2 design enables deeper reach into regions of the genome not previously accessible through standard WES.

What are the disease-associated targets and how are they defined?

Disease-associated targets are genes linked to disorders. These were identified through the gene curation effort led by Emory University and CHOP, with data aggregated through large-scale literature and database curation efforts, deep sequencing of genes, functional validation of disease causality of gene variants through cDNA sequencing and breakpoint sequencing of variants.

When should I use CRE V2 instead of V6?

With its optimized bait selection and the newest curated disease-associated content, CRE V2 focuses additional sequencing power where it matters most, providing the most comprehensive coverage of clinical targets.

Which library prep solutions are CRE V2 compatible with?

The Clinical Research Exome V2 is compatible with best in class SureSelect library prep options (XT, XT2, and QXT).