Stem-Seq™ Plus

stemgenomics cell integrity

Achieve optimum genomic knowledge in one single assay, without the data overload

The *Stem-Seq™ Plus* is a unique and comprehensive NGS test designed especially for cell therapy scientists. It detects both copy number variations (CNVs) across the genome and uses a custom-made, targeted panel composed of 361 genes to identify Single-Nucleotide Variants (SNVs). In short, *Stem-Seq™ Plus* provides a comprehensive and powerful genomic assessment in one single assay.

Stem-Seq™ Plus key features and benefits:

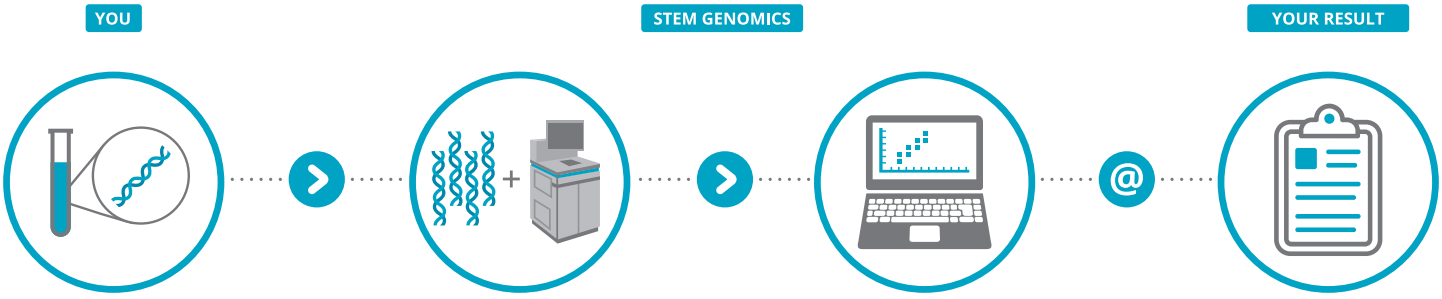
- **A comprehensive solution** that combines both **SNV and CNV detection in one assay**.
- **High sensitivity**, offering detection at **1000 x resulting in 2% mosaicism for SNVs and indels, and 20% mosaicism for CNV detection (300kb)**.
- **361 genes** selected for their association with cancer (including TP53, BCOR, etc.) but also selected variants **specific to pluripotent stem cells** for their impact on the natural development of cells in culture.
- Use of a **backbone** and a **Pool of Normal (PON)** to enable a **more accurate analysis** of the large regions covered by **CNVs** and **reduce false positives**.
- **Filtered or interpreted report** to assist in the understanding of the sequencing analysis.
- Delivery in 4 to **5 weeks depending on the selected report**.
- Analysis available starting from **1 sample** so you do not need to wait for other samples before processing begins!

Technology used

The library is built using Twist capture technology and the sequencing is performed on Illumina NovaSeq as paired-end reads.

How does it work?

All you need to do is send ≥ 30 µL of DNA at a concentration of ≥ 20 ng/µL if dosed by Qubit or ≥ 50 ng/µL if dosed by Nanodrop, at room temperature. We'll take it from there!



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FAQs

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Is it really necessary to check for both CNVs and SNVs in stem cells in culture?

Both variants can interfere with your cells in culture. Case in point, the first human trial using hPSCs at the RIKEN Institute in Japan was suspended due to the late identification of CNVs and SNVs in the cells that were about to be injected into patients.

What is the use of the backbone and PON in the *Stem-Seq™ Plus* assay?

As CNVs represent large regions of the genome, they are complex to analyze. Consequently, Stem Genomics introduced a backbone and a Pool of Normal (PON) in the *Stem-Seq™ Plus* assay to enable a more robust analysis of significant variants. The backbone of probes covers the entire genome. Combined with the PON, they enable data normalization between the target sample and the normal sample and effectively reduce background noise.

Regarding the *Stem-Seq™* final analysis report, how are the variants interpreted?

Our specialists are committed to providing a comprehensive interpretation of single nucleotide variants (SNVs) by meticulously examining each variant in multiple databases such as Cosmic and ClinVar, as well as conducting an extensive literature review. In addition, for copy number variation (CNV) analysis, our team will prioritize your variant by comparing it against our proprietary database, the SMART database and the ACMG (American College of Medical Genetics and Genomics) classification standards.

Is it possible to obtain the list of excluded variants as well as the rationale behind the exclusion?

Yes, it is. We offer a transparent and comprehensive analysis process, starting with the provision of the raw data containing all the variants identified in your samples.

Is the assay relevant to all stem cell types?

The *Stem-Seq™* Plus Assay has been designed to provide pertinent information to all stem cell scientists working on human stem cells. It is particularly suited to pluripotent stem cell scientists who encounter the highest level of mutations in their cells.

Is your assay range focused on genomic stability or can you support stem cell researchers with other useful assays that we can integrate into our QC?

In accordance with the ISSCR's latest quality standard recommendations, we strongly recommend regularly performing STR and mycoplasma tests. We can perform both for you in complement to genomic stability testing.

For research use only.

For more information, please contact us at

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