Stem-Seq™ Panel

stemgenomics cell integrity

In-depth genomic knowledge without the data overload

The *Stem-Seq™ Panel* is a custom-made, targeted NGS panel composed of 361 genes that have been selected for their relevance to stem cell scientists. It detects Single-Nucleotide Variants (SNVs) associated with cancer (including TP53, BCOR, etc.) but also selected variants specific to pluripotent stem cells and their impact on the natural development of cells in culture. Based on innovative NGS technology, the *Stem-Seq™ Panel* enables scientists to look deeper into targeted regions of interest.

Stem-Seq™ Panel key features and benefits:

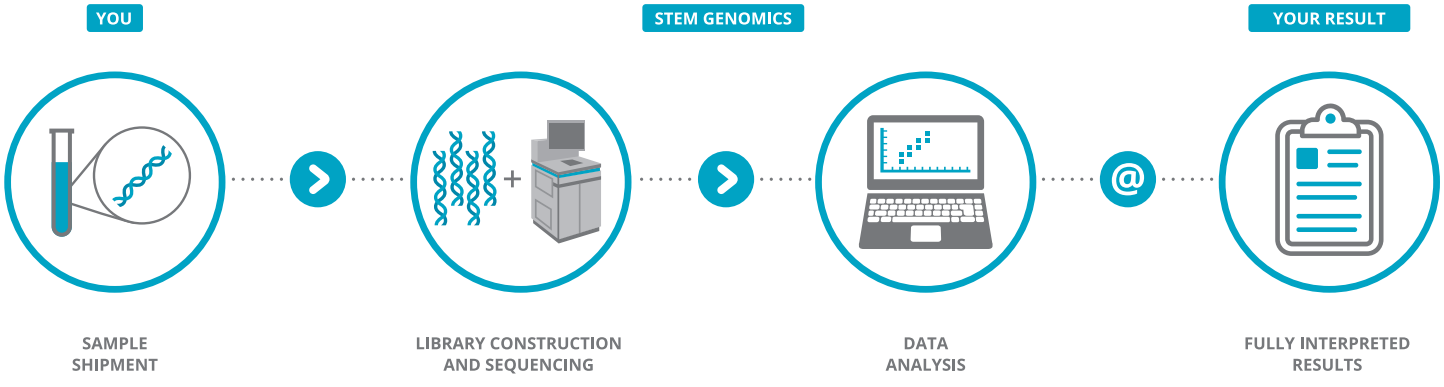
- **361 genes** selected for their relevance to human stem cell scientists
- **Report interpreted** by stem cell scientists in order to assist in the understanding of the sequencing analysis
- **High sensitivity** offering detection of **SNVs and indels** (1000 x, 1% mosaicism)
- Delivery in **4 to 5 weeks** (depending on selected report format)

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 a DNA concentration of ≥ 20 ng/µL if dosed by Qubit or ≥ 50 ng/µL if dosed by Nanodrop, at room temperature. Volume: ≥ 30 µL. We'll take it from there!



Stem Genomics
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FAQs

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Can I combine the *iCS-digital*™ assay range with the *Stem-Seq*™ *panel*?

These are complementary assays that together will strengthen your stem cell workflow genomic stability. The *iCS-digital*™ range is ideal for regular in-process checks during amplification and maintenance and detects CNVs. As for the *Duo iCS-Karyo*, it will de facto detect CNVs, but will also show aneuploidies or chromosomal structural abnormalities such as translocations and inversions. The *Stem-Seq*™ *panel* range will complement these two tests at acquisition, banking characterization or end of workflow. It will identify potential SNVs (punctual mutations) and small insertions/deletions (indels).

What is the difference between the two levels of reports available?

The first level of reporting is automatically interpreted. The variants identified are classified according to the ACMG (American College of Medical Genetics and Genomics) criteria. The second level of reporting is called "fully interpreted" according to the following internal classification: in-silico variant interpretation (the ACMG classification), analysis of specialized databases, manual validation of predictions and review against scientific publications by a stem cell research scientist.

How much does it cost?

The price will depend on the level of interpretation you require for the reports. Discounts are also available for large volume orders.

Is the assay relevant to all stem cell types?

The *Stem-Seq*™ *Panel* 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 there an NGS solution able to also detect CNVs in stem cells?

We have a brand new solution that will do that for you. For more information, contact us directly for a detailed presentation of the solution.

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 checking the identity of your stem cells during their time in culture with our STR assay. Mycoplasma testing is also critical for robust science and we have a digital PCR solution called *Myco-digital* that can do that for you.

For research use only.

For more information, please contact us at

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