ProgeneDX
CIRS Assays

GENIE TEST DESCRIPTION

Your GENIE test uses a statistical method called normalization to adjust your gene expression values so they are comparable and consistent across time and specimens. Normalization provides a baseline between all GENIE testing. We use special genes to calculate this statistical normalization, these genes are called "Housekeeping genes" and they are not listed on your report. Housekeeping genes are defined as genes expressed at approximately the same level regardless of physiological condition. So, both CIRS patients and healthy individuals have approximately the same expression levels of these genes.

Your report consists of 18 categories of molecular pathways and 1 statistical measure called dispersion. The categories contain groups of genes or gene families that are related to the category heading. These genes are represented in the bubbles within the category. The bubble contains both the name of the gene and your gene expression value represented by Z score for categories 2-18, while category 1 is an average of multiple genes. The Z score represents how many standard deviations your score is from the mean, or average, of the normal value. The coloring of the bubble is used to represent whether your score is above or below normal, red is above and blue is below normal, with the intensity of coloring indicating the magnitude of change. Z scores greater than 2 would indicate your gene value is abnormal, values between 2 and 1 are normal but should be watched, values less than 1 are normal and uncolored. The values here have not undergone what is called multiple test correction, which means, with so many measurements, it is likely to have a few abnormal values, even in healthy people.

The very first value on your report is called **Absolute IF**, which stands for absolute impact factor. This factor considers several variables and should be used as a reference to a patients overall metabolic output when looking at the metabolic section of the report. For instance, a patient with an impact factor around 1 indicates the metabolic output is normal in terms of RNA output, even though the rest of the metabolic section may show up or down regulation. The absolute IF provides an idea of where the metabolic output is currently, while the other measurements in the section provide an idea of where the output is heading, either up, down, or neutral.

The **Dispersion** score on your report indicates how well your Housekeeping genes match the levels found in healthy individuals. The dispersion is close to zero if all your housekeeping genes are the same as levels found in normal healthy individuals and increases as the values become more diverse. Values up to 1 are normal. Dispersion values greater than 1 indicate that the housekeeping genes used for your GENIE normalization are starting to drift out of normal ranges. This means some of your GENIE scores could become exaggerated (slightly higher or lower than their actual value) since the baseline for measurement is starting to skew. If the Dispersion score goes above 2, we rerun the test using your duplicate blood sample to verify our results are as accurate as possible.