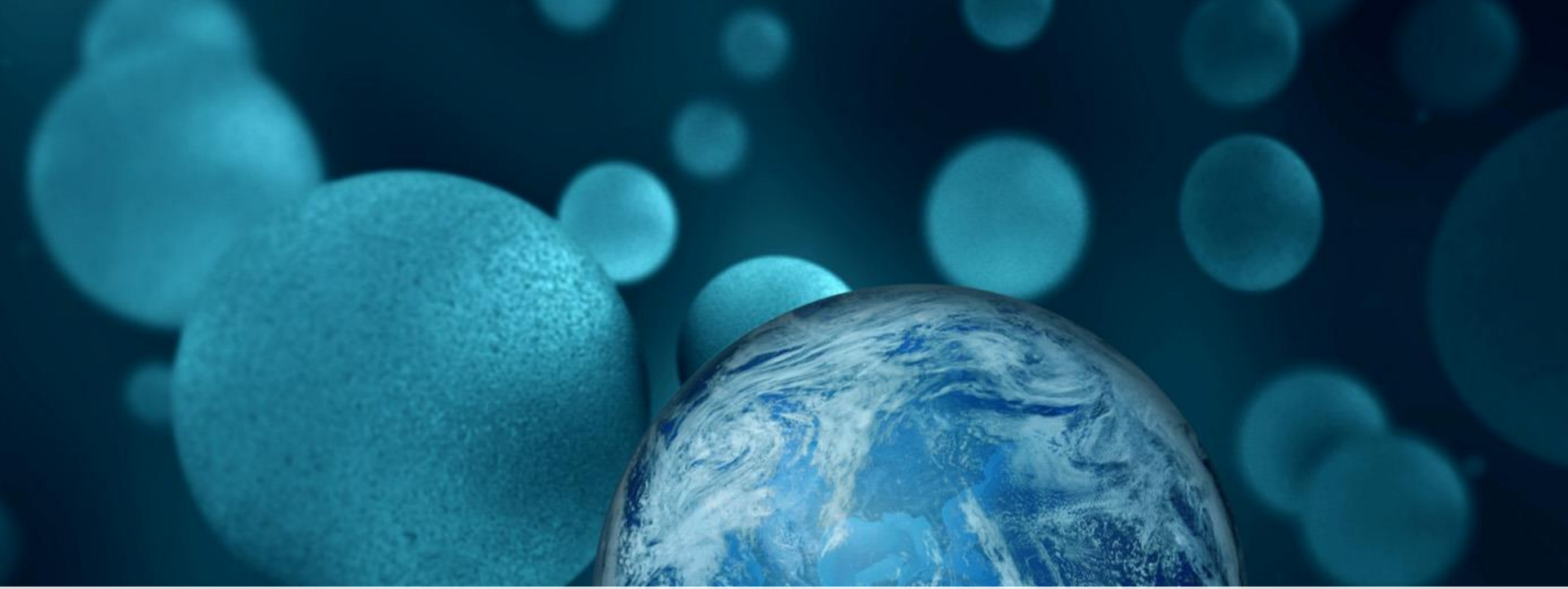

ThermoFisher SCIENTIFIC

KaryoStat™ Report

Client Name: Stanford
Quote No: CUB16307.2
Date: 12 July 2021
Prepared by: Jackie Webb

Summary of services

Project Summary:

- Stanford (Client) is interested in services provided by the Life Technologies Corporation in the analysis of fourteen (14) client-provided samples using the KaryoStat™ assay.

Service Description:

- The KaryoStat™ assay allows for digital visualization of chromosome aberrations with a resolution similar to G-banding karyotyping. The size of structural aberration that can be detected is > 2 Mb for chromosomal gains and > 1 Mb for chromosomal losses (the resolution depends on the location of the aberration in the chromosome. Due to a lower probe density on the telomere ends and centromeres, the resolution in those locations may be closer to 5Mb). The KaryoStat™ array is optimized for balanced whole-genome coverage with a low-resolution DNA copy number analysis, the assay covers all 36,000 RefSeq genes, including 14,000 OMIM® targets. The assay enables the detection of aneuploidies, submicroscopic aberrations, and mosaic events.

Materials & Methods:

Genomic DNA purification

Cells were prepared according to the Genomic DNA Purification Kit (Catalog #: K0512) and quantified using the Qubit™ dsDNA BR Assay Kit (Catalog #: Q32850)

GeneChip® Preparation

250 ng total gDNA was used to prepare the GeneChip® for KaryoStat™ according to the manual and is an array that looks for copy number variants and single nucleotide polymorphisms across the genome.

KaryoStat™ Results: Sample information

#	Sample ID	Status
KS-7214	2134-c1	Complete
KS-7215	2134-c2	Complete
KS-7216	849	Complete
KS-7217	968	Complete
KS-7218	630	Complete
KS-7219	407	Complete
KS-7220	466	Complete
KS-7221	741	Complete
KS-7222	973	Complete
KS-7223	248	Complete
KS-7224	672	Complete
KS-7225	500	Complete
KS-7226	2266	Complete
KS-7227	2355	Complete

Table 1. Customer-provided sample information

KaryoStat™ Results: KS-7217 (SCVIi031-A)

1. KaryoStat™ analysis of KS-7217 revealed the sample originated from a male individual.
2. No chromosomal aberrations were found when comparing against the reference dataset (Figure 4)

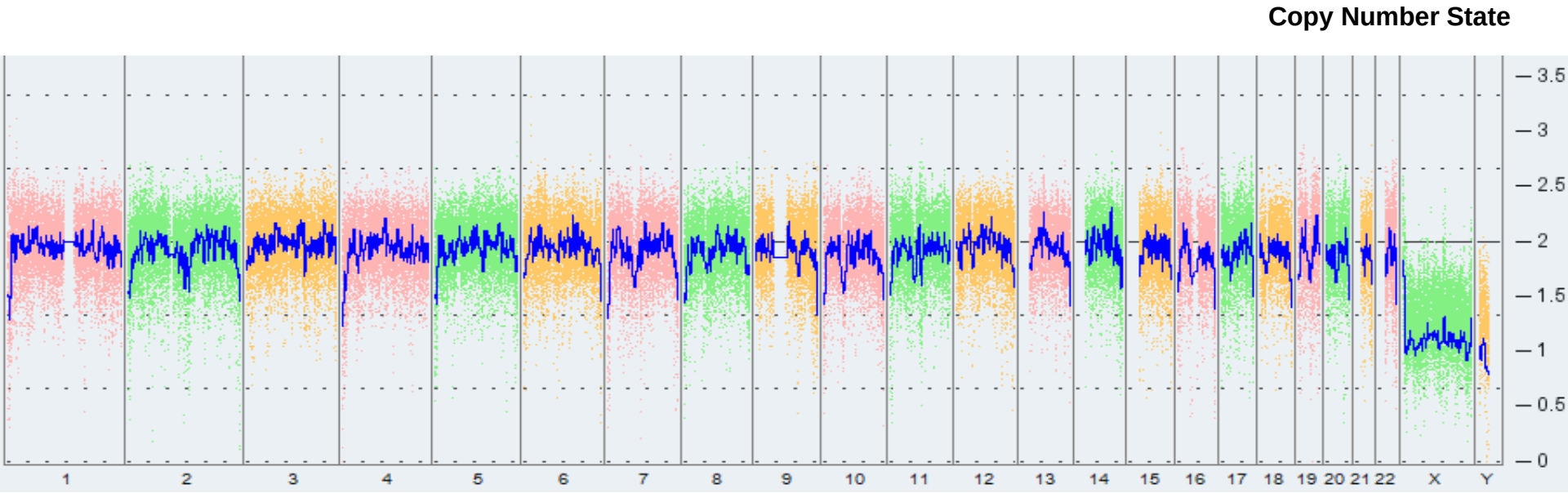

Figure 4: Whole genome view. The whole genome view displays all somatic and sex chromosomes in one frame with high level copy number. The smooth signal plot (right y-axis) is the smoothing of the log2 ratios which depict the signal intensities of probes on the microarray. A value of 2 represents a normal copy number state (CN = 2). A value of 3 represents chromosomal gain (CN = 3). A value of 1 represents a chromosomal loss (CN = 1). The pink, green and yellow colors indicate the raw signal for each individual chromosome probe, while the blue signal represents the normalized probe signal which is used to identify copy number and aberrations (if any).*

**If a deletion in Chr. Y is found, it is possible that this sample is derived from the WTC cell lines, which is known to have this genotype, and is originating from the donor the cell line was derived from.*