Summary of services

Project Summary:

- Stanford University is interested in services provided by the Life Technologies Corporation in the analysis of twelve (12) client-provided sample using the KaryoStat™ assay for human cells.

Service Description:

- The KaryoStat™ assay allows for digital visualization of chromosome aberrations with a resolution similar to g-banding karyotyping by relying on 150k SNP probes across the human genome. 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 assay enables the detection of aneuploidies, submicroscopic aberrations, and mosaic events.
- Using the same array as the Karyostat Assay, the Cell ID assay allows for DNA fingerprint matching of human cell lines through correlation analysis of 150k SNPs between samples. The detection of 150k SNPs across the genome allows for unique DNA based signatures of the genetic background of a cell, which can then be compared with others.

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 SNPs, copy number variants and single nucleotide polymorphisms across the genome.

KaryoStat™ Results: Sample information

#	Sample ID	Status
KS-7474	856	Complete
KS-7475	868	Complete
KS-7476	975	Complete
KS-7477	2211	Complete
KS-7478	815-3	Complete
KS-7479	815-4	Complete
KS-7480	815-6	Complete
KS-7481	42	Complete
KS-7482	43	Complete
KS-7483	171	Complete
KS-7484	322	Complete
KS-7485	765	Complete

Table 1. Customer-provided sample information

*Cell ID Samples **Reference Sample

KaryoStat™ Results: KS-7476

1. KaryoStat™ analysis of KS-7476 revealed the sample originated from a male individual
2. No chromosomal aberrations were found when comparing against the reference dataset (Figure 3)

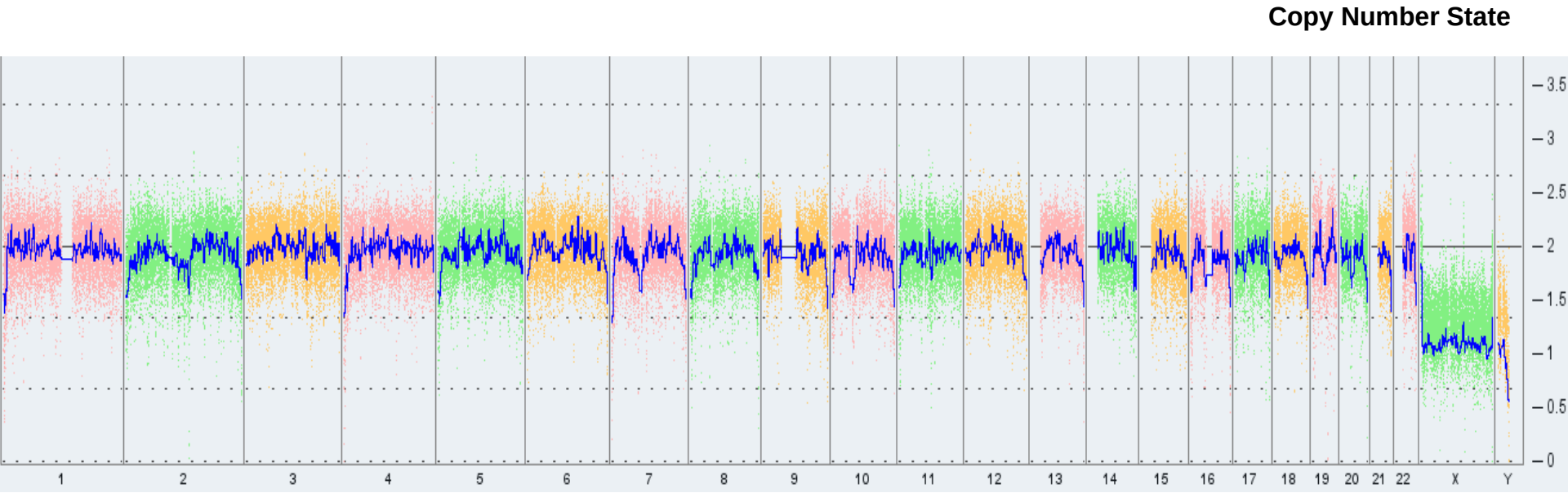

Figure 3: Whole genome view. The whole genome view displays all somatic and sex chromosomes in one frame with high level copy number. The smooth signal plot (right y-axis) is the smoothing of the log2 ratios which depict the signal intensities of probes on the microarray. A value of 2 represents a normal 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).*

Disclaimer: This assay was conducted solely for the listed investigator/institution. The results of this assay are for research use only.