

Sample Information



#	Sample ID	Status
KS-19309	iPSC MTARC1 SEC XC p18	Complete
KS-19310	PBMC patient 2	Complete

Table 1: Karyostat⁺ Sample ID. Customer provided sample information

Cell ID Results Comparison Between All Samples

	KS-19309	KS-19310
KS-19309	100.00%	98.77%
KS-19310	98.77%	100.00%

Table 2: Cell ID Correlation Plot. 1.1M SNPs spread across the genome of cell lines are analyzed and compared between indicated samples. A correlation in analysis of all SNP calls was performed to match samples with one another. The correlation between a sample and itself has a value of 100, correlations >95% between samples are considered having an identical genetic background (green boxes), correlations <95% indicate different genetic backgrounds (red boxes)

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

KaryoStat+ Results: KS-19309

1. KaryoStat+ analysis of this sample revealed that it originated from a male individual.
2. No chromosomal aberrations were found when comparing against the reference dataset.

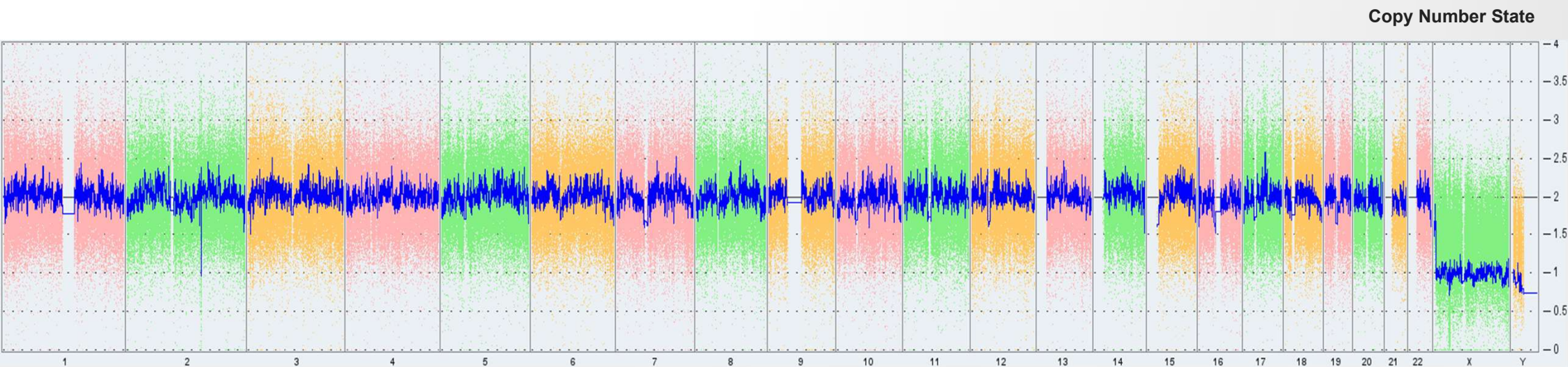


Figure 1: Whole genome view. The whole genome view displays all somatic and sex chromosomes in one frame with high level copy number. The smooth signal plot (right y-axis) is the smoothing of the log₂ ratios which depict the signal intensities of probes on the microarray. A value of 2 represents a normal 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). Aberrations when present are indicated by red arrows.

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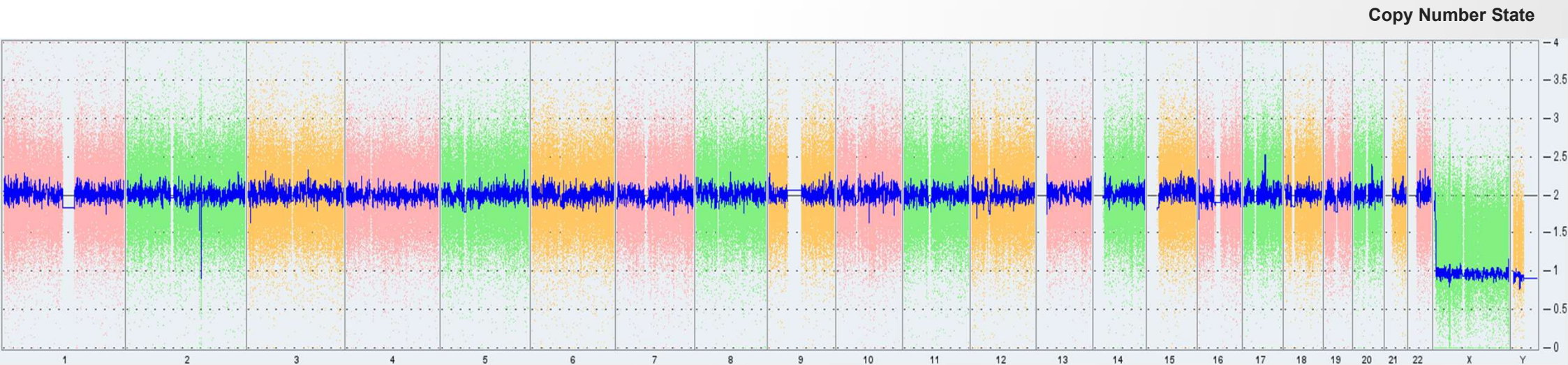


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