

## Chromosome Analysis Report: 098354

Date Reported: Tuesday, August 22, 2023 Cell Line: Sample Report Submitted Passage #: 35 Date of Sample: 8/15/2023 Specimen: Human IPSC Results: 46,XX Cell Line Sex: Female Harvest Date: 8/15/2023 Reason for Testing: LOT\_RELEASE Investigator: WiCell Stem Cell Bank, WiCell Process Description #: WIC001



	Description in the anticelline description is		
Cell: 39	Process Description: WiCell works with client to determine their specific analysis requirements. This number connects those requirements to this final report and can be used for multiple samples or assays.		
Slide: G02			
Slide Type:	Karvotype		
Total Counte	d: 20		
Total Analyze	ed: 8		
-			
Total Karyog	rammed: 4		
Rand Resolut	tion: 425 - 450		

## Interpretation:

Signatures of certified analyst, American Board of Medical Genetics and Genomics (ABMGG) board certified or board-eligible director, and QA.

This is a normal karyotype; no clonal abnormalities were detected at the stated band level of resolution.

Deviation:	No deviations occurred.	Description of any deviations, if applicable.	
Completed by: Director Review:	SAMPLE		
Report Review: QA Review:			
For internal use on <b>Date:</b>	ly Sent By: Se	nt To:	Compliance statement

This assay was completed in compliance with the U.S. FDA Current Good Manufacturing Practice for Finished Pharmaceuticals (21 CFR part 211) and the EU Good Manufacturing Practice guidelines (EC EudraLex Volume 4) where applicable.

Limitations: This assay allows for microscopic visualization of numerical and structural chromosome abnormalities. The size of structural abnormality that can be detected is >3-10Mb, dependent upon the G-band resolution obtained from this specimen. For the purposes of this report, band level is defined as the number of G-bands per haploid genome. It is documented here as "band level", i.e., the range of bands determined from the four karyograms in this assay. Detection of heterogeneity of clonal cell populations in this specimen (i.e., mosaicism) is limited by the number of metaphase cells examined, documented here as "# of cells counted".

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