

**Date Reported:** Monday, June 24, 2019

**Cell Line:** iPSC SNP-1

**Passage#:** 30

**Date of Sample:** 6/13/2019

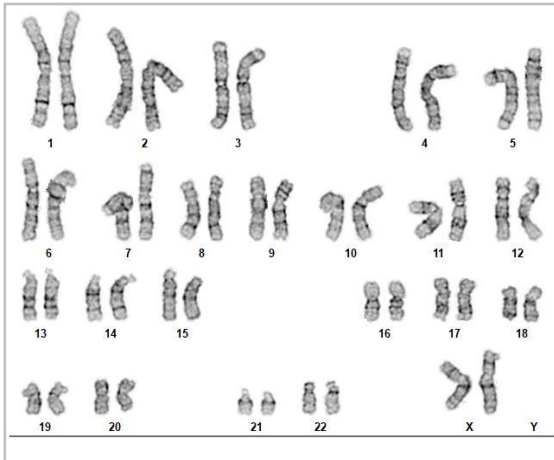
**Specimen:** Human IPS

**Results:** 46,XX

**Cell Line Sex:** Female

**Reason for Testing:** none given

**Investigator:** Guibin Chen, NIH



**Cell:** 34

**Slide:** G03

**Slide Type:** Karyotype

**Total Counted:** 20

**Total Analyzed:** 8

**Total Karyogrammed:** 4

**Band Resolution:** 400 - 525

**Interpretation:**

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

**Completed by:** Pam Mill

**Reviewed and Interpreted by:** Jennifer Laffin, PhD, FACMG

**Date:** \_\_\_\_\_ **Sent By:** \_\_\_\_\_ **Sent To:** \_\_\_\_\_ **QC Review By:** \_\_\_\_\_

*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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