



WiCell Characterization

Guidelines for characterization testing of cell lines

Assay	What it Detects	What it Doesn't Detect	TAT ¹	When to Use
Fluorescence In Situ Hybridization (FISH)	<ul style="list-style-type: none"> Genomic sequence of interest <ul style="list-style-type: none"> Duplications or deletions >20 Kb >2% mosaicism (for example: cultures where >2 of 100 cells are trisomy 12) Chromosomal location of genomic gains Chromosome fusions (breakaparts) 	<ul style="list-style-type: none"> Changes in regions other than the probe-specific sequence 	10-15 days	<ul style="list-style-type: none"> To confirm findings and refine breakpoints detected by g-banded karyotyping To confirm findings and localize genomic gains detected by SNP microarray As a screen for microdeletions/duplications of known targets
G-Banded Karyotyping	<ul style="list-style-type: none"> Microscopic genomic abnormalities (>5-10 Mb) <ul style="list-style-type: none"> Inversions Duplications/deletions Balanced and unbalanced translocations Aneuploidies >10% mosaicism (for example: cultures where >1 of 10 cells are trisomy 12) 	<ul style="list-style-type: none"> Submicroscopic genomic abnormalities (<5 Mb) <~10% culture mosaicism (for example: cultures where 1 of 10 cells is trisomy 12) 	7-10 days (4-6 days expedited)	<ul style="list-style-type: none"> As a baseline genomic screen <ul style="list-style-type: none"> At derivation of cell lines At the start of experimental protocols To assess and monitor genomic stability (for example: every 5-10 passages of cell culture) At conclusion of experiments (prior to publication) For cell line banking When publication-quality karyotypes are needed
Mycoplasma Detection by PCR	<ul style="list-style-type: none"> 96 species of mycoplasma contamination from stem cell cultures. <ul style="list-style-type: none"> Sensitivity (5-100 CFU/ml) 	<ul style="list-style-type: none"> This system does not allow for the amplification of DNA originating from other sources, such as bacteria. 	5-7 days	<ul style="list-style-type: none"> To monitor the health of your cell line To monitor for contamination in shared lab spaces To assure that mycoplasma is not interfering with your experiments To rule out mycoplasma as the culprit of chromosomal aberrations
Short Tandem Repeat Analysis (STR)	<ul style="list-style-type: none"> STR polymorphisms for 15 loci plus amelogenin (Promega® PowerPlex® 16) Probability of matching identity to an existing STR profile 	<ul style="list-style-type: none"> STR polymorphisms in areas other than those represented in Promega® PowerPlex® 16 	10-20 days	<ul style="list-style-type: none"> To monitor identity of a cell line To confirm relationship of iPS cells to their parent line To establish an STR profile of a newly derived or reprogrammed cell line To rule out culture cross-contamination
Single nucleotide polymorphism (SNP) Microarray	<ul style="list-style-type: none"> Submicroscopic genomic abnormalities (>5-10 Mb) Genomic gains and losses (>50 Kb) <ul style="list-style-type: none"> Copy number variants Duplications/deletions Unbalanced translocations Aneuploidies Copy neutral Loss of Heterozygosity (LOH) / Absence of Heterozygosity (AOH) (>5 Mb) >~10% mosaicism (for example: cultures where >1 of 10 cells are trisomy 12) 	<ul style="list-style-type: none"> Balanced translocations <ul style="list-style-type: none"> Robertsonian Balanced insertions Inversions <~10% culture mosaicism (for example: cultures where 1 of 10 cells is trisomy 12) Chromosomal position of genomic gains 	14-21 days	<ul style="list-style-type: none"> As a baseline genomic screen <ul style="list-style-type: none"> To detect submicroscopic (<5 Mb) abnormalities To identify amplified or deleted genes of interest To assess and monitor genomic stability (for example: every 5-10 passages of cell culture) In conjunction with G-banded karyotyping <ul style="list-style-type: none"> To define unbalanced translocation breakpoints For research of genomic copy number change <ul style="list-style-type: none"> To identify structural variation within populations or disease cohorts To develop a cell line copy number variant profile
Spectral Karyotyping (SKY)	<ul style="list-style-type: none"> Microscopic genomic abnormalities (>5-10 Mb) <ul style="list-style-type: none"> Balanced and unbalanced translocations Aneuploidies 	<ul style="list-style-type: none"> Submicroscopic genomic abnormalities (<5 Mb) Inversions Duplications/deletions 	14-21 days	<ul style="list-style-type: none"> As an adjunct to g-banded karyotyping <ul style="list-style-type: none"> To define complex rearrangements To identify marker chromosomes When publication-quality spectral karyotypes are needed

¹ Turn-around-times (TAT) provided are based on provision of sufficient mitotically active hES or iPS cultures grown in Matrigel/TeSR or MEF/hES media conditions.

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