Supplementary Table 1. Summary of genomic aberrations that can occur during prolonged culturing for both human embryonic stem cells and induced pluripotent stem cells.

Genomic Aberrations	**ESCs**	**iPSCs**	**References**
Trisomy 12 or amplification of 12p	+	+	[21, 22, 29, 33, 34]
Trisomy X	+	+	[21]
Trisomy 17	+	-	[21, 26, 29, 83]
Isodicentric X chromosome	+	-	[35]
Amplification of 20q11.21	+	+	[30, 31, 33]
Deletions of 15q11.2, 18q12.1, 22q11.21	+	-	[27, 31]
Deletions of 8q24.3, 17q21.1	-	+	[54]
Amplifications of 1p36.13, 1p36.33, 2p11.2, 7q35, 14q32.32, 21q11.2, 22q11.22	+	-	[27]
Amplification of 1q31.3	-	+	[54]
Trisomy 8 and Trisomy 20q	+	+	[32]
LOH of 16q	+	-	[27]

LOH = Loss of heterozygosity

Supplementary Table 2. Comparison of methods for evaluating the genomic integrity of pluripotent stem cells.

Method	Advantages	Disadvantages
GTG karyotyping	• Detects gross abnormalities quickly • Can detect mosaicism and structural aberrations or inversions	• Limited to the detection of larger chromosomal aberrations (>5 Mb) • Cannot detect functions of affected genes
FISH and SKY	• Identify structural chromosomal aberrations	• Limited to the detection of larger chromosomal aberrations (>2 Mb) • Cannot detect functions of affected genes
CGH and SNP arrays	• Highly sensitive • Can detect small regions of changes (>25 Kb) • Can detect mosaicism • SNP arrays can detect loss of heterozygosity	• Expensive • Cannot detect functions of affected genes • Samples can only be compared when run on the same platform
Whole genome sequencing	• Highly sensitive • Can detect single base changes • Can detect mosaicism	• Expensive • Cannot detect functions of affected genes • Samples can only be compared when run on the same platform
Global gene expression meta-analysis	• Can detect the function of affected genes	• Limited to the detection of larger chromosomal aberrations (>10 Mb) • Cannot detect mosaicism

CGH = Comparative genomic hybridization
FISH = Fluorescent in situ hybridization
SKY = Spectral karyotyping
SNP = Single nucleotide polymorphism