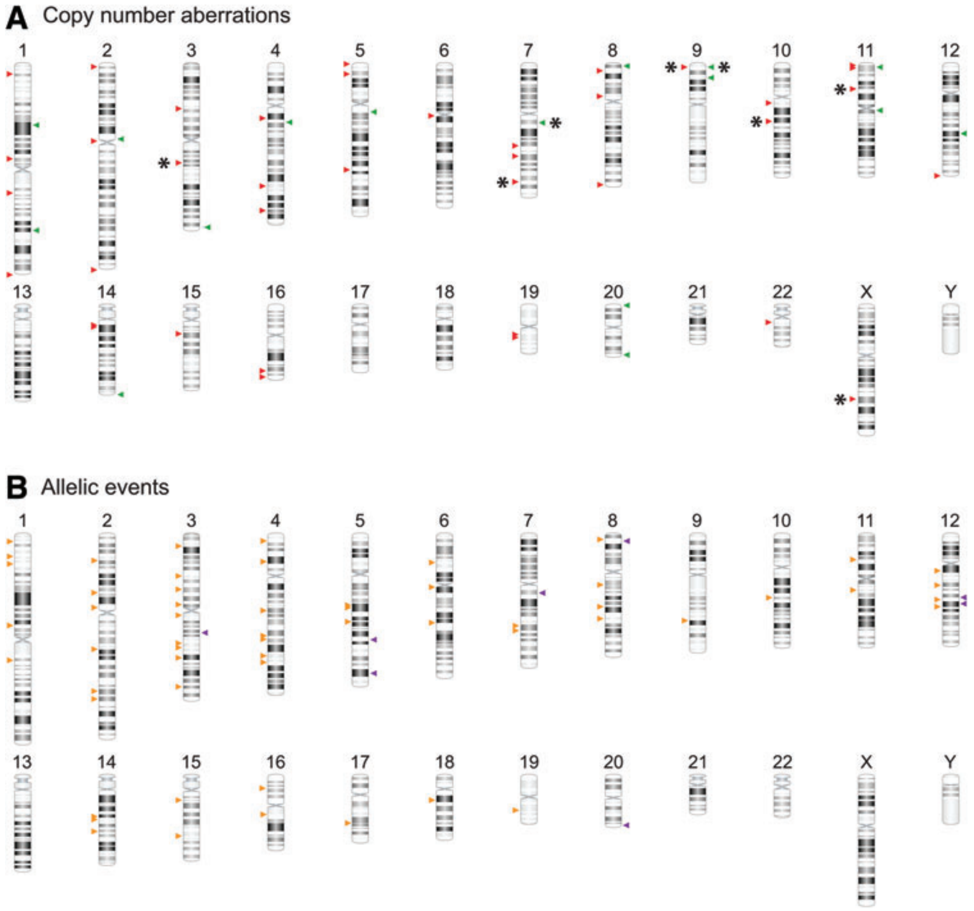

SUPPLEMENTARY FIG. S3. Characterization of the iMSC#3 genome after long-term culturing (155 PDs) using high-resolution array CGH. **(A)** Regions with increased and decreased copy numbers are shown in *green* and *red*, respectively. Aberrations that showed less than 25% overlap with regions of known copy number variations are indicated with an *asterisk* (*). **(B)** Regions with loss of heterozygosity or allelic imbalance (more copies of one allele over another) are shown in *yellow* or *purple*, respectively. Affymetrix Genome-Wide Human SNP Array 6.0 was used in the analysis (Affymetrix).