Table S1. Sequences of the primers used for reverse transcription-quantitative PCR

	Gene (aliases)	Primer sequence
iPSC	*POU5F1* (OCT4)	F: GAC AGG GGG AGG GGA GGA GCT AGG R: CTT CCC TCC AAC CAG TTG CCC CAA AC
Mesoderm	*ISL1* (ISL-1)	F: AGA TCA GCC TGC TTT TCA GC R: AGG ACT GGC TAA CCA TGC TGT
Cardiomyocyte	*MYH7* (β-MHC)	F: ACA TGC TGC TGA TCA CCA AC R: AAG CGT TAT CAG TGG CCA TG
	MYL2 (MLC-2v)	F: ACA GGG ATG GCT TCA TTG AC R: ATG CGT TGA GAA TGG TTT CC
	ACTC1 (cardiac muscle alpha chain)	F: CTT CAT TGG TAT GGA ATC TGC TG R: TAC TCT TGC TTG CTA ATC CAC
	TNNT2 (cTnT)	F: ATG AGC GGG AGA AGG AGC GGC AGA AC R: TCA ATG GCC AGC ACC TTC CTC CTC TC
	HCN4 (HCN4)	F: GGG GAA TTC GCA ACT GAA GC R: TGC TGC GCC CTT AAA TCT CT
	RYR2 (RYR2)	F: GCT ATT CTG CAC ACG GTC ATT R: ATT TCC GTG CCA CTT CCT TT
Endogenous control	18S rRNA	F: AGG AAT TGA CGG AAG GGC ACC A R: GTG CAG CCC CGG ACA TCT AAG

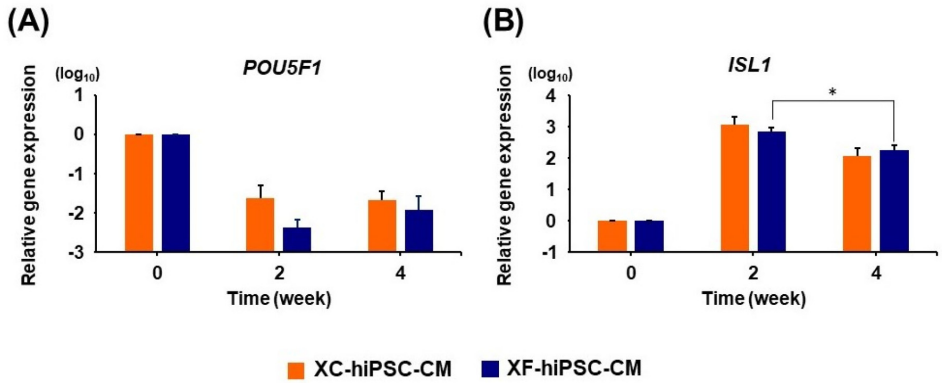

Fig. S1. Changes in the mRNA expression in CM that differentiated from hiPSC. hiPSC-CM were generated using the Gibco™ PSC Cardiomyocyte Differentiation Kit (XF). The expression of genes related to stemness (*OCT4*) (A) and cardiac progenitor cells (*ISL1*) (B) was evaluated by quantitative PCR at 0, 2, and 4 weeks of differentiation. The expression values were normalized to that of 18S rRNA, which was used as a housekeeping gene. The values are presented in terms of mean±S.E.M. *$p<0.05$, $n=3\sim4$ per group.

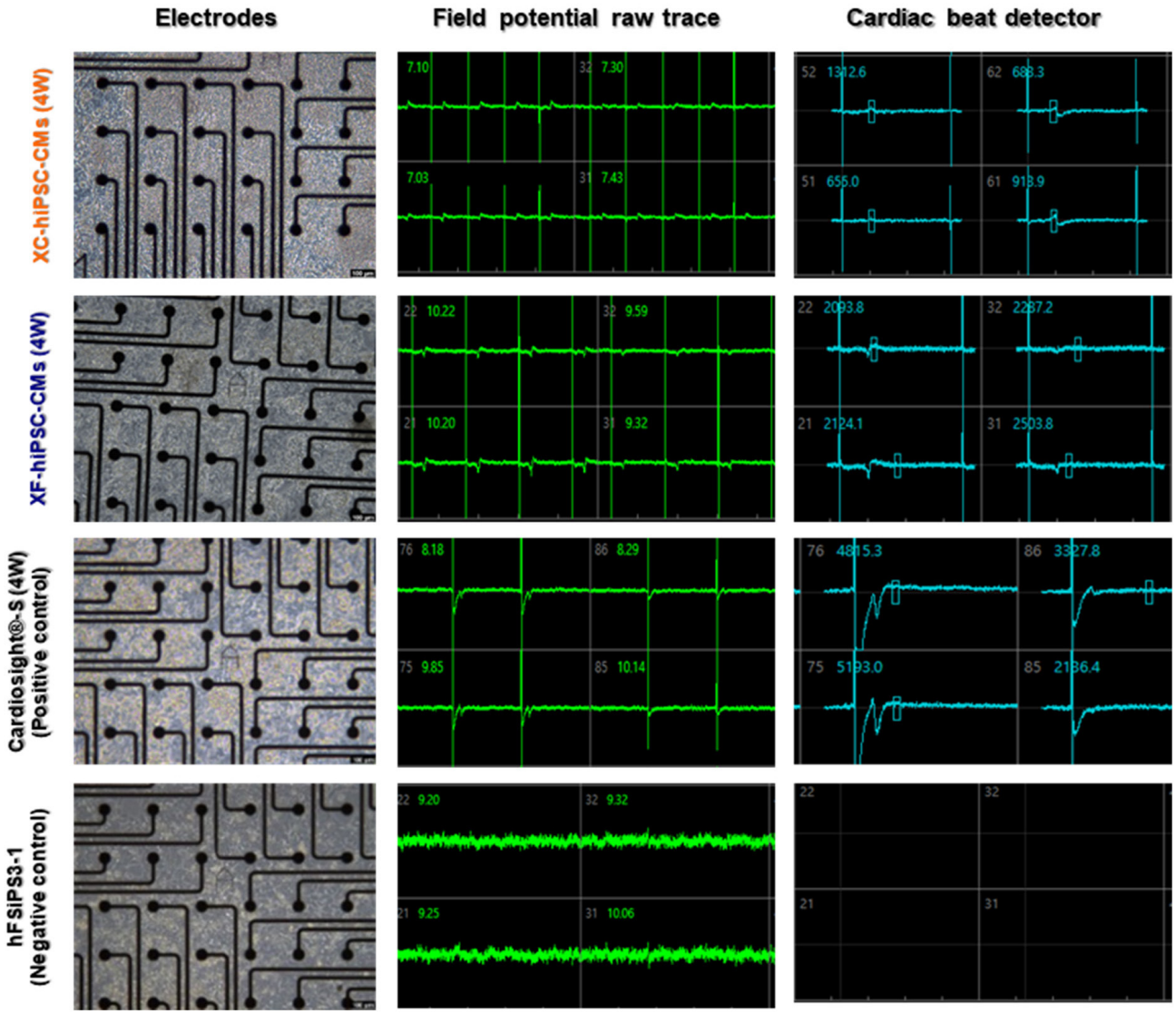

Fig. S2. Representative raw images of electrophysiological records from hiPSC-CM and Cardiosight®-S) and hiPSC. Electrophysiological activity of XC- or XF-hiPSC-CM at 2 to 4 weeks after differentiation from hiPSC was measured using the multi-electrode array assay.