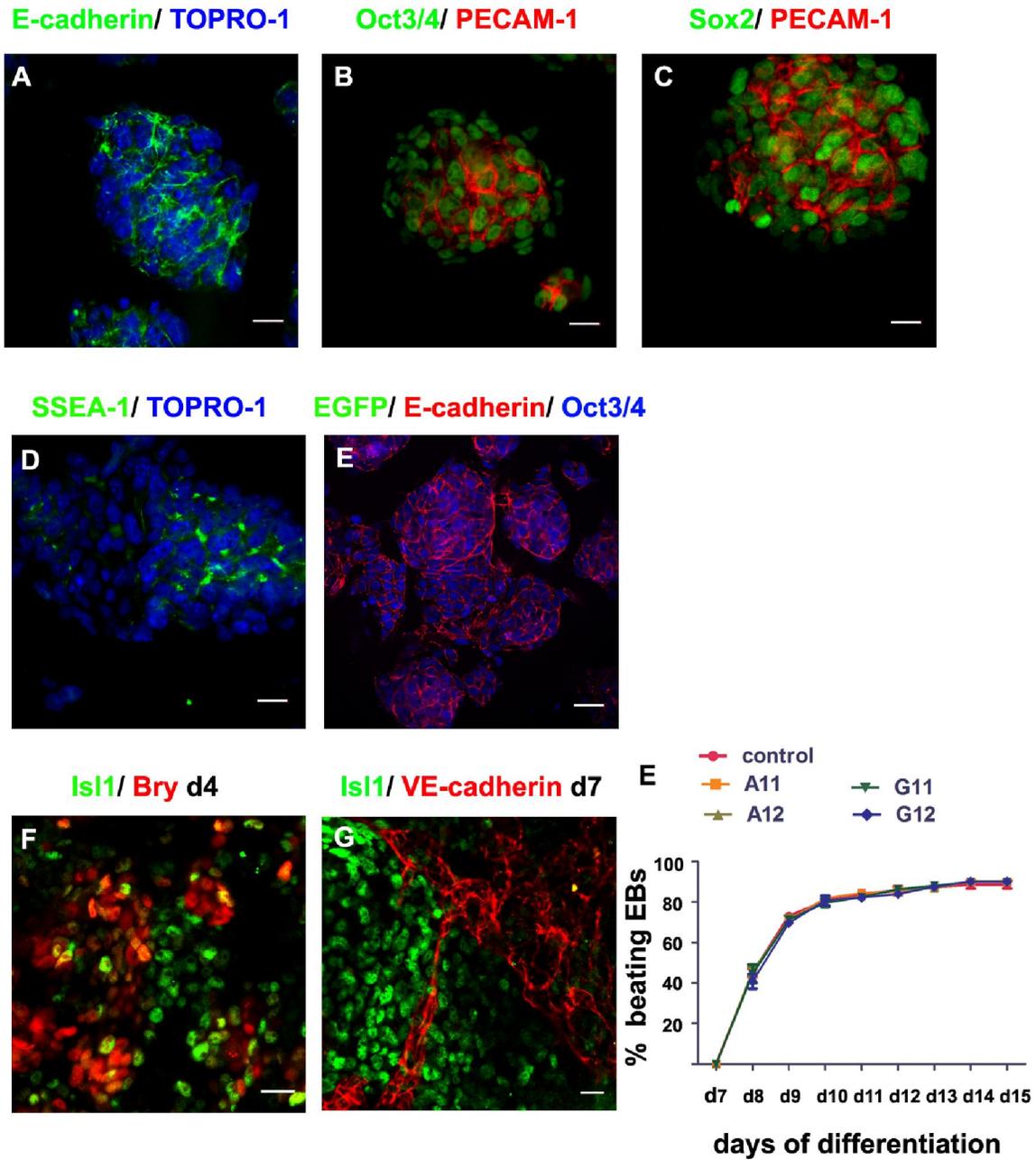


Supplementary Table 1 is presenting the PCR primer list used.

Gene name	forward primer 5->3	reverse primer 5->3	product size cDNA
VE-Cadherin	GTAACCCTGTAGGGAAAGAG TCCATT	GCATGCTCCCGATTAAACT GCCATA	260bp
PECAM-1	GTCATGGCCATGGTCGAGTA	CTCCTCGGCGATCTTGCTG AA	260bp
Flk1	TTTGGCAAATACAACCCTTCA GA	GCAGAAGATACTGTCACCA CC	133bp
Nfatc1	AGGTGCAGCCCAAGTCTCAC	GTGGCCATCTGGAGCCTTC T	620bp
Nrg1	CCAATGGCCACATTGCCAATA GGT	AGCCTGGCCTGTAATTCTTC CTGT	229bp
Isl-1	GCAGCTCCAGCAGCAGCAAC CCA	TGGGAGCTGCGAGGACATC GATGC	253bp
Nkx2.5	AGCCGCCCCACATTTTACC CG	GCGAGAAGAGCACGCGTG GCT	178bp
Gata4	GCGGAAGGAGGGGATTCAAA	TGAATGTCTGGGACATGGA GC	230bp
cTnT	AGCCCACATGCCTGCTTAAA	TCTCGGCTCTCCCTCTGAA C	115bp
MLC2v	ACTTCACCGTGTTCCCTCACGA TGT	TCCGTGGGTAATGATGTGG ACCAA	254bp

MLC2a	AAGGGAAGGGTCCCATCAAC TTCA	AACAGTTGCTCTACCTCAG CAGGA	202bp
AFP	CTTCCCTCATCCTCCTGCTAC	ACAAACTGGGTAAAGGTGA TGG	234bp
FOXA2	CCGTGAAGATGGAAGGGCAC	TCATTCCAGCGCCACATA G	210bp
Pdx1	CCTTTCCCGAATGGAACCGA G	GGTCAAGTTCAACATCACT GCC	264bp
Nestin	CATACAGGACTCTGCTGGAG G	AGGTGCTGGTCTCTGGTA T	130bp
Tubb3	CTTTTCGTCTCTAGCCGCGT	TCCCAGAACTTGGCCCCTA T	94bp
Pax6	TGAGAAGTGTGGGAACCAGC	CACTCCGCTGTGACTGTTC T	214bp
NANOG	CCAGTGGAGTATCCCAGCAT	GTTGGTCCAGGTCTGGTTG T	159bp
SOX2	AAAGGGTTCTTGCTGGGTTT	AAACAAGACCACGAAAACG G	156bp
b-actin	GTGACGTTGACATCCGTAAA G	GCCGGACTCATCGTACTC	244bp
gapdh	AGGTCGGTGTGAACGGATTT G	GGGGTCGTTGATGGCAACA	94bp

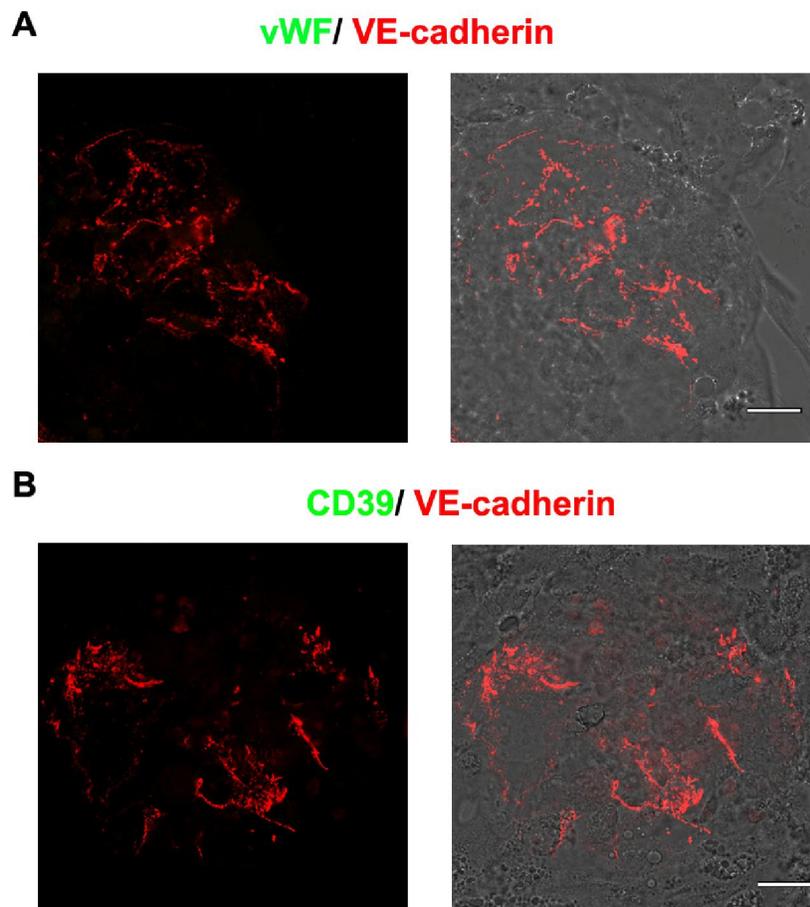
Supplementary Figure S1.



Supplementary Figure S1: Characterization of Pvec- and Pvec-EGFP- genetically modified ESCs. (A-E) Undifferentiated cells from clone A11 and G11 express pluripotency markers Oct3/4, Sox2, PECAM-1, SSEA-1 and E-cadherin but not EGFP, as shown by immunostaining.

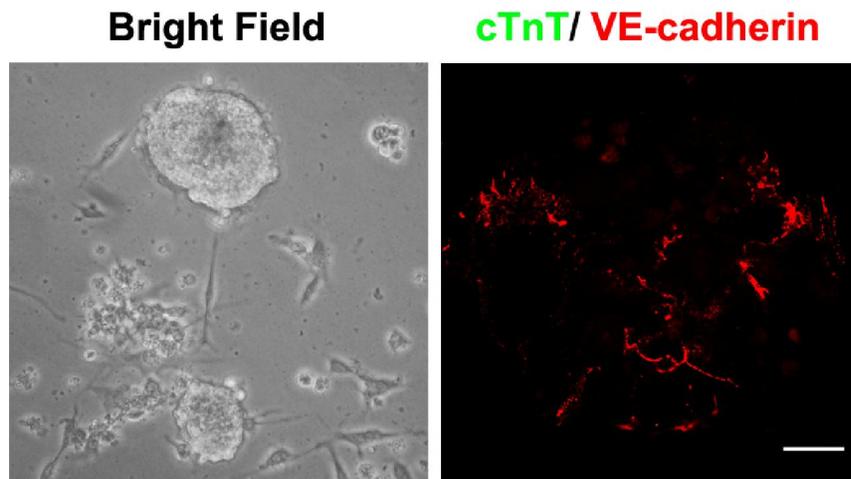
DNA was stained with TOPRO-1. (F) Mesodermal Bry^+ cells and $Isl1^+$ cardiovascular progenitor cells in A11 derived-EBs at d4. (G) Endothelial VE-cadherin $^+$ cells were typically located adjacent to $Isl1^+$ progenitor cells in A11 derived-EBs at d7. (H) Statistical analysis of beating activity in clones A11, A12, G11, G12 and control (E14T ESCs) during differentiation days 7-15 (an EB was considered as beating if contained one or more beating areas). *** $P < 0,001$ vs control. Data were evaluated by Repeated-measures two-way ANOVA, followed by Bonferroni post-hoc analysis for multiple comparisons. Probability values $P < 0.05$ were considered significant. Scale bars: 20 μm

Supplementary Figure S2.



Supplementary Figure S2: Pvec+ cells express VE-cadherin but not vWF or CD39 after double immunostaining with anti-VE-cadherin and anti- vWF (A) or anti- CD39 (B). Right panels are the immunofluorescence images superimposed on the background of phase-contrast optics. Scale bars: (A-B) 20 μ m

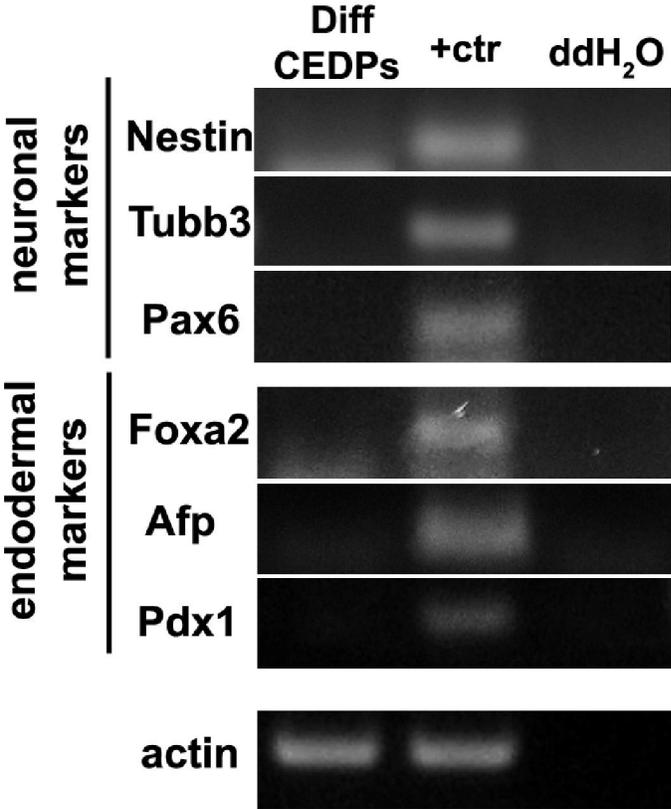
Supplementary Figure S3.



Supplementary Figure S3: (A) Typical image of spheres formed in the presence of SB-216763 after 5 days of CEDPs differentiation. (B) cTnT⁺ cells did not form under these conditions after 10 days of CEDPs differentiation, after immunostaining with anti-cTnT and anti-VE-cadherin. Scale bar: (B) 20 μ m

Supplemental video of a beating area after 15 days of CEDPs differentiation.

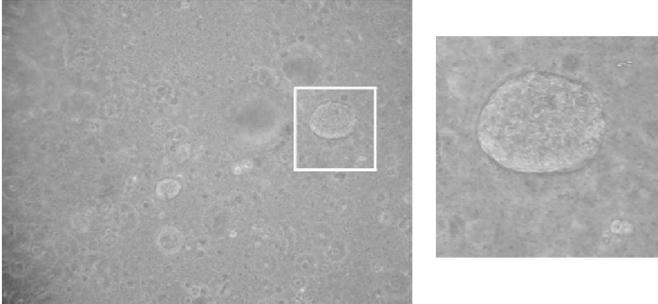
Supplementary Figure S4.



Supplementary Figure S4: RT-PCR analysis of CEDPs differentiation products at d10 showed absence of neuroectodermal and endodermal markers.

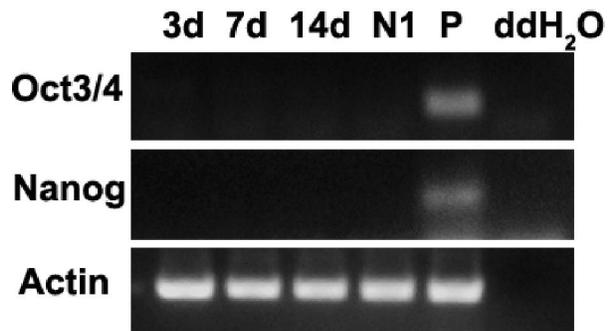
Supplementary Figure S5.

Spheres in alginate



Supplementary Figure S5: Optical microscope image of spheres formed in gelatinised alginate hydrogel at day 5 of CEDPs differentiation (magnification corresponds to marked area).

Supplementary Figure S6.



Supplementary Figure S6: Absence of pluripotency markers Oct3/4 and Nanog in transplanted animals by RT-PCR analysis.

Supplementary Figure S7.

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Mus musculus myosin, light polypeptide 2, regulatory, cardiac, slow (MyI2), mRNA

Sequence ID: [ref|NM_010861.3|](#) Length: 633 Number of Matches: 1

Range 1: 280 to 303 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
48.1 bits(24)	1e-04	24/24(100%)	0/24(0%)	Plus/Plus

```

Query 1   ACTTCACCGTGTTCCTCACGATGT 24
          |||
sbjct 280 ACTTCACCGTGTTCCTCACGATGT 303
  
```

[Download](#) [GenBank](#) [Graphics](#)

Mus musculus myosin, light polypeptide 2, regulatory, cardiac, slow (MyI2), mRNA

Sequence ID: [ref|NM_010861.3|](#) Length: 633 Number of Matches: 1

Range 1: 510 to 533 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
48.1 bits(24)	1e-04	24/24(100%)	0/24(0%)	Plus/Minus

```

Query 1   TCCGTGGGTAATGATGTGGACCAA 24
          |||
sbjct 533 TCCGTGGGTAATGATGTGGACCAA 510
  
```

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Rattus norvegicus myosin light chain 2 (MyI2), mRNA

Sequence ID: [ref|NM_001035252.2|](#) Length: 677 Number of Matches: 1

[See 1 more title\(s\)](#)

Range 1: 262 to 285 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	0.84	22/24(92%)	0/24(0%)	Plus/Plus

[Download](#) [GenBank](#) [Graphics](#)

Rattus norvegicus myosin light chain 2 (MyI2), mRNA

Sequence ID: [ref|NM_001035252.2|](#) Length: 677 Number of Matches: 1

[See 1 more title\(s\)](#)

Range 1: 492 to 515 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	0.84	22/24(92%)	0/24(0%)	Plus/Minus

```

Query 1   TCCGTGGGTAATGATGTGGACCAA 24
          |||
sbjct 515 TCCGTGGGTGATGATGTGAACCAA 492
  
```

Supplementary Figure S7: Sequence alignment data supporting species-selectivity of the MLC2v primer set used to identify putative mouse-derived ventricular myocytes in the rat heart.

Supplementary Table S2 is presenting the mean of Isl1⁺ cells counted in two non-sequential sections.

sampled sections #	Isl1 ⁺ number of cells counted # mean
110 (108 and 112)	65
140 (138 and 142)	472
190 (188 and 192)	736
240 (238 and 242)	755
280 (278 and 282)	435
330 (328 and 332)	356
370 (368 and 372)	71