



Supplementary Figure 1. Immunofluorescent characterization of Dct-expressing cells in the heart. Sections from e17.5 hearts stained with an anti-Dct antibody (a, d, g, j, m, p, s, v) do not co-express markers of the cardiac conduction system (b), fibroblasts (e), neurons (h, k), cardiac myocytes (n, q), vascular smooth muscle (t) or secondary heart field (w). Filled arrows show Dct-positive cells while open arrows show cells stained by the marker of interest. Merged images of Dct and each individual marker are shown in the panels on the right (c, f, i, l, o, r, u, x). Note there is no overlap seen between Dct and any of these markers.

**Supplementary Table 1. Real-time RT-PCR Primer Sequences**

Transcript	Primer Sequence	PCR Product Size
GAPDH	5'-gcatggactgtggtcatgag-3' 5'-ccatcaccatctccaggag-3'	280
Troponin-I, type 3	5'-tgggcttgaagagcttcaggact-3' 5'-tggcatctgcagagatcctcact-3'	199
Triadin	5'-tcattctgacaaaggccaaacacgc-3' 5'-tctggaactctgggtctcccttt-3'	161
Cx43	5'-tcattctcatgctgggtgtcct-3' 5'-tggtagaggagcagcattgaagt-3'	194
Cardiac $\alpha$ -actin	5'-accatgtaccctggattgccgat-3' 5'-atgggcctgcctcatcactctt-3'	193
Dct	5'-actggcaatgagtcctttgcgttg-3' 5'-agtccgactaatcagcgttgggt-3'	127
Tyrosinase	5'-agtcgtatctggccatggcttct-3' 5'-acagcaagctgtgtagtctt-3'	172
Phospholamban	5'-ttgaaatgcctcagcaagcacgtc-3' 5'-cggctttaagctgagttggcatgt-3'	157
Ryr2	5'-tgtgctgctacatcggcagtatga-3' 5'-gcgaagcaagcagattgatggtgt-3'	113
L-type Ca <sup>2+</sup> $\alpha$ 1C-subunit	5'-agggctcttctgccgaaactact-3' 5'-ccacaaacacgcactgaaccacat-3'	192
Cx45	5'-ggcaaaccaattccaccacatg-3' 5'-gacaatcagcacagttagccag-3'	111

**Supplementary Table 2. Real-time RT-PCR Results**

Transcript	$\Delta C(t)$ A-Myo /GAPDH	$\Delta C(t)$ C-Mel /GAPDH	A-Myo vs. C-Mel Fold Change
Troponin-I	23.1±0.4	33.6±1.3 <sup>A</sup>	>1,000
Triadin	22.6±1.1	34.0±2.1 <sup>A</sup>	>1,000
Cx43	25.5±0.6	36.6±1.0 <sup>A</sup>	>1,000
Cardiac $\alpha$ -actin	22.2±0.9	32.3±0.8 <sup>A</sup>	>1,000
Dct	37.8± 0.8	26.1±0.6 <sup>A</sup>	<0.001
Tyrosinase	34.5±0.3	27.9±0.7 <sup>A</sup>	0.01
Cx45	28.4±0.4	25.5±0.9 <sup>A</sup>	0.13
Phospholamban	25.2±0.7	23.9±1.0 <sup>A</sup>	0.41
Ryr2	28.2±1.0	28.8±1.7	1.5
L-type Ca <sup>2+</sup> $\alpha$ 1C	22.9±0.2	23.8±0.3 <sup>A</sup>	1.9

A-Myo=Atrial myocyte; C-Mel=Cardiac melanocyte; <sup>A</sup>p<0.05 compared to A-Myo. Data are presented as the mean  $\pm$  standard deviation and tests of statistical difference were computed using 2-tailed Student's *t* test.

### Supplementary Table 3.

#### Genes Identified by 1-Way ANOVA with Normalized Values Greater or Less than Median Atrial Myocyte Expression by 2-fold

Common Name	Fold Change	Genbank #	Description
Neo1	54.14	BB350308	neogenin
Trim2	27.68	BB466780	tripartite motif-containing 2
2310076L09Rik	26.88	BB717485	RIKEN cDNA 2310076L09 gene
1700012D01Rik	24.93	AV040390	RIKEN cDNA 1700012D01 gene
Cds2	16.63	BB027654	CDP-diacylglycerol synthase 2
Ints5	13.3	AV014698	integrator complex subunit 5
Mapre2	11.57	BC027056	microtubule-associated protein, RP/EB family, member 2
Bex1	11.33	NM_009052	brain expressed gene 1
2310061F22Rik	10.4	BB253397	RIKEN cDNA 2310061F22 gene
Insig2	10.12	AV257512	insulin induced gene 2
Fat1	7.795	AV088463	FAT tumor suppressor homolog 1 (Drosophila)
Ccni	7.513	NM_017367	cyclin I
---	7.305	BB115446	Transcribed locus
Mtap	7.24	BG075139	methylthioadenosine phosphorylase
Hipk2	6.55	AK003718	homeodomain interacting protein kinase 2
D0H4S114	6.45	BB369191	DNA segment, human D4S114
Prkci	6.073	NM_008857	protein kinase C, iota
Pln	6.027	AK002622	phospholamban
2410004B18Rik	5.631	NM_025555	RIKEN cDNA 2410004B18 gene
Usp47	4.763	BG069271	ubiquitin specific peptidase 47
Sdhc	4.685	NM_025321	succinate dehydrogenase complex, subunit C
Mrps14	4.618	BI246587	mitochondrial ribosomal protein S14
Arf3	4.494	AI987871	ADP-ribosylation factor 3
Actc1	4.433	NM_009608	actin, alpha, cardiac
Pfn2	4.391	NM_019410	profilin 2
1110031B06Rik	4.382	AV217222	RIKEN cDNA 1110031B06 gene
Map2k7	4.364	AW541674	mitogen-activated protein kinase kinase 7
Chchd4	4.322	NM_133928	coiled-coil-helix-coiled-coil-helix domain containing 4
Tmem41b	4.272	BB508081	transmembrane protein 41B
---	4.038	AV162270	CDNA clone IMAGE:40048701

Tmem41b	4.007	BB311030	transmembrane protein 41B
1110002E22Rik	3.931	BE991102	RIKEN cDNA 1110002E22 gene
Strn	3.893	BG519214	striatin, calmodulin binding protein
Sod2	3.874	BQ174944	superoxide dismutase 2, mitochondrial
Trub2	3.843	BG064045	TruB pseudouridine (psi) synthase homolog 2 (E. coli)
Cryz1	3.724	BC010479	crystallin, zeta (quinone reductase)-like 1
D0H4S114	3.686	D45203	DNA segment, human D4S114
Mul1	3.575	BC019516	mitochondrial ubiquitin ligase activator of NFKB 1
Tmem41b	3.523	AA589282	transmembrane protein 41B
Acadvl	3.521	BC026559	acyl-Coenzyme A dehydrogenase, very long chain
2310014D11Rik	3.436	AK009333	RIKEN cDNA 2310014D11 gene
Ndrg2	3.428	NM_013864	N-myc downstream regulated gene 2
1810013L24Rik	3.399	BM230552	RIKEN cDNA 1810013L24 gene
Ube2h	3.386	BB447627	ubiquitin-conjugating enzyme E2H
Ube2l3	3.367	BG066549	ubiquitin-conjugating enzyme E2L 3
Ctgf	3.358	NM_010217	connective tissue growth factor
Csnk2a1	3.312	BB283759	casein kinase 2, alpha 1 polypeptide
Myh7	3.305	NM_080728	myosin, heavy polypeptide 7, cardiac muscle, beta
Insig2	3.262	AV257512	insulin induced gene 2
Trub2	3.259	BG064045	TruB pseudouridine (psi) synthase homolog 2 (E. coli)
Ap1s2	3.17	BB185861	adaptor-related protein complex 1, sigma 2 subunit
Snx4	3.117	NM_080557	sorting nexin 4
Hmgn3	3.102	AV018952	high mobility group nucleosomal binding domain 3
Insig2	3.083	AV257512	insulin induced gene 2
Abi1	3.06	AV330821	abl-interactor 1
Rab11fip5	3.046	BQ177085	RAB11 family interacting protein 5 (class I)
Hdlbp	3.018	AI118566	high density lipoprotein (HDL) binding protein
Bms1	3.006	BB007109	BMS1 homolog, ribosome assembly protein (yeast)
Ccng1	3.004	BG065754	cyclin G1
Lpp	2.973	BB557975	LIM domain containing preferred translocation partner in lipoma
Ndrg4	2.93	AI837704	N-myc downstream regulated gene 4
Tbx20	2.882	AK020409	T-box 20
Dnaja3	2.881	AK004575	DnaJ (Hsp40) homolog, subfamily A, member 3
Parl	2.862	BQ174254	presenilin associated, rhomboid-like
Timm10/Timm13	2.819	NM_013899	translocase of inner mitochondrial membrane 13 homolog (yeast) ///

			10 homology (yeast)
NdrG4	2.815	AV006122	N-myc downstream regulated gene 4
Mdh1	2.806	NM_008618	malate dehydrogenase 1, NAD (soluble)
Sorbs2	2.794	BB251748	sorbin and SH3 domain containing 2
---	2.787	AV324454	---
1110002E22Rik	2.765	BB099116	RIKEN cDNA 1110002E22 gene
Uqcrh	2.762	AK019085	ubiquinol-cytochrome c reductase hinge protein
Nfu1	2.693	BC018355	NFU1 iron-sulfur cluster scaffold homolog ( <i>S. cerevisiae</i> )
Ube2b	2.686	AK010432	ubiquitin-conjugating enzyme E2B, RAD6 homology
Trdn	2.677	AF223416	triadin
Rusc1	2.669	BB145073	RUN and SH3 domain containing 1
Ldb3	2.626	BB479063	LIM domain binding 3
Apoo	2.622	AK002320	apolipoprotein O
Plag1	2.62	AF147785	pleiomorphic adenoma gene-like 1
Pigq	2.603	BB546727	phosphatidylinositol glycan anchor biosynthesis, class Q
Dynll1	2.58	NM_019682	dynein light chain LC8-type 1 /// predicted gene, EG627788
Grpel1	2.547	NM_024478	GrpE-like 1, mitochondrial
MsrB3	2.546	AV286522	methionine sulfoxide reductase B3
Actr6	2.543	AK008409	ARP6 actin-related protein 6 homolog (yeast)
Slc7a1	2.531	BB264620	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
Myl3	2.524	AK002312	myosin, light polypeptide 3
Ccdc47	2.507	AB040489	coiled-coil domain containing 47
Ung	2.504	BC004037	uracil DNA glycosylase
Ube2g1	2.489	NM_025985	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, <i>C. elegans</i> )
Ckm	2.487	NM_007710	creatine kinase, muscle
Acta2	2.483	NM_007392	actin, alpha 2, smooth muscle, aorta
Eif3j	2.474	BB379268	eukaryotic translation initiation factor 3, subunit J
Myl3	2.464	X67685	myosin, light polypeptide 3
Atp6v1c1	2.462	AA987147	ATPase, H <sup>+</sup> transporting, lysosomal V1 subunit C1
Trim63	2.454	BG817292	tripartite motif-containing 63
Phip	2.45	AK012667	pleckstrin homology domain interacting protein
Gbas	2.436	NM_008095	glioblastoma amplified sequence
Hadhb	2.405	BG866501	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase, beta subunit
Tmcc1	2.399	AI506779	transmembrane and coiled coil domains 1

Tfr	2.386	AK011596	transferrin receptor
Arfp1	2.376	AV087417	ADP-ribosylation factor interacting protein 1
Ptdss2	2.374	BB490580	phosphatidylserine synthase 2
D10Ert322e	2.368	NM_026065	DNA segment, Chr 10, ERATO Doi 322, expressed
Msn	2.364	NM_010833	moesin
Atp5h	2.357	AF354051	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit d
Rcan1	2.345	AF282255	regulator of calcineurin 1
---	2.342	C79511	---
Ablim1	2.339	BG065289	actin-binding LIM protein 1
4931406P16Rik	2.336	BG067664	RIKEN cDNA 4931406P16 gene
Taf13	2.336	NM_025444	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor
Myl3	2.323	X67685	myosin, light polypeptide 3
Spsb4	2.32	BC023083	splA/ryanodine receptor domain and SOCS box containing 4
6530403A03Rik	2.305	BC021443	RIKEN cDNA 6530403A03 gene
Got2	2.301	U82470	glutamate oxaloacetate transaminase 2, mitochondrial
Ankrd1	2.294	AK009959	ankyrin repeat domain 1 (cardiac muscle)
Ghr	2.288	NM_010284	growth hormone receptor
Pigq	2.287	BB248089	phosphatidylinositol glycan anchor biosynthesis, class Q
Dscr3	2.284	NM_007834	Down syndrome critical region gene 3
R3hdm1	2.281	BQ174018	R3H domain 1 (binds single-stranded nucleic acids)
Usp39	2.273	BB446580	ubiquitin specific peptidase 39
Nudt19	2.27	BG070689	nudix (nucleoside diphosphate linked moiety X)-type motif 19
2310003L22Rik	2.269	AK009123	RIKEN cDNA 2310003L22 gene
Ltbp3	2.264	BB324823	latent transforming growth factor beta binding protein 3
Sri	2.263	AK008404	sorcin
Strn	2.243	BG070684	striatin, calmodulin binding protein
Prmt2	2.233	BB357347	protein arginine N-methyltransferase 2
Nrp1	2.233	AK011144	neuropilin 1
Xpr1	2.222	AV337591	xenotropic and polytropic retrovirus receptor 1
Aco1	2.218	BB504570	aconitase 1
Tpm1	2.207	AK002271	tropomyosin 1, alpha
Gapdh	2.199	NM_008084	glyceraldehyde-3-phosphate dehydrogenase
Synpo2l	2.189	BB322227	synaptopodin 2-like
Myom1	2.187	NM_010867	myomesin 1
Pkp2	2.187	AA516617	plakophilin 2

Phldb2	2.183	AV253284	pleckstrin homology-like domain, family B, member 2
Popdc2	2.183	NM_022318	popeye domain containing 2
Usp46	2.177	BM231854	Ubiquitin specific peptidase 46
Fhl2	2.175	NM_010212	four and a half LIM domains 2
Arpc2	2.164	BG967632	actin related protein 2/3 complex, subunit 2
Psmc11	2.149	AV136581	Proteasome 26S subunit, non-ATPase, 11
Sspn	2.138	BC021484	sarcospan
Tmem106b	2.136	AV025807	transmembrane protein 106B
Nola2	2.134	BC024944	nucleolar protein family A, member 2
Ptpla	2.129	BB014781	protein tyrosine phosphatase-like, member a
---	2.129	BF682509	CDNA clone IMAGE:5721202
Rps17	2.128	AA030209	Ribosomal protein S17
Cap2	2.127	AV261931	CAP, adenylate cyclase-associated protein, 2 (yeast)
Pdk4	2.115	NM_013743	pyruvate dehydrogenase kinase, isoenzyme 4
Atp5a1	2.111	C78762	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subunit, isoform 1
Nars	2.11	AK013880	asparaginyl-tRNA synthetase
Gsto1	2.095	AV003026	glutathione S-transferase omega 1
Pls3	2.093	BC005459	plastin 3 (T-isoform)
1110003E01Rik	2.093	NM_133697	RIKEN cDNA 1110003E01 gene
Sdsl	2.092	NM_133902	serine dehydratase-like
2700023E23Rik	2.092	BB822655	RIKEN cDNA 2700023E23 gene
Sars	2.09	BC008612	seryl-aminoacyl-tRNA synthetase
Pln	2.089	AK002622	phospholamban
Dnajb4	2.086	BC017161	DnaJ (Hsp40) homolog, subfamily B, member 4
Cdc42ep3	2.073	BB012489	CDC42 effector protein (Rho GTPase binding) 3
Chchd2	2.065	BI694986	coiled-coil-helix-coiled-coil-helix domain containing 2
Ola1	2.061	AK019142	Obg-like ATPase 1
Larp5	2.051	BM200204	La ribonucleoprotein domain family, member 5
Arl6ip2	2.05	NM_019717	ADP-ribosylation factor-like 6 interacting protein 2
2310050B05Rik	2.048	AV381718	RIKEN cDNA 2310050B05 gene
Eif2s3x	2.041	BC006682	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked
Ppp2ca	2.033	BB053843	protein phosphatase 2, catalytic subunit, alpha isoform
Ndufab1	2.032	AV092283	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1
Slc25a39	2.025	BB514802	solute carrier family 25, member 39



Col4a1	2.023	BF158638	collagen, type IV, alpha 1
Trp53inp2	2.018	AK003956	transformation related protein 53 inducible nuclear protein 2
Smpx	2.014	NM_025357	small muscle protein, X-linked
---	2.011	BB752393	Transcribed locus, strongly similar to NP_037393.1 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
Mrpl2	2.006	NM_025302	mitochondrial ribosomal protein L2
Slco3a1	0.499	NM_023908	solute carrier organic anion transporter family, member 3a1
Skp1a	0.496	AV347477	S-phase kinase-associated protein 1A
Luc7l2	0.493	BG075618	LUC7-like 2 ( <i>S. cerevisiae</i> )
Trdn	0.492	AF223417	triadin
Hfe2	0.491	AK009636	hemochromatosis type 2 (juvenile) (human homolog)
Ube2d3	0.489	AK009276	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)
AU016916	0.487	AU016916	expressed sequence AU016916
Tomm7	0.485	BB609428	translocase of outer mitochondrial membrane 7 homolog (yeast)
Creb3	0.483	AU044960	cAMP responsive element binding protein 3
Tmtc1	0.472	BQ174442	transmembrane and tetratricopeptide repeat containing 1
Cnn3	0.471	BB833102	calponin 3, acidic /// similar to calponin 3, acidic
Csrp2	0.466	NM_007792	cysteine and glycine-rich protein 2
Gja1	0.462	BB142324	gap junction protein, alpha 1
Dedd	0.459	BE199280	death effector domain-containing
Rragd	0.456	BF462770	Ras-related GTP binding D
Gng12	0.452	NM_025278	guanine nucleotide binding protein (G protein), gamma 12
Prkag2	0.451	BB756794	protein kinase, AMP-activated, gamma 2 non-catalytic subunit
Ccm2	0.449	BI903794	cerebral cavernous malformation 2 homolog (human)
Impdh2	0.444	M33934	inosine 5'-phosphate dehydrogenase 2
Spnb2	0.438	BQ174069	spectrin beta 2
Urod	0.437	AV292769	uroporphyrinogen decarboxylase
---	0.431	AV006589	---
Slc38a1	0.419	BF165681	solute carrier family 38, member 1
Zfp91	0.419	U05343	zinc finger protein 91
Litaf	0.415	AV360881	LPS-induced TN factor
Sap18	0.408	AV023865	Sin3-associated polypeptide 18 /// similar to SAP18
G3bp2	0.403	BG069656	GTPase activating protein (SH3 domain) binding protein 2
Cryz	0.403	BB793369	crystallin, zeta
Prepl	0.393	BB005298	prolyl endopeptidase-like

Slc2a1	0.392	BM209618	solute carrier family 2, member 1
Mrpl39	0.39	NM_017404	mitochondrial ribosomal protein L39
Arhgap21	0.376	BM213829	Rho GTPase activating protein 21
Xpo7	0.375	BB111454	exportin 7
Finc	0.373	AV014577	filamin C, gamma (actin binding protein 280)
Fndc3b	0.372	BG064539	fibronectin type III domain containing 3B
Dsg2	0.329	BG092030	desmoglein 2
Slc38a10	0.299	BB315716	solute carrier family 38, member 10
Polrmt	0.28	BB739221	polymerase (RNA) mitochondrial (DNA directed)
Zdhhc6	0.249	AV142865	zinc finger, DHHC domain containing 6
Clu	0.226	BB433678	clusterin
Clu	0.209	AV152288	clusterin
Clu	0.201	AV075715	clusterin
Pcyox1	0.121	BB785407	prenylcysteine oxidase 1

**Supplementary Table 4. Baseline ECG Intervals**

	Sedated 6-lead ECG		Telemetry ECG	
	<i>Dct</i> <sup>-/-</sup> (n=11)	<i>Dct</i> <sup>+/-</sup> (n=12)	<i>Dct</i> <sup>-/-</sup> (n=6)	<i>Dct</i> <sup>+/-</sup> (n=6)
SCL (ms)	160.1 ± 33.7	192.3 ± 62.2	119.8 ± 51.0	116.2 ± 46.5
HR (bpm)	394.0 ± 66.7	320.9 ± 90.3	497.6 ± 72.4	516.1 ± 67.4
PR (ms)	41.8 ± 4.9	40.3 ± 2.4	34.7 ± 4.1	33.9 ± 2.8
QRS (ms)	11.1 ± 1.8	10.8 ± 1.3	10.6 ± 1.4	10.3 ± 1.6
QT (ms)	26.2 ± 3.1	24.0 ± 7.0	22.1 ± 2.8	21.9 ± 3.2
QTm (ms)	19.6 ± 2.5	21.4 ± 2.8	20.5 ± 2.2	19.8 ± 2.0

<sup>A</sup>p<0.05 compared to *Dct*<sup>-/-</sup>; SCL = sinus cycle length; HR = heart rate; PR = PR interval; QRS = QRS duration; QT = QT interval; QTm = QT interval corrected for murine physiology. Data are presented as the mean ± standard deviation and tests of statistical difference were computed using 2-tailed Student's *t* test for ECG parameters measured by telemetry or sedated 6-limb leads, separately

**Supplementary Table 5. Baseline Echocardiographic Data**

	<i>Dct</i> <sup>-/-</sup> (n=4)	<i>Dct</i> <sup>+/-</sup> (n=4)	<i>W/Wv</i> (n=5)	<i>Dct</i> <sup>-/-</sup> , <i>W/Wv</i> <sup>/</sup> (n=5)
Heart Rate (bpm)	426.2 ± 42.6	465.7 ± 50.7	425.6 ± 42.6	465.9 ± 50.7
LV FS (%)	36.5 ± 4.6	37.5 ± 3.1	36.5 ± 4.6	37.5 ± 3.1
Simpson EF (%)	55.5 ± 5.0	56.5 ± 5.3	55.5 ± 5.0	56.5 ± 5.3
LV Mass (mg)	81.9 ± 25.8	68.2 ± 22.0	81.9 ± 25.8	68.2 ± 22.0
IVS (mm)	0.88 ± 0.1	0.77 ± 0.1	0.88 ± 0.1	0.77 ± 0.1
LV PW (mm)	0.73 ± 0.1	0.77 ± 0.1	0.73 ± 0.1	0.77 ± 0.1
Ao V <sub>max</sub> (mm/s)	830.4 ± 161	877.5 ± 204	830.3 ± 161	878.8 ± 204
MV E at A (mm/s)	645.2 ± 143	745.7 ± 148	645.4 ± 143	746.0 ± 148
PA V <sub>max</sub> (mm/s)	746.8 ± 98.3	647.9 ± 77.6	747.2 ± 98.3	646.0 ± 77.6

<sup>A</sup>p<0.05 compared to *Dct*<sup>-/-</sup>; <sup>B</sup>p<0.05 compared to *Dct*<sup>+/-</sup>; <sup>C</sup>p<0.05 compared to *W/Wv*, <sup>D</sup>p<0.05 compared to *Dct*<sup>-/-</sup>, *W/Wv*; LV FS = left ventricular fractional shortening; Simpson EF = ejection fraction determined by Simpson's method; LV Mass = left ventricular mass; IVS = interventricular septum width; LV PW = left ventricular posterior wall width; Ao V<sub>max</sub> = maximal velocity across the aortic valve; MV E at A = mitral valve "E" wave at "A" wave; PA V<sub>max</sub> = Pulmonary artery velocity maximum. Data are presented as the mean ± standard deviation and tests of statistical difference were computed using 1-way ANOVA followed by Tukey post-hoc analysis.

**Supplementary Table 6. EP Phenotypes of Mouse Lines Studied**

Mouse Line	Cardiac Melanocytes	Observed EP Phenotype
Homozygous <i>DctCre</i> <sup>A</sup>	Yes	Inducible and spontaneous atrial arrhythmias
Heterozygote <i>DctCre</i> <sup>A</sup>	Yes	No abnormal EP phenotype
Homozygote <i>DctCre</i> crossed with <i>Z/EG</i> <sup>A</sup>	Yes	Isolated cardiac melanocytes have prolonged repolarization with afterdepolarizations and calcium oscillations
Heterozygote <i>DctCre</i> crossed with <i>Z/EG</i> <sup>A</sup>	Yes	No abnormal EP phenotype
Kit mutant ( <i>W/W<sup>v</sup></i> )	No	No abnormal EP phenotype
Kit mutant crossed with homozygous <i>DctCre</i>	No	No abnormal EP phenotype
<i>Dct-LacZ</i> transgenic	Yes	No abnormal EP phenotype

<sup>A</sup>We employed *DctCre* knockin mice for *in vivo* electrophysiological studies and used *DctCre* mice crossed with *Z/EG* transgenic mice as a source of cardiac melanocytes and myocytes for single cell electrophysiology studies.