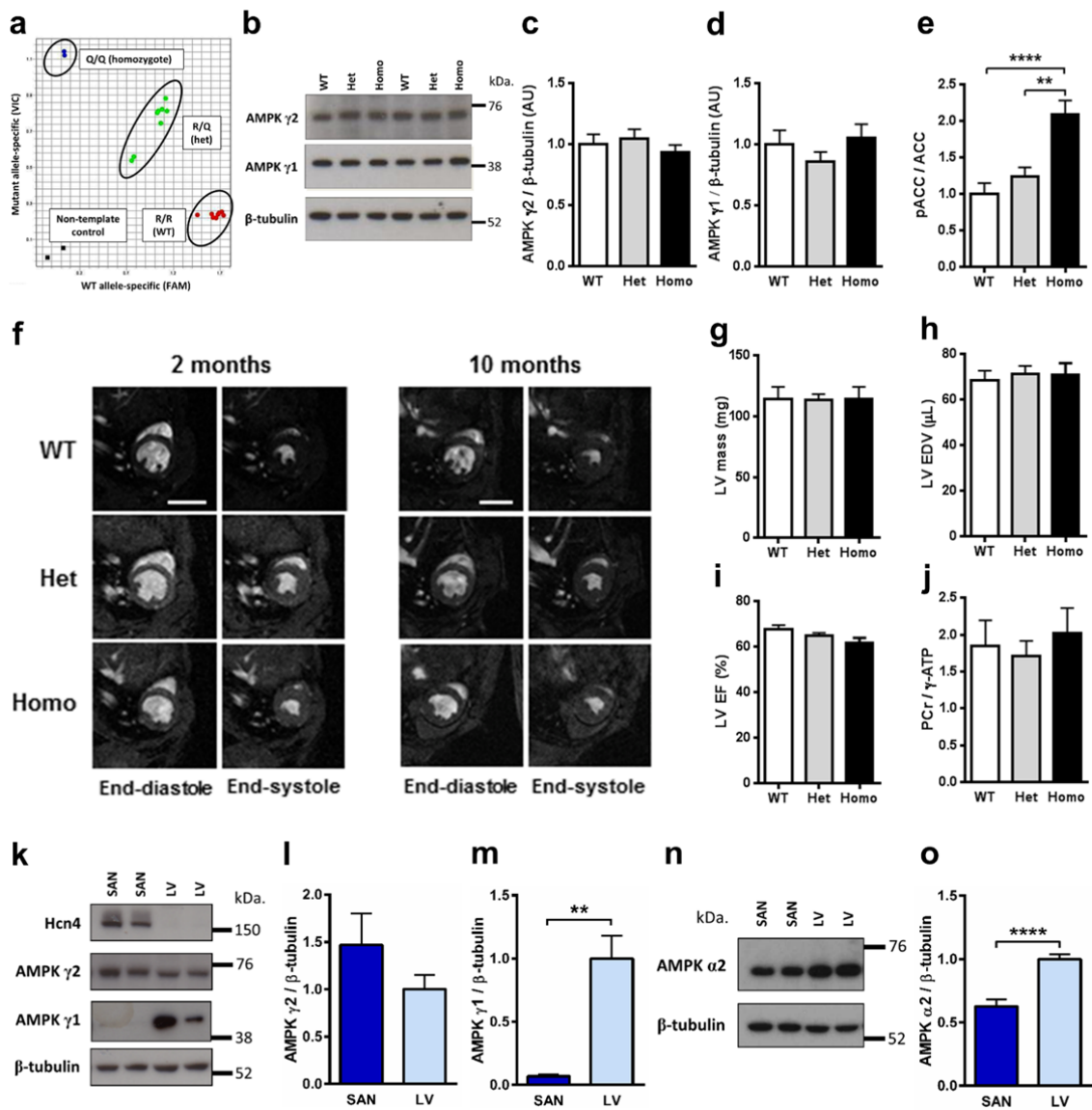
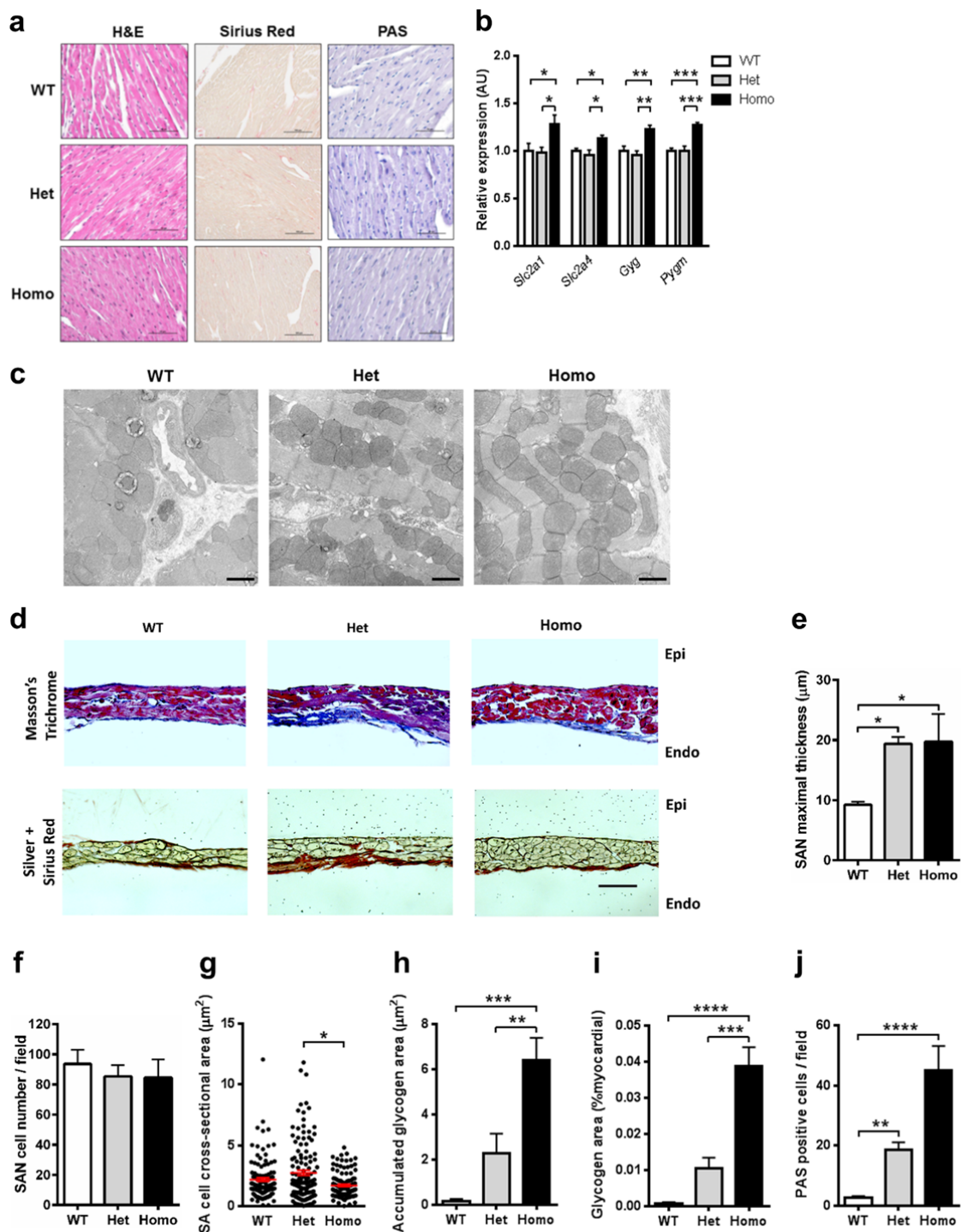


1 SUPPLEMENTARY FIGURES AND LEGENDS



5 **Supplementary Figure 1. Validation and cardiac phenotype of the R299Q γ 2 AMPK knock-in mouse**
6 **model. (a)** Allelic discrimination plot obtained using WT γ 2- and R299Q γ 2-specific probes on whole
7 heart cDNA. **(b)** Representative western blot of whole heart tissue for γ AMPK isoforms from R299Q
8 γ 2 (Het, heterozygous; Homo, homozygous) mice and wild-type (WT) controls, with β -tubulin as
9 loading control. **(c, d)** Densitometry analysis of western blot of whole heart tissue from R299Q γ 2
10 and WT mice for **(c)** γ 2 and **(d)** γ 1 AMPK isoforms. Relative protein levels are presented normalised
11 to β -tubulin ($n = 11-15$). **(e)** Densitometry analysis of western blots of whole heart tissue from R299Q
12 γ 2 and WT mice for phospho-acetyl-CoA Carboxylase (pACC) ($n = 11-15$). **(f)** Representative mid-
13 ventricular, end-diastolic and end-systolic short-axis cine-MRI images at 2 and 10 months of age
14 (scale bar 5 mm). **(g-i)** Cine MRI analysis of left ventricular (LV) mass **(g)**, end-diastolic volume (EDV)
15 **(h)** and ejection fraction (EF) **(i)** in R299Q γ 2 and WT mice aged 10 months ($n = 8-19$). **(j)** *In vivo*
16 myocardial PCr/ γ -ATP ratio determined by ^{31}P MRS (Magnetic Resonance Spectroscopy) ($n = 7-19$).
17 **(k-m)** Western blot **(k)** and densitometry **(l, m)** of γ 2 and γ 1 AMPK in normal murine SA node and LV,
18 together with SA node positive (HCN4) and loading (β -tubulin) controls ($n = 6-8$). **(n, o)** Western blot
19 **(n)** and densitometry **(o)** of α 2 AMPK in normal murine SA node and LV ($n = 4-10$). Uncropped
20 western blots are shown in Supplementary Fig. 10. In **c-e, g-j**, one-way analysis of variance (ANOVA)
21 followed by Holm-Sidak's multiple comparisons test was performed; in **l, m, o** Student's *t*-test was
22 performed. ** $P < 0.01$, **** $P < 0.0001$. In **c-e, g-j, l,m,o** data are shown as means $\pm$ s.e.m.

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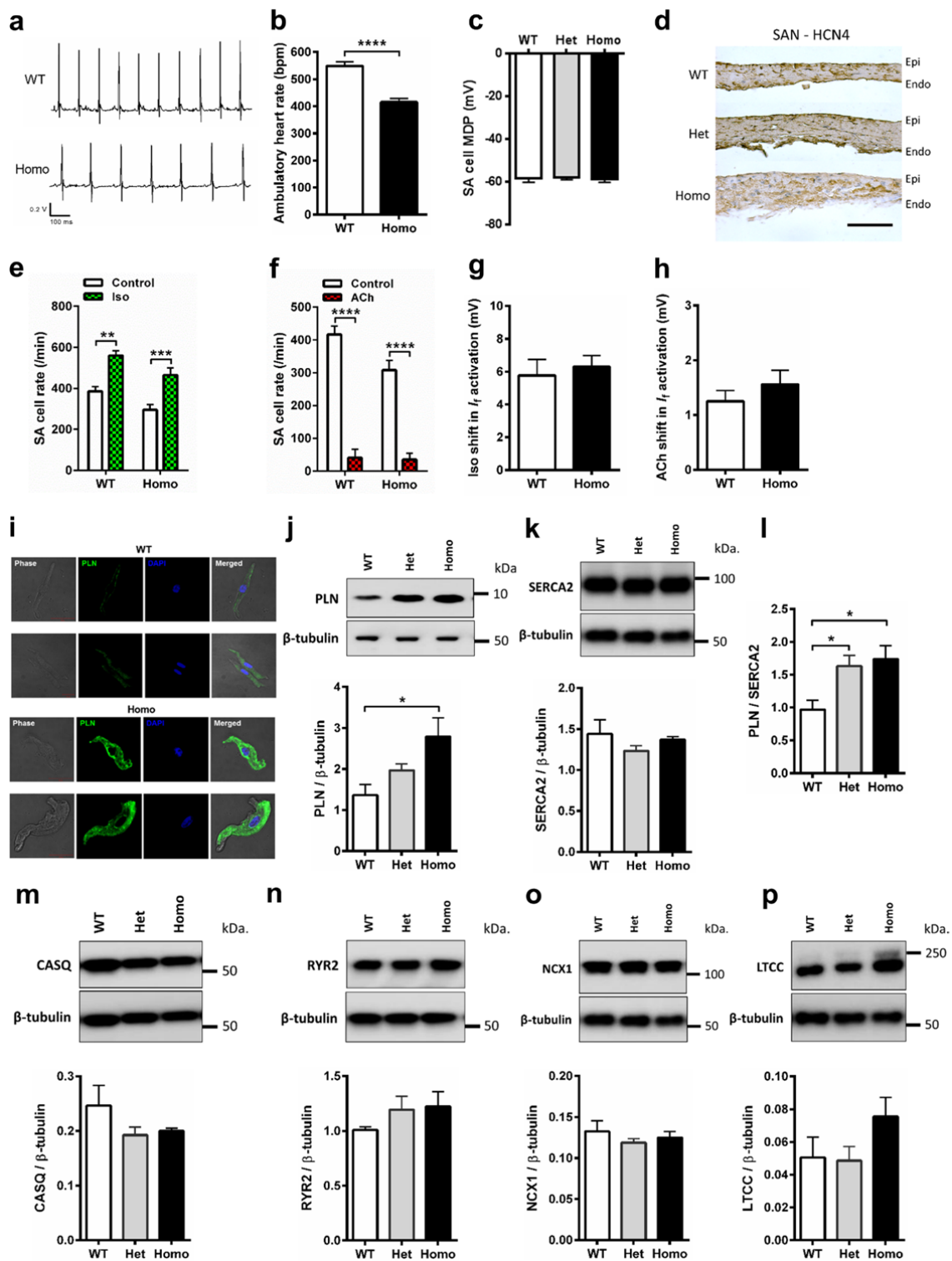
26 **Supplementary Figure 2. Cardiac histology and glycogen content of R299Q γ 2 AMPK knock-in mice.**

27 (a) Histological appearances of hearts from R299Q γ 2 and WT mice aged 12 months stained for
28 haematoxylin and eosin (H&E, scale bar 50 μ m), sirius red (scale bar 100 μ m) and periodic acid-Schiff
29 (PAS, scale bar 50 μ m). (b) Cardiac relative expression of genes (by qRT-PCR) involved in glucose
30 uptake and glycogen metabolism from R299Q γ 2 and WT mice ($n = 7-8$). (c) Cardiac ultrastructure of
31 R299Q γ 2 and WT mice aged 12 months by transmission electron microscopy (scale bar 1 μ m). (d)
32 Representative SA node sections stained with Masson's trichrome (upper row) or silver staining with
33 sirius red (lower row) (scale bar 10 μ m). (e, f) Maximal SA node thickness (e) and SA node cell
34 number per field (f) in R299Q γ 2 and WT mice. (g) Cross-sectional area of individual SA cells from
35 R299Q γ 2 and WT mice. (h-j) Quantification of glycogen content from PAS-stained SA node sections
36 of R299Q γ 2 and WT mice ($n = 12$). In b, e, f, h-j, one-way analysis of variance (ANOVA) followed by
37 Holm-Sidak's multiple comparisons test was performed; in g, the Kruskal-Wallis test followed by
38 Dunn's multiple comparisons test was performed. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P <$
39 0.0001. In b, e-j, data are shown as means $\pm$ s.e.m.

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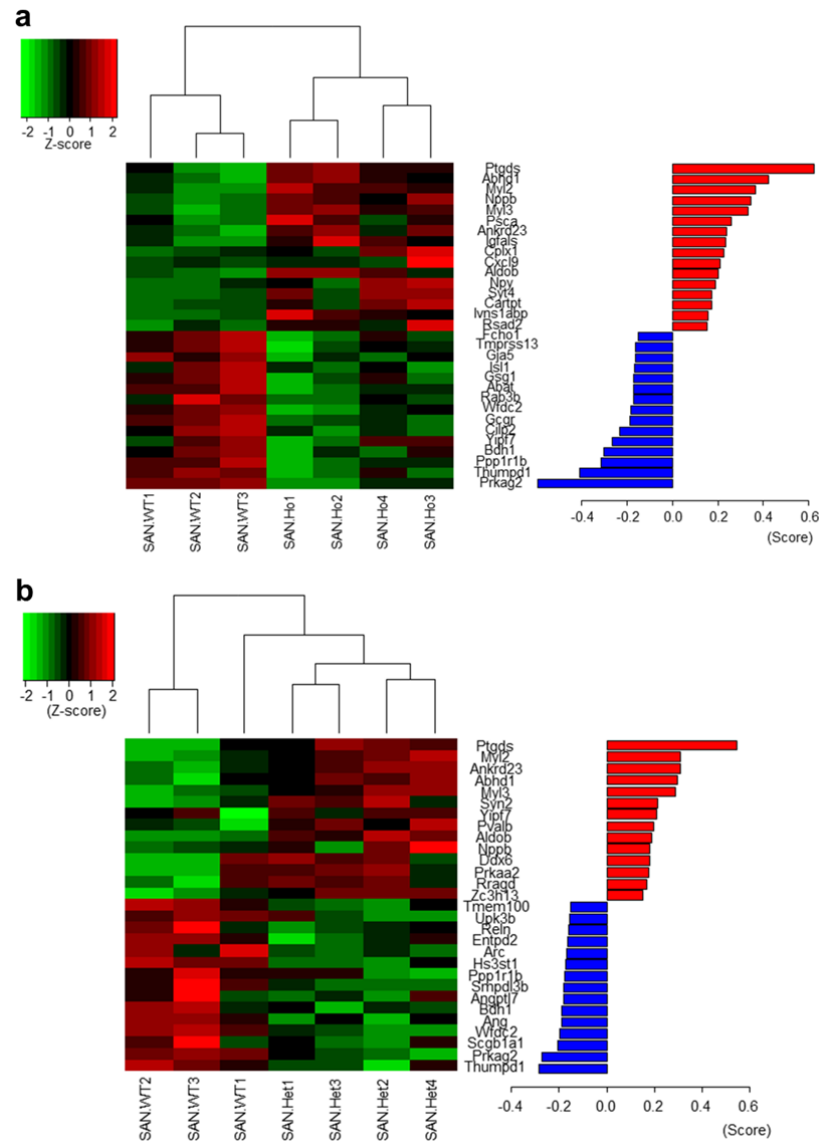
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Supplementary Figure 3. SA cell electrophysiology, HCN4 and Ca²⁺ clock component expression in R299Q γ 2 mice. (a, b) Representative ambulatory telemetry-derived ECG recordings (a) and mean ambulatory HR (b) of WT and homozygous R299Q γ 2 mice ($n = 8$ per genotype). (c) Maximum diastolic potential (MDP) of isolated SA cells from R299Q γ 2 and WT mice ($n = 5-11$). (d) SA node sections stained with anti-HCN4 (scale bar 5 μ m). (e, f) Mean SA cell spontaneous rate under control conditions or in response to stimulation with 30 nM isoproterenol (Iso, e) or 30 nM acetylcholine (ACh, f) ($n = 6-8$). (g, h) Mean shifts of the I_f activation curve induced by 30 nM Iso (g) or 30 nM ACh (h). Iso and ACh shifts are depolarizing and hyperpolarizing, respectively ($n = 5-8$). (i) Immunohistochemistry for total phospholamban (PLN, green) in freshly isolated SA cells from WT and homozygous R299Q γ 2 mice (scale bar 20 μ m). Nuclei were counterstained with DAPI (blue). (j-p) Western blot (and accompanying densitometry) of isolated SA node from WT and R299Q γ 2 mice for the calcium clock components: phospholamban (PLN, j), sarco(endo)plasmic reticulum Ca²⁺-ATPase (SERCA, k), calsequestrin (CASQ, m), cardiac ryanodine receptor (RYR2, n), Na⁺/Ca²⁺ exchanger (NCX1, o) and L-type Ca²⁺ channel (LTCC, p), together with the PLN/SERCA2 ratio (l). Uncropped western blots with location of molecular weight markers are shown in Supplementary Fig. 10. In b, g, h, the Student's t -test was performed; in c, j-p, one-way analysis of variance (ANOVA) was performed; in e, f, two-way ANOVA was performed. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$. In b, c, e-h, j-p, data are shown as means $\pm$ s.e.m.



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67 **Supplementary Figure 4. Hierarchical cluster analysis of SA node microarray from R299Q $\gamma 2$ mice.**

68 **(a, b)** Heat map plot of differentially expressed genes from SA node of **(a)** homozygous R299Q $\gamma 2$ vs

69 WT and **(b)** heterozygous R299Q $\gamma 2$ vs WT mice. Genes were selected with the Kolmogorov-Smirnov

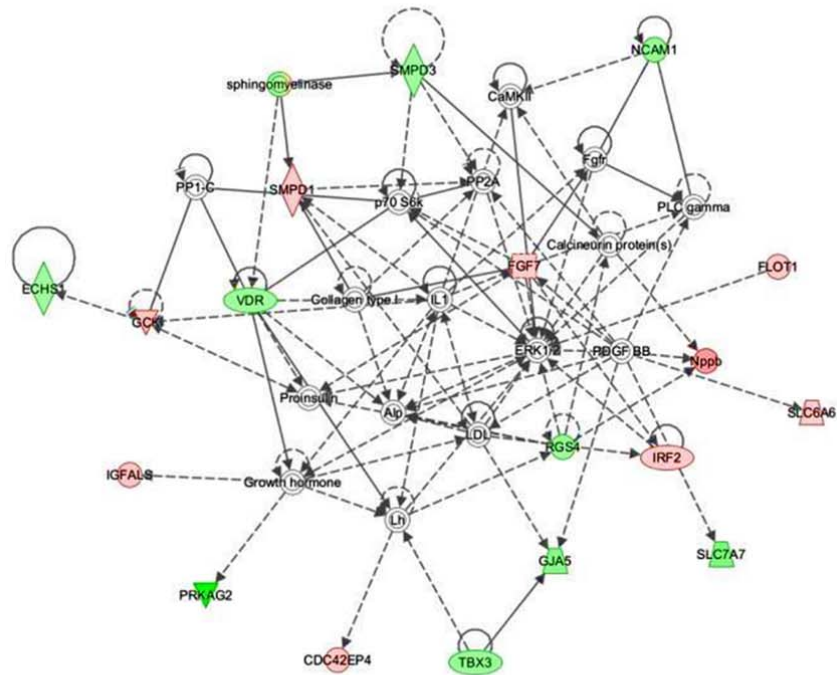
70 test (score >0.15 or <-0.15). The Z-score is the standardized level of expression obtained by

71 subtracting the mean from each value and dividing the results by the standard deviation. GSEA

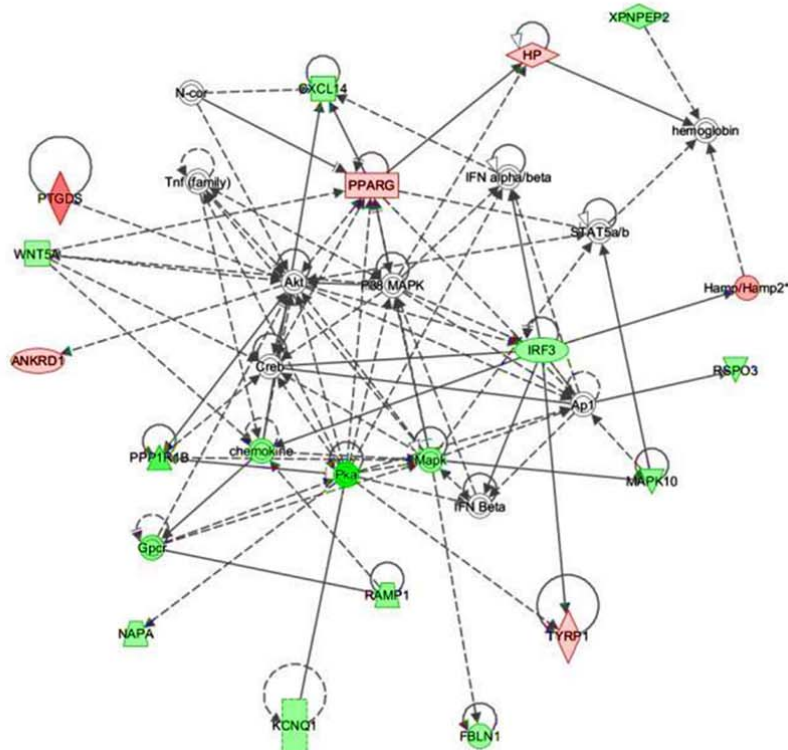
72 software was used to compute scores for each gene. Red and blue bars indicate up- and down-

73 regulation, respectively.

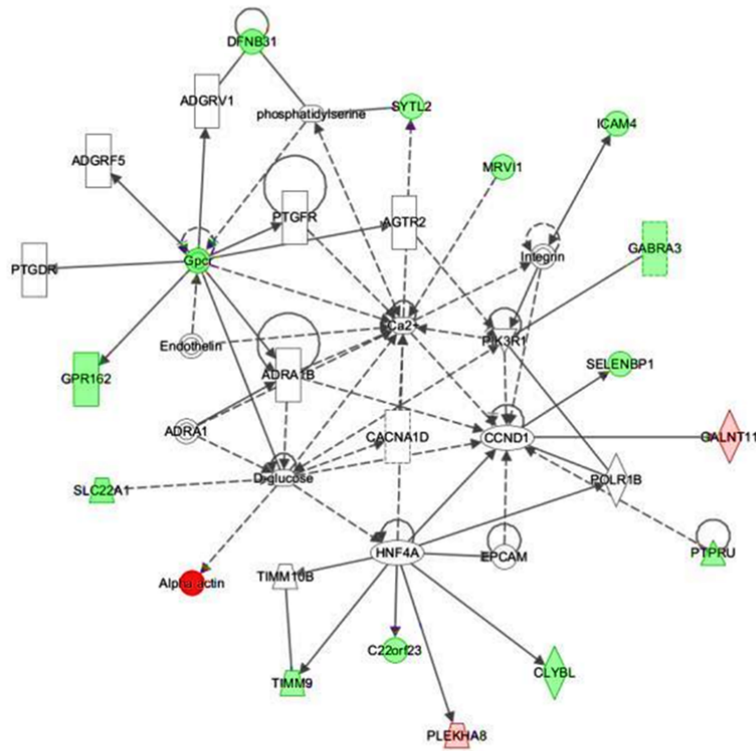
Network 1 – Homo vs WT



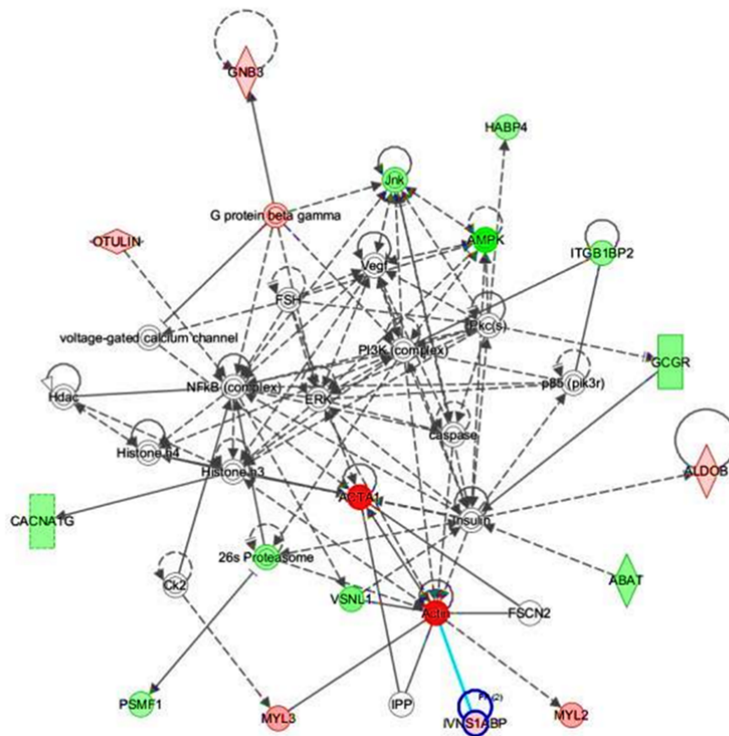
Network 2 – Homo vs WT



Network 3 – Homo vs WT



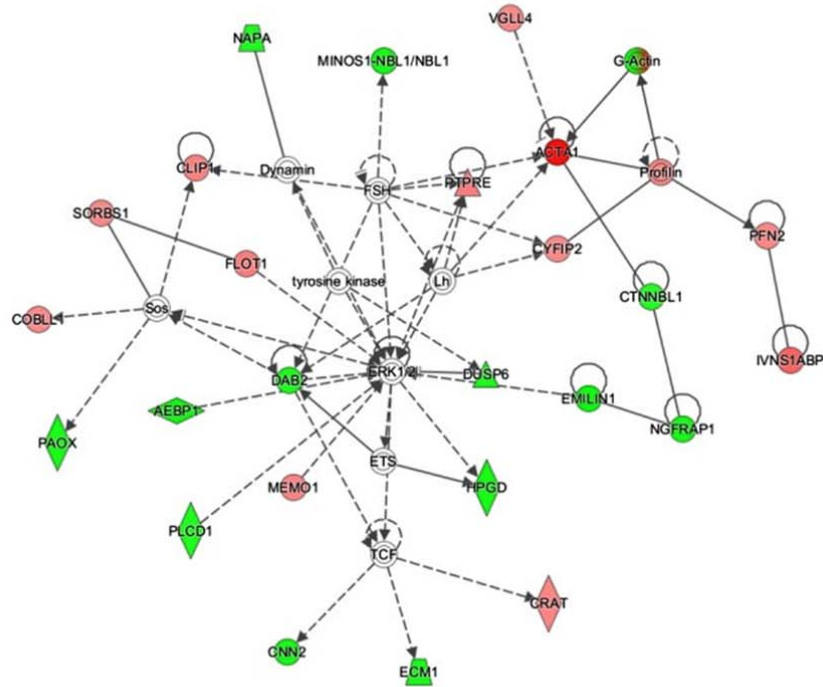
Network 4 – Homo vs WT



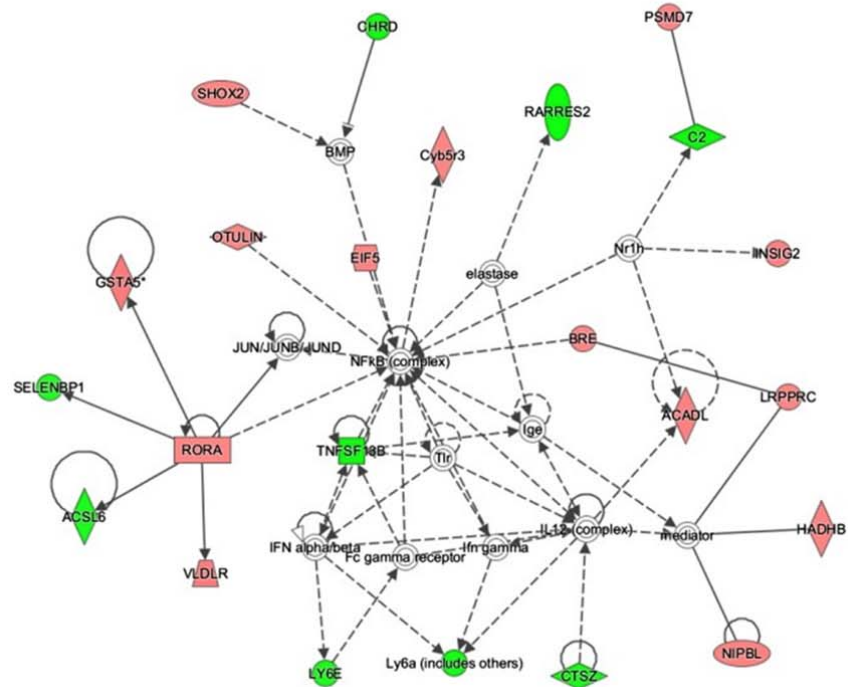
77 **Supplementary Figure 5. Ingenuity pathway network analysis of homozygote R299Q γ 2 versus WT**
78 **differential SA node transcriptome.** Red/green are genes up/down-regulated, respectively, in SA
79 node of homozygous R299Q γ 2 mice vs WT; dashed line - indirect interactions; solid lines - direct
80 interactions. Detailed legend for symbols given in:
81 http://ingenuity.force.com/ipa/articles/Feature_Description/Legend.

82

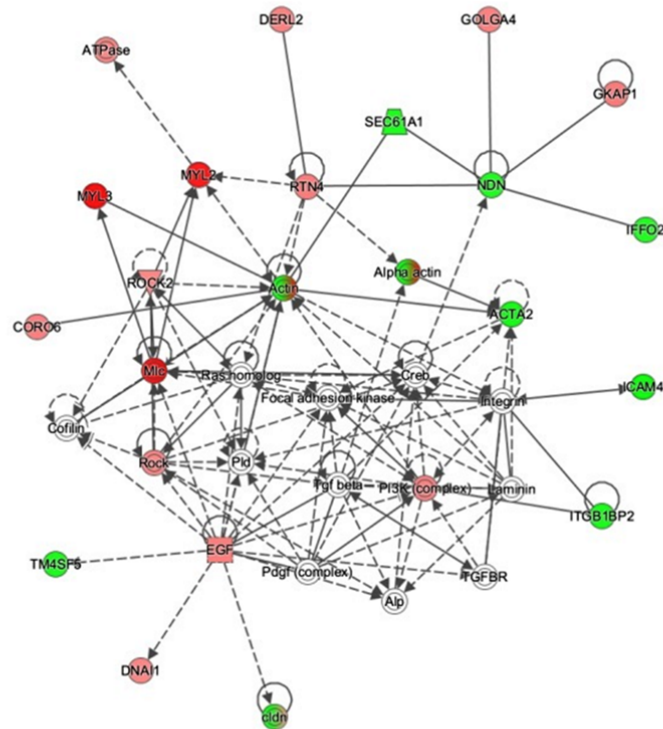
Network 1 – Het vs WT



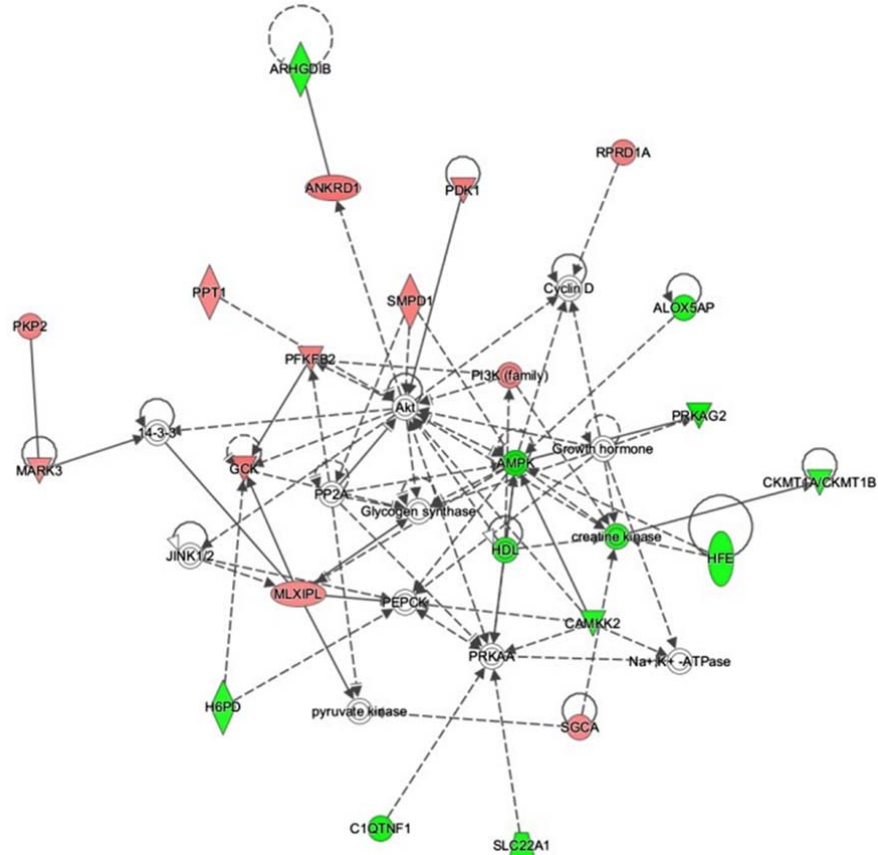
Network 2 – Het vs WT



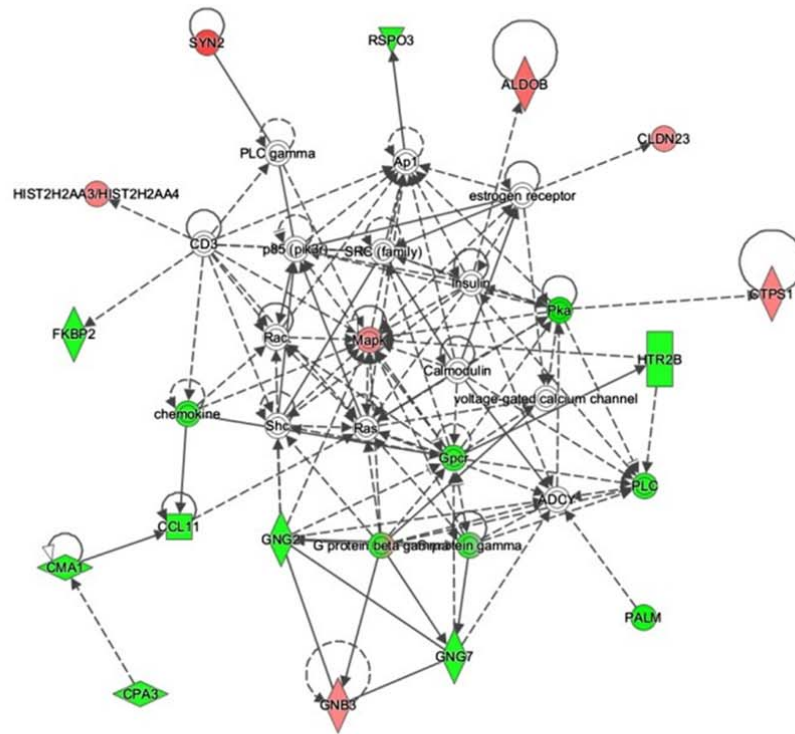
Network 3 – Het vs WT



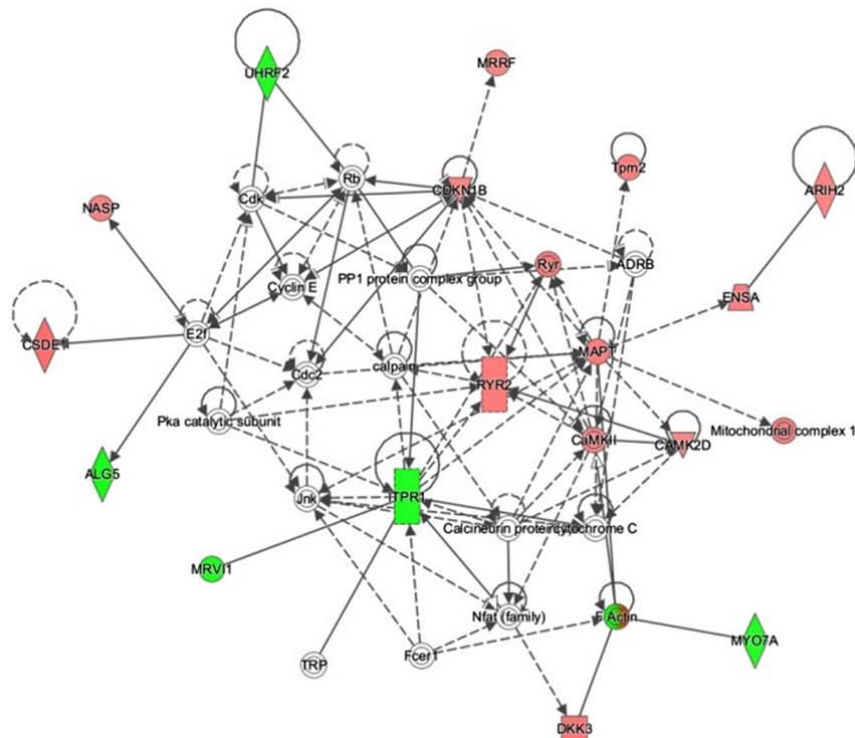
Network 4 – Het vs WT



Network 5 – Het vs WT



Network 6 – Het vs WT

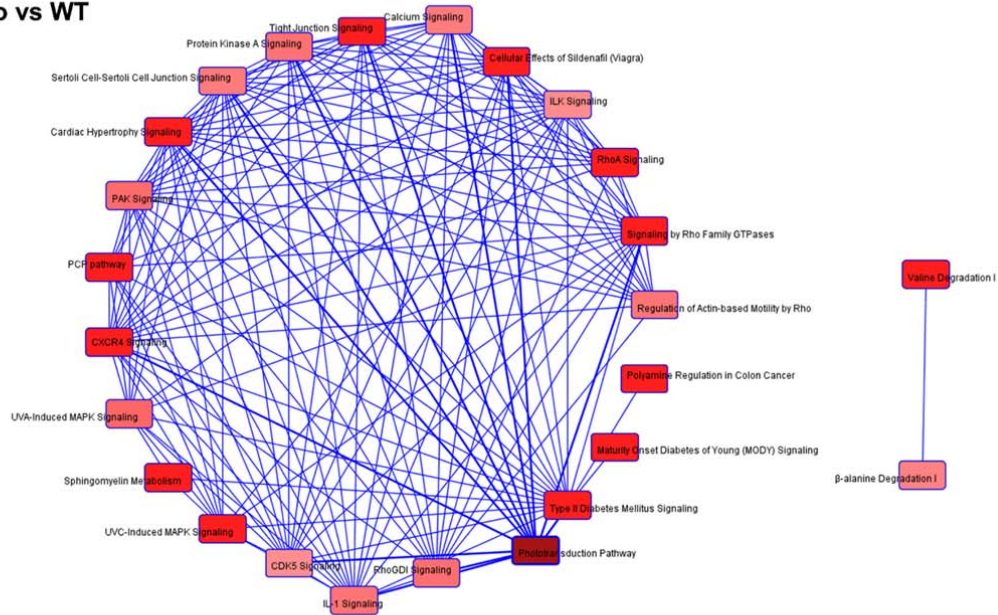


86 **Supplementary Figure 6. Ingenuity pathway network analysis of heterozygote R299Q γ 2 versus WT**
87 **differential SA node transcriptome.** Red/green are genes up/down-regulated, respectively, in SA
88 node of heterozygous R299Q γ 2 mice vs WT; dashed line - indirect interactions; solid lines - direct
89 interactions. Detailed legend for symbols given in:

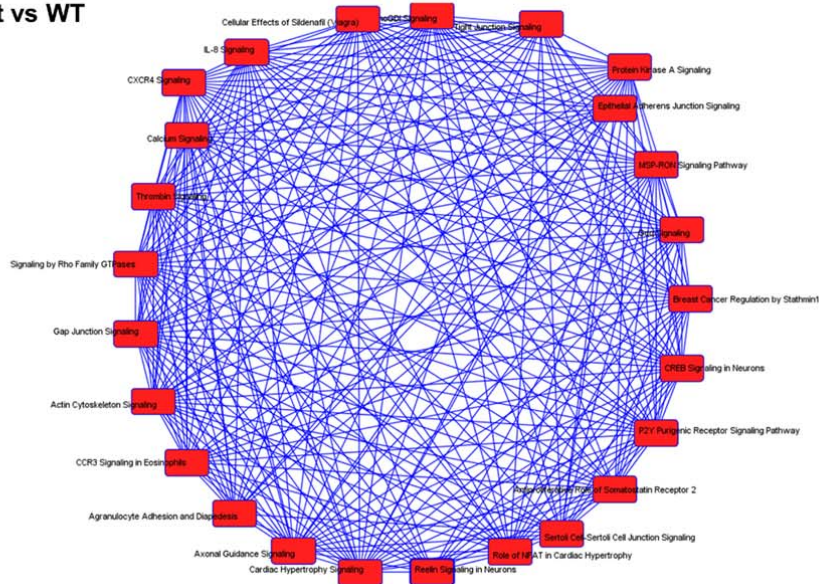
90 http://ingenuity.force.com/ipa/articles/Feature_Description/Legend.

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a Homo vs WT



b Het vs WT



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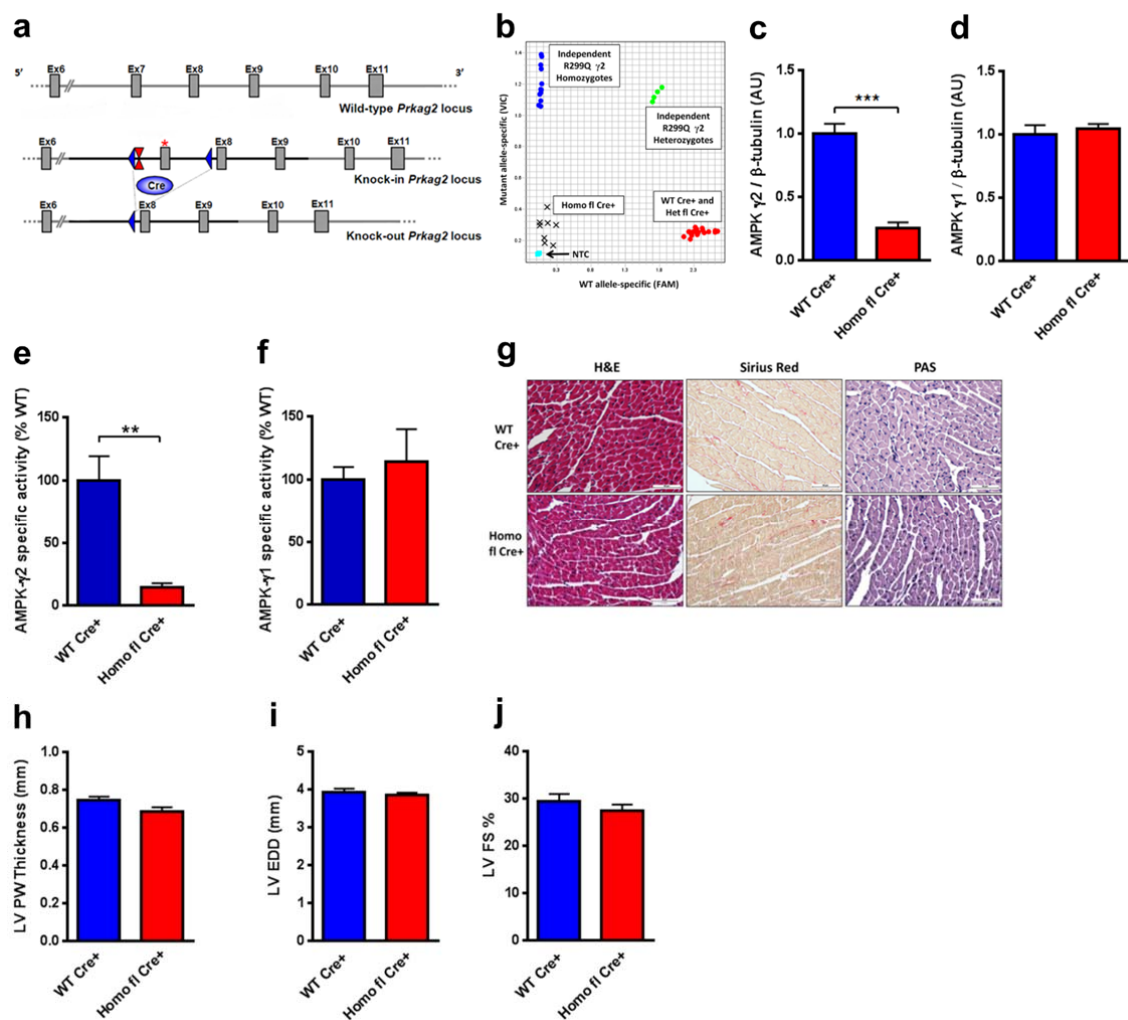
94 **Supplementary Figure 7. Ingenuity pathway analysis identification of canonical pathways**

95 **associated with R299Q γ 2 AMPK differential SA node transcriptome. (a, b) Ingenuity pathway**

96 **analysis identification of canonical pathways associated with R299Q γ 2 AMPK differential SA node**

97 **transcriptome. (a) Hmozygote R299Q γ 2 versus WT SA node comparison. (b) Heterozygote R299Q γ 2**

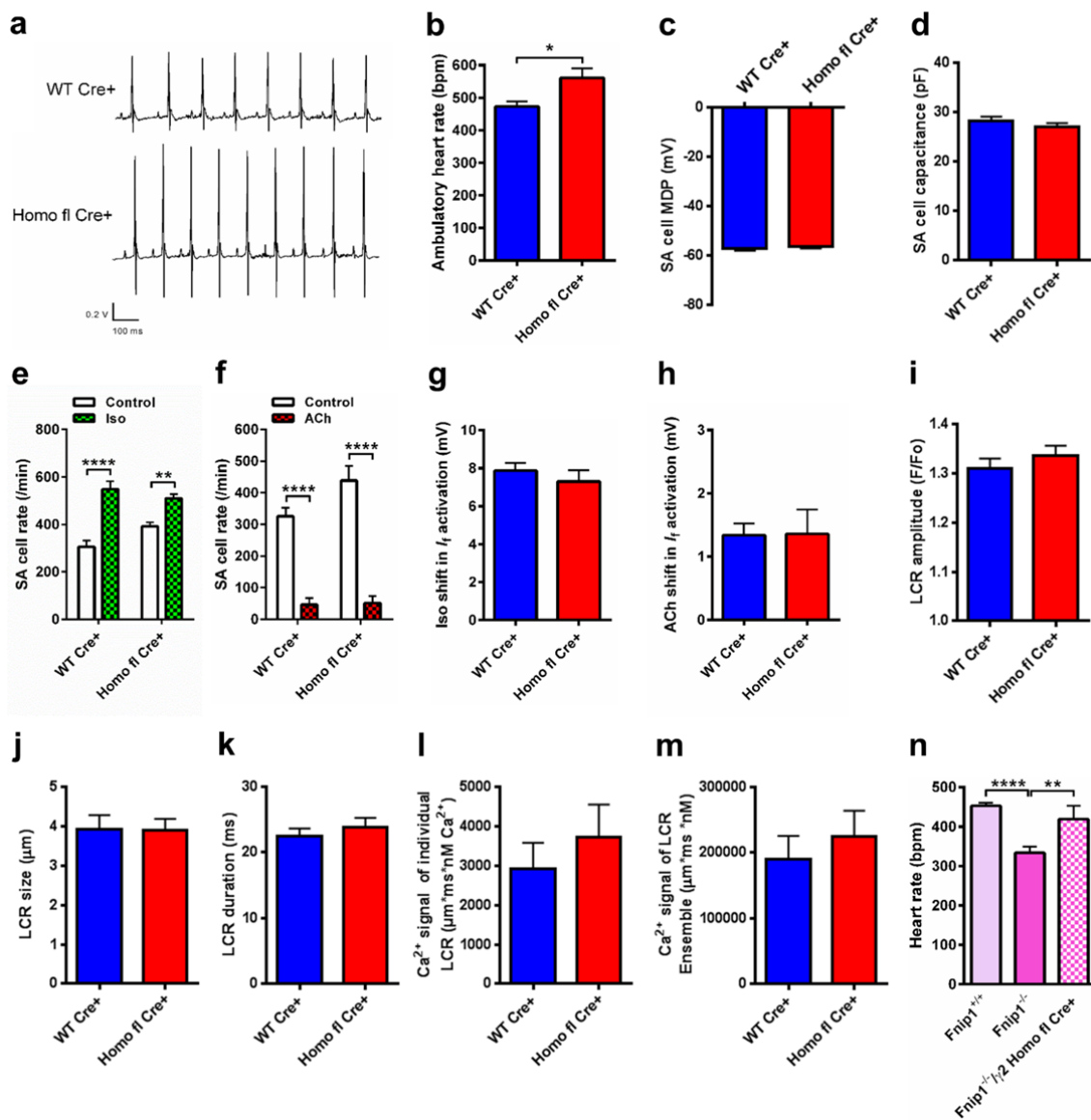
98 **versus WT SA node comparison.**



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Supplementary Figure 8. $\gamma 2$ AMPK knock-out mouse model validation and gross cardiac phenotype. (a) Illustration of strategy used to generate Sox2cre $\gamma 2$ AMPK knock-out mice by Cre-mediated excision of R299Q mutated exon 7 of *Prkag2*. (b) Allelic discrimination plot illustrating absence of R299Q $\gamma 2$ -specific transcript in Sox2cre $\gamma 2$ AMPK knock-out mice (Homo fl Cre+) and clustering with non-template controls (NTC). (c, d) Densitometry analysis of western blot of whole heart tissue from Homo fl Cre+ and Sox2cre+ control (WT Cre+) mice for $\gamma 2$ (c) and $\gamma 1$ (d) AMPK isoforms. Relative protein levels are presented normalised to β -tubulin ($n = 4$). (e, f) AMPK $\gamma 2$ - (e) and $\gamma 1$ - (f) specific activity of freeze-clamped, Langendorff-perfused whole hearts measured by SAMS peptide phosphorylation assay in the presence of AMP ($n = 5$). (g) Histological appearances of hearts from Homo fl Cre+ and WT Cre+ mice aged 3 months stained with haematoxylin and eosin (H&E), sirius red and PAS (scale bar 50 μ m). (h-j) Echocardiographic assessment of cardiac structure and function of Homo fl Cre+ mice versus WT Cre+ controls, with depiction of mean left ventricular (LV) posterior wall (PW) thickness (h), end-diastolic dimension (EDD) (i) and fractional shortening (FS) of LV mid-cavity (j). In c-f, h-j, the Student's *t*-test was performed. ** $P < 0.01$, *** $P < 0.001$. In c-f, h-j, data are shown as means $\pm$ s.e.m.



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Supplementary Figure 9. Ambulatory heart rate and SA cell electrophysiology of $\gamma 2$ AMPK knock-out mice. (a, b) Representative ambulatory telemetry-derived ECG recordings (a) and mean ambulatory HR (b) of Homo fl Cre+ and WT Cre+ mice ($n = 6$ per genotype). (c, d) SA cell maximum diastolic potential (MDP) (c) and capacitance (d) from Homo fl Cre+ and WT Cre+ mice. (e, f) Mean SA cell spontaneous rate under control conditions or in response to stimulation with 30 nM isoproterenol (Iso, e) or 30 nM acetylcholine (ACh, f) ($n = 7-9$). (g, h) Mean shifts of the I_f activation curve induced by 30 nM Iso (g) or 30 nM ACh (h). Iso and ACh shifts are depolarizing and hyperpolarizing, respectively ($n = 5-8$). (i-k) Mean spontaneous LCR amplitude (i), size (j) and duration (k) of isolated SA cells from Homo fl Cre+ and WT Cre+ mice ($n = 28$ cells/5 mice). (l, m) Ca^{2+} signal of individual LCRs (l) and LCR ensemble (m). (n) HR of WT FNIP (*Fnip1*^{+/+}), homozygous FNIP1 null (*Fnip1*^{-/-}) and compound homozygous FNIP1 null /Sox2cre $\gamma 2$ AMPK knock-out mice (FNIP1^{-/-} / $\gamma 2$ Homo fl Cre+) mice under general anesthesia ($n = 8-15$). In b-d, g-m, the Student's *t*-test was performed; in e, f, two-way ANOVA was performed; in n, one-way ANOVA was performed. * $P < 0.05$, ** $P < 0.01$, **** $P < 0.0001$. In b-n, data are shown as means $\pm$ s.e.m.

Fig. 1d

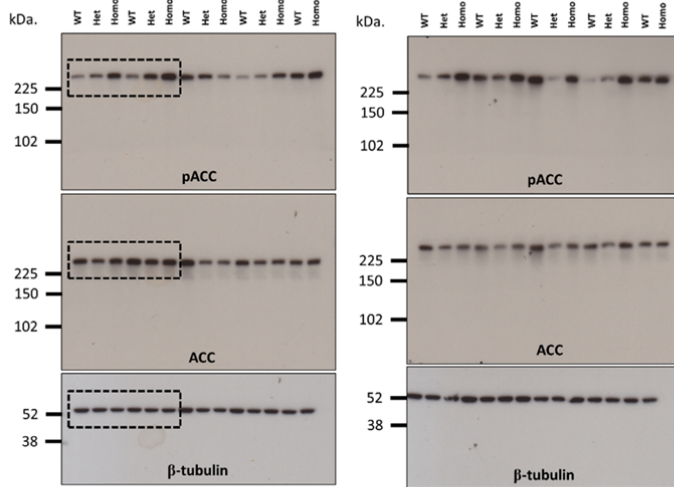


Fig. 1m

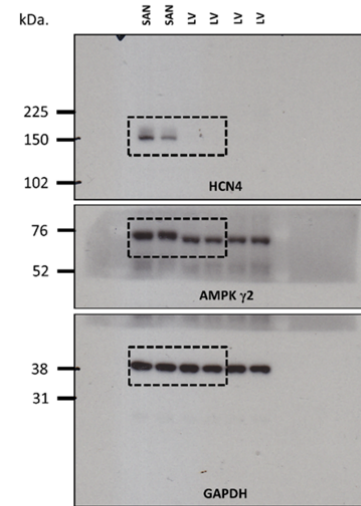


Fig. 1m

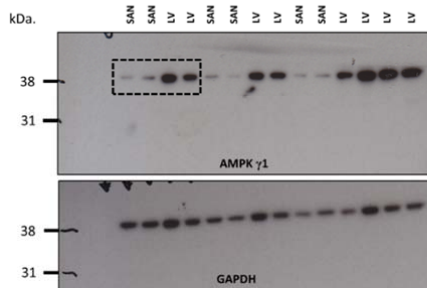


Fig. 1m

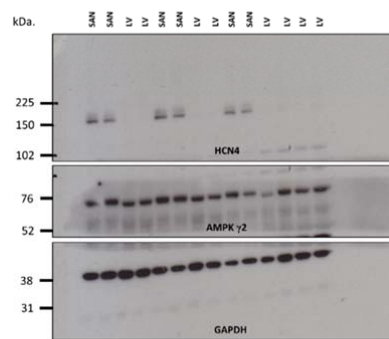


Fig. 1m

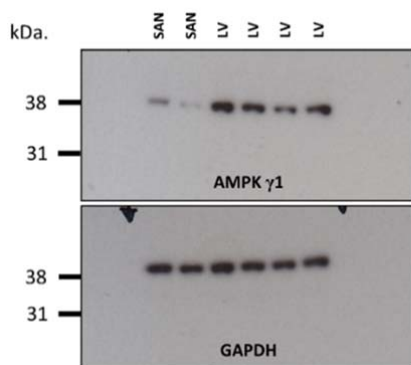
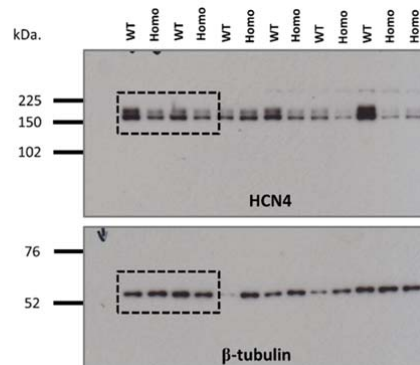


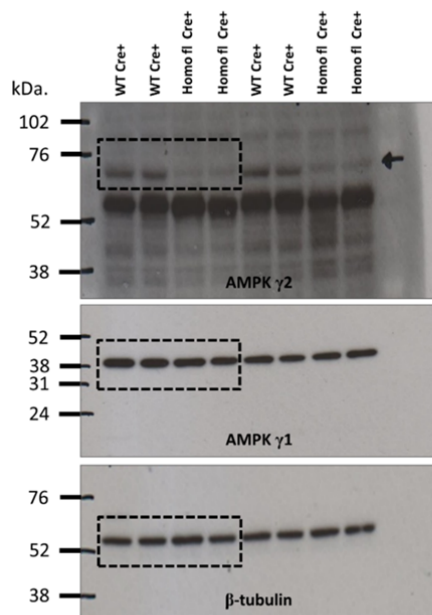
Fig. 2f



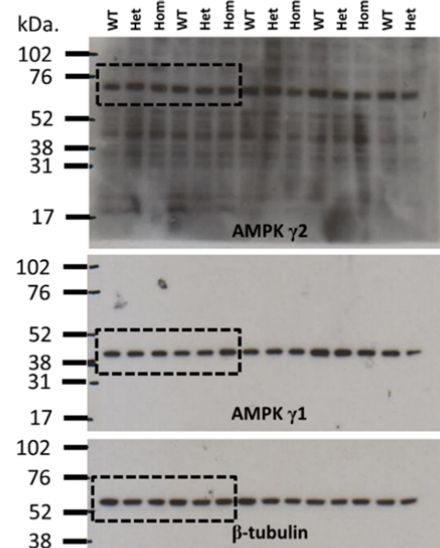
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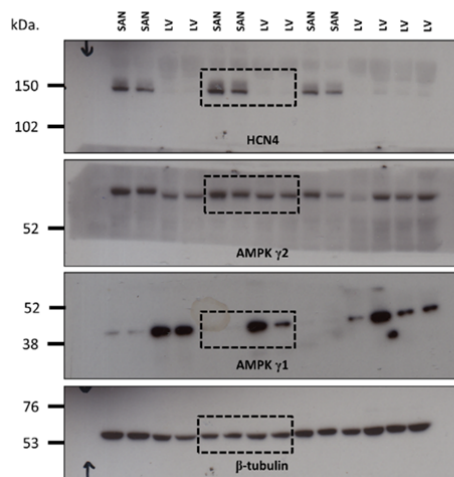
Fig. 7a



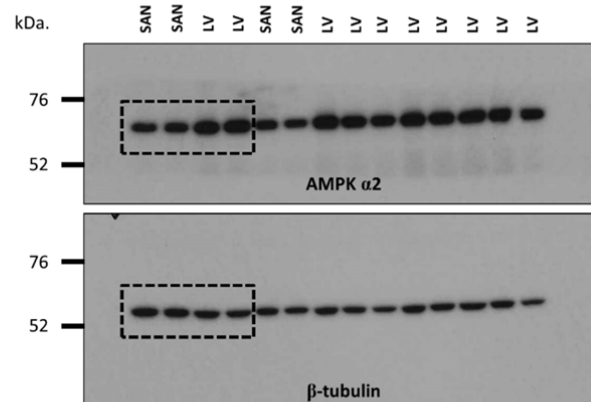
Supplementary Fig. 1b



Supplementary Fig. 1k



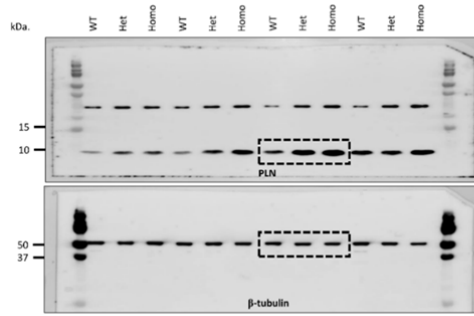
Supplementary Fig. 1n



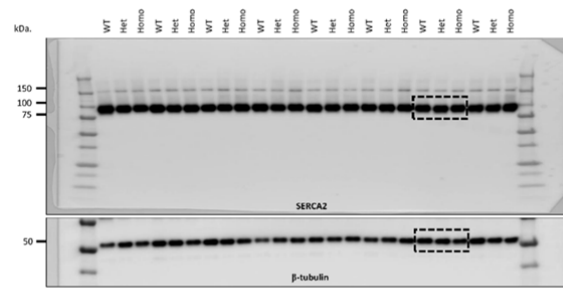
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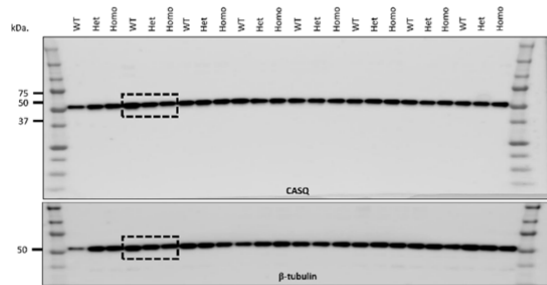
Supplementary Fig. 3j



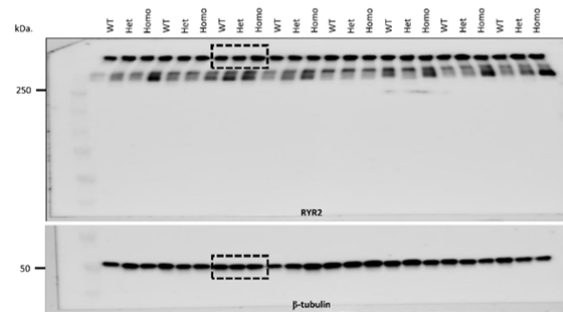
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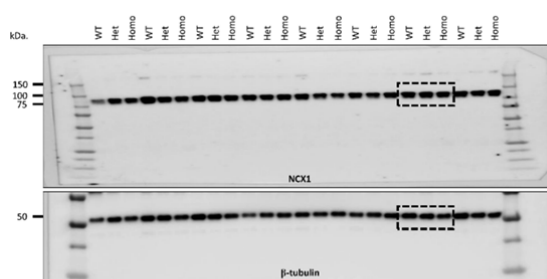
Supplementary Fig. 3m.



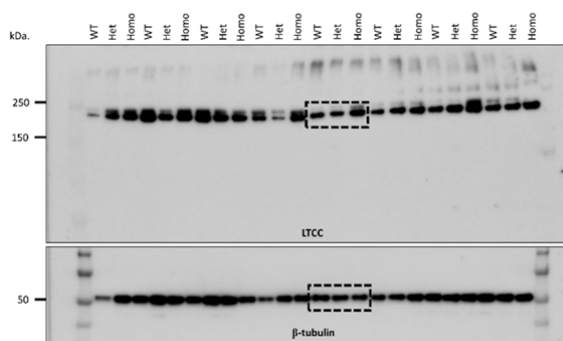
Supplementary Fig. 3n



Supplementary Fig. 3o



Supplementary Fig. 3p



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141 **Supplementary Figure 10. Full length Western blots shown in main and Supplementary Figures.**

142 Cropped areas shown in the corresponding figure are indicated by dashed boxes.

143

144 **Supplementary Table 1. Conduction parameters at invasive electrophysiology study of R299Q γ 2**
145 **mice.**

Intervals (in ms)	WT (n = 11)	Het (n = 7)	Homo (n = 13)
Baseline SCL	104.4 $\pm$ 2.7	112.3 $\pm$ 3.9	126.9 $\pm$ 3.6 *
SNRT	104.3 $\pm$ 11.2	110.1 $\pm$ 7.5	115.6 $\pm$ 6.3
AVW	67.6 $\pm$ 4.3	63.4 $\pm$ 3.7	67.3 $\pm$ 1.3
AV 2:1	53.1 $\pm$ 3.2	48.1 $\pm$ 2.8	52.5 $\pm$ 1.7
AVNERP	43.9 $\pm$ 4.6	39.2 $\pm$ 2.8	40.8 $\pm$ 2.4

146
147 SCL, Sinus cycle length; SNRT, sinus node recovery time; AVW, atrioventricular (AV) Wenckebach
148 cycle length; AV 2:1, AV 2:1 cycle length; AVNERP, AV nodal effective refractory period. * P < 0.05 vs
149 Het and P < 0.001 vs WT. Data are shown as mean $\pm$ s.e.m.

150 **Supplementary Table 2. Top 50 genes downregulated in SA node of R299Q γ 2 homozygote versus**
151 **WT mice.**

Gene	Gene Title	Score
<i>Prkag2</i>	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	-0.594
<i>Thumpd1</i>	THUMP domain containing 1	-0.409
<i>Ppp1r1b</i>	dopamine and cAMP regulated phosphoprotein, DARPP-32	-0.315
<i>Bdh1</i>	3-hydroxybutyrate dehydrogenase, type 1	-0.300
<i>Yipf7</i>	Yip1 domain family, member 7	-0.266
<i>Cilp2</i>	cartilage intermediate layer protein 2	-0.230
<i>Gcgr</i>	glucagon receptor	-0.188
<i>Wfdc2</i>	WAP four-disulfide core domain 2	-0.182
<i>Rab3b</i>	RAB3B, member RAS oncogene family	-0.170
<i>Abat</i>	4-aminobutyrate aminotransferase	-0.170
<i>Gsg1</i>	germ cell associated 1	-0.170
<i>Isl1</i>	ISL1 transcription factor, LIM/homeodomain, (islet-1)	-0.166
<i>Gja5</i>	gap junction protein, alpha 5, 40kDa (connexin 40)	-0.163
<i>Tmprss13</i>	transmembrane protease, serine 13	-0.162
<i>Fcho1</i>	FCH domain only 1	-0.152
<i>Hist1h2be</i>	histone cluster 1, H2be	-0.146
<i>Lrrc49</i>	leucine rich repeat containing 49	-0.142
<i>Ramp1</i>	receptor (calcitonin) activity modifying protein 1	-0.141
<i>Tmem35</i>	transmembrane protein 35	-0.138
<i>Tmem100</i>	transmembrane protein 100	-0.137
<i>Xrcc2</i>	X-ray repair complementing defective repair in Chinese hamster cells 2	-0.132
<i>Olfm1</i>	olfactomedin 1	-0.130
<i>Sfrp5</i>	secreted frizzled-related protein 5	-0.126
<i>Tef</i>	thyrotrophic embryonic factor	-0.126
<i>Fmod</i>	fibromodulin	-0.125
<i>Rpp25</i>	ribonuclease P 25kDa subunit	-0.122
<i>Dapk2</i>	death-associated protein kinase 2	-0.119
<i>Tmem63b</i>	transmembrane protein 63B	-0.118

<i>Rassf2</i>	Ras association (RalGDS/AF-6) domain family 2	-0.117
<i>Pi16</i>	peptidase inhibitor 16	-0.116
<i>Hs3st1</i>	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	-0.115
<i>Cuedc1</i>	CUE domain containing 1	-0.114
<i>Unc13b</i>	unc-13 homolog B (C. elegans)	-0.113
<i>Arc</i>	activity-regulated cytoskeleton-associated protein	-0.112
<i>Gstm2</i>	glutathione S-transferase M2 (muscle)	-0.112
<i>Chrm2</i>	cholinergic receptor, muscarinic 2	-0.112
<i>Tbx3</i>	T-box 3 (ulnar mammary syndrome)	-0.112
<i>Mmp9</i>	matrix metalloproteinase 9	-0.111
<i>Junb</i>	jun B proto-oncogene	-0.111
<i>Gstt1</i>	glutathione S-transferase theta 1	-0.110
<i>Trappc5</i>	trafficking protein particle complex 5	-0.110
<i>Pdlim4</i>	PDZ and LIM domain 4	-0.110
<i>Ncam1</i>	neural cell adhesion molecule 1	-0.110
<i>Cxcl14</i>	chemokine (C-X-C motif) ligand 14	-0.110
<i>Rps15a</i>	ribosomal protein S15a	-0.110
<i>Mapk10</i>	mitogen-activated protein kinase 10	-0.110
<i>Gnao1</i>	guanine nucleotide binding protein, alpha activating activity polypeptide O	-0.109
<i>Gng2</i>	guanine nucleotide binding protein (G protein), gamma 2	-0.108
<i>Clec10a</i>	C-type lectin domain family 10, member A	-0.108
<i>Igfbpl1</i>	insulin-like growth factor binding protein-like 1	-0.108

153 **Supplementary Table 3. Top 50 genes upregulated in SA node of R299Q γ 2 homozygote versus WT**
154 **mice.**

Gene	Gene Title	Score
<i>Ptgds</i>	prostaglandin D2 synthase 21kDa (brain)	0.6245
<i>Abhd1</i>	abhydrolase domain containing 1	0.4233
<i>Myl2</i>	myosin, light chain 2, regulatory, cardiac, slow	0.3654
<i>Nppb</i>	natriuretic peptide precursor B	0.3467
<i>Myl3</i>	myosin, light chain 3, alkali; ventricular, skeletal, slow	0.3325
<i>Psca</i>	prostate stem cell antigen	0.2587
<i>Ankrd23</i>	ankyrin repeat domain 23	0.2378
<i>Igfals</i>	insulin-like growth factor binding protein, acid labile subunit	0.2337
<i>Cplx1</i>	complexin 1	0.2246
<i>Cxcl9</i>	chemokine (C-X-C motif) ligand 9	0.2112
<i>Aldob</i>	aldolase B, fructose-bisphosphate	0.2025
<i>Npy</i>	neuropeptide Y	0.1891
<i>Syt4</i>	synaptotagmin IV	0.1745
<i>Cartpt</i>	CART prepropeptide	0.1722
<i>Ivns1abp</i>	influenza virus NS1A binding protein	0.1559
<i>Rsad2</i>	radical S-adenosyl methionine domain containing 2	0.1542
<i>Lrrc10</i>	leucine rich repeat containing 10	0.1498
<i>Stmn2</i>	stathmin-like 2	0.1419
<i>Pfkfb2</i>	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	0.1399
<i>Ddit4</i>	DNA-damage-inducible transcript 4	0.1374
<i>Tyrp1</i>	tyrosinase-related protein 1	0.1362
<i>Fgf7</i>	fibroblast growth factor 7 (keratinocyte growth factor)	0.1361
<i>Apoc1</i>	apolipoprotein C-I	0.1356
<i>Phkb</i>	phosphorylase kinase, beta	0.1346
<i>Sox17</i>	SRY (sex determining region Y)-box 17	0.1345
<i>Pten</i>	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	0.1334
<i>Tmem106b</i>	transmembrane protein 106B	0.1327
<i>Asb10</i>	ankyrin repeat and SOCS box-containing 10	0.1323

<i>Gpr158</i>	G protein-coupled receptor 158	0.1307
<i>Sult4a1</i>	sulfotransferase family 4A, member 1	0.1276
<i>Arrdc4</i>	arrestin domain containing 4	0.1269
<i>Cidec</i>	cell death-inducing DFFA-like effector c	0.1261
<i>Vgll2</i>	vestigial like 2 (Drosophila)	0.1240
<i>Slc10a6</i>	solute carrier family 10 (sodium/bile acid cotransporter family), member 6	0.1238
<i>Rtn4</i>	reticulon 4	0.1229
<i>Ndfip2</i>	Nedd4 family interacting protein 2	0.1223
<i>Adamts8</i>	ADAM metalloproteinase with thrombospondin type 1 motif, 8	0.1185
<i>Rtn1</i>	reticulon 1	0.1178
<i>Pcdh7</i>	BH-protocadherin (brain-heart)	0.1171
<i>Psmc6</i>	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	0.1168
<i>Per2</i>	period homolog 2 (Drosophila)	0.1160
<i>Eif4e</i>	eukaryotic translation initiation factor 4E	0.1150
<i>Slc38a2</i>	solute carrier family 38, member 2	0.1146
<i>Pccb</i>	propionyl Coenzyme A carboxylase, beta polypeptide	0.1142
<i>Stat1</i>	signal transducer and activator of transcription 1, 91kDa	0.1140
<i>Jak1</i>	Janus kinase 1 (a protein tyrosine kinase)	0.1139
<i>Fkbp5</i>	FK506 binding protein 5	0.1135
<i>Ptprb</i>	protein tyrosine phosphatase, receptor type, B	0.1127
<i>Slc40a1</i>	solute carrier family 40 (iron-regulated transporter), member 1	0.1116
<i>Pparg</i>	peroxisome proliferative activated receptor, gamma	0.1109

Supplementary Table 4. Network screening analysis evaluation of sample genes associated positively with the green co-expression module.

Gene	<i>P</i> value	<i>q</i> value	Z-score
<i>Prkag2</i>	0.011	0.016	4.47
<i>Tbx3</i>	0.002	0.010	6.85
<i>Tbx18</i>	0.012	0.017	4.24
<i>Hcn2</i>	0.002	0.010	7.23
<i>Hcn4</i>	0.005	0.011	5.58
<i>Prkar1a</i>	0.004	0.010	6.08
<i>Prkar2b</i>	0.004	0.010	5.99
<i>Prkcdbp</i>	0.007	0.012	5.17
<i>Plcb3</i>	0.003	0.010	6.73
<i>Camk2</i>	0.003	0.010	6.68
<i>Camkk2</i>	0.002	0.010	6.92
<i>Camk4</i>	0.002	0.010	6.82
<i>Calml4</i>	0.002	0.010	6.84
<i>Calcr1</i>	0.002	0.010	6.84
<i>Calhm2</i>	0.002	0.010	7.20
<i>Prkci</i>	0.009	0.014	-4.67
<i>Camta1</i>	0.026	0.026	-3.47
<i>Prkab1</i>	0.008	0.013	-4.83

Supplementary Table 5. Primer sequences.

Genotyping primers		
Name	Forward 5' – 3'	Reverse 5' – 3'
R299Q <i>Prkag2</i>	CACCTGAAGTTGCCGTGTGACCTCC	GAGGCATTTCTCAAGGGAGGCTCC
Sox2cre	CTGGTGTAGCTGATGATCCG	CTCAGTGGTATTTGTGAGCC
Intact exon 7	TGTTTCTGGTTTCTTCCAGGTCAA	TGCAAAAGCCAGAAAGTTCTTCAAC
Excised exon 7	GGTGTGCACAGCATCCAGCAACA	AGGCTGAGCTCACCGTTACTCGTG
Allelic discrimination primers		
Name	Forward 5' – 3'	Reverse 5' – 3'
Exon- spanning	CTTCTTTGCCTTGGTAGCCAAC	CATTCTACAAAGCTCTGCTTTTACTT
SA node microarray validation primers		
Gene	Forward 5' – 3'	Reverse 5' – 3'
<i>Acta1</i>	CCACAGCTGAACGTGAGATTGT	TGGCCATCTCATTCTCGAAGT
<i>Hcn1</i>	CACAGTGCCACAACGTGTCA	CTGCATCTGGGTCTGTATTTAGGA
<i>Hcn4</i>	CCACCCCTACAGTGACTTCAGAT	CCCACGGGTATGATGATCAGA
<i>Isl1</i>	TGACTCCTGTCTGTCCAAGAACTT	CCAGAAAGAGCGAAAACAGTCATT
<i>Myl3</i>	CCCAAGGGCGAGATGAAGAT	TCTGCCTGGGTAGGATTCTGA
<i>Nppb</i>	GGTCTGGCCGGACACTCA	AGCTTGTCAGTGGTGTCTTCA
<i>Pln</i>	GTAGTTGGCCATGCTGAGAGAA	TGTGGTAGTGAGCAATATAACAAATGC
<i>Ppp1r1b</i>	GTCTCTGTTTGCTTTGGCTGAA	CCCTACTCCCACCGGGTAAA
<i>Ptgds</i>	CAAAGCTGGAGGGTGTAGAGGTA	ACTCCTTGCTCTGTCACTCTCAA
<i>Tbx3</i>	TGCCTATCAGAATGACAAGATAACTCA	TGTCTCGAAAACCCCTTTGCAA