Extended Methods:

Mice: All animal care and surgeries were in accordance with UVA ACUC Policy on Rodent Surgery and Perioperative Care under ACUC-approved animal protocol (UVA ACUC Wolf Laboratory protocol No. 4080). *αMHC -MerDreMer-Ki67p-RoxedCre::Rox-Lox-tdTomato-eGFP* (*αDKRC::RLTG*) mice were previously described.[1] *C57BL/6J* (JAX stock #000664), *αMHC-Cre* (*B6.FVB-Tg(Myh6-cre)2182Mds/J*)[2], *C57BL/6-Dyrk1a*$^{tm1Jdc/J}$ (DYRK1a$^{flox/flox}$) mice[3] , and ROSA-DTA (*B6.129P2-Gt(ROSA)*$^{26Sortm1(DTA)Lky}$*/J*) were purchased from Jackson labs. *CAG-STOP-Fucci2aR*[4] was obtained from the European Mouse Mutant Archive. CAG-STOP-Fucci2aR and αMHC-Cre were backcrossed nine generations into *C57BL/6J* before establishing *αMHC-Cre/+::CAG-STOP-Fucci2aR/CAG-STOP-Fucci2aR* and *αMHC-Cre/+::CAG-STOP-Fucci2aR/CAG-STOP-Fucci2aR::DYRK1a*$^{fl/fl}$ mice. For experiments using *αDKRC::RLTG* mice, twelve to fifteen week-old male and female mice were treated with Tamoxifen (1 mg/kg) IP daily for two five-day periods with a two-day rest between rounds (i.e., five days “on”, two days “off”, and five days “on”) followed by a two-week recovery period prior to indicated experiments.

I/R MI protocol: We used an I/R MI protocol previously described in our recent publication.[1] Briefly, all animal care and surgeries were in accordance with UVA ACUC Policy on Rodent Surgery and Perioperative Care under ACUC approved animal protocol (UVA ACUC Wolf Lab protocol #4080). The individual performing surgeries was blinded to the mouse genotypes and treatments. In sham control mice, the entire procedure was identical except for the ligation of the LAD. The mortality rate associated with surgeries was ~10%.

Harmine minipump protocol: Harmine Sigma (SMB00461) solution was prepared aseptically in a sterile vial the day of the procedure, by dissolving 35 mg of Harmine in 1mL of sterile USP grade DMSO (Sigma #D1435) and water to give a Harmine dose of 10 mg/kg/day. The pH of

the solution was in the physiological range. The Harmine solution was filtered using a 0.22 micron filter prior to loading into sterile, pre-packaged Azlet mini-pumps (#1002) that was subcutaneously implanted into mice.

Echocardiography: Mice were anesthetized with Isoflurane and gently restrained on a Vevo integrated rail system. The system included a physiological monitoring unit consisting of a heating board with integrated ECG electrodes. The table temperature was maintained at ~38^{o}C using a rectal probe for temperature feedback. Hair was gently removed, and ultrasound contact gel (warmed to 37^{o}C) was applied to the chest. Echocardiography was performed using a high frequency 30 mHz linear transducer and a Vevo 1100 (Visual Sonics) system similar to previously described methods. Initial B-mode images were obtained in the parasternal long axis with the apex and aortic valves visualized. Next, B-mode short axis images were obtained by turning the ultrasound probe ~90 degrees and identifying the mitral valve papillary muscles. The parasternal long axis images were analyzed using VevoView software to calculate left ventricular dimensions. The individuals performing and analyzing the echocardiography were blinded to the genotypes and treatment groups.

Isolation of Cardiomyocytes: Cardiomyocytes from twelve-week old *αMHC-Cre::Fucci2aR* and *αMHC-Cre::Fucci2aR::DYRK1a$^{fl/fl}$* mice controls were isolated by retro-aortic cannulation and collagenase treatment by Langendorff isolated heart perfusion as described by Simpson[5], seven days after Sham or I/R MI surgeries. Briefly, mice were injected with Heparin (100 IU, intraperitoneally) ten minutes before undergoing anesthesia with 3% Isoflurane. After the mouse was fully anesthetized, the hearts were dissected from surrounding tissues and attached via the proximal aorta to a 22-gauge cannula fixed to 1mL syringe loaded with perfusion buffer (10 mM HEPES (pH 7.0) containing 120 mM NaCl, 15 mM KCl, 0.1 mM KH2PO4, 0.6 mM Na2HPO4,

1.2 mM MgSO4-7H2O, 4.6 mM NaHCO3, 30 mM Taurine, 10 mM 2,3-butanedione monoxime, and 5.6 mM Glucose). Notably, the perfusion buffer was maintained at 37oC during all perfusion steps. The heart was then carefully removed from the chest and surrounding tissues, and the canular was attached to the perfusion system with attention to avoid the introduction of air into the circulation lines. Then, the canulated heart was perfused with digestion buffer (perfusion buffer containing collagenase (Worthington Collagenase2, 300 units/ml) and 50 uM Calcium chloride) at a rate of 4ml/min for 20 minutes. A pressure monitor was used to measure resistance pressure during the perfusion. After perfusion, the heart was removed from the apparatus and placed in a petri dish containing 5 ml of digestion buffer. The atria were removed leaving only the ventricles that were placed in a new petri dish containing 3 ml of digestion buffer. The ventricles were mechanically dissociated using micro-forceps and then 5 ml of perfusion buffer containing 10% fetal calf serum and 25 uM Calcium chloride. The tissues were transferred to a 15 ml comical tube along with an additional 2 ml of perfusion buffer containing 10% fetal calf serum and 25 uM Calcium chloride. The tissue was further mechanically dissociated by repeated gentle pipetting and then the myocytes were separated from non-myocytes by centrifugation at 300 RPM for 3 minutes. The supernatant containing non-myocytes was discarded and the myocyte pellet was resuspended in 10 ml of fresh perfusion buffer containing 10% fetal calf serum and 25 uM Calcium chloride, followed by centrifugation at 300 RPM for 3 minutes. After centrifugation, the supernatant was discarded, and the myocyte pellet was frozen at -80oC for subsequent RNAseq and qPCR experiments.

Quantitative PCR (qPCR): Cardiomyocytes from eight-week old *αMHC-Cre::Fucci2aR* (5 hearts) and *αMHC-Cre:: Fucci2aR::DYRK1a*$^{fl/fl}$ mice (3 hearts) were isolated by retrograde perfusion of collagenase using a Langendorff apparatus. RNA was extracted from the heart tissue using the RNeasy kit from Qiagen. For reverse transcription, random primers (1µg) and

10 ng of total RNA were used in a final reaction volume of 20µl containing 100 units of Superscript II (Invitrogen). PCR was performed in duplicate for 40 cycles using 10% of the volume of the reverse transcription in a total volume of 25µl that included 12.5µl of TaqMan Gene Expression Master Mix (4369016 Applied Biosystems) and a 1x final concentration of the following TaqMan Gene Expression Assays (Applied Biosystems) from ThermoFisher Scientific. Dyrk1a (Mm01209881_m1), Dyrk1b (Mm00599813_m1), Dyrk2 (Mm01166529_m1), Dyrk3 (Mm00523595_m1), and Dyrk4 (Mm01183103_m1) probes were obtained from ThermoFisher Scientific. mRNA was quantified by real-time PCR analysis using the CFX96 Real Time System coupled with the C1000 Touch Thermal Cycler (BioRad, Inc.). Thermocycler conditions were 40 cycles of denaturation at 95oC for 15 seconds, and annealing and extension step of 60^{o}C for 60 seconds. The ΔCT method was used to quantify all relative mRNA levels using 18S RNA as the reference and internal standard. The TaqMan primer-probe set for 18S RNA (4310893e) with the Vic/Tamra detection system was used to measure 18S RNA in replicate samples to those taken for the above listed mRNA quantifications.

For experiments of *C57BL/6J*, hearts were collected at P1, P3, P5, P7, P10, P14, and P28 (seven to nine hearts per time point) and used to isolate total RNA as described above. The following probes were used in TaqMan Gene Expression Assays (Applied Biosystems): E2F1 (Mm00432939_m1), E2F2 (Mm00624964_m1), E2F3 (Mm01138833_m1), E2F4 (Mm00514160_m1), E2F5 (Mm00468171_m1), E2F6 (Mm00519030_m1), tfDP1 (Mm00833674_g1), tfDP2 (Mm00618407_m1), Lin9 (Mm00613517_m1), Lin37 (Mm00650488_gh), Lin52 (Mm00848895_g1), Lin54 (Mm00554788_m1), Myb (Mm00501741_m1), Mybl1 (Mm00485327_m1), Mybl2 (Mm00485340_m1), Rb1 (Mm00519030_m1), RBL1 (Mm01250721_m1), RBL2 (Mm01242468_m1), Rbbp4 (Mm00771401_g1).

Histology and Immunohistochemistry: Hearts were excised and fixed in 10% Neutral Buffered Formalin (Fisher, Inc.) for a minimum of four hours prior to embedding in paraffin. Ten micron sections were prepared in short axis orientation by microtome with 8 sections per glass slide. Paraffin was removed and the tissue sections were rehydrated using Xylene and serial ethanol wash steps, respectively. Antigen retrieval was performed by incubating tissue sections in boiling 1x Unmasking solution (Vector Labs H-3300) for 22 minutes. After cooling to room temperature, the tissue sections were treated with Sudan Black to quench auto-fluorescence if slides were used to immunofluorescence. Briefly, tissue sections were incubated in 0.1% Sudan Black (Sigma, Cat# 199664) in 1x PBS and 70% ethanol at room temperature for 20 minutes to quench auto fluorescence, followed by 3 x five minute washes in 1x PBS containing 0.02% Tween 20, and a final five minute wash in 1x PBS. For immunofluorescence staining, tissue sections were blocked in 1X PBS containing fish skin gelatin oil (FSG) + Donkey Serum (serum : buffer, 1:10) for 1 hour at room temperature. For primary antibodies derived from mice, an additional step to block endogenous mouse IgG was performed using 1X PBS containing Goat F(ab) Anti-Mouse IgG H&L (Abcam-ab6668) for 1 hour at room temperature. After washing 3 x 2min in 1x PBS containing FSG and 0.1 %Tween-20, tissue sections were incubated in primary antibodies (see table for dilutions) in 1x PBS contacting FSG overnight at 4oC. Tissue sections were washed with 1x PBS containing FSG and 0.1 %Tween-20 for 5 minutes followed by 1X PBS for 5 min prior to incubation with secondary antibodies (see table for dilutions) in 1x PBS containing FSG and 0.1 %Tween-20. Secondary antibodies were removed and sections were washed with 1x PBS containing FSG and 0.1 %Tween-20 for 5 minutes followed by 1X PBS for 5 min prior to imaging. For immunostaining experiments, controls included heart 6 sections

stained with primary antibodies only and secondary antibodies only. The controls were used to determine background signals and exposure times for subsequent experiments.

To quantify cardiomyocyte cross-sectional areas, ten micron short-axis paraffin embedded sections of hearts of *αMHC-Cre::Fucci2aR* and *αMHC-Cre:: Fucci2aR::DYRK1a*$^{fl/fl}$ mice were stained with anti-mCherry antibody (Origene, Inc. Cat. # TA150125), wheat germ agglutinin (Thermofisher, Inc. Cat # W32466), and DAPI nuclear stain (Abcam, Ab104139). Images were obtained using a Leica DM2500 Fluorescence microscopy system with a Leica DFC7000 T fluorescence color camera and Leica LAS X Multi Channel Acquisition software. Cardiomyocytes in cross-section that had centrally-located mCherry positive nuclei were quantified using ImageJ software, normalized to a 25 micron scale bar for each image. For quantification of infarcted myocardium, paraffin embedded 10 micron thick short-axis sections were stained with Masson Trichrome. ImageJ software was used to measure the areas of the infarct and myocardium.

Quantification of cardiomyocyte cycling: We quantified eGFP positive cardiomyocytes as previously described by immunohistochemistry with colorimetric detection using a Rabbit specific HRP/AEC detection kit (Abcam, Inc. Cat# ab64260). Images were obtained using a Leica DM2500 microscopy system with a Leica DFC7000 T fluorescence color camera or a Leica THUNDER imaging system and Leica LAS X Multi Channel Acquisition software. For fluorescence imaging, the channels were calibrated to background of control sections stained with secondary antibodies alone. eGFP+ cardiomyocytes visualized using an YFP filter and quantified from 6-8 ten-micron short axis sections of three slides per animal separated by ~400 microns per slide. The infarct zone was identified by WGA. The non-infarct zone was divided into thirds with the two regions adjacent to the infarct defined as the border zones and the middle

region defined as the remote zone. eGFP+ cardiomyocytes present in the same location on sequential slides were counted once among all sections to avoid over-representation of eGFP+ cells. Cardiomyocyte endoreplication was defined as single GFP+ cells, indicative of cell cycle reentry without replication, and proliferation as two neighboring GFP+ cardiomyocytes separated by cell membranes stained by WGA.

TTC staining protocol. Mice were given Heparin (1000 Units by intraperitoneal injection) ten minutes before administration of Isoflurane excision of hearts. Briefly, the descending aorta was cross-clamped and a small incision was made in the right atrium. Then, 500 ul of 30 mM KCl in 0.9% normal saline containing 100 Units per ml of Heparin was injected into the apex to stop the heart in diastole. Hearts were then cannulated *in vivo* using a 22 gauge blunt needle, dissected from the surrounding tissue, placed on a clamp stand, and slowly perfused with 300 ul of 30 mM KCl in normal saline. The LAD ligature was then rebuilt, and a one ml syringe containing phthalocyanine blue/saline solution (Copper (III) phthalocyanine (Sigma# 252980-5G) 5% (wt:vol) in 0.9% normal saline containing a drop of Dawn dish detergent) was attached to the cannulation needle and ~200 ul of the solution was used to gently perfuse the heart. The heart was then de-cannulated and washed in cold 0.9% normal saline. The atrial appendage and aorta were removed from the base of the heart and a cotton-tipped applicator was used to expel liquid form the ventricles. The heart was then placed in a Rat Heart Slicer Matrix (Zivic Instruments, Model # HSRS001-1) that contained 3%wt:vol low gelling agarose (Alfa Aesar, Inc, Catalog number J66319) at 42^{o}C. Liquid agarose was then injected into the LV using a 3 ml syringe equipped with a 20 gauge needle. After the mold was filled with agarose, the mold containing the heart was placed in a -20^{o}C freezer on the large steel block and the agarose was allowed to solidify for ~4 minutes. After the agarose was solidified, the heart was cut into 1 mm short-axis sections using microtome blades and each section was placed in an individual 1.5 ml Eppendorf

tube containing TTC solution (2,3,5-Triphenyltetrazolium chloride (TTC) (Sigma# T8877-10G) 1% (wt:vol) in 100mM Tris-base in 0.9% normal saline, pH 7.4), pre-warmed to 42^{o}C. The heart slices were incubated at 42^{o}C for 20 minutes. Then, each slice was transferred to an individual 1.5 ml Eppendorf tube containing 10% NBF for 60 minutes. Each slice was then removed, had excess buffer removed, and was weighed before imaging using a stereoscope. The AAR and AON were calculated as previously described.[6]

RNA sequencing. Twelve-week old male *αMHC-Cre::Fucci2aR* and *αMHC-Cre::Fucci2aR::DYRK1a$^{fl/fl}$* mice underwent sham or I/R MI surgeries. Cardiomyocytes were isolated seven days after the surgeries (3 hearts per group, 12 hearts total). RNA extraction, cDNA library preparation with adapter ligation, and sequencing using an Illumina® HiSeq® system were performed by Genewiz, Inc. Sequence quality was determined by MultiQC and one sham *αMHC-Cre::Fucci2aR* set and one sham *αMHC-Cre::Fucci2aR::DYRK1a$^{fl/fl}$* set was excluded because of overlap after PCA analyses. Differential gene expression was determined using R and DEseq2. Volcano plots were generated using Prism. Venn diagrams were generated using Bioinformatics & Evolutionary Genomics program (http://bioinformatics.psb.ugent.be/webtools/Venn/). Pathway analyses were performed using Reactome (https://reactome.org/)[7] and Enrichr (https://maayanlab.cloud/Enrichr/).[8, 9]

For analyses of gene expression data from Walsh[10], et al, raw data were downloaded from GEO NCBI repository, accession number 17020. The data were subsequently subjected to quality control using lumi package (version 2.24.0) for the R programming language (http://bioconductor.org/packages/release/bioc/html/lumi.html). The data were then background-corrected, variance-stabilized, normalized and count matrix extracted using the same package. Then unexpressed genes were removed as well as entries not mapped to gene symbols. For

the heat map, genes with variance larger than 0.04 across all samples were extracted and the correlation heat map was produced using the R programming language. Clusters clearly separating the conditions were marked.

Statistics: GraphPad Prism 8 (GraphPad Software, Inc.) was used for statistical analyses. The data was analyzed for normal distribution using Anderson-Darling, D'Agostino & Pearson, Shapiro-Wilk, and Kolmogorov-Smirnov tests in GraphPad. When N was too small to determine normality, we performed the Mann-Whitney test for comparisons between two groups and Kruskal-Wallis for ANOVAs with a Dunn's multiple comparison test. Student's t-tests were used to calculate p-values of qPCR data. All mice that survived until the pre-specified endpoint of the experiments were used in the analyses. The number of mice used in experiments was based on our prior publication and a calculator from the IACUC at Boston University, including an Excel template for calculation based on means/standard deviations and proportions (https://www.bu.edu/researchsupport/compliance/animal-care/working-with-animals/research/sample-size-calculations-iacuc/). For the echocardiography experiments, we assumed a Type I (alpha) error of 0.05, a difference (delta) of ~30% (EF ~35% in the MI control group and ~25% in the DYRK1a knockout group), a standard deviation of 5%, and a Power of 0.95. We calculated that ~seven mice would be needed in each group. Representative figures were chosen based on the representative of the mean.

Supplemental Material

Online Supplemental Figure 1. Schematic of DYRK1a and the MuvB/Dream Complex.

Online Supplemental Figure 2. DYRK1a is a potential regulator of postnatal cardiomyocyte growth. (A) Heat map of gene expression using GSE17020 dataset from Walsh *et al.* showing seven clusters from embryonic, neonatal, and adult hearts. Genes in each cluster are provided in Supplemental Table I. **(B)** Molecular Signatures Database (MSigDB) Gene Set Enrichment analysis of genes corresponding to clusters 1-3 and 6-7. Gene set names, p-values, adjusted p-values, Odds Ratios, and combined scores from analyses using Enrichr are shown. **(C)** Analyses of pathway enrichment using Reactome are shown for genes corresponding to clusters 1-3 and 6-7. **(D)** Analysis of supplemental data from Talman *et al.* showing changes in the relative expression of 214 genes predicted to be regulated by the DREAM complex in P1, P4, P9, and P23 hearts. The genes predicted to be regulated by the DREAM complex were derived from Fisher *et al.* and are listed in Supplemental Table III. Values are the average counts for each gene at the denoted time points, normalized to each gene's expression at P1. **(E)** Quantitative PCR (qPCR) of the expression of seventeen transcripts corresponding to the MuvB/DREAM complex genes from *C57B6J* hearts isolated at P1, P3, P5, P7, P10, P14, P21, and P28. Values are means ± SD for transcript expression of each gene normalized to 18S housekeeping gene expression. N=3 samples per time point using 2-9 pooled mouse hearts per sample.

Online Supplemental Figure 3. Immunofluorescent and immunohistochemical stating of GFP positive cardiomyocytes of *αDKRC::RLTG* mice. (A) Immunofluorescent staining of

paraffin embedded heart from *αDKRC::RLTG*. Anti-cardiac troponin (Red) and anti-GFP (Green) are shown. Scale bar (white) is 25 microns. **(B and C)** Isolated GFP+ cardiomyocyte from *αDKRC::RLTG* showing bright field (B) and endogenous GFP signal (C). Scale bar (white) is 5o microns. **(D)** Immunohistochemical staining of eGFP+ cardiomyocytes from *αDKRC::RLTG*. Cells stationed with anti-GFP antibody are denoted by black arrows. The infarct and border zones are labeled. **(E)** Inset from panel D showing two neighboring eGFP positive cardiomyocytes denoted by black arrows. **(F - H)** Immunofluorescent staining of hearts of *αDKRC::RLTG* mice treated with Harmine. Panel F shows two pairs of GFP positive cardiomyocytes in the border zone. Anti-GFP (green), wheat germ agglutinin (WGA) (red), and DAPI (blue) are shown. Scale bar (white) is 25 microns. Panels G and H show representative GFP positive cardiomyocytes. Anti-GFP (green), wheat germ agglutinin (WGA) (red), and DAPI (blue) are shown. Scale bar (white) is 25 microns.

Online Supplemental Figure 4. Comparison of LVEF at four weeks after I/R MI in *αDKRC::RLTG/DTA* and *+::RLTG/DTA* mice. Comparison of *αDKRC::RLTG/DTA* and *+::RLTG/DTA* littermate controls treated with harmine to previously published *αDKRC::DTA* and *+::DTA* mice not treated with harmine (Bradley, L. et al. *Circ Res* (2021)). The absolute values (%) of left ventricular (LV) ejection fraction (EF) of mice are shown. Open circles are values for individual animals. Bars are group means ± SD. p = 0.0001 for *+::RLTG/DTA* (harmine-treated) vs. *αDKRC::RLTG/DTA* (harmine-treated), p = 0.0001 for *+::DTA* (no harmine) vs. *αDKRC::DTA* (no harmine), p = 0.001 for *+::RLTG/DTA* (harmine-treated) vs. *+::DTA* (no harmine), and p = 0.13 for *αDKRC::RLTG/DTA* (harmine-treated) vs. *αDKRC::DTA* (no harmine). p-values were calculated by one-way ANOVA with Tukey's multiple comparison test. N = 7 in the

αDKRC::RLTG/DTA (harmine-treated) group, N = 6 in the *+::RLTG/DTA* (harmine-treated*), N = 6 in the αDKRC::DTA* (no harmine), and N = 8 in the *+::DTA* (no harmine) group*.*

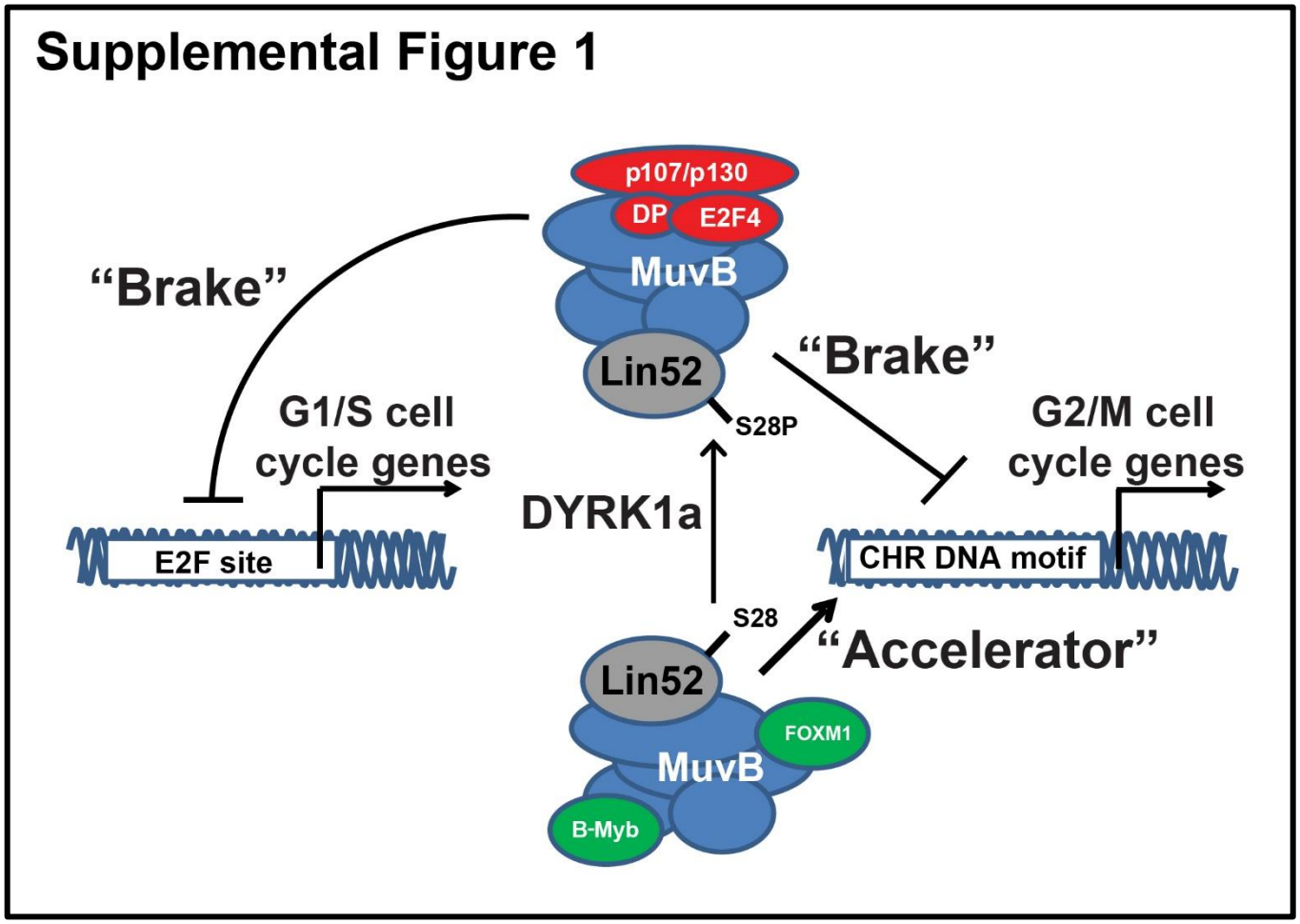
Online Supplemental Figure 5. Triphenyl Tetrazolium Chloride (TCC) staining of *αMHC-Cre::Fucci2aR::DYRK1a*$^{flox/flox}$ and *αMHC-Cre::Fucci2aR* animals after I/R MI. (A) Overview of the experimental protocol for Triphenyl Tetrazolium Chloride (TCC) staining. **(B)** The Area-at-risk (AAR) and Area-of-necrosis (AON) for *αMHC-Cre::Fucci2aR* (open bars) and *αMHC-Cre::Fucci2aR::DYRK1a*$^{flox/flox}$ (gray bars). The values are weight (mg x 10^{-2}) and expressed as the mean ± SD. Open circles are individual animals. p=0.47 for the AAR *αMHC-Cre::Fucci2aR::DYRK1a*$^{flox/flox}$ vs. *αMHC-Cre::Fucci2aR* animals. p=0.19 for the AON *αMHC-Cre::Fucci2aR::DYRK1a*$^{flox/flox}$ vs. *αMHC-Cre::Fucci2aR* animals. P-values calculated by student's t-test. N=6 animals in the *αMHC-Cre::Fucci2aR::DYRK1a*$^{flox/flox}$ group and N=4 animals in the *αMHC-Cre::Fucci2aR* group**. (C)** Representative sections corresponding to panel D of *αMHC-Cre::Fucci2aR* and *αMHC-Cre::Fucci2aR::DYRK1a*$^{flox/flox}$ hearts stained with TTC. Blue stain corresponds to viable myocardium. Red stain corresponds to AAR. Pale beige stain corresponds to the AON.

Online Supplemental Figure 6. Gene Ontology (GO) Biological Terms 2021 corresponding to differentially expressed genes identified from RNAseq.

Online Supplemental Figure 7. Heatmap of the eighty-nine genes unique to DYRK1a k/o cardiomyocytes after MI showing the expression of each gene in individual cardiomyocyte

samples from Control Sham, Control MI, DYRK1a k/o Sham, and DYRK1a k/o MI. Red asterisks denote genes regulated by the DREAM complex (see Table III).

Online Supplemental Figure 8. Comparison of the MSigDB gene expression analyses for Clusters 1-3 of Supplemental Figure 2A and the eighty-nine genes unique to DYRK1a k/o cardiomyocytes after MI.


Supplemental Figure 1
p107/p130
DP
E2F4
MuvB
Lin52
S28P
"Brake"
G1/S cell
cycle genes
E2F site
"Brake"
G2/M cell
cycle genes
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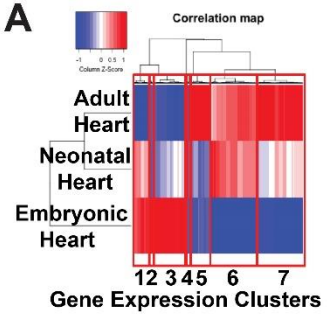
DYRK1a
S28
"Accelerator"
Lin52
FOXM1
MuvB
B-Myb

Supplemental Figure 2

A



B

MSigDB Hallmark 2020 Clusters 1-3
(Increased in embryo and decreased in neonate and adult)

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	Myogenesis	1.47E-10	2.28E-09	15.54	351.78
2	E2F Targets	1.47E-10	2.28E-09	15.54	351.78
3	G2-M Checkpoint	4.28E-06	4.42E-05	9.66	119.47
4	Mitotic Spindle	4E-05	0.00031	8.36	84.65

MSigDB Hallmark 2020 Clusters 6-7
(Decreased in embryo and increased in neonate and adult)

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	Epithelial Mesenchymal Transition	4.33E-26	1.86E-24	15.1	881.8
2	TNF-alpha Signaling via NF-kB	1.84E-10	3.96E-09	7.32	164.04
3	Apoptosis	2.68E-09	3.85E-08	7.63	150.49

C

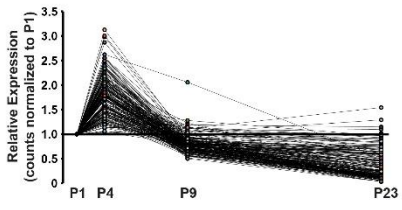
Reactome Analysis of Clusters 1-3 (Increased in embryo and decreased in neonate and adult)

Pathway name	Entities Found	Entities Total	Entities Ratio	Entities p-Value	Entities FDR	Reactions Found	Reactions Total	Reactions Ratio
Striated Muscle Contraction	12	40	0.003	3.33E-16	1.35E-13	4	4	0
Muscle contraction	18	224	0.015	5.15E-14	1.04E-11	15	42	0.003
Cell Cycle, Mitotic	15	596	0.04	2.54E-05	3.43E-03	93	350	0.026

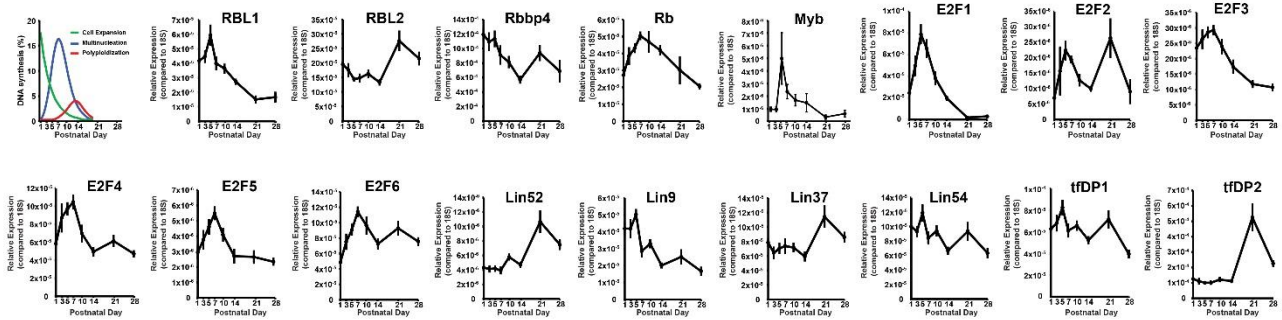
Reactome Analysis of Clusters 6-7 (Decreased in embryo and increased in neonate and adult)

Pathway name	Entities Found	Entities Total	Entities Ratio	Entities p-Value	Entities FDR	Reactions Found	Reactions Total	Reactions Ratio
Extracellular matrix organization	39	330	0.022	6.81E-14	5.83E-11	153	319	0.024
Interleukin-10 signaling	17	86	0.006	6.01E-10	2.57E-07	3	15	0.001
Interleukin-4 and Interleukin-13 signaling	25	216	0.015	3.63E-09	1.04E-06	18	47	0.004

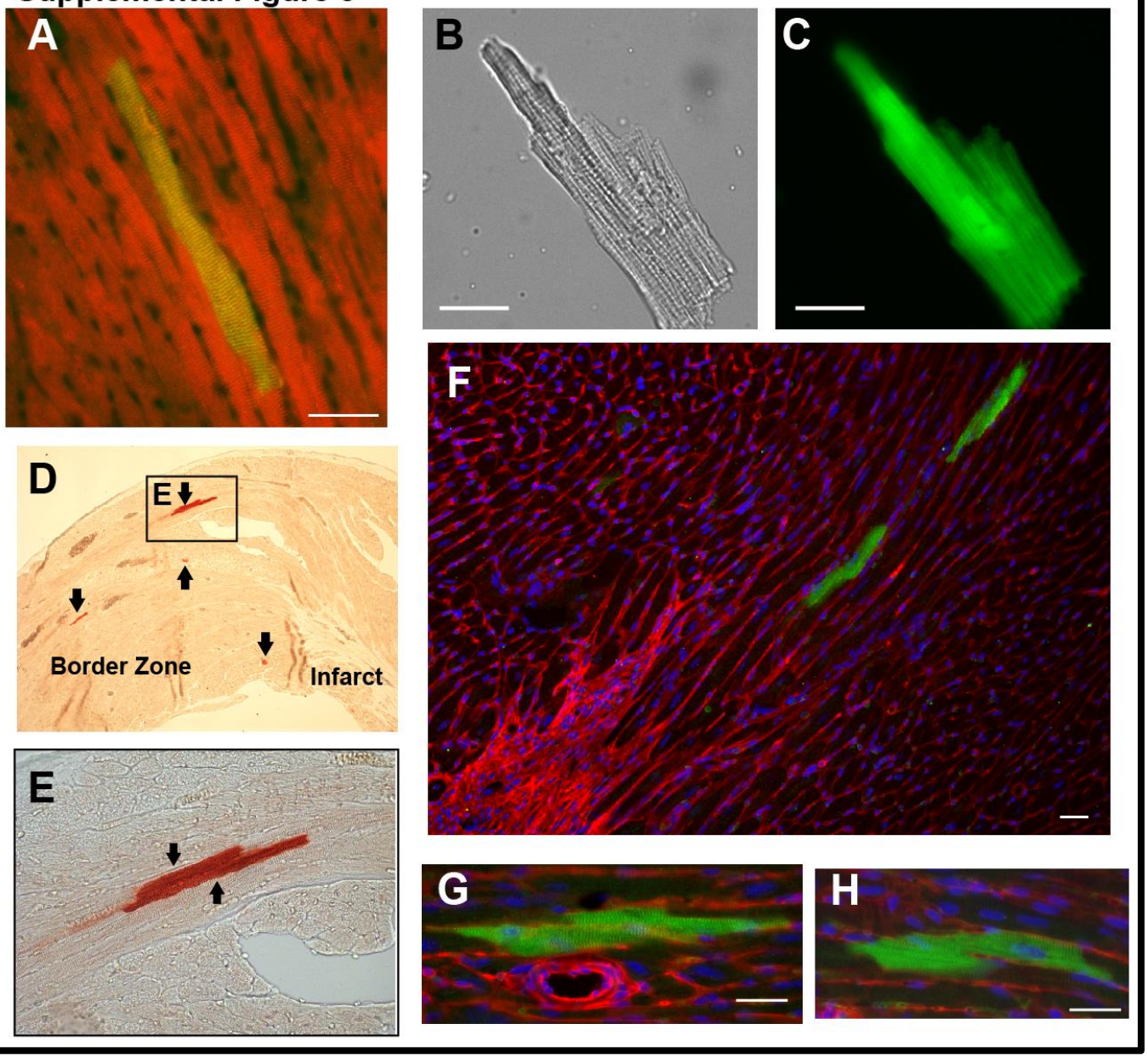
D

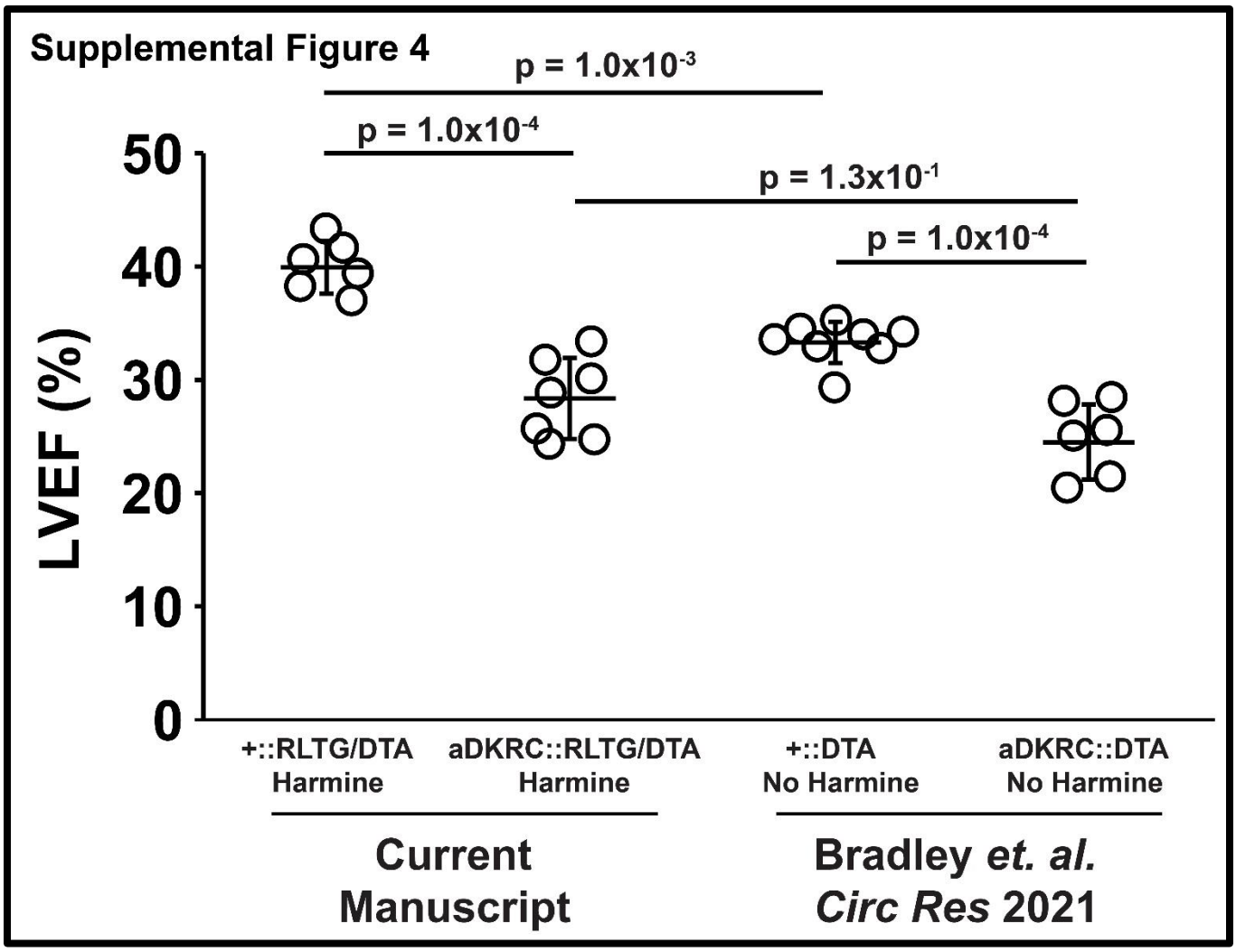


E

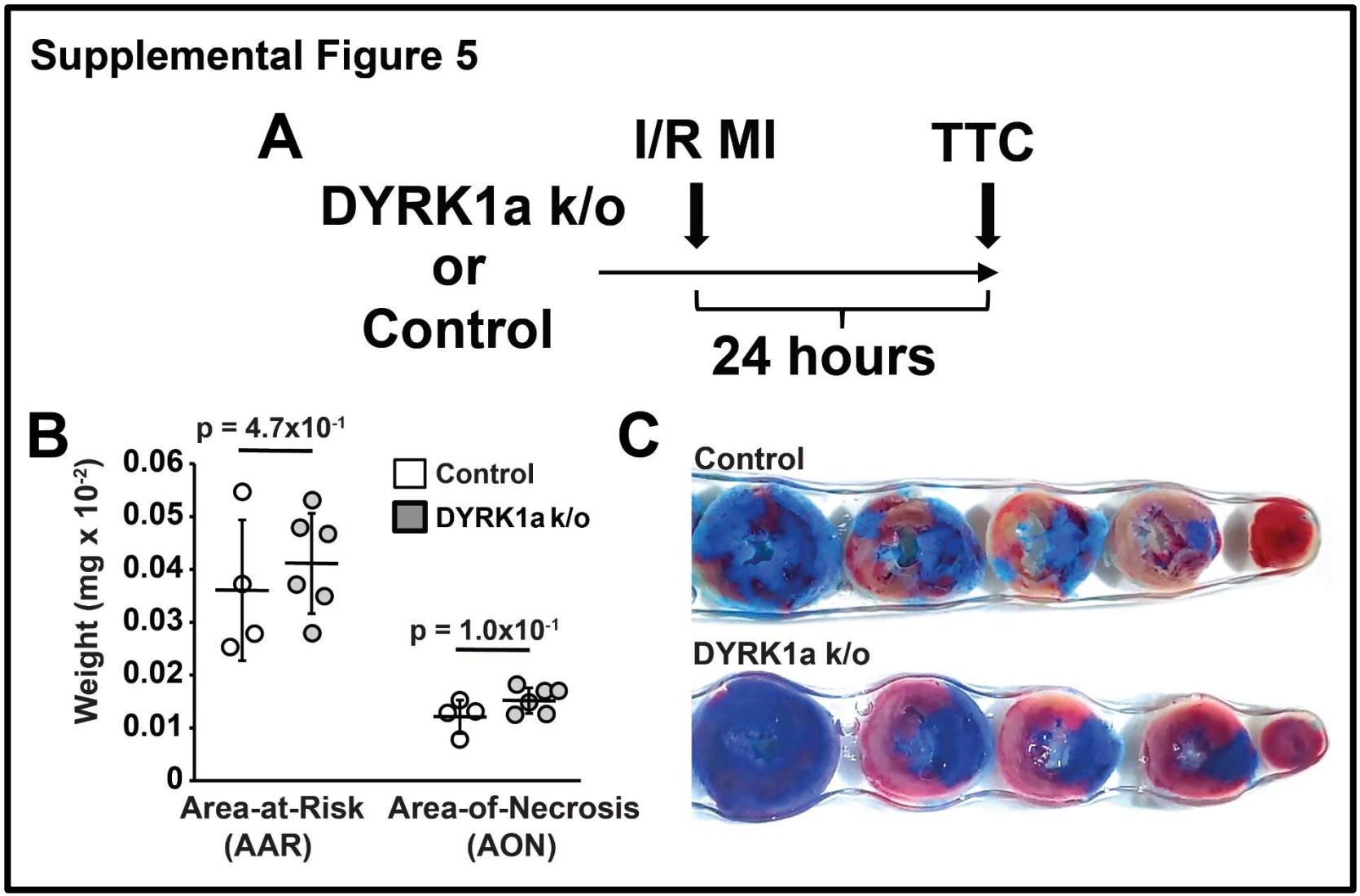


Supplemental Figure 3

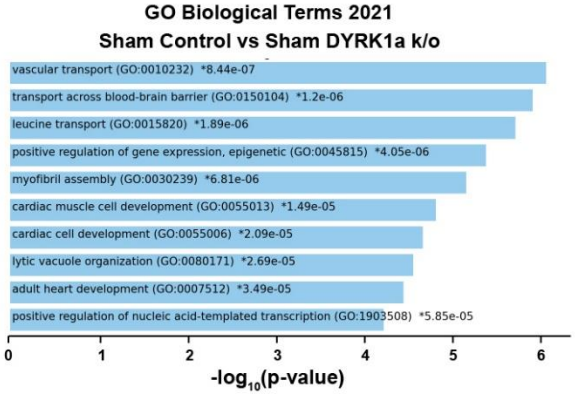


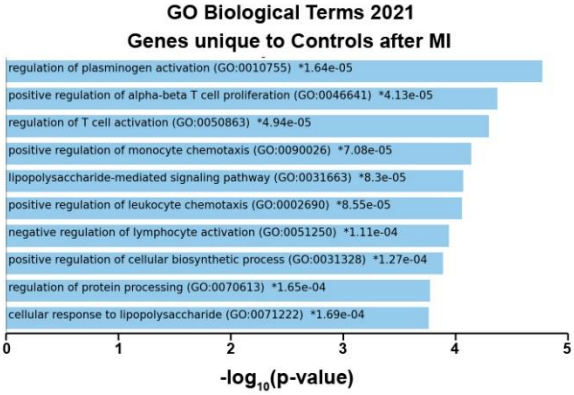

Supplemental Figure 4
p = 1.0x10-3
p = 1.0x10-4
p = 1.3x10-1
p = 1.0x10-4
LVEF (%)
50
40
30
20
10
0
+::RLTG/DTA Harmine
aDKRC::RLTG/DTA Harmine
+::DTA No Harmine
aDKRC::DTA No Harmine
Current Manuscript
Bradley et. al. Circ Res 2021

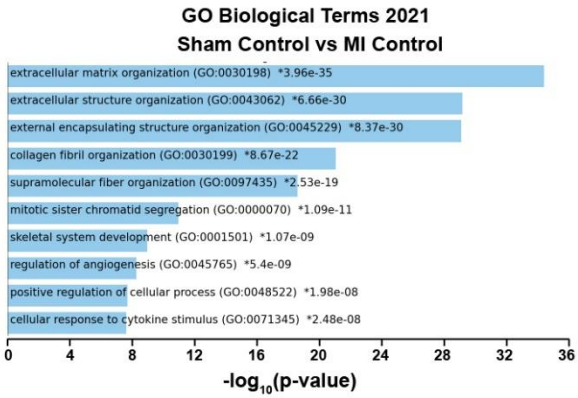
Supplemental Figure 5

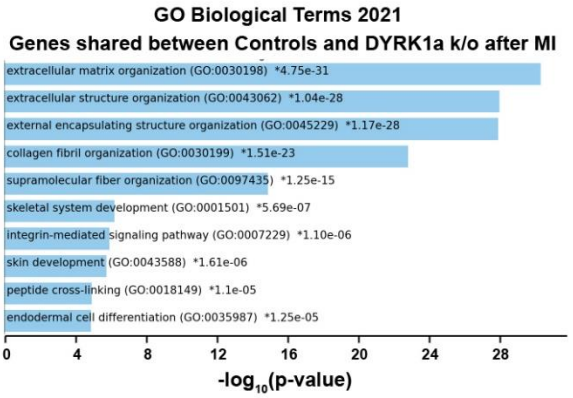


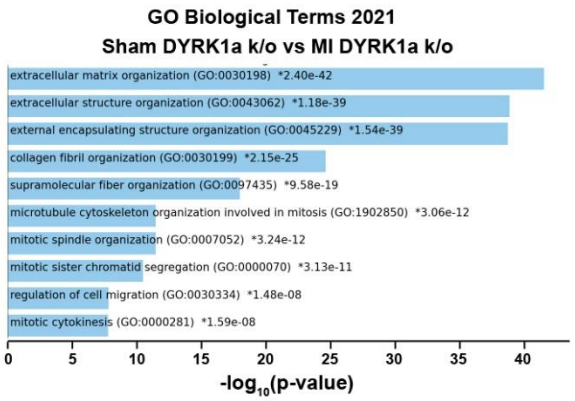
Supplemental Figure 6

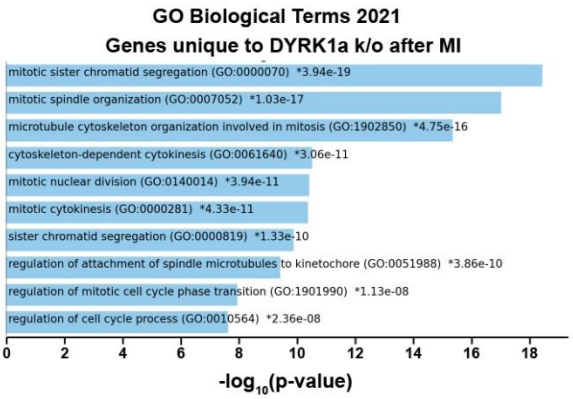


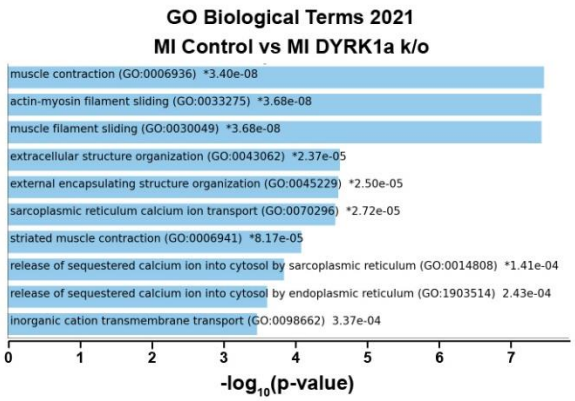


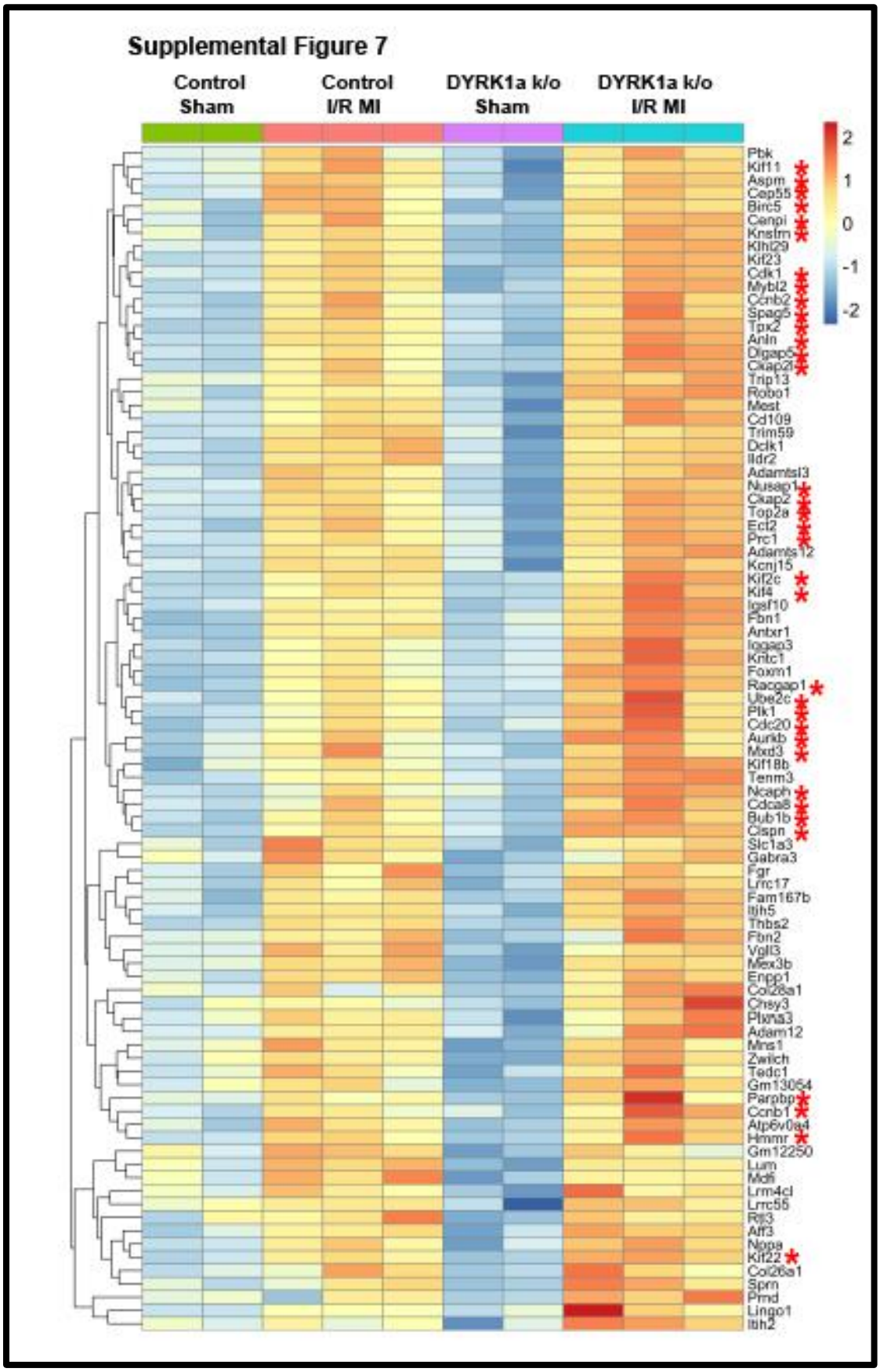











Supplemental Figure 7
Control Sham
Control I/R MI
DYRK1a k/o Sham
DYRK1a k/o I/R MI
2
1
0
-1
-2
Pbk
Kif11
Aspm
Cep55
Birc5
Cenpi
Knstrn
Klhl29
Kif23
Cdk1
Mybl2
Ccnb2
Spag5
Tpx2
Anln
Dlgap5
Ckap2l
Trip13
Robo1
Mest
Cd109
Trim59
Dclk1
Ildr2
Adamtsl3
Nusap1
Ckap2
Top2a
Ect2
Prc1
Adamts12
Kcnj15
Kif2c
Kif4
Igsf10
Fbn1
Antxr1
Iqgap3
Knltc1
Foxm1
Racgap1
Ube2c
Plk1
Cdc20
Aurkb
Mxd3
Kif18b
Tenm3
Ncaph
Cdca8
Bub1b
Clspn
Slc1a3
Gabra3
Fgr
Lrrc17
Fam167b
Itih5
Thbs2
Fbn2
Vgll3
Mex3b
Enpp1
Col28a1
Chsy3
Plxna3
Adam12
Mns1
Zwilch
Tedc1
Gm13064
Parpbp
Ccnb1
Atp6v0a4
Hmmr
Gm12250
Lum
Mdfi
Lrm4cl
Lrrc55
Rtl3
Aff3
Nppa
Kif22
Col26a1
Sprn
Prnd
Lingo1
Itih2

Supplemental Figure 8

MsigDB Hallmark 2020
(Clusters 1-3 : Embryonic/Neonatal/Adult Hearts)

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	Myogenesis	1.47E-10	2.28E-09	15.54	351.78
2	E2F Targets	1.47E-10	2.28E-09	15.54	351.78
3	G2-M Checkpoint	4.28E-06	4.42E-05	9.66	119.47
4	Mitotic Spindle	4E-05	0.00031	8.36	84.65

MsigDB Hallmark 2020
(Unique to DYRK1a k/o cardiomyocytes after MI)

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	G2-M Checkpoint	2.58E-20	2.84E-19	29.59	1334.53
2	E2F Targets	2.58E-20	2.84E-19	29.59	1334.53
3	Mitotic Spindle	1.86E-17	1.36E-16	25.59	985.99

Supplemental Table 1

Gene clusters derived from NCBI Gene Expression Omnibus (GEO) http://www.ncbi.nlm.nih.gov/geo/ Accession number GSE17020

Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
Actc1	1700006H03Rik	Nkx2-5	A630052E07Rik	LOC100044430	1200009O22Rik	1200002N14Rik
Actn2	2410076I21Rik	Nppb	Actg2	LOC100045680	1200016E24Rik	2310043N10Rik
Capn6	3632451O06Rik	Pdlim5	Col24a1	LOC100047583	1500015O10Rik	2310051E17Rik
Cdc20	Alpk2	Pkp2	Cthrc1	LOC100047628	4930533K18Rik	9030024J15Rik
Cdca3	Bmp7	Plk1	Dlk1	LOC100048554	5033414K04Rik	Abca8a
Cdca8	Cited1	Popdc2	Eln	LOC433943	6330406I15Rik	Abca9
Cdkn3	Col2a1	Ppargc1a	Emid2	LOC638301	9030425E11Rik	Acbd4
Cox6a2	Esrrg	Ppp1r14c	Nov	LOC641240	Adamts12	Ace
Eif2s3y	Fbxw5	Ppp1r1a	Nrk	LOC667277	Adamts2	Adamtsl3
Eno3	Got2	Prox1	Postn	Lsamp	Adamts4	Adcyap1r1
H19	Hba-x	Rragd	Prss35	Ly6a	Antxr1	Ahnak2
Hist1h2ab	Hbb-bh1	Rrm2	Slc38a5	Ly6c1	Anxa1	Aldh1a1
Hist1h2ad	Hbb-y	scl000959.1_2	Stfa1	Lyz2	Aoc3	Angptl1
Hist1h2af	Hspd1	Scn5a		Mgl2	Atp2a3	Angptl7
Hist1h2ah	LOC623031	Sept6		Mgst1	B230343A10Rik	Anpep
Hist1h2ak	Rcan1	Slc4a1		Mmp3	B3gnt9	Apoe
Hist1h2an	Slitrk5	Sox11		Pcolce2	Bgn	Bcl2a1a
Hspb7		Spc25		Podn	Bicc1	Bcl2a1b
Igf2bp3		Srpk3		Ppap2b	C1qtnf2	Bcl6
Kif22		Synpo2l		Ppl	Camk2n1	Blnk
Kif23		Tfrc		Ptgs2	Ccdc3	C1qa
LOC100039888		Tmod1		Retnla	Cd34	C1qb
LOC230899		Tnni1		Sod3	Cd93	C1qc
LOC640739		Tnni2		Tmem195	Cdc42ep5	C1qtnf1
Mest		Tnnt1		Tnfaip2	Clip2	C1qtnf5
Mybphl		Top2a		Tnfsf13b	Cnrip1	C3
Myh6		Upp1		Vit	Col14a1	Capg
Myl3				Xdh	Col15a1	Casp4
Myl7					Col1a1	Cbr2
Myoz2					Col1a2	Ccl2
Nppa					Col3a1	Ccl3
Nusap1					Col5a2	Ccl4
Pgam2					Col6a1	Ccl7
Prc1					Col6a2	Ccl9
Rp23-480b19.10					Col6a3	Cd14
Ryr2					Coro1a	Cd55
Slc38a4					Ctsk	Cd83
Smyd1					Ctss	Ch25h

Spag5					Cxcl1	Chrd
Spc24					Cygb	Clec2d
Srl					Cyth4	Col8a1
Stab1					Dcn	Comp
Tmem108					Dpt	Cp
Tnnc1					E430002G05Rik	Crispld2
Tnni3					Ebf1	Csf1r
Tnnt2					Ebf3	Ctsa
Ttn					Emilin1	Cxcl16
Uhrf1					Emp1	Cyp1b1
Vash2					Emp3	Cyp2d22
					Emr1	D12Ertd647e
					Eng	Dpep1
					Esam	Ebf2
					Fap	Ecm1
					Fbn1	Efemp1
					Fcgrt	Efhd1
					Fcrls	EG245190
					Fer1l3	EG630499
					Foxs1	Egfr
					Galntl1	Egr2
					Gdf10	Entpd2
					Gja4	Ephx1
					Heyl	Fbln1
					Hic1	Fbln2
					Higd1b	Fcgr3
					Ifi27	Fosb
					Igfbp4	Fxyd5
					Igfbp7	Gfpt2
					Irf8	Gstm1
					Kcnk2	Gstt3
					Laptm5	H2-D1
					Leprel2	Has1
					LOC100039175	Hmgcs2
					LOC100048332	Hs3st1
					LOC100048436	Htra3
					LOC100048556	Htra4
					LOC673251	Icam1
					LOC98434	Ifitm1
					Lox	Ifitm3
					Lrrc17	Igfbp3
					Ltbp2	Igfbp6
					Lum	Il1b

					Man2a1	Il33
					Matn4	Il6
					Meox1	Irak3
					Mfap4	Islr
					Mfap5	Itga11
					Mgp	Itgbl1
					Mmp2	Junb
					Mmp23	Klf2
					Mrc1	Klf4
					Mrc2	Klf9
					Mrgprf	Larp6
					Msc	Lgals3
					Mustn1	Lgals3bp
					Mxra7	Lgals9
					Myh11	LOC100044190
					Mylk	LOC100045864
					Naalad2	LOC674135
					Nfix	Lrp1
					Nid1	Lrrn4cl
					Notch1	Ltbp4
					Ogn	Lypd1
					Olfml1	Mmp13
					Olfml3	Mpeg1
					P2ry2	Mxra8
					P2ry6	Nfkbiz
					Parp3	Ngfb
					Pcsk6	Nupr1
					Pde1a	Omd
					Pdgfra	Osmr
					Pdgfrb	Pde4b
					Pdgfrl	Pdlim2
					Plat	Pi16
					Pmp22	Pla1a
					Prelp	Plac9
					Ptgis	Plscr4
					Ramp2	Prg4
					Rarres2	Pros1
					Rasl12	Psmb8
					Rbp1	Ptgir
					Rgma	Ptx3
					Rgs5	Rab3d
					Rhoj	Rnase4
					S100a10	S100a4

					S100a6	Samd9l
					Scara3	Scara5
					scl0003799.1_2	Scd1
					Serpinf1	Scn7a
					Sertad4	Selplg
					Sfrp2	Serpina3n
					Slc43a3	Serping1
					Sox9	Slamf9
					Sparcl1	Slc10a6
					Sphk1	Slco2b1
					Srpx	Smoc2
					Srpx2	Srgn
					Sulf1	Sult1a1
					Synpo	Svep1
					Tek	Tap2
					Tgfbr2	Tgfbi
					Thbs2	Tlr4
					Thy1	Tmem100
					Tmod3	Tmem204
					Tnxb	Tmem45a
					Tpst1	Tna
					Ttyh2	Tppp3
					Twist2	Trf
					Ybx3	Ugt1a10
						Vgll3
						Wfdc1
						Wisp2

Supplemental Table 2

List of genes with increased or decreased expression from DYRK1a k/o and Control Cardiomyocytes after I/R MI

GENES INCREASED UNIQUE TO CONTROL AFTER I/R MI	GENES INCREASED IN COMMON BETWEEN CONTROL AND DYRK1a K/O AFTER I/R MI	GENES INCREASED UNIQUE TO DYRK1A k/o AFTER I/R MI		GENES DECREASED UNIQUE TO CONTROL AFTER I/R MI		GENES DECREASED UNIQUE TO DYRK1a k/o AFTER I/R MI
4833412C05Rik	1500015O10Rik	Adam12		Gm10108		Actn3
Aebp1	Abi3bp	Adamts12		Gm11808		Arg1
AL591207.1	Acan	Adamtsl3		Gm12033		Atp2a1
Aqp2	Adamts16	Aff3		Gm15920		Car3
Arhgap22	Adamts2	Anln		Gm2225		Chil3
Bgn	Angptl7	Antxr1		Gm9385		Cyp1a1
C1qtnf6	Aspn	Aspm		Rpl10a-ps1		Ear2
Ccl12	C1qtnf3	Atp6v0a4				F7
Ccl5	Capn6	Aurkb				Gm12070
Ccl8	Ccna2	Birc5				Gm43281
Ccr2	Cemip	Bub1b				Lcn2
Cd24a	Cilp	Ccnb1				Mmp13
Cdca5	Cilp2	Ccnb2				Mybpc1
Cdh3	Col11a1	Cd109				Myh1
Cenpe	Col12a1	Cdc20				Myh2
Chaf1b	Col14a1	Cdca8				Myh4
Clec11a	Col16a1	Cdk1				Mylpf
Clec4n	Col1a1	Cenpi				Pvalb
Cyp26a1	Col1a2	Cep55				Retnla
Ddah1	Col22a1	Chsy3				Ryr1
Depdc1a	Col3a1	Ckap2				Tmem26
Dio3	Col5a1	Ckap2l				Tnnc2
Diras2	Col5a2	Clspn				Tnni2
Dnm3os	Col8a1	Col26a1				Tnnt3
Dok1	Col8a2	Col28a1				Xist
Esco2	Col9a2	Dclk1				
Fam105a	Comp	Dlgap5				
Fam83d	Crlf1	Ect2				
Fcrls	Cthrc1	Enpp1				
Fst	Cx3cr1	Fam167b				
Gcnt4	Cxcl10	Fbn1				
Gdf15	Dclk3	Fbn2				

Gli2	Dkk3	Fgr				
Gm15867	Eln	Foxm1				
Gng8	Etv4	Gabra3				
H1fx	Fibin	Gm12250				
Hck	Fmod	Gm13054				
Il6	Fn1	Hmmr				
Islr2	Fndc1	Igsf10				
Kif15	Frem1	Ildr2				
Krt18	Frzb	Iqgap3				
Loxl1	Fstl1	Itih2				
Lrp8	Garem2	Itih5				
Lrrc25	Gdf6	Kcnj15				
Mfap2	Gm4841	Kif11				
Ms4a7	Gm4951	Kif18b				
Neil3	Gpr176	Kif22				
Ngef	Gpr39	Kif23				
Nkd2	Gxylt2	Kif2c				
Oas3	Ism1	Kif4				
Pif1	Itga11	Klhl29				
Pou2f2	Itgbl1	Knstrn				
Prrx2	Lox	Kntc1				
Ptpn22	Loxl3	Lingo1				
Ptprv	Ltbp2	Lrrc17				
Ptx3	Matn4	Lrrc55				
Rasal3	Mdk	Lrrn4cl				
Rbp1	Melk	Lum				
Rflna	Mfap4	Mdfi				
Rhoh	Mfap5	Mest				
Runx1	Mki67	Mex3b				
Runx2	Myh7	Mns1				
Samsn1	Ncapg	Mxd3				
Serpina3i	Nek2	Mybl2				
Serpina3n	Nox4	Ncaph				
Serpinb1a	Nuf2	Nppa				
Serpinb1c	Nupr1	Nusap1				
Serpine1	P4ha3	Parpbp				
Serpine2	Pamr1	Pbk				
Serpinf1	Pclaf	Plk1				
Shcbp1	Pdgfrl	Plxna3				
Siglece	Piezo2	Prc1				
Slc13a3	Pimreg	Prnd				
Slfn10-ps	Plac8	Racgap1				
Slitrk4	Postn	Robo1				
Srpx2	Ptn	Rtl3				

Ssc5d	Sertad4	Slc1a3				
Star	Sfrp1	Spag5				
Susd3	Sfrp2	Sprn				
Tmem119	Sox9	Tedc1				
Tmem45a	Sprr1a	Tenm3				
Tnfaip8l2	Stil	Thbs2				
Tpbg	Thbs1	Top2a				
Vav1	Thbs4	Tpx2				
Wfdc18	Timp1	Trim59				
Wscd2	Tnc	Trip13				
	Tnfrsf11b	Ube2c				
	Wisp1	Vgll3				
	Wisp2	Zwilch				
	Zfp185					

Supplemental Table 3

List of 214 Genes predicted to be regulated by the DREAM Complex

Ensembl gene id	Gene name	Description
ENSMUSG00000036777	Anln	anillin, actin binding protein [Source:MGI Symbol;Acc:MGI:1920174]
ENSMUSG00000015749	Anp32e	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E [Source:MGI Symbol;Acc:MGI:1913721]
ENSMUSG00000041219	Arhgap11a	Rho GTPase activating protein 11A [Source:MGI Symbol;Acc:MGI:2444300]
ENSMUSG00000051517	Arhgef39	Rho guanine nucleotide exchange factor (GEF) 39 [Source:MGI Symbol;Acc:MGI:3036286]
ENSMUSG00000030654	Arl6ip1	ADP-ribosylation factor-like 6 interacting protein 1 [Source:MGI Symbol;Acc:MGI:1858943]
ENSMUSG00000005470	Asf1b	anti-silencing function 1B histone chaperone [Source:MGI Symbol;Acc:MGI:1914179]
ENSMUSG00000033952	Aspm	asp (abnormal spindle)-like, microcephaly associated (Drosophila) [Source:MGI Symbol;Acc:MGI:1334448]
ENSMUSG00000022360	Atad2	ATPase family, AAA domain containing 2 [Source:MGI Symbol;Acc:MGI:1917722]
ENSMUSG00000027496	Aurka	aurora kinase A [Source:MGI Symbol;Acc:MGI:894678]
ENSMUSG00000020897	Aurkb	aurora kinase B [Source:MGI Symbol;Acc:MGI:107168]
ENSMUSG00000017716	Birc5	baculoviral IAP repeat-containing 5 [Source:MGI Symbol;Acc:MGI:1203517]
ENSMUSG00000030528	Blm	Bloom syndrome, RecQ helicase-like [Source:MGI Symbol;Acc:MGI:1328362]
ENSMUSG00000022070	Bora	bora, aurora kinase A activator [Source:MGI Symbol;Acc:MGI:1924994]
ENSMUSG00000017146	Brca1	breast cancer 1, early onset [Source:MGI Symbol;Acc:MGI:104537]
ENSMUSG00000034329	Brip1	BRCA1 interacting protein C-terminal helicase 1 [Source:MGI Symbol;Acc:MGI:2442836]
ENSMUSG00000027379	Bub1	BUB1, mitotic checkpoint serine/threonine kinase [Source:MGI Symbol;Acc:MGI:1100510]
ENSMUSG00000040084	Bub1b	BUB1B, mitotic checkpoint serine/threonine kinase [Source:MGI Symbol;Acc:MGI:1333889]
ENSMUSG00000066979	Bub3	BUB3 mitotic checkpoint protein [Source:MGI Symbol;Acc:MGI:1343463]
ENSMUSG00000014226	Cacybp	calcyclin binding protein [Source:MGI Symbol;Acc:MGI:1270839]
ENSMUSG00000029836	Cbx3	chromobox 3 [Source:MGI Symbol;Acc:MGI:108515]
ENSMUSG00000027160	Ccdc34	coiled-coil domain containing 34 [Source:MGI Symbol;Acc:MGI:1915451]
ENSMUSG00000027715	Ccna2	cyclin A2 [Source:MGI Symbol;Acc:MGI:108069]
ENSMUSG00000041431	Ccnb1	cyclin B1 [Source:MGI Symbol;Acc:MGI:88302]
ENSMUSG00000032218	Ccnb2	cyclin B2 [Source:MGI Symbol;Acc:MGI:88311]
ENSMUSG00000024791	Cdca5	cell division cycle associated 5 [Source:MGI Symbol;Acc:MGI:1915099]

ENSMUSG00000028873	Cdca8	cell division cycle associated 8 [Source:MGI Symbol;Acc:MGI:1196274]
ENSMUSG00000019942	Cdk1	cyclin-dependent kinase 1 [Source:MGI Symbol;Acc:MGI:88351]
ENSMUSG00000096472	Cdkn2d	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4) [Source:MGI Symbol;Acc:MGI:105387]
ENSMUSG00000037628	Cdkn3	cyclin-dependent kinase inhibitor 3 [Source:MGI Symbol;Acc:MGI:1919641]
ENSMUSG00000006585	Cdt1	chromatin licensing and DNA replication factor 1 [Source:MGI Symbol;Acc:MGI:1914427]
ENSMUSG00000029177	Cenpa	centromere protein A [Source:MGI Symbol;Acc:MGI:88375]
ENSMUSG00000045328	Cenpe	centromere protein E [Source:MGI Symbol;Acc:MGI:1098230]
ENSMUSG00000026605	Cenpf	centromere protein F [Source:MGI Symbol;Acc:MGI:1313302]
ENSMUSG00000026708	Cenpl	centromere protein L [Source:MGI Symbol;Acc:MGI:1917704]
ENSMUSG00000031756	Cenpn	centromere protein N [Source:MGI Symbol;Acc:MGI:1919405]
ENSMUSG00000075266	Cenpw	centromere protein W [Source:MGI Symbol;Acc:MGI:1913561]
ENSMUSG00000068394	Cep152	centrosomal protein 152 [Source:MGI Symbol;Acc:MGI:2139083]
ENSMUSG00000046111	Cep295	centrosomal protein 295 [Source:MGI Symbol;Acc:MGI:2442521]
ENSMUSG00000024989	Cep55	centrosomal protein 55 [Source:MGI Symbol;Acc:MGI:1921357]
ENSMUSG00000002835	Chaf1a	chromatin assembly factor 1, subunit A (p150) [Source:MGI Symbol;Acc:MGI:1351331]
ENSMUSG00000032113	Chek1	checkpoint kinase 1 [Source:MGI Symbol;Acc:MGI:1202065]
ENSMUSG00000029521	Chek2	checkpoint kinase 2 [Source:MGI Symbol;Acc:MGI:1355321]
ENSMUSG00000029516	Cit	citron [Source:MGI Symbol;Acc:MGI:105313]
ENSMUSG00000037725	Ckap2	cytoskeleton associated protein 2 [Source:MGI Symbol;Acc:MGI:1931797]
ENSMUSG00000048327	Ckap2l	cytoskeleton associated protein 2-like [Source:MGI Symbol;Acc:MGI:1917716]
ENSMUSG00000040549	Ckap5	cytoskeleton associated protein 5 [Source:MGI Symbol;Acc:MGI:1923036]
ENSMUSG00000028044	Cks1b	CDC28 protein kinase 1b [Source:MGI Symbol;Acc:MGI:1889208]
ENSMUSG00000062248	Cks2	CDC28 protein kinase regulatory subunit 2 [Source:MGI Symbol;Acc:MGI:1913447]
ENSMUSG00000002718	Cse1l	chromosome segregation 1-like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1339951]
ENSMUSG00000033411	Ctdspl2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2 [Source:MGI Symbol;Acc:MGI:1196405]
ENSMUSG00000029366	Dck	deoxycytidine kinase [Source:MGI Symbol;Acc:MGI:102726]
ENSMUSG00000024472	Dcp2	decapping mRNA 2 [Source:MGI Symbol;Acc:MGI:1917890]
ENSMUSG00000030641	Ddias	DNA damage-induced apoptosis suppressor [Source:MGI Symbol;Acc:MGI:1921291]
ENSMUSG00000021377	Dek	DEK oncogene (DNA binding) [Source:MGI Symbol;Acc:MGI:1926209]
ENSMUSG00000021697	Depdc1b	DEP domain containing 1B [Source:MGI Symbol;Acc:MGI:2145425]

ENSMUSG00000021707	Dhfr	dihydrofolate reductase [Source:MGI Symbol;Acc:MGI:94890]
ENSMUSG00000037544	Dlgap5	discs, large (Drosophila) homolog-associated protein 5 [Source:MGI Symbol;Acc:MGI:2183453]
ENSMUSG00000027490	E2f1	E2F transcription factor 1 [Source:MGI Symbol;Acc:MGI:101941]
ENSMUSG00000027699	Ect2	ect2 oncogene [Source:MGI Symbol;Acc:MGI:95281]
ENSMUSG00000051220	Ercc6l	excision repair cross-complementing rodent repair deficiency complementation group 6 like [Source:MGI Symbol;Acc:MGI:2654144]
ENSMUSG00000022034	Esco2	establishment of sister chromatid cohesion N-acetyltransferase 2 [Source:MGI Symbol;Acc:MGI:1919238]
ENSMUSG00000058290	Espl1	extra spindle pole bodies 1, separase [Source:MGI Symbol;Acc:MGI:2146156]
ENSMUSG00000039748	Exo1	exonuclease 1 [Source:MGI Symbol;Acc:MGI:1349427]
ENSMUSG00000027752	Exosc8	exosome component 8 [Source:MGI Symbol;Acc:MGI:1916889]
ENSMUSG00000029687	Ezh2	enhancer of zeste 2 polycomb repressive complex 2 subunit [Source:MGI Symbol;Acc:MGI:107940]
ENSMUSG00000020808	Fam64a	family with sequence similarity 64, member A [Source:MGI Symbol;Acc:MGI:1924434]
ENSMUSG00000027654	Fam83d	family with sequence similarity 83, member D [Source:MGI Symbol;Acc:MGI:1919128]
ENSMUSG00000032815	Fanca	Fanconi anemia, complementation group A [Source:MGI Symbol;Acc:MGI:1341823]
ENSMUSG00000047757	Fancb	Fanconi anemia, complementation group B [Source:MGI Symbol;Acc:MGI:2448558]
ENSMUSG00000034023	Fancd2	Fanconi anemia, complementation group D2 [Source:MGI Symbol;Acc:MGI:2448480]
ENSMUSG00000039187	Fanci	Fanconi anemia, complementation group I [Source:MGI Symbol;Acc:MGI:2384790]
ENSMUSG00000004018	Fancl	Fanconi anemia, complementation group L [Source:MGI Symbol;Acc:MGI:1914280]
ENSMUSG00000055884	Fancm	Fanconi anemia, complementation group M [Source:MGI Symbol;Acc:MGI:2442306]
ENSMUSG00000019773	Fbxo5	F-box protein 5 [Source:MGI Symbol;Acc:MGI:1914391]
ENSMUSG00000024742	Fen1	flap structure specific endonuclease 1 [Source:MGI Symbol;Acc:MGI:102779]
ENSMUSG00000020235	Fzr1	fizzy/cell division cycle 20 related 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1926790]
ENSMUSG00000035293	G2e3	G2/M-phase specific E3 ubiquitin ligase [Source:MGI Symbol;Acc:MGI:2444298]
ENSMUSG00000074802	Gas2l3	growth arrest-specific 2 like 3 [Source:MGI Symbol;Acc:MGI:1918780]
ENSMUSG00000027454	Gins1	GINS complex subunit 1 (Psf1 homolog) [Source:MGI Symbol;Acc:MGI:1916520]
ENSMUSG00000031821	Gins2	GINS complex subunit 2 (Psf2 homolog) [Source:MGI Symbol;Acc:MGI:1921019]
ENSMUSG00000027883	Gpsm2	G-protein signalling modulator 2 (AGS3-like, C. elegans) [Source:MGI Symbol;Acc:MGI:1923373]
ENSMUSG00000050107	Gsg2	germ cell associated 2, haspin [Source:MGI Symbol;Acc:MGI:1194498]
ENSMUSG00000022385	Gtse1	G two S phase expressed protein 1 [Source:MGI Symbol;Acc:MGI:1352755]
ENSMUSG00000049932	H2afx	H2A histone family, member X [Source:MGI Symbol;Acc:MGI:102688]

ENSMUSG00000037894	H2afz	H2A histone family, member Z [Source:MGI Symbol;Acc:MGI:1888388]
ENSMUSG00000038047	Haus6	HAUS augmin-like complex, subunit 6 [Source:MGI Symbol;Acc:MGI:1923389]
ENSMUSG00000035439	Haus8	4HAUS augmin-like complex, subunit 8 [Source:MGI Symbol;Acc:MGI:1923728]
ENSMUSG00000064168	Hist1h2bh	histone cluster 1, H2bh [Source:MGI Symbol;Acc:MGI:2448387]
ENSMUSG00000096807	Hist1h2bm	histone cluster 1, H2bm [Source:MGI Symbol;Acc:MGI:2448404]
ENSMUSG00000069310	Hist1h3c	histone cluster 1, H3c [Source:MGI Symbol;Acc:MGI:2448320]
ENSMUSG00000099583	Hist1h3d	histone cluster 1, H3d [Source:MGI Symbol;Acc:MGI:2448322]
ENSMUSG00000060678	Hist1h4c	histone cluster 1, H4c [Source:MGI Symbol;Acc:MGI:2448421]
ENSMUSG00000063689	Hist2h2ab	histone cluster 2, H2ab [Source:MGI Symbol;Acc:MGI:2448314]
ENSMUSG00000044783	Hjurp	Holliday junction recognition protein [Source:MGI Symbol;Acc:MGI:2685821]
ENSMUSG00000054717	Hmgb2	high mobility group box 2 [Source:MGI Symbol;Acc:MGI:96157]
ENSMUSG00000020330	Hmmr	hyaluronan mediated motility receptor (RHAMM) [Source:MGI Symbol;Acc:MGI:104667]
ENSMUSG00000007836	Hnrnpa0	heterogeneous nuclear ribonucleoprotein A0 [Source:MGI Symbol;Acc:MGI:1924384]
ENSMUSG00000004980	Hnrnpa2b1	heterogeneous nuclear ribonucleoprotein A2/B1 [Source:MGI Symbol;Acc:MGI:104819]
ENSMUSG00000027778	Ift80	intraflagellar transport 80 [Source:MGI Symbol;Acc:MGI:1915509]
ENSMUSG00000024660	Incenp	inner centromere protein [Source:MGI Symbol;Acc:MGI:1313288]
ENSMUSG00000012443	Kif11	kinesin family member 11 [Source:MGI Symbol;Acc:MGI:1098231]
ENSMUSG00000041498	Kif14	kinesin family member 14 [Source:MGI Symbol;Acc:MGI:1098226]
ENSMUSG00000036768	Kif15	kinesin family member 15 [Source:MGI Symbol;Acc:MGI:1098258]
ENSMUSG00000027115	Kif18a	kinesin family member 18A [Source:MGI Symbol;Acc:MGI:2446977]
ENSMUSG00000024795	Kif20b	kinesin family member 20B [Source:MGI Symbol;Acc:MGI:2444576]
ENSMUSG00000030677	Kif22	kinesin family member 22 [Source:MGI Symbol;Acc:MGI:109233]
ENSMUSG00000028678	Kif2c	kinesin family member 2C [Source:MGI Symbol;Acc:MGI:1921054]
ENSMUSG00000079553	Kifc1	kinesin family member C1 [Source:MGI Symbol;Acc:MGI:109596]
ENSMUSG00000027326	Knl1	kinetochore scaffold 1 [Source:MGI Symbol;Acc:MGI:1923714]
ENSMUSG00000027331	Knstrn	kinetochore-localized astrin/SPAG5 binding [Source:MGI Symbol;Acc:MGI:1289298]
ENSMUSG00000018362	Kpna2	karyopherin (importin) alpha 2 [Source:MGI Symbol;Acc:MGI:103561]
ENSMUSG00000001440	Kpnb1	karyopherin (importin) beta 1 [Source:MGI Symbol;Acc:MGI:107532]
ENSMUSG00000035310	Lin54	lin-54 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:2140902]

ENSMUSG00000058729	Lin9	lin-9 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:1919818]
ENSMUSG00000024590	Lmnb1	lamin B1 [Source:MGI Symbol;Acc:MGI:96795]
ENSMUSG00000029910	Mad2l1	MAD2 mitotic arrest deficient-like 1 [Source:MGI Symbol;Acc:MGI:1860374]
ENSMUSG00000026779	Mastl	microtubule associated serine/threonine kinase-like [Source:MGI Symbol;Acc:MGI:1914371]
ENSMUSG00000002870	Mcm2	minichromosome maintenance complex component 2 [Source:MGI Symbol;Acc:MGI:105380]
ENSMUSG00000041859	Mcm3	minichromosome maintenance complex component 3 [Source:MGI Symbol;Acc:MGI:101845]
ENSMUSG00000022673	Mcm4	minichromosome maintenance complex component 4 [Source:MGI Symbol;Acc:MGI:103199]
ENSMUSG00000005410	Mcm5	minichromosome maintenance complex component 5 [Source:MGI Symbol;Acc:MGI:103197]
ENSMUSG00000026355	Mcm6	minichromosome maintenance complex component 6 [Source:MGI Symbol;Acc:MGI:1298227]
ENSMUSG00000029730	Mcm7	minichromosome maintenance complex component 7 [Source:MGI Symbol;Acc:MGI:1298398]
ENSMUSG00000027353	Mcm8	minichromosome maintenance 8 homologous recombination repair factor [Source:MGI Symbol;Acc:MGI:1913884]
ENSMUSG00000061607	Mdc1	mediator of DNA damage checkpoint 1 [Source:MGI Symbol;Acc:MGI:3525201]
ENSMUSG00000035683	Melk	maternal embryonic leucine zipper kinase [Source:MGI Symbol;Acc:MGI:106924]
ENSMUSG00000047534	Mis18bp1	MIS18 binding protein 1 [Source:MGI Symbol;Acc:MGI:2145099]
ENSMUSG00000031004	Mki67	antigen identified by monoclonal antibody Ki 67 [Source:MGI Symbol;Acc:MGI:106035]
ENSMUSG00000005370	Msh6	mutS homolog 6 [Source:MGI Symbol;Acc:MGI:1343961]
ENSMUSG00000021485	Mxd3	Max dimerization protein 3 [Source:MGI Symbol;Acc:MGI:104987]
ENSMUSG00000019982	Myb	myeloblastosis oncogene [Source:MGI Symbol;Acc:MGI:97249]
ENSMUSG00000033186	Mzt1	mitotic spindle organizing protein 1 [Source:MGI Symbol;Acc:MGI:1924039]
ENSMUSG00000028693	Nasp	nuclear autoantigenic sperm protein (histone-binding) [Source:MGI Symbol;Acc:MGI:1355328]
ENSMUSG00000038252	Ncapd2	non-SMC condensin I complex, subunit D2 [Source:MGI Symbol;Acc:MGI:1915548]
ENSMUSG00000035024	Ncapd3	non-SMC condensin II complex, subunit D3 [Source:MGI Symbol;Acc:MGI:2142989]
ENSMUSG00000015880	Ncapg	non-SMC condensin I complex, subunit G [Source:MGI Symbol;Acc:MGI:1930197]
ENSMUSG00000042029	Ncapg2	non-SMC condensin II complex, subunit G2 [Source:MGI Symbol;Acc:MGI:1923294]
ENSMUSG00000034906	Ncaph	non-SMC condensin I complex, subunit H [Source:MGI Symbol;Acc:MGI:2444777]
ENSMUSG00000028614	Ndc1	NDC1 transmembrane nucleoporin [Source:MGI Symbol;Acc:MGI:1920037]
ENSMUSG00000024056	Ndc80	NDC80 kinetochore complex component [Source:MGI Symbol;Acc:MGI:1914302]
ENSMUSG00000039396	Neil3	nei like 3 (E. coli) [Source:MGI Symbol;Acc:MGI:2384588]
ENSMUSG00000026622	Nek2	NIMA (never in mitosis gene a)-related expressed kinase 2 [Source:MGI Symbol;Acc:MGI:109359]
ENSMUSG00000026020	Nop58	NOP58 ribonucleoprotein [Source:MGI Symbol;Acc:MGI:1933184]

ENSMUSG00000026434	Nucks1	nuclear casein kinase and cyclin-dependent kinase substrate 1 [Source:MGI Symbol;Acc:MGI:1934811]
ENSMUSG00000026683	Nuf2	NUF2, NDC80 kinetochore complex component [Source:MGI Symbol;Acc:MGI:1914227]
ENSMUSG00000052798	Nup107	nucleoporin 107 [Source:MGI Symbol;Acc:MGI:2143854]
ENSMUSG00000038759	Nup205	nucleoporin 205 [Source:MGI Symbol;Acc:MGI:2141625]
ENSMUSG00000020739	Nup85	nucleoporin 85 [Source:MGI Symbol;Acc:MGI:3046173]
ENSMUSG00000027306	Nusap1	nucleolar and spindle associated protein 1 [Source:MGI Symbol;Acc:MGI:2675669]
ENSMUSG00000072980	Oip5	Opa interacting protein 5 [Source:MGI Symbol;Acc:MGI:1917895]
ENSMUSG00000028587	Orc1	origin recognition complex, subunit 1 [Source:MGI Symbol;Acc:MGI:1328337]
ENSMUSG00000044702	Palb2	partner and localizer of BRCA2 [Source:MGI Symbol;Acc:MGI:3040695]
ENSMUSG00000035365	Parpbp	PARP1 binding protein [Source:MGI Symbol;Acc:MGI:1922567]
ENSMUSG00000026873	Phf19	PHD finger protein 19 [Source:MGI Symbol;Acc:MGI:1921266]
ENSMUSG00000041064	Pif1	PIF1 5'-to-3' DNA helicase [Source:MGI Symbol;Acc:MGI:2143057]
ENSMUSG00000030867	Plk1	polo-like kinase 1 [Source:MGI Symbol;Acc:MGI:97621]
ENSMUSG00000025758	Plk4	polo-like kinase 4 [Source:MGI Symbol;Acc:MGI:101783]
ENSMUSG00000023345	Poc1a	POC1 centriolar protein A [Source:MGI Symbol;Acc:MGI:1917485]
ENSMUSG00000038644	Pold1	polymerase (DNA directed), delta 1, catalytic subunit [Source:MGI Symbol;Acc:MGI:97741]
ENSMUSG00000030726	Pold3	polymerase (DNA-directed), delta 3, accessory subunit [Source:MGI Symbol;Acc:MGI:1915217]
ENSMUSG00000007080	Pole	polymerase (DNA directed), epsilon [Source:MGI Symbol;Acc:MGI:1196391]
ENSMUSG00000034206	Polq	polymerase (DNA directed), theta [Source:MGI Symbol;Acc:MGI:2155399]
ENSMUSG00000060288	Ppih	peptidyl prolyl isomerase H [Source:MGI Symbol;Acc:MGI:106499]
ENSMUSG00000038943	Prc1	protein regulator of cytokinesis 1 [Source:MGI Symbol;Acc:MGI:1858961]
ENSMUSG00000025395	Prim1	DNA primase, p49 subunit [Source:MGI Symbol;Acc:MGI:97757]
ENSMUSG00000026134	Prim2	DNA primase, p58 subunit [Source:MGI Symbol;Acc:MGI:97758]
ENSMUSG00000020493	Prr11	proline rich 11 [Source:MGI Symbol;Acc:MGI:2444496]
ENSMUSG00000068744	Psrc1	proline/serine-rich coiled-coil 1 [Source:MGI Symbol;Acc:MGI:1913099]
ENSMUSG00000023015	Racgap1	Rac GTPase-activating protein 1 [Source:MGI Symbol;Acc:MGI:1349423]
ENSMUSG00000030254	Rad18	RAD18 E3 ubiquitin protein ligase [Source:MGI Symbol;Acc:MGI:1890476]
ENSMUSG00000022314	Rad21	RAD21 cohesin complex component [Source:MGI Symbol;Acc:MGI:108016]
ENSMUSG00000027323	Rad51	RAD51 recombinase [Source:MGI Symbol;Acc:MGI:97890]
ENSMUSG00000028702	Rad54l	RAD54 like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:894697]
ENSMUSG00000022391	Rangap1	RAN GTPase activating protein 1 [Source:MGI Symbol;Acc:MGI:103071]

ENSMUSG00000033762	Recql4	RecQ protein-like 4 [Source:MGI Symbol;Acc:MGI:1931028]
ENSMUSG00000038555	Reep2	receptor accessory protein 2 [Source:MGI Symbol;Acc:MGI:2385070]
ENSMUSG00000048668	Rhno1	RAD9-HUS1-RAD1 interacting nuclear orphan 1 [Source:MGI Symbol;Acc:MGI:1915315]
ENSMUSG00000021932	Rnaseh2b	ribonuclease H2, subunit B [Source:MGI Symbol;Acc:MGI:1914403]
ENSMUSG00000029110	Rnf4	ring finger protein 4 [Source:MGI Symbol;Acc:MGI:1201691]
ENSMUSG00000028884	Rpa2	replication protein A2 [Source:MGI Symbol;Acc:MGI:1339939]
ENSMUSG00000037846	Rtkn2	rhotekin 2 [Source:MGI Symbol;Acc:MGI:2158417]
ENSMUSG00000027959	Sass6	SAS-6 centriolar assembly protein [Source:MGI Symbol;Acc:MGI:1920026]
ENSMUSG00000023940	Sgol1	shugoshin-like 1 (S. pombe) [Source:MGI Symbol;Acc:MGI:1919665]
ENSMUSG00000026039	Sgol2a	shugoshin-like 2a (S. pombe) [Source:MGI Symbol;Acc:MGI:1098767]
ENSMUSG00000022322	Shcbp1	Shc SH2-domain binding protein 1 [Source:MGI Symbol;Acc:MGI:1338802]
ENSMUSG00000036223	Ska1	spindle and kinetochore associated complex subunit 1 [Source:MGI Symbol;Acc:MGI:1913718]
ENSMUSG00000054115	Skp2	S-phase kinase-associated protein 2 (p45) [Source:MGI Symbol;Acc:MGI:1351663]
ENSMUSG00000054099	Slc25a40	solute carrier family 25, member 40 [Source:MGI Symbol;Acc:MGI:2442486]
ENSMUSG00000028312	Smc2	structural maintenance of chromosomes 2 [Source:MGI Symbol;Acc:MGI:106067]
ENSMUSG00000034349	Smc4	structural maintenance of chromosomes 4 [Source:MGI Symbol;Acc:MGI:1917349]
ENSMUSG00000024054	Smchd1	SMC hinge domain containing 1 [Source:MGI Symbol;Acc:MGI:1921605]
ENSMUSG00000061479	Snrpa	small nuclear ribonucleoprotein polypeptide A [Source:MGI Symbol;Acc:MGI:1855690]
ENSMUSG00000002055	Spag5	sperm associated antigen 5 [Source:MGI Symbol;Acc:MGI:1927470]
ENSMUSG00000005233	Spc25	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913692]
ENSMUSG00000069910	Spdl1	spindle apparatus coiled-coil protein 1 [Source:MGI Symbol;Acc:MGI:1917635]
ENSMUSG00000028718	Stil	Scl/Tal1 interrupting locus [Source:MGI Symbol;Acc:MGI:107477]
ENSMUSG00000017548	Suz12	suppressor of zeste 12 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1261758]
ENSMUSG00000037313	Tacc3	transforming, acidic coiled-coil containing protein 3 [Source:MGI Symbol;Acc:MGI:1341163]
ENSMUSG00000024498	Tcerg1	transcription elongation regulator 1 (CA150) [Source:MGI Symbol;Acc:MGI:1926421]
ENSMUSG00000039994	Timeless	timeless circadian clock 1 [Source:MGI Symbol;Acc:MGI:1321393]
ENSMUSG00000025574	Tk1	thymidine kinase 1 [Source:MGI Symbol;Acc:MGI:98763]
ENSMUSG00000019961	Tmpo	thymopoietin [Source:MGI Symbol;Acc:MGI:106920]
ENSMUSG00000020914	Top2a	topoisomerase (DNA) II alpha [Source:MGI Symbol;Acc:MGI:98790]
ENSMUSG00000027469	Tpx2	TPX2, microtubule-associated [Source:MGI Symbol;Acc:MGI:1919369]

ENSMUSG00000032586	Traip	TRAF-interacting protein [Source:MGI Symbol;Acc:MGI:1096377]
ENSMUSG00000032783	Troap	trophinin associated protein [Source:MGI Symbol;Acc:MGI:1925983]
ENSMUSG00000038379	Ttk	Ttk protein kinase [Source:MGI Symbol;Acc:MGI:1194921]
ENSMUSG00000001403	Ube2c	ubiquitin-conjugating enzyme E2C [Source:MGI Symbol;Acc:MGI:1915862]
ENSMUSG00000060860	Ube2s	ubiquitin-conjugating enzyme E2S [Source:MGI Symbol;Acc:MGI:1925141]
ENSMUSG00000026429	Ube2t	ubiquitin-conjugating enzyme E2T [Source:MGI Symbol;Acc:MGI:1914446]
ENSMUSG00000029591	Ung	uracil DNA glycosylase [Source:MGI Symbol;Acc:MGI:109352]
ENSMUSG00000028560	Usp1	ubiquitin specific peptidase 1 [Source:MGI Symbol;Acc:MGI:2385198]
ENSMUSG00000031016	Wee1	WEE 1 homolog 1 (S. pombe) [Source:MGI Symbol;Acc:MGI:103075]
ENSMUSG00000028180	Zranb2	zinc finger, RAN-binding domain containing 2 [Source:MGI Symbol;Acc:MGI:1858211]