Meis transcription factors regulate cardiac conduction system development and adult function

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1. ABSTRACT

AIMS: The Cardiac Conduction System (CCS) is progressively specified during development by interactions among a discrete number of Transcriptions Factors that ensure its proper patterning and the emergence of its functional properties. Meis genes encode homeodomain transcription factors (TFs) with multiple roles in mammalian development. In humans, Meis genes associate with congenital cardiac malformations and alterations of cardiac electrical activity, however the basis for these alterations has not been established. Here we studied the role of Meis transcription factors in cardiomyocyte development and function during mouse development and adult life.

METHODS AND RESULTS: We studied *Meis1* and *Meis2* conditional deletion mouse models that allowed cardiomyocyte-specific elimination of Meis function during development and inducible elimination of Meis function in cardiomyocytes of the adult CCS. We studied cardiac anatomy, contractility and conduction. We report that Meis factors are global regulators of cardiac conduction, with a predominant role in the CCS. While constitutive Meis deletion in cardiomyocytes led to congenital malformations of the arterial pole and atria, as well as defects in ventricular conduction, Meis elimination in cardiomyocytes of the adult CCS produced sinus node dysfunction and delayed atrio-ventricular conduction. Molecular analyses unraveled Meis-controlled molecular pathways associated with these defects. Finally, we studied in transgenic mice the activity of a *Meis1* human enhancer related to an SNP associated by GWAS to PR elongation and found that the transgene drives expression in components of the atrio-ventricular conduction system.

CONCLUSIONS: Our study identifies Meis TFs as essential regulators of the establishment of cardiac conduction function during development and its maintenance during adult life. In addition, we generated animal models and identified molecular alterations that will ease the study of Meis-associated conduction defects and congenital malformations in humans.

2. INTRODUCTION

Meis transcription factors (TFs) belong to the TALE (Three Aminoacid Loop Extension) family and are highly conserved in evolution at the molecular and functional level[1]. *Meis1* (myeloid ecotropic viral integration site 1) was the first gene of the family to be identified[2]. In mammals, two additional highly similar genes have been identified; *Meis2* and *Meis3*[3,4]. Except in the head, the embryonic expression patterns of *Meis1* and *Meis2* are highly coincident and both genes encode very similar proteins with redundant functions[5]. In contrast, Meis3 expression is mainly restricted to the hindbrain, although it can be also detected in the heart, spleen and lung at later stages[4]. Understanding Meis roles in cells in which Meis1 and Meis2 are co-expressed therefore involves the elimination of both genes.

Meis TFs function as cofactors of other TFs, such as Pbx, Prep or Hox factors[6]. They can form dimers or trimers, modifying the cofactors' affinity and selectivity for DNA-binding sites. Thus, there is increased difficulty in understanding Meis TFs function, because it is highly context-dependent. *Meis1* knockout mice die around E14.5 due to failing hematopoiesis[7-9]. Additional defects in *Meis1*-deficient embryos include eye hypoplasia, cardiac interventricular septum defects and overriding aorta[7,9-11]. *Meis2*-deficient mice also die around E14.5 and show hematopoietic defects and persistent truncus arteriosus[12].

Meis TFs also play roles in postnatal life. *Meis1* is important for the maintenance of hematopoietic stem cell quiescence in the bone marrow hematopoietic niche[13-15]. In the postnatal heart, Meis1 is important for the cell cycle arrest that takes place after birth in mouse cardiomyocytes[16]. In humans, a rare germline heterozygous *Meis2* mutation is associated with palatal defects, intellectual disability and congenital heart defects, including ventricular septal defect and overriding aorta[17-19]. In addition, *Meis1* genetic variants are associated with PR elongation in humans, suggesting a Meis role in atrio-ventricular conduction[20,21]. These results indicate that Meis TFs are not only involved in human heart morphogenesis, but also in the regulation of cardiomyocyte specialized functions, however this aspect has not been explored in animal models.

Genetic analyses in mouse models have advanced our knowledge on the transcriptional control of Cardiac Conduction System (CCS) development. Members of the Tbx-, GATA- and Irx-family, Isl1, Nkx2.5, Shox2 and other TFs have been found essential for the specification and regional specialization of the CCS (reviewed in[22]). In contrast, the study of the role of developmental transcriptional regulatory networks during the maintenance of CCS physiology in the adult heart has remained less studied[23,24].

Here, we studied the roles of *Meis1* and *Meis2* in cardiomyocytes using genetic mouse models. We report that Meis TFs are required for cardiac conduction with a predominant role in the cardiomyocytes of the CCS, including the sinoatrial node and the atrio-ventricular and ventricular conduction systems. Interestingly, Meis function is not restricted to CCS development but also required for the maintenance of

adult CCS physiology, including sinoatrial node pacemaker function and atrio-ventricular conduction. In particular, in the mouse models generated we observed elongation of the PR interval, which reproduces the GWAS association between *Meis1* and PR prolongation in humans. In addition, our study identifies congenital defects partially overlapping those reported in patients that carry *Meis2* mutations. Our study identifies Meis TFs as essential regulators of cardiac conduction development and adult physiology and provides animal models for *Meis*-associated conduction defects and congenital malformations.

3. METHODS

Mouse strains

All animal procedures in the MT laboratory were approved by the CNIC Animal Experimentation Ethics Committee, by the Community of Madrid (Ref. PROEX 144.1/21) and conformed to EU Directive 2010/63EU and Recommendation 2007/526/EC regarding the protection of animals used for experimental and other scientific purposes, enforced in Spanish law under Real Decreto 1201/2005. In this study mice were maintained on a mixed genetic background. Mice were euthanized by CO_2 inhalation according to the European Commission recommendations for the euthanasia of experimental animals.

Mouse lines used were *Meis1*^{ECFP} and *Meis1*^{CreER} [11], *R26R*^{TdTomato} [25], *Meis1*^{flox} [13], *Meis2*^{flox} [26], *α-MHC*^{Cre}[27], *Hcn4*^{CreERT2} [28], and *617-HCRE* [29].

For the generation of M1M2KO mice, we crossed *Meis1*$^{flox/flox}$*; Meis2*$^{flox/flox}$ females with *Meis1*$^{flox/+}$*; Meis2*$^{flox/flox}$*; α-MHC*$^{Cre/+}$ males in order to obtain 25% of embryos with Meis1 and Meis2 double homozygous deletion. Animals resulting from the same crosses that did not inherit the Cre allele were used as controls.

For the generation of M1M2 CSiKO mice, we crossed *Meis1*$^{flox/flox}$*; Meis2*$^{flox/flox}$ females with *Meis1*$^{flox/+}$*; Meis2*$^{flox/flox}$*; Hcn4*$^{CreERT2/+}$ males in order to obtain 25% of embryos with Meis1 and Meis2 double homozygous deletion in the conduction system following Tamoxifen exposure. Animals resulting from the same crosses that did not inherit the CreERT2 allele were used as controls. For experimens, all animals received the same Tamoxifen dose, as described below.

Tamoxifen administration

200 mg of tamoxifen (Sigma-T5648-1G) were dissolved in 20 ml of corn oil (Sigma-C8267) for a final concentration of 10 mg/ml. A daily dose of 100 µl from this solution was administered by oral-gavage to adult mice for 5 consecutive days.

Immunofluorescence

Hearts dissected and fixed overnight at 4ºC in 2% paraformaldehyde (PFA) in PBS and whole/mount stained or embedded in gelatin or paraffin for sectioning. Primary antibodies used were anti-Meisa (1:500)[30], anti-Meis2 (1:500)[30], cTnT (1:200, MS-295 Thermo Scientific), Cx43 (1:200, Sigma C6219), GFP (1:200, Acris R1091P), Hcn4 (1:100, Abcam ab85023 and 1:200 Sigma-Aldrich AB5808), Cx40 (1:200, Invitrogen 378900), Scn5a (1:200, Alomone Labs ASC-005). Cryosections or paraffin sections were permeabilized with PBT (PBS with 0.5% Triton X-100) and blocked with universal TNB blocking reagent FP1012-Perkin Elmer. Primary antibodies were incubated at 4°C overnight and secondary antibodies for 1 h at room temperature. Secondary antibodies were anti-rabbit Alexa633 and 594 (Life technologies A21071 and A11012), anti-rabbit-HRP (Dako P0448), anti-mouse Alexa488 (Life technologies A11029) and anti-goat-biotin (Jackson 705-065-003) all at 1:500 concentration. Sections were mounted using Dako fluorescence mounting medium (s3023). Whole-mount atria were stained with Wheat Germ Agglutinin (WGA-Thermo Scientific-W21404) and optically cleared using Abberior TDE Mounting Medium.

***In situ* hybridization on sections**

Paraffin sections were rehydrated from xylol to PBS passing through sterile solutions with decreasing concentrations of ethanol. Sections were digested with proteinase K (10µg/ml) at 37ºC for 10 minutes. Riboprobe hybridization was performed at 65ºC overnight. The next day, sections were washed and incubated with anti-DIG antibody at 4ºC overnight. Then, sections were developed with BM-purple (Roche, ref 11442074001) at room temperature or 37ºC. Time of development was about 5 days.

Image acquisition and analysis

Images of the *in situ* hybridization were acquired with a Nikon Eclipse 90i microscope. H&E and Sirius Red stained sections were scanned with Hamamatsu Nanozoomer 2.0 RS and NDP. Scan 2.5 software. Analysis and quantifications were performed with the NDP Analyzer software.

Immunofluorescence images were acquired with a Zeiss LSM 700 confocal microscope using 405, 458, 488, 568 and 633 nm wavelengths and 10x/0.45 dry, 25x/0.8 and 40x/1.3 oil objectives. Whole-mount atria 3D images were obtained with the Leica TCS SP8 coupled to a DMi8 inverted confocal microscope Navigator module equipped with light laser. Z-stacks were captured every 4 µm using a 10x/0.4 dry objective. To estimate ploidy in isolated cardiomyocytes, nuclear volumes and DAPI intensity were measured with acquired confocal z-stacks at high magnification (63x/1.4, oil) with 2µm Z-steps using a Zeiss LSM 700 confocal microscope. Image J (https://imagej.nih.gov/ij/) was used for image analysis.

Echocardiography

For prenatal echocardiography, pregnant females were anesthetized with 2% isofluorane in oxygen. Abdominal surgery was then performed for uterus exposure. After surgery, isoflurane was adjusted to maintain a heart rate at 450±50 bpm and fetuses were exposed one at a time to keep them as warm as possible. An infrared heat lamp was used for the same purpose during acquisition. Echocardiography was performed by an expert operator using a high-frequency ultrasound system (Vevo 2100, Visualsonics, Canada) with a 50-MHz probe on a heating platform. Bidimensional (2D), M-Mode echocardiography was used to visualize the hearts in long and short axis view (LAX and SAX, respectively). Left and right ventricular ejection fraction (EF), wall thickness and diastolic and systolic chamber dimensions were assessed from the M-Mode SAX view. Ejection fraction was calculated from the short axis view at the level of the papillary muscles and using the Teichholz method[31]. Heart rate was calculated using three consecutive outflow waves. Corrected ventricular masses were calculated from M-mode images according to the following formula for the left ventricle: $1.053 \times [(LVIDd + LVPWd + VSTd)^3 - (LVIDd)^3] \times 0.8$, where LVIDd: diastolic left ventricle inner dimension, LVPW: diastolic left ventricle posterior wall thickness and VSTd: ventricular septum thickness. The procedure for RV mass estimation was similar, taking into account that before birth both ventricles are rather similar and both serve the systemic circulation. The position of the fetuses was recorded, so that fetal identity could be tracked for genotyping. This procedure was therefore blinded to the genotype of the fetuses. A similar procedure was performed for adult mouse heart echography without surgery.

Optical mapping

Pregnant females at ED14.5 or ED16.5 were sacrificed by cervical dislocation and the embryos were harvested. Heart isolation from the embryos was performed in a petri dish with ice-cold Tyrode's Buffer to prevent ischemic damage. Harvested hearts were placed in wells of a P12 dish on ice and incubated for 15 minutes in 500 µL of ice-cold Tyrode's Buffer with 25 µL of di-4-ANEPPS (stock solution in DMSO, 1.25 mg/ml, Invitrogen) and 2 µL of blebbistatin (14 mM stock in DMSO, Sigma) in darkness. After staining, hearts were pinned in a custom-made heated dish (37 ºC) with continuously oxygenated Tyrode's Buffer with 14 µM blebbistatin. Membrane voltage changes were recorded as fluorescence changes over time at 1 kHz from both anterior and posterior aspect of the heart using Ultima L high-speed camera (SciMedia, Japan) and bundled software (BV_Analyzer) was used to generate epicardial activation maps as described[32].

Electrocardiogram

Electrocardiogram (ECG) recordings were obtained in sedated animals as reported elsewhere[33]. Briefly, mice were anesthetized with 1.5% isoflurane in oxygen, inhaled through a facial mask. To avoid night-day

circadian variations, ECGs were performed in the morning. Expert operators (V.C. and S.T.) gently handled the animals to insert subcutaneously ECG electrodes in the terminal end of the four limbs. Additional ECG gel was used to improve signal-to-noise ratio. Then, ECG recordings were acquired for 60-second at 2 KHz sweep-speed using a MP36R data acquisition workstation (Biopac Systems). Data were stored for off-line analysis using custom MatLab scripts for pre-processing, visualization and quantification of electrophysiological intervals and heart rate[34] (Figure S1).

After band-pass filtering between 0.5-200 Hz, baseline wander was removed using a bidirectional filtering strategy. We removed and excluded ECG segments with noise artifacts manually using sequential previsualization of 10-s segments. To detect the R-peak of the QRS complex (green dots in Figure S1), we used parabolic fitting of the Coiflet wavelet transformation and further detection of the maximum magnitude point. All R-peak detections were supervised to ensure accuracy of ECG segmentations. After detection of the QRS complex, P and T waves, and ECG intervals were extracted using adaptive windowing depending on beat-to-beat R-R changes. More specifically: i) PR intervals were measured from the beginning of the P wave to the beginning of the R wave/Q wave; ii) QRS intervals were measured from the beginning of the Q wave until the point where the S wave crosses the baseline; and iii) QT intervals were measured from the beginning of the Q wave until the point where the T-wave declines to 90% (T90) from the peak. Adaptive heart-rate-corrected QT values (QTc) were derived using a modification of Bazzet's formula for murine electrocardiography[35]. From the evaluation of control mice at 2 and 6 months of age, we established a sub-domain of normal RR variability among all ECG traces. Then, we defined the presence of sinus node dysfunction when the animal-specific RRn+1 vs RRn domain fell partially or completely out of the normal RR variability sub-domain identified in controls. Dimensionless R-R intervals were also plotted over the 60-second electrogram recordings to detect sinus rhythm alterations. A free copy of the custom-made ECG tool for semiautomatic analysis of large amounts of data from long-duration ECG recordings in mice can be obtained from D.F. upon request.

RNA sequencing

4 control and 4 M1M2DKO fetuses were harvested at E15.5 from four independent litters. Hearts were dissected in ice-cold sterile PBS. Atria and ventricles were separated and OFT removed. Then, atria and ventricles were separated and all other tissues removed. Tissue lysis was performed with TissueLyser LT (Quiagen) or TriReagent (Trizol, Sigma-T9424) and RNA isolation with RNeasy Mini or Midi Kit (Quiagen) for embryonic and adult tissues respectively. Library and sequencing were performed at CNIC Genomic Unit. 20ng of total RNA were used to generate barcoded RNA-seq libraries using the NEBNext Ultra RNA Library preparation kit (New England Biolabs). The size and the concentration of the libraries was checked using the TapeStation 2200 DNA 1000 chip. Libraries were sequenced on a HiSeq2500

(Illumina) to generate 60-base single reads. FastQ files for each sample were obtained using bcltofastQ software 2.20. Gene Set Enrichment Analysis was performed with genes differentially expressed using the Broad Institute GSEA "Molecular Signatures Database" computing overlaps with KEGG and Gene Ontology gene sets. RNAseq data are available from the GEO database with accession number GSE213356.

Bioinformatic analysis

Public Meis1 ChIP-seq data[36] was integrated with available ATAC-seq data from right atrial CMs and pacemaker CMs[37]. Raw ATAC-seq sequencing data was processed in order to obtain a list of accessible DNA regions. Adapters were trimmed using Cutadapt v.1.7.1[38] and reads were mapped against mouse mm10 reference genome using bowtie2 v.2.2.5[39]. Duplicated sequences were annotated with Markduplicates v.1.97 from the "Picard Tools", Broad Institute GitHub repository (http://broadinstitute.github.io/picard/). Unmapped sequences, secondary alignments and low quality reads were filtered out. Peaks were called using MACS2 v.2.2.9.1[40] callpeaks function with the parameters --nomodel --shift -100 --extsize 200 commonly used for ATAC-seq data. Overlapping peaks between ChIP-seq and ATAC-seq data were obtained using the GenomicRanges[41] package in R. ATAC reads inside Meis1 peaks were quantified using the samtools v.0.1.18[42] bedcov function, and normalized by mapped library size.

Statistical analysis

All statistical analyses are detailed in the figure legends.

4. RESULTS

Meis1 and Meis2 expression in the developing and adult mouse heart

To characterize Meis function in cardiomyocytes, we studied the expression of *Meis1* and *Meis2* in the developing and adult mouse heart. In the embryonic heart, up to embryonic day of development 10.5 (E10.5), *Meis1* and *Meis2* mRNA expression was detected in the second heart field, epicardium and endocardium, but not in the heart tube, indicating that Meis TFs associate at these early stages with a cardiac progenitor phenotype (Figure 1A). In contrast, from mid-gestation towards birth, Meis proteins revealed with a pan-Meis antibody were detected in differentiating cardiomyocytes (Figure 1B; 1C-E). Specific detection of *Meis1* expression using an ECFP knock-in reporter[11] showed at mid-gestation strong expression in the sino-atrial node, atrio-ventricular bundle, trabecular myocardium and atrial myocardium (Figure 1C'-E'). Lower expression levels were detected in the ventricular working myocardium (Figure

1D'). Specific detection of Meis2 showed generalized expression in cardiomyocytes, with higher expression in the atrio-ventricular bundle (AVB) (Figure 1F-H'). In the adult heart, both the *Meis1* reporter and the pan-Meis antibody showed a strong signal the sino-atrial node (SAN), atrio-ventricular node (AVN) and AVB (Figure 1I-K, M, N), a lower level of expression in atrial cardiomyocytes (Figure 1L-O) and very low expression in ventricular working cardiomyocytes (Figure 1P). Consistent with these results, tracing *Meis1*-expressing cells using knock-in *Meis1*^{CreERT2} tracer line showed high density of labelled cells in the SAN, a medium density in atria and the bundle branches, and very low density in the working myocardium (Figure 1Q-S).

Characterization of *Meis1* and *Meis2* function in cardiomyocytes

To study the function of Meis TF in cardiomyocytes we recombined floxed *Meis1* and *Meis2* alleles with *αMHC-Cre*, generating double *Meis1* and *Meis2* disruption in cardiomyocytes (M1M2DKO) (Figure 2A, B). We did not recover any live M1M2DKO animal at postnatal day 1 (P1), while 60% were found alive at E18.5 (Figure 2C), indicating that most deaths took place at the end of gestation or perinatally. Anatomically, mutant hearts showed Ventricular Septum Defect (VSD), with inter-ventricular communication (60% of mutants) and overriding aorta (80% of hearts with VSD) (Figure 2D, G). In addition, atria were strongly dysmorphic, showing hypoplasia and finger like protrusions (Figure 2F). Evaluation of interventricular septum (IVS) thickness and ventricular mass by echocardiography at E18.5 (Figure 2H) suggested mild hypoplasia of mutant hearts, while left ventricular function was preserved. Mutant hearts at E18.5 showed as well a higher beat rate than control hearts, suggesting alterations of the sino-atrial node.

We then studied by RNA-seq how the elimination of Meis function affects the cardiomyocyte molecular profile. For this, we separately analyzed the atria and ventricles of E15.5 M1M2DKO hearts. We found a high number of differentially expressed genes between mutants and controls in E15.5 atria and a lower number in ventricles at E15.5 (Figure 3A and Supplementary Datasets 1 and 2). This observation matches the expression profile of Meis genes and the strong dysmorphology of the atria in M1M2DKO hearts.

Pathway analysis of the differentially expressed genes (Figure 3B, C) identified an association with pathological conditions like Arrhythmogenic Right Ventricular Cardiomyopathy (ARVC), Hypertrophic Cardiomyopathy (HCM) and Dilated Cardiomyopathy (DCM). In relation to biological processes, "cardiac contraction" and "calcium signaling" were detected. The most prominent molecular pathways detected related to "GAP junction", "Focal adhesion", "ECM receptor interaction" and "Wnt signaling", suggesting the cell-cell and cell-ECM interactions were the most affected pathways.

To determine the validity of this analysis, we studied whether the differentially expressed genes were enriched for Meis1/2-bound genes, comparing our data with previously reported ChIP-seq data[36] that identified the distribution of Meis protein binding in the chromatin. We found a significant association between the genes differentially repressed or activated upon Meis inactivation and those genes that have nearby Meis1/2-binding sites in the heart[36] (Figure 3D and Supplementary Dataset 3). These results show that the RNA-seq analysis identifies direct Meis targets.

Association of *Meis1* and *Meis2* function with CCS development and fetal function

These previous observations, together with the preferential expression of *Meis1* and *Meis2* in various components of the adult CCS, led us to specifically address the role of Meis TFs in cardiac conduction. We therefore studied the correlation between Meis-regulated genes and a list of genes functionally associated with progressive CCS disease in humans[43] and found a strong association (Figure 4A). In addition, other studies identified Meis binding sites enriched in open chromatin regions in mouse sinoatrial node cardiomyocytes[37] and in human pacemaker-like cardiomyocytes derived from IPSCs[44]. We then mapped the co-occurrence of ATACseq peaks in RA and Pacemaker cardiomyocytes from[37] and Meis ChIPseq binding sites from[36] and associated them to specific genes by mapping their presence within -1Kb to +1Kb from the transcription units. We then identified the overlap between these genes and those that change expression in M1M2DKO mutants (Supplementary Dataset 4). This study showed that of the 1282 genes affected by Meis mutation in atria, 32% contained a Meis peak coincident with an ATACseq peak in RA CMs (Supplementary Dataset 4). This proportion was 35% for genes with Meis and ATACseq peaks in Pacemaker CMs. The identified genes represent good candidates for direct Meis targets in atrial and sinoatrial node CMs. There was a strong overlap between these candidate Meis targets in atrial and pacemaker CMs, with very few genes specific for atria, but a group of 50 genes specific for pacemaker CMs (Supplementary Dataset 4). Although the proportion of genes with ATACseq + Meis peaks was only slightly higher in Pacemaker CMs than in RA CMs, the opening of the ATACseq peaks coincident with Meis peaks was on average higher in Pacemaker CMs than in RA CMs, as measured by the number of reads in each peak (Figure 4B and Supplementary Dataset 5). The presence of ATACseq + Meis peaks was about double as frequent within the group of genes downregulated in mouse mutants than in the upregulated ones. This suggest that Meis is predominantly an activator rather than a repressor on direct targets in CMs. These results indicate Meis roles and target genes in both atrial and pacemaker CMs.

To more specifically study the correlation between genes regulated by Meis TF and the transcriptional signature of the CCS, we compared a published single-cell RNAseq analysis of the different components of the E16 CCS[45] with the set of genes de-regulated in E15.5 M1M2DKO hearts. We found a very strong

association between the genes downregulated in M1M2DKO (genes activated by Meis) and those found in the single-cell analysis to have preferential expression in the SAN, the AVN and the Purkinje (PKJ) cardiomyocytes (Figure 4C, left superior quadrant of each graph and Supplementary Datasets 6, 7 and 8). In contrast, genes downregulated in M1M2DKO are not found among those whose expression level in SAN, AVN or PKJ cardiomyocytes is similar or lower to that to surrounding non-CCS cardiomyocytes (Figure 4C, left inferior quadrant of each graph + genes grouping around 0 in the vertical axis and Supplementary Datasets 6, 7 and 8). In contrast, genes upregulated in M1M2DKO (genes repressed by Meis) were found in both, the set of genes with higher expression in the SAN and AVN cardiomyocytes and the set of genes with lower expression in the SAN and AVN cardiomyocytes compared to surrounding non-CCS cardiomyocytes (Figure 4C, right upper and lower quadrants of each graph and Supplementary Datasets 6 and 7). In the case of PKJ cardiomyocytes, genes upregulated in M1M2KO only showed clear association with genes preferentially expressed in PKJ cardiomyocytes (Figure 4C, right upper quadrant and Supplementary Dataset 8). A study of the distribution of Meis ChIPseq peaks[36] showed that only genes with higher expression in SAN, AVN, or PKJ cardiomyocytes than in non-CCS cardiomyocytes strongly associate with Meis-bound genes (Figure 4D). To determine whether some of these findings correlate with expression changes at the level of protein expression, we characterized by immunocytochemistry the expression of SH2D4a, an adapter protein that regulates several signaling pathways[46-48], is preferentially expressed in the SAN (Figure 4C and[45]) and shows lower expression in M1M2DKO atria by RNAseq (Figure 4C). We found widespread low expression of SH2D4a in cardiomyocytes of control mice, with the exception of the SAN, in which a strong expression was found (Figure S1). In M1M2DKO mutants, SH2D4a expression was strongly reduced in general and specifically in the SAN, where the strong expression was lost (Figure S1). We also tested the expression of the EPHB3 protein, a receptor involved in cell-cell communication that is preferentially expressed in the VCS (Figure 4C and [45, 49]) and shows reduced expression in M1M2DKO mutants by RNAseq (Figure 4C). In control hearts, we found expression of EPHB3 in the AVB, BB and subendothelial cardiomyocytes (Figure S1), the latter being coincident with the location of the Purkinje fibers. In M1M2DKO mutants we could not detect any EPHB3 expression (Figure S1). Together, these findings show that Meis controls the gene regulatory network typical of cardiomyocytes in various components of the CCS, with predominance of activating interactions, but also performing some repressive activities.

Next, we studied whether these changes in gene expression translate into functional alterations of cardiac conduction. For this, we first studied fetal cardiac conduction at E14.5 using an optical mapping approach to record epicardial voltage activation maps (Figure 4E). We found prolonged activation time in both, the right and the left ventricle (Figure 4E, F). No alterations were found in atrial conduction velocity in these analyses (not shown). The functional maturation of the His-Purkinje system can be monitored during

development by the progressive displacement of the breakthrough activation point from the base to the apex of the ventricles[50,51]. We therefore mapped the breakthrough point and found that in the LV it was more basally located in mutants compared to controls, while in the RV a non-significant but similar tendency was observed (Figure 4G). These observations indicate delayed maturation of the VCS, in agreement with the alterations found in gene expression.

Meis1 and *Meis2* maintain CCS function during adult life

The previous results suggest a predominant role of Meis transcription factors in the development and adult physiology of components of the CCS; however, the M1M2DKO model does not sort out functions in working versus CCS cardiomyocytes and does not allow functional analyses in the adult heart. To overcome this limitation, we generated a model in which we used *Hcn4*^{CreERT2}[28] to specifically recombine the floxed Meis alleles in the CCS of adult mice (M1M2 CSiKO, Figure 5A-C). We administered Tamoxifen at 2 months of age and then followed the time-course of several ECG parameters (Figure 5D-K, S1) up to 24 months. As expected, the Tamoxifen treatment led to elimination of Meis expression in components of the CCS without obvious anatomical alterations (Figure S4). The analysis of the ECG showed an early (starting 1 month after tamoxifen administration) and statistically significant prolongation of the PR interval in mutants (Figure 5D). Time-course comparisons using a mixed model ANOVA also showed higher amplitude values of the P-wave in the M1M2 CSiKO mice compared to controls (Figure 5E), without significant changes in P-wave duration between groups (Figure 5F). The prolongation of the PR interval suggests an underlying impairment of atrio-ventricular conduction in M1M2 CSiKO. In contrast, all analyses involving the QRS complex (QRS duration and amplitude) were not statistically different between mutants and controls (Figure 5G, H). The latter suggests no impairment in the VCS. Overall, heart rate values assessed using RR intervals were not statistically different between groups (Figure 5I). However, further analysis using RR interval variability to address SAN function (in the absence of atrial or ventricular premature complexes) identified overt differences in RR interval variability between groups (Figure 5J, K). The latter was compatible with higher prevalence of sinus node dysfunction in mutants compared to controls. Such rhythm alterations were characterized by rapid oscillations in R-R intervals due to irregular P waves (with sinus node morphology) in singular or periodic episodes (Figure 5L and S3). Moreover, further analysis of the time-course incidence of such alterations in RR interval variability showed early onset in M1M2CSiKO mice (already detected at 2 and 6 months after tamoxifen treatment in 5 out of 17 animals) compared to controls, in which only one animal showed abnormal RR interval variability at 24 months of age (Figure 5M and S3). In all animals, once sinus node disfunction was detected, the alteration was present during the follow-up if the animal was still alive.

The elongation of the PR interval in M1M2 CSiKO mice evokes the human GWAS analyses in which *Meis1* SNPs located in intron 8 associate with PR interval elongation[20, 21] (Figure 6A). Interestingly, SNP variants in intron 8 associate as well with the Restless Legs Syndrome (RLS) in humans[52] (Figure 6A), and a highly conserved regulatory element (*617-HCRE*) of the human *Meis1* intron 8 shows enhancer activity related to RLS[29] (Figure 6A). This regulatory element is nearby the lead SNP associated with PR interval elongation (rs10865355); however no functional SNP has been related yet to PR elongation in this region. Examination of previously described functional genomics data sets[44, 53] shows that the only genomic segment with cardiac enhancer marks in the genomic region that contains SNPs in high linkage disequilibrium with rs10865355 is coincident with *617-HCRE* (Figure 6A). We thus studied the cardiac expression of a mouse transgene with the *LacZ* reporter under the control of the *617-HCRE* enhancer (Figure 6B). We found cardiac expression of the reporter in 6 out of 9 specimens. Expression was detected in small cell patches, which suggests variable mosaic expression of the transgene. In all 6 specimens, we found patches of cells potentially affecting the atrial and atrio-ventricular conduction system, including the SAN (Figure 6B, specimens #1, #2 and #5), the internodal tracks (Figure 6B, specimen #3) and the AVN (Figure 6B, specimen #4). Co-detection of ß-Galactosidase with Hcn4 in sections confirmed the expression of the transgene in cardiomyocytes of the SAN, AVN, AVB and adjacent regions (Figure 6C-E'). These results demonstrate that the *617-HCRE* activity contributes to *Meis1* expression in various components of the CCS, providing a potential mechanistic basis for the observed *Meis1*-linked PR elongation in humans.

5. DISCUSSION

Although *Meis2* is involved in human congenital malformations[17-19] and *Meis1* has been associated to PR elongation in humans[20, 21] and to regenerative ability in mice[16], a systematic analysis of *Meis1* and *Meis2* functions during the cardiomyocyte life cycle had not been performed. Given the strong similarity between Meis1 and Meis2 proteins and their frequent co-expression, we decided to perform a combined deletion of both genes in cardiomyocytes. A third gene encoding a transcription factor of the family, *Meis3*, is expressed at low levels in cardiomyocytes[54] and does not get activated in *Meis1/2* mutants (see RNAseq results). Therefore, the models reported here largely eliminate Meis function in cardiomyocytes. A detailed expression analysis revealed the preferential expression of Meis1 and Meis2 in the SAN, AVN and AVB cardiomyocytes and deletion of Meis genes showed alterations in cardiac conduction, both during development and in adult life. Interestingly, the observations in adult mice correlate well with the association of *Meis1* with PR elongation by GWAS in humans. Furthermore, we found that a mechanistic basis can be proposed between the activity of human *Meis1* enhancer *617-HCRE* and Meis function in cardiac conduction. In addition, we found alterations on sinus node function and impulse propagation in

the deletion of *Meis1* and *Meis2* from the adult CCS. These results suggest a wide involvement of Meis activity in regulating different components of the CCS, not only during development but, more intriguingly, during the maintenance of SAN pacemaker activity and atrio-ventricular conduction in adulthood. These observations suggest that not only congenital Meis mutations but alterations of Meis expression during adult life in cardiomyocytes of the SAN and atrio-ventricular conduction system may lead to progressive CCS disease. Interestingly, previous studies during limb induction have shown functional cooperation between Meis factors and Tbx5 through binding to common DNA sites[55], while Tbx5 is required for VCS development and adult function maintenance[56]. Similarly, Shox2, which is needed for SAN development is also important for limb proximal-to-distal patterning and Meis TFs are upstream regulators of *Shox2* transcription during limb development[55]. In addition, Nkx2.5 needs to be repressed from the prospective sinus node head for its proper specification[57] and Meis1 has been shown to antagonize Nkx2.5 on DNA binding sites during anterior SHF differentiation[58]. These correlations suggest that transcriptional regulatory modules involving Meis and other transcription factors co-opted during patterning of different organs.

In addition, VSD and atrial malformations were observed following Meis genes deletion during gestation, indicating functions beyond the development and function of the CCS. Although these morphological alterations could be envisioned as the cause of perinatal death of the mutants, functional analyses of fetuses at term do not detect heart failure, which suggests that perinatal electrical failure may underlie the observed lethality. The morphological alterations in atria are striking and suggest strong alteration of atrial patterning mechanisms. One of the pathways strongly altered in fetal hearts was the Wnt pathway and the factors involved preferentially contained those related to the planar cell polarity (PCP) pathway[59], including ligands Wnt5a and Wnt11 and receptors Fzd1, 4 and 7. Since the PCP pathway is generally involved in morphogenesis, it is likely involved in the morphological alterations found in the atria. Furthermore, deletion of Wnt5a[60], Wnt11[61] and Fzd1[62] and Fdz7[63] leads to outflow tract defects including VSD, DORV, persistent truncus arteriosus and transposition of the great arteries, which suggests that the alterations of outflow tract patterning in Meis mutants are also related to failure in proper regulation of the PCP pathway.

Our study identifies multiple roles of Meis transcription factors during cardiomyocyte development and adult life and shows that they play a predominant role in the development and adult physiology of the SAN and atrio-ventricular conduction, providing models to explain the association between *Meis1* and cardiac conduction alterations in humans.

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7. AUTHOR CONTRIBUTIONS

N.M. Conceptualization, Experimentation, Methodology, Data Analysis, Manuscript Writing, Manuscript Correction

A.S. Data Analysis, Manuscript Correction

C.D. Immunofluorescence analyses

S.T. Methodology

V.C. Methodology

I.E. Methodology

A.L. Provision of transgenic mouse line

B.S. GWAS and LD data curation

J.W. Provision of transgenic mouse line, GWAS and LD data curation, and Manuscript Correction

V.O. Experimentation, Methodology

D.S. Conceptualization, Experimentation, Methodology, Data Analysis, Manuscript Correction

D.F. Conceptualization, Data Analysis, Manuscript Correction

M.T. Conceptualization, Experimentation, Methodology, Data Analysis, Manuscript Writing, Manuscript Correction

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Conflict of interest: none declared.

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10. FIGURE LEGENDS

Figure 1. Expression of Meis1 and Meis2 in the developing and adult heart. (A) *Meis1* and *Meis2* mRNA in situ hybridization showing expression in the second heart field (SHF), pericardium, endocardium (Ec) and epicardium (Ep) at E10.5. Boxed regions indicate magnifications shown in the panels to the right side. (B) Confocal images of ventricles at the indicated embryonic days. Anti-Meisa immunofluorescence shown in red and myocardium autofluorescence in green. Boxed areas are magnified in the panels below. (C-E') Confocal images from sections of E16.5 hearts with the *Meis1*^{ECFP} line combined with anti-Meisa. (F-H') Confocal images from sections of E16.5 hearts showing anti-Meis2 and anti-cTNT immunofluorescence. Boxes in C and F indicate magnified regions in D-E' and G-H'. CM, ventricular

compact myocardium; TM, trabecular myocardium (TM); MS, membranous septum (MS); AVB, atrio-ventricular bundle (AVB). **(**I-L) Confocal images showing the distribution of ECFP in the CCS and atrial myocardium of *Meis1*^{ECFP} adult hearts. **(**M-P) Anti-Meisa and anti-Hcn4 immunofluorescence in the SAN (M) and AVN (N), right atrium (O) and ventricular CMs (P). Dotted lines indicate magnified areas and arrowheads within show anti-Meisa-positive CMs. (Q-Q') Whole-mount brightfield and fluorescent confocal images of *Meis1*^{CreER}*;R26R*^{TdTomato} adult hearts showing strong recombination in the SAN following Tamoxifen administration. Tamoxifen was administered by oral gavage to 10 week old mice at a dose of 1mg/day for 5 consecutive days. Hearts were harvested two days after tamoxifen administration. **(**R-S) 200µm-thick sections of the same heart, stained with DAPI and acquired by confocal microscopy (maximum projection). (R) shows expression in RA and SAN and (S) expression in the bundle branches (BB). CM, ventricular compact myocardium; TM, trabecular myocardium; MS, membranous septum; AVB, atrio-ventricular bundle; OFT, Outflow tract; V, Ventricle; M, Myocardium; RA, Right Atrium; LA, Left Atrium; LV, Left Ventricle; RV, Right Ventricle; SAN, Sinoatrial node; RBB, right and left bundle branch; LBB left bundle branch. Scale bars: 100µm, except in Q (1 mm) and R (300 µm).

Figure 2. Anatomical and functional consequences of the elimination of *Meis1* and *Meis2* function in cardiomyocytes during embryonic development. (A) Model for simultaneous constitutive deletion of *Meis1* and *Meis2* in CMs. (B) Confocal images of control and M1M2DKO embryos showing the loss of Meis expression in mutant cardiomyocytes by immunofluorescence with anti-Meisa and cTNT. Boxes indicate the magnified regions shown in the panels on the right side. Arrowheads point to cardiomyocyte nuclei with or without Meis expression. Scale bars, 100 µm. (C) Expected and observed frequencies of M1M2DKO fetuses at different embryonic days. E.14.5 n=72; E16.5 n=66; E18.5, n=130; P1, n=27**.** One-Tailed Fischer's test. (D) Four-chamber view of E16.5 control and mutant embryonic heart sections stained with H&E. Arrowheads point to VSD and RA morphology. Scale bar 200µm. (E) Ventral view of representative whole-mount E18.5 hearts from control and mutant littermates. Arrowhead points to finger-like projections in the left atrium. Scale bar 500µm. Panels on the right side show magnification of left atria for better appreciation of the altered morphology. Scale bar 200um. (F) 3D reconstruction of whole-mount confocal images from E18.5 control and mutant atria stained with WGA. Arrowheads indicate finger-like projections in the mutant atrium. Panels on the right side show individual confocal sections the reconstructed specimens. Scale bar: 400µm. (G) Classification of M1M2DKO fetuses at E16.5 according to the presence of ventricular septal defects (VSD). n=12. **(**H) Results from transuterine echocardiography of control and mutant fetuses at 18.5. n=15 control and 9 mutant specimens for all graphs except for bmp, in which 26 control and 18 mutant specimens were used. IVS, Interventricular septum thickness; LV, RV

mass, left and right ventricular mass corrected; LVEF left ventricular ejection fraction. Unpaired two-tailed Mann-Whitney Test. Lines show the mean and dots, individual measurements on different specimens.

Figure 3. Transcriptomic analysis of mutant hearts with cardiomyocyte-specific *Meis1* and *Meis2* deletion. (A) Volcano plots showing transcriptome changes in atria (blue, above) and ventricles (red, below) of E15.5 M1M2DKO hearts. n=4 control and 4 mutant specimens. Some genes potentially relevant in cardiac biology are highlighted. For the analysis in atria, genes of the Gene Ontology class "Wnt signaling pathway" are shown in green. (B-C) Gene ontology plots summarizing results from gene set enrichment analysis in E15.5 M1M2DKO ventricles (B) and atria (C). Genes and fold changes are represented on the left side, and the associated disease categories on the right side. (D) Graph showing the overrepresentation of genes bound by Meis1/2 (ChIPseq peaks from 3kb upstream to 1kb downstream; data from[36]) within the genes activated (≥1.5 fold) or repressed (≤ -1.5 fold) in the RNA-seq analysis in E15.5 atria and ventricles. Chi-square test with two-tailed P values.

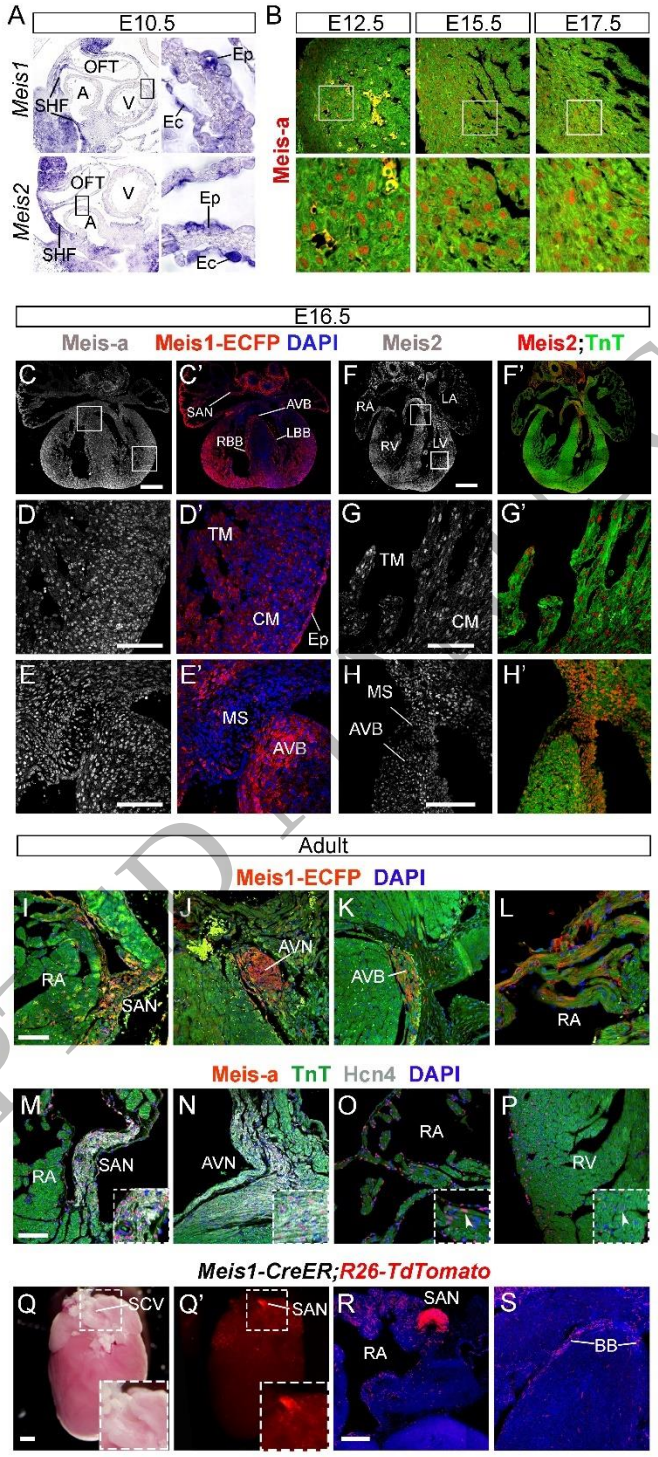
Figure 4. Elimination of Meis function affects the cardiac conduction system during heart development. (A) Graphic table shows the incidence of Meis regulation and binding to genes associated to progressive cardiac conduction disease. Blue filling indicates repression in M1M2DKO and red filling activation in M1M2DKO of the indicated gene in the colored heart region. The presence of a Meis1/2 ChIPseq peak[36] from 3kb upstream to 1kb downstream of the transcription unit is represented by a ChIPseq "peak" icon. Chi-square test with Yate's correction and two-tailed P-values. (B) Violin plot representing the distribution of reads/peak in ATACseq peaks[37] coincident with Meis ChIPseq binding sites[36] in RA CMs (RACMs) and pacemaker CMs (PCMs). The dotted lines show the median and quartiles. Wilcoxon matched-pairs signed rank test. Two tailed p-value <0.0001. (C) Plots correlating single-cell RNA-seq fold-change between CCS cardiomyocytes and nearby non-CCS cardiomyocytes from[45], with RNA-seq fold change upon Meis1/2 elimination in cardiomyocytes. n=4 control and 4 mutant specimens for RNAseq of Meis mutants. Dots highlighted in red indicate genes that change significantly in the Meis1/2 mutant hearts. From left to right, graphs show the comparison of Meis1/2 mutant atria with the SAN region, Meis1/2 mutant atria with the AVN region and Meis1/2 mutant ventricles with the VCS region. (D) Volcano plots showing the distribution of single-cell RNA-seq fold-change between CCS cardiomyocytes and nearby non-CCS cardiomyocytes from[45] with highlight of the genes bound by Meis1/2 in ChIPseq adult heart experiments from[36]. Line graphs below indicate the local enrichment in Meis-bound genes according to the fold enrichment in the single-cell RNA-seq analyses. Data are shown from left to right for the SAN, AVN and VCS regions. Chi-square test with Yate's correction and two-sided P-values. (E) Representative optical maps of ventricular depolarization (dorsal side) in control and M1M2DKO hearts at E14.5. (*) indicates

the area where the first signal appears. Color bar shows the temporal scale (each color = 1ms). Scale bar, 200 µm. (F) Left and right ventricular activation curves showing depolarized area percentage per millisecond obtained from the maps (n=8/group). Graphs show the mean ±SEM. Two-way ANOVA with Sidak's correction for multiple measurements and two-sided p-value. (G) Map of the ventricular conduction activation points (or breakthrough point), indicated with an asterisk for each control and mutant hearts, including representation of the geometric center and a standard deviation ellipse (dorsal view). n=6 control and 7 mutant specimens. Type II MANOVA Test with Pillai statistics was applied to the orthogonal coordinates defining the position of each activation point.

Figure 5. Conditional elimination of Meis function in the adult cardiac conduction system produces progressive dysfunction of sinus rhythm function and PR elongation. (A) Model for double deletion of *Meis1* and *Meis2* in the conduction system using *Hcn4*^{CreERT2}. (B) Experimental timeline showing tamoxifen treatment and the schedule for the electrocardiographic analyses. (C) Dorsal views in brightfield and epifluorescence of a tamoxifen-induced newborn heart in which Tomato reports the sites of Cre activity provided by the *Hcn4*^{CreERT2} allele. SAN, sinoatrial node; AVN, atrioventricular node. Scale bar, 1 mm. (D-I) Representation of the values for different parameters of the ECG analyses in control and mutant M1M2 CSiKO mice before tamoxifen administration (basal) and at different times after tamoxifen administration. Each dot represents the average value for a single specimen. n=10 control and 16 mutant in Basal, 10 control and 16 mutant at 1 and 2 months, 9 control and 17 mutant at 6 months and 3 control and 10 mutant at 24 months. Mixed model ANOVA with Sidak's correction for multiple measurements and two-tailed P values. Adjusted P-values are shown for each individual comparison. The P-value for the global analysis of the "genotype" variable is shown only in case of significance. (J) Examples of ECGs of control and M1M2 CSiKO showing sinus rhythm dysfunction. (K) Poincaré plot of the RRn to RRn+1 correlation in relative terms for all analyzed data in D-I (right). The domain for "no sinus node dysfunction" was determined from control animals of up to 6 months of age, whereas all points outside this domain correspond to mutants up to 6 months of age. (L) Example of sinus rhythm alteration in the same mutant specimen 6 months and 2 years after tamoxifen administration. (M) Bar plot showing the incidence of sinus node dysfunction in control and mutant M1M2 CSiKO mice at different times after tamoxifen administration for all analyzed data in D-I.

Figure 6. A Meis1 human enhancer in a GWAS-identified intron associated with PR elongation drives expression in CCS cardiomyocytes. (A) The Meis1 genomic region showing SNPs in different degrees of linkage disequilibrium with the lead SNP associated with PR elongation (rs10865355). SNP linkage data were retrieved from LD information from the European ancestry (EUR) dataset of the 1000Genomes Phase

3 project for rs10865355 using the LDproxy Tool provided by LDLink (https://ldlink.nci.nih.gov/?tab=ldproxy). The full list of SNPs is provided in Supplementary Dataset 9. Below, a zoom-in to intron 8, where the PR elongation-associated SNPs are located. Potential regulatory elements are indicated by epigenetic marks and detection of open chromatin by ATAC-seq in pace maker-like CMs and ventricular-like CMs derived from hIPSCs and the developing human heart. The location of the *617-HCRE* enhancer, previously characterized in the context of the RLS syndrome[29], is also shown. (B) Scheme showing the transgene carrying *LacZ* gene under the control of *617-HCRE* and brightfield images of 5 different E17.5 transgenic hearts stained for LacZ. Arrowheads indicate the areas of LacZ expression. Ao, Aorta; Pa, pulmonary artery; SV, sinus venosus; AVVs, atrio-ventricular valves. Scale bars, 500 µm. (C-E) Confocal images of co-immunofluorescence of ß-Galactosidase (green) and Hcn4 (red) in sections from transgenic hearts at E17.5. Arrowheads indicate the areas of co-expression at the sino-atrial node (SAN), atrio-ventricular node (AVN) and atrio-ventricular bundle (AVB). (C'-E') Single channel images from panel C-E with ß-Galactosidase expression.



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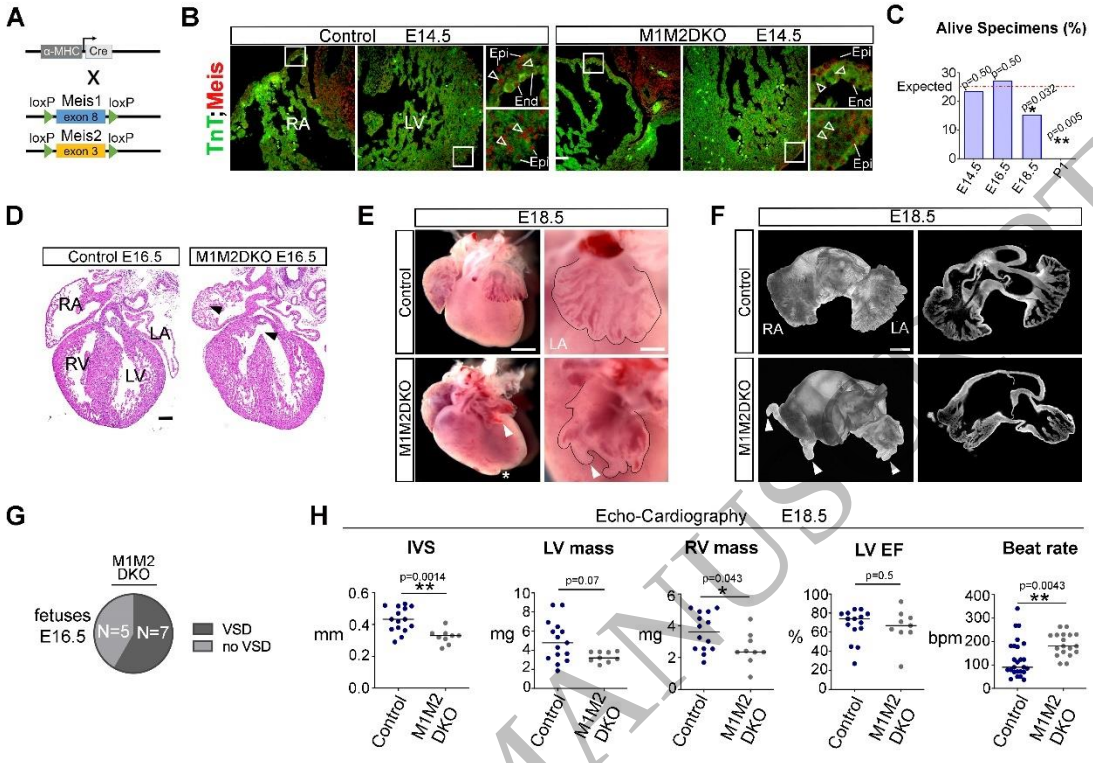

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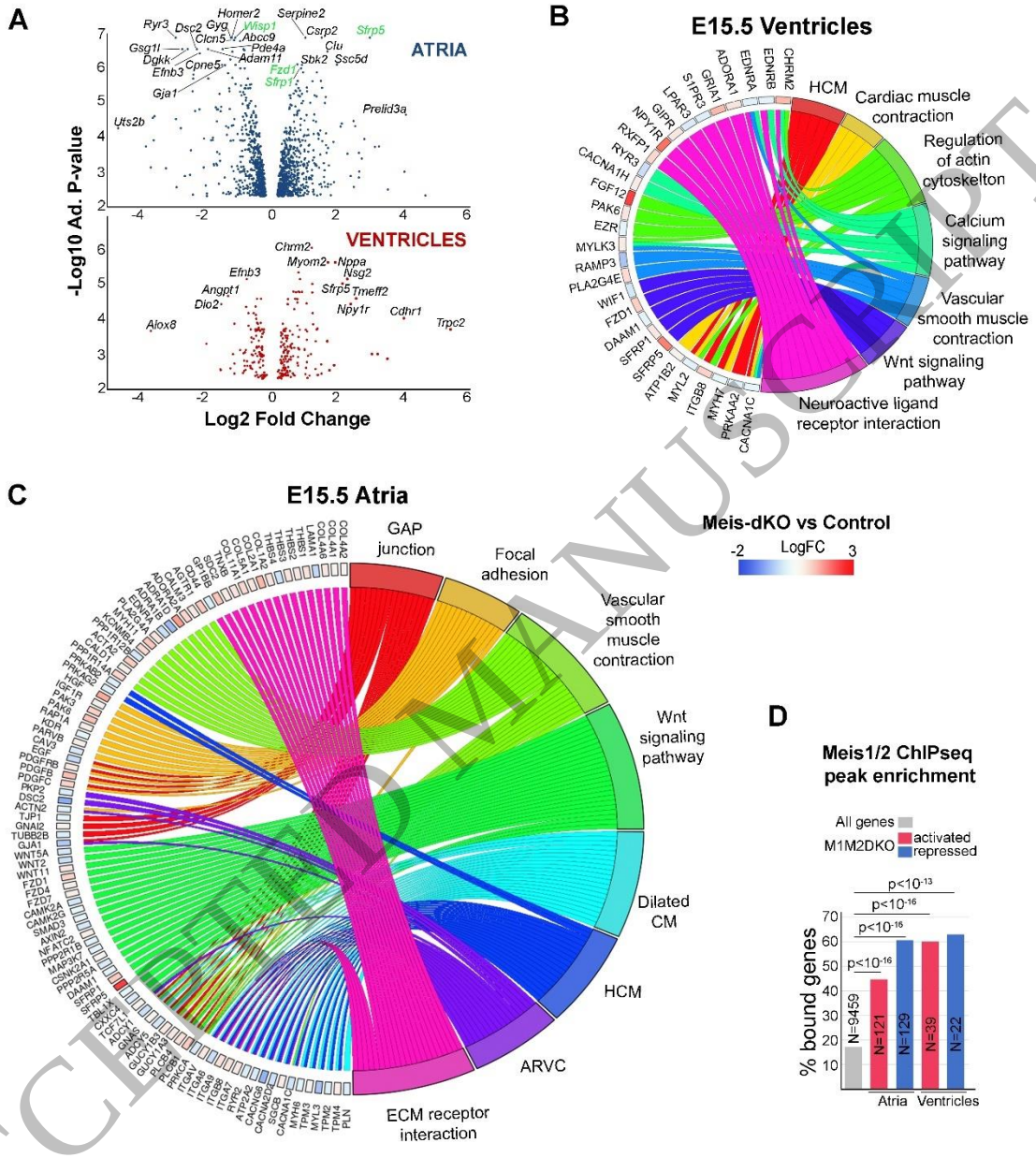

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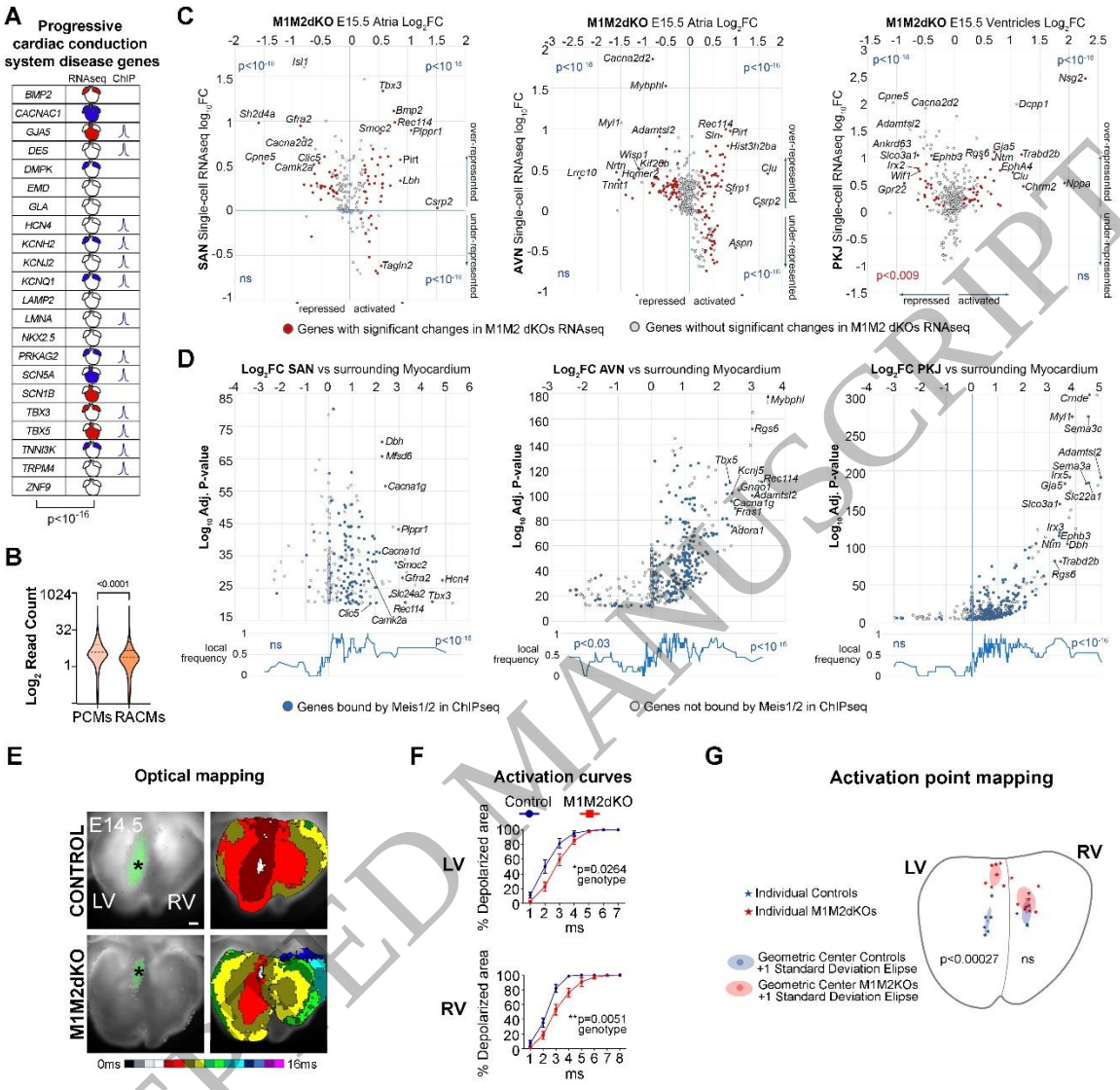

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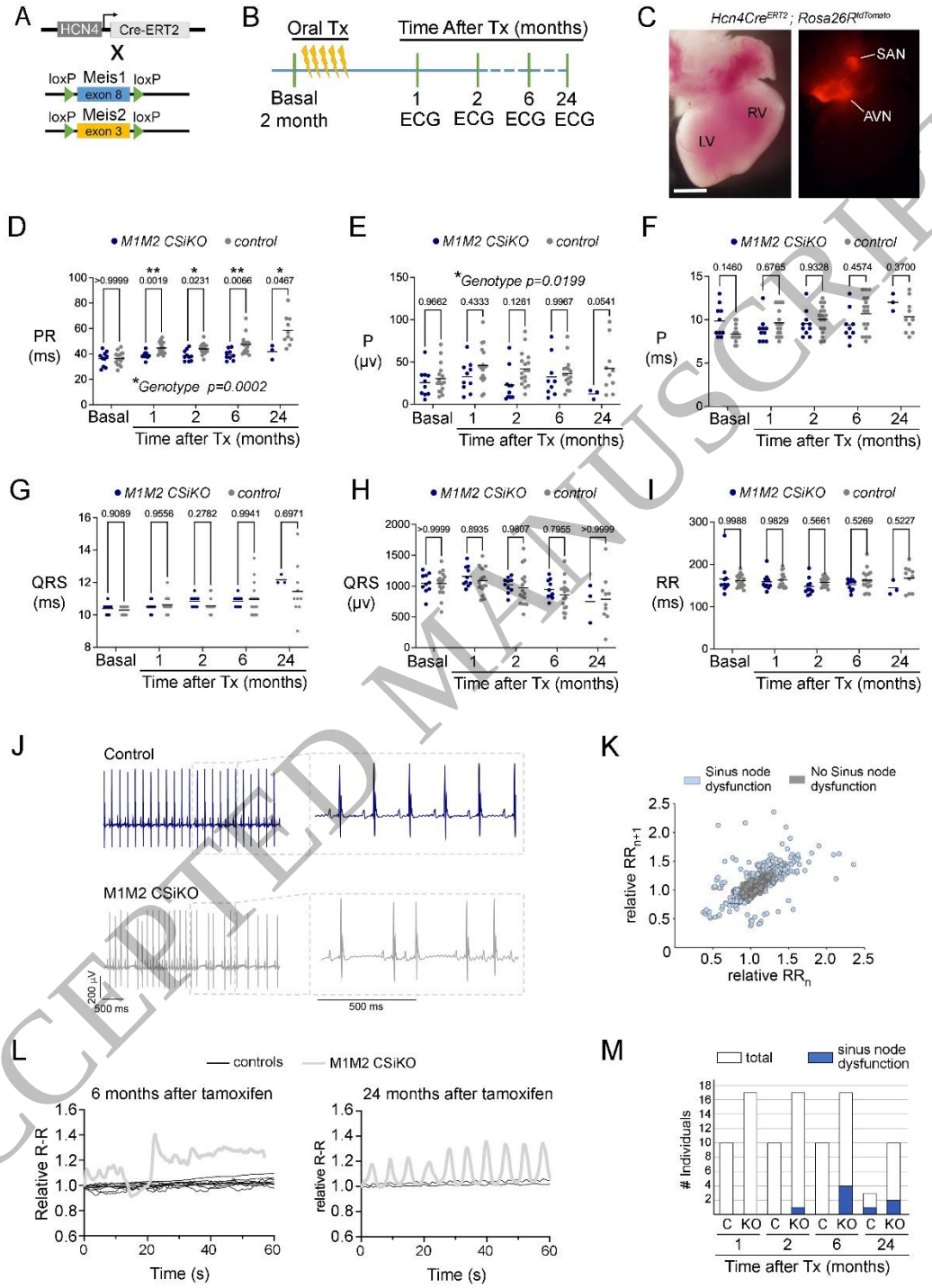

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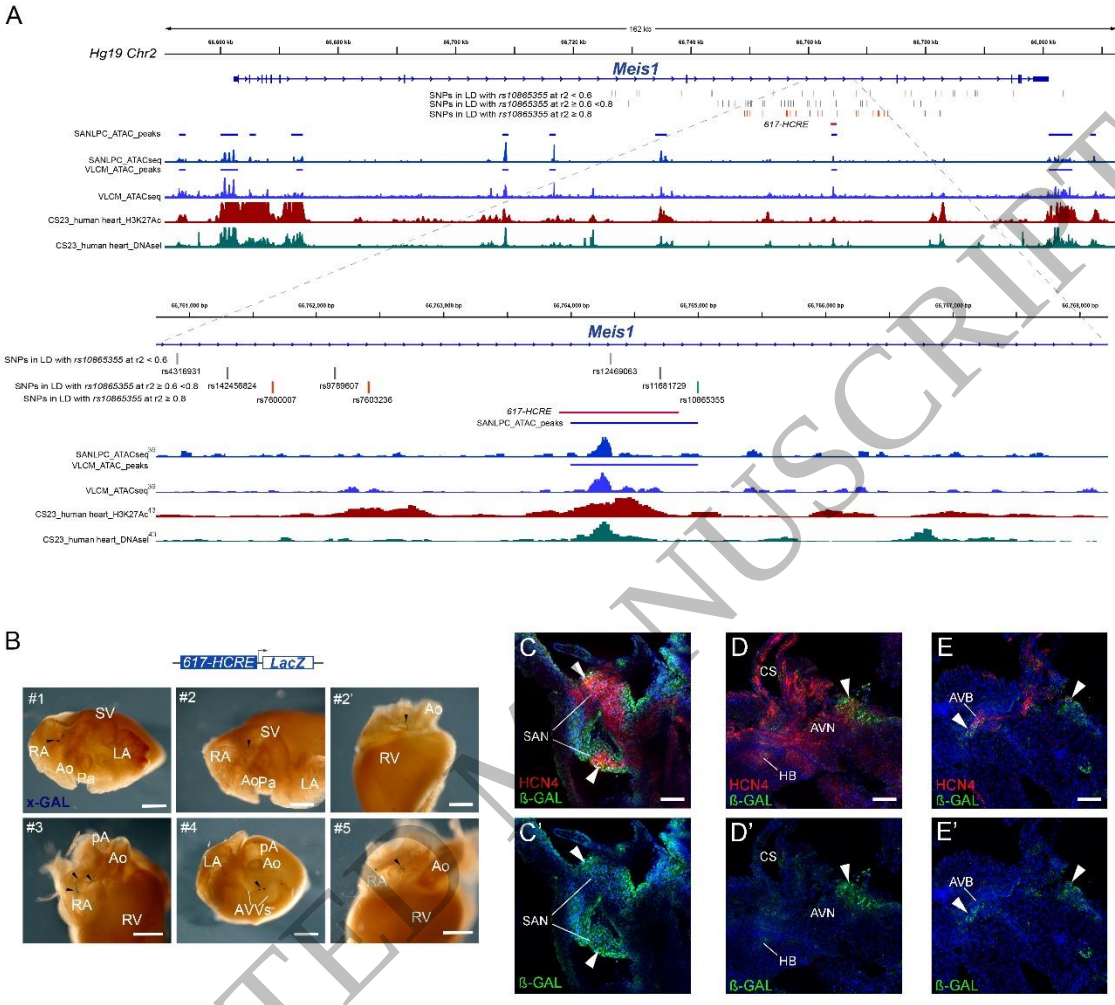

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