**Original Articles**

- Diminished PRRX1 Expression Is Associated With Increased Risk of Atrial Fibrillation and Shortening of the Cardiac Action Potential
  
  **Editorial:** Connecting the Dots in Atrial Fibrillation

- Genome-Wide Association Study to Find Modifiers for Tetralogy of Fallot in the 22q11.2 Deletion Syndrome Identifies Variants in the GPR88 Locus on 5q14.3
  
  **Editorial:** Modifying Mendel Reduc: Unbiased Approaches Can Find Modifiers

- New Blood Pressure–Associated Loci Identified in Meta-Analyses of 475,000 Individuals
  
  **Editorial:** Blood Pressure Genome-Wide Association Studies, Missing Heritability, and Omniphenics

- Transcriptome and Functional Profile of Cardiac Myocytes Is Influenced by Biological Sex
  
  **Editorial:** Sex Determines Cardiac Myocyte Stretch and Relaxation

- MicroRNA Signature of Cigarette Smoking and Evidence for a Putative Causal Role of MicroRNAs in Smoking-Related Inflammation and Target Organ Damage
  
  **Editorial:** A Smoking-Associated miRNA-mRNA Coexpression Network

- Reduced Cardiac Calcineurin Expression Mimics Long-Term Hypoxia-Induced Heart Defects in Drosophila
  
  **Editorial:** High Heart: A Role for Calcineurin Signaling in Hypoxia-Influenced Cardiac Growth

- Body Height and Incident Risk of Venous Thromboembolism: A Coisabiling Design
  
  **Editorial:** Insights From the Positive Association of Height With Incident Venous Thromboembolism

- Heritability of Mitral Regurgitation: Observations From the Framingham Heart Study and Swedish Population
  
  **Editorial:** Inheritance Impacts Mitral Valve Insufficiency

- Validation of Polygenic Scores for QT Interval in Clinical Populations
  
  **Editorial:** QT Interval Determinant: Mutations, Rare Variants, or Single-Nucleotide Polymorphisms?

- Prediction for Intravenous Immunoglobulin Resistance by Using Weighted Genetic Risk Score Identified From Genome-Wide Association Study in Kawasaki Disease

**Editorial:** One Size Does Not Fit All: Genetic Prediction of Kawasaki Disease Treatment Response in Diverse Populations

- Impact of Selection Bias on Estimation of Subsequent Event Risk

- **Editorial:** Biases in Genetic Association of Coronary Heart Disease Events May Be Less Likely Than Suspected: Here Is When to Check for Them

- Predicting the Functional Impact of KCNQ1 Variants of Unknown Significance
  
  **Editorial:** Machine Learning and Rare Variant Adjudication in Type 1 Long QT Syndrome

- Characterization of a Human Induced Pluripotent Stem Cell–Derived Cardiomyocyte Model for the Study of Variant Pathogenicity: Validation of a KCNJ2 Mutation
  
  **Editorial:** Commercially Available Human-Induced Pluripotent Stem Cell–Derived Cardiomyocytes: Another Piece in Our Tool Box, but Not a Swiss Army Knife Yet

- α-Galactosidase A Genotype N215S Induces a Specific Cardiac Variant of Fabry Disease
  
  **Editorial:** Clinical Characteristics of the GLA N215S Variant and Implications for the Diagnosis and Management of Nonclassic Fabry Disease

- A Comparison of Whole Genome Sequencing to Multigene Panel Testing in Hypertrophic Cardiomyopathy Patients
  
  **Editorial:** Hypertrophic Cardiomyopathy Gene Testing: Go Big?

- Genomic Triangulation and Coverage Analysis in Whole-Exome Sequencing–Based Molecular Autopsies
  
  **Editorial:** Genomic Triangulation in Sudden Unexplained Death in the Young: The Way to Go?

- Care in Specialized Centers and Data Sharing Increase Agreement in Hypertrophic Cardiomyopathy Genetic Test Interpretation
  
  **Editorial:** Pathogenicity of Hypertrophic Cardiomyopathy Variants: A Path Forward Together

**Perspective**

What Do We Really Think About Human Germline Genome Editing, and What Does It Mean for Medicine?

**Clinical Genomic Cases**

Heterozygous Null LDLR Mutation in a Familial Hypercholesterolemia Patient With an Atypical Presentation Because of Alcohol Abuse
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