

## Online Appendix

### International Bicuspid Aortic Valve Consortium (BAVCon)

BAVCon is a collaborative registry that consists of 16 institutions and also includes data from the National Registry of Genetically Triggered Thoracic Aortic Aneurysms and Cardiovascular Conditions (GenTAC, <https://gentac.nhlbi.nih.gov>). The authors thank Barbara Kroner, PhD, for assistance with GenTAC data. Demographic, clinical and imaging data on all patients who are enrolled at participating sites are collected using standardized forms. All data elements were prospectively defined, and study protocols were approved by institutional review boards at each site. Images from each enrolled patient are reviewed by local principal investigators to ensure data accuracy. Imaging modalities and medications are determined by treating physicians according to clinical guidelines and institutional policies.

<b>BAVCon Sites and Investigators</b>
<b>Harvard Medical School</b>
Simon Body, MBCHB, MPH
Eric Isselbacher, MD
Frederick Schoen, MD, PhD
Christine Seidman, MD
Jonathan Seidman, PhD
Thor Sundt, MD
Jochen Daniel Muehlschlegel, MD
Calum A. MacRae, MD, PhD
Michael Francke, BS
<b>Laval University</b>
Yohan Bossé, PhD
Patrick Mathieu, MD, FRCSC
Philippe Pibarot, DVM, PhD
<b>University of Ottawa</b>
Mona Nemer, PhD
<b>Vanderbilt University</b>
Joshua C Denny, MD, MS
Peter Weeke, MD

Huan Mo, MD, MS
<b>University of Salerno</b>
Eduardo Bossone, MD, PhD
Rodolfo Citro, MD, PhD
<b>Monaldi Hospital</b>
Giuseppe Limongelli, MD, PhD
Maria Giovanna Russo, MD
<b>Second University of Naples</b>
Alessandro DellaCorte, MD, PhD
Gianantonio Nappi, MD
Marisa De Feo, MD, PhD
Ciro Bancone, MD, PhD
Giovanni Dialetto, MD
Franco E. Covino, MD
Sabrina Manduca, MD
Marianna Buonocore, MD
Amalia Forte, PhD
<b>Mayo Clinic</b>
Hector Michelena, MD
Maurice Sarano, MD
Nandan Anavekar, MD
Rakesh Suri, MD, DPhil
<b>University of Michigan</b>
Kim Eagle, MD
Bo Yang, MD
Nickole Carlson, RN, BSN
Michael Ranella, BS
<b>Tufts Medical Center</b>
Gordon Huggins, MD
<b>University of Texas Health Science Center at Houston</b>
Dianna M. Milewicz, MD, PhD
Siddharth Prakash, MD, PhD
Truc Baccam, RN
Ellen Regalado, MS
<b>University Hospital Vall d'Hebron</b>
Arturo Evangelista, MD

Jose Rodriguez-Palomares, MD
Gisela Teixidó-Tura, MD
Giuliana Maldonado
<b>Oxford University</b>
Malenka Bissell, MD, BM, MRCPCH
<b>Istituto Policlinico San Donato</b>
Alessandro Frigiola, MD
Andrea Ballotta, MD
Francesca Pluchinotta, MD
<b>University of Pennsylvania</b>
Joseph Bavaria, MD
Rita Milewski, RPh, MD, PhD
<b>University of Liège Hospital</b>
Patrizio Lancelotti, MD, PhD
Raluca Dulgheru, MD
<b>Hadassah University Medical Center</b>
Dan Gilon, MD

## Glossary of Terms

**Penetrance** : the proportion of individuals with a mutation who exhibit clinical symptoms

**Linkage analysis** : the formal study of the association between the inheritance of a condition in a family and a particular chromosomal locus

**Pedigree** : genetic representation of a family tree that diagrams the inheritance of a trait or disease through several generations

**Heritability** : the proportion of observable differences in a trait between individuals within a population that is due to genetic differences

**Epigenetic** : the study of changes in [gene expression](#) or [cellular phenotype](#), caused by mechanisms other than changes in the underlying [DNA](#) sequence

**LOD score** : logarithm (base 10) of odds, a statistical test often used for [linkage analysis](#) that compares the likelihood of obtaining the test result if the phenotype and genetic locus are indeed linked, to the likelihood of observing the same data purely by chance

**Expressivity** : variations in a [phenotype](#) among individuals carrying a particular [genotype](#)

**Positional cloning** : a method of gene identification in which a gene for a specific phenotype is identified only by its approximate chromosomal location

**Proband** : the first affected family member who seeks medical attention for a [genetic disorder](#)

**Alleles** : variant forms of the same gene

**Genome-wide association study** : an approach that involves rapidly scanning markers across the entire genomes of many people to find genetic variations associated with a particular disease

**Intron** : nucleotide sequence within a [gene](#) that does not code for a protein

**Segregation analysis** : statistical test to determine the pattern of inheritance of a trait

**Exome** : the protein-coding portion of the genome, approximately 1% of the total genomic sequence

