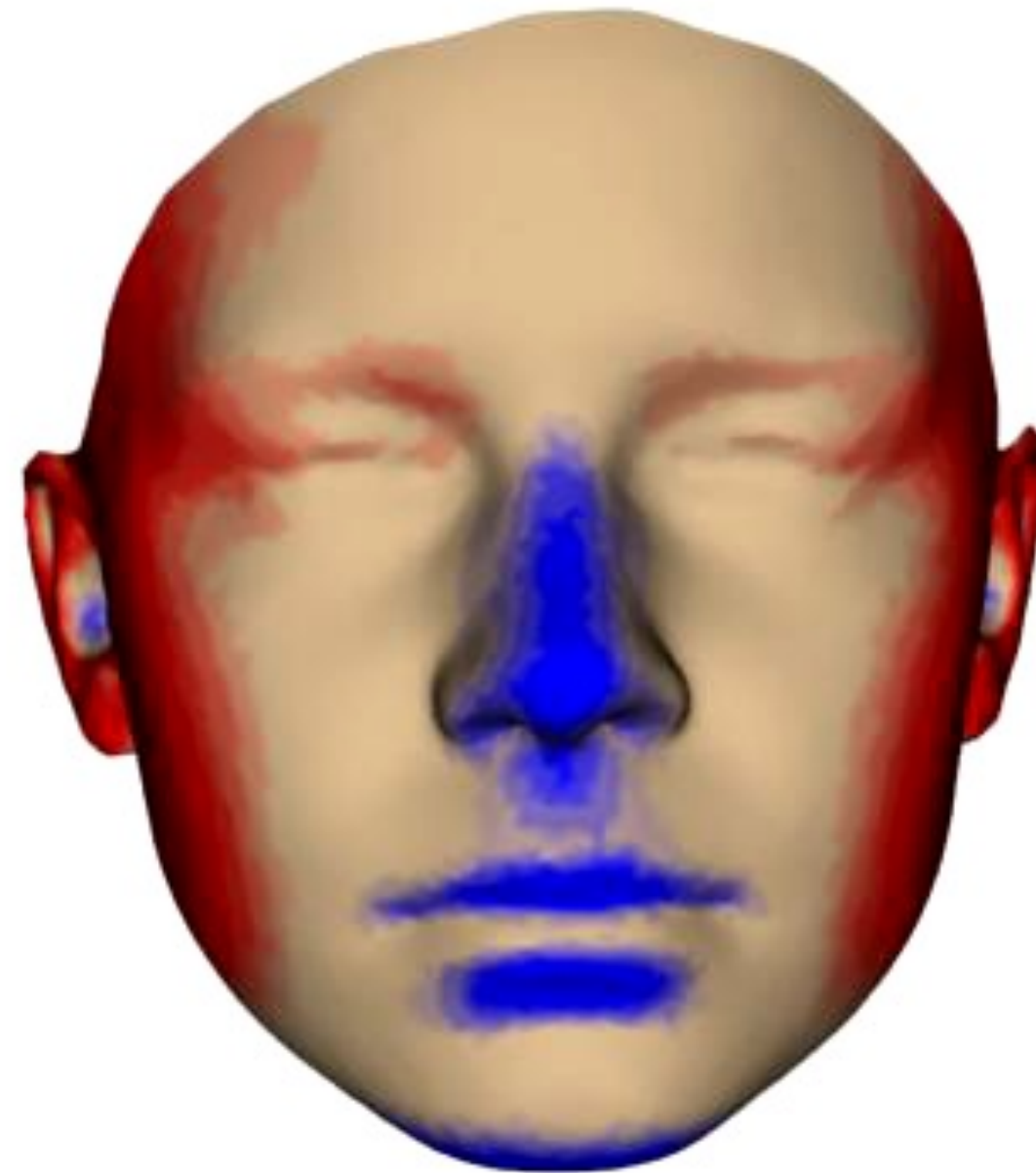


Facial Imaging and Genetic Disease



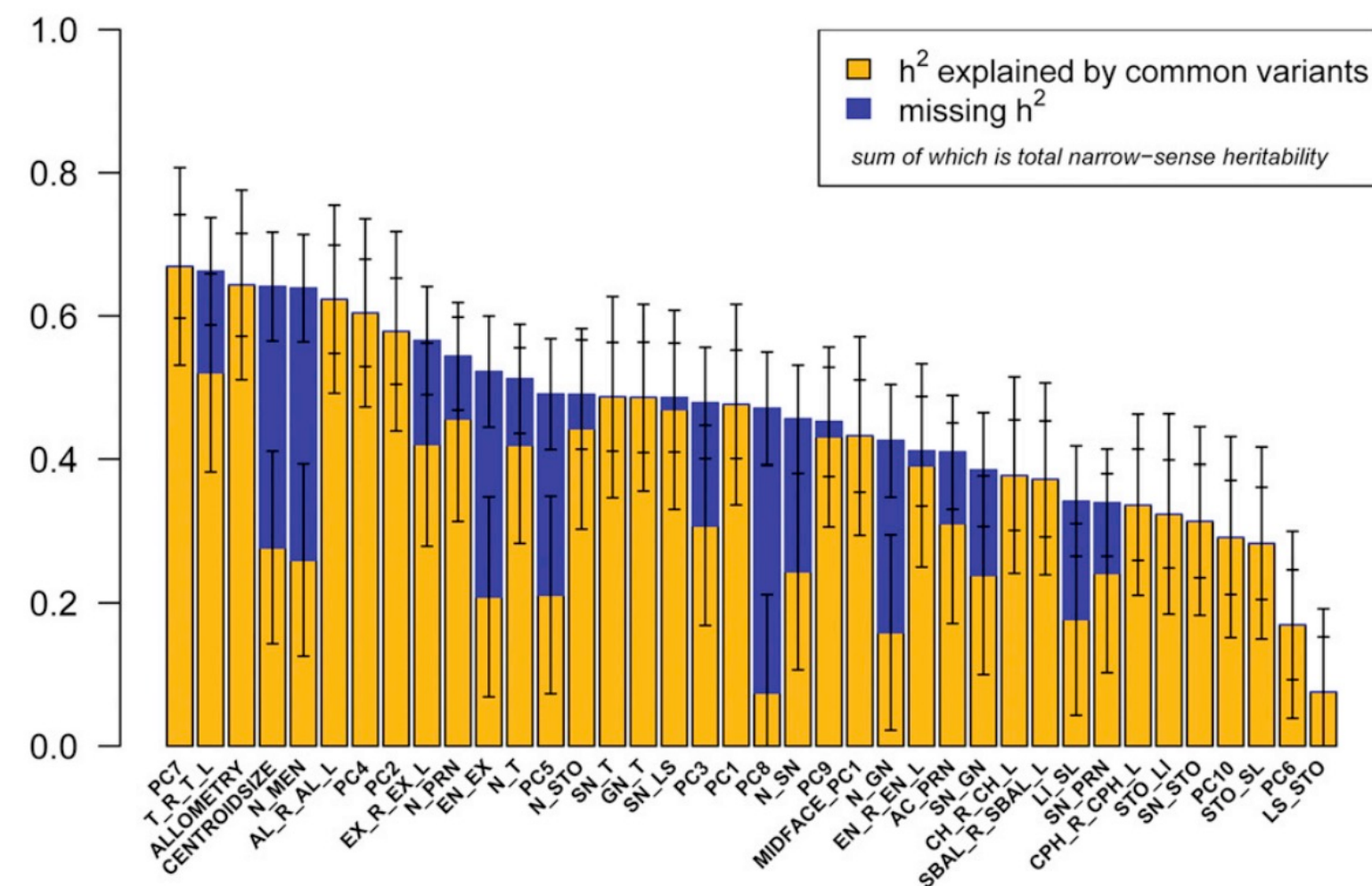
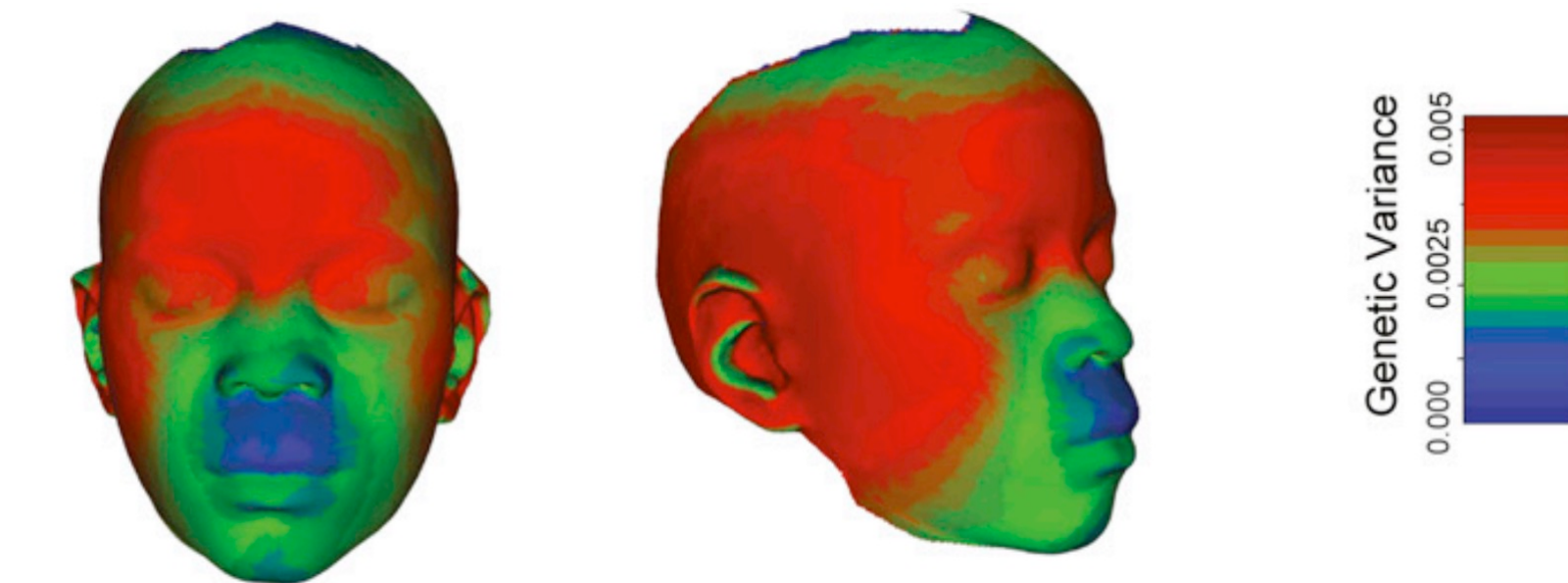
**Benedikt Hallgrímsson, Dept. of Cell Biology & Anatomy,
Alberta Children's Hospital Research Institute**



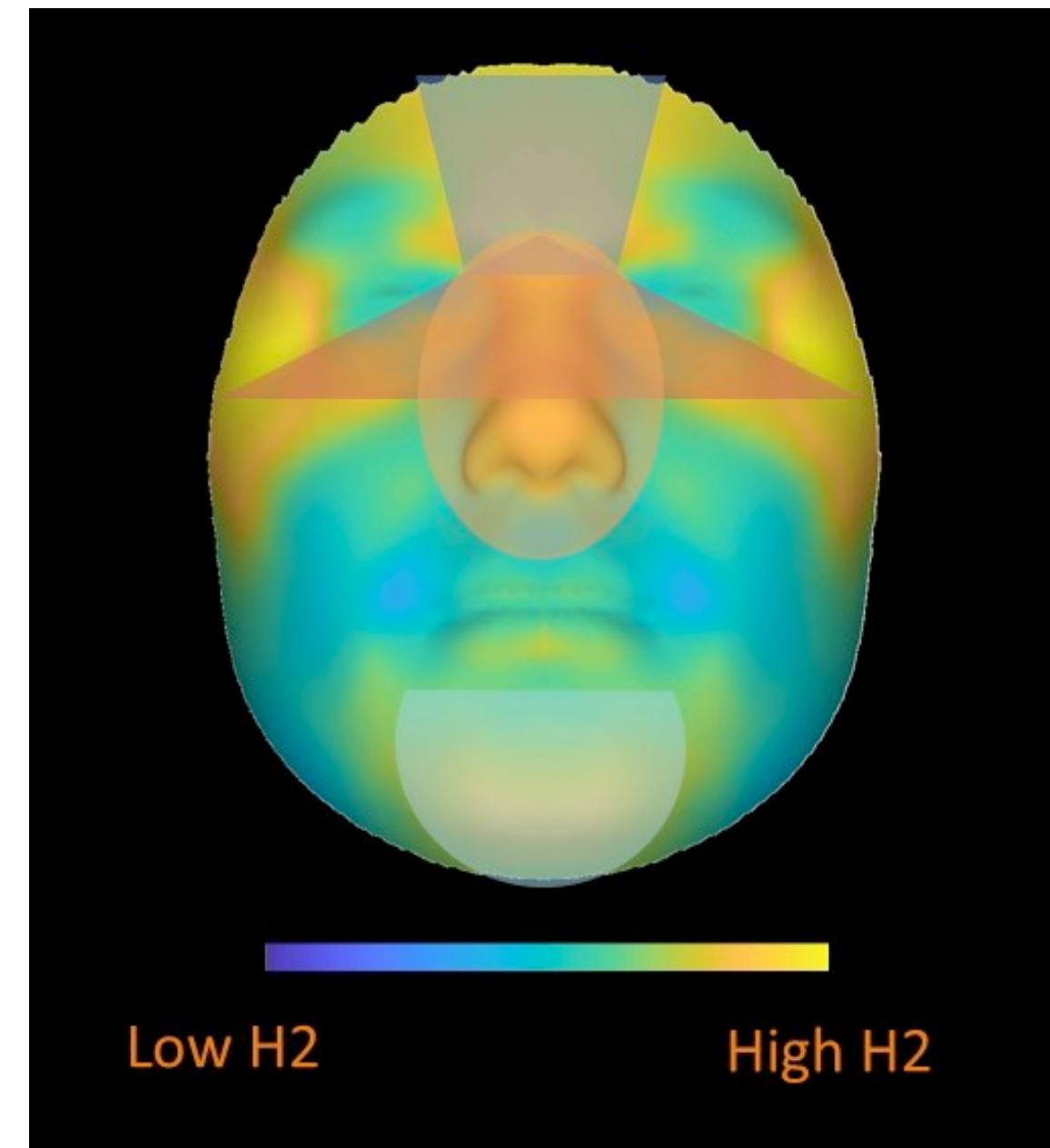
Why would facial shape variation be useful for syndrome diagnosis?

1. Facial shape is heritable and also highly polygenic

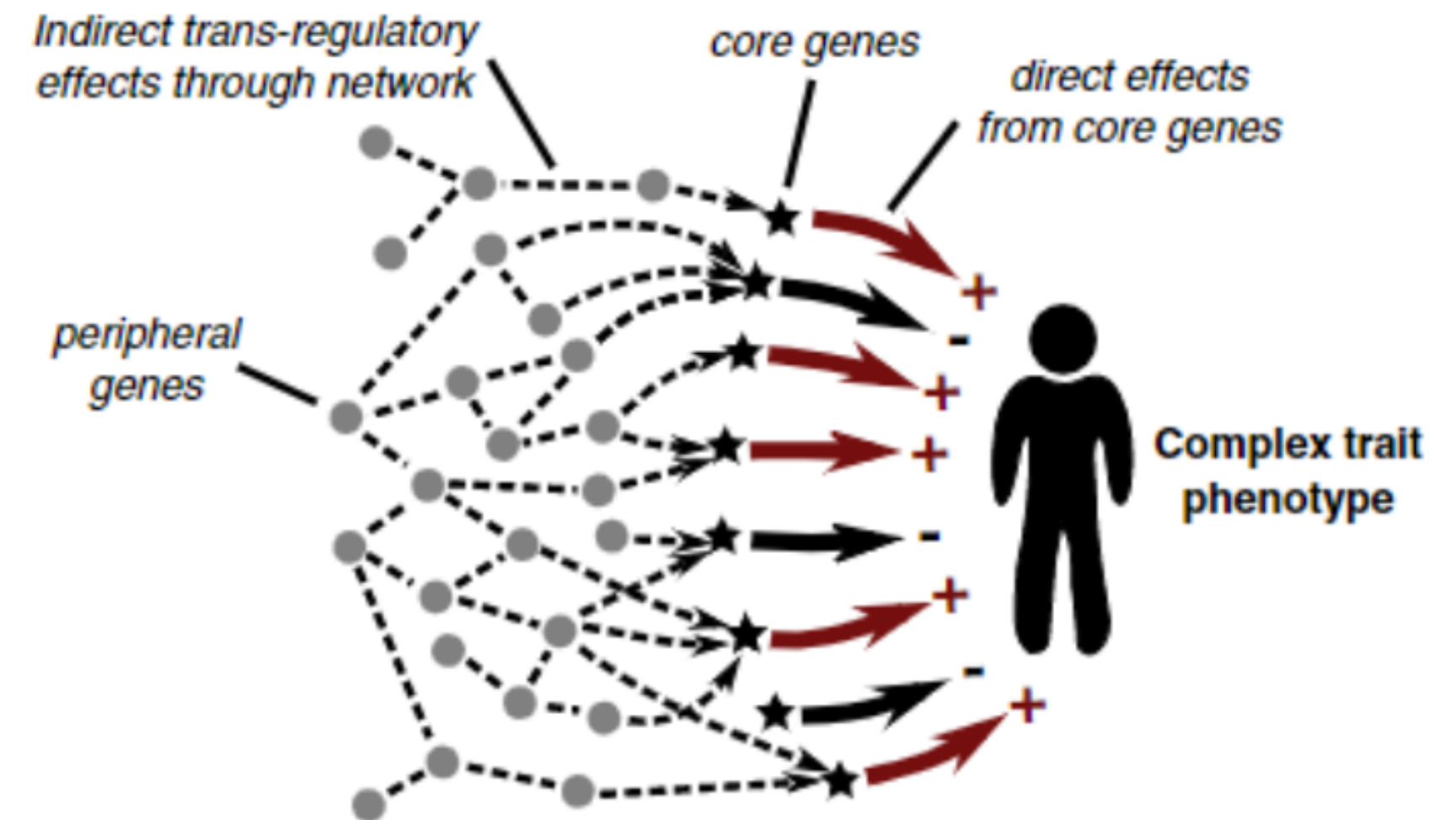
Cole *et al.*. 2017 *Genetics*



Hoskens *et al.*. 2018 *Frontiers in Genetics*



Liu, Yang and Pritchard. 2019 *Cell*



Facial shape is *at least* as polygenic as stature. Perhaps more so (figure depicts the “omnigenic” model for complex traits).

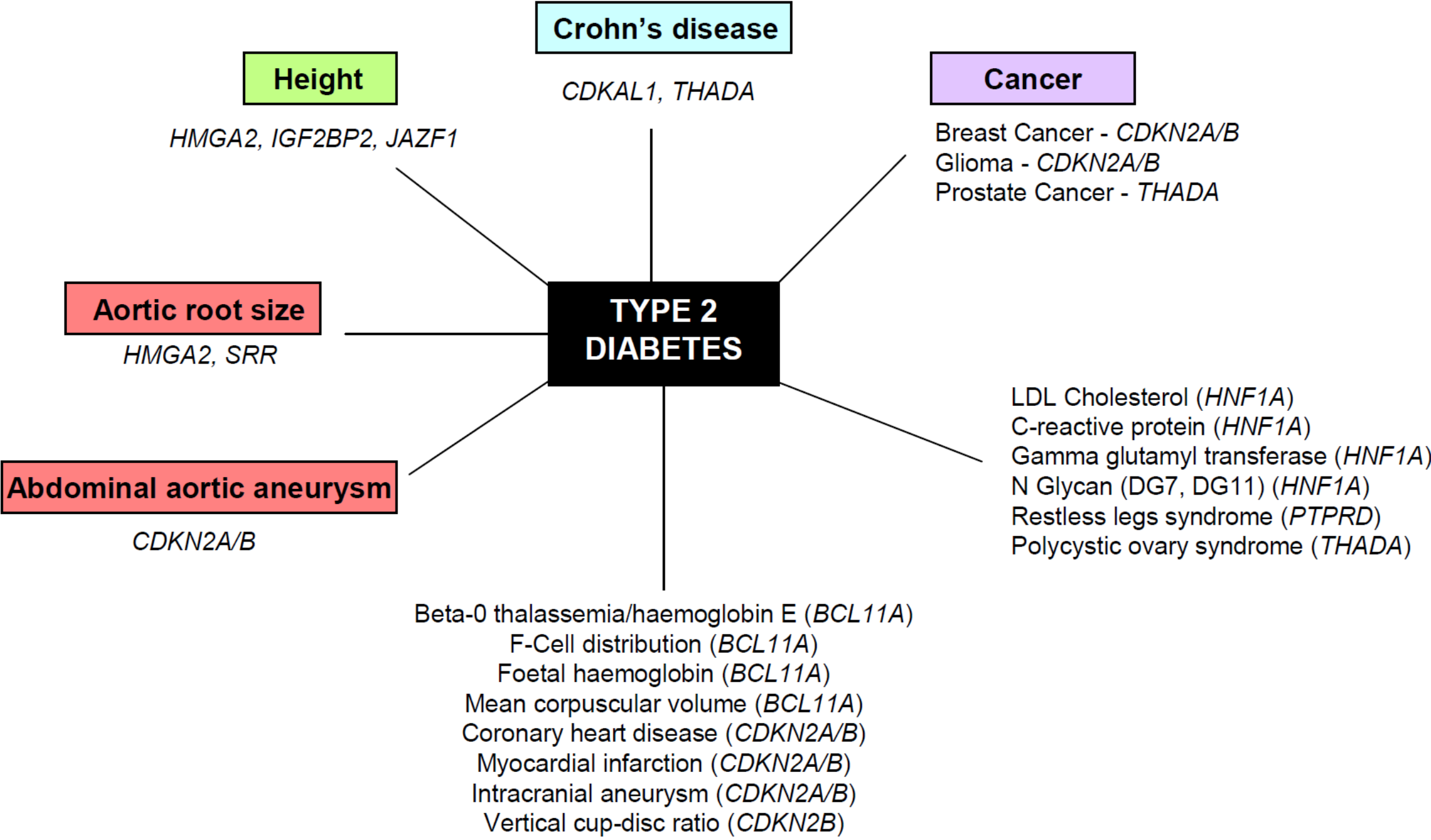
High polygenicity means that many genes/genetic disorders can impact facial shape

2. Pleiotropy is very common. This means that many mutations that cause disease may also affect facial shape.

Example: Patient with acrofacial dysostosis. tuberous sclerosis. and polycystic kidney disease.



J G Dauwerse et al. J Med Genet 2002;39:136-141
©2002 by BMJ Publishing Group Ltd

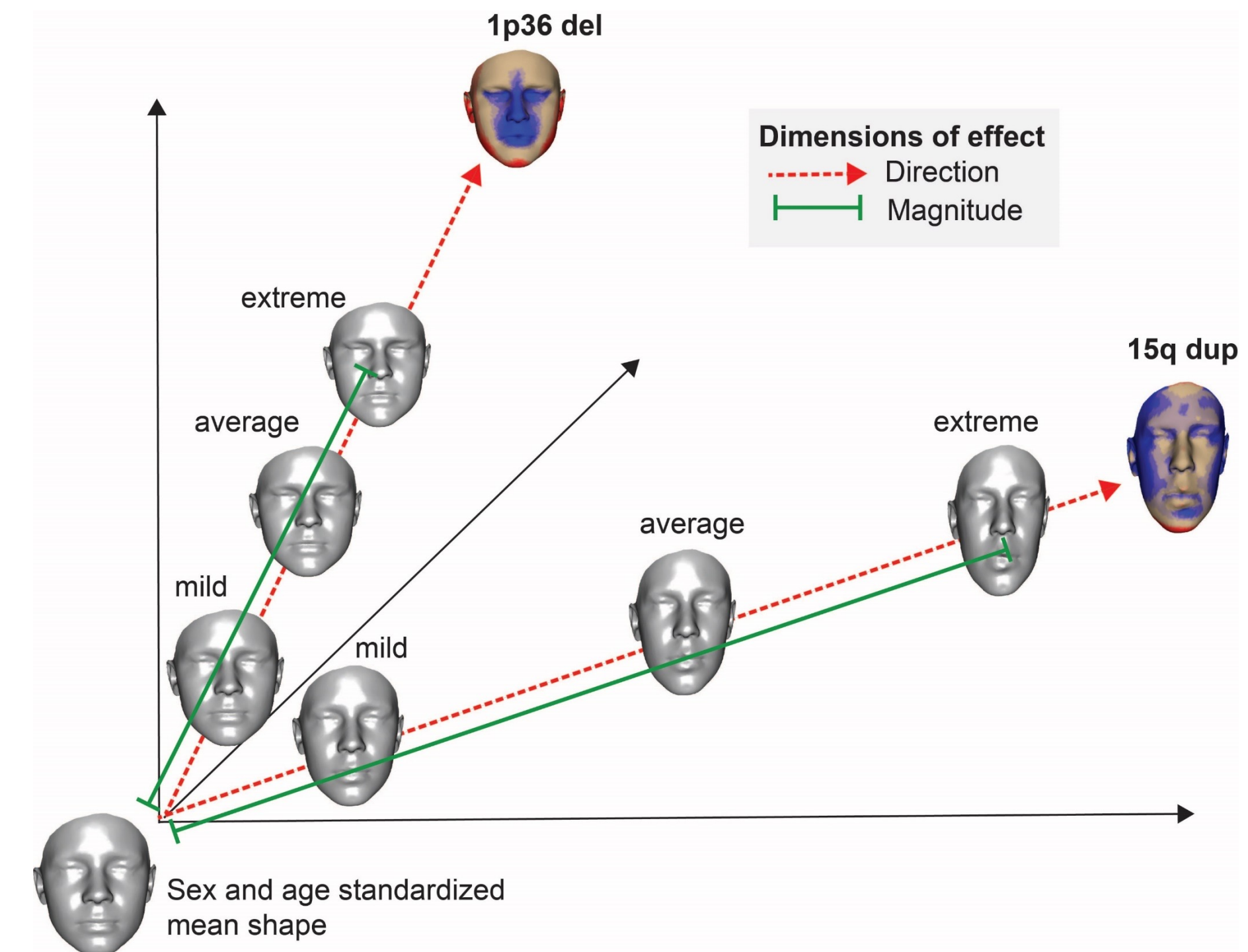
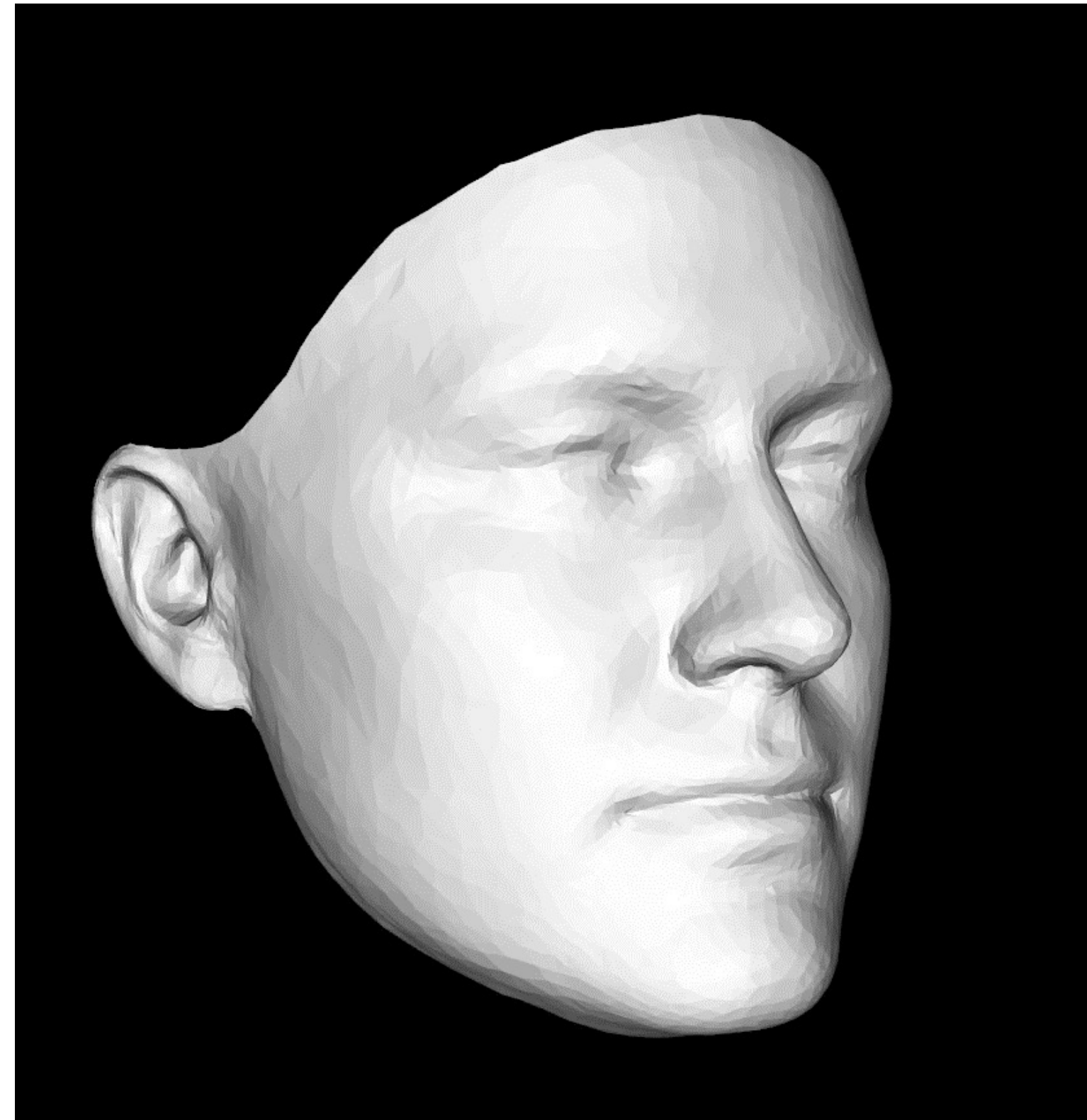


Sivakumaran et al. 2011. Am. J. Hum Gen.

3. Facial shape is a high dimensional trait – thus. genetic variants can have specific and highly distinctive effects

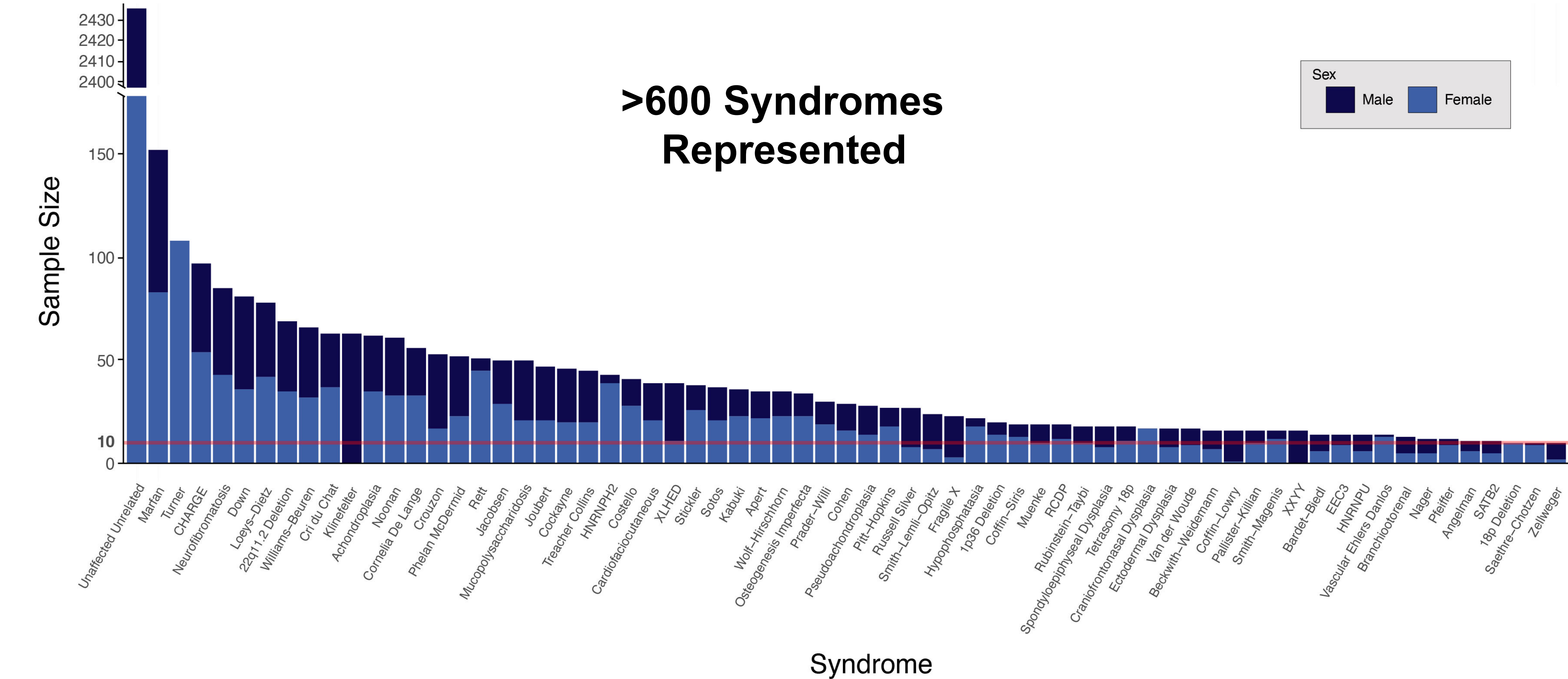
Facial shape can vary in many ways. This creates many. potentially distinctive. directions of genetic effects.

This contrasts with a trait like stature that varies only along a single dimension. While also heritable. polygenic and subject to pleiotropy. this makes stature less useful for disease diagnosis.



Facebase 2 (2014-Present): *Developing 3D Craniofacial Morphometry Data and Tools to Transform Dysmorphology*

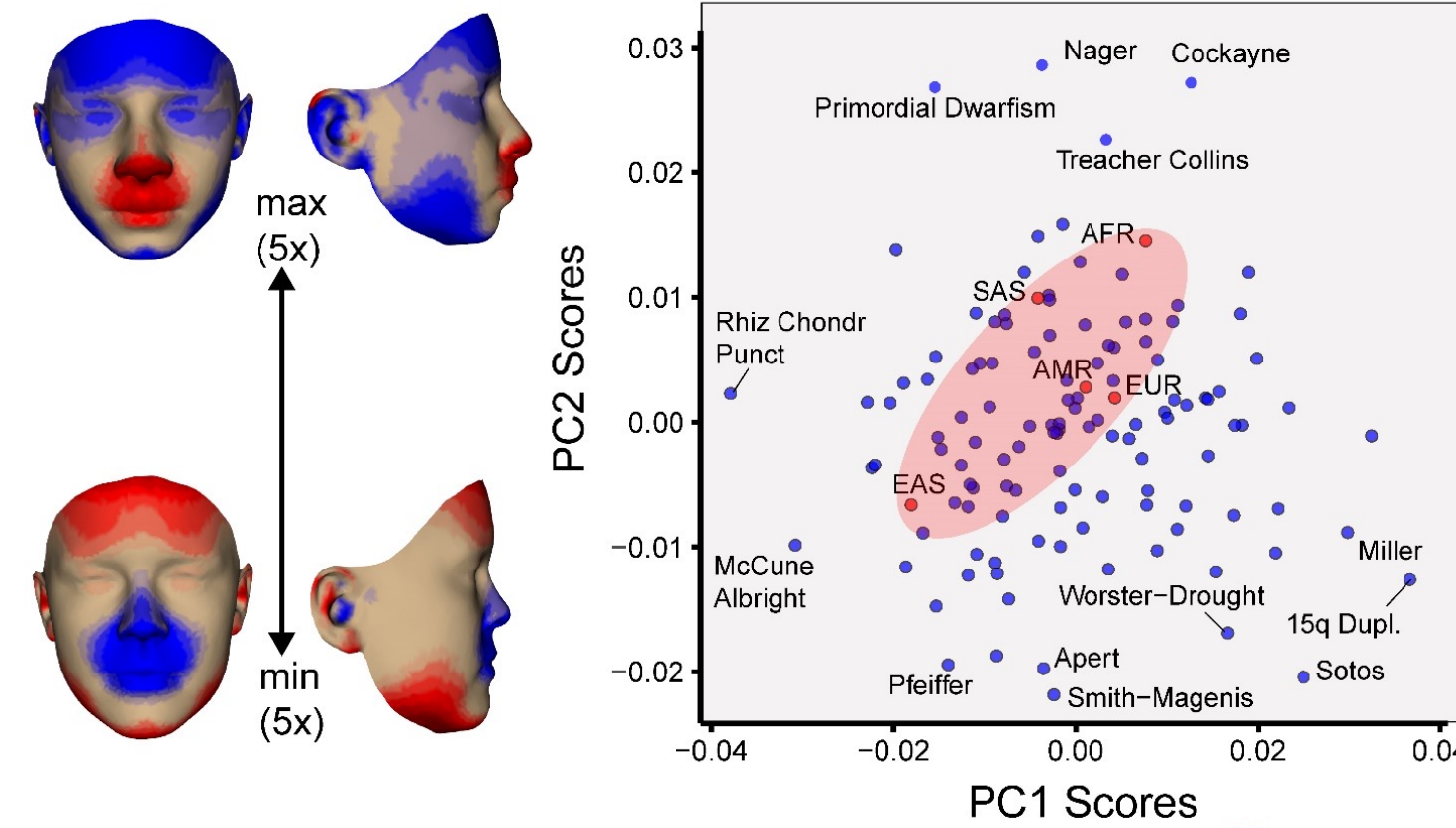
Library of 3D Facial Scans



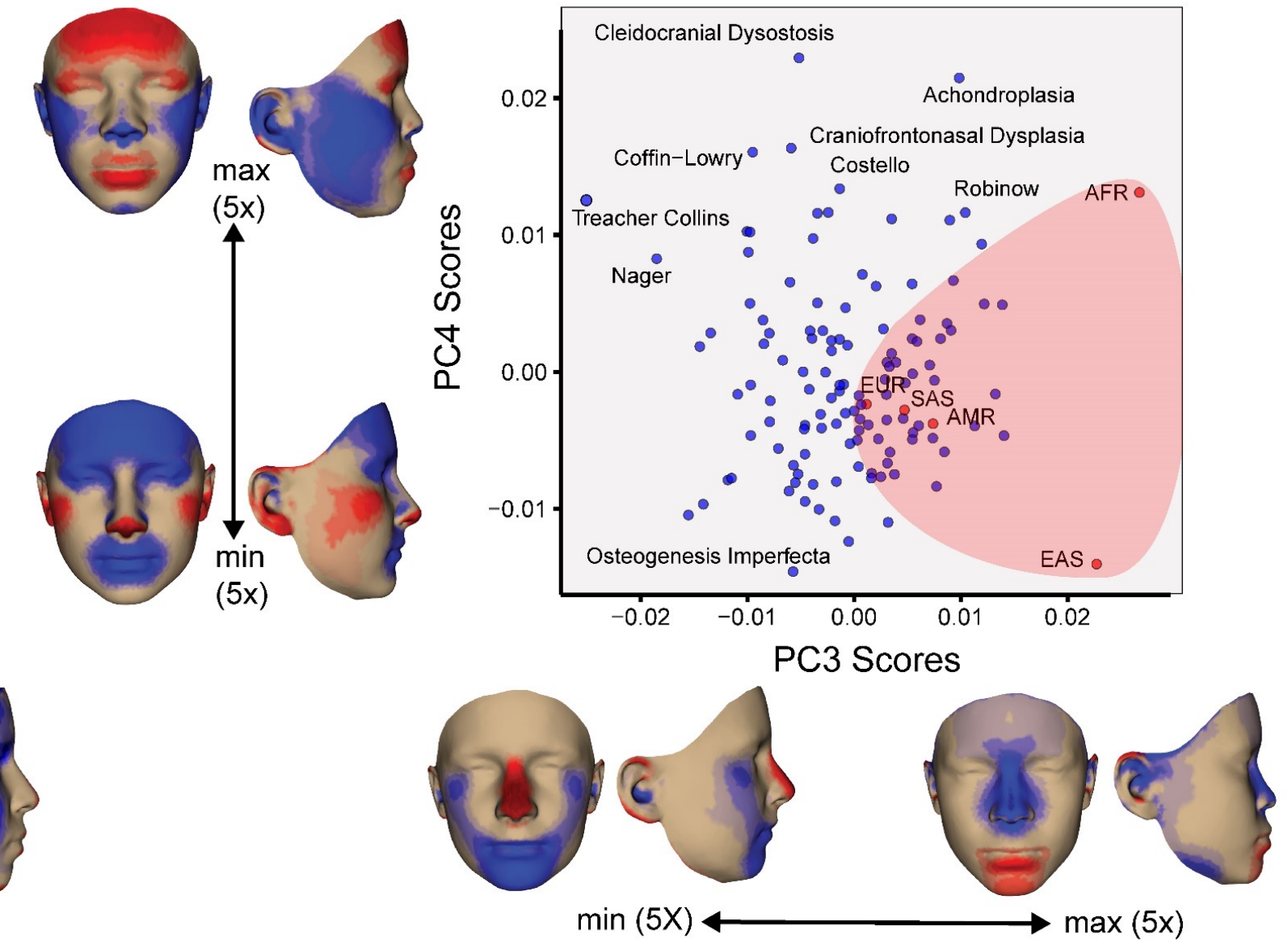
Facial shape is altered in many genetic syndromes

>7000 human syndromes; 30-40% involve facial dysmorphology

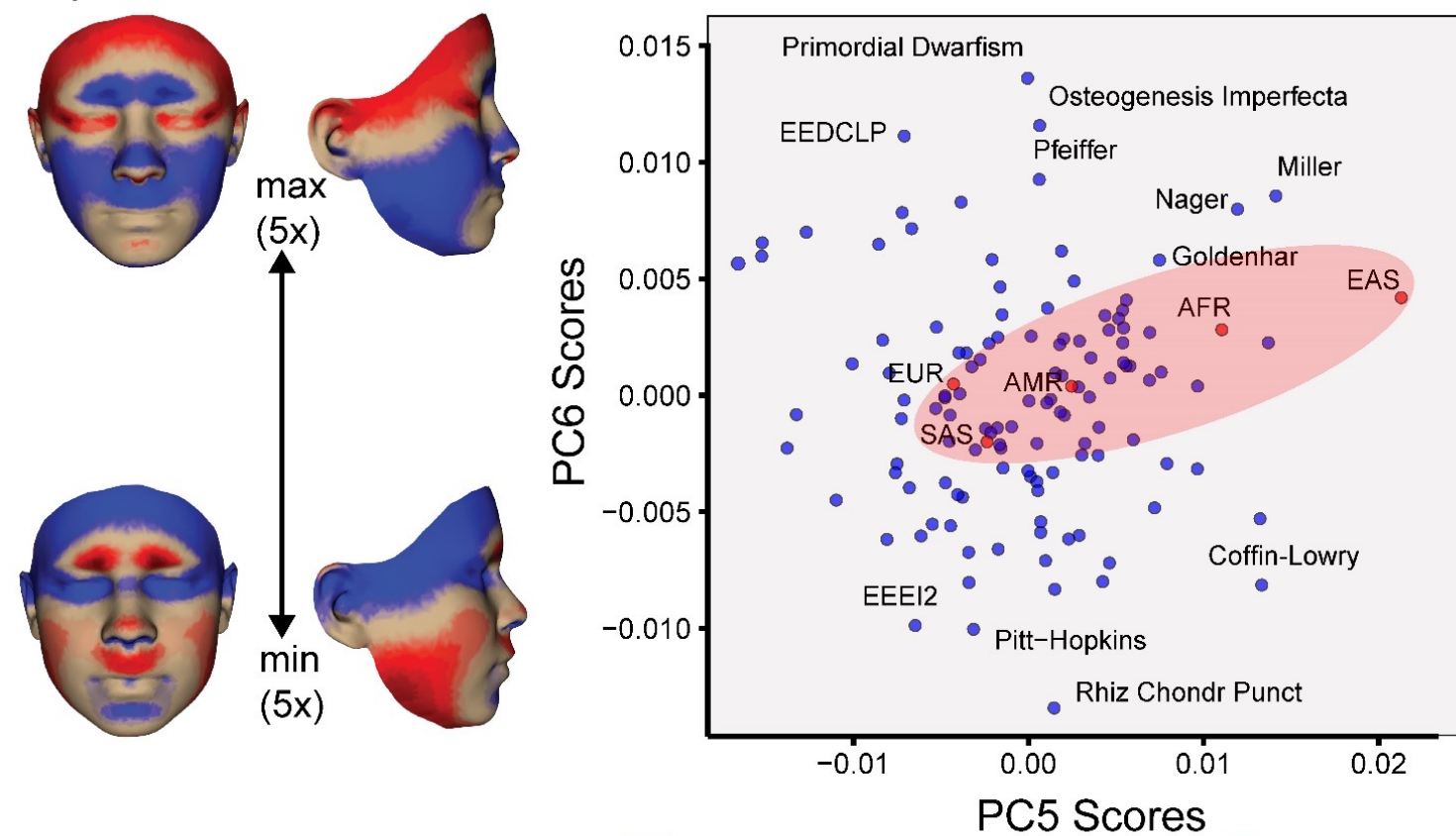
A) PC2 vs PC1



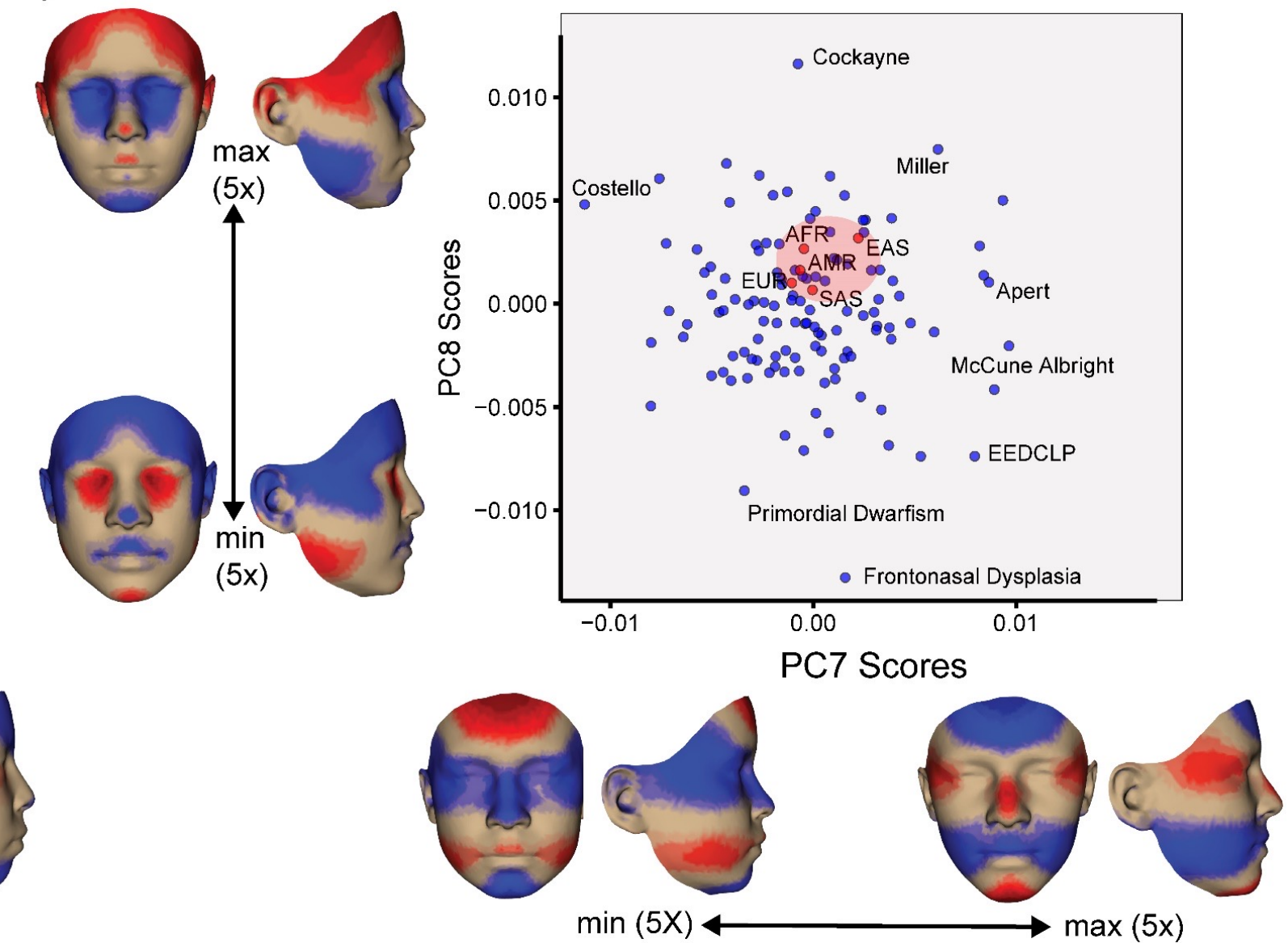
B) PC4 vs PC3



C) PC6 vs PC5



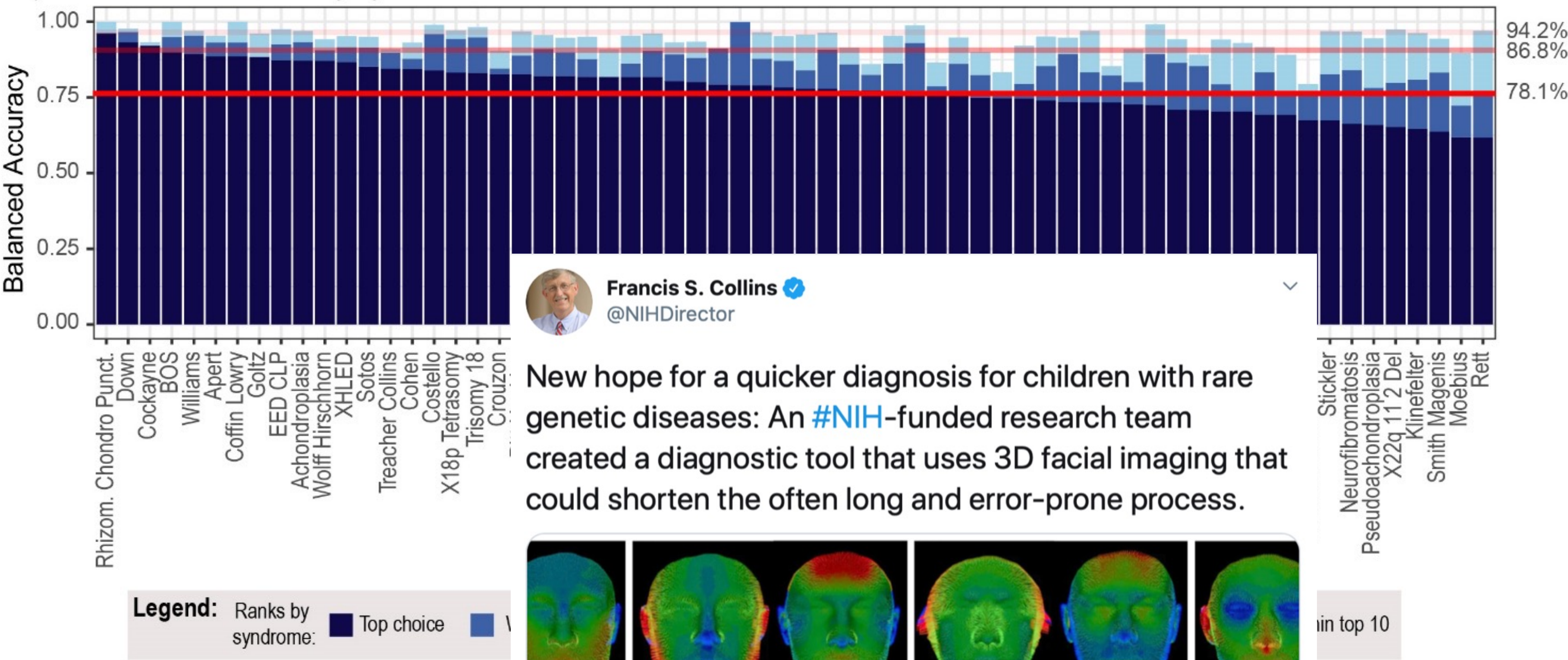
D) PC8 vs PC7



***Collaboration with Francois Bernier,
Ophir Klein, Rich Spritz, and Peter
Claes.***

Machine-Learning Based Classification

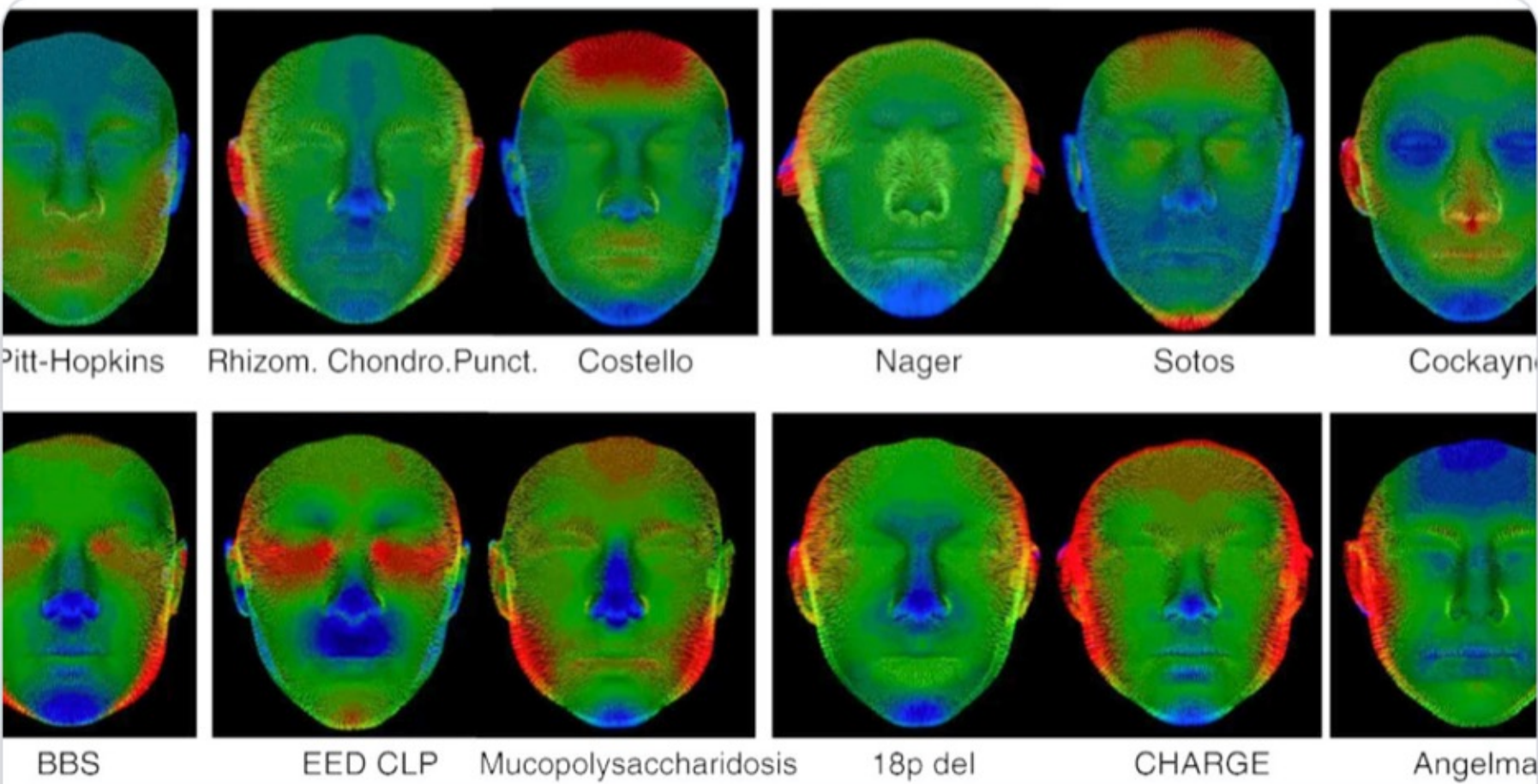
ii) Balanced Accuracies by syndrome



Open

Automated syndrome diagnosis by three-dimensional facial imaging

Benedikt Hallgrímsson, PhD¹, J. David Aponte, MSc¹, David C. Katz, PhD¹, Jordan J. Bannister, BSc², Sheri L. Riccardi, BSc³, Nick Mahasuwan, BSc⁴, Brenda L. McInnes, MSc⁵, Tracey M. Ferrara, PhD³, Danika M. Lipman, BSc¹, Amanda B. Neves, BHSc¹, Jared A. J. Spitzmacher, BSc¹, Jacinda R. Larson, PhD¹, Gary A. Bellus, MD, PhD^{6,16}, Anh M. Pham, BSc⁷, Elias Aboujaoude, MD, MA⁸, Timothy A. Benke, MD⁶, Kathryn C. Chatfield, MD⁶, Shanlee M. Davis, MD⁶, Ellen R. Elias, MD⁶, Robert W. Enzenauer, MD⁹, Brooke M. French, MD¹⁰, Laura L. Pickler, MD⁶, Joseph T. C. Shieh, MD, PhD¹¹, Anne Slavotinek, MBBS, PhD¹¹, A. Robertson Harrop, MD, MSc¹², A. Micheil Innes, MD⁵, Shawn E. McCandless, MD⁶, Emily A. McCourt, MD⁶, Naomi J. L. Meeks, MD⁶, Nicole R. Tartaglia, MD⁶, Anne C.-H. Tsai, MD⁶, J. Patrick H. Wyse, MD, PhD¹³, Jonathan A. Bernstein, MD, PhD¹⁴, Pedro A. Sanchez-Lara, MD, MSCE⁷, Nils D. Forkert, PhD¹⁵, Francois P. Bernier, MD⁵, Richard A. Spritz, MD³ and Ophir D. Klein, MD, PhD^{4,11}



3D Facial Scans Could Speed Diagnoses for Children with Rare Genetic Disea...
Scientists have developed a prototype tool based on 3D facial imaging that could shorten years undergoing medical tests and waiting for a diagnosis for ...

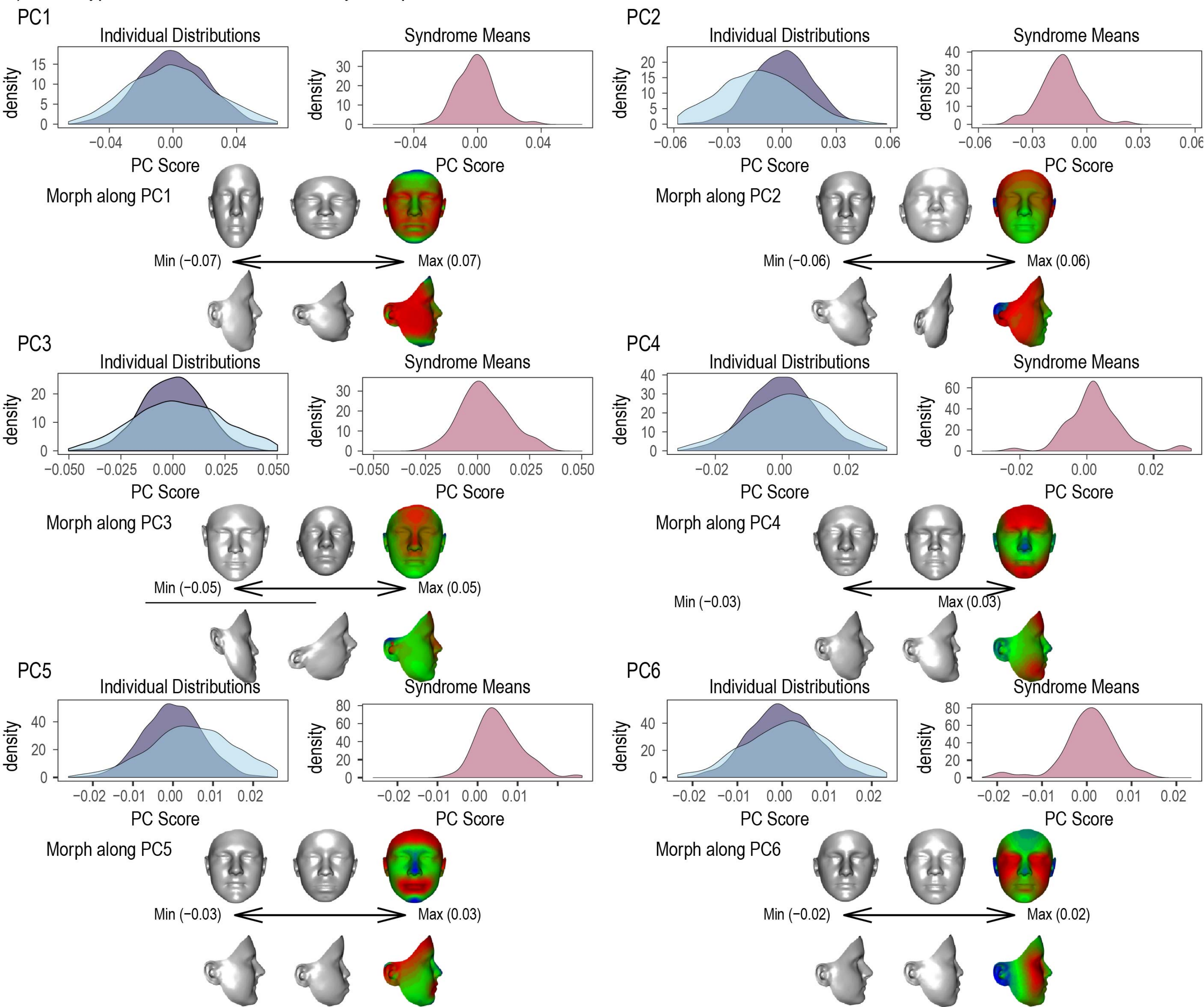
Syndromic influences on craniofacial shape follow the same covariance structure as the background variation

The covariance structure for syndromic faces is virtually identical (random skewers and Mantel's tests $r>0.88$) to the control sample.

The covariance structure for syndromic means is also very similar.

Syndromic faces vary along the same axes as normal variation but do a greater extent.

D) Phenotypic Distribution for PCs 1–6 by Group



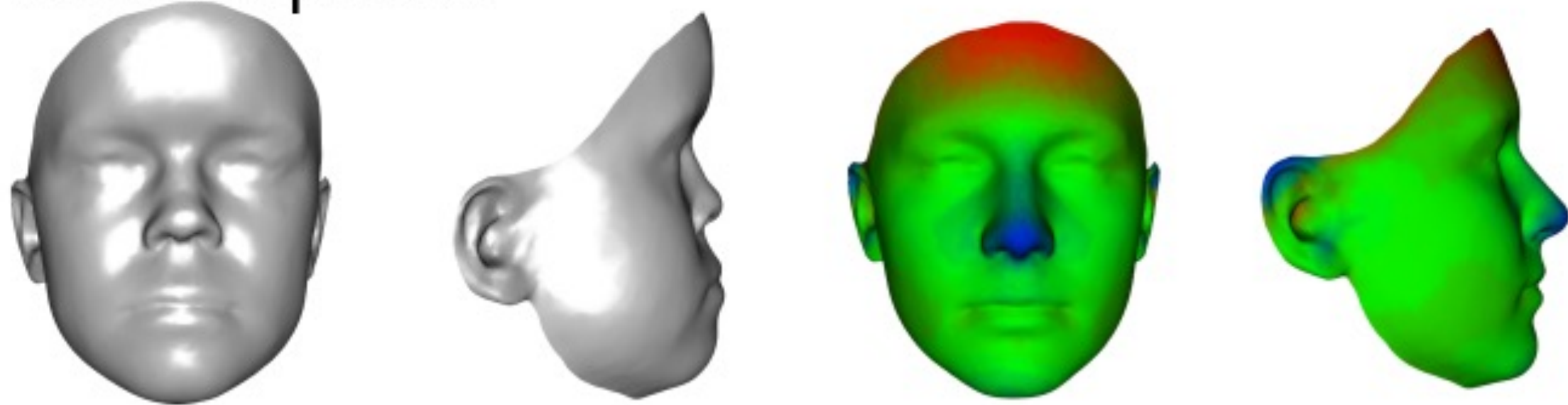
- David Aponte. PDF
- David Katz. PDF
- Jordan Bannister. Ph.D Student

Collaboration with Francois Bernier, Ophir Klein, Rich Spritz, and Peter Claes.

Morphological Integration

Integration refers to the *tendency* for traits to covary.

Achondroplasia



Peter Dinklage

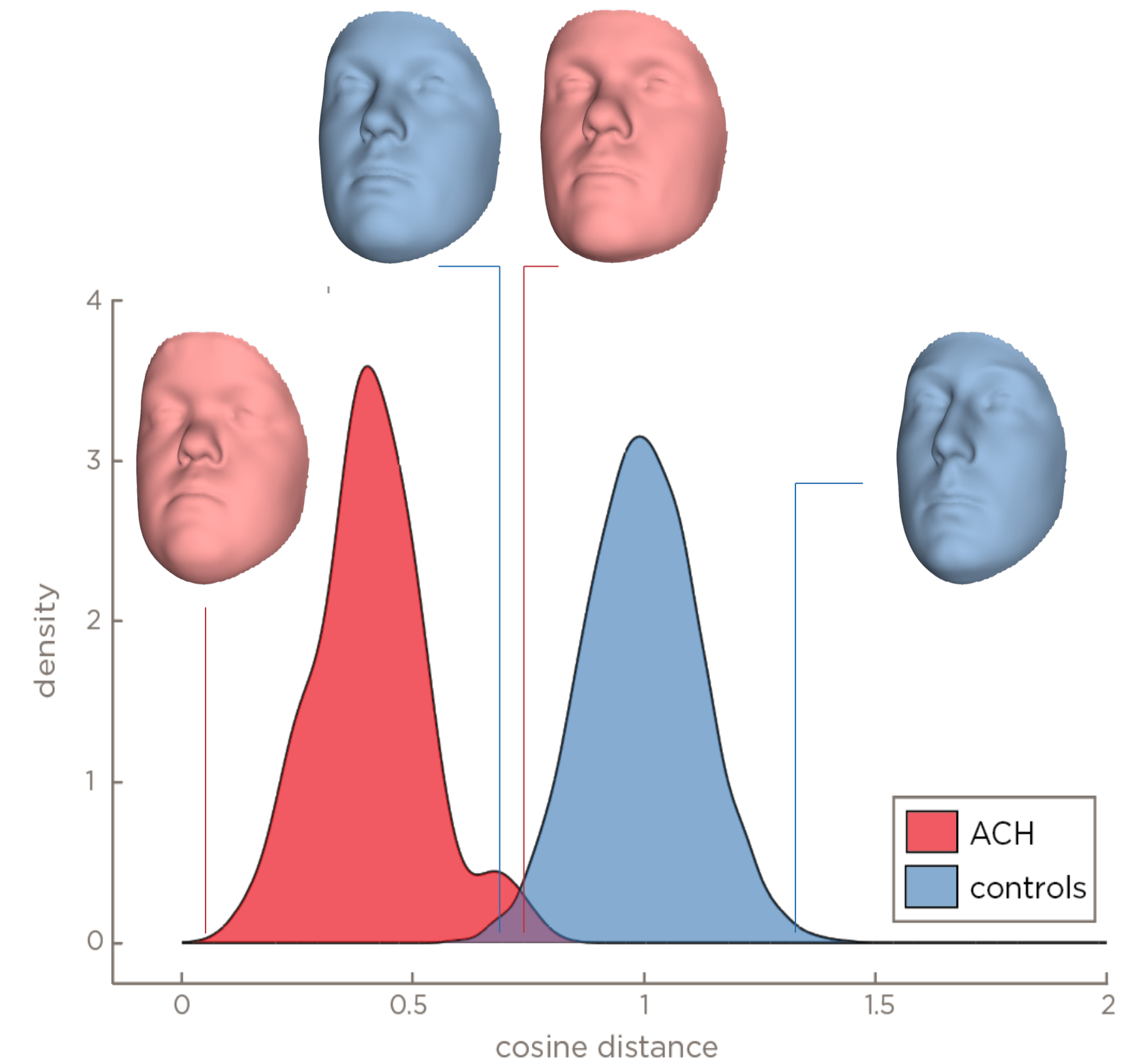
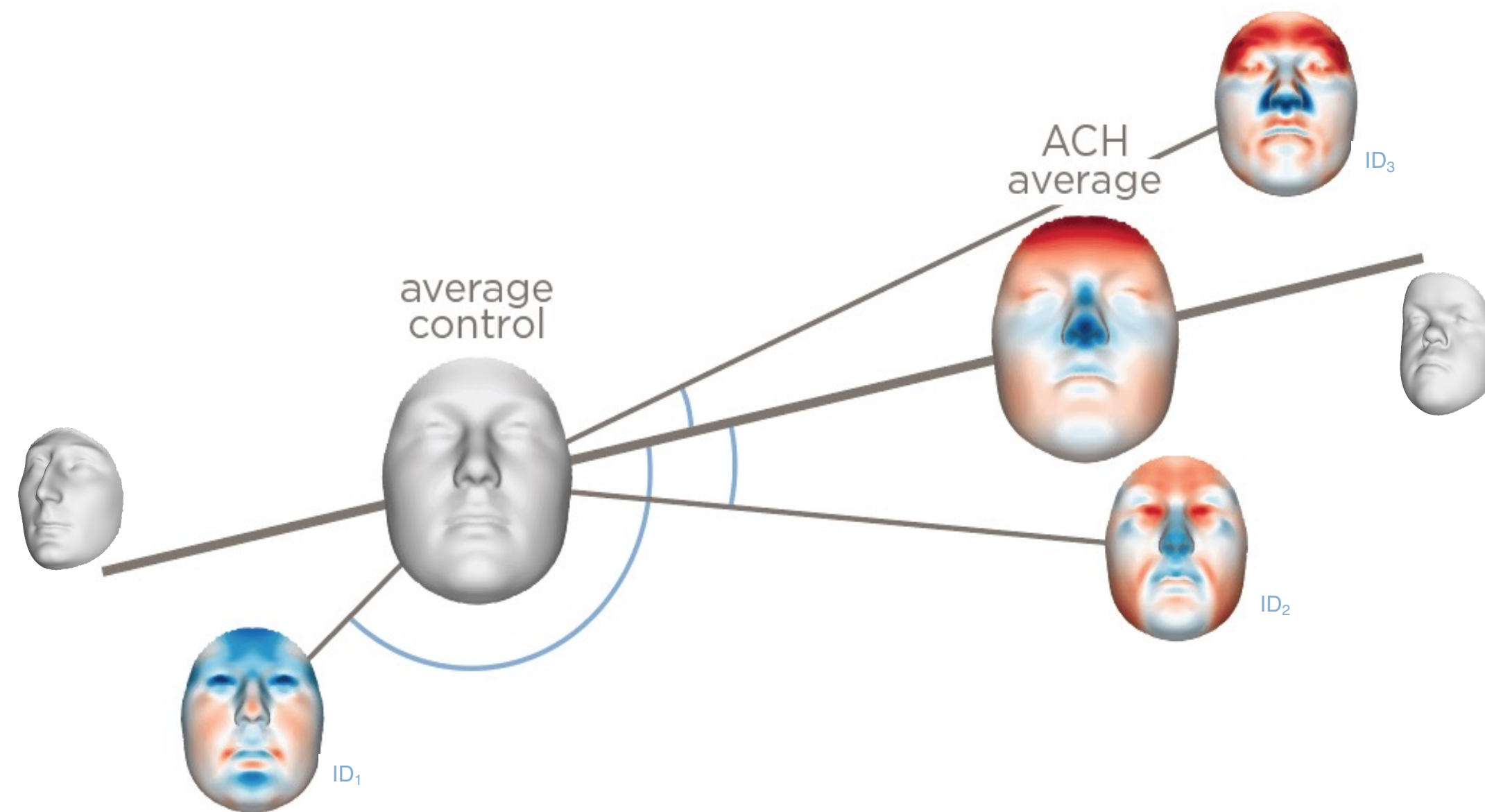
Many syndromes, such as achondroplasia, produce a correlated suite of phenotypic effects because of **integration**. Often, such traits covary along an axis of penetrance for a disease-related mutation or severity for an environmental effect.

Syndromic phenotypes as traits. E.g. Achondroplasia

Hanne Hoskens. Postdoc

Michiel Vanneste. Resident (Leuven)

Collaboration with Hilde Peeters and Peter Claes



Achondroplasia

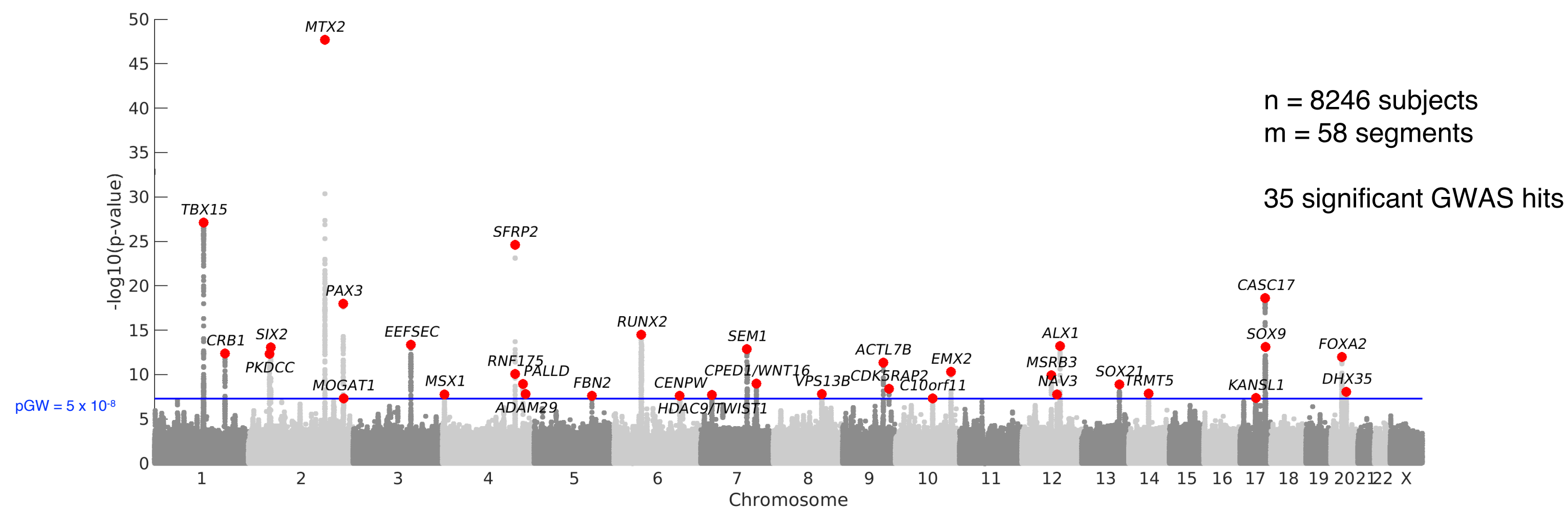
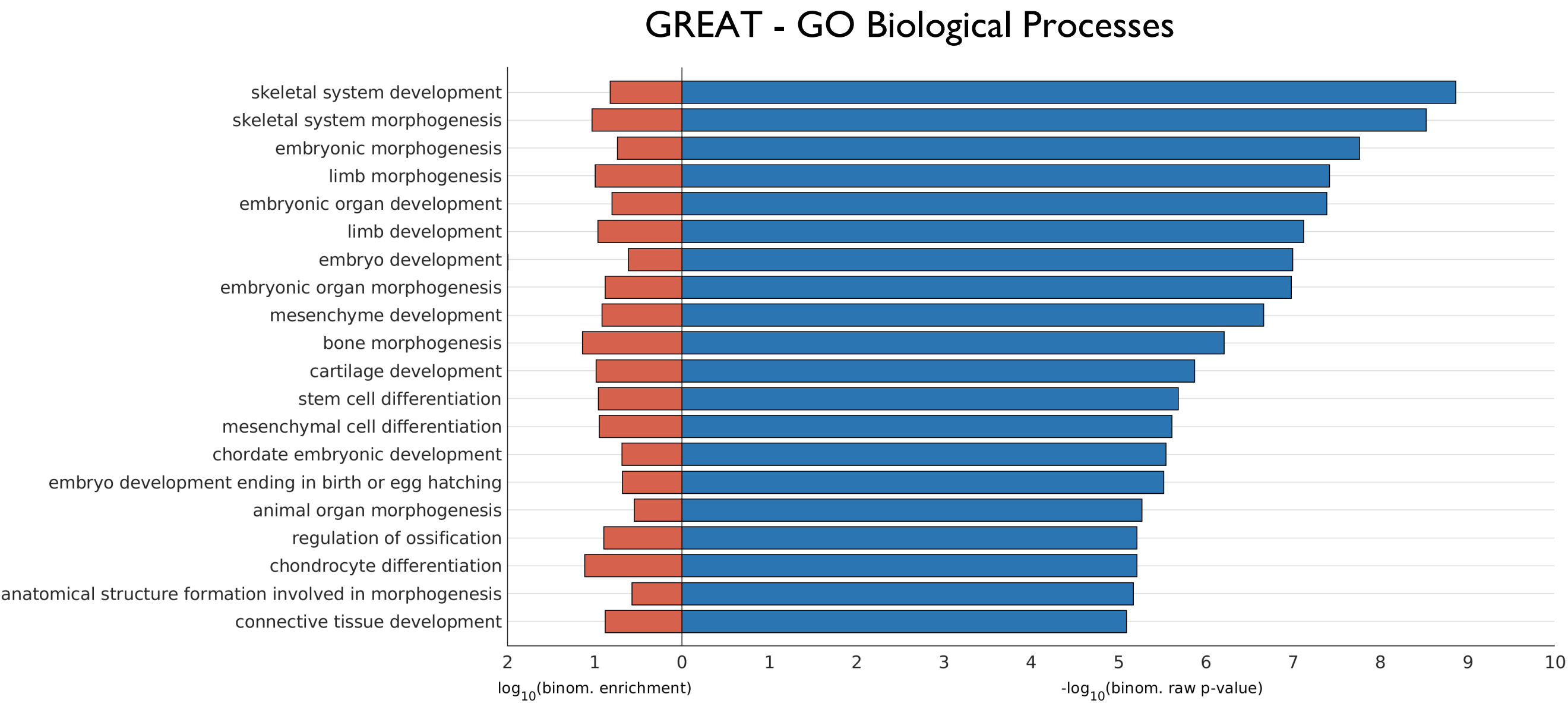
GWAS Result

Hanne Hoskens. Postdoc
Michiel Vanneste. Resident (Leuven)

Collaboration with Hilde Peeters and Peter Claes

- We performed a GWAS for the achondroplasia axis in individuals who do not have achondroplasia.

Overlap with achondroplasia-related genes



nature communications

Article <https://doi.org/10.1038/s41467-024-54839-1>

Syndrome-informed phenotyping identifies a polygenic background for achondroplasia-like facial variation in the general population

Received: 29 November 2023
Accepted: 21 November 2024
Published online: 02 December 2024

Check for updates

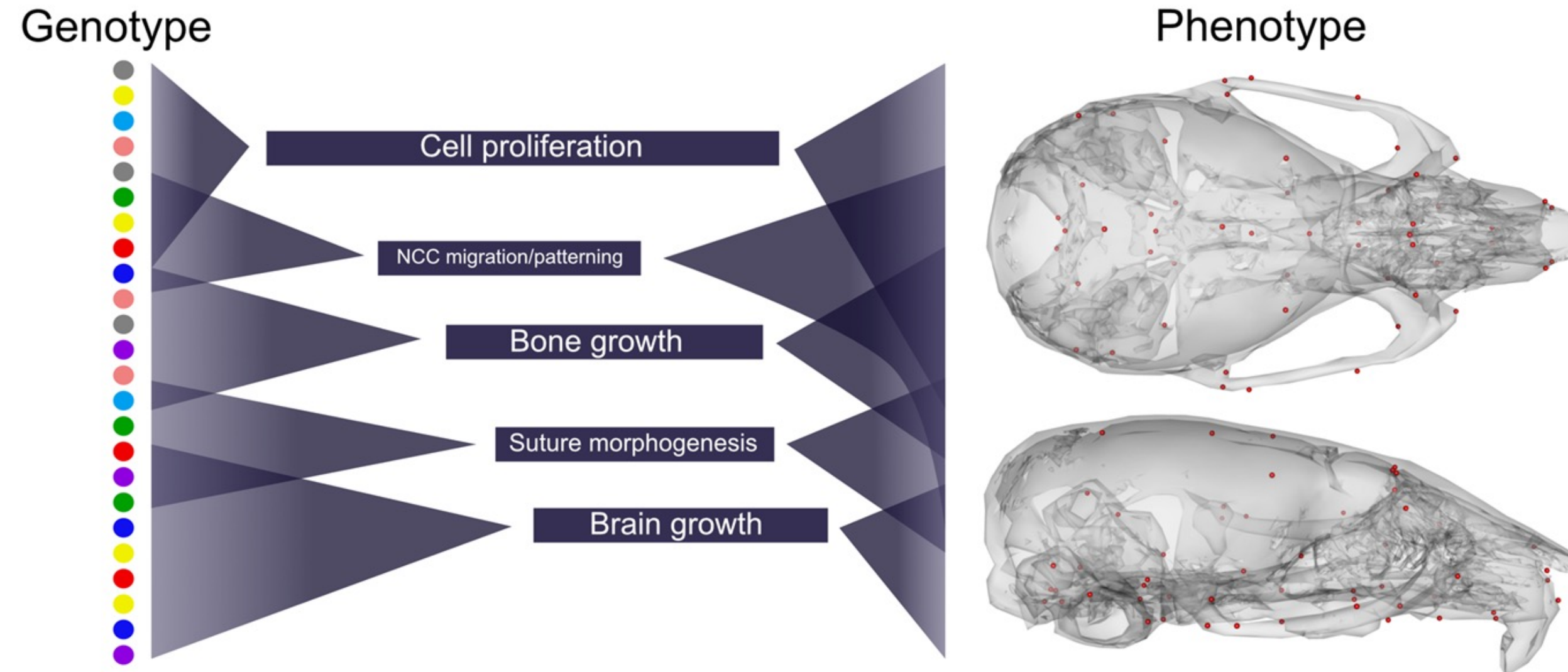
Michiel Vanneste^{1,15}, Hanne Hoskens^{2,3,4,15}, Seppe Goovaerts^{1,5}, Harold Matthews^{1,5}, Jay Devine^{5,6}, Jose D. Aponte^{2,3,4}, Joanne Cole⁷, Mark Shriver⁸, Mary L. Marazita^{9,10}, Seth M. Weinberg^{9,10}, Susan Walsh¹¹, Stephen Richmond¹², Ophir D. Klein¹³, Richard A. Spritz¹⁴, Hilde Peeters¹, Benedikt Hallgrímsson^{2,3,4} & Peter Claes^{1,5,6}

Hanne Hoskens. Postdoc
Michiel Vanneste. Resident (Leuven)

Collaboration with Hilde Peeters and Peter Claes

Multivariate Genotype-Phenotype Mapping

David Aponte PhD student



- We used the Mitteroecker *et al.* method (MGP)
- The method relates latent variables from the genetic and phenotypic variance-covariance matrices to perform a multivariate to multivariate mapping of genotype to phenotype.

Collaboration with Ralph Marcucio, Daniel Graf, Steve Murray, Jim Cheverud

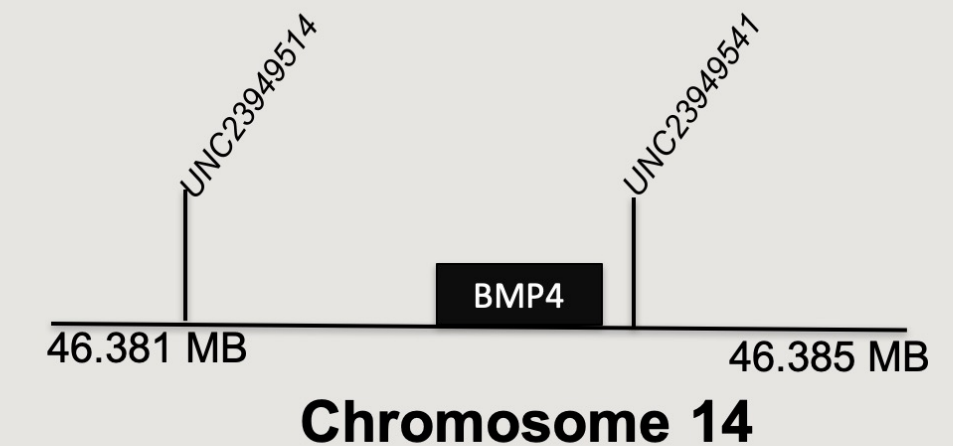
Aponte *et al.* 2021 *eLife*

Process:
Chondrocyte differentiation

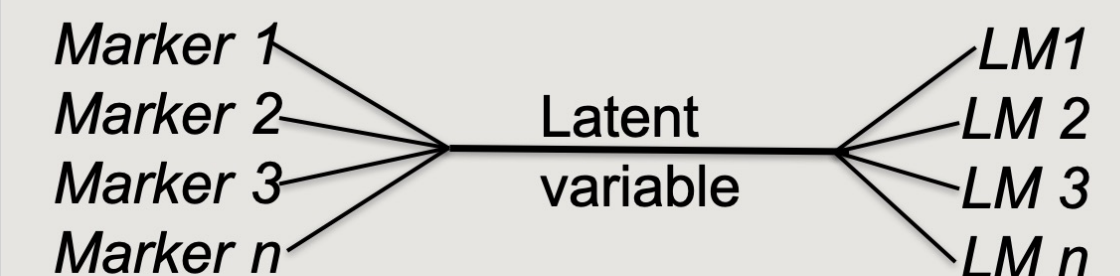
Associated genes:

- 1) *Adam*
- 2) *BMP2*
- 3) *BMP4*
- 4) *Etc.*

Find nearest MegaMUGA marker:

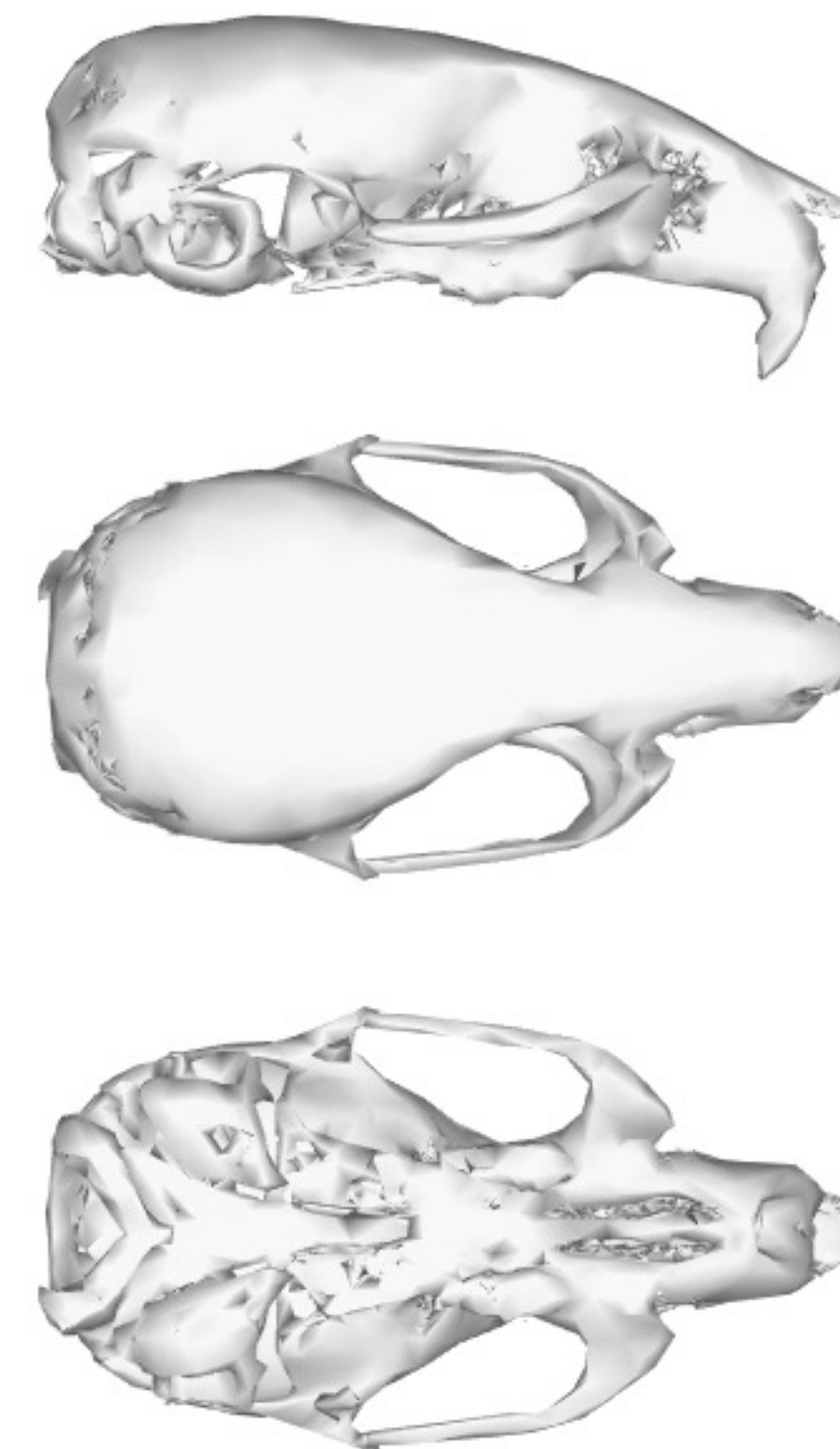
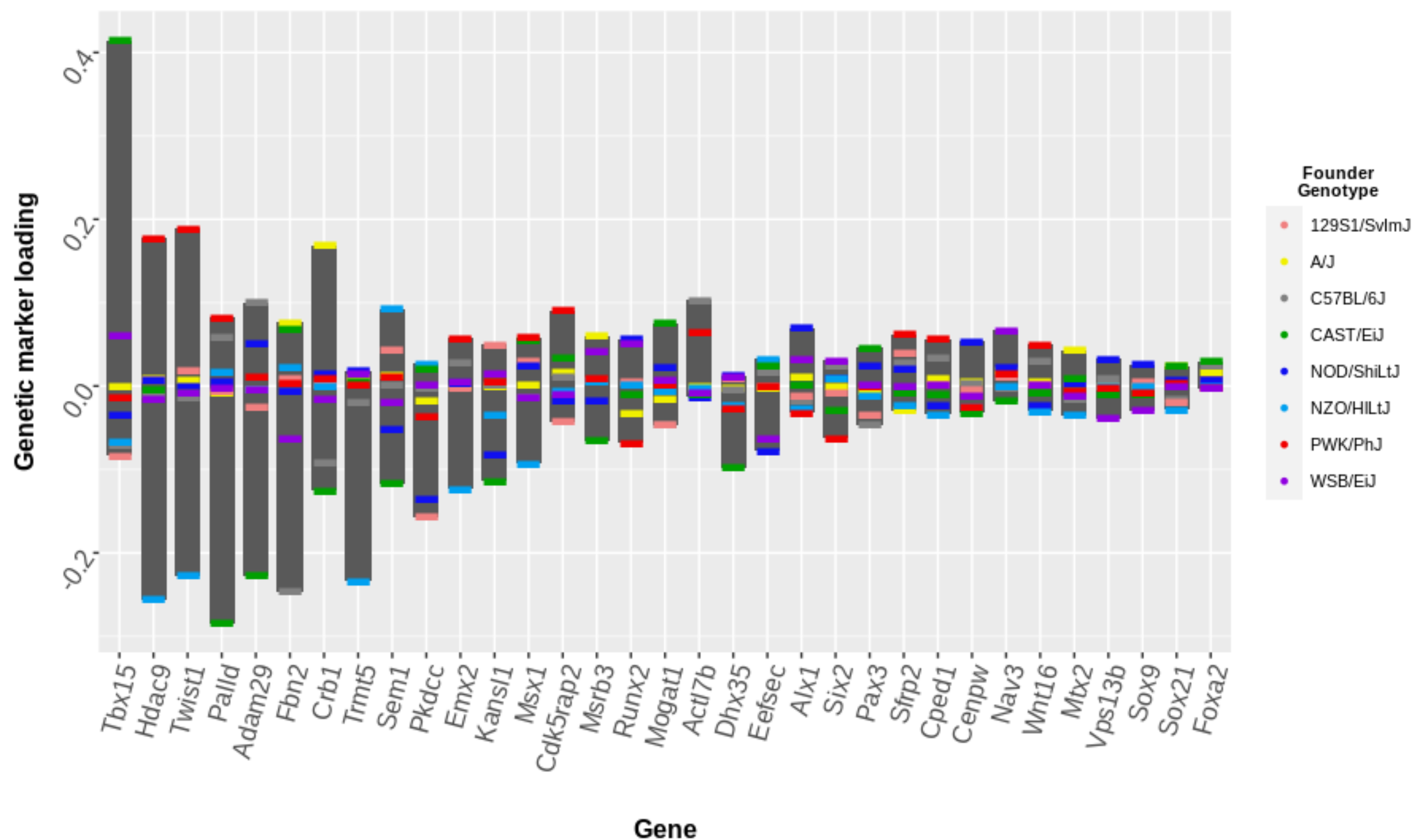


Compute and decompose covariance matrix:

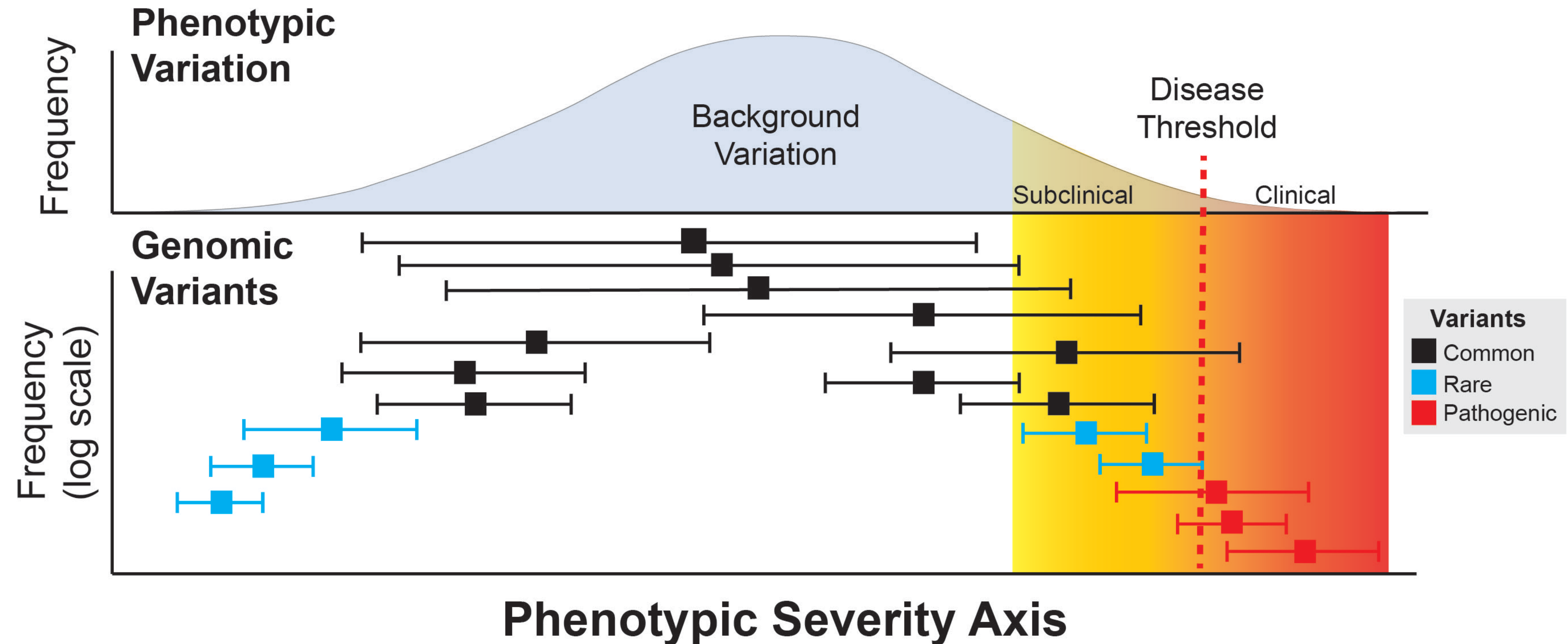


Multivariate Geno-Pheno (MGP) method

We then ran the 35 hits from the human GWAS on Diversity-Outbred mice using MGP



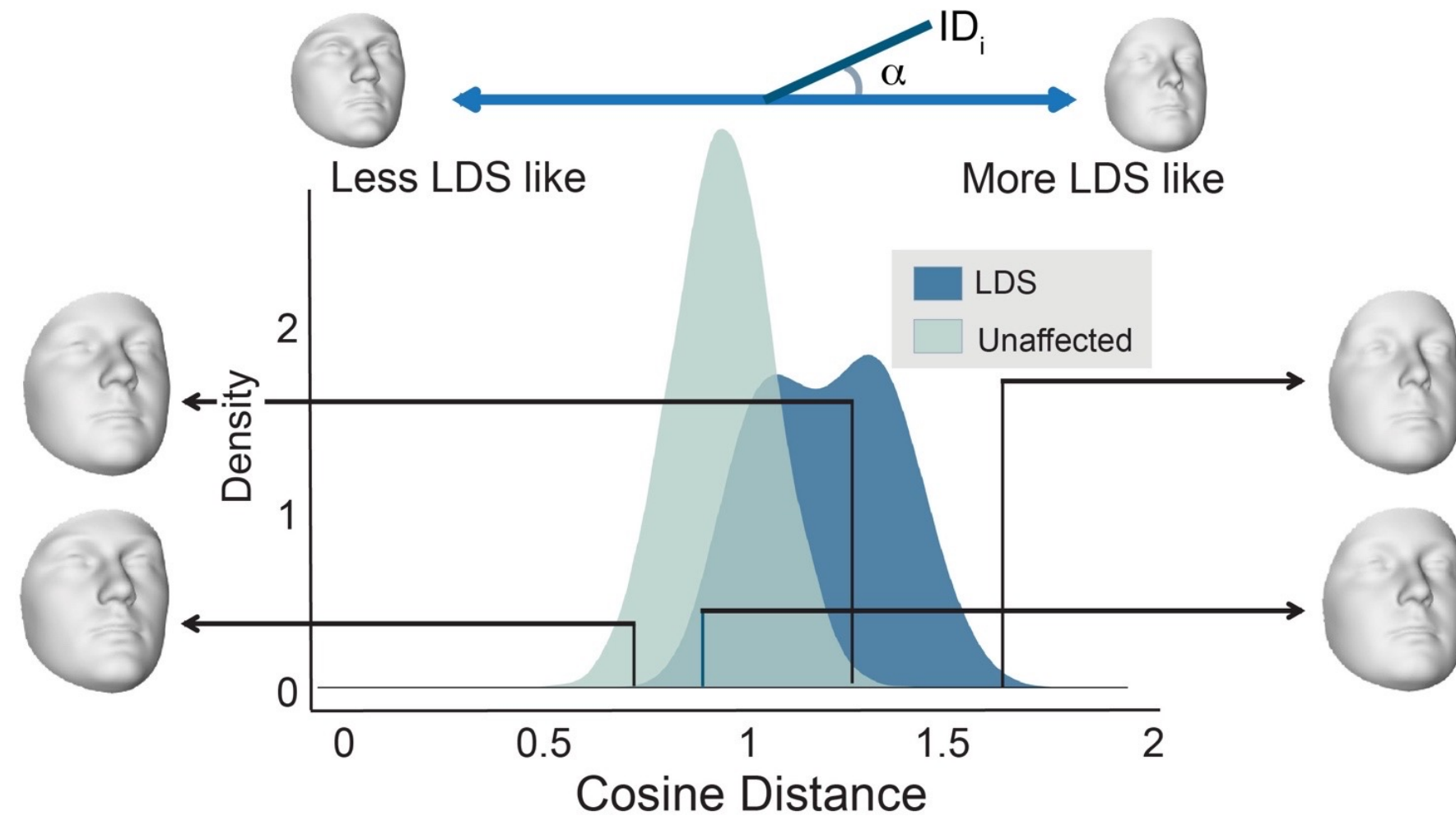
Integration and the genetics of Mendelian disorders



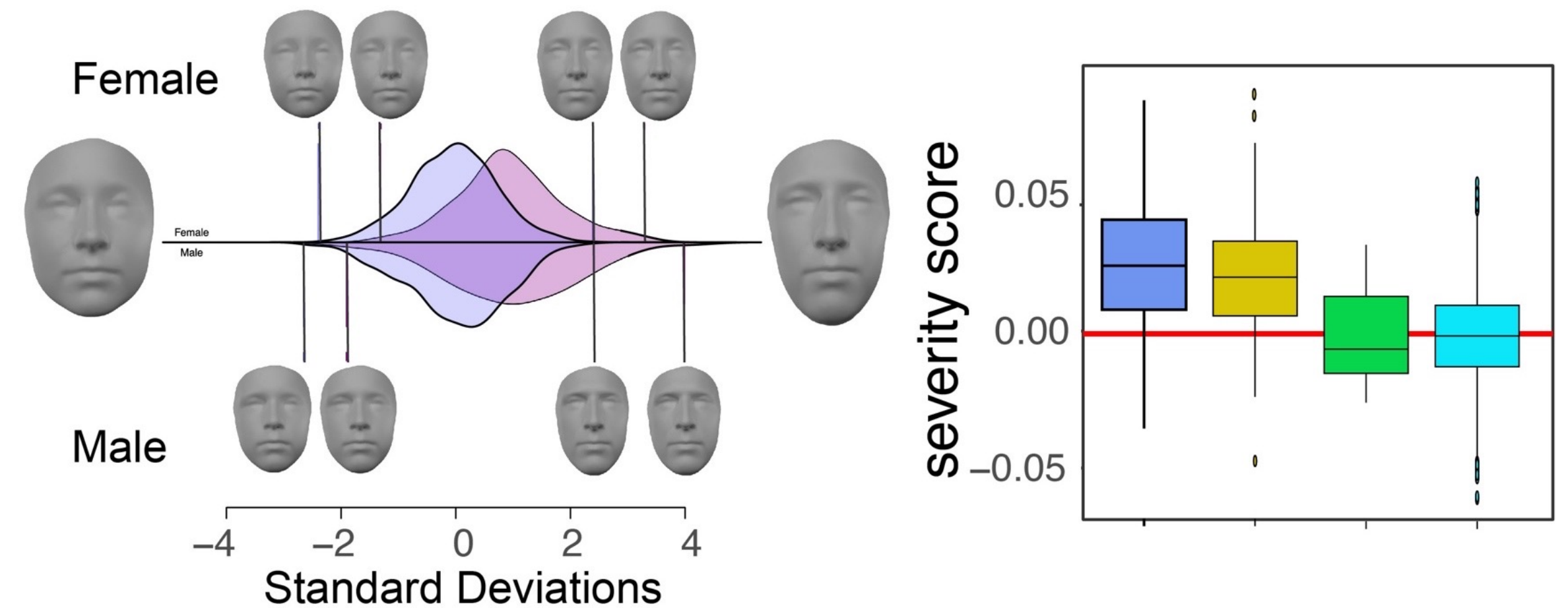
If the genes that drive variation along facial shape severity axes have similar patterns of pleiotropy to the disease-associated variants, then such axes have predictive value in clinical context.

Axes of Facial Shape Severity for HTADs

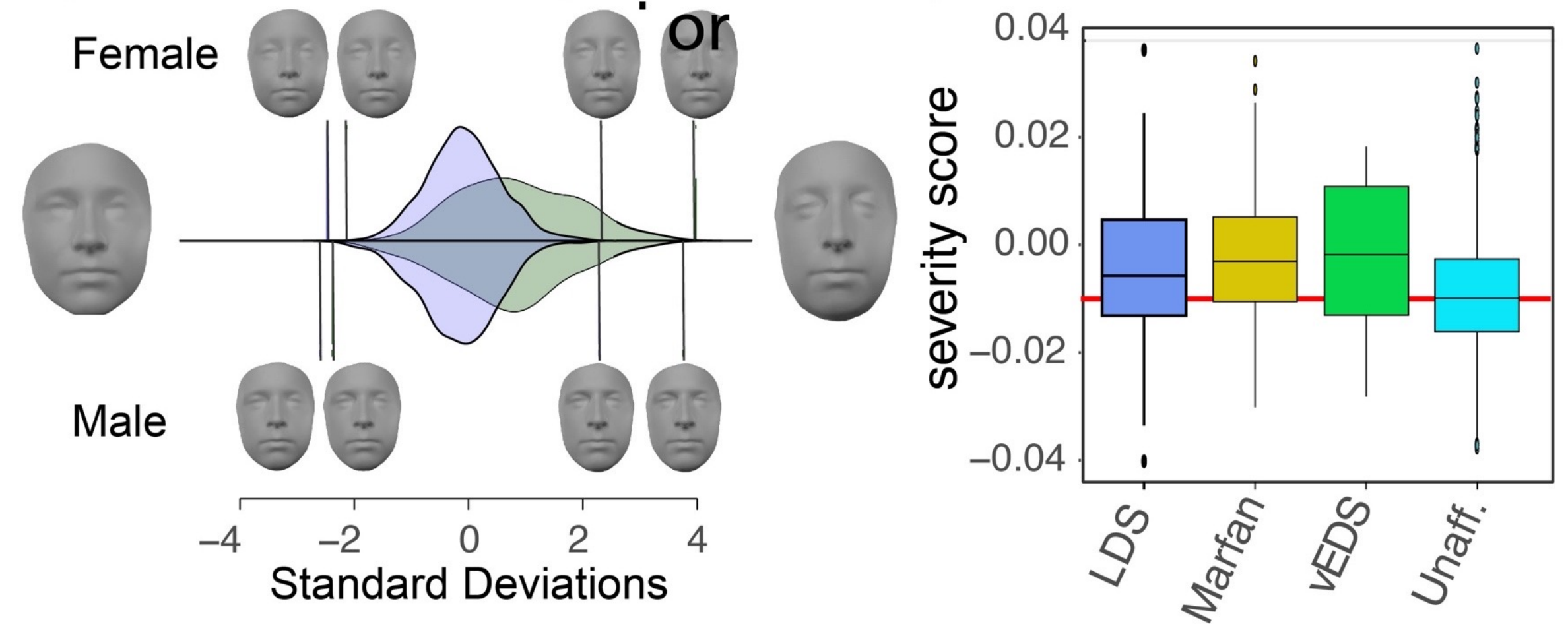
A) Calculation of Facial Shape Severity Score



B) Distributions for Marfan Severity Score

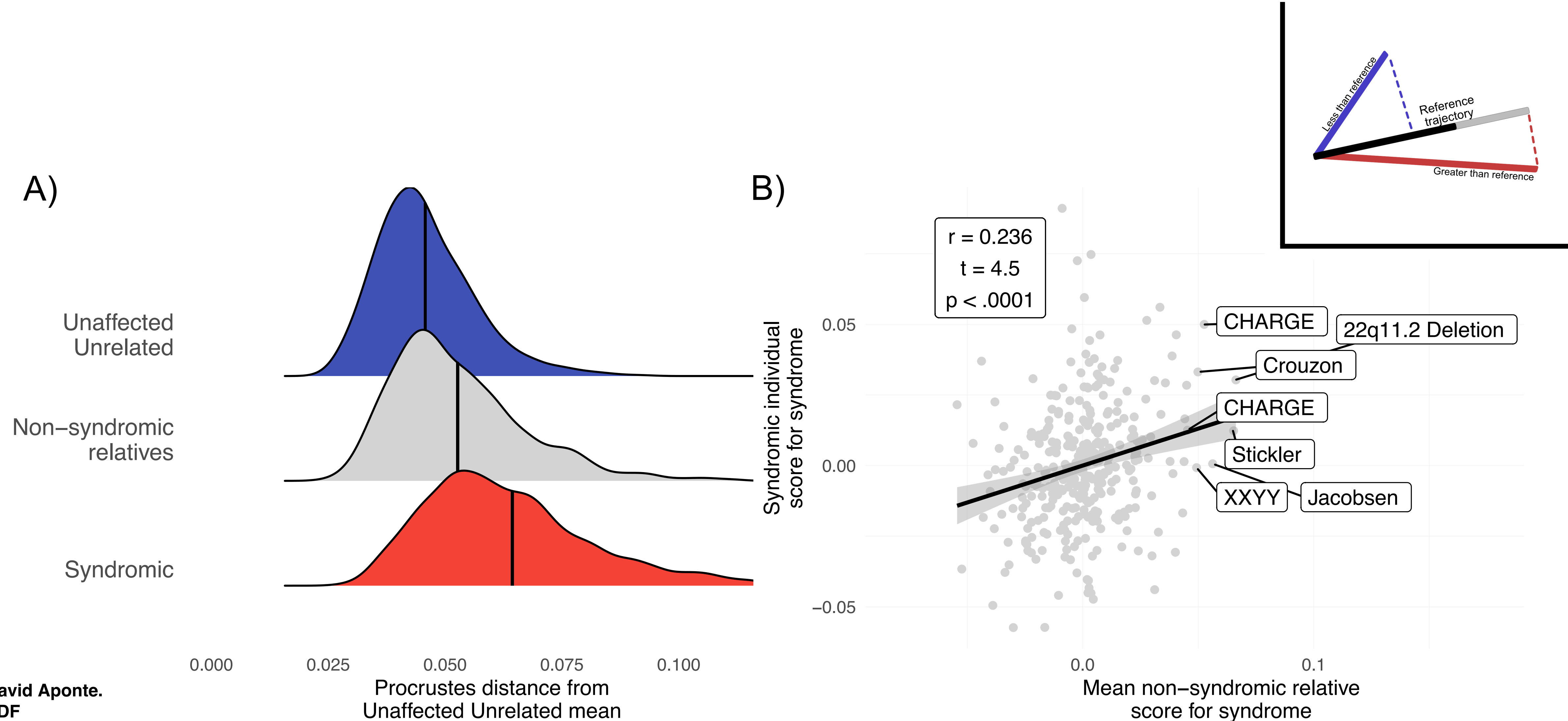


C) Distributions for Loeys-Dietz Severity Score

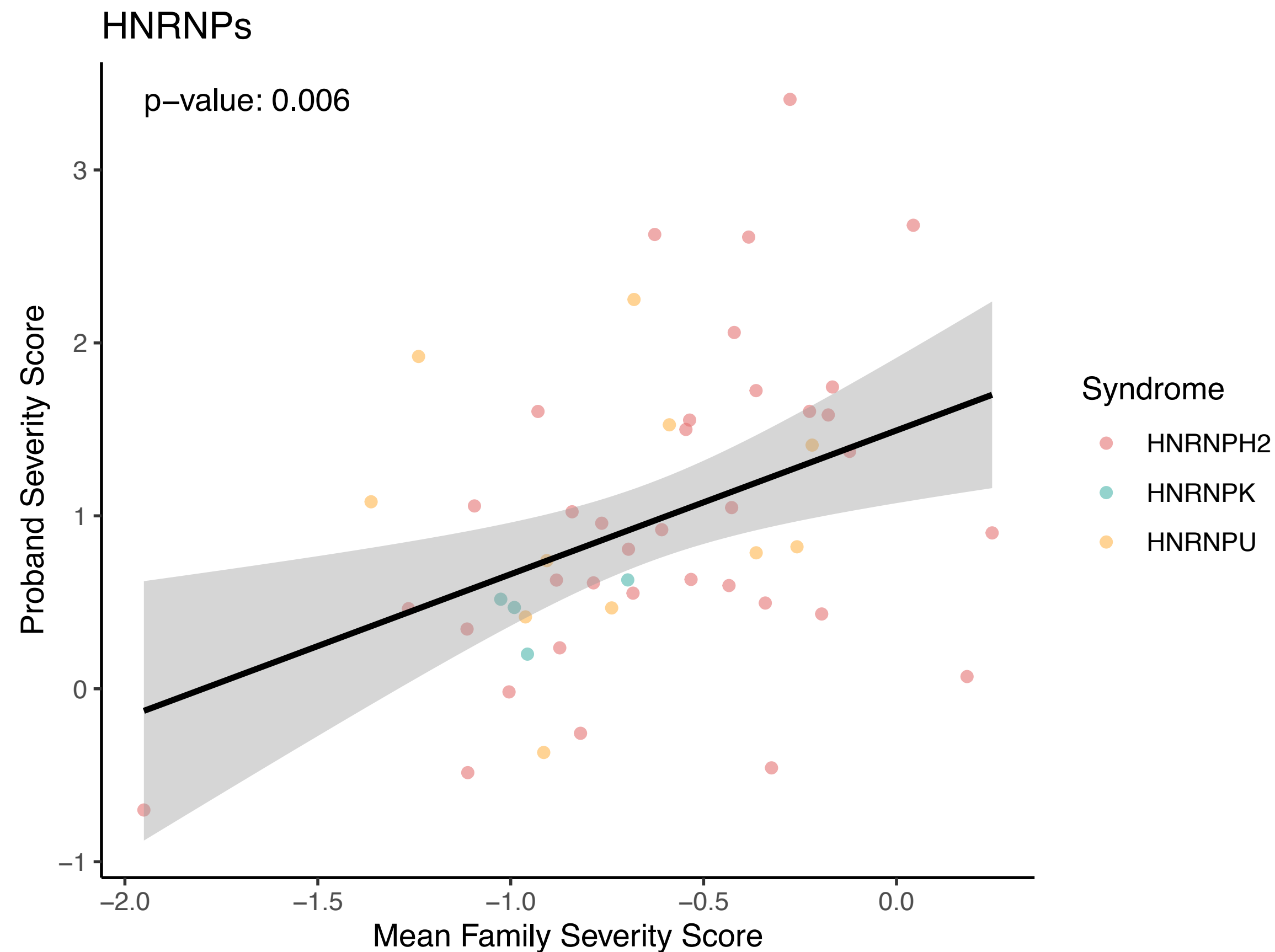


Connective tissue syndromes also fall along axes of severity that have a polygenic basis. These syndromes are associated with dramatically increased risk of sudden death due to aortic dissection

Non-syndromic relatives harbor signs of syndromic morphology



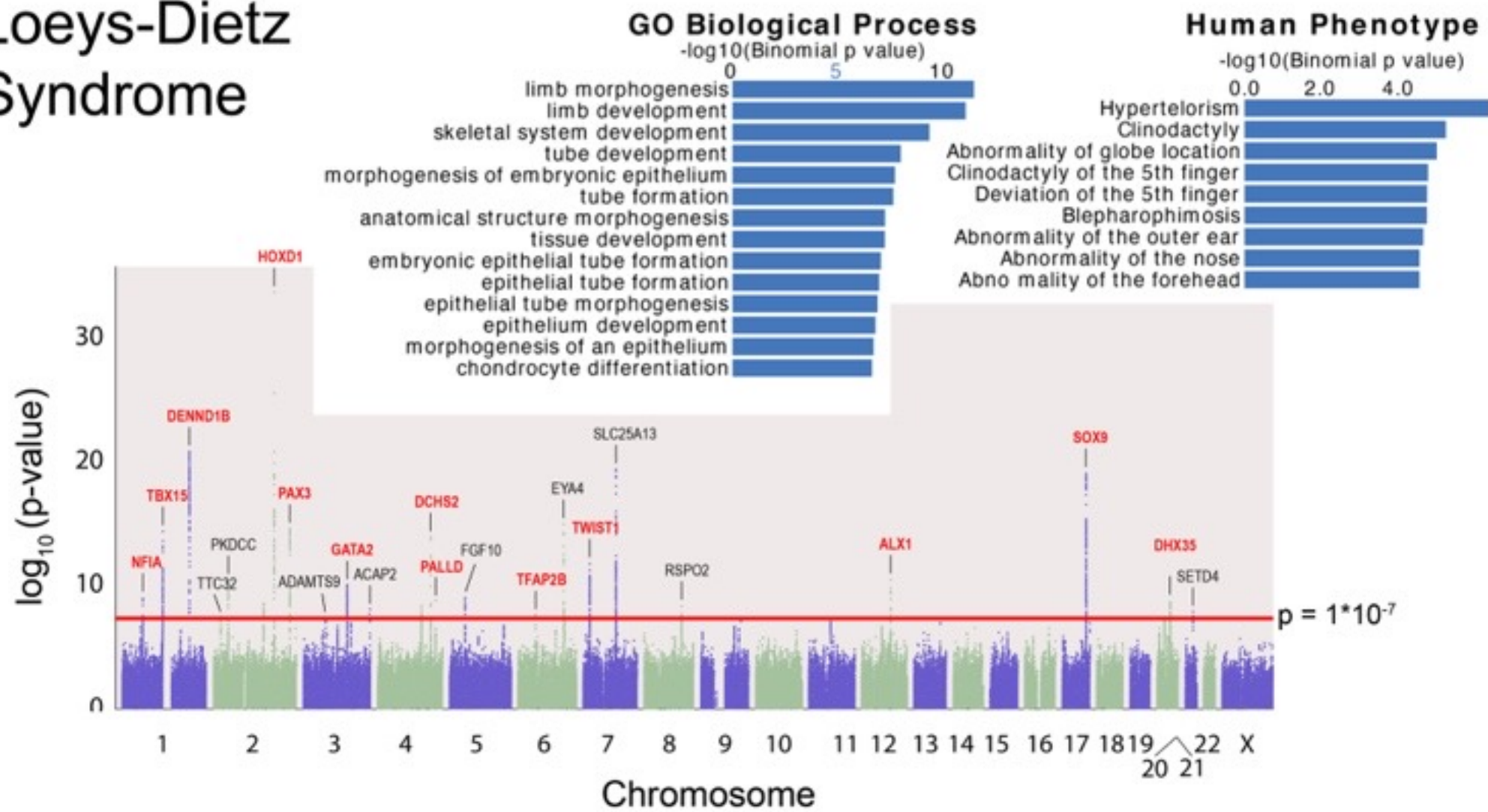
Does familial resemblance to a syndrome predict severity?



Is variation in facial shape severity meaningful?

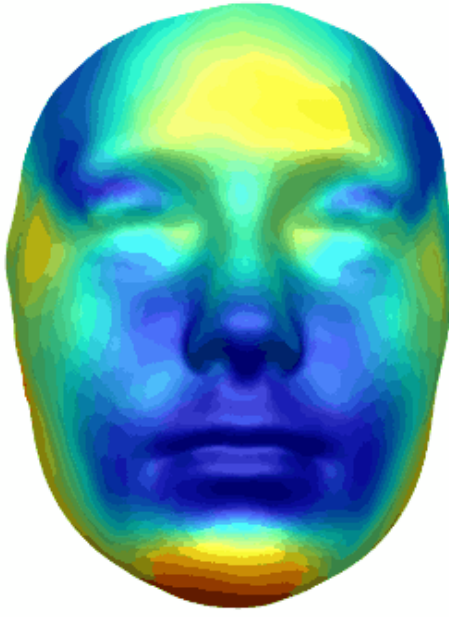
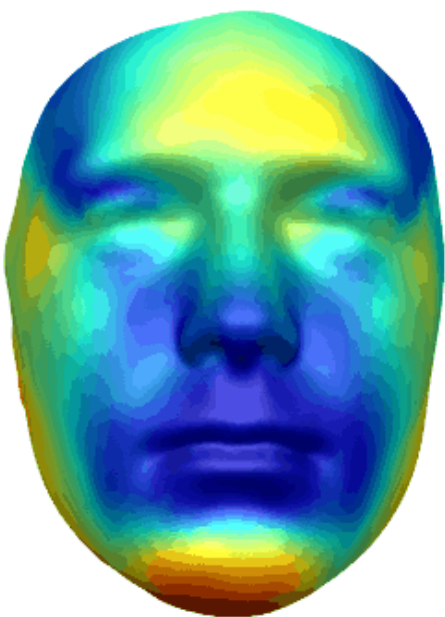
Syndrome-Informed GWAS for Loeys-Dietz

Loeys-Dietz Syndrome

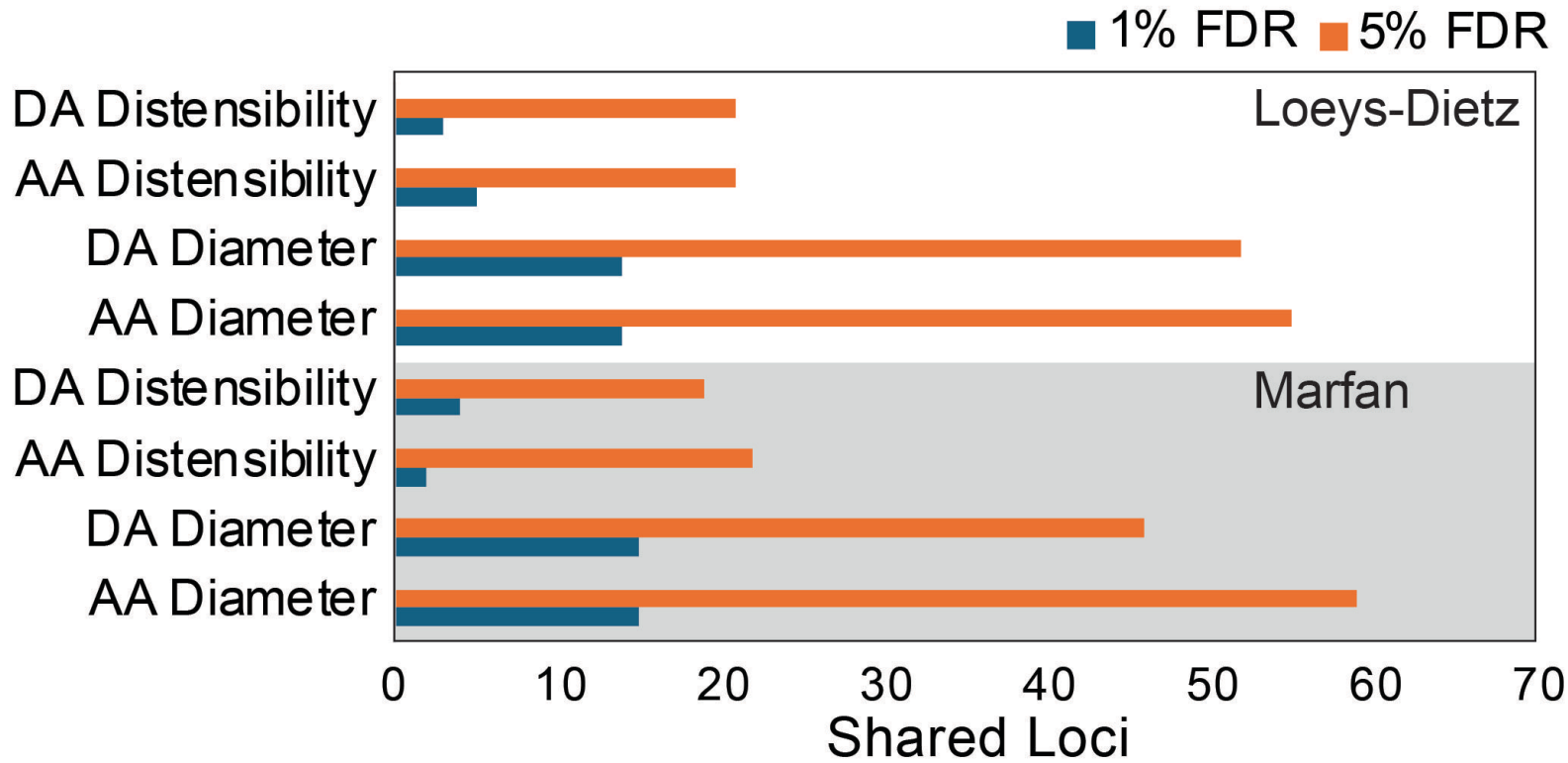


Male

Female

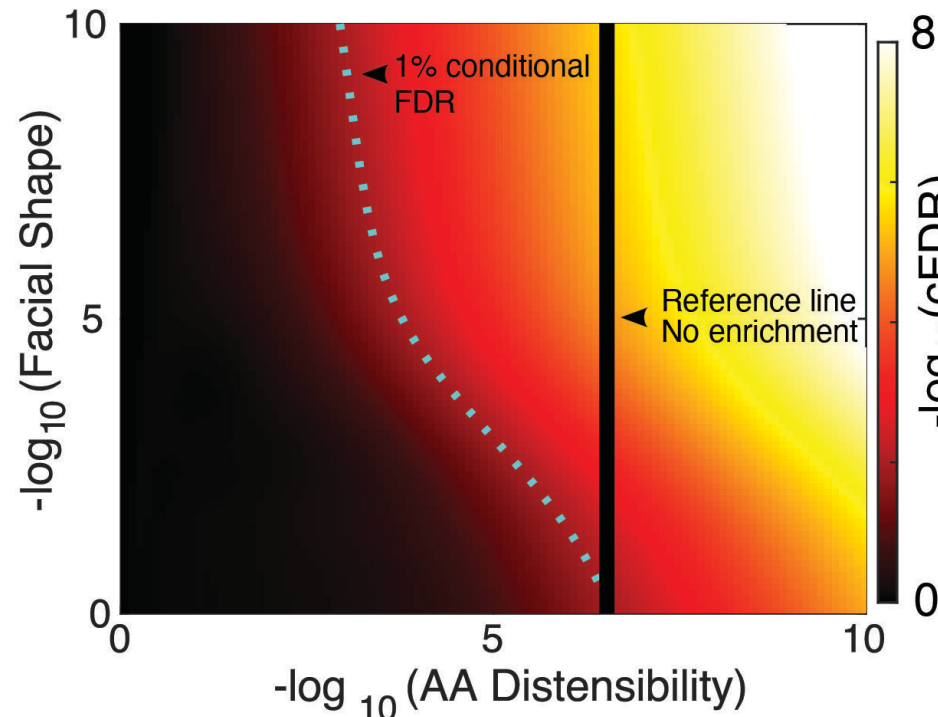


A) Shared loci between TAD and Syndrome-Informed GWAS

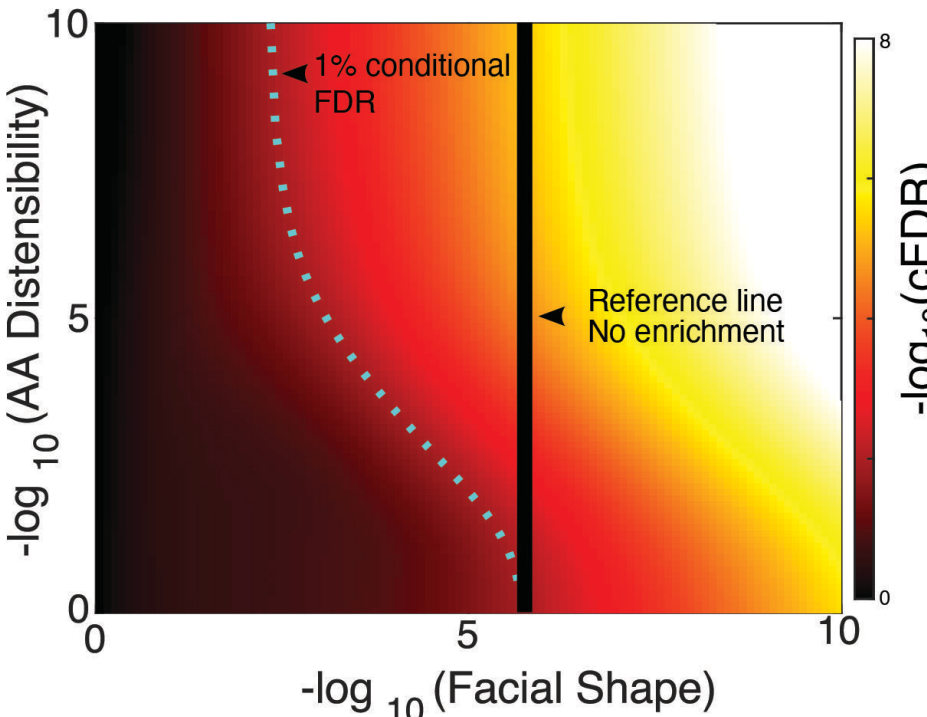


B) Conditional False Discovery Rate Heatmaps

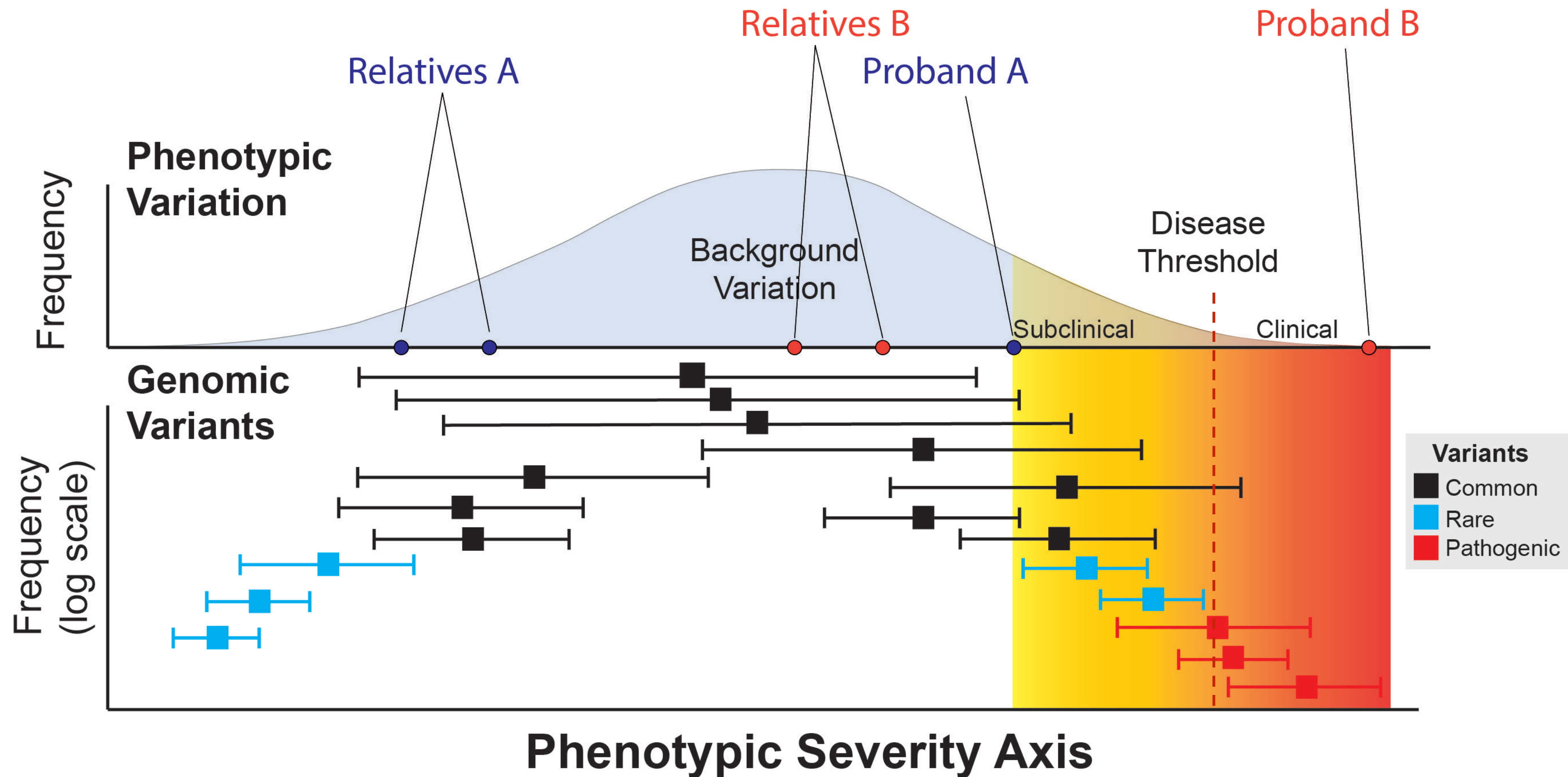
i) Aortic Distensibility GWAS on Marfan



i) Marfan GWAS on Aortic Distensibility



For heritable aortopathies, preliminary analyses reveal significant overlap between the genetics of facial shape severity for these syndromic axes and the genetics of Thoracic Aortic Dissection.



Relatives of probands who have been diagnosed with a disease are more likely to have a genetic background that elevates disease-related severity even when they don't have the pathogenic variant.

Conclusions

- Many pathogenic mutations influence the face due to pleiotropy and the massive polygenicity of facial shape variation.
- Variation in facial shape is high dimensional but also highly structured or *integrated*. This means that many pathogenic variants alter facial shape along directions of variation that are present in the background population.
- This feature can be used to construct axes of phenotypic severity or penetrance. Such axes can have a polygenic basis in the background population. It is not known whether axes of facial shape severity predict underlying disease severity for specific diseases, but this is an issue of current concern.



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one child 
every child



Canada First Research
Excellence Fund



National Institute of Dental
and Craniofacial Research



syndrome-atlas.ca

- Model-driven visualizations of age/sex/severity
- Simulated skin texture
- Directly compare syndromes

