Parabon® Snapshot™ Phenotype Report

#OPD-FL-2001-380051-Snapshot

Agency: ORLANDO POLICE DEPARTMENT

Agency Case #: 2001-380051

Evidence ID #: EN3828A

Subject DNA Vial #: 15-08830.02

Report Preparation Date: 11 NOV 2015

PNL Document #15K11P55-5BE8XMUM9E

Snapshot DNA PHENOTYPING

PARABON® NANOLABS

Snapshot Prediction Results
Introduction

For additional information about the contents of this report, please refer to the **Parabon Snapshot Phenotype Report Guide**.

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Sample Description and Genotyping Results

7.56 ng of DNA extracted from a swab with suspected semen was sent to AKESOgen for genotyping on the Illumina CytoSNP-850k chip. The overall genotyping call rate was 98.95% (842,350 SNPs), which indicates that the sample was most likely single-source.

Analysis of the sex chromosomes showed the subject is male.

Snapshot Prediction Results
Skin Color

Snapshot™
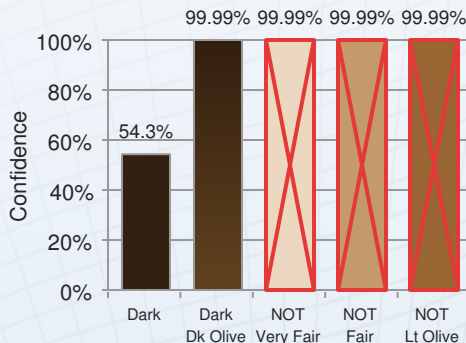DNA PHENOTYPING

#OPD-FL-2001-380051-Snapshot

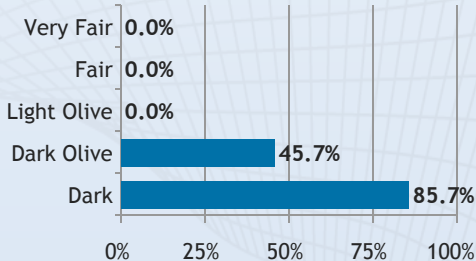PNL Document #15K11P55-5BE8XMUM9E

Background

The skin color model is based on 502 unrelated individuals from a range of ethnic backgrounds. The categorical trait values are coded from lightest to darkest, such that:

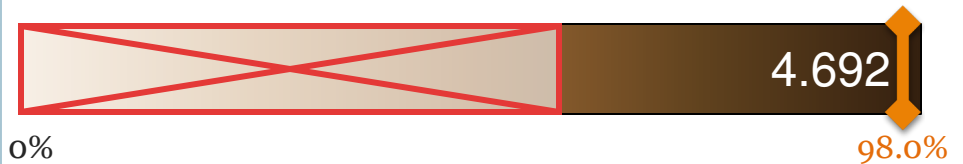|	
Very Fair	= 1
Fair	= 2
Light Olive	= 3
Dark Olive	= 4
Dark	= 5

Predictions

Skin Color
Consistency Values

The subject is predicted to have **skin color = 4.692**.

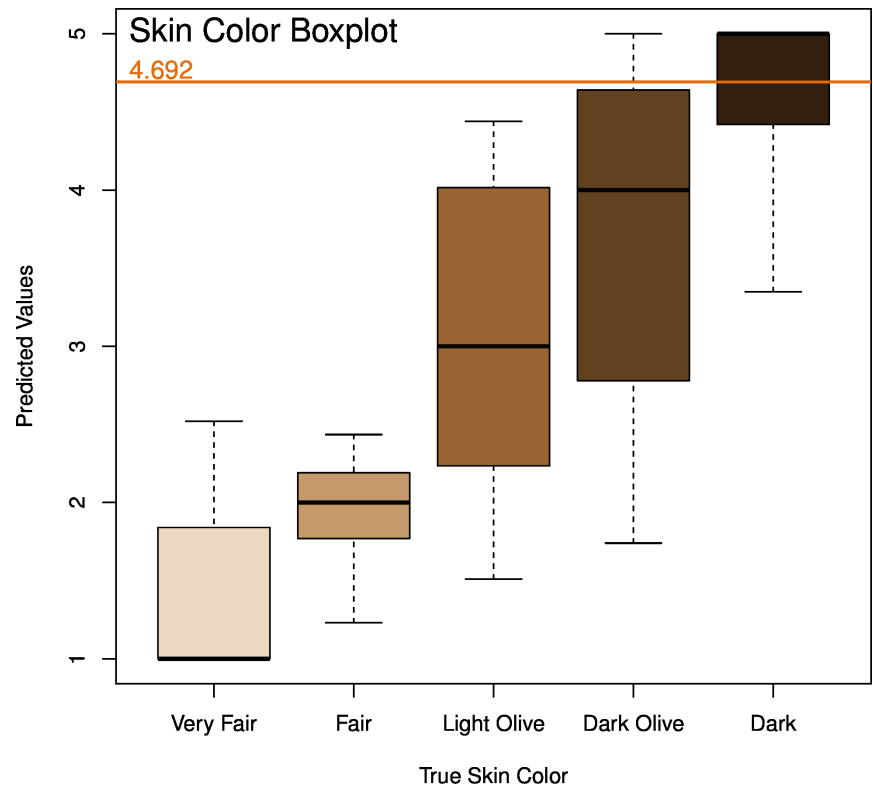In the range of previously observed prediction values for skin color, this value falls at 98.0%.

0%   98.0%

Based on these results, this subject:

- Has **Dark** skin color with 54.3% confidence
- Has **Dark or Dark Olive** skin color with 99.99% confidence
- Does <u>not</u> have **Very Fair** skin color with 99.99% confidence
- Does <u>not</u> have **Fair** skin color with 99.99% confidence
- Does <u>not</u> have **Light Olive** skin color with 99.99% confidence

Consistency of this value with the five possible trait values for skin color is shown below.

Skin Color Boxplot

Snapshot Prediction Results
Eye Color

Snapshot ™
DNA PHENOTYPING

Background

The eye color model is based on 2565 unrelated individuals from a range of ethnic backgrounds. The categorical trait values are coded from lightest to darkest, such that:

Blue	= 1
Green	= 2
Hazel	= 3
Brown	= 4
Black	= 5

The subject is predicted to have **eye color = 4.078**.

In the range of previously observed prediction values for eye color, this value falls at 93.3%.

0%   4.078   93.3%

Based on these results, this subject:

- Has **Brown** eye color with 52.0% confidence
- Has **Brown or Hazel** eye color with 56.2% confidence
- Does not have **Blue** eye color with 99.99% confidence
- Does not have **Green** eye color with 99.99% confidence

Consistency of this value with the five possible trait values for eye color is shown below.

Predictions

Eye Color
Consistency Values

Blue	0.0%
Green	0.0%
Hazel	48.0%
Brown	96.1%
Black	43.8%

Eye Color Boxplot

Snapshot Prediction Results
Hair Color

Snapshot
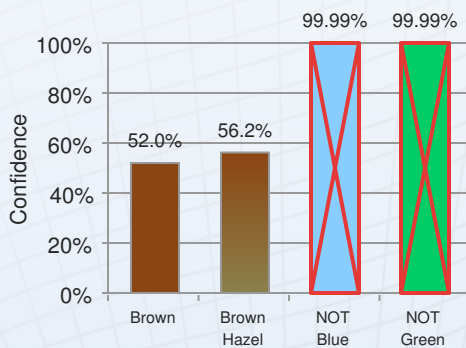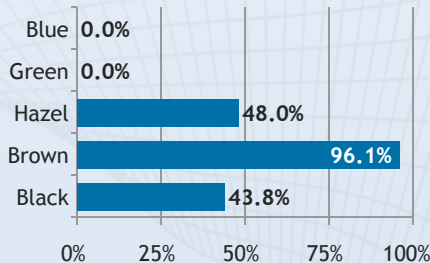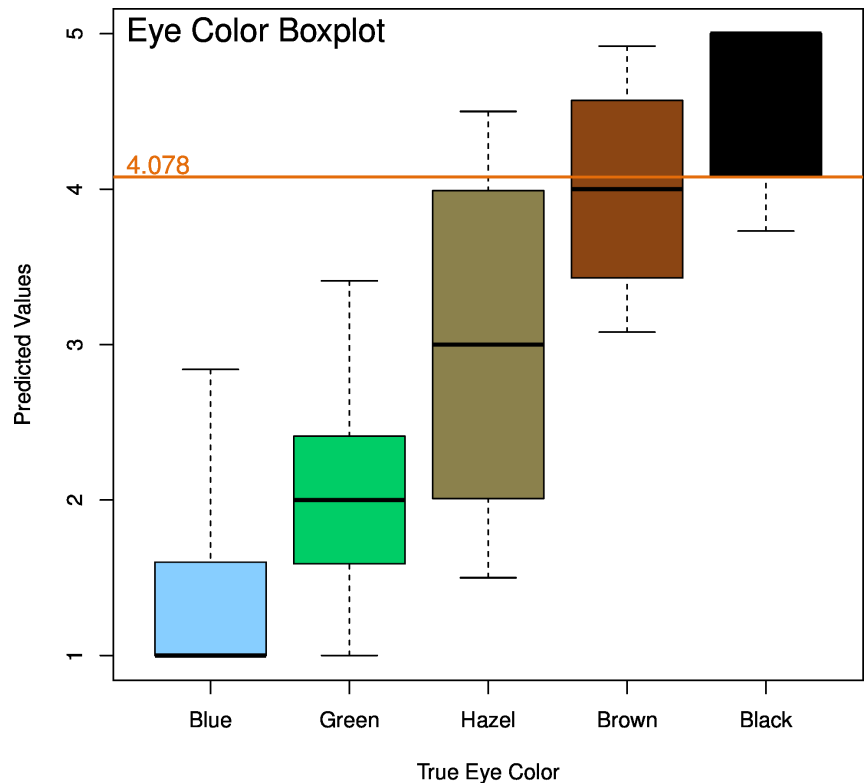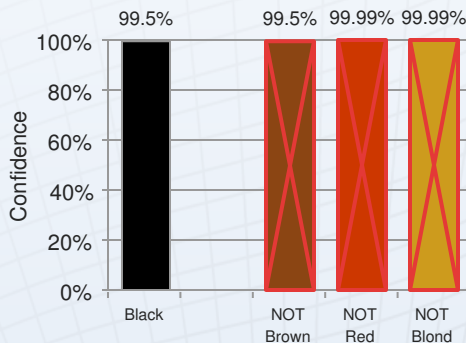DNA PHENOTYPING™

#OPD-FL-2001-380051-Snapshot
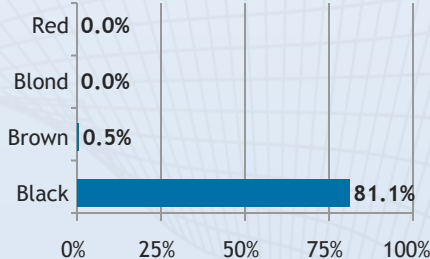PNL Document #15K11P55-5BE8XMUM9E

Background

The hair color model is based on 2534 unrelated individuals from a range of ethnic backgrounds. The categorical trait values are coded from lightest to darkest, such that:
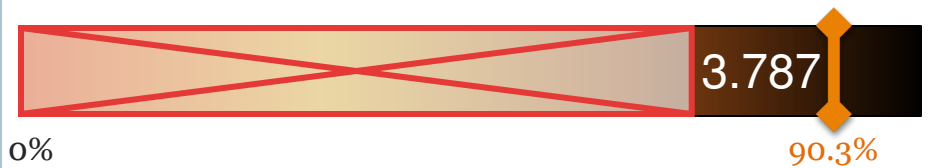
Red	= 1
Blond	= 2
Brown	= 3
Black	= 4

The subject is predicted to have **hair color = 3.787**.

In the range of previously observed prediction values for hair color, this value falls at 90.3%.

0%
3.787
90.3%

Based on these results, this subject:

- Has **Black** hair color with 99.5% confidence
- Does not have **Brown** hair color with 99.5% confidence
- Does not have **Red** hair color with 99.99% confidence
- Does not have **Blond** hair color with 99.99% confidence

Consistency of this value with the four possible trait values for hair color is shown below.

Predictions

Hair Color
Consistency Values

Red	0.0%
Blond	0.0%
Brown	0.5%
Black	81.1%

Hair Color Boxplot
3.787
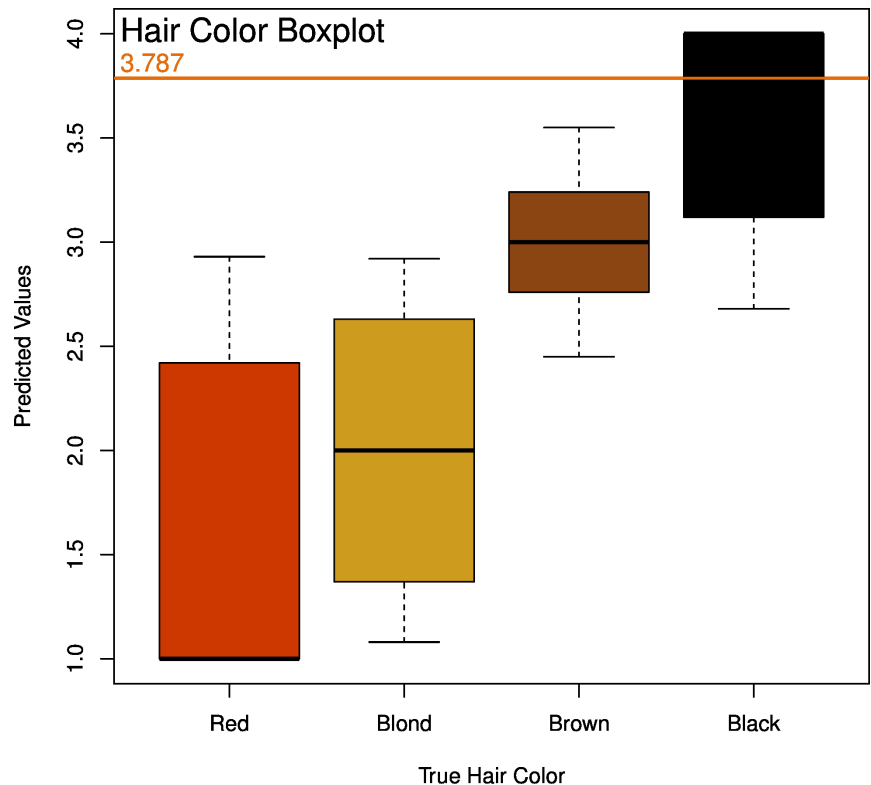
Snapshot Prediction Results
Freckles

Background

The freckles model is based on 581 unrelated individuals from a range of ethnic backgrounds. The categorical trait values are coded from lightest to darkest, such that:

Zero	= 1
Few	= 2
Some	= 3
Many	= 4

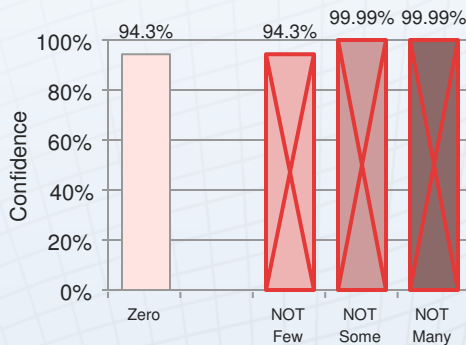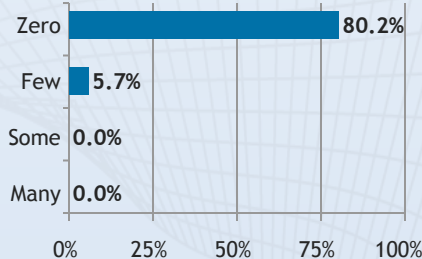The subject is predicted to have **freckles = 1.468**.

In the range of previously observed prediction values for freckles, this value falls at 18.9%.

1.468

0%   18.9%   100%

Based on these results, this subject:

- Has **Zero** freckles with 94.3% confidence
- Does <u>not</u> have **Few** freckles with 94.3% confidence
- Does <u>not</u> have **Some** freckles with 99.99% confidence
- Does <u>not</u> have **Many** freckles with 99.99% confidence

Consistency of this value with the four possible trait values for freckles is shown below.

Predictions

Freckles
Consistency Values

Zero	80.2%
Few	5.7%
Some	0.0%
Many	0.0%

Freckles Boxplot

1.468
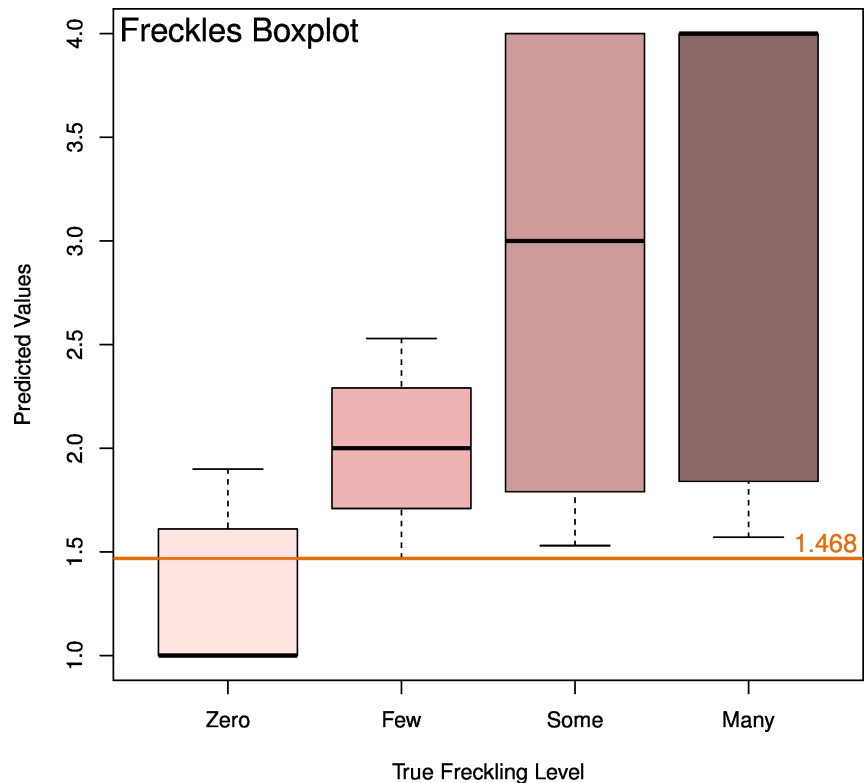
Snapshot Prediction Results
Genomic Ancestry #OPD-FL-2001-380051-Snapshot

The genome for this subject best matches African-American ancestry. The evidence supporting this conclusion follows.

Partitioning this genome according to its proportional membership in the seven continental regions yields:

Region	Percent
Africa	90.2%
Europe	9.5%
Americas	**
Central Asia	**
East Asia	**
Middle East	**
Oceania	**

** - No significant ancestry from this population

On a global scale, this genome (crosshairs) clusters with known African and African-American individuals (red and blue points, respectively, on top right plot).

This subject shows primarily African ancestry with some European ancestry. These proportions are also shown on the map to the right. This ancestry is common in African-American individuals.

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Partitioning analysis within Africa and Europe yields the following results:

Region	Percent
Africa - West	82.07%
Europe - Southwest	4.57%
Europe - Northwest	3.59%
Europe - Southeast	3.07%

The individual shows ancestry primarily from West Africa. Various regions of Europe (Southwest, Northwest, and Southeast) each show very small contributions (less than 5% each). In the Snapshot ancestry database of nearly 10,000 subjects, this pattern is typically seen in African-American subjects.

The principal component plot at the left shows only subjects from Africa and Europe, as well as admixed individuals. It can be interpreted as showing increasing African ancestry from left to right. This subject (crosshairs) clusters with known African-American and African-Caribbean subjects (green points).

West Africa includes subjects from the Bambara, Dogon, Esan, Gambian, Mandinka, Mende, and Yoruba populations.

Population
- Africa–East
- Africa–Indigenous
- Africa–South
- Africa–West
- African–American
- African–Caribbean
- Europe–Caucasus
- Europe–Central_East
- Europe–Central_West
- Europe–East
- Europe–Northeast
- Europe–Northwest
- Europe–South
- Europe–Southeast
- Europe–Southwest

Below is the predicted face for this subject from the front and from the side. This prediction was compared to the average predicted face for subjects with the same sex and ancestry. The heat maps show how the predicted face differs from this average face in area and X, Y, and Z displacement. In all heat maps, red indicates an increase in value of the prediction as compared to the average, and blue indicates a decrease. X displacement is relative to the center of the face — i.e., red means farther from the center — whereas Y displacement is relative to the bottom of the chin.
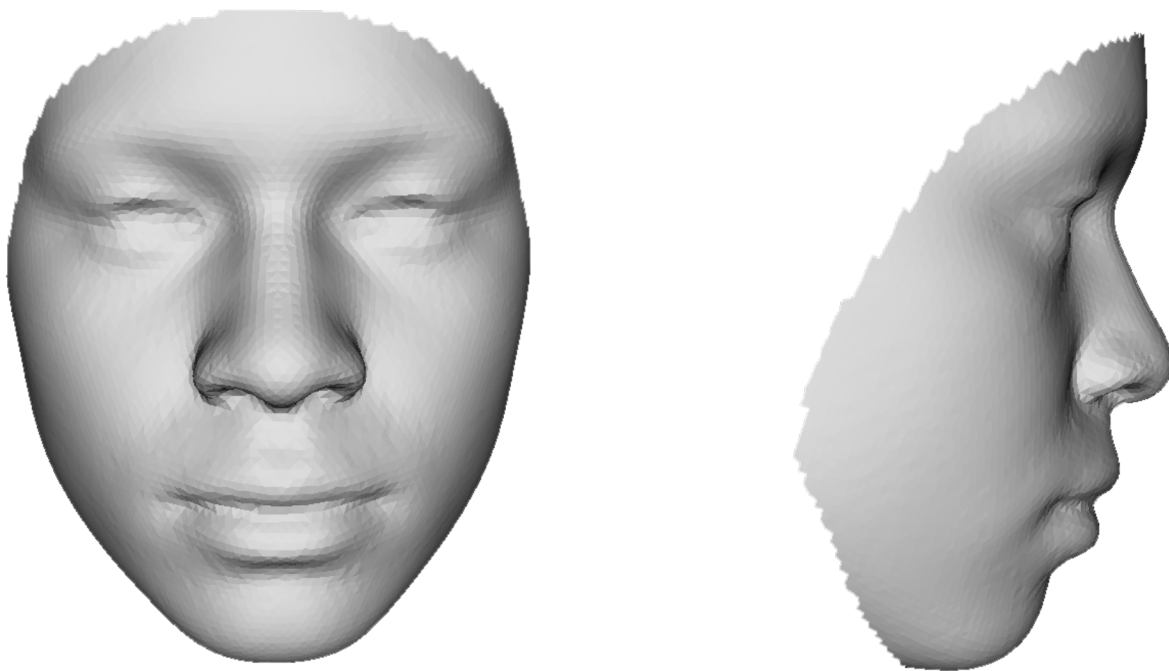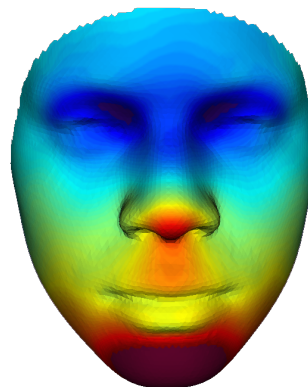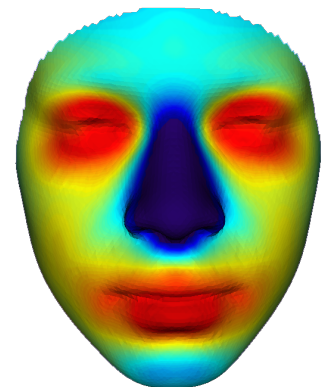
Predicted face for this subject
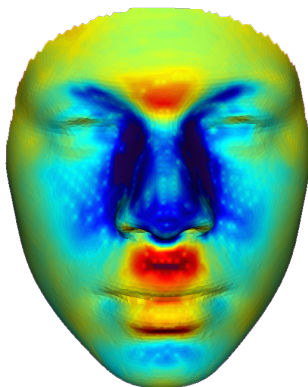
Area: Larger mouth and brow; smaller nose and eyes
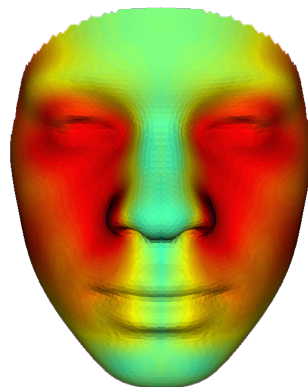
X Displacement: Wider face, mouth, nostrils, and jaw; slightly narrower chin

Y Displacement: Shorter chin; higher nose tip; lower eyes and brow

Z Displacement: More protruding eyes and mouth; flatter nose and chin

Magnitude

Relative to the average male with African ancestry

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Snapshot Prediction Results
Composite Profile

Width
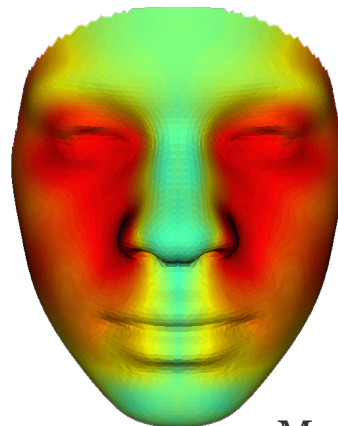
Depth
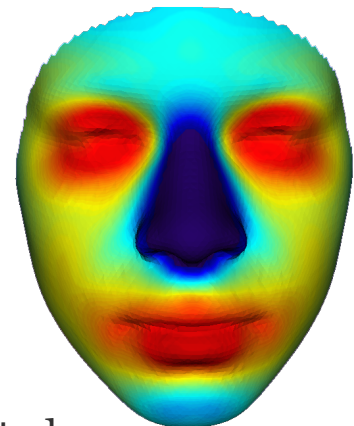
Magnitude

Wider face, nostrils, mouth, and jaw; shorter chin; more protruding eyes and mouth with a flatter nose

Predicted (⬛) & Excluded (⊠) Phenotypes

Skin Color   98.0

Dark / Dark Olive (99.99% confidence)
NOT Very Fair / Fair / Light Olive (99.99% confidence)

Eye Color   93.3

Brown / Hazel (56.2% confidence)
NOT Blue / Green (99.99% confidence)

Hair Color   90.3

Black (99.5% confidence)
NOT Brown / Red / Blond (99.5% confidence)

Freckles   18.9

Zero (94.3% confidence)
NOT Few / Some / Many (94.3% confidence)

Sex: Male ♂
Age: Unknown
(Composite shown at age 25)
Body Mass: Unknown
(Composite shown at BMI 22, Normal)
Ancestry: African-American

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Snapshot Prediction Results Disclaimer

The Parabon® Snapshot™ DNA Phenotyping Service provides predictions of human appearance from DNA. The Snapshot phenotype prediction models are derived from the application of statistical methods and machine learning algorithms to Parabon's reference database of genotype and phenotype (trait) information, which has been provided by self-consented individuals representing a diverse set of ancestry groups. The Snapshot composite images presented in this report are algorithmic predictions of face morphology, based on the sex, ancestry and genotype of the tested subject, onto which individually predicted pigmentation traits are superimposed. The shape of the head is inferred from the predicted face shape and ear shape is currently not predicted. The predictions depict the tested subject at approximately twenty-five (25) years of age and average body-mass index (BMI), unless otherwise indicated. Trait variations due to age, weight, or personal choice, such as dyed hair or facial hair, are not captured.

The Snapshot reference database and the Snapshot prediction models derived therefrom do not represent the full range of human genetic diversity, as they do not include subjects from all human populations and necessarily reflect only a subset of the total genetic variation within any given population. Moreover, environmental factors, such as nutrition, can affect appearance in ways that are inherently unpredictable. Accordingly, discretion should be used when attempting to include or exclude individuals in an investigation by comparison of appearance with Snapshot predictions. Mixture deconvolution is under active development, and results are offered provisionally. Confidence intervals have been calculated using the corresponding subset of SNPs during cross-validation.

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Snapshot Prediction Results
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Snapshot
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