NOTICE: Contains Sensitive Information
For Lead Generation Only

Parabon® Snapshot® Phenotype Report

Snapshot #SAMPLE

Agency Case #: SAMPLE

DNA Vial #: SAMPLE

Report Preparation Date: 01 Jan 2024

PNL Document #15B13K10-814

Snapshot® DNA ANALYSIS

Snapshot Prediction Pipeline Assembly Software v6.3.5

PARABON® NANOLABS

Snapshot Prediction Results
Introduction

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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

19.2 ng of DNA was extracted from a saliva sample from the rim of an empty water bottle, and 2 ng was subsampled for SNP genotyping on the Illumina OmniExpressExome chip. The overall genotyping call rate for this sample was 97.0%. Within the SNPs needed for Snapshot, 97.4% had called genotypes. Confidence intervals were calculated using this same set of SNPs.

Based on the SNPs available on this chip, this individual's most likely Y chromosome haplogroup is E1b1b1b, which is most common in North Africa.

The genetic genealogy (GG) assessment resulted in top matches sharing 100 cM with the subject in FTDNA and 120 cM in GEDmatch. A centimorgan (cM) is a measure of genetic distance. Closer relatives share larger amounts of DNA (more cM). Based on an expert assessment of the match results, this sample was assigned a Level 4 on Parabon's genetic genealogy assessment scale. Please see pages 4-6 for a full description of the assessment levels. Based on this assessment, Parabon will proceed with genetic genealogy analysis.

Snapshot Prediction Results
Basic Ancestry

Snapshot DNA ANALYSIS

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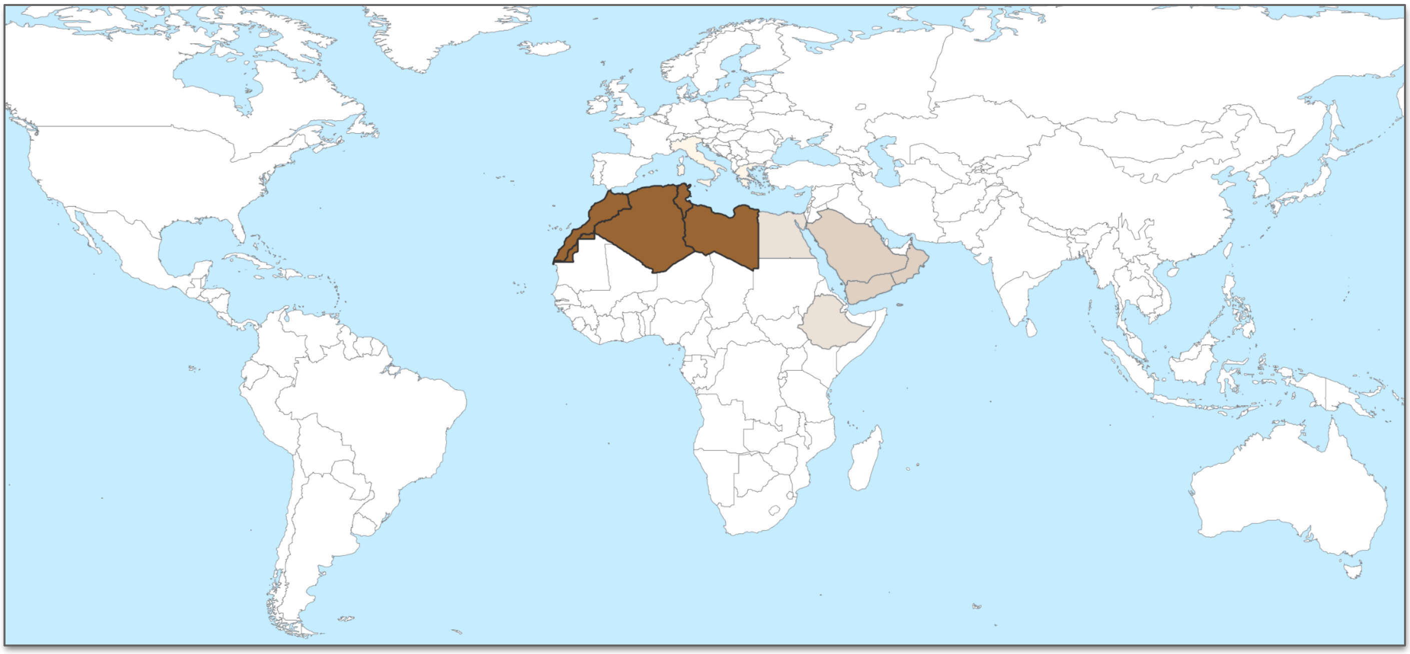
The map and tables below show this subject's predicted ancestry proportions (bottom left) and the populations in the Snapshot ancestry database where those proportions are most common (bottom right). Population similarity is expressed as the number and percentage of individuals in each population who have ancestry proportions similar to the subject. If no populations are listed, or all the percentages are small, the subject is likely admixed or from a population not yet sampled by Parabon.



Region	Percent
Middle East - NW Africa	60.32%
Middle East - Arabia	18.51%
Middle East - NE Africa	11.81%
Europe - South	5.26%

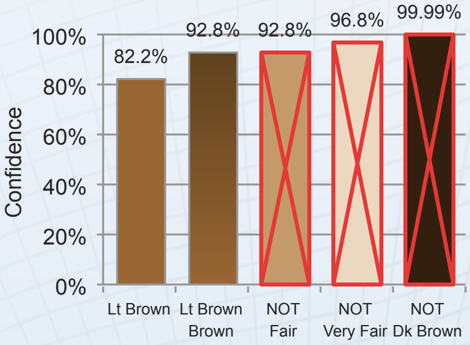
Population	Num	Percent
Middle East - NW Africa	18	10.30%

Snapshot Prediction Results
Skin Color

Background

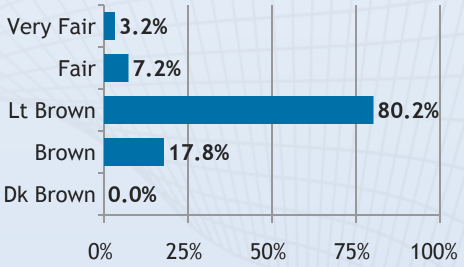
The skin color model is based on unrelated individuals from a range of ethnic backgrounds. Each subject's melanin index (M-index, a measure of the amount of light absorbed by skin, or skin darkness) was measured objectively using three separate measurements from a reflectance spectrophotometer on the forehead. Outlier values were discarded, and each subject's remaining measurements were averaged. Larger numbers mean darker skin color, with an overall range of 10.367 – 111.033.

Predictions



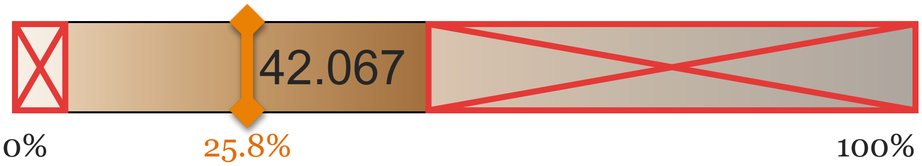
Skin Index

Consistency Values



The subject is predicted to have **M-index** = **42.067**.

In the range of previously observed prediction values for M-index, this value falls at 25.8%.

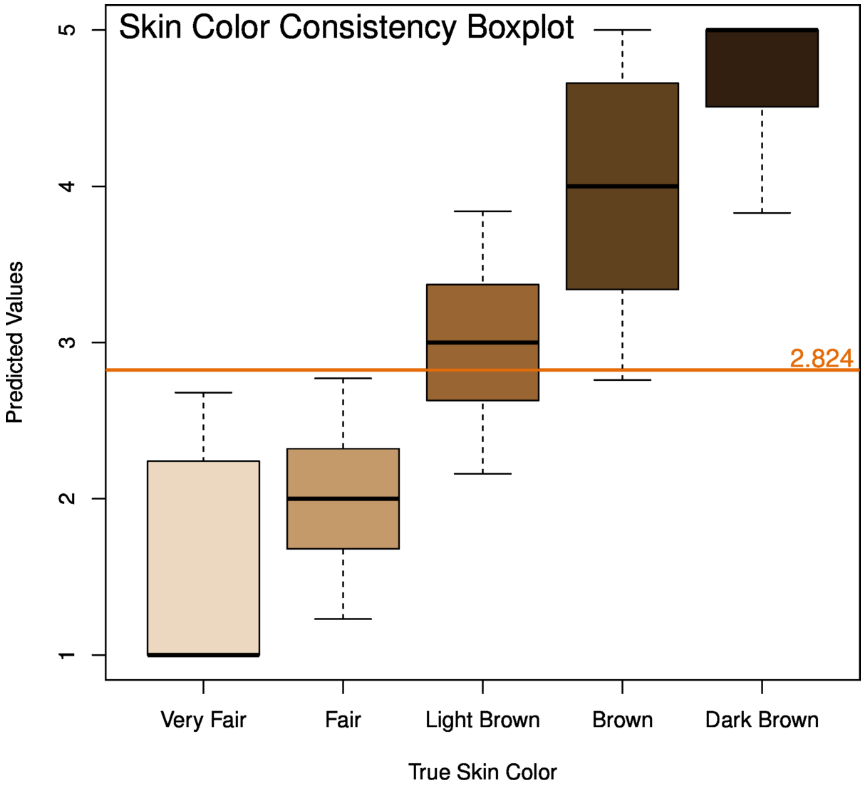


This M-index value corresponds to a skin color value of **2.824**.

Based on these results, this subject likely self-describes as:

- Has **Light Brown** skin color with 82.2% confidence
- Has **Light Brown or Brown** skin color with 92.8% confidence
- Does <u>not</u> have **Fair** skin color with 92.8% confidence
- Does <u>not</u> have **Very Fair** skin color with 96.8% confidence
- Does <u>not</u> have **Dark Brown** skin color with 99.99% confidence

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



Snapshot Prediction Results
Eye Color

Snapshot DNA ANALYSIS

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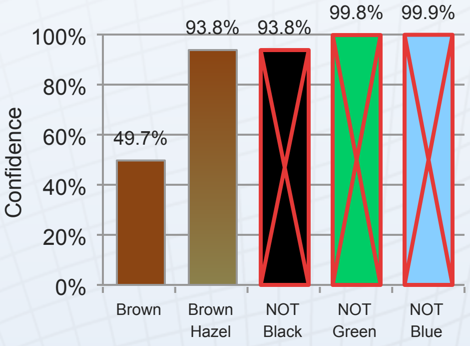
Background

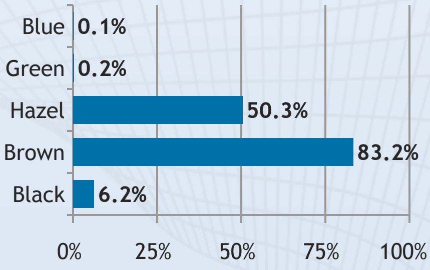
The eye color model is based on unrelated individuals from a range of ethnic backgrounds. The categorical trait values are coded from lightest to darkest, such that:

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

Predictions



Eye Color
Consistency Values



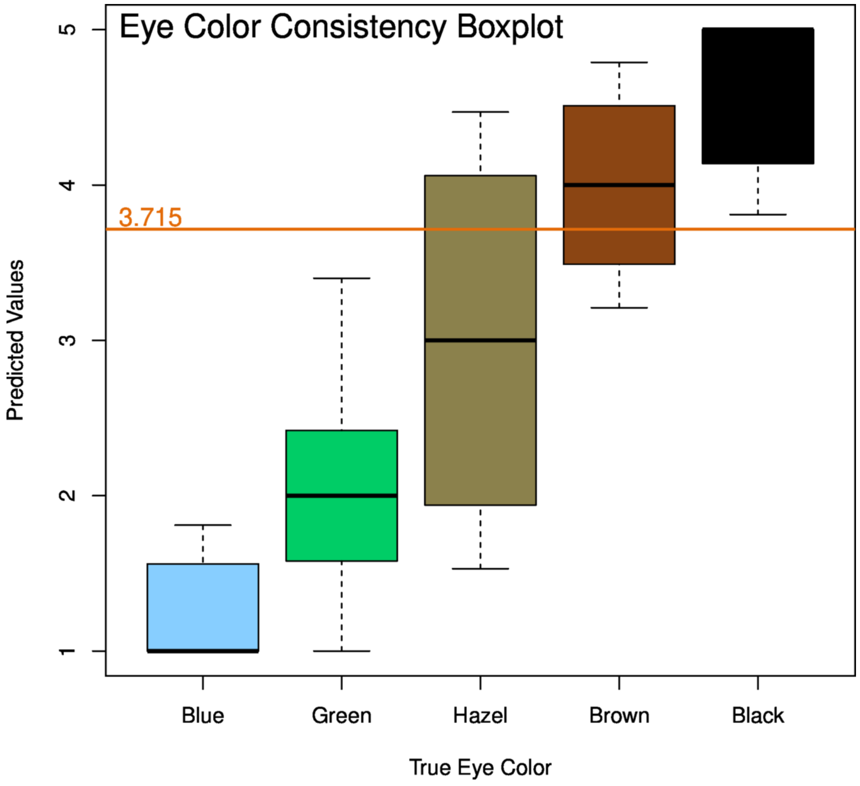
The subject is predicted to have **eye color** = **3.715**.

In the range of previously observed prediction values for eye color, this value falls at 82.1%.

Based on these results, this subject:

- Has **Brown** eye color with 49.7% confidence
- Has **Brown or Hazel** eye color with 93.8% confidence
- Does not have **Black** eye color with 93.8% confidence
- Does not have **Green** eye color with 99.8% confidence
- Does not have **Blue** eye color with 99.9% confidence

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



Snapshot Prediction Results

Hair Color

Snapshot #SAMPLE

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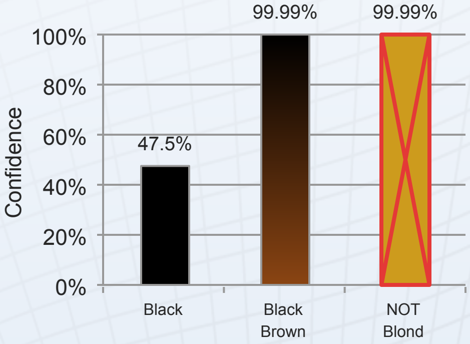
Background

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

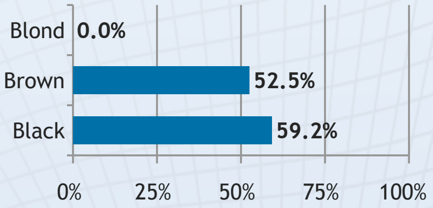
The hair redness model is also based on unrelated individuals. The binary trait values are coded as Red = 1 and Not Red = 0.

Predictions



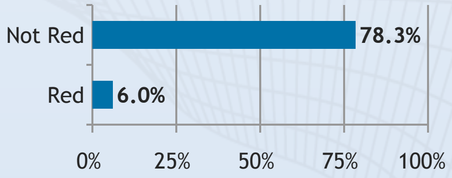
Hair Darkness

Consistency Values

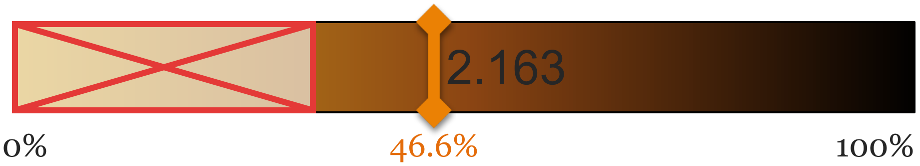


Hair Redness

Consistency Values



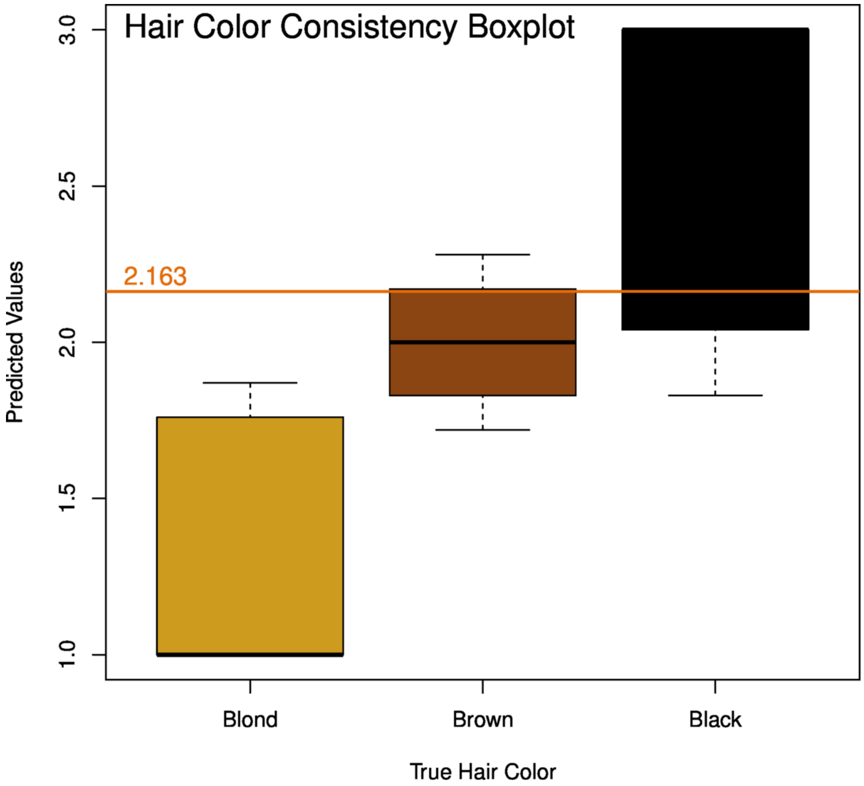
The subject is predicted to have **hair darkness** = **2.163**. In the range of previously observed prediction values, this falls at 46.6%.



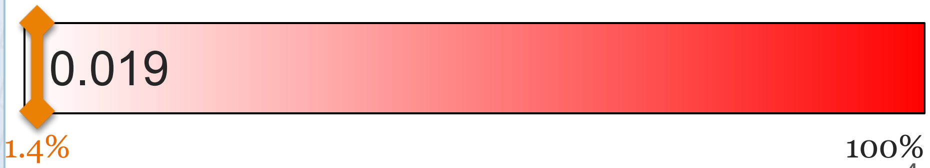
Based on these results, this subject:

- Has **Black** hair darkness with 47.5% confidence
- Has **Black or Brown** hair darkness with 99.99% confidence
- Does not have **Blond** hair darkness with 99.99% confidence

Consistency of this value with the three possible trait values for hair darkness is shown below.



The subject is predicted to have **hair redness** = **0.019**. In the range of previously observed prediction values, this falls at 1.4%.



Snapshot Prediction Results
Freckles

Snapshot #SAMPLE

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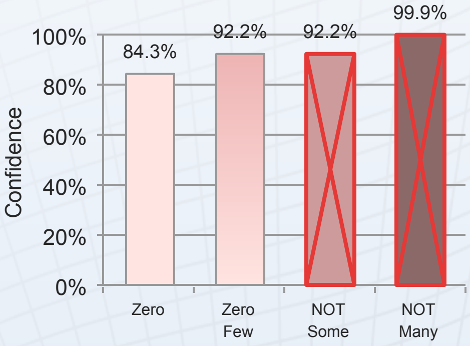
Background

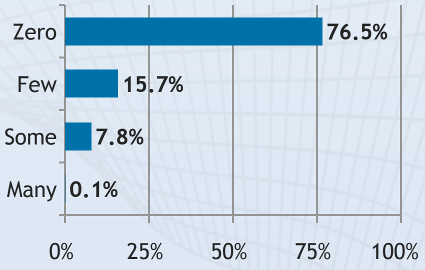
The freckles model is based on unrelated individuals from a range of ethnic backgrounds. The categorical trait values are coded from lightest to darkest, such that:

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

Predictions

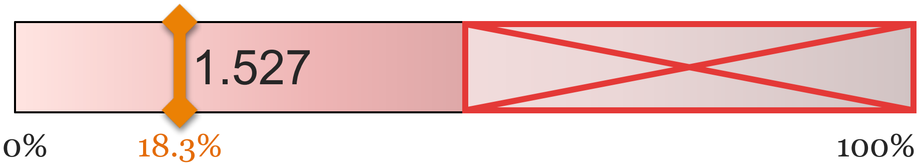


Freckles
Consistency Values



The subject is predicted to have **freckles = 1.527**.

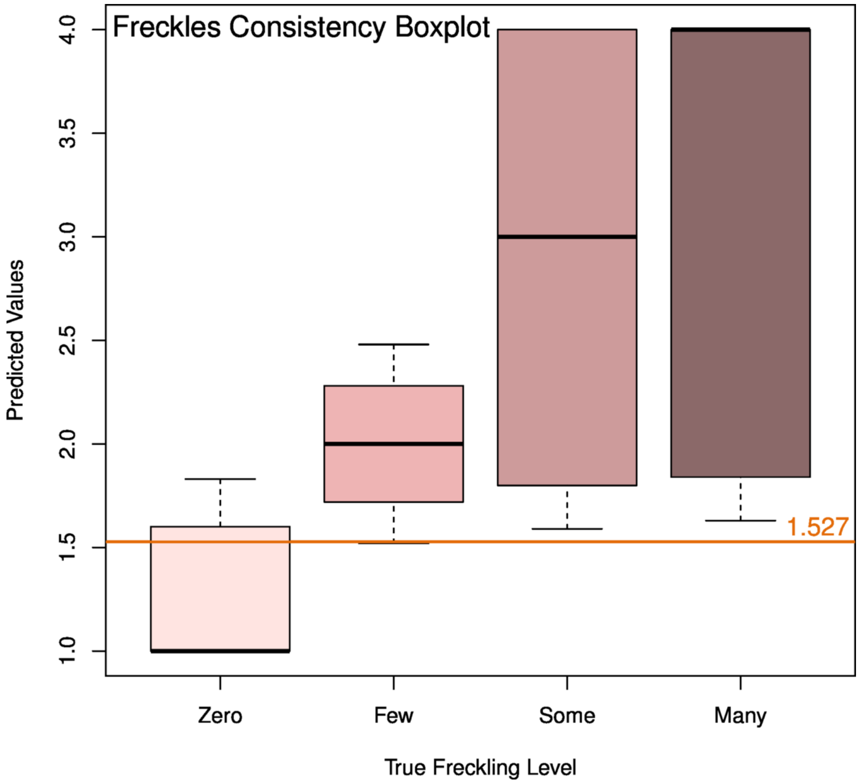
In the range of previously observed prediction values for freckles, this value falls at 18.3%.



Based on these results, this subject:

- Has **Zero** freckles with 84.3% confidence
- Has **Zero or Few** freckles with 92.2% confidence
- Does not have **Some** freckles with 92.2% confidence
- Does not have **Many** freckles with 99.9% confidence

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



Snapshot Prediction Results

Face Morphology

Snapshot #SAMPLE

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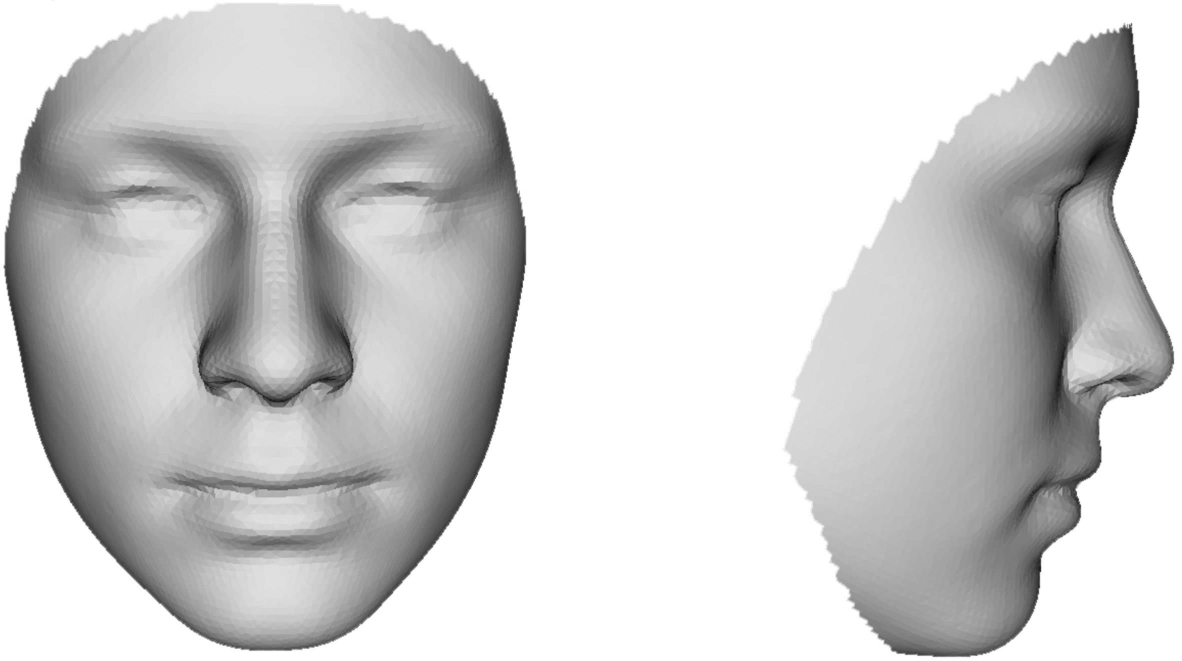
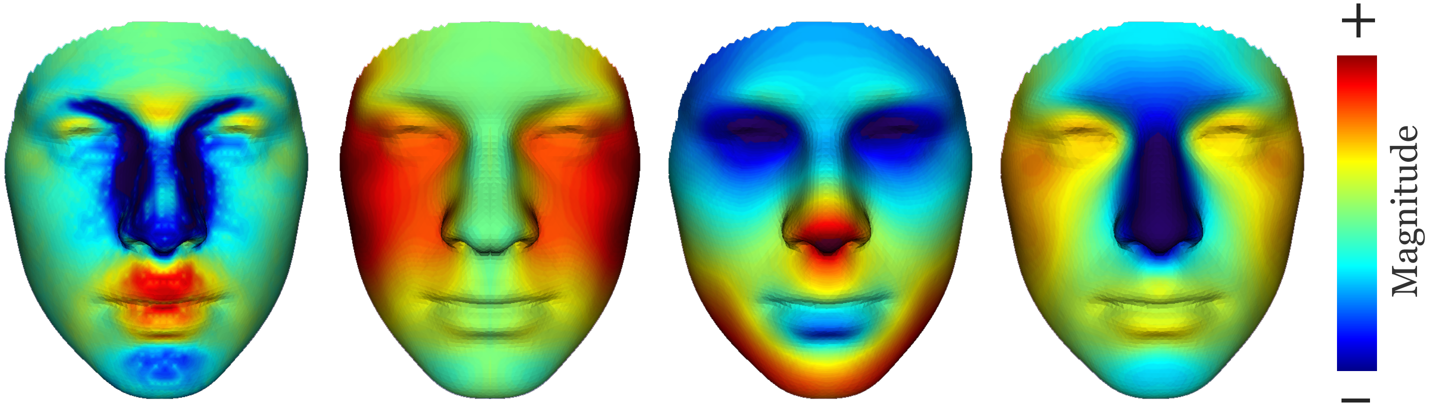
Below is the predicted face for this subject from the front and from the side. This prediction — which was generated using sex, ancestry, *and* thousands of SNP genotypes — was compared to a baseline prediction based *solely* on sex and ancestry. The heat maps at the bottom show how the subject's prediction differs from the simpler model in area and in X, Y, and Z displacement. In all heat maps, red indicates an increase in the value of the prediction as compared to this baseline face, and blue indicates a decrease. X displacement is measured relative to the center of the face, so red means "wider" and blue means "narrower". Y and Z displacement are measured absolutely — i.e., red means "higher" in Y and "more protruding" in Z.



Predicted face for this subject



Area
Red = Larger
Blue = Smaller

X Displacement
Red = Wider
Blue = Narrower

Y Displacement
Red = Higher
Blue = Lower

Z Displacement
Red = Protruding
Blue = Recessed

Relative to a face predicted using only matching sex and ancestry

Snapshot Prediction Results
Composite Profile

Snapshot #SAMPLE

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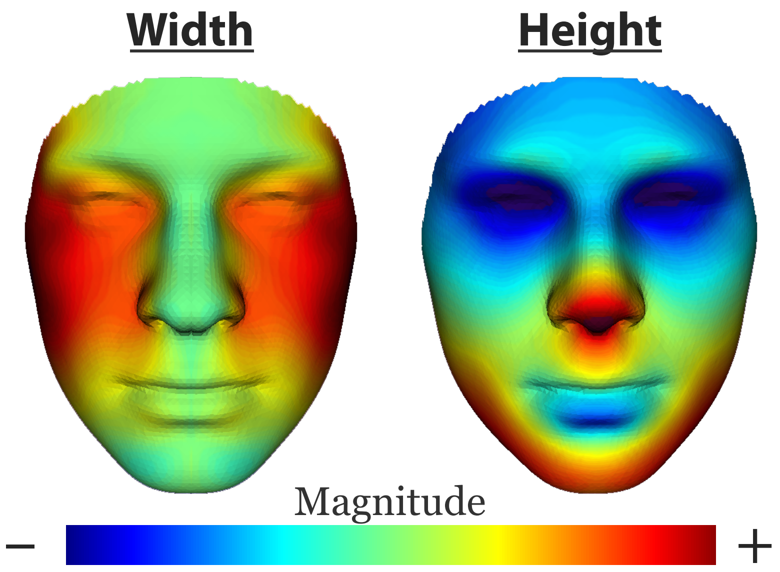
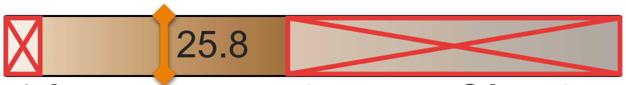


Face morphology differences are emphasized relative to a baseline face prediction made using only sex and ancestry.

Predicted (▨) & Excluded (☒) Phenotypes

Skin Color



Light Brown / Brown (92.8% confidence)

NOT Fair / Very Fair / Dk Brown (92.8% confidence)

Eye Color

Brown / Hazel (93.8% confidence)

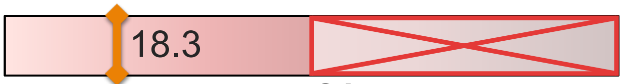
NOT Black / Green / Blue (93.8% confidence)

Hair Color

Black / Brown (99.99% confidence)

NOT Blond (99.99% confidence)

Freckles



Zero / Few (92.2% confidence)

NOT Some / Many (92.2% confidence)

Sex: Male ♂

Age: Unknown
(Shown at age 25)

Body Mass: Unknown
(Shown at BMI 22, Normal)

Ancestry: Middle Eastern from Northwest Africa

Snapshot Prediction Results

GG Assessment Guide

Snapshot #SAMPLE

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Your case has been assigned a Genetic Genealogy (GG) assessment level ranging from 1–5, depending on our estimation of whether it can potentially be solved using GG analysis — i.e., result in a list of highly promising candidate subjects — with one (1) being the most promising and five (5) being the least promising. This assessment is based on the match information currently available and could drastically improve if the data is uploaded to another database and/or new matches appear.

NOTE: The majority of Parabon's solved cases received an assessment of 4, and many cases that were originally assessed at level 5 became workable once new matches became available. Parabon's goal is to be as straightforward as possible about what kind of results you can expect to get in your case, and very few cases receive an assessment better than a 4.

1. **Extremely high probability**
2. **High probability**
3. **High probability of being solved by GG analysis, with some potential challenges**
4. **Medium probability of being solved by GG analysis with agency collaboration**
5. **Low probability of generating actionable information**

+ If your assessment includes a plus sign — e.g., "4+" — this indicates that your case is more promising than most cases at this level.

- If your assessment includes a minus sign — e.g., "4-" — this indicates that your case is less promising than most cases at this level. For these, additional research is needed to confidently determine if it belongs in this category or not.

e If your assessment includes an "e" — e.g., "4e" — this means that the subject was found to come from an endogamous population (one in which there has historically been a higher than average degree of intermarrying). Endogamy is the high background relatedness present in small, isolated populations, which increases the amount of DNA shared by unrelated people. This means that many of the matches are more distantly related than would be expected from the amount of shared DNA observed, decreasing the informativeness of each match.

Purpose of the Assessment, Unforeseen Challenges, and Results

Parabon's assessments are based on the number and relatedness of the matches found during the GG screening process and incorporate our experience with and considerations of working within specific population groups. These assessments are intended as estimates to help you decide whether or not to proceed, but they are not guarantees, as it is very difficult to know how challenging a case will be until significant genealogy work is undertaken. If you approve a GG analysis and we find unforeseen obstacles that halt our progress or otherwise cause a significant reassessment, we will inform you immediately, and you will only be charged a pro rata amount based on the time expended.

If you authorize Parabon to proceed with the GG research, Parabon's expert genetic genealogists will combine genetic analysis with traditional genealogical research to trace the family tree of the unknown subject. A custom report will be created for your case that includes a detailed summary of Parabon's research methods and findings. This may include family trees, common ancestors, contact information for distant and close relatives, names within the subject's family tree, proposed target testers, and, ultimately, the names of potential persons of interest. All cases come with the caveat that there is a chance that the subject may have been adopted, abandoned, or of unknown paternity, and that the subject's existence may be unknown to those with whom there is a close genetic relationship.

For cases that are not solved, Parabon will continue to monitor the case on your behalf at no charge in the hope that closer matches will turn up over time as new people join the genetic genealogy databases. If new, promising matches appear, GG analysis for this case may become workable in the future.

Level 1: Extremely high probability of being solved by GG analysis

There is a very close relative — e.g., a child — in the GG database with an available name and family history. This case therefore has a very high probability of being solved — i.e., resulting in an identification of the person-of-interest.

Level 2: High probability of being solved by GG analysis

This case is expected to produce highly actionable information for your agency. It has an above average probability of identifying the unknown subject or narrowing down their identity to a list of possibilities from within a specifc extended family through GG analysis alone. This case has an above average probability of being solved (i.e., resulting in an identification of the person-of-interest).

Level 3: High probability of being solved by GG analysis, with some potential challenges

This case is expected to produce actionable information for your agency. It may even be possible to identify the unknown subject or narrow down their identity to a list of possibilities from within a specific extended family through GG analysis alone. However, this analysis has additional risk, either because 1) the number of unique, potentially informative matches is small, increasing the probability that detailed family information may not be discoverable — e.g., due to adoption — or, 2) a significant amount of family tree building will be required, which may not be able to be completed within a standard GG analysis.

Level 4: Medium probability of being solved by GG analysis with agency collaboration

This case was determined to be workable and may even be solvable with standard GG analysis alone. A collaborative investigation that combines Parabon's genetic genealogy expertise with your investigative capabilities is likely to generate actionable information for your case. We will begin GG analysis and produce the richest set of family trees possible with our resources to kickstart your investigation, often pausing research to produce an intermediate report and briefing with recommendations to more efficiently advance the case, including requesting assistance from you — e.g., searching records to which we do not have access.

After this research is concluded, we will write a summary report with our findings. This may include ancestors who have been identified for the person-of-interest, the likely regional origin of the subject, contact information for distant and/or close relatives, and/or surnames likely to be present in the subject's family tree. In many cases, we are even able to provide a list of one or more potential persons-of-interest. We will also provide concrete recommendations for how your agency can work with our genetic genealogists to continue this research, such as suggestions for contacting relatives and/or additional tests needed to include or exclude individuals and/or branches of the family tree. In such cases, **Snapshot DNA Phenotyping** and **Kinship Inference** services may optionally be employed to help significantly narrow the list of potentially included individuals.

Level 5: Low probability of generating actionable information

Based on our experience, an extraordinary level of effort would be required to make meaningful progress on this case, and the probability of failure is very high. Either the matches were all very distant, which implies that any common ancestor lived so long ago that there could be many thousands of living descendants, and/or the matches were not traceable, which could be due to factors such as adoption or recent immigration. However, if the data is uploaded to another database and/or new matches appear, this case could immediately become workable. This does not mean that Parabon does not want to work on this case, but rather that we believe it is in the agency's best interest to refrain from investing their resources in a full genetic genealogy analysis at this time.

It is highly likely that a large amount of time would be spent on this research with little in the way of results. However, there is a possibility that, with Parabon's GG expertise and your agency's investigative skills, we may be able to work together to generate useful information on this case. If you would like, You may choose to wait for better matches to appear — either from a new database or new matches uploading — or, upon your request, we can start with a preliminary GG analysis to more fully determine the amount of genealogical information available and establish the best path forward. The initial results will be delivered in a report with concrete recommendations for how we can collaborate with your agency to continue this research, if viable. As you use these recommendations to make progress, Parabon's genetic genealogists will be available to guide you and ensure you stay on the most efficient path.

Regardless, Parabon will continue to monitor the case on your behalf at no charge in the hope that closer matches will turn up over time as new people join the genetic genealogy databases. If new, promising matches appear, GG analysis for this case may become more workable in the future. If you would like to discuss how Parabon's **Snapshot DNA Phenotyping** or **Kinship Inference** services might assist you in your investigation, please contact a Snapshot Case Manager to discuss additional DNA analysis options.

Autosomal DNA Statistics

cM (centiMorgans)^		Percentage (%) of Shared DNA^^		Group	Relationship	Notes
Average	Range	Average	Range			
3,600		50%			Parent/Child	
3,600	2,300 – 3,900	50%	32% – 54%	Group A	Full Sibling	23andMe (FIR included)
2,650		37%				Ancestry, FTDNA, and GEDmatch (HIR only)
1,800	1,300 – 2,300	25%	18% – 32%	Group B	Half Sibling Aunt/Uncle/Niece/Nephew Double First Cousin Grandparent/Grandchild	3/4 Siblings^^^
900	575 – 1,330	12.5%	8% – 18.5%	Group C	First Cousin (1C) Half Aunt/Uncle/Niece/Nephew Great-Grandparent/Great-Grandchild Great-Aunt/Uncle/Niece/Nephew	
450	215 – 650	6.25%	3% – 9%	Group D	First Cousin Once Removed (1C1R) Half First Cousin (½ 1C) Half Great-Aunt/Uncle/Niece/Nephew	
224	75 – 360	3.125%	1% – 5%	Group E	Second Cousin (2C) First Cousin Twice Removed (1C2R) Half First Cousin Once Removed (½ 1C1R)	
112	30 – 215	1.56%	0.42% – 3%	Group F	Second Cousin Once Removed (2C1R) Half Second Cousin (½ 2C) First Cousin Three Times Removed (1C3R) Half First Cousin Twice Removed (½ 1C2R)	
56	0 – 109*	0.78%	0% – 1.52%	Group G	Third Cousin (3C) Second Cousin Twice Removed (2C2R)	~10% of 3Cs will not share DNA*
30	0 – 75**	0.4%	0% – 1%	Group H	Third Cousin Once Removed (3C1R) Other Distant Cousins	~50% of 4Cs will not share DNA**

^ cM = Ancestry.com & FTDNA
^^ Percentage of DNA = 23andMe
^^^ 3/4 Siblings are a combination of half-siblings and 1st cousins; FIRs are included.

Groups A & B: 99% within the ranges given
Groups C – I: 95% within the ranges given

Created by Christa Stalcup

Snapshot Prediction Results Disclaimer

Snapshot #SAMPLE

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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. Unless otherwise indicated, the predictions depict the tested subject at approximately twenty-five (25) years of age and average body-mass index (BMI). Trait variations due to age, weight, or personal choice, such as dyed hair or facial hair, are not captured. Mixture deconvolution determines the most likely genotype for the unknown contributor and is expected to achieve ≥99% accuracy. However, if an error occurs in a SNP that is significant for phenotyping, it could impact the predictions.

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. Confidence intervals have been calculated using the corresponding subset of SNPs during cross-validation.

Parabon® Snapshot® services ("Service" or "Services") provided by Parabon NanoLabs, Inc. ("Parabon") are subject to the following terms and conditions. *Last updated 7 Jun 2019.*

ACKNOWLEDGEMENTS
By requesting or ordering Services, whether acting individually or on behalf of your organization, you acknowledge the following: (1) You are responsible for knowing and complying with the laws of your jurisdiction, if any exist, pertaining to the use of DNA for the following forensic purposes: genetic genealogy, kinship inference, and phenotyping; and (2) the products resulting from the Services are strictly limited to reports in PDF format for genetic genealogy, kinship inference, and phenotyping ("Materials").

NO WARRANTIES
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PARABON MAKES NO REPRESENTATIONS OR WARRANTIES THAT THE SERVICES WILL BE UNINTERRUPTED OR THAT THE MATERIALS WILL BE ERROR-FREE.

LIMITATIONS AND INTENDED USE
Snapshot Materials are intended to help investigators operate more efficiently, for example, by providing information about an unknown subject that has the potential to generate new leads, narrow a suspect list, or jog witnesses' memories. It is your obligation, acting individually or on behalf of your organization, to use the information provided to you responsibly and only for lawful purposes.

IMPORTANT: Snapshot Materials are for **Lead Generation Only**.

Snapshot DNA phenotyping composites are provided as approximations of appearance that summarize predicted ancestry and traits. Because many environmental influences can affect an individual's appearance that are not contained within DNA (and thus cannot be predicted through DNA phenotyping), Snapshot composites cannot be expected to represent a subject's exact appearance. Examples of environmental influences that affect an individual's appearance include, but are not limited to age, weight, scars, exposure to smoking, exposure to sun, tattoos, hairstyles, and presence of facial hair.

By default, Snapshot composites are generated at a target age of 25 years and a body mass index (BMI) of 22, which is the average of the 'Normal' BMI range. However, if additional information about the lifestyle or age of the unknown subject is known, such information can be incorporated into a composite by Parabon's Forensic Art Department.

IMPORTANT: Snapshot composites are **NOT** intended for use with facial recognition software.

Furthermore, Snapshot composites must be used, at all times, in conjunction with their associated phenotype and ancestry predictions. Accordingly, Snapshot composites may NOT be distributed as standalone images ("faces"), either within your organization or externally to any third party.

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You acknowledge that the Materials are accessible by you via a web-based account. You are responsible for providing all hardware, system software, access devices, networks and telecommunications or other connections required to access the account and for paying all telephony, data transmission and other costs associated with such access. You are responsible for maintaining the confidentiality of your account password and you are solely responsible for all activities that occur through your account, including the activities of others, regardless of whether such activities are authorized. You agree to immediately notify Parabon of any breach or unauthorized use of your account. Parabon reserves the right to require you to alter your password if Parabon believes that your password is no longer secure. You agree that you will be solely responsible for any loss or damage you suffer as a result of your failure to adequately safeguard your account information.

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