## **NOTICE: Contains Sensitive Information**

# Parabon<sup>®</sup> Snapshot<sup>®</sup> Phenotype Report

#PBCSO-FL-05-056017-Snapshot

Agency: Palm Beach County Sheriff's Office

Agency Case #: 05-056017

Evidence ID #: 9Ds

**Report Preparation Date:** 21 Mar 2019

PNL Document #19C21M19-WK4FYT7S





## 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**

3.85 ng of DNA extracted from pubic hair was sent to AKESOgen for genotyping on the Illumina CytoSNP-850K chip. The overall genotyping call rate for this sample was 70.8%. Within the SNPs needed for Snapshot, 72% had called genotypes. Confidence intervals were calculated using this same set of SNPs.

The genetic genealogy (GG) assessment resulted in o promising matches from a genealogy perspective (> 300 cM of shared DNA; second cousin or closer) and o potentially helpful matches (70 cM - 300 cM; third cousin or closer). A centimorgan (cM) is a measure of genetic distance. Closer relatives share larger amounts of DNA (more cM).

This sample was assigned a Level 5 on Parabon's genetic genealogy assessment scale. Please see pages 3-5 for a full description of the assessment levels.

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## Snapshot Prediction Results Genomic Ancestry #P



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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
Europe - Southeast	57.88%
Europe - North	15.23%
Europe - Caucasus	13.19%
Europe - Northeast	11.18%

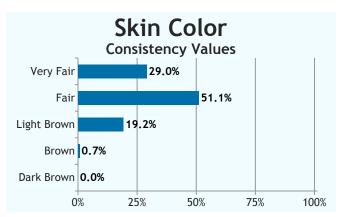
Population	Num	Percent
Europe - Central East	13	26.00%
Europe - Southeast	58	15.10%
Europe - Admixed	4	1.20%
Europe - Northeast	3	0.60%
Europe - North	3	0.40%
Middle East - North	1	0.20%

## Snapshot Prediction Results Pigmentation



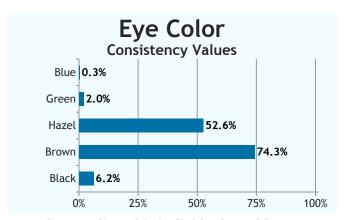
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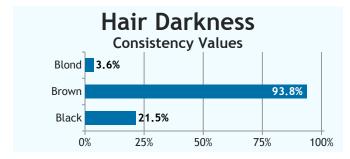
Snapshot predicts this individual would report their skin color as:

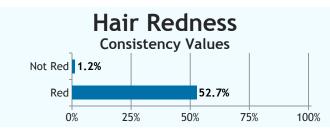
- Fair (71.0% confidence)
- Fair / Very Fair (80.8% confidence)
- **NOT Brown** (99.3% confidence)
- <u>NOT</u> Dark Brown (99.99% confidence)



Snapshot predicts this individual would report their eye color as:

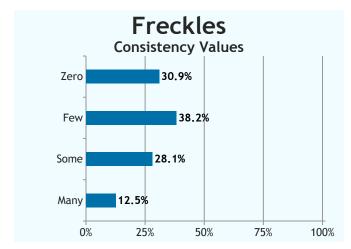
- **Brown** (47.4% confidence)
- Brown / Hazel (93.8% confidence)
- **NOT Black** (93.8% confidence)
- **NOT Green** (98.0% confidence)
- **NOT Blue** (99.7% confidence)





Snapshot predicts this individual would report their hair color as:

- **Reddish Brown** (78.5% confidence)
- Reddish Brown / Black (96.4% confidence)
- **NOT Blond** (96.4% confidence)



Snapshot predicts this individual would report their level of freckling as:

- Few (69.1% confidence)
- Few / Zero (71.9% confidence)

## Snapshot Prediction Results GG Assessment Guide #P



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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 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:

- 1. Extremely high probability
- 2. High probability
- 3. Medium probability
- 4. Low probability of being solved through GG, but likely to generate actionable info
- 5. Unlikely to generate 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 inter-marrying). 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 promising and potentially helpful matches found during the GG screening process. 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 summary of Parabon's research methods and findings, as well as sources and documentation to support the findings. This may include family trees, contact information for distant and close relatives, and/or names within the subject's family tree. All cases come with the caveat that there is a chance that the subject may have been adopted, abandoned, or of unknown paternity and 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.

## Snapshot Prediction Results GG Assessment Guide #P



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## 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: Medium probability of being solved by GG analysis

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 likely will not be able to be completed within a standard GG analysis.

Level 4: Low probability of being solved by GG analysis, but likely to generate actionable info This case was determined to be workable, but highly unlikely to be solvable with standard GG analysis alone. However, 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 start with GG analysis and produce the richest set of family trees possible with our resources to kickstart your investigation. Periodically, we will ask you for information to advance the GG analysis — e.g., searching records to which we do not have access.

After this initial research, we will write a report with our findings, such as a 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. We will also provide concrete recommendations for how your agency can work with our genetic genealogists to continue this research, such as regions to target when asking the public for information, scripts for contacting relatives, and/or additional tests needed to include or exclude 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 matching individuals.

## Level 5: Unlikely to generate actionable information from GG analysis

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, or all closer matches lacked sufficient family history information to build a viable family tree, which could be due to factors such as adoption or recent immigration.

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, we can start

## Snapshot Prediction Results GG Assessment Guide #P



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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. 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%	3270 - 5470	Group A	run Sibiling	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	o – 75**	0.4%	0% – 1%	Group H	Third Cousin Once Removed (3C1R) Other Distant Cousins	~50% of 4Cs will not share DNA**

<sup>^</sup> cM = Ancestry.com & FTDNA

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

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Created by Christa Stalcup © 2016 The DNA Detectives

<sup>^^</sup> Percentage of DNA = 23andMe

<sup>^^ 3/4</sup> Siblings are a combination of half-siblings and 1st cousins; FIRs are included.

## Snapshot Prediction Results Disclaimer



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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. 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.

## **Snapshot Prediction Results**



**Terms of Service** 

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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.

Snapshot DNA Phenotyping composites are provided as approximations of appearance that summarize predicted ancestry and phenotypes. 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. Such environmental influences on 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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