TruDiagnostic™

The Epigenetic Company

Provider Summary Report

A *Glimpse* of Patient's Results
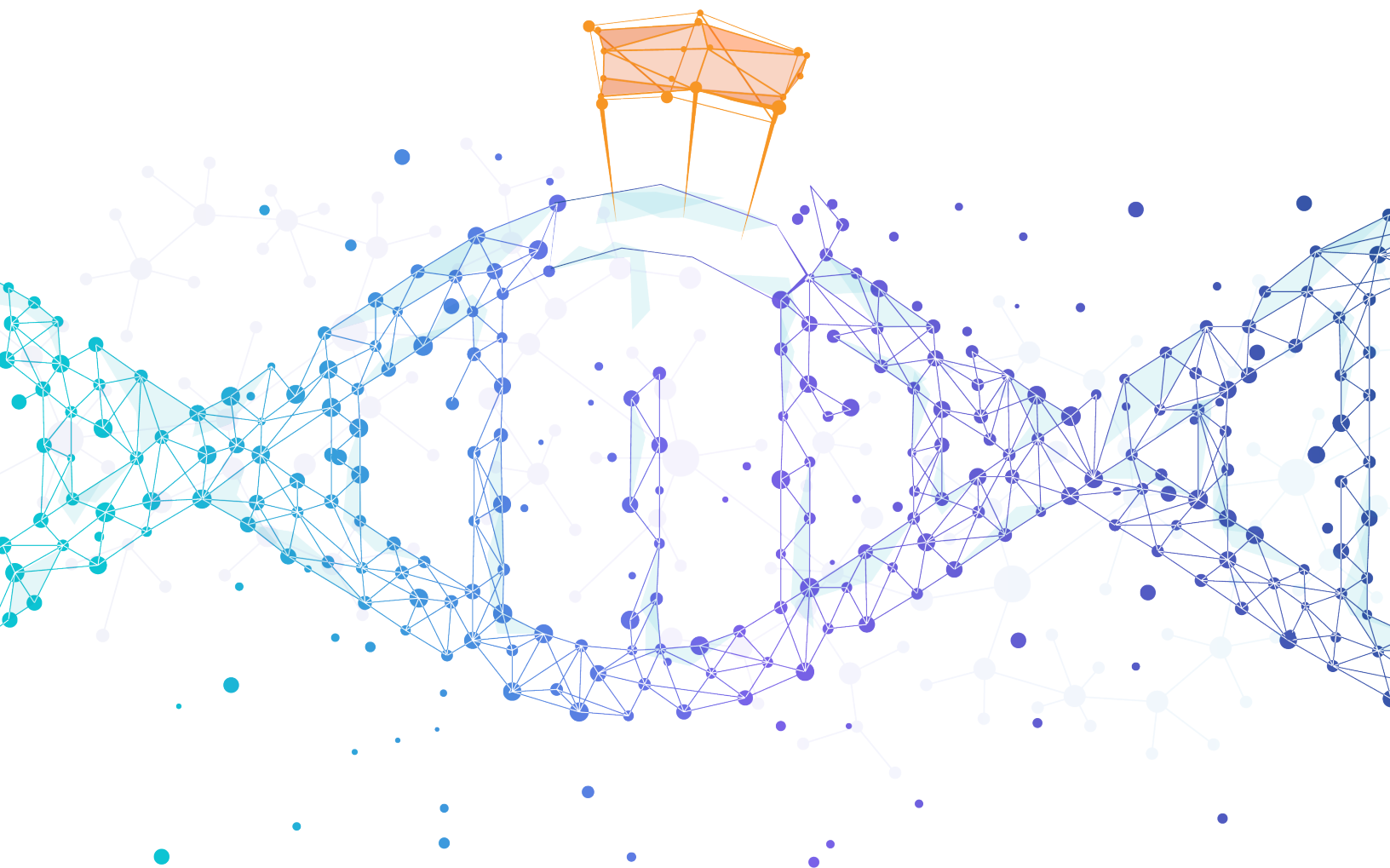
Click Here
to Log In to
Your Portal

KEY

— Population Median   ● Your Result

TruDiagnostic™
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Intrinsic Age

Intrinsic

42.50

3.49 Years

Chronological Age

39.01

Change Over Time
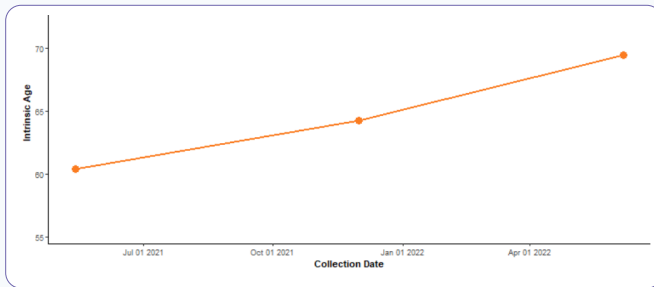
Population

Extrinsic Age

Extrinsic

41.50

2.49 Years

Chronological Age

39.01
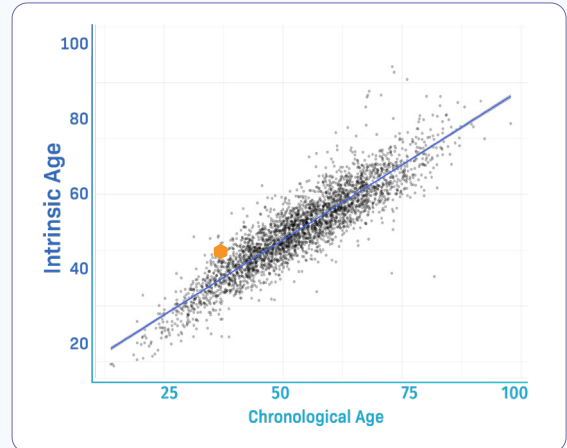
Population
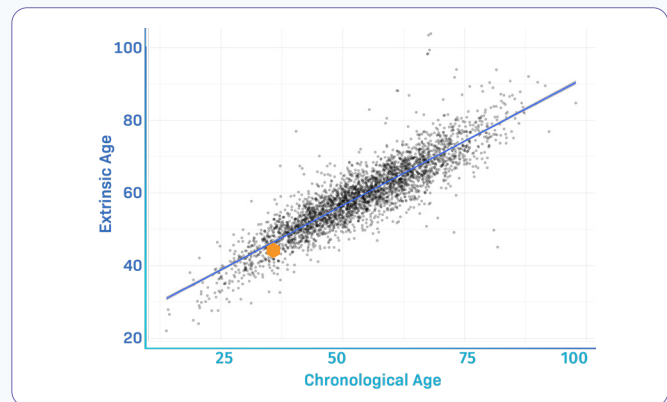
Immune Cell Measurement

Parameters	Reference Range	Percentage Values (%)
Bcell		0%
CD4T		17.47%
CD8T	20% to 40%	4.60%
NK		2%
Lymphocyte Total		24.07%
Neutrophils	40% to 60%	66.85%
Monocytes	2% to 8%	12.71%
Eosinophils	1% to 4%	0.93%
CD4T/CD8T Cell Ratio	1 to 4	4.25

Change Over Time
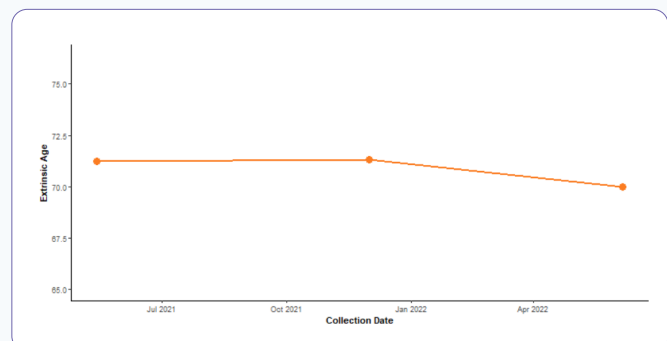
DunedinPACE

DunedinPACE Value

DunedinPACE Value:

1.05
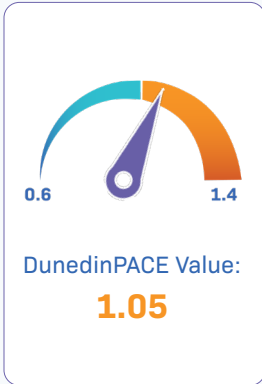
Population
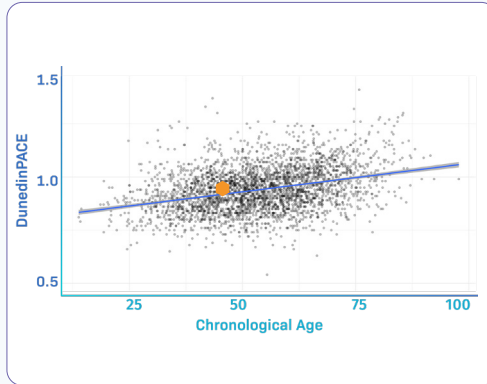
Change Over Time
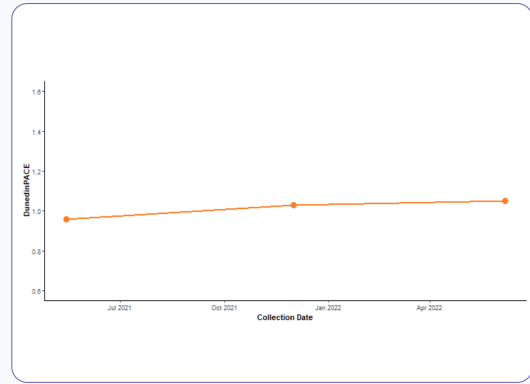
Algorithm	Patient Data	Morbidity and Mortality Associations	Risk Statement
DunedinPACE	**1.05** Biological years per year	**All-Cause Mortality** (Belsky et al., 2020)	If you are aging above a rate of 1.00, you would increase risk of death by 56% over the next 7 years.
		Chronic Disease (Belsky et al., 2020)	If you are aging above a rate of 1.00, you would increase risk of chronic disease diagnosis by 54% over the next 7 years.

The following graphs are **NOT** your personal data. These graphs are showing how the increased rate of aging affects performance from the Dunedin cohort.
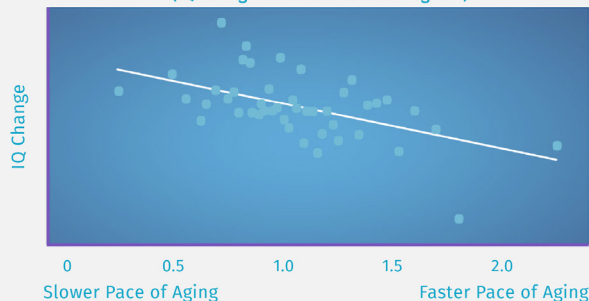
One-Leg Balance Test
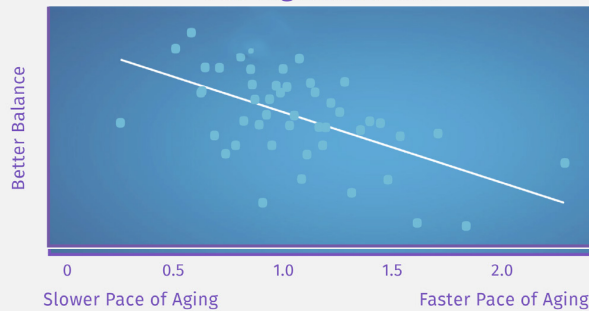
Grip Strength
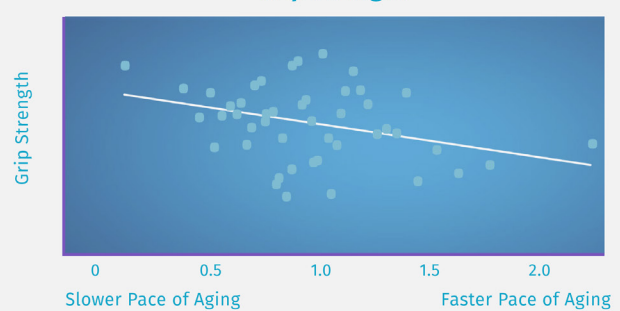
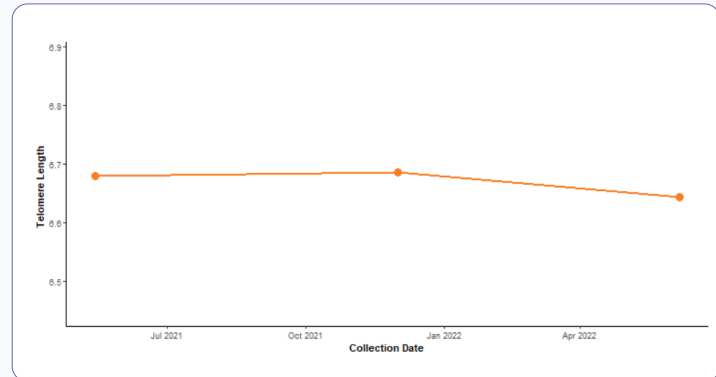### Cognitive Decline
(IQ Change from Childhood to Age 45)

Significant Variation in Facial Aging

Telomere Length

Change Over Time

Telomere Length
7.1
Kb

5   6   7   8
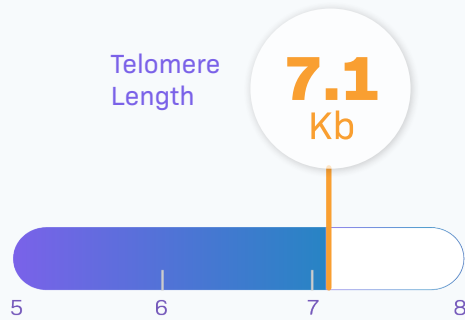
Telomere Length Based Biological Age Prediction
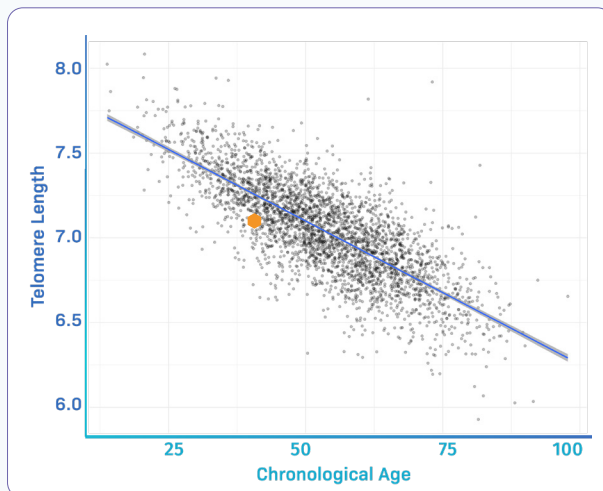
Your Average telomere prediction length:

7.1 kilobases (Kb)

Telomere length compared to population:

70th Percentile

Telomere length compared to people your age:

70% Longer

Algorithm	Patient Data	Morbidity and Mortality Associations	Risk Statement
Telomere	**7.1 Kilobase Unit**	Your Telomere length puts you in the **70th** percentile. This means that your telomeres are longer than **70%** of people your age.	Shorter telomeres are not only associated with age but with disease too. Shorter telomere length and low telomerase activity are correlated with several chronic preventable diseases.

Mitotic Clock

Cumulative number of stem cell divisions per stem cell per year:
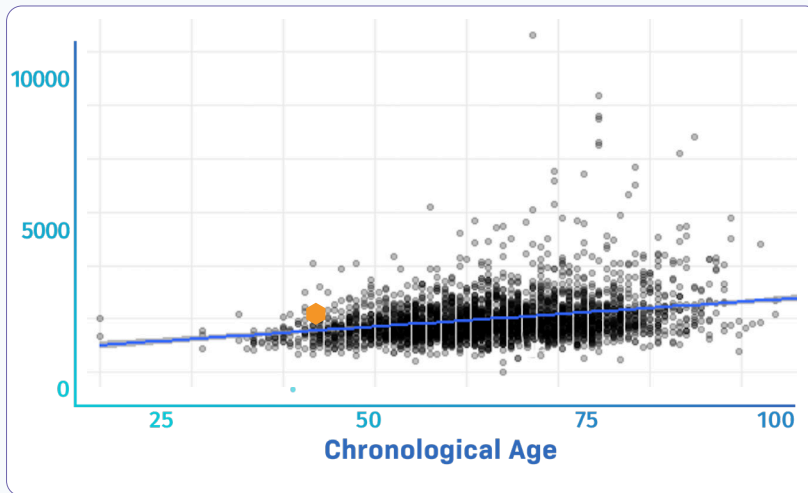
Stem cell divisions per stem cell per year:

3001

This puts you in the:

60th Percentile

Average estimate for the intrinsic rate of stem-cell division for the tissue:

Average estimate for intinsic rate of stem-cell division:

4004

This puts you in the:

50th Percentile

Loci Reports

Type 2 Diabetes Risk

ABCG1 (Cg06500161)
Average Beta Value:

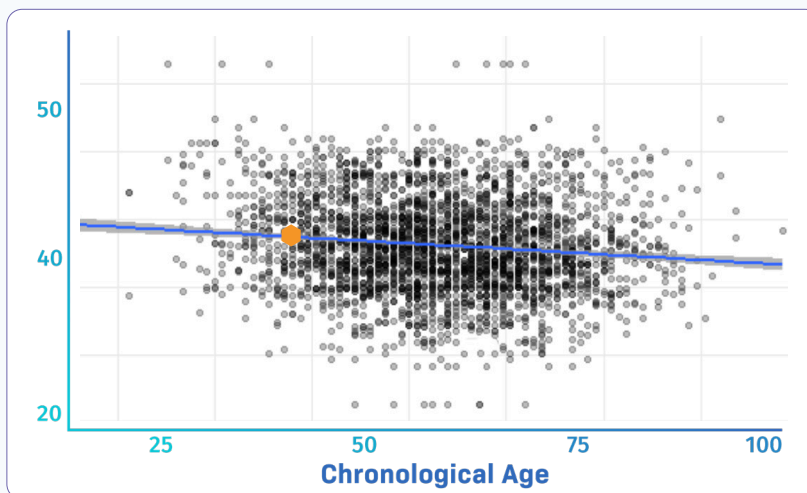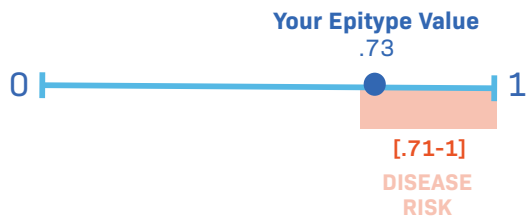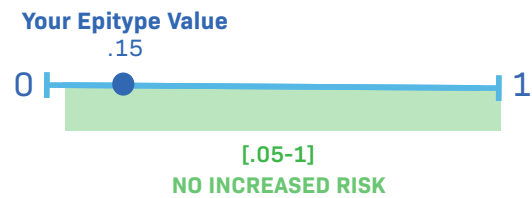**Your Epitype Value**
.73

0 |————————●————| 1

[.71-1]
DISEASE RISK

PHOSPHO1 (Cg02650017)
Average Beta Value:

Your Epitype Value
.15

0 |——●————————————| 1

[.05-1]
NO INCREASED RISK

Risk Report	Patient Outcomes	Summary	Impact	Additional Note
Type 2 Diabetes	**High Risk**	Your DNA methylation score was **0.73** at the ABCG1 locus and **0.15** at the PHOSPHO1 locus.	Your DNA methylation score at ABCG1 and PHOSPHO1 gives an indication of your level of risk for type 2 diabetes. If your score is 73% or greater at the ABCG1 locus, it is associated with a 9% increased risk for future type 2 diabetes occurrence. A DNA methylation score of 4% or greater at the PHOSPHO1 locus is associated with a 15% decreased risk for future type 2 diabetes occurrence.	DNA methylation at these loci is associated with cholesterol levels, triglyceride levels, ischemic stroke, and risk of T2D. Studies on these particular CpG loci have suggested that fasting and low carb diets can reduce methylation at these loci to lower your risk. Please consult your doctor to discuss this and more treatment options.

Loci Reports

Obesity Risk

FGFRL1 (cg25932599)
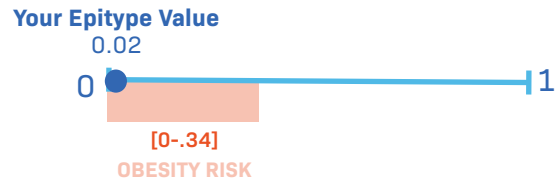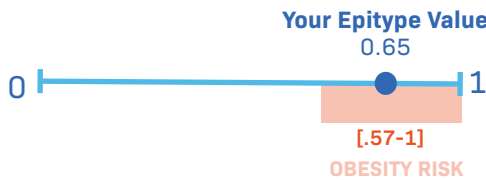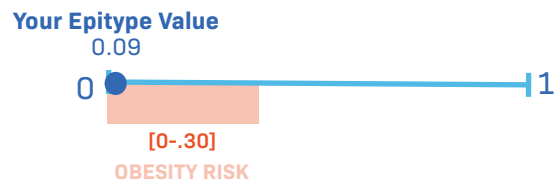### Average Beta Value:

Your Epitype Value
0.22

0 |——●——————————————| 1

[0-.24]
OBESITY RISK
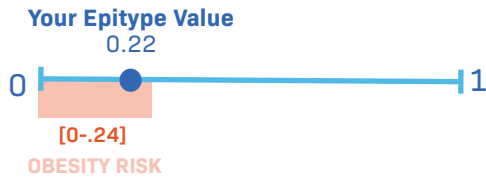
NCAPH2 (cg25152348)
Average Beta Value:

Your Epitype Value
0.02

0 |●——————————————————| 1

[0-.34]
OBESITY RISK

PNKD (cg22712983)
Average Beta Value:

Your Epitype Value
0.65

0 |———————————————●———| 1

[.57-1]
OBESITY RISK

SMAD3 (cg07576222)
Average Beta Value:

Your Epitype Value
0.09

0 |●——————————————————| 1

[0-.30]
OBESITY RISK

| Risk Report	Patient Outcomes	Summary	Impact	Additional Notes
Obesity	**High Risk**	Your DNA methylation score was **0.22** at the FGFRL1 locus, **0.02** at the NCAPH2 locus, **0.65** at the PNKD locus, and **0.09** at the SMAD3 locus.	Based on your DNA methylation scores at these four gene loci means that you are at **high risk** for developing obesity.	Many metabolic alterations, such as obesity, are due to the interplay between environmental, lifestyle, and genetic factors. The alteration of epigenetic mechanisms can modify the activity of genes related to metabolism that triggers metabolic disorders.

Weight Loss Response

	CpG site	Gene	ß-value Responders	Your Score	Response Status
1	cg15500865	PON3	0.072	0.63	Hypermethylated
2	cg25161512	PON3	0.115	0.111	Hypomethylated
3	cg11435506	PON3	0.165	0.161	Hypomethylated
4	cg03301582	PON3	0.120	0.117	Hypomethylated
5	cg08898155	PON3	0.163	0.167	Hypermethylated
6	cg04080282	PON3	0.324	0.321	Hypomethylated
7	cg26457160	PON3	0.490	0.494	Hypermethylated
8	cg10329418	PON3	0.252	0.250	Hypomethylated
9	cg27166921	PON3	0.253	0.251	Hypomethylated
10	cg24750391	PON3	0.355	0.359	Hypermethylated
11	cg08461772	PON3	0.418	0.417	Hypomethylated

| Risk Report	Patient Outcomes	Summary	Impact	Additional Note
Weight Loss Response	**Intermediate Response**	Your DNA methylation scores at the above loci indicate you are a **Intermediate Responder** for weight loss treatment utilizing a hypocaloric diet. This means a calorie deficit diet *passably works* as your weight loss strategy.	If your DNA methylation score puts you in the category of non-responder or intermediate responder then a hypocaloric diet might not be the best treatment option for you. If you are a responder, that means a hypocaloric diet has a greater chance of positively impacting your weight loss goals.	Studies on these particular CpG loci have concluded that some individuals have a better response to a calorie deficit diet than others. This may indicate why weight loss has been difficult to achieve and can provide insight into finding the best weight loss strategy.

Loci Reports

Smoking & Disease Risk

AHHR (cg05575921)
Average Methylation %:

Your Epitype Value
88%

0 ├─────────────────●────┤ 100

[64%-100%]
NO EPIGENETIC RISK
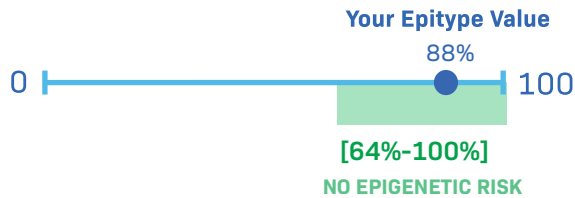
The impact that tobacco smoke exposure has on the epigenome is based on the level of methylation at the AHRR gene locus cg05575921.

Your DNA methylation score was **88%** at the AHRR locus, meaning that your methylation score aligns with the status of **non-smokers,** putting you at **low risk** for developing smoking-related conditions.

Alcohol Consumption and DNA Methylation
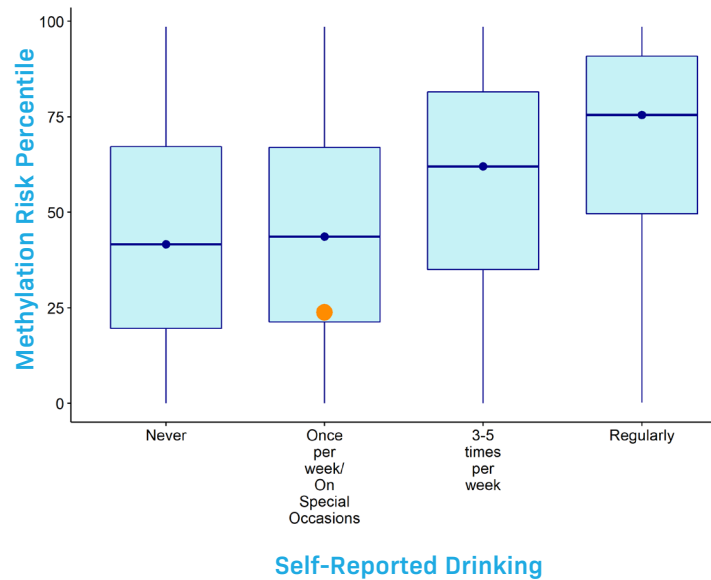
On your intake survey, you self-reported your drinking status as **3-5 Times Per Week**. With our custom methylation risk score, you are in the **80th** percentile. This means your score is higher than **80%** of the population we have tested.

Those who marked self-reported drinking as "Not Applicable" were assumed to have no drinking status and have been combined with data from "Never" status.