

# Salivary DNA Genotyping - Final Report

## **Study Objective:**

The goal of this project was to isolate high quality genomic DNA from 24 salivary samples and genotype them for several single nucleotide polymorphisms (SNPs) and variable number tandem repeats (VNTRs).

### Materials:

24 frozen SalivaBio Oral Swabs containing human saliva samples were received in swab storage tubes (SSTs). Saliva was tested for hormones prior to DNA isolation. The corresponding hormone testing roster number is XXXXX.

### Methods:

### DNA isolation from SalivaBio Swabs

A Salimetrics modified Genomic DNA extraction method was used to isolate DNA from saliva containing swabs. Swabs were centrifuged to remove saliva then incubated with Cell Lysis Buffer containing Proteinase K and incubated at 55 °C. After cell lysis, DNA was purified on PureLink genomic DNA silica based membrane columns. DNA was eluted from the columns using Tris HCI-EDTA, quantitated, and the purity and yield determined for each sample by measuring the absorbance of the purified DNA at A260 and A280 by spectrophotometry. Samples were aliquoted and stored at -20 °C until further analysis.



# Summary and Interpretation:

# **DNA** Isolation

DNA was successfully extracted from (24 of 24, 100%) saliva samples. The DNA quality and quantity data along with a summary of the genotyping results are represented Table2.

| Roster ID | Sample ID | Conc. (ng/uL) | 260/280 | 260/230 |
|-----------|-----------|---------------|---------|---------|
|           | 031       | 9.00          | 1.73    | 1.04    |
|           | 032       | 39.44         | 1.81    | 1.17    |
|           | 033       | 18.96         | 1.71    | 0.95    |
|           | 034       | 43.73         | 1.83    | 1.19    |
|           | 037       | 13.40         | 2.05    | 1.50    |
|           | 038       | 14.58         | 1.55    | 0.76    |
|           | 042       | 19.44         | 1.81    | 1.17    |
|           | 043       | 59.96         | 1.96    | 1.90    |
|           | 044       | 21.74         | 1.75    | 1.04    |
|           | 045       | 24.73         | 1.97    | 1.60    |
|           | 046       | 24.32         | 1.83    | 0.88    |
|           | 047       | 53.51         | 1.86    | 1.45    |
|           | 048       | 9.49          | 2.05    | 1.03    |
|           | 049       | 20.30         | 1.70    | 0.83    |
|           | 050       | 21.24         | 1.58    | 0.80    |
|           | 051       | 6.26          | 1.55    | 0.71    |
|           | 052       | 6.97          | 1.64    | 0.74    |
|           | 053       | 5.82          | 1.89    | 0.64    |
|           | 054       | 9.24          | 1.63    | 0.58    |
|           | 055       | 40.30         | 1.83    | 1.54    |
|           | 056       | 24.43         | 1.97    | 1.69    |
|           | 057       | 15.18         | 1.76    | 1.01    |
|           | 058       | 27.31         | 1.90    | 1.32    |
|           | 059       | 25.56         | 1.93    | 1.50    |

# Table 2. DNA data summary



## Footnotes:

Concurrent with the subject samples tested, several control samples were also assayed to provide data quality assurance. These controls include:

- "Empty" samples which are treated the same as all subject samples during extraction, but contain no saliva;
- For quality assurance, some samples may be repeated.

### **References:**

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