Report Contents

1. Coriell Personalized Medicine Collaborative Research Study Report. This report includes all data included in the clinical report as well as supplemental interpretations and educational material. This research report is based on Questionnaires Finalized on 08/01/2010

2. Clinical Report. This report was generated and approved by Coriell's CLIA certified genotyping laboratory.
Sample Results

CPMC Research Study Report

Name: STEVE CPMC  Gender: Male  
Date of Birth:  Date Collected: 11-30-2016  
Coriell ID: DEMOSTEVE  Date Received: 11-30-2016  
Lab Accessioning Number: DEMOSTEVE  Date of Report: 09-22-2011  
Ordering Physician: Dr. Edward Viner

Risk of Developing Rheumatoid Arthritis Based on:

- CPMC Rheumatoid Arthritis Variant 1 (rs6920220)
- Family History
- Smoking Status

The CPMC is a research study investigating the utility of personalized genomic information on health and health behavior. Most common health conditions are caused by an interaction between multiple genetic variants and non-genetic risk factors such as lifestyle and environment. The genetic variant risk in this report is based on one genetic variant, but does not represent your complete genetic risk for rheumatoid arthritis. These results were generated as part of this research study in a CLIA-approved laboratory.

More information about the study, how to interpret CPMC results, and how we calculate risk is available on our website http://cpmc.coriell.org or by contacting our genetic counselor. Participants may schedule an appointment with our board-certified genetic counselor through the web portal by clicking on "request an appointment". Our genetic counselor also can be reached by email at cpmgc@coriell.org or by phone at 888-580-8028.

This research report includes all data included in the clinical report as well as supplemental interpretations and educational material. Please see the report that follows for the official clinical report.
Rheumatoid Arthritis
Risk factors may be related to each other and risk estimates cannot be combined.
This graph provides a summary of the relative risks for one genetic variant, family history and smoking status.

<table>
<thead>
<tr>
<th>Chart Color</th>
<th>Relative Risk Due To:</th>
<th>Your Risk</th>
<th>Minimum Risk</th>
<th>Maximum Risk</th>
<th>Interpretation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genetic Variant</td>
<td>1.20</td>
<td>1.00</td>
<td>1.60</td>
<td></td>
<td>You have 1 copy of the non-risk variant and 1 copy of the risk variant. Based on this result, you are 20% more likely (or 1.20 times as likely) to develop rheumatoid arthritis as someone with no copies of this variant. <em>Having this risk variant contributes to your risk of rheumatoid arthritis.</em></td>
</tr>
<tr>
<td>Family History</td>
<td>3.00</td>
<td>1.00</td>
<td>9.30</td>
<td></td>
<td>Based on your family history, you are 3.00 times more likely to develop rheumatoid arthritis than someone who does not have a parent with rheumatoid arthritis. <em>Having a parent with rheumatoid arthritis contributes to your risk of rheumatoid arthritis.</em></td>
</tr>
<tr>
<td>Smoking Status</td>
<td>1.90</td>
<td>1.00</td>
<td>1.90</td>
<td></td>
<td>Because you are a current smoker you are 90% more likely (or 1.90 times as likely) to develop rheumatoid arthritis compared to former and never smokers. <em>Being a current smoker contributes to your risk of rheumatoid arthritis.</em></td>
</tr>
</tbody>
</table>

You reported you are a Caucasian man, between 65 and 74 years old; an estimated 7 in 10,000 Caucasian men in your age group have rheumatoid arthritis.
**Rheumatoid Arthritis**  
Risk Due To Genetic Variant #1 (rs6920220)  
Your Result: 1 copy of the non-risk variant and 1 copy of the risk variant were detected (GA)  
Non-Risk Variant = G   Risk Variant = A

<table>
<thead>
<tr>
<th>Chart Color</th>
<th>Your Risk</th>
<th>Minimum Risk</th>
<th>Maximum Risk</th>
<th>Interpretation</th>
</tr>
</thead>
</table>
| 1.20        | 1.00      | 1.60         |              | You have 1 copy of the non-risk variant and 1 copy of the risk variant. Based on this result, you are 20% more likely (or 1.20 times as likely) to develop rheumatoid arthritis as someone with no copies of this variant.  
*Having this risk variant contributes to your risk of rheumatoid arthritis.* |

Genetic Variant Risk is based on the number of copies of this genetic risk variant.  
People with one or two copies of the risk variant are compared to people with no copies of the risk variant to determine relative risk.  
A relative risk greater than 1.00 indicates an increased risk.

These results are based on a single study.
Based on your family history, you are 3.00 times more likely to develop rheumatoid arthritis than someone who does not have a parent with rheumatoid arthritis.

Having a parent with rheumatoid arthritis contributes to your risk of rheumatoid arthritis.

Risk is compared based on family history.

People with one or more parents or siblings with rheumatoid arthritis were compared to people with no parents or siblings with rheumatoid arthritis to determine relative risk of developing rheumatoid arthritis.

A relative risk greater than 1.00 indicates an increased risk.

These results are based on a single study.
Rheumatoid Arthritis
Risk Due To Smoking Status
You reported that you are a current smoker.

<table>
<thead>
<tr>
<th>Chart Color</th>
<th>Your Risk</th>
<th>Minimum Risk</th>
<th>Maximum Risk</th>
<th>Interpretation</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.90</td>
<td>1.00</td>
<td>1.90</td>
<td></td>
<td>Because you are a current smoker you are 90% more likely (or 1.90 times as likely) to develop rheumatoid arthritis compared to former and never smokers. Being a current smoker contributes to your risk of rheumatoid arthritis.</td>
</tr>
</tbody>
</table>

Risk is compared based on smoking habits.
People who are current smokers or former smokers are compared to people who have never smoked to determine relative risk.
A relative risk of greater than 1.00 indicates an increased risk.

These results are based on multiple studies.
Rheumatoid Arthritis - Variant #1 (rs6920220)

We all have 2 copies of every gene, one from each of our parents. Each copy may have small changes called genetic variants. Some genetic variants are associated with an increased risk of disease. Some genetic variants are associated with a decreased risk of disease.

Having one or two copies of this variant increases your risk for rheumatoid arthritis.

<table>
<thead>
<tr>
<th>How Common Is This Variant?</th>
<th>GG - 68 in 100 people have 2 copies of the non-risk variant</th>
<th>GA - 30 in 100 people have 1 copy of the non-risk variant and 1 copy of the risk variant</th>
<th>AA - 2 in 100 people have 2 copies of the risk variant</th>
</tr>
</thead>
<tbody>
<tr>
<td>Non-Risk Variant = G</td>
<td>Risk Variant = A</td>
<td>This frequency is based on data from European populations</td>
<td></td>
</tr>
</tbody>
</table>

Gene: near TNFAIP3  
Chromosome: 6q23
Rheumatoid arthritis can be caused by both genetic factors and non-genetic (or environmental) risk factors.

It is estimated that non-genetic factors (like smoking) account for about 47% of the risk of rheumatoid arthritis.

It is estimated that 53% of the risk for rheumatoid arthritis is based on genetic risk factors. This estimate accounts for both known and unknown gene variants.

There are many different genetic and non-genetic risk factors that contribute to the risk of rheumatoid arthritis. We are only able to tell you about your family history risk, 1 genetic and 1 non-genetic risk factor at this time.
Age and gender contribute to your risk of rheumatoid arthritis.

You reported you are a Caucasian man, between 65 and 74 years old; an estimated 7 in 10,000 Caucasian men in your age group have rheumatoid arthritis.
Limitations

Rheumatoid Arthritis

- This result alone does NOT diagnose rheumatoid arthritis. Rheumatoid arthritis must be diagnosed by your health care provider.
- This result does NOT mean that you have or will absolutely develop rheumatoid arthritis.
- This result does NOT mean that you will not develop rheumatoid arthritis in the future.
- This result ONLY assesses your risk for developing rheumatoid arthritis due to the factors presented in this report and does not mean that other genetic variants or risk factors for rheumatoid arthritis are present or absent.
- Personal risk factors, such as age, family history or lifestyle, may have a greater impact on your risk to develop rheumatoid arthritis than any individual genetic variant.
- Risk estimates are based on current available literature.
- Although rare, it is possible that you may receive an incorrect result; 100% accuracy of reported results cannot be guaranteed.
- Occasionally there may be a specific variant on a gene chip that is not able to be read or interpreted. In this case you will not receive a result for that variant. It is expected that you will receive results for about 95% of variants approved by the ICOB.
- Relative risks used to estimate risk of disease for CPMC participants are based on groups of people with the same risk or protective factor as the individual CPMC participant. In some cases, the relative risk is estimated based upon an odds ratio and known or assumed disease prevalence.
- Separate risk estimates for each risk or protective factor have been given. Risk or protective factors may be related to each other and risk estimates cannot be combined.
- Risk information for non-genetic factors is based on information you provided in your medical, family, lifestyle questionnaire. If you did not provide answers or if you answered “do not know”, risk estimates for some factors may not be available.
- Risk information for non-genetic factors is based on information you provided in your medical, family, lifestyle questionnaire and may not be reflective of your current risk if any of these factors have changed. You will be given the opportunity to update your medical, family and lifestyle questionnaire responses periodically.
- Every effort will be made to provide you with risk information based on your reported race/ethnicity. However, data may not be available for all races/ethnicities for all risk factors. Please see your individual results to determine which race/ethnicity the data given is based on.
- For some risk factors data may be provided by gender. Every effort will be made to provide you with risk information based on your reported gender. However, when risk data is not available for both genders, risk results for the available gender will be provided.
Methods

Rheumatoid Arthritis

This condition and genetic variant were approved by the Informed Cohort Oversight Board (ICOB)

Test Methodology
Saliva samples were collected using Oragene DNA Collection Kits (DNA Genotek) and DNA was extracted manually according to the manufacturer’s instructions. Purified DNA was quantified using UV absorbance at 260 nm. Five hundred nanograms of the resulting DNA from each sample were used as template in the Affymetrix Genome-Wide Human SNP Nsp/Sty 6.0 GeneChip assay. Data analysis was performed using Affymetrix Genotyping Console software.

See CPMC Technical Paper for genetic variant selection and reporting methodology.

[Risk interpretation based on Coriell's Rheumatoid Arthritis Risk Algorithm Version 1 (September 1, 2011)]


**Clinical Report for Rheumatoid Arthritis Genetic Variant 1 (rs6920220)**

<table>
<thead>
<tr>
<th>Name:</th>
<th>STEVE CPMC</th>
<th>Sample Type:</th>
<th>Saliva</th>
</tr>
</thead>
<tbody>
<tr>
<td>Race/Ethnicity:</td>
<td>White (Caucasian)</td>
<td>Gender:</td>
<td>Male</td>
</tr>
<tr>
<td>Date of Birth:</td>
<td></td>
<td>Date Collected:</td>
<td>11-30-2016</td>
</tr>
<tr>
<td>Coriell ID:</td>
<td>DEMOSTEVE</td>
<td>Date Received:</td>
<td>11-30-2016</td>
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<tr>
<td>Lab Accessioning Number:</td>
<td>DEMOSTEVE</td>
<td>Date of Report:</td>
<td>09-22-2011</td>
</tr>
<tr>
<td>Ordering Physician:</td>
<td>Dr. Edward Viner</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Name of Gene/Region:** This variant is not found within a gene

**Chromosomal Location:** 6q23

<table>
<thead>
<tr>
<th>Variants tested</th>
<th>Result</th>
<th>Reference Genotype</th>
</tr>
</thead>
<tbody>
<tr>
<td>rs6920220</td>
<td>GA</td>
<td>GG</td>
</tr>
</tbody>
</table>

**Interpretation**

Individuals with this result are 20% more likely (or 1.20 times as likely) to develop rheumatoid arthritis as someone with no copies of this variant.

These risk estimates are based on studies in a European population. When race/ethnicity specific risk estimates are not available, risk estimates based on Caucasian populations are provided.

**Other Risks**

Other genetic variants and other risk factors including co-morbidities, lifestyle and family history may contribute to the risk of rheumatoid arthritis. For additional information on other risk factors please see the accompanying CPMC research report.

Risk interpretation based on Coriell's Rheumatoid Arthritis Risk Algorithm Version 2 (October 27, 2014)

**Test Limitations**

DNA-based testing is highly accurate, however there are many sources of potential error including: mis-identification of samples, rare technical errors, trace contamination of PCR reactions, and rare genetic variants that interfere with analysis. There may be other variants, not included in this test, that influence the risk to develop rheumatoid arthritis. This test is not diagnostic for rheumatoid arthritis and cannot rule out the risk of developing rheumatoid arthritis in the future. Risk estimates are based on current available literature (see reference). This test or one or more of its components was developed and its performance characteristics determined by the Coriell Institute for Medical Research. It has not been approved by the Food and Drug Administration (FDA). The FDA has determined that such approval is not necessary. The Coriell Institute is regulated under the Clinical Laboratory Improvement Amendments (CLIA) of 1988 as qualified to perform high-complexity testing.

**Test Methodology**

Saliva samples were collected using Oragene DNA Collection Kits (DNA Genotek) and DNA was extracted manually according to the manufacturer’s instructions or automatically using a DNAAdvance Kit (Agencourt). Purified DNA was quantified using UV absorbance at 260 nm. Five hundred nanograms of the resulting DNA from each sample were used as template in the Affymetrix Genome-Wide Human SNP Nsp/Sty 6.0 GeneChip assay. Data analysis was performed using Affymetrix Genotyping Console software.

**Electronically signed by**

Marie Hoover, PhD, Laboratory Director

This clinical report only includes data generated in the CLIA approved genotyping laboratory, for additional information please see the CPMC research report.

**References**