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



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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: 09-05-2013

Ordering Physician: Dr. Edward Viner

Risk of Developing Bladder Cancer Based on:

• CPMC Bladder Cancer Variant 1 (rs9642880)

· Family History

Smoking

The CPMC is a research study investigating the utility of personalized genomic information on health and health behavior. At this time, the CPMC is reporting one genetic variant per health condition. Since most common health conditions are caused by an interaction between more than one genetic factor and non-genetic factors such as lifestyle, the genetic variant risk in this report does not represent your complete genetic risk for bladder cancer. 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 counselors. Participants may schedule an appointment with one of our board-certified genetic counselors through the web portal by clicking on "request an appointment". Our genetic counselors also can be reached by email at cpmcgc@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.

Genetic Variant Result, Details and Population Data

Bladder Cancer

Risk factors may be related to each other and risk estimates cannot be combined.

This graph provides a summary of the relative risks for genetic variant, family history, and smoking.



You reported you are a Caucasian man, between 60 and 69 years old; 6 in 1,000 Caucasian men in your age group have bladder cancer.

Chart Color	Relative Risk Due To:	Your Risk	Minimum Risk	Maximum Risk	Interpretation
	Genetic Variant	1.20	1.00	1.50	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 1.2 times as likely) to develop bladder cancer as someone with no copies of this variant. Having this risk variant contributes to your risk of bladder cancer.
	Family History 2.00 1.00 Based on your family history, you are 2 times more likely to develop bladder cancer than have a parent with bladder cancer. Having a parent with bladder cancer contributes to your risk of bladder cancer.		·		
	Smoking Status	3.90	1.00	3.90	Because you are a current smoker you are 3.9 times more likely to develop bladder cancer compared to never smokers. Being a current smoker contributes to your risk of bladder cancer.

Bladder Cancer

Risk Due To Genetic Variant #1 (rs9642880)

Your Result: 1 copy of the non-risk variant and 1 copy of the risk variant were detected (GT)

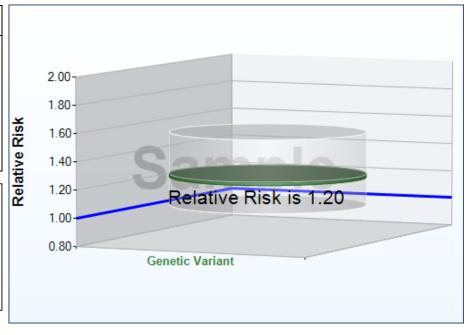
Non-Risk Variant = G Risk Variant = T

Chart Color		_	Maximum Risk	Interpretation
	1.20	1.00	1.50	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 1.2 times as likely) to develop bladder cancer as someone with no copies of this variant. Having this risk variant contributes to your risk of bladder cancer.

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 1.0 indicates an increased risk.



These risk estimates are based on a study conducted in a Caucasian population.

Bladder Cancer

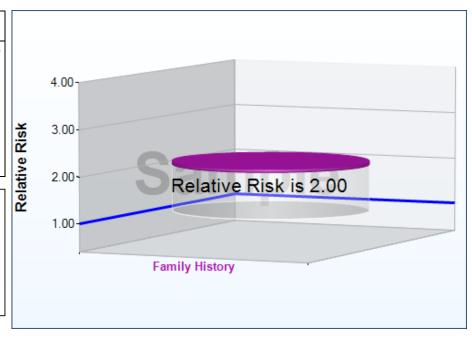
Risk Due To Family History
You reported that one or both of your parents have bladder cancer.

Chart Color		_	Maximum Risk	Interpretation
	2.00	1.00	2.00	Based on your family history, you are 2 times more likely to develop bladder cancer than someone who does not have a parent with bladder cancer. Having a parent with bladder cancer contributes to your risk of bladder cancer.



People with a parent with bladder cancer were compared to people without a parent with bladder cancer to determine relative risk of developing bladder cancer.

A relative risk greater than 1.0 indicates an increased risk.



These risk estimates are based on a study conducted in a Caucasian population.

Bladder Cancer

Risk Due To Smoking Status

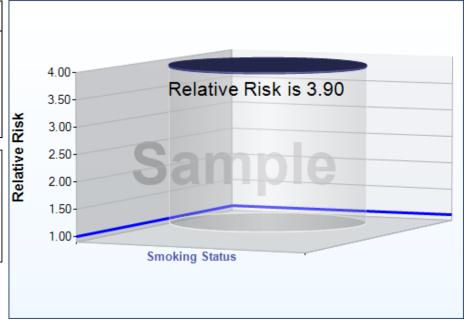
You reported that you are a current smoker.

Chart Color		_	Maximum Risk	Interpretation
	3.90	1.00		Because you are a current smoker you are 3.9 times more likely to develop bladder cancer compared to never smokers. Being a current smoker contributes to your risk of bladder cancer.



Men who are current smokers or former smokers are compared to men who have never smoked to determine relative risk.

A relative risk of greater than 1.0 indicates an increased risk.



These risk estimates are based on a study conducted on multiple populations of differing racial and ethnic backgrounds.

Bladder Cancer - Variant #1 (rs9642880)

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 bladder cancer.

How Common Is This Variant?

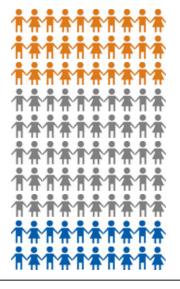
Non-Risk Variant = G Risk Variant = T

GG - 30 in 100 people have 2 copies of the non-risk variant

GT - 50 in 100 people have 1 copy of the non-risk variant and 1 copy of the risk variant

TT - 20 in 100 people have 2 copies of the risk variant

This data is based on studies in Caucasian populations.



Gene: MYC Chromosome: 8q24.21

Causes

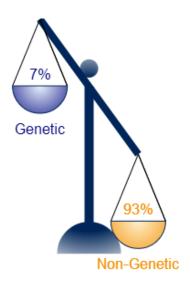
Genetic vs. Non-Genetic Risk Factors

Bladder cancer 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 **93%** of the risk of bladder cancer.

It is estimated that **7%** of the risk for bladder cancer 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 bladder cancer. We are only able to tell you about your family history risk, 1 genetic and 1 non-genetic risk factor at this time.

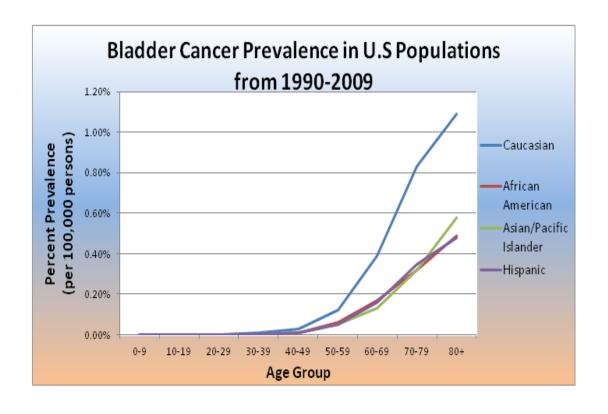


How Common

The risk of having bladder cancer increases with age. Men have a slightly greater risk of developing bladder cancer than women. Caucasians have a greater risk of bladder cancer than individuals of other races.

You reported you are a Caucasian man, between 60 and 69 years old; 6 in 1,000 Caucasian men in your age group have bladder cancer.

Age, race, and gender contribute to your risk of bladder cancer.



Limitations

Bladder Cancer

- This result alone does NOT diagnose bladder cancer. Bladder cancer must be diagnosed by your health care provider.
- This result does NOT mean that you have or will absolutely develop bladder cancer.
- This result does NOT mean that you will not develop bladder cancer in the future.
- This result ONLY assesses your risk for developing bladder cancer due to the factors presented in this report and does not mean that other genetic variants or risk factors for bladder cancer are present or absent.
- The relative risk information presented in this report represents the risk of developing bladder cancer for individuals who do not have a history of bladder cancer.
- Personal risk factors, such as age, family history or lifestyle, may have a greater impact on your risk to develop bladder cancer 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

Bladder Cancer

This condition and genetic variant(s) 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 Bladder Cancer Risk Algorithm Version 1 (September 10, 2013)]

- 1. Stack, C. et al (2011). Genetic risk estimation in the Coriell Personalized Medicine Collaborative. Genet Med. 13(2):131-139.
- 2. Rothman, N. et al (2010). A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. Nat Genet. 42(11):978-985.
- 3. Czene, K. et al (2002). Environmental and heritable causes of cancer among 9.6 million individuals in the Swedish family-cancer database. Int J Cancer. 99:260-266.
- 4. Kharazmi, E. et al (2012). Familial risk of early and late onset cancer: nationwide prospective cohort study. BMJ. 345:e8076.
- 5. Freedman, ND. et al (2011). Association between smoking and risk of bladder cancer among men and women. JAMA. 306(7):737-745.
- 6. Daugherty, SE. et al (2013). Reproductive factors and menopausal hormone therapy and bladder cancer risk in the NIH-AARP Diet and Health Study. Int J Cancer. Accepted article, doi:10.1002/ijc28022
- 7. Howlader, N. et al. SEER Cancer Statistics Review, 1975-2009 (Vintage 2009 Populations), National Cancer Institute. Bethesda, MD, http://seer.cancer.gov/csr/1975_2009_pops09/, based on November 2011 SEER data submission, posted to the SEER web site, April 2012.
- 8. Wang, M. et al (2009). Common genetic variants on 8q24 contribute to susceptibility to bladder cancer in a Chinese population. Carcinogenesis. 30(6):991-996.

Sample Results



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Clinical Report for Bladder Cancer Genetic Variant 1 (rs9642880)

Name:STEVE CPMCSample Type:SalivaRace/Ethnicity:White (Caucasian)Gender:Male

Date of Birth: Date Collected: 11-30-2016

Coriell ID:DEMOSTEVEDate Received:11-30-2016Lab Accessioning Number:DEMOSTEVEDate of Report:09-05-2013

Ordering Physician: Dr. Edward Viner

Name of Gene/Region:	MYC	Chromosomal Location: 8q24.21		
Variants tested	Result	Reference Genotype		
rs9642880	GT	GG		
Interpretation	Individuals with this result are 20% more likely (or 1.2 times as likely) to develop bladder cancer as someone with no copies of this variant. These risk estimates are based on studies in Caucasian populations. When race/ethnicity specific risk estimates are not available, risk estimates based on Caucasian populations are provided.			
Other Risks	-morbidities, lifestyle and family history may contribute to the risk of bladder cancer. For sk factors please see the accompanying CPMC research report.			

Risk interpretation based on Coriell's Bladder Cancer Risk Algorithm Version 1 (September 10, 2013)

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 bladder cancer. This test is not diagnostic for bladder cancer and cannot rule out the risk of developing bladder cancer 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 DNAdvance 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

References

1. Rothman, N. et al (2010). A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. Nat Genet. 42(11):978-985.

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