



# disease risk

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23andMe Discoveries were made possible by 23andMe members who took surveys.

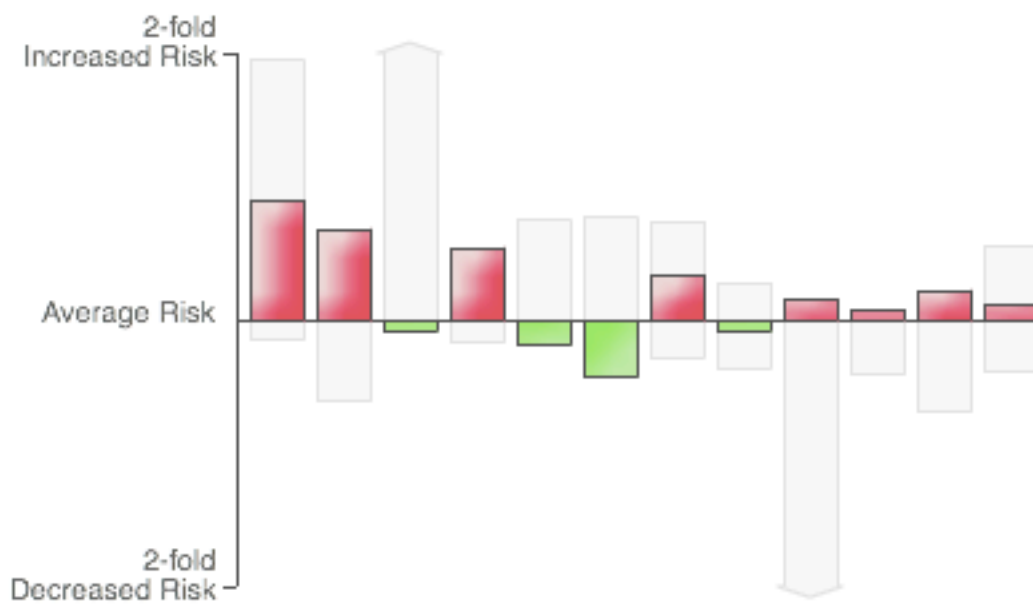
## Elevated Risk ?

Name	Confidence	Your Risk	Avg. Risk	Compared to Average
<a href="#">Prostate Cancer</a> ♂	★★★★★	31.9%	17.8%	1.79x
<a href="#">Psoriasis</a>	★★★★★	22.4%	11.4%	1.98x
<a href="#">Alzheimer's Disease</a>	★★★★★	14.2%	7.2%	1.98x
<a href="#">Ankylosing Spondylitis</a>	★★★			↑
<a href="#">Asthma</a>	★★★			↑
<a href="#">Bipolar Disorder: Preliminary Research</a>	★★★			↑
<a href="#">Chronic Lymphocytic Leukemia</a>	★★★			↑
<a href="#">Follicular Lymphoma</a>	★★★			↑
<a href="#">High Blood Pressure (Hypertension)</a>	★★★			↑

## Talk with a genetic counselor

A genetic counselor specializes in helping people understand genetic disorders and genetic test results. Learn more about gen

### Marker Effects



What does this chart show?

The chart shows the approximate effects of the selected genotype at the 12 reported markers. Higher, **red bars** indicate **increased risk** from the average, while lower, **green bars** indicate **decreased risk** from the average. The light gray bars show the maximum possible effects for the possible genotypes at t

Mouse over individual bars to view additional information about the marker. Click on a bar to view detailed information about the marker below. You can read more about all markers in the [technical report](#).

### 8q24 (region 1)

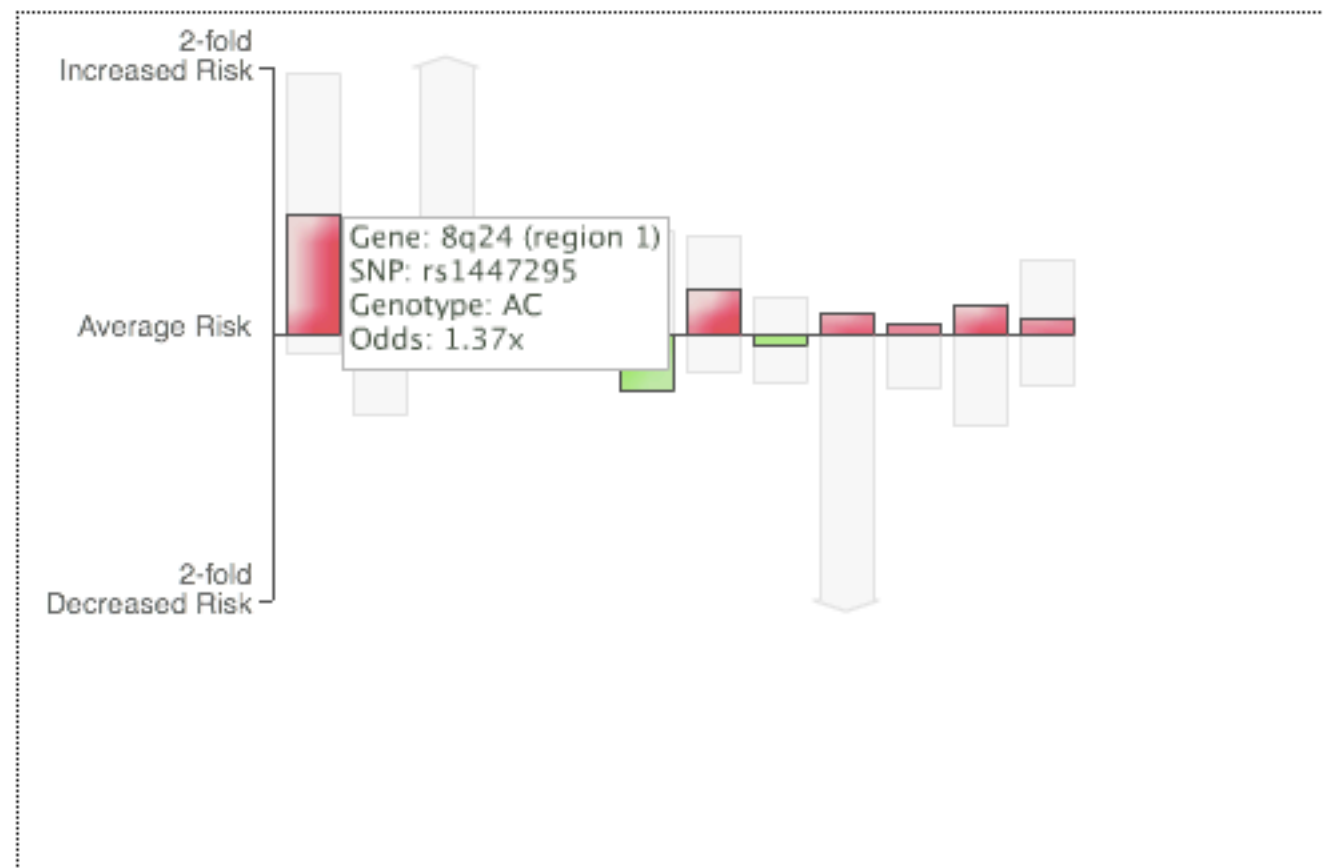
Three SNPs in the same area of the genome have recently been found to be independently associated with prostate cancer risk at 8q24, because it lies within band 24 on the long arm (named the "q" arm) of chromosome 8. The three SNPs are not close to known genes (though there are others located farther away). But other studies have looked at DNA from prostate tumors and found that in the cancer genome the genome often has unusual duplications, or extra copies of DNA.

the genetic things that  
shouldn't be obscured  
(because biology)

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“eat less and exercise”



## jtw's page



jtw has uploaded genotyping rawdata.

-  [Download this set \(23andme\)](#)

### Description

This user has not entered a description yet.

### jtw's variations

This user has not entered any phenotypes yet.

Contact openSNP: [Blog](#) | [Twitter](#) | [Mail](#) | [Privacy Policy](#) | [openSNP in the press](#)

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<http://opensnp.org/users/615>

[rs144](#)

4 Magnitude  
20120916 Geno time



**Male Male.**

[rs5186\(C;C\)](#) **7.3x increased risk of hypertension...more...**

Bad Repute  
4 Magnitude  
0.1575 GMAF  
54 References  
AGTR1 Gene  
3 Chromosome  
148459988 Position  
20120810 Rs time

[High blood pressure, Pre-eclampsia](#)

[rs6152\(A;A\)](#) **won't go bald** This genotype seems to prevent baldness  
...more...

Good Repute  
4 Magnitude  
0.214587 GMAF  
11 References  
AR Gene  
X Chromosome  
66765627 Position  
20120812 Rs time


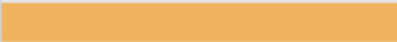
[Baldness](#)

Search...

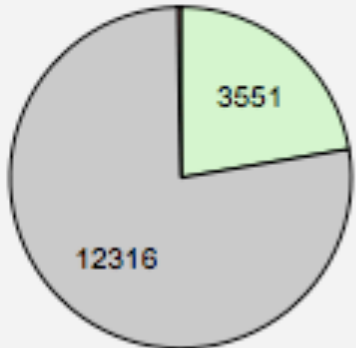
[Graph](#) [Table](#) [Help](#)

[Show All](#)

Sort by Magnitude

Show: ☒ SNPs ☒ Genosets  
Repute: ☒ Good ☒ Not Set ☒ Bad  
Magnitude:    
References:    
UI: ☒ Tooltips ☐ Editor Mode  
Allow  [2x more](#)  
Visible  Offscreen

Repute



3551  
12316  
15903

Good  
Not Set  
Bad

# 'JTW'

## MINOR ALLELE PROGRAM REPORT

=====

'JTW'      'jw' '615'      23andMe Results      Chromosomes 1-22      4 October 2012

The program finds about 60 'rare/uncommon' SNPs from the 900,000+ tested by 23andMe.

There is just a single 'homozygous-recessive' result:

'AA'      rs11869580      Intergenic

but as this occurs in an Intergenic region it is unlikely to be of significance.

There are no SNPs of special note.

## RESULTS

=====

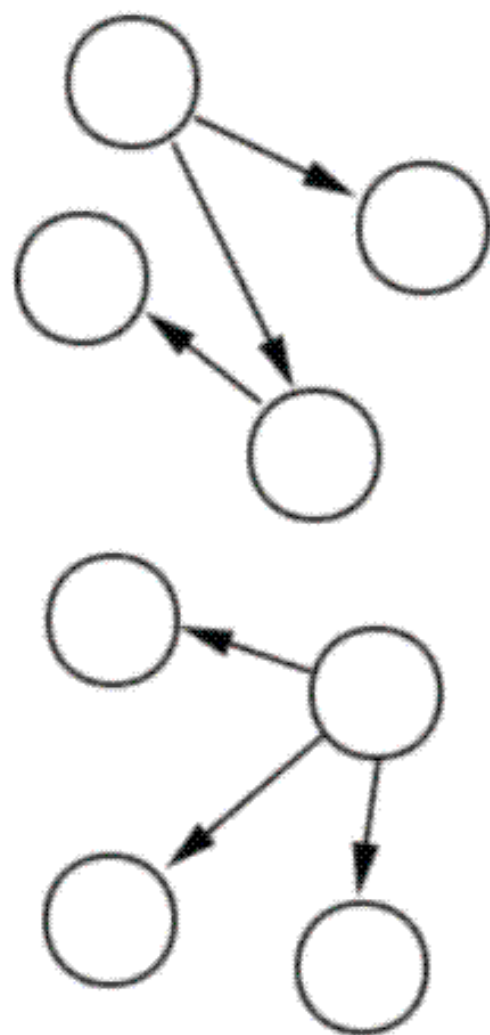
=====

rs56367069	at Chr1a:17326767	gave 'CT'	The minor allele is 'T' with a MAF = 0.00776.
rs4949212	at Chr1a:31961711	gave 'GT'	The minor allele is 'G' with a MAF = 0.00959
rs1181088	at Chr1a:54563039	gave 'AG'	The minor allele is 'G' with a MAF = 0.00959
rs1109918	at Chr1a:67862482	gave 'AG'	The minor allele is 'G' with a MAF = 0.00822.
rs12751479	at Chr1b:98056007	gave 'GT'	The minor allele is 'T' with a MAF = 0.00228
rs35669708	at Chr1b:156851382	gave 'AG'	The minor allele is 'A' with a MAF = 0.00999
rs35698797	at Chr1c:229665958	gave 'CT'	The minor allele is 'T' with a MAF = 0.00502
rs45471294	at Chr2a:31600017	gave 'CT'	The minor allele is 'T' with a MAF = 0.00914.
rs17776702	at Chr2b:103317676	gave 'AG'	The minor allele is 'G' with a MAF = 0.00868
rs17760364	at Chr2c:189631806	gave 'AG'	The minor allele is 'G' with a MAF = 0.00959
rs279552	at Chr3a:9976159	gave 'AG'	The minor allele is 'A' with a MAF = 0.00639
rs460965	at Chr3a:10122927	gave 'CT'	The minor allele is 'T' with a MAF = 0.00594.
rs2067466	at Chr3a:11300780	gave 'CG'	The minor allele is 'C' with a MAF = 0.00319

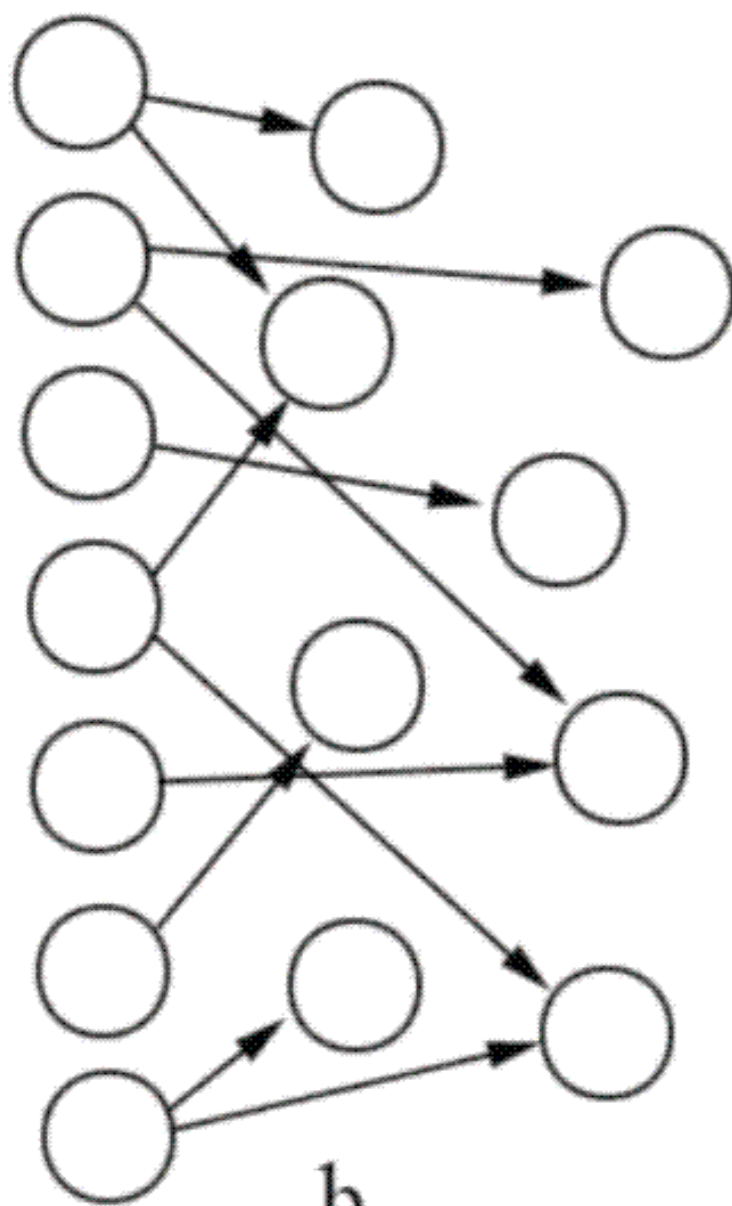


“Also there is no suggestion of consanguinity in your pedigree.”

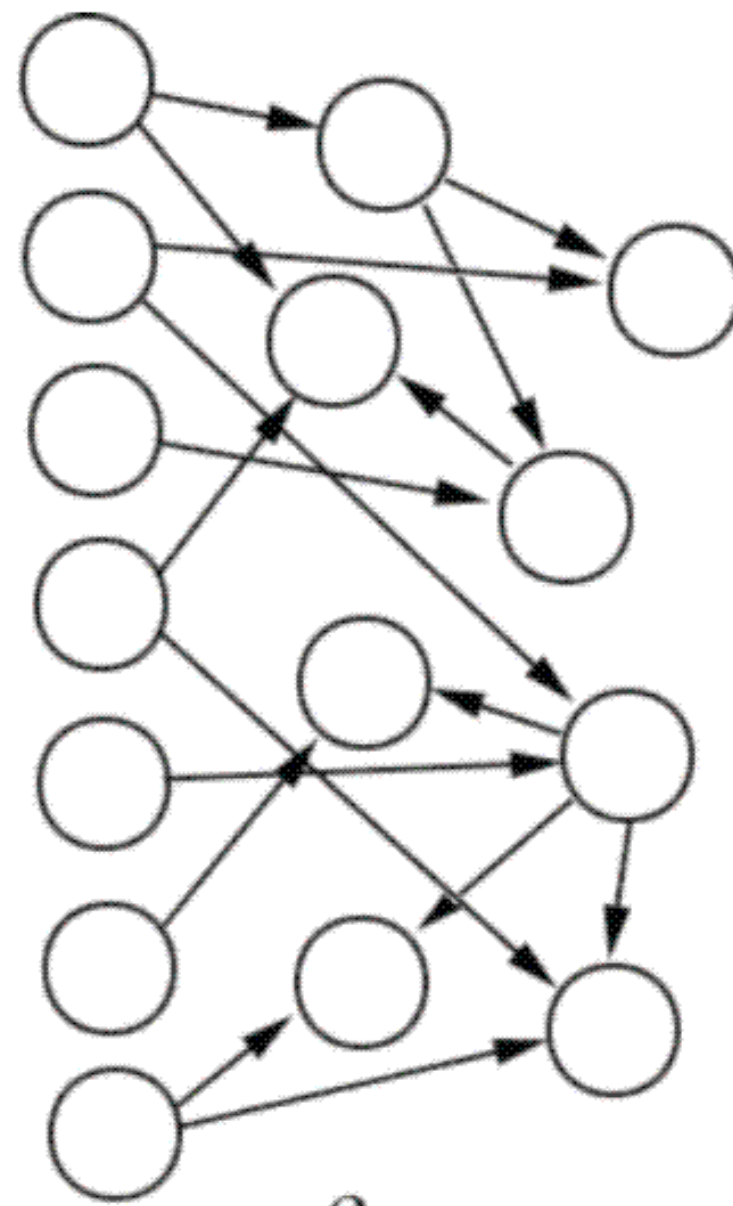
<http://www.ianlogan.co.uk/>



a.



b.



c.





TESTS	RESULTS	FLAG	UNITS	REFERENCE INTERVAL	LAB
<b>Hepatic Function Panel (7)</b>					
Protein, Total, Serum	6.5		g/dL	6.0-8.5	01
Albumin, Serum	4.5		g/dL	3.5-5.5	01
Bilirubin, Total	0.7		mg/dL	0.0-1.2	01
Bilirubin, Direct	0.20		mg/dL	0.00-0.40	01
Alkaline Phosphatase, S	72		IU/L	25-150	01
AST (SGOT)	20		IU/L	0-40	01
ALT (SGPT)	19		IU/L	0-44	01
<b>Lipid Panel w/ Chol/HDL Ratio</b>					
Cholesterol, Total	161		mg/dL	100-199	01
Triglycerides	75		mg/dL	0-149	01
HDL Cholesterol	65		mg/dL	>39	01
According to ATP-III Guidelines, HDL-C >59 mg/dL is considered a negative risk factor for CHD.					
VLDL Cholesterol Cal	15		mg/dL	5-40	01
LDL Cholesterol Calc	81		mg/dL	0-99	01
T. Chol/HDL Ratio	2.5		ratio units	0.0-5.0	01



# access controls possible

## Consent to Research Getting Consent

[LOGIN](#)

These are the rights you are granting to **qualified researchers**

- ☐ Right to **do research** with my data
- ☐ Right to **redistribute** my data
- ☐ Right to **publish the results of research** from my data
- ☐ Right to **commercialize products derived from research** on my data

All boxes must be checked to move forward in the consent process

[Next](#)

### GET INFORMED

- ✓ Welcome
- ✓ Willingness to Participate
- ✓ Researcher Terms of Use
- **Grant Rights**
- Watch Video
- Checkpoint
- Acknowledge Understanding

### CONSENT TO RESEARCH

- Consent Form
- Generate ID

### UPLOAD YOUR DATA

- User Profile
- Sign In
- Upload Data

potential for harm  
economic  
social  
and more we don't know

You must finish watching the video to advance in the consent process.

volunteer cannot skip video

# Consent to Research

Getting Consent

LOGIN

Tell us that you understand this informed consent process.

- ☒ I understand [the uncertainty and risk of public genetic research](#).
- ☒ I provide [consent](#) for my data to be used in public genetic research
- ☒ I understand that although I can [withdraw](#) at any time, I cannot withdraw data that has [already been distributed](#).

All boxes must be checked to create informed consent.

I want to give consent

## GET INFORMED

- ✓ Welcome
- ✓ Willingness to Participate
- ✓ Researcher Terms of Use
- ✓ Grant Rights
- ✓ Watch Video
- ✓ Checkpoint
- Acknowledge Understanding

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- User Profile
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### 7. You choose what data to upload.

		Response Percent	Response Count
True		100.0%	118
False		0.0%	0
	answered question		118
	skipped question		2

### 8. You can decide to withdraw at any time.



		Response Percent	Response Count
True		98.3%	116
False		1.7%	2
	answered question		118
	skipped question		2

### 9. If you withdraw, it's certain that all your data can be cleared from the system.



		Response Percent	Response Count
True		7.6%	9
False		92.4%	109
	answered question		118
	skipped question		2





### 10. You are guaranteed confidentiality.

		Response Percent	Response Count
True		41.5%	49
False		58.5%	69
		answered question	118
		skipped question	2

### 11. Researchers have to sign terms of use to access your data.

		Response Percent	Response Count
True		96.6%	114
False		3.4%	4
		answered question	118
		skipped question	2

### 12. Your data will be redistributed to qualified researchers.

		Response Percent	Response Count
True		97.4%	114
False		2.6%	3
		answered question	117
		skipped question	3

