

# 1 Search by Gene

## General Instruction

You can search the Colorado Biobank Portal (CBP) using your favorite gene.

The easiest way to try this out to **Search by gene**, click the **NRAS** link

Colorado Biobank Portal

Gene, transcript, variant

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## Colorado Biobank Portal

### Welcome to the development version of the Colorado Biobank Portal

**Note:** This engine presents case-control GWAS results from the Colorado Center for Personalized Medicine Biobank.

#### Supported queries

By gene: [NRAS](#)

By transcript: [ENST00000310581](#)

By variant: [rs965513](#)

By region: [chr22:17440016-17459999](#)

By phenotype: [Thyroid cancer](#)

## 2 Insert Gene Symbols

### General Instruction

Alternatively, you can type the **Gene Symbols** in the **Search Box** blank space.



Colorado Biobank Portal

Gene, transcript, variant

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Search Box

# Colorado Biobank Portal

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**Note:** This engine presents case-control GWAS results from the Colorado Center for Personalized Medicine Biobank.

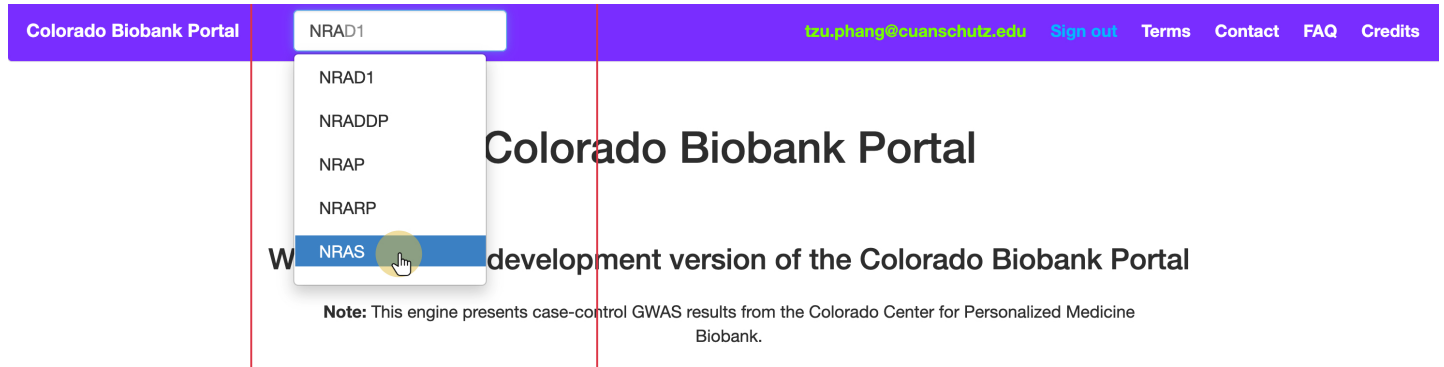
### Supported queries

- By gene: [NRAS](#)
- By transcript: [ENST00000310581](#)
- By variant: [rs965513](#)
- By region: [chr22:17440016-17459999](#)
- By phenotype: [Thyroid cancer](#)

### 3 Gene Symbol Suggestion

#### General Instruction

While you type, an auto-complete feature will take over to match your Gene Symbol name. Please select one of the entry from the auto-complete list.



The screenshot shows the Colorado Biobank Portal search interface. A search bar contains the text 'NRAD1'. A dropdown menu is open, displaying a list of suggestions: 'NRAD1', 'NRADDP', 'NRAP', 'NRARP', and 'NRAS'. The 'NRAS' option is highlighted with a blue bar and a mouse cursor. The background of the portal shows the title 'Colorado Biobank Portal' and a subtitle 'development version of the Colorado Biobank Portal'. A note below the subtitle reads: 'Note: This engine presents case-control GWAS results from the Colorado Center for Personalized Medicine Biobank.'

#### Supported queries

By gene: [NRAS](#)

By transcript: [ENST00000310581](#)

By variant: [rs965513](#)

By region: [chr22:17440016-17459999](#)

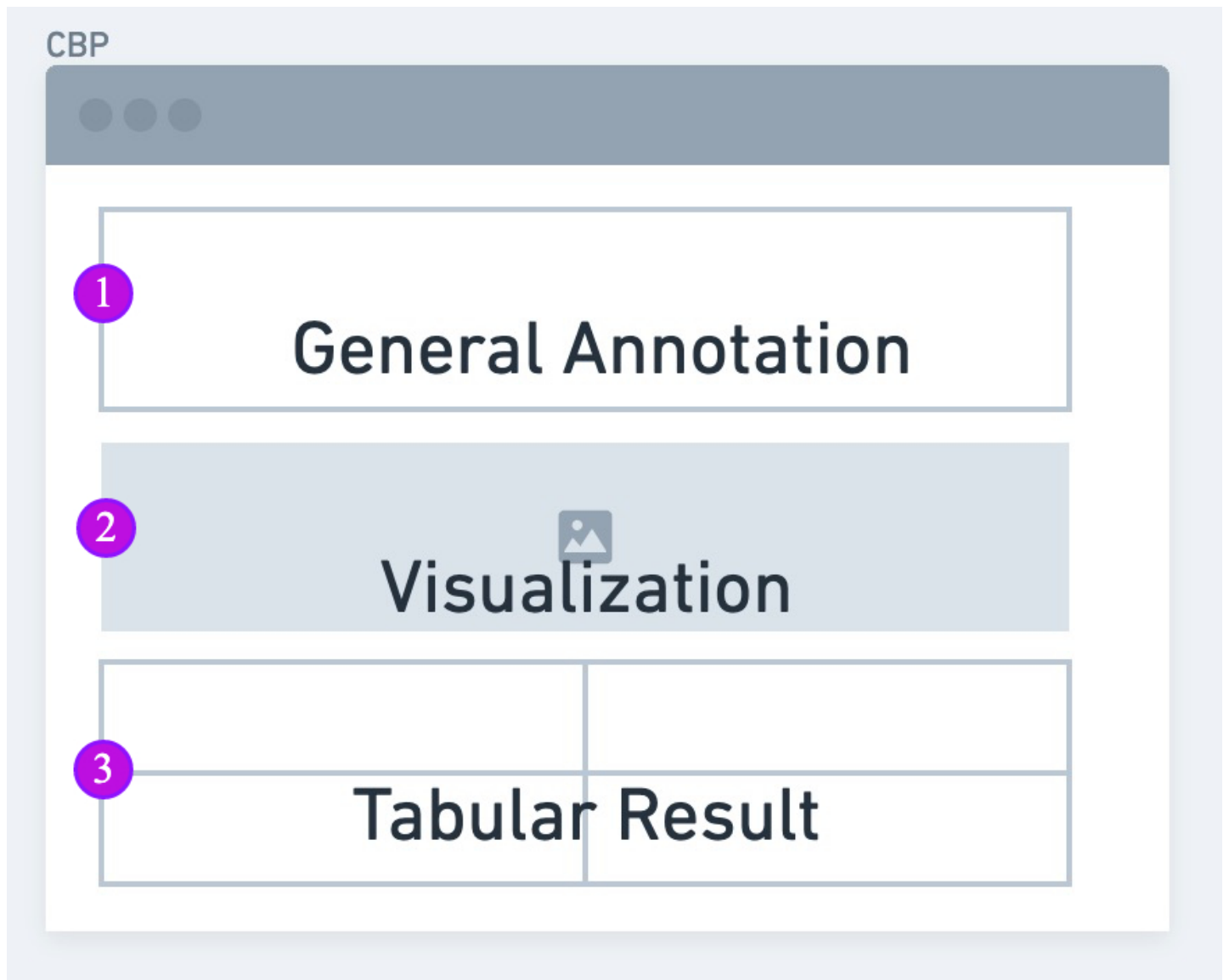
By phenotype: [Thyroid cancer](#)

## 4 Results Layout

### General Instruction

The search result will be displayed in this general layout that consists of three segments:

1. General Annotation: information on the search results and relevant external links
2. Visualization: graphical representation of the search results
3. Tabular Result: table layout of search results summary statistics.



## 5 General Annotation

### General Instruction

The top segment of the result page lists general gene info and external links pertaining to the gene

1. Click on the **External References** to reveal more external links option

Colorado Biobank Portal Gene, transcript, variant, Sign out Downloads Terms Contact FAQ Credentials

# Gene: MMP11

Gene Annotation and External Links

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**MMP11** matrix metallopeptidase 11

**Number of variants** 419

**UCSC Browser** [22:23768225-23784315](#)

**gnomAD** [MMP11](#)

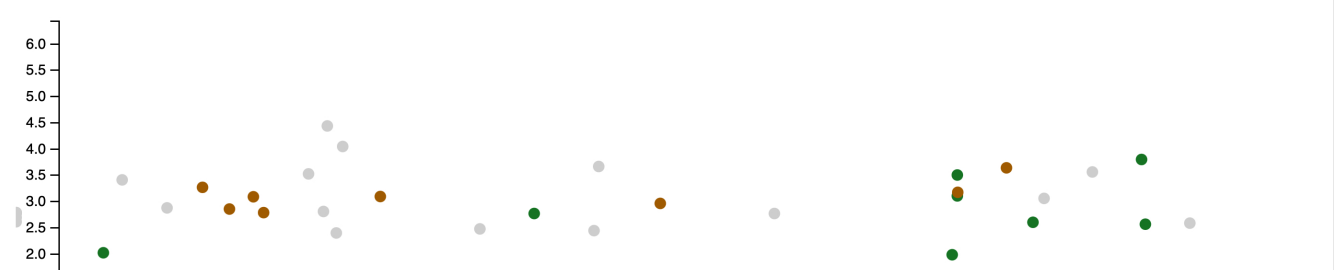
**Other**

[External References](#)

1

### Gene summary

Display: Overview Detail
Association statistic: -log<sub>10</sub>(P-value) Odds Ratio



r4ds-master.zip WT4-html (1).html WT4-html.html Gapminder-de...html KeyCastr.app.zip Show All

## 6 More external link

### General Instruction

More external links pertaining to the gene can be found under the pull down manu

### Scroll for more ...

Scroll down to see more result

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# Gene: MMP11

**MMP11** matrix metallopeptidase 11  
**Number of variants** 419  
**UCSC Browser** [22:23768225-23784315](#)  
**gnomAD** [MMP11](#)  
**Other** External References ▾

UCSC Browser  
GeneCards  
Ensembl  
PubMed Search  
GTEx (Expression)

Gene sum    Display: Overview    Association statistic: -log10(P-value)    Odds Ratio

↑ r4ds-master.zip    WT4-html (1).html    WT4-html.html    Gapminder-de...html    KeyCastr.app.zip    Show All ×

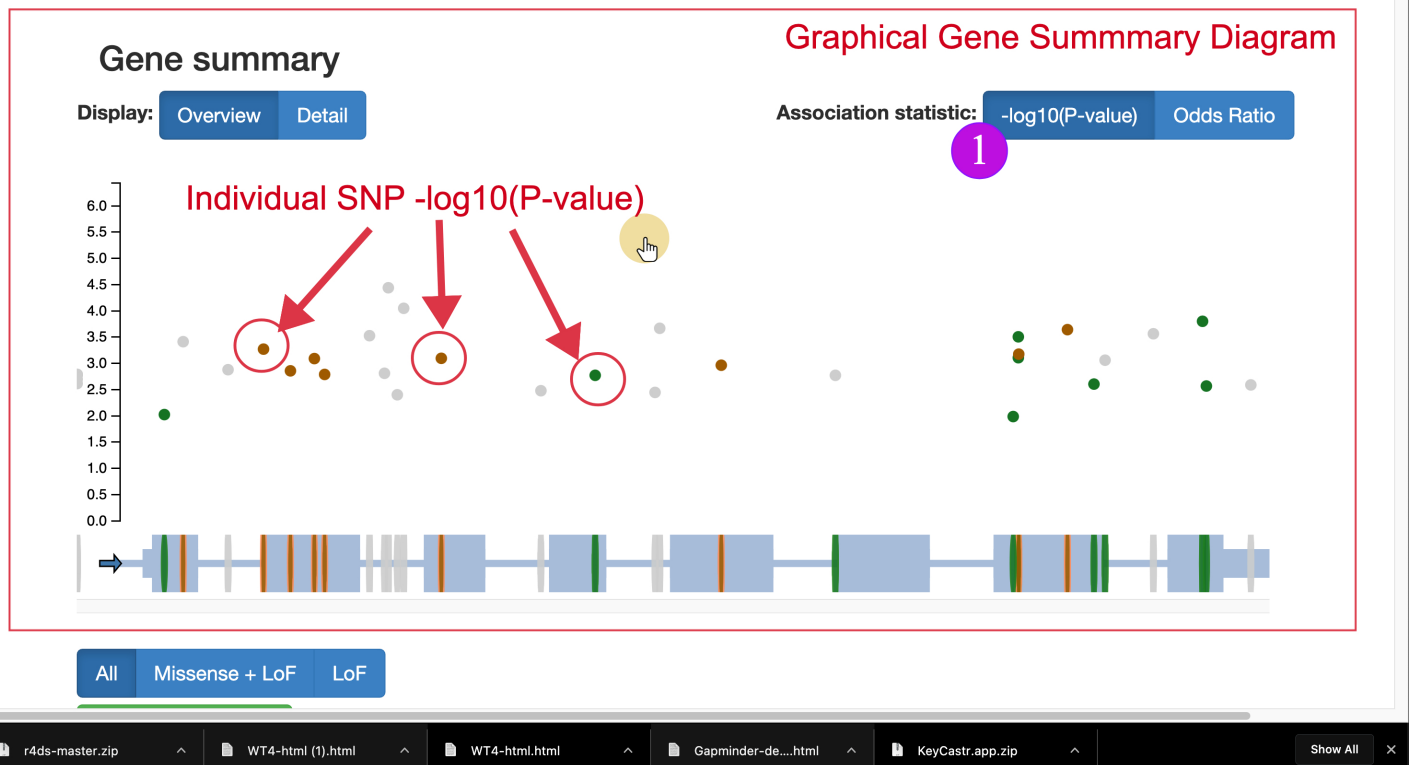
## 7 Visualization: $-\log(p\text{-value})$

### General Instruction

This segment reveal the graphical representation of the gene of interest.

1. By default, each dot represents a SNP in  $-\log(p\text{-value})$ . You can also click on the " $-\log_{10}(P\text{-value})$ " box to activate it.

UCSC Browser [22:23768225-23784315](#)  
gnomAD [MMP11](#)  
Other



## 8 Visualization: Odds Ratios

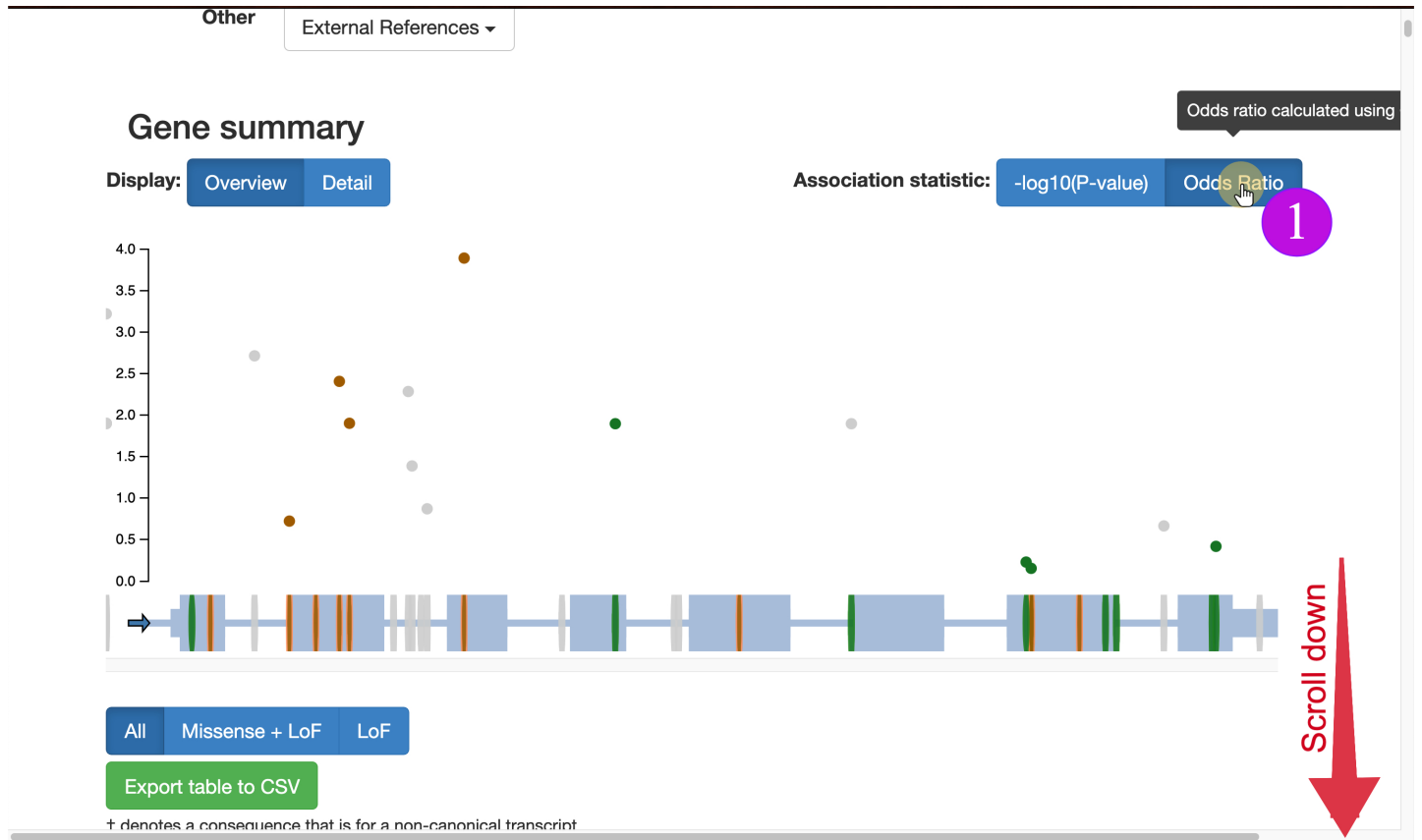
### General Instruction

You can also view the result in "Odds Ratios" unit value

1. Click on the "Odds Ratio" box will activate this feature too.

### Scroll for more

Scroll down to reveal more result





## 9 Tabular Summary Statistics

### General Instruction

The table shows summary statistics for all the SNPs

1. **Variant:** Single Nucleotide Polymorphism (SNP), labeled with these genetic info:
  - a. Chromosome location (here: Chromosome 22, position 23,763,464)
  - b. Genetic alteration (here: altered from nucleotide G to A)
  - c. rsID (here: rs575501011)
2. **Position:** SNP genomic coordinate position for hg38
3. **Gene Symbol:** official Gene Symbol
4. **Consequence:** the repercussion of the genetic alteration (mutation) which could be either benign or damaging
5. **Annotation:** additional information about the SNP as it relates to gene(s)
6. **Minor AF:** Minor Allele Frequency: the frequency at which the second most common allele occurs in a given population (here it is based on CCPM Biobank samples)
7. **Phenotype:** the phenotype used to calculate summary statistics
8. **Odds Ratio:** the ratio of the odds of phenotype (disease) among the exposed to the odds of phenotype among the unexposed.
9. **P-value:** Genome Wide Association Study (GWAS) analysis based on the phenotype which tells us how likely a putative phenotype (disease) associated variant is due to random chance

Variant	Position	Gene symbol	Consequence	Annotation	Minor AF	Phenotype	Odds Ratio	P-value
22:23763464 G / T (rs575501011)	23763464	MMP11		upstream gene	0.000691584	Intracranial hemorrhage (injury)	19.7	0.00140
22:23763602 G / A (rs73396542)	23763602	MMP11		upstream gene	0.194672	Iron deficiency anemia secondary to blood loss ...	1.25	0.00190
22:23763630 G / A (rs114418367)	23763630	MMP11		upstream gene	0.000861755	Malignant neoplasm of ovary	22.7	0.00147
22:23763660 A / C (rs866456155)	23763660	MMP11		upstream gene		Leukemia	10.7	0.00107
22:23763748 G / A (rs906072089)	23763748	MMP11		upstream gene		Rheumatic disease of the heart valves	23.5	0.00169
22:23763821 G / C (rs179465)	23763821	MMP11		upstream gene	0.0916575	Concussion	0.303	0.000118
22:23763985 G / A (rs2298374)	23763985	MMP11		upstream gene		Skin cancer	29.6	0.00247

# 10 Tabular Summary Statistics: Consequence Example

## General Instruction

An example of consequence output

All Missense + LoF LoF

Export table to CSV

† denotes a consequence that is for a non-canonical transcript

Variant	Position	Gene symbol	Consequence	Annotation	Minor AF	Phenotype	Odds Ratio	P-value
1:114708192 T / C (rs909455480)	114708192	NRAS	c.*5A>G	splice region		Myopia	14.6	0.00712
1:114713865 G / A (rs142739534)	114713865	NRAS	p.Gly75/189Gly	synonymous		Other and unspecified complications of birth, p...	31.9	0.00301
1:114709659 C / T (rs143020946)	114709659	NRAS	p.Leu120/189Leu	synonymous	0.000645953	Dysmetabolic syndrome X	7.62	0.00371
1:114708552 G / A (rs374061873&COSV65739652)	114708552	NRAS	p.Pro185Ser	missense		Early or threatened labor, hemorrhage in early ...	22.0	0.00255
1:114705879 CT / C (rs770180355)	114705879	NRAS		3' UTR		Acute bronchitis and bronchiolitis	53.7	0.00380
1:114704375 A / C (rs886259422)	114704375	NRAS		downstream gene		Abnormal findings on mammogram or breast exam	9.36	0.00192
1:114706928 A / C (rs774604143)	114706928	NRAS		3' UTR		Other immunological findings	41.6	0.00727
1:114707511 A / C (rs555171083)	114707511	NRAS		3' UTR		Psychogenic and somatoform disorders	37.9	0.00124
1:114714742 A / G (rs9724624)	114714742	NRAS		intron	0.0433714	Nontoxic multinodular goiter	1.58	0.00122
1:114712736 A / T (rs573797597)	114712736	NRAS		intron	0.000312664	Other disorders of thyroid	8.57	0.00220
1:114708093 A / T (rs769896264)	114708093	NRAS		intron		Influenza	51.2	0.00434
1:114716848 A / T (rs2273267)	114716848	NRAS		upstream gene	0.00909405	Hypotension NOS	2.92	0.00261
1:114708698 C / T (rs9724641)	114708698	NRAS		intron	0.0089222	Schizophrenia and other psychotic disorders	2.59	0.00184
1:114709234 C / T (rs1016348904)	114709234	NRAS		intron		Gram negative septicemia	77.4	0.00224
1:114709312 G / A (rs115405784)	114709312	NRAS		intron	0.000340101	Mood disorders	0.126	0.00194
1:114704595 G / A (rs147926293)	114704595	NRAS		3' UTR	0.00114319	Disturbances of sensation of smell and taste	8.85	0.000817
1:114713267 G / A (rs975060114)	114713267	NRAS		intron		Congestive heart failure, nonhypertensive	14.7	0.000710