

CIBERER Spanish Variant Server

Valencia, 28-30 Sep 2015



PRINCIPE FELIPE
CENTRO DE INVESTIGACION

Computational • Genomics



Introduction

- 1) CSVS provides information about the variability of the Spanish.
- 2) It is useful for filtering polymorphisms and local variations.
- 3) CSVS currently stores information on 578 unrelated Spanish individuals.
- 4) URL: csvs.babelomics.org
- 5) Github: <https://github.com/babelomics/pvs>

CSVS

 CIBERER Spanish Variant Server [Search](#) [Stats](#)

 **BIER**

CSVS

[Try it now](#)

Overview

Welcome to the CIBERER Spanish Variant Server. CSVS was created to provide information about the variability of the Spanish population to the scientific/medical community. It is useful for filtering polymorphisms and local variations in the process of prioritizing candidate disease genes. CSVS currently stores information on 578 unrelated Spanish individuals. We accept submissions from WES or WGS. See the protocol for sending samples.

[Submission Protocol](#)

Supported by



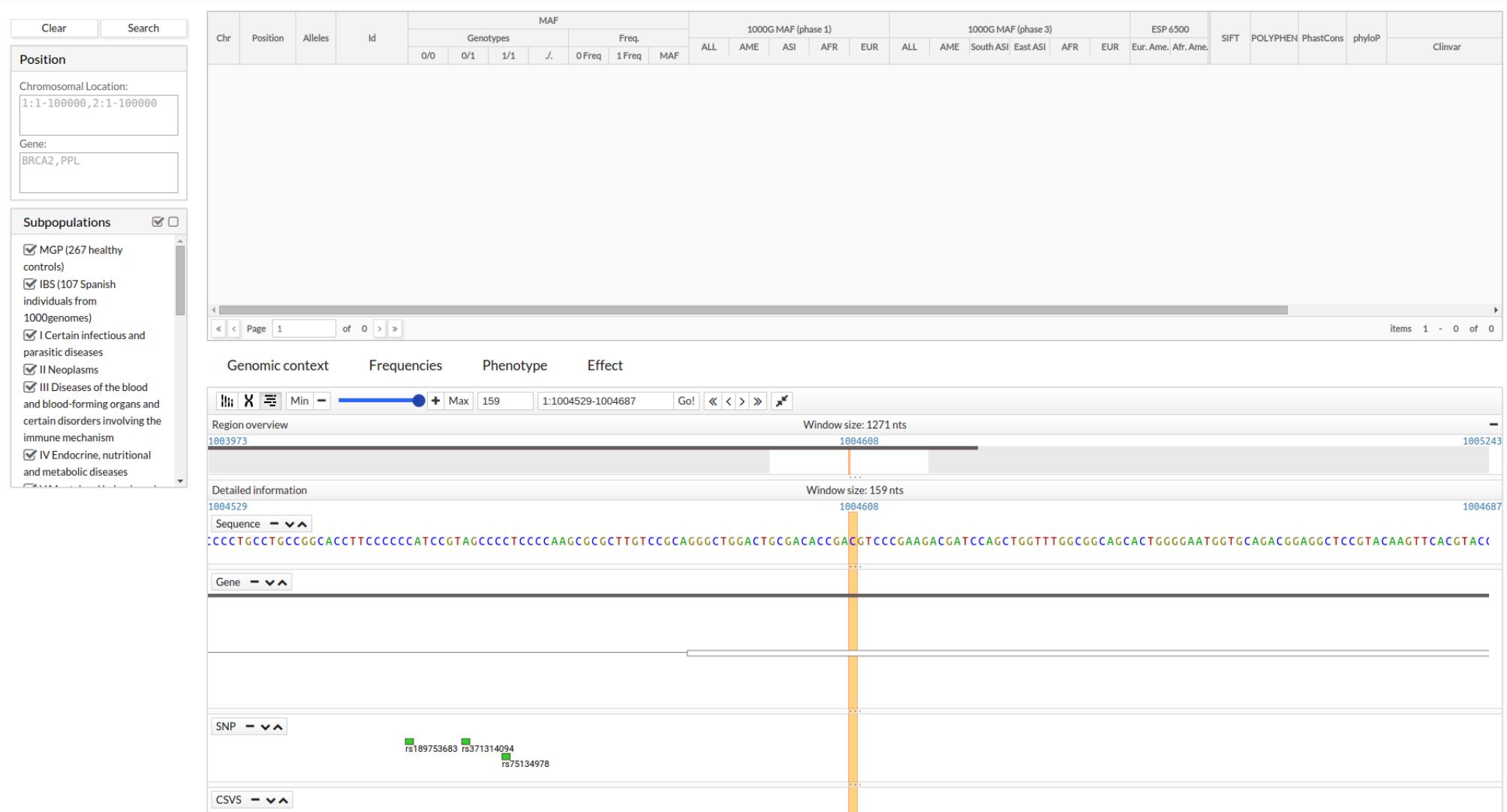


Note:

CSVS web application makes an intensive use of the HTML5 standard and other cutting-edge web technologies such as Web Components, so only modern web browsers are fully supported, these include Chrome 36+, Firefox 32+, IE 10+, Safari 7+ and Opera 24+.

CSVS: created by Computational Genomics Department
Príncipe Felipe Research Center
2015

CSVS



CSVS

Clear **Search**

Position				MAF													ESP 6500					SIFT	POLYPHEN	PhastCons	phyloP	Clinvar		
Chr	Position	Alleles	Id	Genotypes						Freq.						1000G MAF (phase 1)					1000G MAF (phase 3)							
				0/0	0/1	1/1	J.	0 Freq	1 Freq	MAF	ALL	AME	ASI	AFR	EUR	ALL	AME	South ASI	East ASI	AFR	EUR	Eur. Ame. Afr. Ame.						
11	92085508	G>T	COSM545692	577	1	0	0	0.999	0.001	0.001	0.21	0.016	0.978	0.533				
11	92085623	C>T	rs76685441	566	11	0	1	0.99	0.01	0.01	0.010	0.010	0.000	0.000	0.010	0.002	0.007	0.000	0.000	0.007	0.005	0.002	.	.	0.992	0.655		
11	92085905	G>A	.	577	1	0	0	0.999	0.001	0.001	0.994	0.655		
11	92086301	C>A	.	576	2	0	0	0.998	0.002	0.002	0.708	-0.444		
11	92086458	G>A	.	577	1	0	0	0.999	0.001	0.001	0.23	0.063	0.538	-0.768	
11	92086472	A>C	rs139731877	577	1	0	0	0.999	0.001	0.001	0.001	0.000	0.000	0.002	0.001	0.002	0.000	.	.	0.256	0.533	
11	92086496	T>A	.	576	1	0	1	0.999	0.001	0.001	0.66	0.131	0.841	0.533	
11	92086513	C>T	rs10830902	523	47	2	6	0.955	0.045	0.045	0.050	0.040	0.000	0.130	0.040	0.055	0.039	0.004	0.001	0.150	0.044	0.056	0.138	0.01	0.182	0.929	0.533	
11	92086649	G>A	rs10830903	531	44	1	2	0.96	0.04	0.04	0.050	0.040	0.000	0.110	0.040	0.050	0.036	0.004	0.001	0.135	0.044	0.056	0.124	.	.	0.056	0.533	
11	92086662	A>G	rs16917409	577	1	0	0	0.999	0.001	0.001	0.030	0.010	0.000	0.140	0.000	0.036	0.009	0.000	0.000	0.133	0.000	0.001	0.098	0.75	0.032	0.167	0.655	

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Genomic context **Frequencies** **Phenotype** **Effect**

Region overview Window size: 1271 nts
1003973 1004608 1005243

Detailed information Window size: 159 nts
1004529 1004608 1004687

Sequence

CCCCCTGCCGGCACCTTCCCCCATCCGTAGCCCCCTCCCCAACGGCGCTTGTCCGAGGGCTGGACTCGCACCCGACCGTCCCAGACGATCCAGCTGGTTGGCGGCAGCACTGGGAATGGTGAGACGGAGGCTCCGTACAAGTTACAGTAC

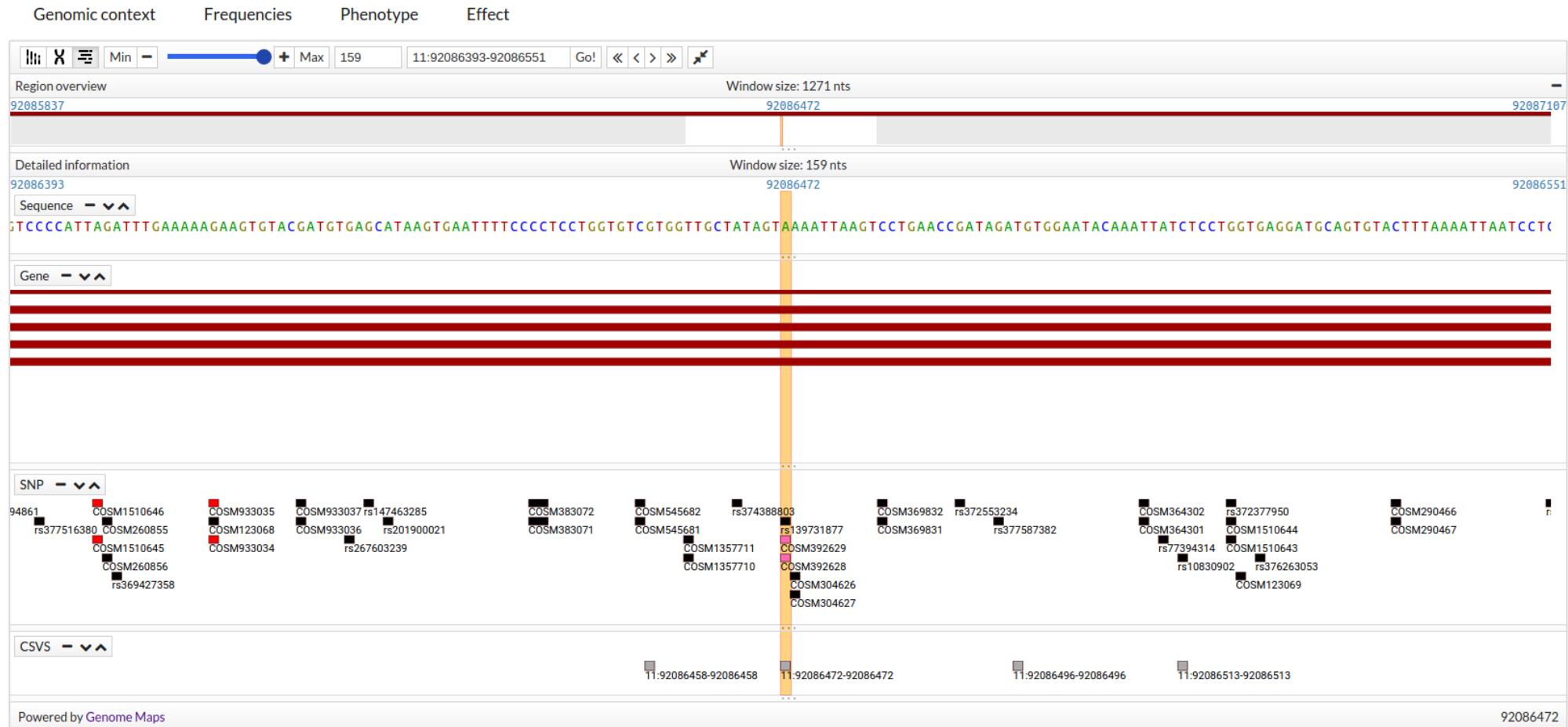
Gene

SNP

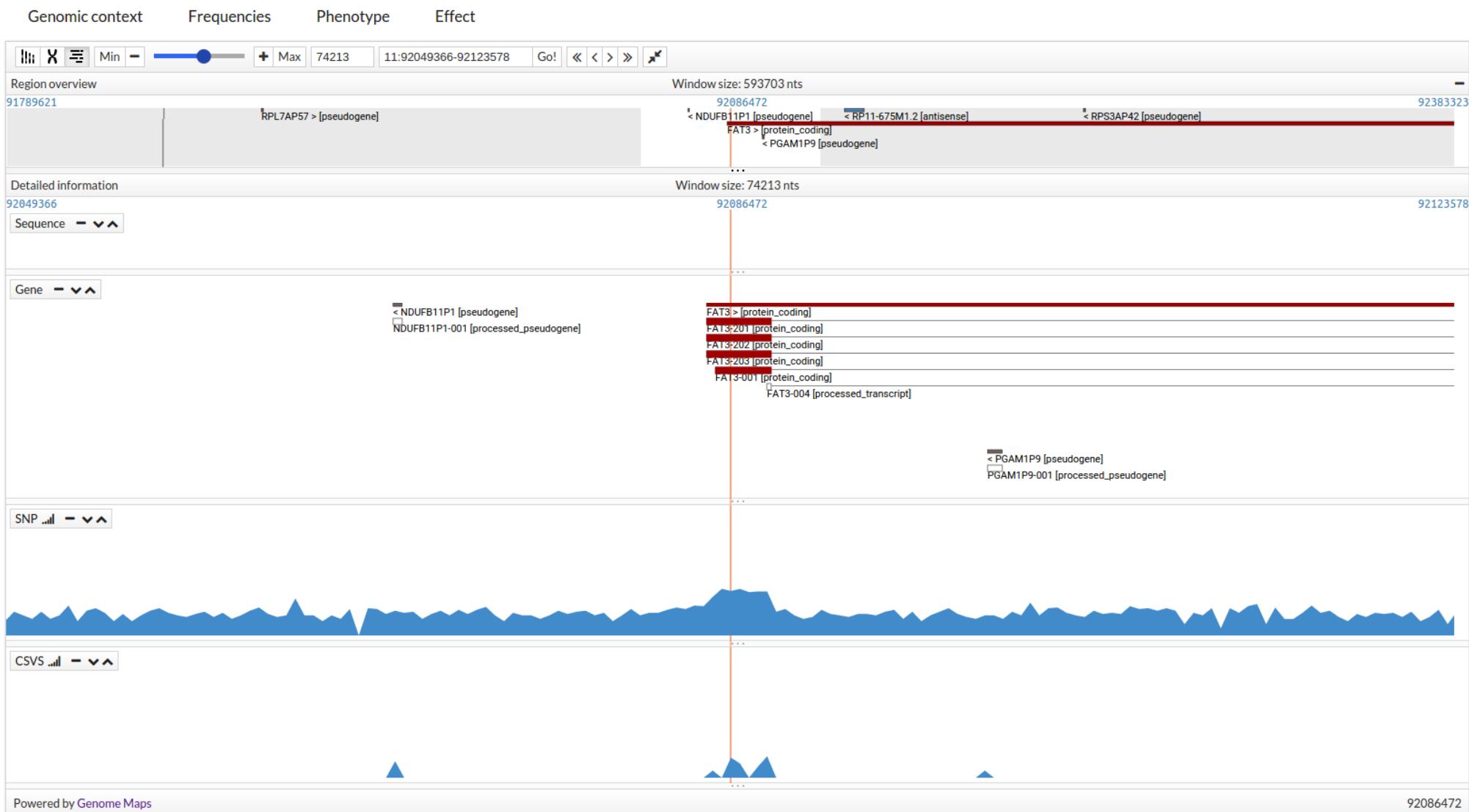
rs189753683 rs371314094 rs75134978

CSVs

CSVS



CSVS



CSVS

