

Accessing the 1000 Genomes Data

Paul Flicek

European Bioinformatics Institute

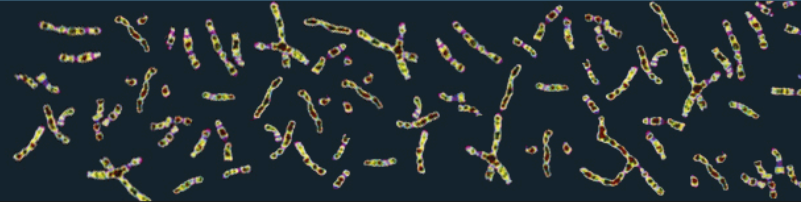
Data access

- General information
- File access
- 1000 Genomes Browser
- Tools
- Where to find help

www.1000genomes.org

1000 Genomes

A Deep Catalog of Human Genetic Variation



[Home](#) [About](#) [Data](#) [Analysis](#) [Participants](#) [Contact](#) [Browser](#) [Wiki](#) [FTP search](#)



Wednesday, 5th October 2011

Please Note: One of our data centres will be offline from Friday 21 October 2011 at 14.00 (GMT+1) to Monday 24 October, 12 noon (GMT+1). As a consequence, this service will remain unavailable for the duration of this planned maintenance.

LATEST ANNOUNCEMENTS

WEDNESDAY OCTOBER 12, 2011

October 2011 Intergrated Variant Set release #ICHG2011

This [October 2011](#) release represents an intergrated set of variant calls and phased genotypes including SNPs, short INDELS and Deletions based on low coverage and exome sequencing data across 1092 individuals.

Our [FAQ](#) contains instructions on how to get [smaller subsections](#) of these files

Data access links: [EBI](#) / [NCBI](#)

Link to additional information:[README file](#)

THURSDAY JUNE 23, 2011

June 2011 Data Release

Genotypes for 1094 individuals for the [May 2011 snp calls](#) from the 20101123 sequence and alignment release of the 1000 genomes project has now been made. This release is based on the GRCh37 assembly of the human genome and are released in the format [VCF 4.0](#)

Our [FAQ](#) contains instructions on how to get [smaller subsections](#) of these files

Data access links: [EBI](#) / [NCBI](#)

Link to additional information:[README file](#)

NAVIGATION

- [Frequently Asked Questions](#)

LINKS



[All Project Announcements](#)



[Sample and Project Information](#)



[Media Archive](#)



[Download the 1000 Genomes Pilot Paper](#)



[Project Contacts](#)

www.1000genomes.org

Recent project announcements

THURSDAY OCTOBER 13, 2011

[New Project Browser #ICHG2011](#)

A new Project browser based on our [Interim 20101123 phase 1 variant calls](#) has been released.

It is based on [Ensembl release 63](#).

Please read our [tutorial document](#) for more information about the browser.

WEDNESDAY OCTOBER 12, 2011

[#ICHG2011 1000 Genomes Project Resources Poster](#)

The Poster which was presented at the ICHG 2011 Poster session on 12th October is available in powerpoint format here

[The 1000 Genomes Project Resources](#)

TUESDAY SEPTEMBER 20, 2011

[New Sequence Data is Available](#)

Additional sequence data from the 1000 Genomes full project are now available. The current sequence.index file can be found at:

[20110920.sequence.index](#)

Data access links: [EBI](#) / [NCBI](#) / [Instructions for data download and Aspera](#)

[Sequence index and Statistics files](#)

[Sequence index file format](#)

[Complete current and previous announcements](#)

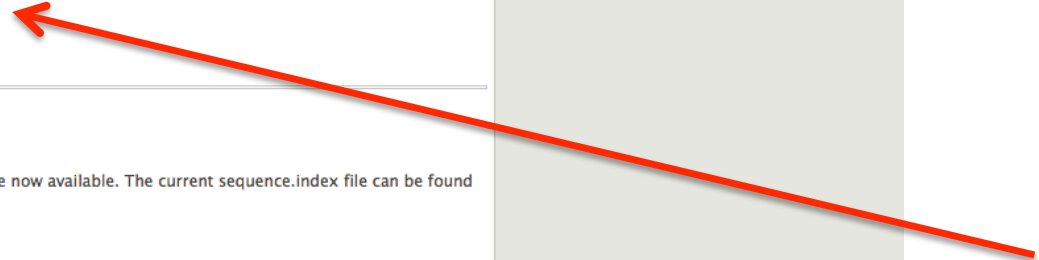
[Information regarding data access](#)



RSS Feed



Twitter



1000 Genomes Project Resources

L. Clarke, H. Zheng-Bradley, R. Smith, E Kuleshea, I Toneva, B. Vaughan, P. Flicek and 1000 Genomes Consortium
European Bioinformatics Institute, Wellcome Trust Genome Campus, Cambridge, CB10 1SA, UK

Introduction

The main goal of the 1000 genomes project is to establish a comprehensive and detailed catalogue of human genome variations; which in turn will empower association studies to identify disease-causing genes. The project now has data and variant genotypes for more than 1000 individuals in 14 populations. The ftp site contains more than 120Tbytes of data in 200,000 files.

DATA TYPE	FILE FORMAT	SIZE
sequence	FASTQ	43 Tbases raw sequence
alignment	BAM	56 Tbytes of BAM files
variants	VCF	38.9M SNPs ~4.7M short indels

Discoverability

Sequence, alignment and variant data is made available as quickly as possible through the project ftp site. (<ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/> | <ftp://ftp-trace.ncbi.nih.gov/1000genomes/>). With more than 200,000 files though discovering new data can be difficult.

The ftp site has a index updated nightly. This index is searchable from our website. <http://www.1000genome.org/ftpsearch>



The search allows users to specify which ftp site to get paths to, to get md5 checksums and also filter out high volume results like bam and fastq files

We also have various routes for users to discover new data.

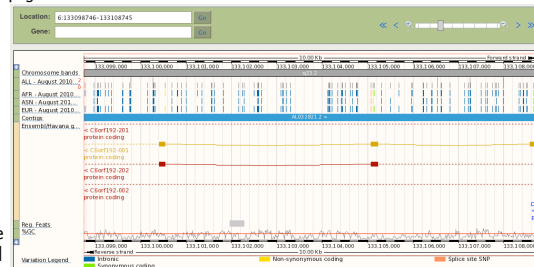
- Website <http://www.1000genomes.org/announcements>
- Twitter [@1000genomes](https://twitter.com/1000genomes)
- RSS <http://www.1000genomes.org/announcements/rss.xml>
- Email 1000announce@1000genomes.org

Visualization

<http://browser.1000genomes.org>

The 1000 Genomes project utilizes the Ensembl Browser to display our variant calls. We provide rapid access to project variant calls through the browser before they become available via dbSNP and DGVA.

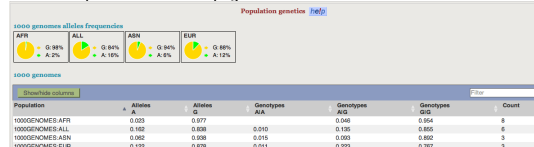
Tracks of 1000 genomes variants by population can be viewed in the location page:



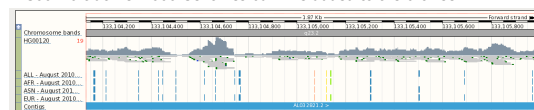
A list of variants can be obtained for any given transcript. In addition to basic information about a variant, PolyPhen and SIFT annotation are displayed to indicate the clinic significance of the variant.

Variant ID	Variant type	Alleles	Annotation	Protein	Consequence	SIFT	PolyPhen
rs1000000	Non-synonymous coding	TGG	stop	A	CTA_C10	Deleterious	Pathogenic
rs1000001	Non-synonymous coding	CTGAG	K	R.L	GGG_TSD	Deleterious	Pathogenic
rs1000002	Non-synonymous coding	GAA	R	F.L	GGG_TSD	Deleterious	Pathogenic
rs1000003	Non-synonymous coding	GAA	R	F.L	GGG_TSD	Deleterious	Pathogenic
rs1000004	Non-synonymous coding	AAG	K	V	TAT_TAD	Deleterious	Pathogenic
rs1000005	Non-synonymous coding	GT	V	E	GAG_TAD	Deleterious	Pathogenic
rs1000006	Non-synonymous coding	GT	K	R.L	GAG_AAC	Deleterious	Pathogenic
rs1000007	Non-synonymous coding	GGTTC	K	L.L	GGG_TAD	Deleterious	Pathogenic
rs1000008	Non-synonymous coding	GT	K	S.E	GAG_GAA	Deleterious	Pathogenic

Aallele frequency for individual variants in different populations is displayed on the 'Population Genetics' page.



Users can Attach remote files as custom tracks. In example below, the HG00120 track is 1000 Genomes bam file added to the browser.



Accessibility

<http://browser.1000genomes.org/tools.html>

The project provides several tools to help users access and interpret the data provided.

Variant Effect Predictor

The predictor takes a list of variant positions and alleles, and predicts the effects of each of these on any overlapping features (transcripts, regulatory features) annotated in Ensembl. An example output is shown below:

Variant ID	Alleles	Gene	Protein	Protein Change	Consequence	Position (chr:pos)	Position (chr:pos)	Transcript	Transcript Change	Effect	Impact
1.146880931	A	ENSG00000262424	ENSG00000262424	Protein	NON_TRANSCRIPT_CODING	100	100	ENSG00000262424	NON_TRANSCRIPT_CODING	None	Low
1.146880932	A	ENSG00000262424	ENSG00000262424	Protein	NON_TRANSCRIPT_CODING	100	100	ENSG00000262424	NON_TRANSCRIPT_CODING	None	Low
1.146880933	A	ENSG00000262424	ENSG00000262424	Protein	NON_TRANSCRIPT_CODING	100	100	ENSG00000262424	NON_TRANSCRIPT_CODING	None	Low
1.146880934	A	ENSG00000262424	ENSG00000262424	Protein	NON_TRANSCRIPT_CODING	100	100	ENSG00000262424	NON_TRANSCRIPT_CODING	None	Low
1.146880935	A	ENSG00000262424	ENSG00000262424	Protein	NON_TRANSCRIPT_CODING	100	100	ENSG00000262424	NON_TRANSCRIPT_CODING	None	Low
1.146880936	A	ENSG00000262424	ENSG00000262424	Protein	NON_TRANSCRIPT_CODING	100	100	ENSG00000262424	NON_TRANSCRIPT_CODING	None	Low
1.146880937	A	ENSG00000262424	ENSG00000262424	Protein	NON_TRANSCRIPT_CODING	100	100	ENSG00000262424	NON_TRANSCRIPT_CODING	None	Low
1.146880938	A	ENSG00000262424	ENSG00000262424	Protein	NON_TRANSCRIPT_CODING	100	100	ENSG00000262424	NON_TRANSCRIPT_CODING	None	Low
1.146880939	A	ENSG00000262424	ENSG00000262424	Protein	NON_TRANSCRIPT_CODING	100	100	ENSG00000262424	NON_TRANSCRIPT_CODING	None	Low
1.146880940	A	ENSG00000262424	ENSG00000262424	Protein	NON_TRANSCRIPT_CODING	100	100	ENSG00000262424	NON_TRANSCRIPT_CODING	None	Low

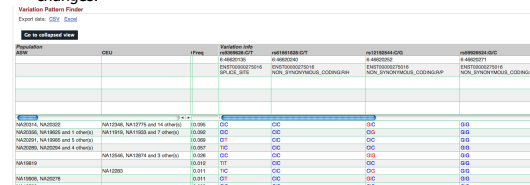
Data Slicer

Many of the 1000 Genomes files are large and cumbersome to handle. The Data Slicer allows users to get data for specific regions of the genome and to avoid having to download many gigabytes of data they don't need samples/populations you choose. Below is the Data Slicer input interface:



Variation Pattern Finder

- The Variation Pattern Finder (VPF) allows one to look for patterns of shared variation between individuals in the a VCF file.
- Within a vcf file different samples have different combination of variation genotypes. The VPF looks for distinct variation combinations within a user specified region, shared by different individuals.
- The VPF only on variations that functional consequences for protein coding genes such as non-synonymous coding SNPs and splice site changes.

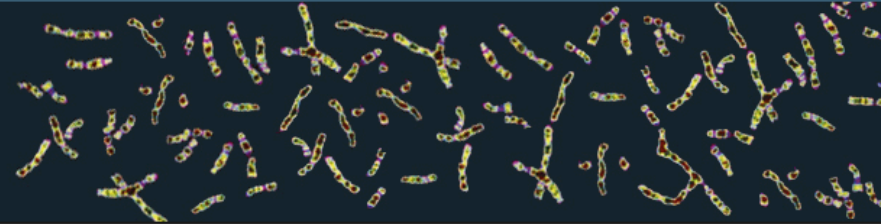


Acknowledgements

We would like to thank the Ensembl variation team for all their help, particularly Will McLaren and Graham Ritchie. Funding: The Wellcome Trust

1000 Genomes

A Deep Catalog of Human Genetic Variation



[Home](#) [About](#) [Data](#) [Analysis](#) [Participants](#) [Contact](#) [Browser](#) [Wiki](#) [FTP search](#)

Search

[Home](#) >

1000 GENOMES DATA AND SAMPLE INFORMATION

The 1000 Genomes Project is a community resource project that aims to release data rapidly for the benefit of the scientific community.

[Description of data released by the project](#)
[How to Access 1000 Genomes Data](#)
[Data Release Policy](#)
[Sample Availability](#)
[Use of the Project data, presentations and publications, and authorship](#)

DATA RELEASED BY THE 1000 GENOMES PROJECT

Sample lists and sequencing progress

A summary of sequencing done for each of the three pilot projects is available [here](#). The list of samples and allocations is provided in a [spreadsheet](#).

Variant Calls

The pilot variant calls are available in [vcf format](#) from [EBI|NCBI](#)

Alignments

The main project alignments are available in [BAM](#) format. A list of the files currently available can be found in the alignment index [EBI|NCBI](#). Alignment statistics can be found in the alignment_indices directory [EBI|NCBI](#). There is also a [README](#) which explains the alignment process and file layout

Raw sequence files

The main project raw sequence data is available in fastq format. A list of files currently available can be found in the sequence.index [EBI|NCBI](#) Sequence statistics can be found in the sequence_indices directory [EBI|NCBI](#). There is also a [README](#) which explains the sequence processing and the file layout

NAVIGATION

- [Frequently Asked Questions](#)

LINKS



[All project announcements](#)



[Files and formats](#)



[Software tools](#)



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[Project Contacts](#)


















Data access

- General information
- File access
- 1000 Genomes Browser
- Tools
- Where to find help

ftp://ftp.1000genomes.ebi.ac.uk
 ftp://ftp-trace.ncbi.nih.gov/1000genomes/ftp

Index of ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/

 Up to higher level directory

Name	Size	Last Modified
 CHANGELOG	109 KB	13/10/2011 00:58:00
 README.alignment_data	12 KB	26/01/2011 00:00:00
 README.ftp_structure <	9 KB	04/04/2011 00:00:00
 README.pilot_data	7 KB	14/08/2010 00:00:00
 README.populations	7 KB	23/07/2011 21:03:00
 README.sequence_data	8543 KB	28/02/2011 00:00:00
 alignment.index		
 alignment_indices		
 changelog_details		13/10/2011 00:59:00
 current.tree	28458 KB	13/10/2011 00:58:00
 data		26/09/2011 19:48:00
 exome_alignment.index		
 pilot_data		27/10/2010 00:00:00
 release <		12/10/2011 15:18:00
 sequence.index		
 sequence_indices		10/10/2011 21:42:00
 technical <		14/07/2011 16:57:00

Site documentation

Sequences & alignments by sample ID

Data sets to accompany the pilot data publication.

Current and archive data set releases

Pre-release data sets and project working materials

1000 Genomes

A Deep Catalog of Human Genetic Variation



[Home](#) [About](#) [Data](#) [Analysis](#) [Participants](#) [Contact](#) [Browser](#) [Wiki](#) [FTP search](#)

[Home](#) >

KEY FILE FORMATS

Information on key file formats is normally provided within README files located near the relevant data on the FTP site. Information on the major formats is also collected here. Tools developed by the 1000 Genomes project or appropriate to work with the data from the project are listed on the [tools](#) page.

[Index file formats](#)
[Data file formats](#)

INDEX FILE FORMATS

Sequence index

The sequence.index file is a tab delimited file containing all the meta data you should need to download and subset the files on this ftp site by individual, library, experiment and sequencing technology.

The columns are:

1. FASTQ_FILE, path to fastq file on ftp site
2. MD5, md5sum of file
3. RUN_ID, SRA/ERA run accession
4. STUDY_ID, SRA/ERA study accession
5. STUDY_NAME, Name of study
6. CENTER_NAME, Submission centre name
7. SUBMISSION_ID, SRA/ERA submission accession
8. SUBMISSION_DATE, Date sequence submitted, YYYY-MM-DAY
9. SAMPLE_ID, SRA/ERA sample accession
10. SAMPLE_NAME, Sample name
11. POPULATION, Sample population
12. EXPERIMENT_ID, Experiment accession
13. INSTRUMENT_PLATFORM, Type of sequencing machine
14. INSTRUMENT_MODEL, Model of sequencing machine
15. LIBRARY_NAME, Library name
16. RUN_NAME, Name of machine run
17. RUN_BLOCK_NAME, Name of machine run sector
18. INSERT_SIZE, Submitter specified insert size
19. LIBRARY_LAYOUT, Library layout, this can be either PAIRED or SINGLE
20. PAIRED_FASTQ, Name of mate pair file if exists (Runs with failed mates will have a library layout of PAIRED but no paired fastq file)
21. WITHDRAWN, 0/1 to indicate if the file has been withdrawn, only present if a file has been withdrawn
22. WITHDRAWN_DATE, date of withdrawal, this should only be defined if a file is withdrawn
23. COMMENT, comment about reason for withdrawal
24. READ_COUNT, read count for the file
25. BASE_COUNT, basepair count for the file
26. ANALYSIS_GROUP, the analysis group of the sequence, this reflects sequencing strategy. Current this includes low coverage, high coverage and exon targeted to reflect the 3 strategies used by the 1000 genomes project.

Any run_id can have up to 3 files associated with it. Single runs have one file. Paired runs can have anywhere from 1 to 3 files depending on the success of the pairing.

NAVIGATION

- [Frequently Asked Questions](#)

LINKS



[All project announcements](#)



[Files and formats](#)



[Software tools](#)



[Download the 1000 Genomes Pilot Paper](#)



[Project Contacts](#)

Data formats and key tools

THE SEQUENCE ALIGNMENT/MAP (SAM) FORMAT

Heng Li^{1,†}, Bob Handsaker^{2,†}, Alec Wysoker², Tim Fennell², Jue Ruan³, Nils Homer⁴, Gabor Marth⁵, Goncalo Abecasis⁶, Richard Durbin^{1,*} and 1000 Genome Project Data Processing Subgroup⁷

¹Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Cambridge, CB10 1SA, UK, ²Broad Institute of MIT and Harvard, Cambridge, MA 02141, USA, ³Beijing Institute of Genomics, Chinese Academy of Science, Beijing 100029, China, ⁴Department of Computer Science, University of California Los Angeles, Los Angeles, CA 90095, ⁵Department of Biology, Boston College, Chestnut Hill, MA 02467, ⁶Center for Statistical Genetics, Department of Biostatistics, University of Michigan, Ann Arbor, MI 48109, USA and ⁷<http://1000genomes.org>

Received on April 28, 2009; revised on May 28, 2009; accepted on May 30, 2009

Advance Access publication June 8, 2009

Associate Editor: Alfonso Valencia

BAM alignment files

ABSTRACT

Summary: The Sequence Alignment/Map (SAM) format is a generic alignment format for storing read alignments against reference sequences, supporting short and long reads (up to 128 Mbp) produced by different sequencing platforms. It is flexible in style, compact in size, efficient in random access and is the format in which alignments from the 1000 Genomes Project are released. SAMtools implements various utilities for post-processing alignments in the SAM format, such as indexing, variant caller and alignment viewer,

2 METHODS

2.1 The SAM format

2.1.1 Overview of the SAM format The SAM format consists of one header section and one alignment section. The lines in the header section start with character '@', and lines in the alignment section do not. All lines are TAB delimited. An example is shown in Figure 1b.

In SAM, each alignment line has 11 mandatory fields and a variable number of optional fields. The mandatory fields are briefly described in Table 1. They must be present but their value can be a '*' or a zero (depending

BIOINFORMATICS APPLICATIONS NOTE

Vol. 27 no. 15 2011, pages 2156–2158
doi:10.1093/bioinformatics/btr330

Sequence analysis

Advance Access publication June 7, 2011

The variant call format and VCFtools

Petr Danecek^{1,†}, Adam Auton^{2,†}, Goncalo Abecasis³, Cornelis A. Albers¹, Eric Banks⁴, Mark A. DePristo⁴, Robert E. Handsaker⁴, Gerton Lunter², Gabor T. Marth⁵, Stephen T. Sherry⁶, Gilean McVean^{2,7}, Richard Durbin^{1,*} and 1000 Genomes Project Analysis Group[†]

¹Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Cambridge CB10 1SA, ²Wellcome Trust Centre for Human Genetics, University of Oxford, Oxford OX3 7BN, UK, ³Center for Statistical Genetics, Department of Biostatistics, University of Michigan, Ann Arbor, MI 48109, ⁴Program in Medical and Population Genetics, Broad Institute of MIT and Harvard, Cambridge, MA 02141, ⁵Department of Biology, Boston College, MA 02467, ⁶National Institutes of Health National Center for Biotechnology Information, MD 20894, USA and ⁷Department of Statistics,

University of Oxford, Oxford OX1 3TG, UK
Associate Editor: John Quackenbush

VCF variant files

Tabix: fast retrieval of sequence features from generic TAB-delimited files

Heng Li

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Associate Editor: Dmitrij Frishman

ABSTRACT

Summary: Tabix is the first generic tool that indexes position sorted files in TAB-delimited formats such as GFF, BED, PSL, SAM and SQL export, and quickly retrieves features overlapping specified regions. Tabix features include few seek function calls per query, data compression with gzip compatibility and direct FTP/HTTP access. Tabix is implemented as a free command-line tool as well as a library in C, Java, Perl and Python. It is particularly useful for manually examining local genomic features on the command line and enables

2 METHODS

Tabix indexing is a generalization of BAM indexing for generic TAB-delimited files. It inherits all the advantages of BAM indexing, including data compression and efficient random access in terms of few seek function calls per query.

2.1 Sorting and BGZF compression

Before being indexed, the data file needs to be sorted first by sequence name and then by leftmost coordinate, which can be done with the standard Unix

All indexed for fast retrieval

1000 Genomes is in the Amazon cloud

1KG pilot content (BAM) is available at
`s3://1000genomes.s3.amazonaws.com`

You can see the XML at

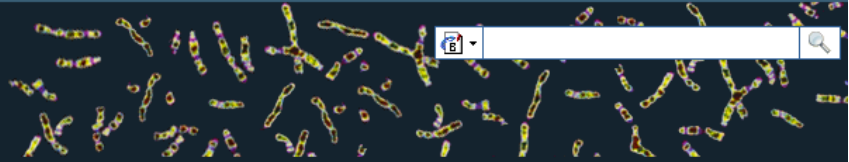
<http://1000genomes.s3.amazonaws.com>

Data access

- General information
- File access
- 1000 Genomes Browser
- Tools
- Where to find help

1000 Genomes

A Deep Catalog of Human Genetic Variation



Tools | Help

Search 1000 Genomes

e.g. gene BRCA2 or Chromosome 6:133098746-133108745

Start Browsing 1000 Genomes data



[Browse Human](#) →
GRCh37

[Protein variations](#) →
View the consequences of sequence variation at the level of each protein in the genome.

[Individual genotypes](#) →
Show different individual's genotype, for a variant.

Browser update September 2011

based on interim Main project data from 20101123 for 1094 individuals and ensembl release 63. The data can be found on [the ftp site](#).

Please see www.1000genomes.org for more information about the data presented here and instructions for downloading the complete data set.

- [View sample data](#)

The 1000 Genomes Browser

Ensembl-based browser provides early access to 1000genomes data

In order to facilitate immediate analysis of the 1000 Genomes Project data by the whole scientific community, this browser (based on Ensembl) integrates the SNP calls from an [interim release 20101123](#). This data has been submitted to dbSNP, and once rsid's have been allocated, will be absorbed into the UCSC and Ensembl browsers according to their respective release cycles. Until that point any non rs SNP id's on this site are temporary and will NOT be maintained.

Links



[1000 Genomes](#) →
More information about the 1000 Genomes Project on the 1000 genomes main site.



[Pilot browser](#) →
This browser is based on Ensembl release 60 and represents the variant set analysed as part of [A map of human genome variation from population-scale sequencing](#), Nature 467, 1061.1073.



[Tutorial](#) →
The 1000 Genomes Browser Tutorial.

The 1000 Genomes Project is an international collaborative project described at www.1000genomes.org.

The 1000 Genomes Browser is based on Ensembl web code.

Ensembl is a joint project of EMBL-EBI  and the [Wellcome Trust Sanger Institute](#)



<http://browser.1000genomes.org>

1000 Genomes

A Deep Catalog of Human Genetic Variation



Human (GRCh37)

Location: 1:114,356,433-114,414,381

Gene: PTPN22

Transcript: PTPN22-001

Tools | Help

Location-based displays

- Whole genome
- Chromosome summary
- Region overview
- Region in detail**
- Genetic Variation
 - Resequencing (20)
 - Linkage Data
 - Markers

Configure this page

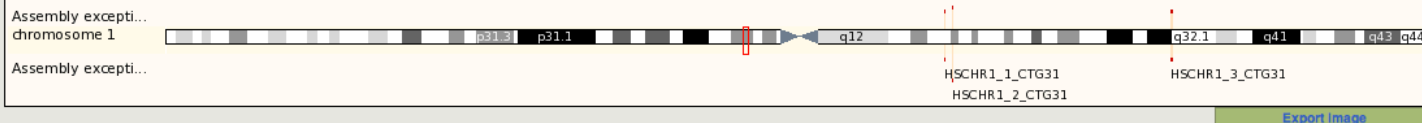
Manage your data

Export data

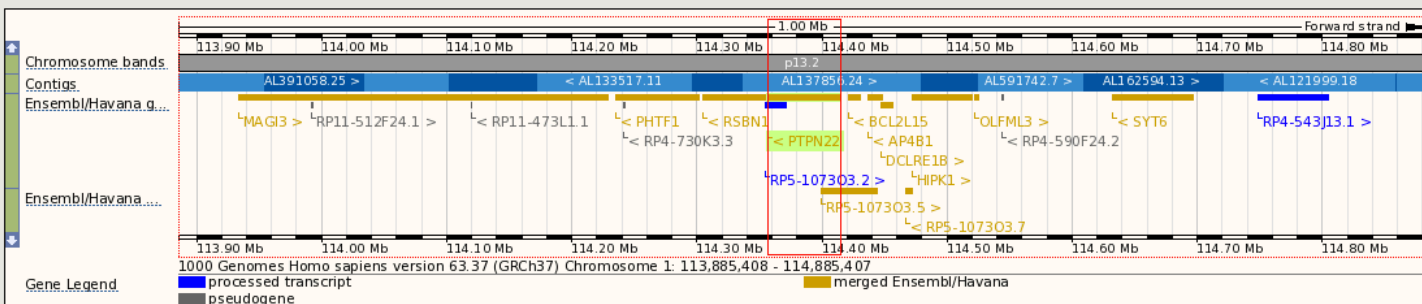
Get VCF data

Bookmark this page

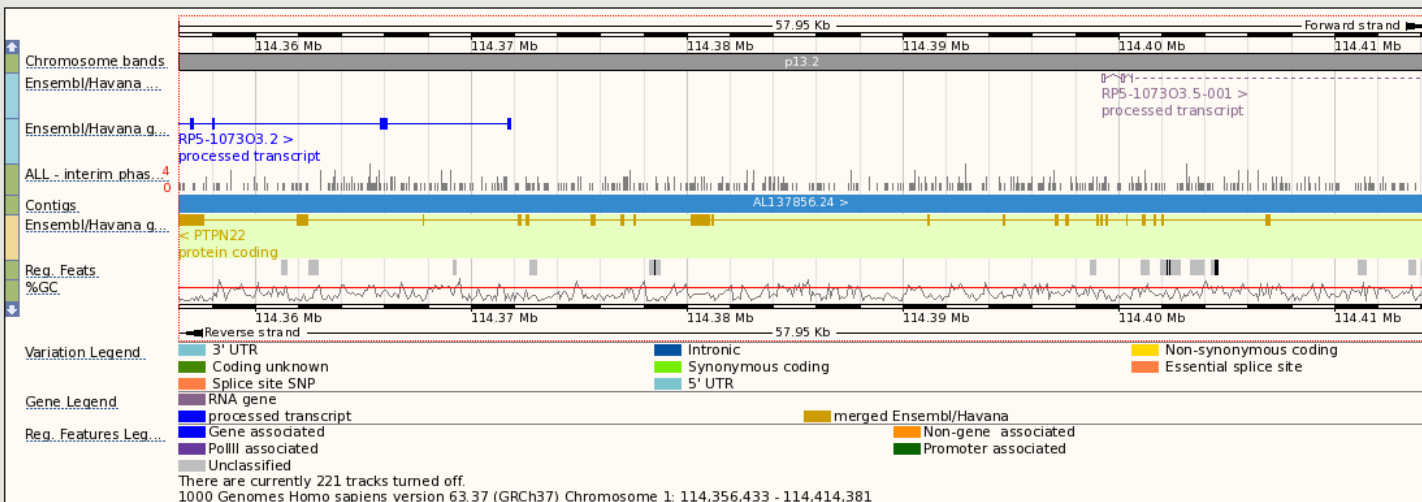
Chromosome 1: 114,356,433-114,414,381



Region in detail [help](#)



Location: Go Gene: Go



Gene-based displays

- Gene summary
- Splice variants (6)
- Supporting evidence
- Sequence
- External references
- Regulation
- Genetic Variation
- Variation Table
- Variation Image
- External Data
- ID History
- Gene history

- Configure this page
- Manage your data
- Export data
- Bookmark this page

Description breast cancer 2, early onset [Source:HGNC Symbol;Acc:1101]
 Location [Chromosome 13: 32,889,811-32,973,805](#) forward strand.
 Transcripts There are 6 transcripts in this gene

Name	Transcript ID	Length (bp)	Protein ID	Length (aa)	Biotype	CCDS
BRCA2-001	ENST00000380152	10930	ENSP00000369407	3418	Protein coding	CCDS9344
BRCA2-003	ENST00000530893	2009	ENSP00000435689	602	Protein coding	-
BRCA2-201	ENST00000544465	10984	ENSP00000439202	3418	Protein coding	CCDS9344
BRCA2-002	ENST00000470094	842	ENSP00000434988	186	Nonsense mediated decay	-
BRCA2-005	ENST00000507792	495	ENSP00000433188	64	Nonsense mediated decay	-
BRCA2-006	ENST00000537776	523	No protein product	-	Retained intron	-

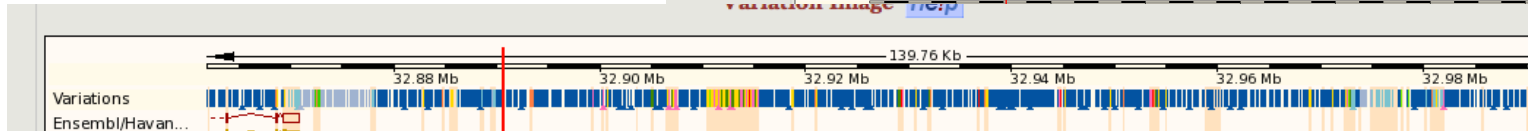
Transcript and Gene level displays

In 1000 Genomes we provide displays at two levels:

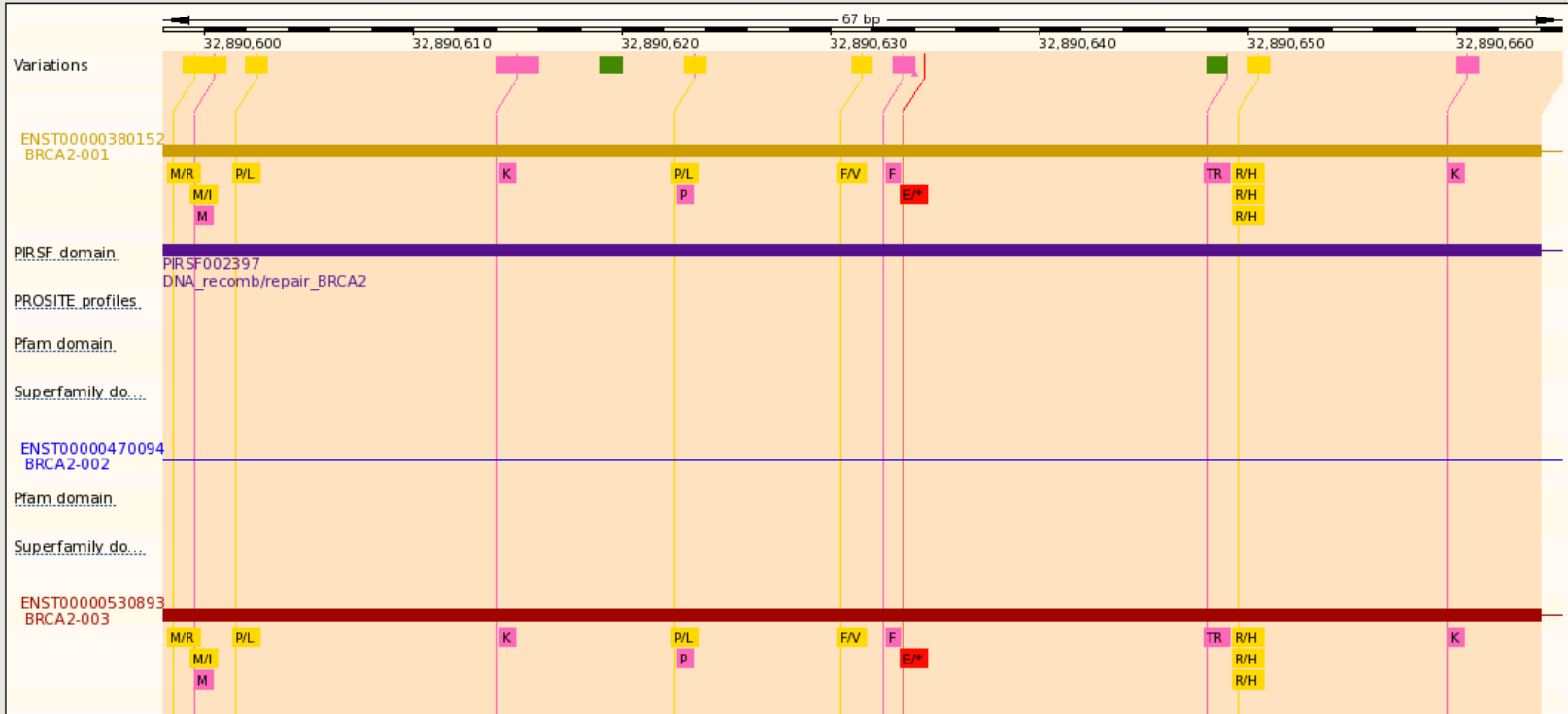
- Transcript views which provide information specific to an individual transcript such as the cDNA and CDS sequences and protein domain annotation.
- Gene views which provide displays for data associated at the gene level such as orthologues, paralogues, regulatory regions and splice variants.

This view is a gene level view. To access the transcript level displays select a Transcript ID in the table above and then navigate to the information you want using the menu at the left hand side of the page. To return to viewing gene level information click on the Gene tab in the menu bar at the top of the page.

Gene variation zoom



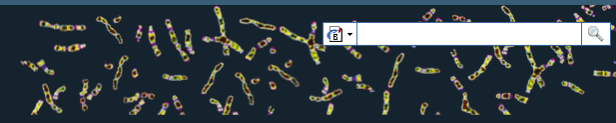
Location: Variation ID:



None of the intronic variations are removed by the Context filter.

1000 Genomes

A Deep Catalog of Human Genetic Variation



Human (GRCh37) Location: 6:74,125,388-74,126,388 Variation: rs311685

- Variation displays
 - Flanking sequence
 - Gene/Transcript (3)
 - Population genetics (46)
 - Individual genotypes (2769)
 - Genomic context
 - Phenotype Data
 - Phylogenetic Context
 - External Data

- Configure this page
- Manage your data
- Export data
- Get VCF data
- Bookmark this page
- Download view as CSV

Variation: rs311685

Variation class SNP (rs311685 source dbSNP_132 - Variants (including SNPs and indels) imported from dbSNP [http://www.ncbi.nlm.nih.gov/projects/SNP/])

Synonyms Affy GeneChip 100K Array SNP_A-1679873
 Affy GenomeWideSNP_6.0 AFFY_6_1M_SNP_A-8668494, SNP_A-8668494
 dbSNP rs58378291, rs17756820, rs2794514, rs524803, rs3173186, rs11567000, rs17421786
 ENSEMBL ENSNP9062281
 Illumina_Human1M-duoV3 rs311685
 Uniprot VAR_057235

Present in 1000 genomes - High coverage - Trios (1000 genomes - High coverage - Trios - CEU, 1000 genomes - High coverage - Trios - YRI), 1000 genomes - Low coverage - CEU, 1000 genomes - Low coverage - CHB+JPT, 1000 genomes - Low coverage - YRI, ALL - interim phase 1 - 1000 Genomes (AFR - interim phase 1 - 1000 Genomes, AMR - interim phase 1 - 1000 Genomes, ASN - interim phase 1 - 1000 Genomes, EUR - interim phase 1 - 1000 Genomes), ENSEMBL:Venter,HapMap

Alleles A/G (Ambiguity code: R)

Ancestral allele A

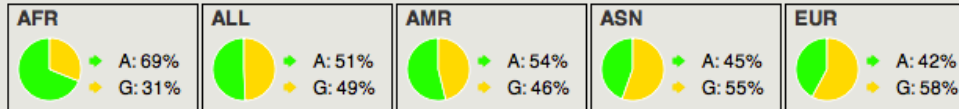
Location This feature maps to 6:74125888 (forward strand) | [View in location tab](#)

Validation status Proven by cluster, frequency, doublehit, 1000Genome HapMap variant

HGVIS names This feature has 4 HGVIS names - click the plus to show

• Population

1000 genomes alleles frequencies



1000 genomes

Population	Alleles A	Alleles G	Genotypes A/A	Genotypes A/G	Genotypes G/G	Count
1000GENOMES:AFR	0.689	0.311	0.463	0.451	0.085	114
1000GENOMES:ALL	0.507	0.493	0.269	0.477	0.254	294
1000GENOMES:AMR	0.539	0.461	0.293	0.492	0.215	53
1000GENOMES:ASN	0.446	0.554	0.199	0.493	0.308	57
1000GENOMES:EUR	0.421	0.579	0.184	0.475	0.341	70

1000 genomes pilot

Population	ssID	Submitter	Alleles A	Alleles G	Count
1000GENOMES:pilot_1_CEU_low_coverage_panel	ss233534774	1000GENOMES	0.458	0.542	
1000GENOMES:pilot_1_CHB+JPT_low_coverage_panel	ss240577229	1000GENOMES	0.400	0.600	
1000GENOMES:pilot_1_YRI_low_coverage_panel	ss222470667	1000GENOMES	0.729	0.271	

CSHL-HAPMAP:HAPMAP-LWK	ss5253350	TSC-CSHL	0.667	0.333	0.400	0.533	0.067	6
CSHL-HAPMAP:HAPMAP-MEX	ss5253350	TSC-CSHL	0.490	0.510	0.245	0.490	0.285	13
CSHL-HAPMAP:HAPMAP-MKK	ss5253350	TSC-CSHL	0.833	0.367	0.410	0.446	0.144	20
CSHL-HAPMAP:HAPMAP-TSI	ss5253350	TSC-CSHL	0.488	0.512	0.226	0.524	0.250	21
CSHL-HAPMAP:HapMap-YRI	ss5253350	TSC-CSHL	0.708	0.292	0.487	0.442	0.071	8
SEATTLESEQ:Eight-Hapmap-Samples	ss159712995	SEATTLESEQ	unknown	unknown				

Other data (26)

1000 Genomes

A Deep Catalog of Human Genetic Variation

Human (GRCh37) Location: 1:114,356,433-114,414,381 Gene: PTPN22 Transcript: PTPN22-001

Transcript: PTPN22-001 (ENST00000359785)

Description protein tyrosine phosphatase, non-receptor type 22 (lymphoid) [Source:HGNC Symbol;Acc:9652]
Location Chromosome 1:114,356,433-114,414,381 reverse strand.
Gene This transcript is a product of gene [ENSG00000134242](#) - There are 12 transcripts in this gene

Name	Transcript ID	Length (bp)	Protein ID	Length (aa)	Biotype	CCDS
PTPN22-001	ENST00000359785	3654	ENSP00000352833	807	Protein coding	CCDS8883
PTPN22-002	ENST00000460620	1794	ENSP00000433141	179	Protein coding	-
PTPN22-004	ENST00000528414	3424	ENSP00000435176	752	Protein coding	-
PTPN22-006	ENST00000420377	2726	ENSP00000388229	795	Protein coding	-
PTPN22-007	ENST00000525799	2118	ENSP00000432674	668	Protein coding	-
PTPN22-201	ENST00000354605	2347	ENSP00000346621	691	Protein coding	CCDS884
PTPN22-202	ENST00000358253	2414	ENSP00000439372	563	Protein coding	-
PTPN22-008	ENST00000532224	2421	ENSP00000431249	135	Nonsense mediated decay	-
PTPN22-010	ENST00000529045	527	ENSP00000434932	92	Nonsense mediated decay	-
PTPN22-009	ENST00000534519	565	-	-	Processed transcript	-
PTPN22-003	ENST00000484147	2258	-	-	Retained intron	-
PTPN22-005	ENST00000469077	562	-	-	Retained intron	-

Transcript and Gene level displays

Views in 1000 Genomes are separated into gene based views and transcript based views according to which level the information is more appropriately associated with. This view is a transcript level view. To flip between the two sets of views you can click on the Gene and Transcript tabs in the menu bar at the top of the page.

Variations [help](#)

Show All entries Show/hide columns Filter

Residue	Variation ID	Variation type	Alleles	Ambiguity code	Residues	Codons	SIFT	PolyPhen
16	rs74163639	Synonymous coding	G/A	R	S	AGC, AGT	-	-
49	rs61745743	Synonymous coding	A/G	R	A	GCT, GCC	-	-
71	rs74163642	Non-synonymous coding	A/G	R	V, A	GTA, GCA	deleterious	probably damaging
141	rs115552198	Non-synonymous coding	G/A	R	R, C	CGC, TGC	deleterious	probably damaging
177	1KG_1_114399013	Synonymous coding	C/T	Y	K	AAG, AAA	-	-
183	rs34590413	Stop gained	G/A	R	R, *	CGA, TGA	-	-
201	rs74163647	Non-synonymous coding	G/A	R	S, F	TCT, TTT	deleterious	probably damaging
206	rs61738614	Non-synonymous coding	A/C	M	L, R	CTT, CGT	deleterious	probably damaging
232	rs78195073	Synonymous coding	T/C	Y	G	GGA, GGG	-	-
247	rs35910094	Synonymous coding	T/G	K	L	CTA, CTC	-	-
263	rs33996649	Non-synonymous coding	C/T	Y	R, Q	CGG, CAG	tolerated	benign
266	rs72650670	Non-synonymous coding	G/A	R	R, W	CGG, TGG	deleterious	probably damaging
277	rs72483511	Stop gained, Splice site	C/A	M	E, *	GAA, TAA	-	-
324	rs113984534	Synonymous coding	A/G	R	Y	TAT, TAC	-	-
366	rs74163654	Synonymous coding	C/T	Y	E	GAG, GAA	-	-
370	rs72650671	Non-synonymous coding	G/T	K	H, N	CAC, AAC	deleterious	possibly damaging
388	rs77913785	Non-synonymous coding	G/T	K	D, E	GAC, GAA	deleterious	benign
413	1KG_1_114380784	Non-synonymous coding	T/G	K	Q, P	CAA, CCA	deleterious	benign
414	1KG_1_114380780	Synonymous coding	A/G	R	S	AGT, AGC	-	-
427	rs112873647	Non-synonymous coding	-/ATT	-	-, N	-, AAT	-	-
444	rs74163655	Non-synonymous coding	T/A	W	I, L	ATA, TTA	tolerated	benign
447	rs112191110	Non-synonymous coding	G/A	R	T, I	ACC, ATC	deleterious	probably damaging
452	rs56174946	Synonymous coding	A/G	R	F	TTT, TTC	-	-
456	rs72650672	Non-synonymous coding	G/C	S	Q, E	CAG, GAG	deleterious	possibly damaging
477	rs74163656	Synonymous coding	A/G	R	L	CAT, CAC	-	-

- SIFT
- PolyPhen

Download view as CSV

File upload to view with 1000 Genomes data

Custom Data

Data Management

- Upload Data
- Attach DAS
- Attach Remote File**
- Manage Data
- Features on Karyotype
- Data Converters
 - Assembly Converter
 - ID History Converter
 - Variant Effect Predictor
 - Data Slicer
 - Variation Pattern Finder

Tip

Accessing data via a URL can be slow unless you use an indexed format such as BAM. However it has the advantage that you always see the same data as the file on your own machine.

We currently accept attachment of the following formats: BAM, BED, bedGraph, GBrowse, Generic, GFF, GTF, PSL, VCF, WIG. VCF files must be indexed prior to attachment.

File URL:
(e.g. <http://www.example.com/MyProject/mydata.gff>)

Data format:

Name for this track:

Next >

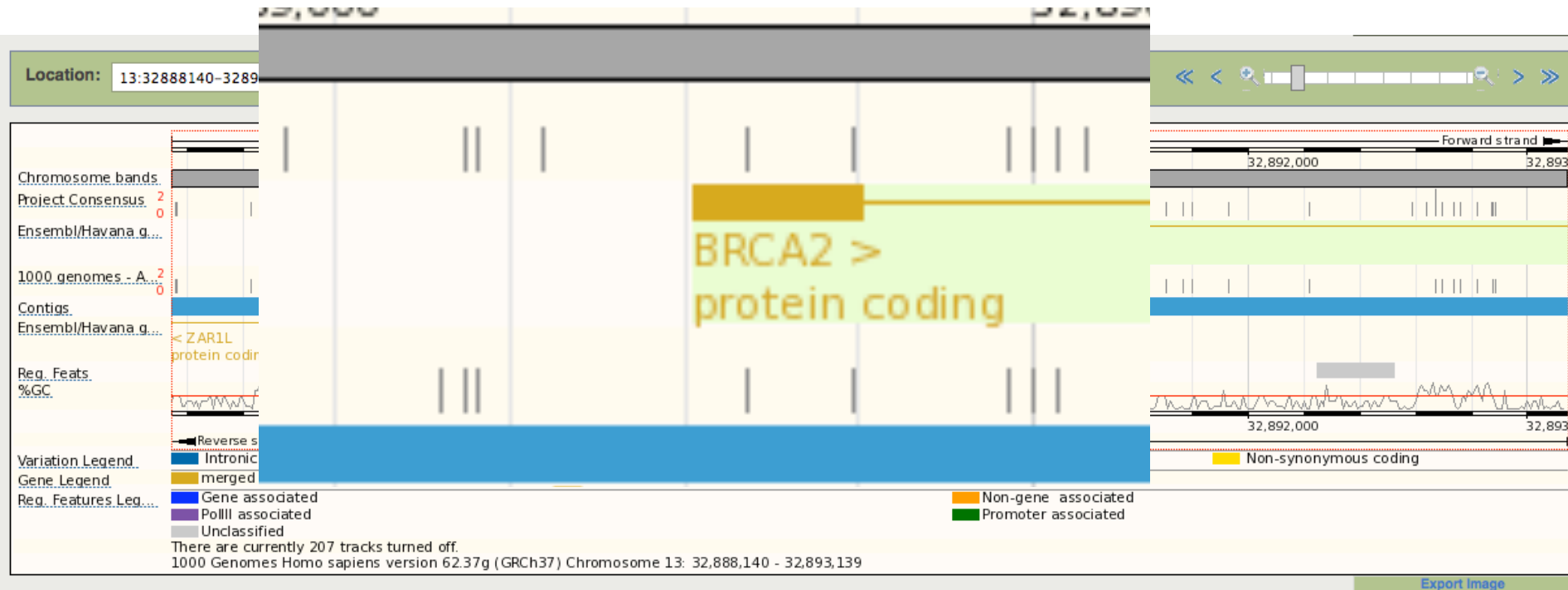
- Supports popular file types:
 - BAM, BED, bedGraph, BigWig, GBrowse, Generic, GFF, GTF, PSL, VCF*, WIG

* VCF must be indexed

Uploaded VCF

Example:

Comparison of August calls and
/technical/working/20110502_vqsr_phase1_wgs_snps/ALL.wgs.phase1.projectConsensus.snps.sites.vcf.gz



1000 Genomes Browser

- For further information on the capabilities of the browser and its use, attend the Ensembl “New Users” Workshop on Saturday at 12:30

SATURDAY, October 15

*12:30 PM - 1:30 PM



Ensembl 'New Users' Workshop: Web site and BioMart
For further information, e-mail xose@ebi.ac.uk

Convention Center
Room 524, Level 5

1000 Genomes Pilot

A Deep Catalog of Human Genetic Variation



Tools | Help

Search 1000 Genomes

Go

e.g. gene BRCA2 or Chromosome 6:133017695-133161157

Start Browsing 1000 Genomes data



[Browse Human](#) →
NCBI 36

[Transcript SNP view](#) →

View the consequences of sequence variation at the level of each transcript in the genome.

[Sequence Alignment View](#) →

Shows read-depth data alongside SNPs

Pilot Browser

based on the full pilot project data described in [A map of human genome variation from population-scale sequencing](#), Nature 467, 1061.1073.

Please see www.1000genomes.org for more information about the data presented here and instructions for downloading the complete data set.

- [View sample data](#)

The 1000 Genomes Browser

Ensembl-based browser provides access to 1000genomes data

This browser represents the variant set analysed as part of [A map of human genome variation from population-scale sequencing](#), Nature 467, 1061.1073. The data behind this browser can be found on [the 1000 Genomes ftp site](#). This data can also be found in Ensembl and UCSC.

Links



[1000 Genomes](#) →

More information about the 1000 Genomes Project on the 1000 genomes main site.

The 1000 Genomes Project is an international collaborative project described at www.1000genomes.org.

The 1000 Genomes Browser is based on Ensembl web code.

Ensembl is a joint project of EMBL-EBI  and the [Wellcome Trust Sanger Institute](#)



The logo image courtesy of [Andy Martin](#)

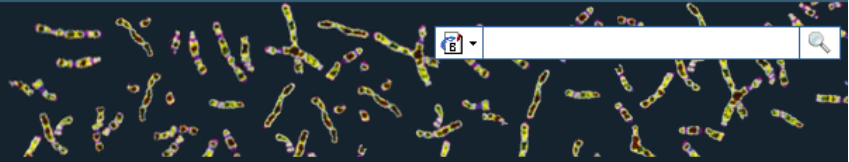
<http://pilotbrowser.1000genomes.org>

Data access

- General information
- File access
- 1000 Genomes Browser
- Tools
- Where to find help

1000 Genomes

A Deep Catalog of Human Genetic Variation



Tools | Help

Search 1000 Genomes

e.g. gene BRCA2 or Chromosome 6:133098746-133108745

Start Browsing 1000 Genomes data



[Browse Human](#) →
GRCh37

[Protein variations](#) →
View the consequences of sequence variation at the level of each protein in the genome.

[Individual genotypes](#) →
Show different individual's genotype, for a variant.

Browser update September 2011

based on interim Main project data from 20101123 for 1094 individuals and ensembl release 63. The data can be found on [the ftp site](#).

Please see www.1000genomes.org for more information about the data presented here and instructions for downloading the complete data set.

- [View sample data](#)

The 1000 Genomes Browser

Ensembl-based browser provides early access to 1000genomes data

In order to facilitate immediate analysis of the 1000 Genomes Project data by the whole scientific community, this browser (based on Ensembl) integrates the SNP calls from an [interim release 20101123](#). This data has been submitted to dbSNP, and once rsid's have been allocated, will be absorbed into the UCSC and Ensembl browsers according to their respective release cycles. Until that point any non rs SNP id's on this site are temporary and will NOT be maintained.

Links



[1000 Genomes](#) →
More information about the 1000 Genomes Project on the 1000 genomes main site.



[Pilot browser](#) →
This browser is based on Ensembl release 60 and represents the variant set analysed as part of [A map of human genome variation from population-scale sequencing](#), Nature 467, 1061.1073.



[Tutorial](#) →
The 1000 Genomes Browser Tutorial.

The 1000 Genomes Project is an international collaborative project described at www.1000genomes.org.

The 1000 Genomes Browser is based on Ensembl web code.

Ensembl is a joint project of EMBL-EBI  and the [Wellcome Trust Sanger Institute](#)

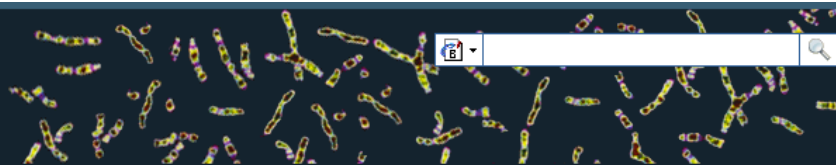


<http://browser.1000genomes.org>

Tools page

1000 Genomes

A Deep Catalog of Human Genetic Variation



[Tools](#) | [Help](#)

We provide a number of ready-made tools for processing your data. At the moment, small datasets can be uploaded to our servers and processed online; for larger datasets, we provide an API script that can be downloaded (you will also need to [install our Perl API](#) to use these).

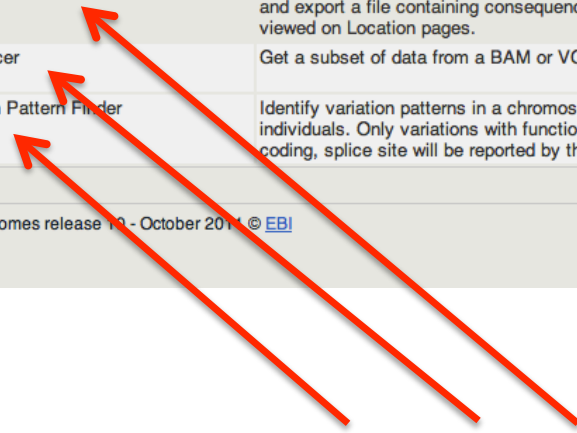
In the near future we aim to offer an intermediate service, whereby medium-to-large data sets can be submitted to a queue, similar to BLAST.

Currently available:

Tool	Description		
Assembly converter	Map your data to the current assembly. Accepted file formats: GFF , GTE , BED , PSL . N.B. Export is currently in GFF only	Online version	API script
ID History converter	Convert a set of Ensembl IDs from a previous release into their current equivalents.	Online version (max 30 ids)	API script
Variant Effect Predictor	(Formerly SNP Effect Predictor). Upload a set of SNPs in our standard format and export a file containing consequence types. Uploaded tracks can also be viewed on Location pages.	Online version (max 750 SNPs)	API script
Data Slicer	Get a subset of data from a BAM or VCF file.	Online version (max 10K region)	
Variation Pattern Finder	Identify variation patterns in a chromosomal region of interest for different individuals. Only variations with functional significance such non-synonymous coding, splice site will be reported by the tool.	Online version	

1000 Genomes release 1.0 - October 2014 © [EBI](#)

[About 1000 Genomes](#) | [Contact Us](#) | [Help](#)



Ensembl Variant Effector Predictor (VEP)

- Takes list of variation and annotates with respect to Ensembl features
- Returns whether the SNP has been seen in the 1000 Genomes and if it has an rs number (if one has been assigned)
- Returns SIFT, PolyPhen and Condel scores
- Extensive filtering options by MAF and populations
- Web and command line versions

Data Management

- Upload Data
- Attach DAS
- Attach Remote File
- Manage Data
- Features on Karyotype
- Data Converters
 - Assembly Converter
 - ID History Converter
 - **Variant Effect Predictor**
 - Data Slicer
 - Variation Pattern Finder

Variant Effect Predictor:

This tool takes a list of variant positions and alleles, and predicts the effects of each of these on overlapping transcripts and regulatory regions annotated in Ensembl. The tool accepts substitutions, insertions and deletions as input, uploaded as a list of [tab separated values](#), [VCF](#) or Pileup format input.

Upload is limited to 750 variants; lines after the limit will be ignored. Users with more than 750 variations can split files into smaller chunks, use the standalone [perl script](#) or the [variation API](#). See also [full documentation](#)

Input file

Species:

Human (Homo sapiens): GRCh37

Name for this upload (optional):

Paste file:

Upload file:

Choose File no file selected

or provide file URL:

Input file format:

Ensembl default

Options

Get regulatory region consequences:

Type of consequences to display:

Ensembl terms

Check for existing co-located variants:

Yes

Return results for variants in coding regions only:

Show HGNC identifier for genes where available:

Show Ensembl protein identifiers where available:

Show HGVS identifiers for variants where available:

No

Non-synonymous SNP predictions (human only)

SIFT predictions:

No

PolyPhen predictions:

No

Condel consensus (SIFT/PolyPhen) predictions:

No

Frequency filtering of existing variants (human only)

Filter variants by frequency:

NB: Enabling frequency filtering may be very slow for large datasets

Filter: Exclude variants with MAF greater than 0.1 in any 1KG low coverage population

Next >

Data slicer for subsets of the data

The screenshot shows the '1000 Genomes' website's 'Data Slicer' tool. The interface is divided into a left sidebar and a main content area. The sidebar includes a 'Custom Data' tab and a 'Data Management' menu with options like 'Upload Data', 'Attach DAS', 'Attach Remote File', 'Manage Data', 'Features on Karyotype', 'Data Converters', 'Assembly Converter', 'ID History Converter', 'Variant Effect Predictor', 'Data Slicer', and 'Variation Pattern Finder'. The main content area features a yellow tip box with instructions on file naming for VCF and BAM files. Below the tip are several input fields: 'VCF / BAM File URL', 'Region', 'Use VCF filters (this doesn't apply to BAM files)', and 'Sample-Population Mapping File URL'. The 'Use VCF filters' section has radio buttons for 'None', 'By individual(s)', and 'By population(s)*'. At the bottom, there are '< Back' and 'Next >' buttons. A red arrow points from the bottom of the page to the 'VCF / BAM File URL' input field.

1000 Genomes
A Deep (

Custom Data

Data Management

- Upload Data
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- Attach Remote File
- Manage Data
- Features on Karyotype
- Data Converters
 - Assembly Converter
 - ID History Converter
 - Variant Effect Predictor
- Data Slicer**
- Variation Pattern Finder

We provide (use these).
In the near
Currently a
Tool
Assembly
ID History
Variant Ef
Data Slice
Variation F
1000 Genom

Tip
When slicing a VCF or BAM file, both the data file and its index file should be present on the web server and named correctly.
The VCF file should have a ".vcf.gz" extension, and the index file should have a ".vcf.gz.tbi" extension, E.g: MyData.vcf.gz, MyData.vcf.gz.tbi
The BAM file should have a ".bam" extension, and the index file should have a ".bam.bai" extension, E.g: MyData.bam, MyData.bam.bai
Click [here](#) for more extensive documentation.

VCF / BAM File URL:

e.g.
ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/release/20101123/interim_phase1_release/ALL.chr6.phase1

Region:

(e.g. 1:1-50000)

Use VCF filters (this doesn't apply to BAM files):

- None
- By individual(s)
- By population(s) *

(to filter by populations please provide URL to a Sample-Population Mapping File in the box below)

Sample-Population Mapping File URL:

e.g.
ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/release/20101123/interim_phase1_release/interim_phase1.2

< Back **Next >**

http://trace.ncbi.nlm.nih.gov/Traces/1kg_slicer/

NCBI 1000 Genomes Data Slicer

Population		Sample	Quality		
<input checked="" type="radio"/> ASW	<input type="radio"/> CEU	NA19625	levels	original	re-calibrated
<input type="radio"/> CHB	<input type="radio"/> CHS	NA19700	full	<input checked="" type="radio"/>	<input type="radio"/>
<input type="radio"/> CLM	<input type="radio"/> FIN	NA19701	8	<input type="radio"/>	<input type="radio"/>
<input type="radio"/> GBR	<input type="radio"/> JPT	NA19703			
<input type="radio"/> LWK	<input type="radio"/> MXL	NA19704			
<input type="radio"/> PUR	<input type="radio"/> TSI	NA19707			
<input type="radio"/> YRI		NA19711			
		NA19712			

Slice		Output	
Reference	1	<input type="radio"/> fasta	<input type="radio"/> fastq
Range (from-to)	1000000-1001000	<input type="radio"/> sam	<input checked="" type="radio"/> bam

Sliced BAM to files

Variation Pattern Finder

- [http://browser.1000genomes.org/
Homo_sapiens/UserData/VariationsMapVCF](http://browser.1000genomes.org/Homo_sapiens/UserData/VariationsMapVCF)
- VCF input
- Discovers patterns of Shared Inheritance
- Variants with functional consequences considered
- Web output with csv and excel downloads

Custom Data

Data Management

- Upload Data
- Attach DAS
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 - Variant Effect Predictor
 - Data Slicer
- Variation Pattern Finder**

Variation Pattern Finder

Export data: [CSV](#) [Excel](#)

Go to collapsed view

Population ASW	CEU	Freq	Variation info			
			rs9369628:C/T	rs61661828:C/T	rs12192544:C/G	rs599
			6:46620135	6:46620240	6:46620252	6:466
			ENST00000275016 SPLICE_SITE	ENST00000275016 NON_SYNONYMOUS_CODING:R/H	ENST00000275016 NON_SYNONYMOUS_CODING:R/P	ENST0 NON_S
NA20314, NA20322	NA12348, N	0.095	CIC	CIC	GIC	GIG
NA20356, NA19625 and 1 other(s)	NA11919, N	0.092	CIC	CIC	CIG	GIG
NA20291, NA19985 and 5 other(s)		0.069	CIT	CIC	CIC	GIG
NA20289, NA20294 and 4 other(s)		0.057	TIC	CIC	CIC	GIG
	NA12546, N	0.026	CIC	CIC	GIG	GIG
NA19819		0.012	TIT	CIC	CIC	GIG
	NA12283	0.011	TIC	CIC	CIG	GIG
NA19908, NA20278		0.011	CIT	CIC	GIC	GIG
NA19703		0.008	CIC	CIC	CIC	GIG
NA20351		0.007	CIC	CIC	CIC	GIG
		0.006	CIC	CIC	CIG	GIG
NA19712		0.004	CIC	CIC	CIC	CIG
		0.003	CIC	CIC	GIC	GIG
		0.003	TIC	CIC	CIC	GIG
		0.002	CIC	CIC	CIC	GIG

Access to backend Ensembl databases

- Public MySQL database at
 - `mysql-db.1000genomes.org` port 4272
- Full programmatic access with Ensembl API
 - More information on the use of the Ensembl API at the Ensembl “Advanced Users” Workshop tomorrow

FRIDAY, October 14

*6:15 PM - 8:00 PM



Ensembl 'Advanced Users' Workshop: API
For further information, e-mail xose@ebi.ac.uk

Convention Center
Room 524, Level 5

Data access

- General information
- File access
- 1000 Genomes Browser
- Tools
- Where to find help

- Does the 1000 genomes project use Hapmap data?
- Can I map your snp coordinates between NCBI36 and GRCh37
- Can I use the 1000 genomes data for imputation?
- How are your alignments generated?
- Are input files available for using 1000 genomes data with the Beagle imputation algorithm?
- Are input files available for using 1000 genomes data with the Impute2 imputation algorithm?
- Are input files available for using 1000 genomes data with the Mach imputation algorithm?
- How can I get the allele frequency of my variant?
- How many individuals will be sequenced?
- How much disk space is used by the 1000 genomes project?
- How much sequence data has been generated for single individuals?
- Is the data for the pilot study still available?
- What Depth of Coverage was used to call the 1000 genomes snps
- What Sequencing Platforms were used for the 1000 genomes project
- What Structural variant data is available for the project?
- What are the targets for your exon targetted pilot study
- What are the targets for your whole exome sequencing?
- What do the names of your bam files mean?
- What do the names of your fastq files mean?
- What do the names of your vcf files mean?
- What does an individual have a genotype in a location where it has no sequence coverage?
- What format are your alignment files in?
- What format are your sequence files in?
- What format are your variant files in?
- What is a bas file?
- What is the difference between your data directory and the pilot_data/data directory
- What is the gender and family relationships of your samples?
- What library insert sizes were used in the 1000 genomes project
- What read lengths are being used by the project
- What tools can I use to download 1000 genomes data
- What version of vcf are your vcf files in?
- What was the source of the DNA for sequencing?
- Where are the pilot structural variants archived?
- Where are the snps for the X/Y/MT chr
- Where are your alignment files located?
- Where are your reference data sets?
- Where are your sequence files located?
- Where are your variant files located?
- Where can I get consequence annotations for the 1000 genome variants
- Where do I get the 1000 genomes data from?
- Where does the Ancestral Allele Information for your variants come from?
- Which samples are you sequencing?
- Why are the coordinates of your pilot variants different to what is displayed in Ensembl or UCSC
- Why do some of your vcf genotype files have genotypes of ./ in them?
- Why is only 85% of the genome assayable?
- Why is the Allele frequency different from Allele Count/Allele Number?
- Why is the sequence data distributed in 2 or 3 files labelled SRR_1, SRR_3 and SRR?
- Why isn't a snp in dbSNP or HapMap
- Why isn't my snp in browser.1000genomes.org

Do I need a password to access 1000 genomes data

>

Credits & Contact

- Eugene Kulesha, Iliana Toneva, Bren Vaughan
- Will McLaren, Graham Ritchie, Fiona Cunningham
- Laura Clarke, Holly Zheng-Bradley, Rick Smith

- Steve Sherry, Chunlin Xiao

For more information contact info@1000genomes.org