

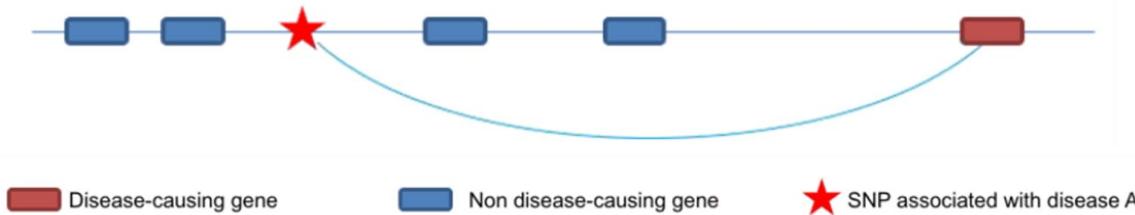
Public bioinformatics resources for GWAS interpretation

HELMHOLTZ RESEARCH FOR
GRAND CHALLENGES

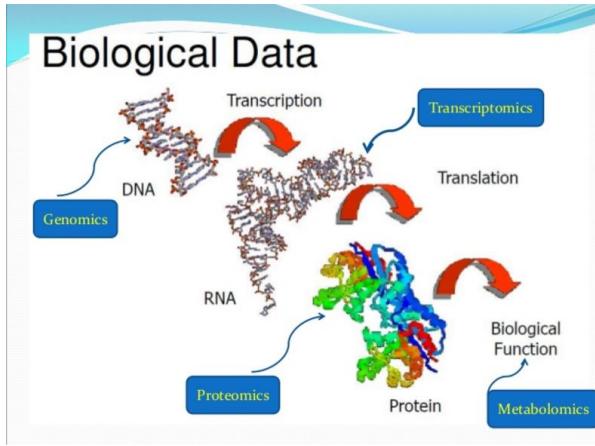
Dr. Konstantinos Hatzikotoulas
Institute of Translational Genomics

Motivation

- Greatest challenge in genetic association studies is to assign functionality (causality) to associated SNPs and genes.
- Predict the most likely genes and variants driving the phenotype associations.
- Need to integrate as much information as possible through genome annotation tools to drive the experimental validation.



What is Bioinformatics?



Computers aid to collect, intergrade and analyse biological data ->
Optimal biological interpretation

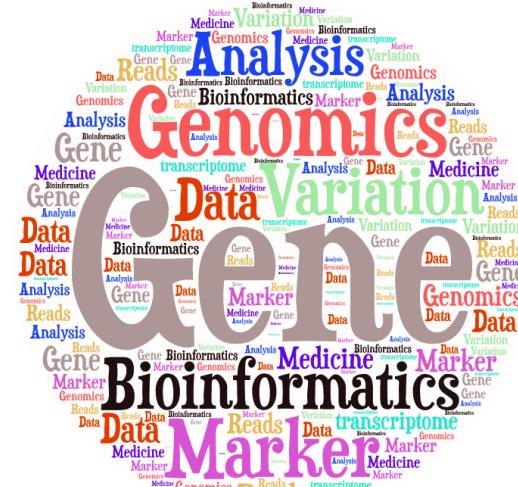
Goal of Bioinformatics

- Develop **databases** and **computational tools** to generate knowledge to better understanding a living cell and how it functions at molecular level.



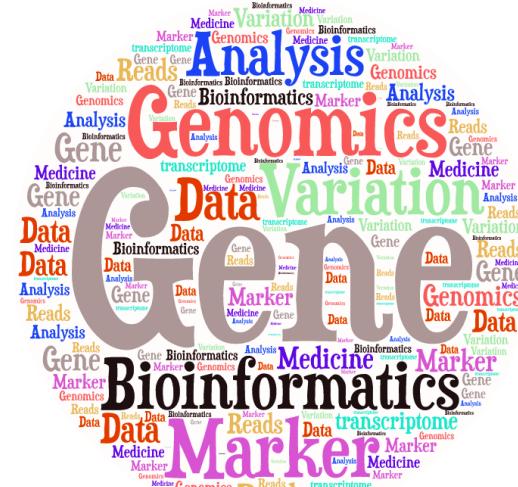
Publicly available bioinformatics resources

- Genome Browsers
 - Nucleotide Sequence Databases
 - Protein Sequence Databases
 - Database Searching by Sequence Similarity
 - Protein Domains: Databases and Search Tools
 - Human Traits & Diseases Databases
 - Phylogeny & Taxonomy
 - Databases of other Organisms
 - Gene Prediction
 - Gene Expression Databases
 - Gene Regulation
 - Metabolic, Gene Regulatory & Signal Transduction Network Databases
 - Publications Database



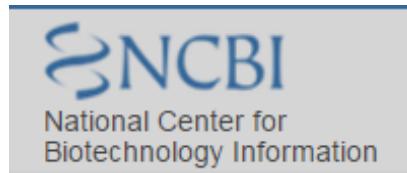
Publicly available bioinformatics resources

- Genome Browsers
 - Nucleotide Sequence Databases
 - Protein Sequence Databases
 - Database Searching by Sequence Similarity
 - Protein Domains: Databases and Search Tools
 - Human Traits & Diseases Databases
 - Phylogeny & Taxonomy
 - Databases of other Organisms
 - Gene Prediction
 - Gene Expression Databases
 - Gene Regulation
 - Metabolic, Gene Regulatory & Signal Transduction Network Databases
 - Publications Database



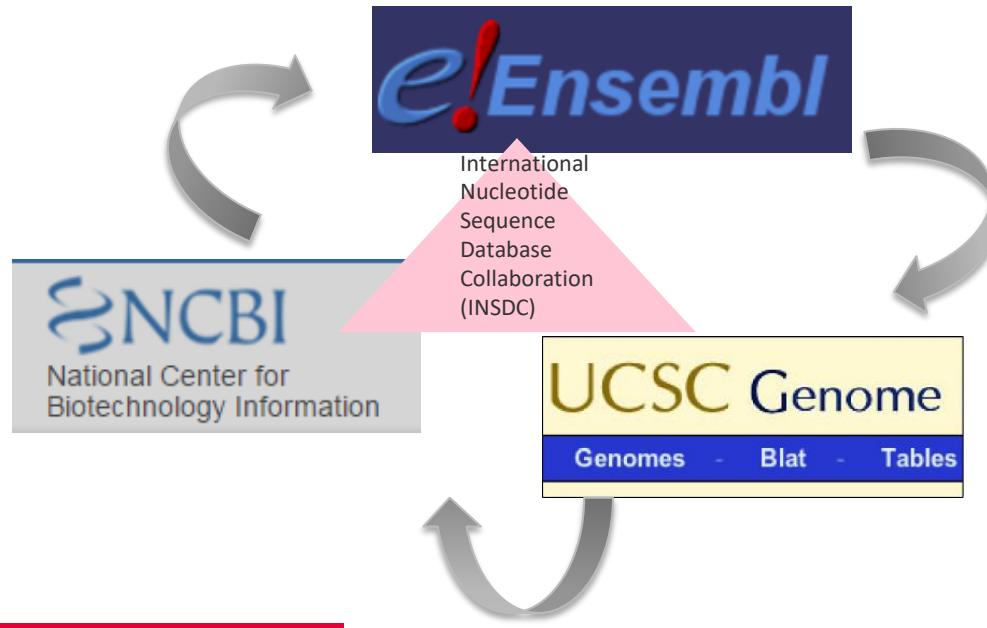
Genome Browsers

- Ensembl : <http://www.ensembl.org>
- UCSC: <http://genome.ucsc.edu/>
- NCBI: <https://www.ncbi.nlm.nih.gov/>



Genome Browsers

- Agreement: To begin bringing all genome assembly data into compliance moving forward



Ensembl ... more than a browser!

- Ensembl is a joint project between the EBI (European Bioinformatics Institute) and the Wellcome Trust Sanger Institute
- **What can I do with Ensembl?**
 - Examine single nucleotide polymorphisms (SNPs) for a gene or chromosomal region.
 - View SNPs across strains (rat, mouse), populations (human) or breeds (dog).
 - View genes with annotations along the chromosome.
 - View alternative transcripts (i.e. splice variants) for a given gene.
 - Upload your own data.
 - Export sequence or create a table of gene information with BioMart.
 - Determine how your variants affect genes and transcripts using the Variant Effect Predictor.
 - Share Ensembl views with your colleagues and collaborators.



Ensembl ... more than a browser!

- Ensembl is a joint project between the EBI (European Bioinformatics Institute) and the Wellcome Trust Sanger Institute
- **What can I do with Ensembl?**
 - Examine single nucleotide polymorphisms (SNPs) for a gene or chromosomal region.
 - View SNPs across strains (rat, mouse), populations (human) or breeds (dog).
 - View genes with other annotation along the chromosome.
 - View alternative transcripts (i.e. splice variants) for a given gene.
 - Upload your own data.
 - Export sequence or create a table of gene information with BioMart.
 - Determine how your variants affect genes and transcripts using the Variant Effect Predictor.
 - Share Ensembl views with your colleagues and collaborators.



Ensembl ... the front page

- It contains lots of information and links to help you navigate Ensembl.

The screenshot shows the Ensembl homepage with several key features highlighted:

- Link back to homepage**: A button in the top left corner.
- Ensembl tools**: A button in the top center.
- Blue bar remains visible on every page**: A speech bubble pointing to the top navigation bar.
- Search**: A search bar at the top right with a "Search" button and a "Login/Register" link.
- See the current release number and what's new**: A callout box pointing to the "Ensembl Release 106 (Apr 2022)" section.
- Search bar**: A search bar with dropdown options for "All species" and a "Go" button.
- Variant Effect Predictor >**: A section for analyzing variants with a "Go" button.
- BioMart >**: A section for exporting custom datasets with a "Go" button.
- BLAST/BLAT >**: A section for searching genomes with a "Go" button.
- Tools**: A sidebar with "All tools" and a "Select a species" dropdown.
- Pig breeds**: A section for pig genome analysis.
- Favourite genomes**: A list of saved genomes:
 - Human (GRCh38.p13)
 - Mouse (GRCm38.p6)
 - Zebrafish (GRCz11)A red arrow points to the "Human" entry, and a blue arrow points to the "Mouse" entry.
- Ensembl Rapid Release**: A section for new assemblies with a "Go" button.
- Other news from our blog**: A list of recent blog posts.
- Footer links**: Six boxes for "Compare genes across species", "Find SNPs and other variants for my gene", "Gene expression in different tissues", "Retrieve gene sequence", "Find a Data Display", and "Use my own data in Ensembl".

Hint: <https://www.ensembl.org/index.html>

Ensembl ... the front page ... Exercise 1

1. Go to the species homepage for **Giant Panda**. What is the name of the genome assembly for Panda?
2. How long is the Panda genome (in bp)? How many coding genes have been annotated?
3. Repeat for **Human**.



Ensembl ... Exploring variants

➤ Let's have a look at a specific variant, rs143383 (chr20:35438203).

e!Ensembl BLAST/BLAT | VEP | Tools | BioMart | Downloads | Help & Docs | Blog

Human (GRCh38.p13) ▾

Location: 20:35,437,703-35,438,703 Variant: rs143383 Jobs ▾

Variant displays

Explore this variant

- Genomic context
 - Genes and regulation
 - Flanking sequence
 - Population genetics
 - Phenotype data
 - Sample genotypes
 - Linkage disequilibrium
 - Phylogenetic context
 - Citations
 - 3D Protein model
- Configure this page
- Custom tracks
- Export data
- Share this page
- Bookmark this page

rs143383 SNP

Most severe consequence | See all predicted consequences

Alleles

Change tolerance

Location

Co-located variants

Evidence status ⓘ

Clinical significance ⓘ

HGVS names

Synonyms

Genotyping chips

Original source

About this variant

Description from SNPedia

Variant information

http://www.ensembl.org/info/genome/variation/prediction/predicted_data.html

This variant has 5 HGVS names - [Show](#) ⓘ

This variant has 9 synonyms - [Show](#) ⓘ

This variant has assays on 5 chips - [Show](#) ⓘ

Variants (including SNPs and indels) imported from dbSNP (release 154) | [View in dbSNP](#) ⓘ

This variant overlaps 2 transcripts, has 3009 sample genotypes, is associated with 11 phenotypes and is mentioned in 201 citations.

This SNP is associated with osteoarthritis ⓘ (OA). It is located in the "five prime untranslated region" (5'UTR ⓘ) of the gene encoding the embryonic stage onwards. GDE5 is also known as "cartilage-derived morphogenic protein 1" or "BMP14" - [Show](#) ⓘ

Explore this variant ⓘ

- Genomic context
- Genes and regulation
- Flanking sequence
- Population genetics
- Phenotype data
- Sample genotypes
- Linkage disequilibrium
- Phylogenetic context
- Citations
- 3D Protein model

Variation icons. These go to the same places as the links on the left

Ensembl ... Exploring variants ...

Variant types

➤ What type of variants is rs143383 (chr20:35438203)?

 Ensembl

Human (GRCh38.p13) ▾

Location: 20:35,437,703-35,438,703 Variant: rs143383 Jobs ▾

Variant displays

- Explore this variant **rs143383 SNP** (highlighted with a red arrow)
- Genomic context
 - Genes and regulation
 - Flanking sequence
 - Population genetics
 - Phenotype data
 - Sample genotypes
 - Linkage disequilibrium
 - Phylogenetic context
 - Citations
 - 3D Protein model
- Configure this page
- Custom tracks
- Export data
- Share this page
- Bookmark this page

Most severe consequence

5 prime UTR variant | See all predicted consequences

G/A | Ancestral: G | Highest population MAF: 0.49

CADD: A:21.4 | GERP: 2.76

Chromosome 20:35438203 (forward strand) | VCF: 20 35438203 rs143383 G A

dbSNP rs1555823599 (G-) ; HGMD-PUBLIC CR072309



This variant has 5 HGVS names - [Show](#)

This variant has 9 synonyms - [Show](#)

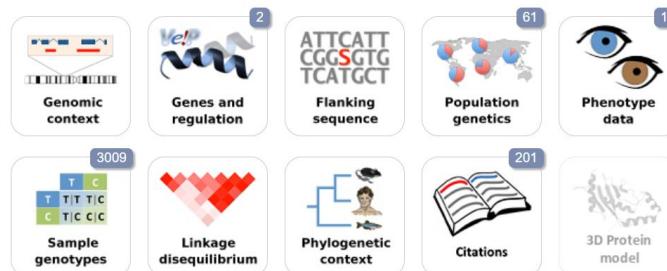
This variant has assays on 5 chips - [Show](#)

Variants (including SNPs and indels) imported from dbSNP (release 154) | [View in dbSNP](#)

This variant overlaps 2 transcripts, has 3009 sample genotypes, is associated with 11 phenotypes and is mentioned in 201 citations.

This SNP is associated with osteoarthritis (OA). It is located in the "five prime untranslated region" (5'UTR) of the gene encoding GDF5. GDF5 is also known as "cartilage-derived morphogenetic protein 1" or "BMP14". ... [Show](#)

Explore this variant



Ensembl ... Exploring variants ...

Variant types

1. Small scale in one or few nucleotides of a gene

Type	Description	Example (Reference / Alternative)	
SNP	Single Nucleotide Polymorphism	Ref: ...TTG A CGTA...	Alt: ...TTG G CGTA...
Insertion	Insertion of one or several nucleotides	Ref: ...TTGACGTA...	Alt: ...TTGA T CGTA...
Deletion	Deletion of one or several nucleotides	Ref: ...TTG AC GT...	Alt: ...TTGGT...
Indel	An insertion and a deletion, affecting 2 or more nucleotides	Ref: ...TTG A CGTA...	Alt: ...TTG GCT CGTA...
Substitution	A sequence alteration where the length of the change in the variant is the same as that of the reference.	Ref: ...TTG AC GT...	Alt: ...TTG TA GT...

2. Large scale in chromosomal structure

CNV

Copy Number Variation: increases or decreases the copy number of a given region

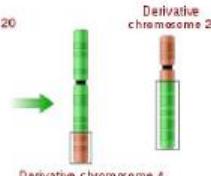
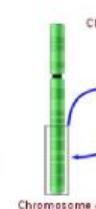
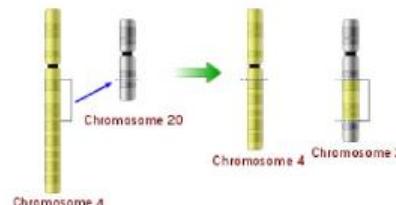
Reference:



"Gain" of one copy:



"Loss" of one copy:



deletion

duplication

insertion

translocation

Ensembl ... Exploring variants ... Calculated variant consequences

➤ Let's have a look at the predicted consequences of the variant.

The screenshot shows the Ensembl Variant displays page for SNP rs143383. The URL is https://www.ensembl.org/Homo_sapiens/Variants/Variant-display?var=rs143383. The page title is "rs143383 SNP". A red circle highlights the "Most severe consequence" link under the "Explore this variant" sidebar. The main content area includes details about the variant being a 5' prime UTR variant, its G/A allele, and its highest population MAF of 0.49. It also lists CADD scores, dbSNP ID, HGMD ID, and various clinical significance icons. Below this, links are provided for HGVS names, synonyms, genotyping chips, original source, and SNPedias. The "Explore this variant" section contains cards for Genomic context, Genes and regulation, Flanking sequence, Population genetics, Phenotype data, Sample genotypes, Linkage disequilibrium, Phylogenetic context, Citations, and 3D Protein model. Each card has a small number indicating the count of associated data points.

Location: 20:35,437,703-35,438,703 Variant: rs143383 Jobs ▾

Variant displays

- Explore this variant
 - Genomic context
 - Flanking sequence
 - Population genetics
 - Phenotype data
 - Sample genotypes
 - Linkage disequilibrium
 - Phylogenetic context
 - Citations
 - 3D Protein model
- Configure this page
- Custom tracks
- Export data
- Share this page
- Bookmark this page

rs143383 SNP

Most severe consequence

5 prime UTR variant | See all predicted consequences

G/A | Ancestral: G | Highest population MAF: 0.49

CADD: A:21.4 | GERP: 2.76

Chromosome 20:35438203 (forward strand) | VCF: 20 35438203 rs143383 G A

dbSNP rs1555823599 (G-) ; HGMD-PUBLIC CR072309

This variant has 5 HGVS names - [Show](#) This variant has 9 synonyms - [Show](#) This variant has assays on 5 chips - [Show](#) Variants (including SNPs and indels) imported from dbSNP (release 154) | [View in dbSNP](#) This variant overlaps 2 transcripts, has 3009 sample genotypes, is associated with 11 phenotypes and is mentioned in 201 citations. This SNP is associated with osteoarthritis (OA). It is located in the "five prime untranslated region" (5'UTR) of the gene encoding the embryonic stage onwards. GDF5 is also known as "cartilage-derived morphogenetic protein 1" or "BMP14".... [Show](#)

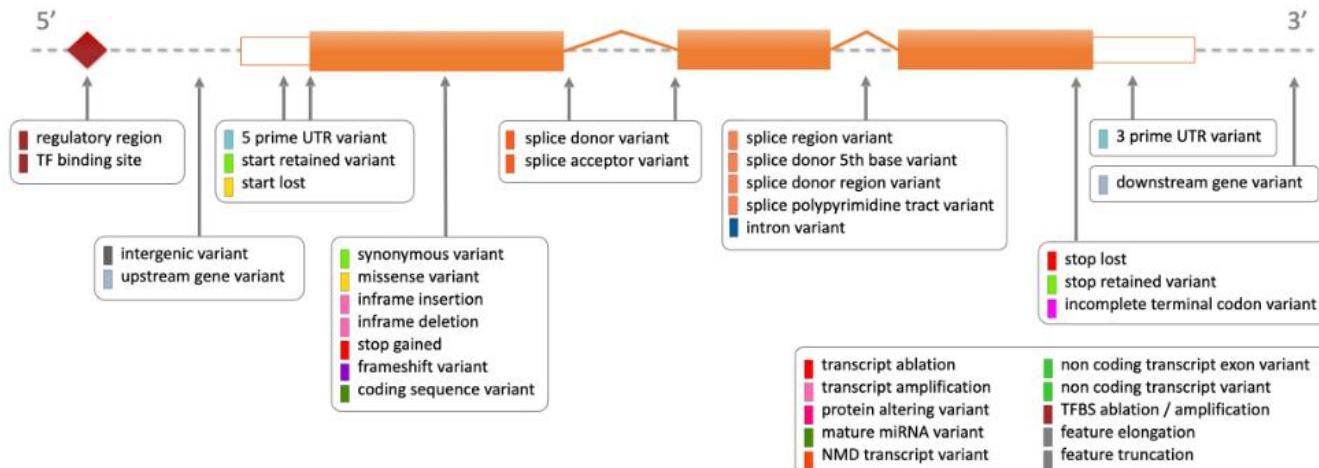
This variant has 5 HGVS names - [Show](#) This variant has 9 synonyms - [Show](#) This variant has assays on 5 chips - [Show](#) Variants (including SNPs and indels) imported from dbSNP (release 154) | [View in dbSNP](#) This variant overlaps 2 transcripts, has 3009 sample genotypes, is associated with 11 phenotypes and is mentioned in 201 citations. This SNP is associated with osteoarthritis (OA). It is located in the "five prime untranslated region" (5'UTR) of the gene encoding the embryonic stage onwards. GDF5 is also known as "cartilage-derived morphogenetic protein 1" or "BMP14".... [Show](#)

Explore this variant

- Genomic context (2)
- Genes and regulation (61)
- Flanking sequence (11)
- Population genetics (61)
- Phenotype data (11)
- Sample genotypes (3009)
- Linkage disequilibrium (201)
- Phylogenetic context (201)
- Citations (3009)
- 3D Protein model (201)

Ensembl ... Exploring variants ... Calculated variant consequences

- A rule-based approach to predict the effects that each allele of the variant may have on the transcript.



Ensembl ... Exploring variants ... Calculated variant consequences

➤ Sequence Ontology (SO) consequence term :

http://www.ensembl.org/info/genome/variation/prediction/predicted_data.html

SO term	SO description	SO accession	Display term	IMPACT
transcript_ablation	A feature ablation whereby the deleted region includes a transcript feature	SO_0001893#F	Transcript ablation	HIGH
splice_acceptor_variant	A splice variant that changes the 2 base region at the 3' end of an intron	SO_0001574#F	Splice acceptor variant	HIGH
splice_donor_variant	A splice variant that changes the 2 base region at the 5' end of an intron	SO_0001575#F	Splice donor variant	HIGH
stop_gained	A sequence variant whereby at least one base of a codon is changed, resulting in a premature stop codon, leading to a shortened transcript	SO_0001587#F	Stop gained	HIGH
frameshift_variant	A sequence variant which causes a disruption of the translational reading frame, because the number of nucleotides inserted or deleted is not a multiple of three	SO_0001589#F	Frameshift variant	HIGH
stop_lost	A sequence variant where at least one base of the terminator codon (stop) is changed, resulting in an elongated transcript	SO_0001578#F	Stop lost	HIGH
start_lost	A codon variant that changes at least one base of the canonical start codon	SO_0002012#F	Start lost	HIGH
transcript_amplification	A feature amplification of a region containing a transcript	SO_0001889#F	Transcript amplification	HIGH
inframe_insertion	An inframe non synonymous variant that inserts bases into the coding sequence	SO_0001821#F	Inframe insertion	MODERATE
inframe_deletion	An inframe non synonymous variant that deletes bases from the coding sequence	SO_0001822#F	Inframe deletion	MODERATE
missense_variant	A sequence variant, that changes one or more bases, resulting in a different amino acid sequence but where the length is preserved	SO_0001583#F	Missense variant	MODERATE
protein_altering_variant	A sequence_variant which is predicted to change the protein encoded in the coding sequence	SO_0001818#F	Protein altering variant	MODERATE
splice_region_variant	A sequence variant in which a change has occurred within the region of the splice site, either within 1-3 bases of the exon or 3-8 bases of the intron	SO_0001630#F	Splice region variant	LOW
splice_donor_5th_base_variant	A sequence variant that causes a change at the 5th base pair after the start of the intron in the orientation of the transcript	SO_0001787#F	Splice donor 5th base variant	LOW
splice_donor_region_variant	A sequence variant that falls in the region between the 3rd and 6th base after splice junction (5' end of intron)	SO_0002170#F	Splice donor region variant	LOW
splice_polyypyrimidine_tract_variant	A sequence variant that falls in the polyypyrimidine tract at 3' end of intron between 17 and 3 bases from the end (acceptor -3 to acceptor -17)	SO_0002169#F	Splice polyypyrimidine tract variant	LOW
incomplete_terminal_codon_variant	A sequence variant where at least one base of the final codon of an incompletely annotated transcript is changed	SO_0001626#F	Incomplete terminal codon variant	LOW
start_retained_variant	A sequence variant where at least one base in the start codon is changed, but the start remains	SO_0002019#F	Start retained variant	LOW
stop_retained_variant	A sequence variant where at least one base in the terminator codon is changed, but the terminator remains	SO_0001567#F	Stop retained variant	LOW
synonymous_variant	A sequence variant where there is no resulting change to the encoded amino acid	SO_0001819#F	Synonymous variant	LOW
coding_sequence_variant	A sequence variant that changes the coding sequence	SO_0001580#F	Coding sequence variant	MODIFIER
mature_miRNA_variant	A transcript variant located with the sequence of the mature miRNA	SO_0001620#F	Mature miRNA variant	MODIFIER
5_prime_UTR_variant	A UTR variant of the 5' UTR	SO_0001623#F	5 prime UTR variant	MODIFIER
3_prime_UTR_variant	A UTR variant of the 3' UTR	SO_0001624#F	3 prime UTR variant	MODIFIER
non_coding_transcript_exon_variant	A sequence variant that changes non-coding exon sequence in a non-coding transcript	SO_0001792#F	Non coding transcript exon variant	MODIFIER
intron_variant	A transcript variant occurring within an intron	SO_0001627#F	Intron variant	MODIFIER
NMD_transcript_variant	A variant in a transcript that is the target of NMD	SO_0001621#F	NMD transcript variant	MODIFIER
non_coding_transcript_variant	A transcript variant of a non coding RNA gene	SO_0001619#F	Non coding transcript variant	MODIFIER
upstream_gene_variant	A sequence variant located 5' of a gene	SO_0001631#F	Upstream gene variant	MODIFIER
downstream_gene_variant	A sequence variant located 3' of a gene	SO_0001632#F	Downstream gene variant	MODIFIER
TFBS_ablation	A feature ablation whereby the deleted region includes a transcription factor binding site	SO_0001895#F	TFBS ablation	MODIFIER
TFBS_amplification	A feature amplification of a region containing a transcription factor binding site	SO_0001892#F	TFBS amplification	MODIFIER
TF_binding_site_variant	A sequence variant located within a transcription factor binding site	SO_0001782#F	TF binding site variant	MODIFIER
regulatory_region_ablation	A feature ablation whereby the deleted region includes a regulatory region	SO_0001894#F	Regulatory region ablation	MODERATE
regulatory_region_amplification	A feature amplification of a region containing a regulatory region	SO_0001891#F	Regulatory region amplification	MODIFIER
feature_elongation	A sequence variant that causes the extension of a genomic feature, with regard to the reference sequence	SO_0001907#F	Feature elongation	MODIFIER
regulatory_region_variant	A sequence variant located within a regulatory region	SO_0001566#F	Regulatory region variant	MODIFIER
feature_truncation	A sequence variant that causes the reduction of a genomic feature, with regard to the reference sequence	SO_0001906#F	Feature truncation	MODIFIER
intergenic_variant	A sequence variant located in the intergenic region, between genes	SO_0001628#F	Intergenic variant	MODIFIER

Ensembl ... Exploring variants ...

Calculated variant consequences

➤ Let's have a look at all the predicted consequences of the variant.

Ensembl BLAST/BLAT | VEP | Tools | BioMart | Downloads | Help & Docs | Blog

Human (GRCh38.p13) ▾

Location: 20:35,437,703-35,438,703 Variant: rs143383 Jobs ▾

Variant displays

- Explore this variant
 - Genomic context
 - Genes and regulation
 - Flanking sequence
 - Population genetics
 - Phenotype data
 - Sample genotypes
 - Linkage disequilibrium
 - Phylogenetic context
 - Citations
 - 3D Protein model
 - Most severe consequence
 - Alleles
 - Change tolerance
 - Location
 - Co-located variants
 - Evidence status ⓘ
 - Clinical significance ⓘ
 - HGVIS names
 - Synonyms
 - Genotyping chips
 - Original source
 - About this variant
 - Description from SNPedia
- Configure this page
- Custom tracks
- Export data
- Share this page
- Bookmark this page

rs143383 SNP

5 prime UTR variant [See all predicted consequences](#) (circled)

G/A | Ancestral: G | Highest population freq = 0.49

CADD: A:21.4 | GERP: 2.76

Chromosome 20:35438203 (forward strand) | VCF: 20 35438203 rs143383 G A

dbSNP rs1555823599 (G-) ; HGMD-PUBLIC CR072309

This variant has 5 HGVIS names - [Show](#) ⓘ

This variant has 9 synonyms - [Show](#) ⓘ

This variant has assays on 5 chips - [Show](#) ⓘ

Variants (including SNPs and indels) imported from dbSNP (release 154) | [View in dbSNP](#) ⓘ

This variant overlaps 2 transcripts, has 3009 sample genotypes, is associated with 11 phenotypes and is mentioned in 201 citations.

This SNP is associated with osteoarthritis ⓘ (OA). It is located in the "five prime untranslated region" (5'UTR ⓘ) of the gene encoding the embryonic stage onwards. GDF5 is also known as "cartilage-derived morphogenetic protein 1" or "BMP14" ... [Show](#) ⓘ

Explore this variant ⓘ

- Genomic context
- Genes and regulation (circled)
- Flanking sequence
- Population genetics
- Phenotype data
- Sample genotypes (3009)
- Linkage disequilibrium
- Phylogenetic context
- Citations (201)
- 3D Protein model

Ensembl ... Exploring variants ... Calculated variant consequences

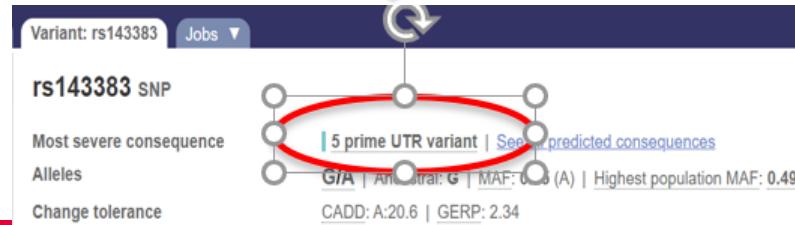
➤ This variant is found in 2 transcripts of the *GDF5* gene.

Genes and regulation ?

Gene and Transcript consequences

Show/hide columns										Filter	Export
Gene	Transcript (strand)	Allele (Tr. allele)	Consequence Type	Position in transcript	Position in CDS	Position in protein	AA	Codons	Detail	Show	
ENSG00000125965 HGNC: GDF5	ENST00000374369.8 (-)	A (T)	5 prime UTR variant	26 (out of 2368)	-	-	-	-	Show		
ENSG00000125965 HGNC: GDF5	ENST00000374372.1 (-)	A (T)	intron variant	-	-	-	-	-	Show		

	coding_sequence_variant	A sequence variant that changes the coding sequence	SO_0001580	Coding sequence variant	MODIFIER
	mature_miRNA_variant	A transcript variant located with the sequence of the mature miRNA	SO_0001620	Mature miRNA variant	MODIFIER
	5_prime_UTR_variant	A UTR variant of the 5' UTR	SO_0001623	5 prime UTR variant	MODIFIER
	3_prime_UTR_variant	A UTR variant of the 3' UTR	SO_0001624	3 prime UTR variant	MODIFIER
	non_coding_transcript_exon_variant	A sequence variant that changes non-coding exon sequence in a non-coding transcript	SO_0001792	Non coding transcript exon variant	MODIFIER
	intron_variant	A transcript variant occurring within an intron	SO_0001627	Intron variant	MODIFIER
	NMD_transcript_variant	A variant in a transcript that is the target of NMD	SO_0001621	NMD transcript variant	MODIFIER
	non_coding_transcript_variant	A transcript variant of a non coding RNA gene	SO_0001619	Non coding transcript variant	MODIFIER



Ensembl ... Exploring variants... Population genetics

➤ Let's have a look at population genetics.

Ensembl BLAST/BLAT | VEP | Tools | BioMart | Downloads | Help & Docs | Blog

Human (GRCh38.p13) ▾

Location: 20:35,437,703-35,438,703 Variant: rs143383 Jobs ▾

Variant displays

- Explore this variant
- Genomic context
 - Genes and regulation
 - Flanking sequence
 - Population genetics
- Phenotype data
- Sample genotypes
- Linkage disequilibrium
- Phylogenetic context
- Citations
- 3D Protein model

Configure this page

Custom tracks

Export data

Share this page

Bookmark this page

rs143383 SNP

Most severe consequence: 5 prime UTR variant | See all predicted consequences

Alleles: G/A | Ancestral: G | Highest population MAF: 0.49

Change tolerance: CADD: A:21.4 | GERP: 2.76

Location: Chromosome 20:35438203 (forward strand) | VCF: 20 35438203 rs143383 G A

SNP rs155582350 (rs143383): HGMD-PUBLIC CR072309

This variant has 5 HGVS names - Show

This variant has 9 synonyms - Show

This variant has assays on 5 chips - Show

Variants (including SNPs and indels) imported from dbSNP (release 154) | View in dbSNP

This variant overlaps 2 transcripts, has 3009 sample genotypes, is associated with 11 phenotypes and is mentioned in 201 citations.

This SNP is associated with osteoarthritis (OA). It is located in the "five prime untranslated region" (5'UTR) of the gene encoding the embryonic stage onwards. GDF5 is also known as "cartilage-derived morphogenetic protein 1" or "BMP14". ... Show

Explore this variant

- Genomic context
- Genes and regulation
- Flanking sequence
- Population genetics
- Phenotype data
- Sample genotypes
- Linkage disequilibrium
- Phylogenetic context
- Citations
- 3D Protein model

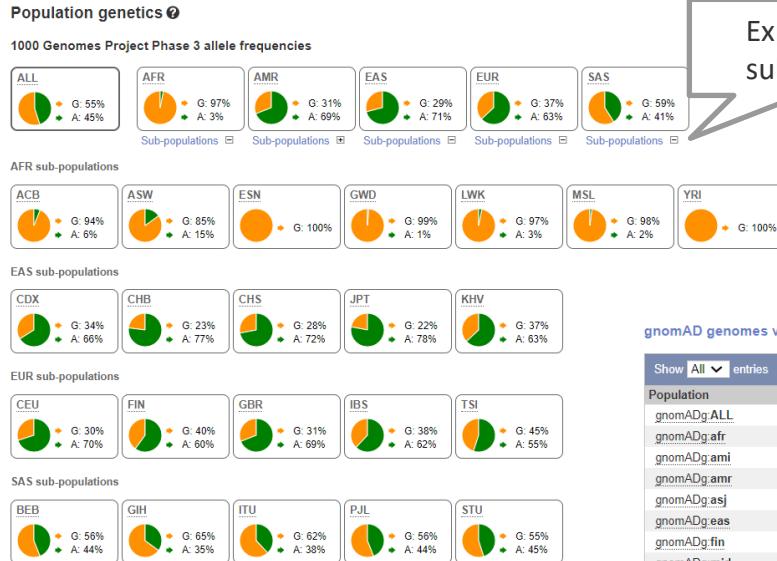
Population genetics (highlighted)

Population genetics (highlighted in sidebar)

Ensembl ... Exploring variants ... Population genetics

- Frequencies are grouped by project for studies with multiple subpopulations.
 - Pie charts can be displayed only for 1000 Genomes allele frequencies.

Pie charts of allele frequencies



Expand
subpopulations

Tables of more detailed data

EAS		G: 0.287 (289)	A: 0.713 (719)	G: 0.085 (43)	A: 0.512 (250)	AIG: 0.403 (203)
CDX		G: 0.344 (64)	A: 0.656 (122)	GIG: 0.140 (13)	AIG: 0.452 (42)	AIG: 0.409 (38)
CHB		G: 0.233 (48)	A: 0.767 (158)	GIG: 0.049 (5)	AIG: 0.583 (60)	AIG: 0.393 (38)
CHS		G: 0.276 (58)	A: 0.724 (152)	GIG: 0.067 (7)	AIG: 0.514 (54)	AIG: 0.419 (44)
JPT		G: 0.221 (46)	A: 0.779 (162)	GIG: 0.067 (7)	AIG: 0.625 (55)	AIG: 0.388 (32)
KHV		G: 0.369 (73)	A: 0.631 (25)	GIG: 0.111 (11)	AIG: 0.374 (37)	AIG: 0.515 (51)

Population	Allele: frequency (count)		
gnomADg_ALL		G: 0.522 (79301)	A: 0.477 (72469)
gnomADg_afr		G: 0.879 (36292)	A: 0.121 (5066)
gnomADg_ami		G: 0.401 (365)	A: 0.599 (545)
gnomADg_amr		G: 0.376 (5729)	A: 0.624 (9491)
gnomADg_asj		G: 0.455 (1576)	A: 0.545 (1890)
gnomADg_eas		G: 0.283 (1462)	A: 0.717 (3710)
gnomADg_fin		G: 0.415 (4371)	A: 0.585 (6163)
gnomADg_mld		G: 0.494 (156)	A: 0.506 (160)
gnomADg_nfe		G: 0.377 (25640)	A: 0.623 (42306)
gnomADg_oth		G: 0.485 (1010)	A: 0.515 (1072)
gnomADg_sas		G: 0.559 (2700)	A: 0.441 (2126)

[Jump to: 1000 Genomes Project Phase 3 \(32\)](#) | [gnomAD genomes v3.1.2 \(11\)](#) | [NCBI ALFA \(12\)](#) | [TOPMed \(1\)](#) | [Gambian Genome Variation Project \(5\)](#)

Ensembl ... Exploring variants... Phenotype/Disease data

➤ Let's have a look at the phenotypes associated with this variant.

The screenshot shows the Ensembl Variant displays page for SNP rs143383. The URL is https://www.ensembl.org/Homo_sapiens/Variants/Variant-display?var=rs143383. The variant is located at GRCh38.p13, position 20:35,437,703-35,438,703. The main content area shows the variant details: rs143383 SNP, 5' prime UTR variant, G/A allele, Ancestral G, Highest population MAF: 0.49, CADD score: 21.4, GERP score: 2.76, Chromosome 20:35438203 (forward strand), VCF ID: 20 35438203 rs143383 G A, dbSNP ID: rs155823599 (G-), HGMD-PUBLIC ID: CR072309. Below this, there are sections for HGVS names (circled in red), Synonyms, Genotyping chips, Original source, About this variant, and Description from SNPedia. The "Explore this variant" sidebar on the left has a section for "Phenotype data" which is also circled in red. At the bottom, there is a grid of icons representing various genomic and phenotypic data sources, with the "Phenotype data" icon (an eye) circled in red.

Variant displays

- Explore this variant
 - Genomic context
 - Flanking sequence
 - Population genetics
 - Phenotype data
 - Sample genotypes
 - Linkage disequilibrium
 - Phylogenetic context
 - Citations
 - 3D Protein model
- Configure this page
- Custom tracks
- Export data
- Share this page
- Bookmark this page

rs143383 SNP

Most severe consequence

Alleles

Change tolerance

Location

Co-located variants

Evidence status ⓘ

Clinical significance ⓘ

HGVS names

Synonyms

Genotyping chips

Original source

About this variant

Description from SNPedia

Explore this variant ⓘ

- Genomic context
- Genes and regulation
- Flanking sequence
- Population genetics
- Phenotype data
- Sample genotypes
- Linkage disequilibrium
- Phylogenetic context
- Citations
- 3D Protein model

5 prime UTR variant | See all predicted consequences

G/A | Ancestral: G | Highest population MAF: 0.49

CADD: A:21.4 | GERP: 2.76

Chromosome 20:35438203 (forward strand) | VCF: 20 35438203 rs143383 G A

dbSNP rs155823599 (G-) ; HGMD-PUBLIC CR072309

This variant has 5 HGVS names - [Show ⓘ](#)

This variant has 9 synonyms - [Show ⓘ](#)

This variant has assays on 5 chips - [Show ⓘ](#)

Variants (including SNPs and indels) imported from dbSNP (release 154) | [View in dbSNP ⓘ](#)

This variant overlaps 2 transcripts, has 3009 sample genotypes, is associated with 11 phenotypes and is mentioned in 201 citations.

This SNP is associated with osteoarthritis (OA). It is located in the "five prime untranslated region" (5'UTR) of the gene encoding GDF5. GDF5 is also known as "cartilage-derived morphogenetic protein 1" or "BMP14". ... [Show ⓘ](#)

HELMHOLTZ RESEARCH FOR GRAND CHALLENGES

Ensembl ... Exploring variants...

Phenotype/Disease data

➤ This variant is associated with 15 phenotypes/diseases.

Phenotype Data

Significant association(s)

Phenotype, disease and trait	Source(s)	Mapped Terms	Ontology Accessions	Supporting evidence	External reference	Clinical significance	Reported gene(s)	Associated allele	Statistics
ACROMESOMELIC DYSPLASIA 2B	ClinVar  [Illumina Laboratory ...]	-	Orphanet:93437 	-	-	    	LOC109461476, GDF5	-	-
Acromesomelic dysplasia 2C, Hunter-Thompson type	ClinVar  [Illumina Laboratory ...]	-	-	-	-	    	LOC109461476, GDF5	-	-
Brachydactyly	ClinVar  [Illumina Laboratory ...]	Brachydactyly	HP:0001156  , Orphanet:294937 	-	-	    	LOC109461476, GDF5	-	-
ClinVar: phenotype not specified	ClinVar  [GeneDx Invitae]	-	-	-	-	    	LOC109461476, GDF5	-	-
Cortical surface area	NHGRI-EBI GWAS catalog 	-	EFO:0010736 	-	PMID:34560273 	-	-		p-value: 1.00e-17
Grebe syndrome	ClinVar  [Illumina Laboratory ...]	-	Orphanet:2098 	-	-	    	LOC109461476, GDF5	-	-
Height	GIANT 	body height	EFO:0004339 	-	-	-	-		p-value: 2.81e-35
Height	NHGRI-EBI GWAS catalog 	body height	EFO:0004339 	-	PMID:34270706 	-	GDF5	-	p-value: 1.00e-9 beta coefficient: 0.48 unit increase
Height	NHGRI-EBI GWAS catalog 	body height	EFO:0004339 	-	PMID:31562340 	-	GDF5	-	p-value: 9.00e-78 beta coefficient: 0.06367727 unit increase
Knee osteoarthritis	NHGRI-EBI GWAS catalog 	Knee osteoarthritis	EFO:0004616  , HP:0005086 	-	PMID:30664745 	-	GDF5	-	p-value: 5.00e-7 odds ratio: 1.0495905
Knee osteoarthritis	NHGRI-EBI GWAS catalog 	Knee osteoarthritis	EFO:0004616  , HP:0005086 	-	PMID:30374069 	-	-		p-value: 8.00e-18 odds ratio: 1.09287
MULTIPLE SYNSTOSES SYNDROME 2	ClinVar  [Illumina Laboratory ...]	-	Orphanet:3237 	-	-	    	LOC109461476, GDF5	-	-
Osteoarthritis of hip	ClinVar  [OMIM]	-	-	PMID:17384641 	MIM:601146 	    	LOC109461476, GDF5	-	-
Vertex-wise cortical surface area	NHGRI-EBI GWAS catalog 	-	EFO:0010736 	-	PMID:34910505 	-	-		p-value: 2.00e-16 beta coefficient: 8.25 z score increase
Whole brain free water diffusion multivariate analysis	NHGRI-EBI GWAS catalog 	brain measurement	EFO:0004464 	-	PMID:35505052 	-	-	-	p-value: 3.00e-15

Ensembl ... Exploring variants... Citations

➤ Let's have a look at the citations of the variant.

The screenshot shows the Ensembl Variant displays page for SNP rs143383. The URL is https://www.ensembl.org/Homo_sapiens/Variants/Variant-display?var=rs143383&db=core. The variant is located at 20:35,437,703-35,438,703. The sidebar on the left has a red circle around the "Explore this variant" section, specifically the "Citations" link. The main content area shows the SNP details, including its consequence as a 5' prime UTR variant, its G/A allele, and its association with dbSNP and HGMD-PUBLIC. Below this, there are links to HGVS names, synonyms, genotyping assays, and clinical significance. A large red circle highlights the "Citations" section in the "Explore this variant" grid at the bottom right.

Variant displays

- Explore this variant
 - Genomic context
 - Flanking sequence
 - Population genetics
 - Sample genotypes
 - Linkage disequilibrium
 - Phylogenetic context
 - Citations
 - 3D Protein model
- Configure this page
- Custom tracks
- Export data
- Share this page
- Bookmark this page

rs143383 SNP

Most severe consequence: 5 prime UTR variant | See all predicted consequences

Alleles: G/A | Ancestral: G | Highest population MAF: 0.49

Change tolerance: CADD: A:21.4 | GERP: 2.76

Location: Chromosome 20:35438203 (forward strand) | VCF: 20 35438203 rs143383 G A

dbSNP: rs1555823599 (G-) ; HGMD-PUBLIC CR072309

This variant has 5 HGVS names - [Show](#)

This variant has 9 synonyms - [Show](#)

This variant has assays on 5 chips - [Show](#)

Variants (including SNPs and indels) imported from dbSNP (release 154) | [View in dbSNP](#)

This variant overlaps 2 transcripts, has 3009 sample genotypes, is associated with 11 phenotypes and is mentioned in 201 citations.

This SNP is associated with osteoarthritis (OA). It is located in the "five prime untranslated region" (5'UTR) of the gene encoding the embryonic stage onwards. GDF5 is also known as "cartilage-derived morphogenetic protein 1" or "BMP14".... [Show](#)

Explore this variant

- Genomic context
- Genes and regulation
- Flanking sequence
- Population genetics
- Phenotype data
- Sample genotypes
- Linkage disequilibrium
- Phylogenetic context
- Citations
- 3D Protein model

Citations (201)

HELMHOLTZ RESEARCH FOR GRAND CHALLENGES

Ensembl ... Exploring variants ...

Citations

➤ This variant is mentioned in 222 citations.

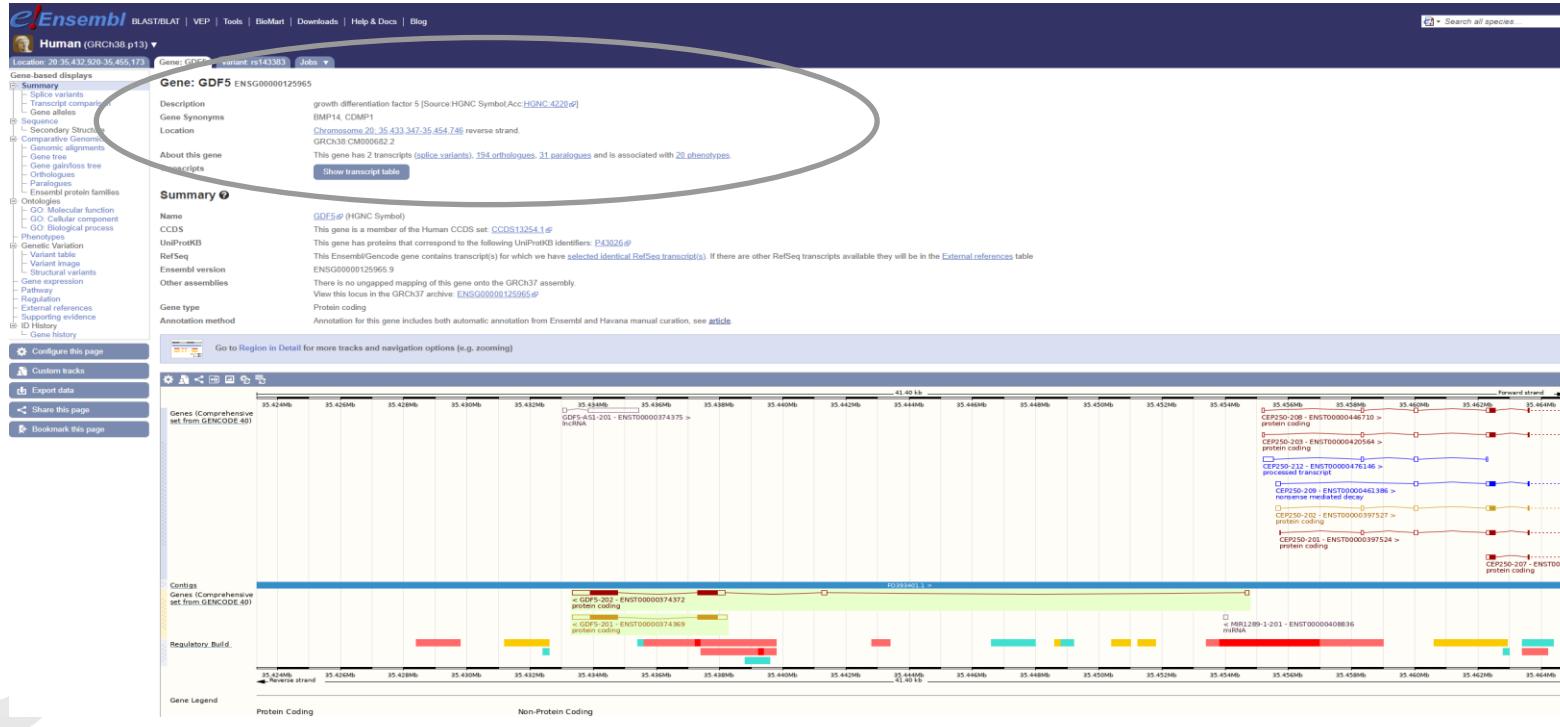
Citations

rs143383 is mentioned in the following publications

Show	All	entries	Show/hide columns	Filter	Print	
Year	PMID	Phenotype	Title	Author(s)	Full text	Citation source
2021	33235627		Identification of key genes in osteoarthritis using bioinformatics, principal component analysis and meta-analysis.	Sun X, Duan H, Xiao L, Yao S, et al	PMC678638	EPMC
2021	34206824		Current Evidence about Developmental Dysplasia of the Hip in Pregnancy.	Simionescu AA, Cirstoiu MM, Cirstoiu C, Stanescu AMA, et al	PMC8305660	EPMC
2021	34210342		The effect of common variants in GDF5 gene on the susceptibility to chronic postsurgical pain.	Yan S, Nie H, Bu G, Yuan W, et al	PMC847225	EPMC
2021	33817978		The Mechanisms and Functions of GDF-5 in Intervertebral Disc Degeneration.	Guo S, Cui L, Xiao C, Wang C, et al	PMC8126946	EPMC
2021	33522652		Growth differentiation factor 5 in cartilage and osteoarthritis: A possible therapeutic candidate.	Sun K, Guo J, Yao X, Guo Z, et al	PMC7941218	EPMC
2021	34203285		Genetic Study of IL6, GDF5 and PAPPA2 in Association with Developmental Dysplasia of the Hip.	Harsanyi S, Zamborsky R, Krajcová L, Kokavec M, et al	PMC8303839	EPMC
2021	33973562		A Case-Control Study of Major genetic pre-disposition risk alleles in developing DDD in the Northeast US population: Effects of Gene-Gene Interactions.	Vatlinchinov VI, Zhai BK, Hida T, Lacson R, et al		EPMC
2021	33861510		Frequency of Growth Differentiation Factor 5 rs143383 and asporin D-repeat polymorphisms in patients with hand and knee osteoarthritis in Kurdistan province, Iran.	Moghimi N, Nasseri S, Ghafouri F, Jalili A		EPMC
2020	31923126		A Meta-analysis Assessing the Association Between COL11A1 and GDF5 Genetic Variants and Intervertebral Disc Degeneration Susceptibility.	Wu F, Huang X, Zhang Z, Shao Z		dbSNP
2020	32103374		A novel variant near LSP1P3 is associated with knee osteoarthritis in the Chinese population.	Li Y, Liu F, Xu X, Zhang H, et al		EPMC, dbSNP
2020	31932746		Regulation of Gdf5 expression in joint remodelling, repair and osteoarthritis.	Kania K, Colella F, Riemen AHK, Wang H, et al	PMC6957535	EPMC
2020	32928309		Association between growth differentiation factor 5 rs143383 genetic polymorphism and the risk of knee osteoarthritis among Caucasian but not Asian: a meta-analysis.	Peng L, Jin S, Lu J, Ouyang C, et al	PMC7488690	EPMC
2020	32244273		Developmental Dysplasia of the Hip: A Review of Etiopathogenesis, Risk Factors, and Genetic Aspects.	Harsanyi S, Zamborsky R, Krajcová L, Kokavec M, et al	PMC7230892	EPMC
2020	32967120		Can Implementation of Genetics and Pharmacogenomics Improve Treatment of Chronic Low Back Pain?	Suntsov V, Jovanovic F, Knezevic E, Candido KD, et al	PMC7558486	EPMC
2020	32144293		Generation and characterization of human induced pluripotent stem cells (iPSCs) from hand osteoarthritis patient-derived fibroblasts.	Castro-Vilà E, Gómez-Quiles R, Sanjurjo-Rodríguez C, Piñeiro-Ramírez M, et al	PMC7060311	EPMC

Ensembl ... Exploring genes

➤ Let's have a look at *GDF5* (growth differentiation factor 5).



Ensembl ... Exploring variants ... Exercise 2

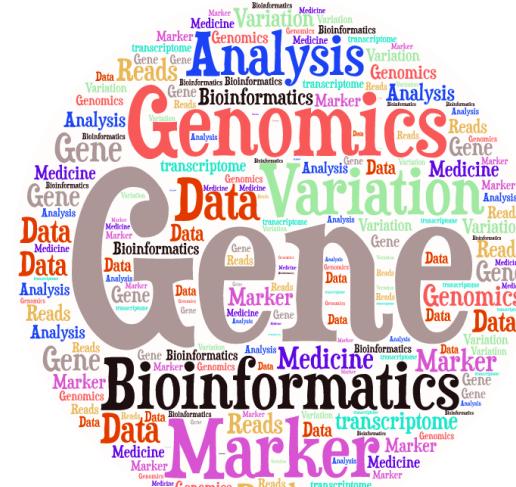
Explore rs2075650 (build 37).

1. What type of variants is?
2. Where is this variant located (chr - position - strand)?
3. Are there big differences in allele frequencies between populations?
4. What is the ancestral allele frequency in the Japanese in Tokyo (JPT) population from the 1000G set?
5. What is the least frequent genotype for this variant in the KHV population from the 1000G set?
6. In how many transcripts is this variant found?
7. Are all transcripts from the same gene?
8. How many and which consequence type are predicted for this variant?
9. How many phenotypes are associated with this variant?
10. How many phenotypes are associated with the gene that this variant is located in?
11. How many publications refer to rs2075650?



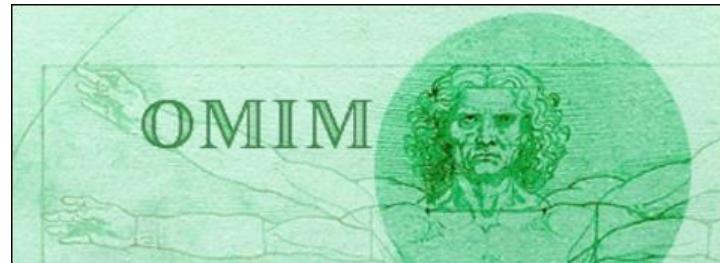
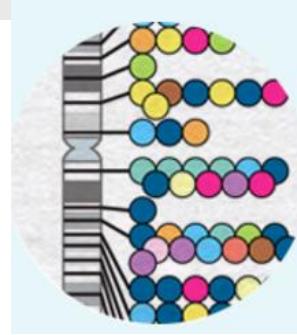
Publicly available bioinformatics resources

- Genome Browsers
 - Nucleotide Sequence Databases
 - Protein Sequence Databases
 - Database Searching by Sequence Similarity
 - Protein Domains: Databases and Search Tools
 - Human Traits & Diseases Databases
 - Phylogeny & Taxonomy
 - Databases of other Organisms
 - Gene Prediction
 - Gene Expression Databases
 - Gene Regulation
 - Metabolic, Gene Regulatory & Signal Transduction Network Databases
 - Publications Database



Human Traits & Diseases Databases

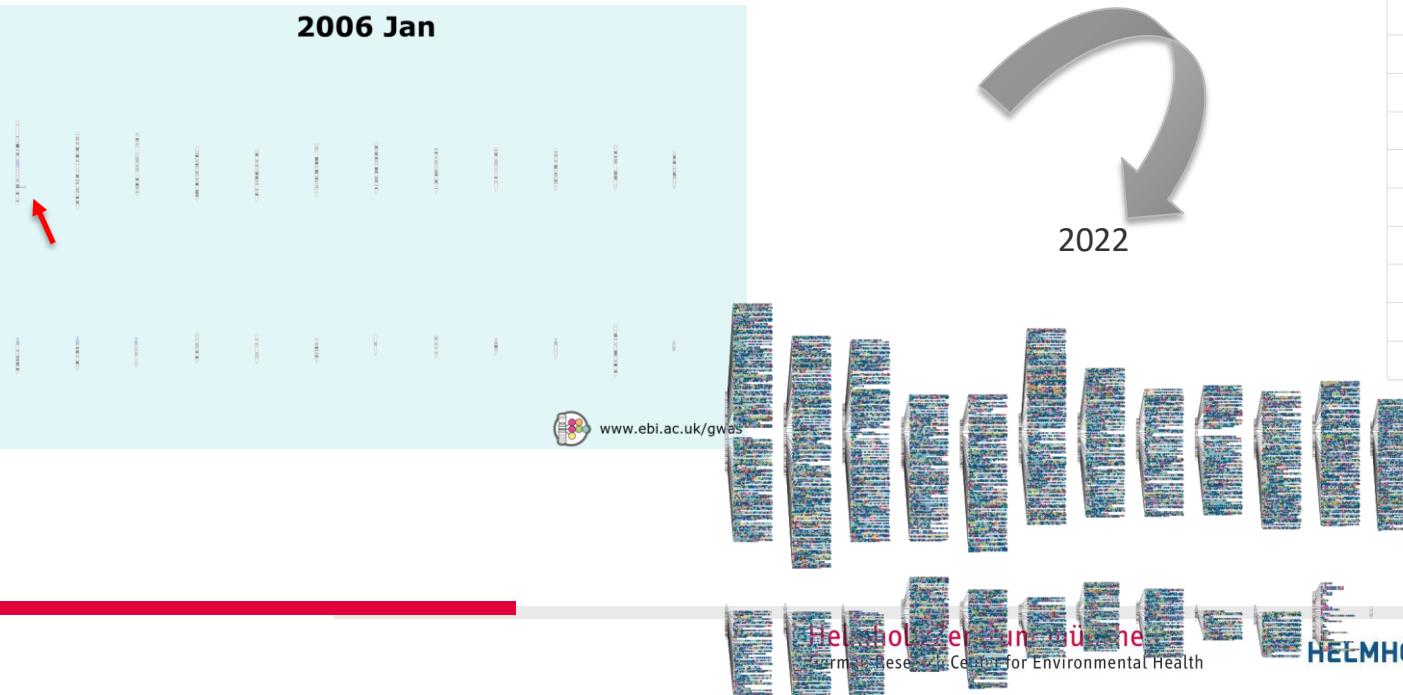
- GWAS catalog (<https://www.ebi.ac.uk/gwas/>)
- OMIM (<http://omim.org/>)
- Orphanet (<http://www.orpha.net>)



Human Traits & Diseases Databases

GWAS catalog

- “GWAS catalog” is a catalog of published/unpublished genome-wide association studies.



Show SNPs for	
Digestive system disease	640
Cardiovascular disease	1607
Metabolic disease	1096
Immune system disease	2380
Nervous system disease	3120
Liver enzyme measurement	1363
Lipid or lipoprotein measurement	4772
Inflammatory marker measurement	469
Hematological measurement	11555
Body weights and measures	3984
Cardiovascular measurement	1875
Other measurement	2764
Response to drug	446
Biological process	2523
Cancer	2713
Other disease	3005
Other trait	2822

Human Traits & Diseases Databases

GWAS catalog



GWAS Catalog

The NHGRI-EBI Catalog of human genome-wide association studies

Search the catalog 🔍

Examples: breast carcinoma, rs7329174, Yao, 2q37.1, HBS1L, 6:16000000-25000000

- Let's have a look at a specific variant, rs143383.

Search results for *rs143383*

V [rs143383](#)

Location: 20:35438203 **Cytogenetic region:** 20q11.22 **Most severe consequence:** 5 prime utr variant **Mapped gene(s):** GDF5

Associations 6 Studies 6

G [GDF5](#)

Description: growth differentiation factor 5

Location: 20:3543347-35454746 **Cytogenetic region:** 20q11.22 **Biotype:** protein coding

Associations 92 Studies 67

Human Traits & Diseases Databases

GWAS catalog

V rs143383

Location: 20:35438203 **Cytogenetic region:** 20q11.22 **Most severe consequence:** 5 prime utr variant **Mapped gene(s):** GDF5

Associations 10 Studies 10

Available data: Associations 10 Studies 10 Traits 5 Linkage disequilibrium (LD)

Download Associations

Associations 10

Show 5 entries

Column visibility Export Clear search

Variant and risk allele	P-value	P-value annotation	RAF	OR	Beta	CI	Mapped gene	Reported trait	Trait(s)	Background trait(s)	Study accession	Location
rs143383-G	2×10^{-16}	-	0.37	-	8.25 z score increase	-	GDF5	Vertex-wise cortical surface area	cortical surface area measurement	-	GCST90095130	20:35438203
rs143383-9	5×10^{-7}	-	NR	1.0495905	-	[1.03-1.07]	GDF5	Knee osteoarthritis	osteoarthritis, knee	-	GCST007090	20:35438203
rs143383-G	1×10^{-17}	-	0.3608	-	-	-	GDF5	Cortical surface area	cortical surface area measurement	-	GCST90091060	20:35438203
rs143383-T	8×10^{-18}	-	0.64	1.09287	-	[NR]	GDF5	Knee osteoarthritis	osteoarthritis, knee	-	GCST006925	20:35438203
rs143383-9	9×10^{-78}	-	NR	-	0.06367727 unit increase	[0.057-0.07]	GDF5	Height	body height	-	GCST008839	20:35438203

Showing 1 to 5 of 10 entries

« 1 2 »

Human Traits & Diseases Databases

GWAS catalog

G

GDF5

Description: growth differentiation factor 5

Location: 20:35433347-35454746 **Cytogenetic region:** 20q11.22 **Biotype:** protein coding

Associations

131

Studies

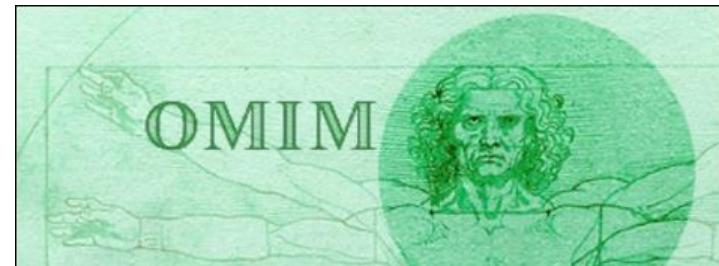
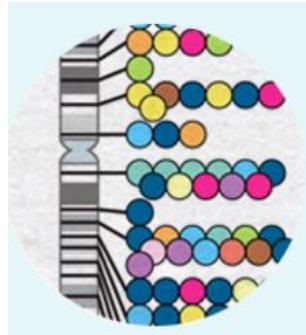
98



Human Traits & Diseases Databases ...

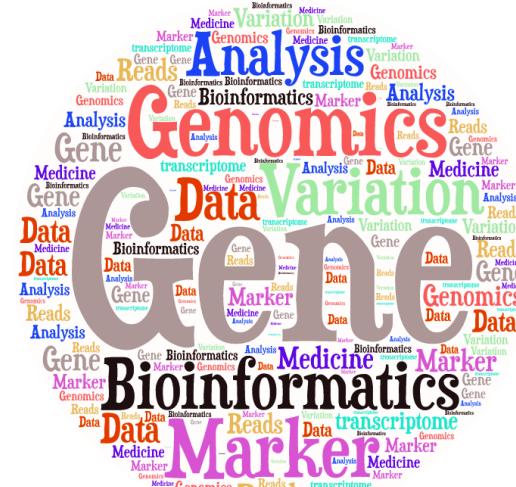
Exercise 3

1. Try to find more information about rs2075650 and the gene that is located in GWAS catalogue and OMIM databases.



Publicly available bioinformatics resources

- Human Genome Browsers
 - Nucleotide Sequence Databases
 - Protein Sequence Databases
 - Database Searching by Sequence Similarity
 - Protein Domains: Databases and Search Tools
 - Human Traits & Diseases Databases
 - Phylogeny & Taxonomy
 - Databases of other Organisms
 - Gene Prediction
 - Gene Expression Databases
 - Gene Regulation
 - Metabolic, Gene Regulatory & Signal Transduction Network Databases
 - Publications Database



Databases of other Organisms

- Mouse: http://www.ensembl.org/Mus_musculus/Info/Index

The screenshot shows the Ensembl gene detail page for **Gdf5** (ENSMUSG00000038259). The top navigation bar includes links for BLAST/BLAT, VEP, Tools, BioMart, Downloads, Help & Docs, and Blog. A search bar at the top right allows searching across all species. The main content area displays the gene's description, gene synonyms (CDMP1), and location (Chromosome 2: 155,941,023-155,945,307 reverse strand). It also lists orthologues, paralogues, and associated phenotypes. A detailed table provides transcript information for Gdf5-201, including Name (Gdf5), Transcript ID (ENSMUST00000040162), bp (2320), Protein (495aa), Biotype (Protein coding), CCDS (CCDS16958.1), UniProt (P43027), and Flags (TSL.1, GENCODE basic, APPRIS P1). The "Summary" section includes links for variants, pathways, regulation, and ID history. Below the table, a "Go to Region in Detail" link leads to a genomic track viewer. This viewer shows the genomic region from 155,932 Mb to 155,954 Mb, highlighting the Gdf5 gene (24.34 kb) and its protein coding region (exons 1-20). Other tracks include CTCF, Open Chromatin, Promoter, and Promoter Flank. A legend at the bottom explains the track colors and symbols.

Databases of other Organisms

- Mouse: <http://www.informatics.jax.org/>

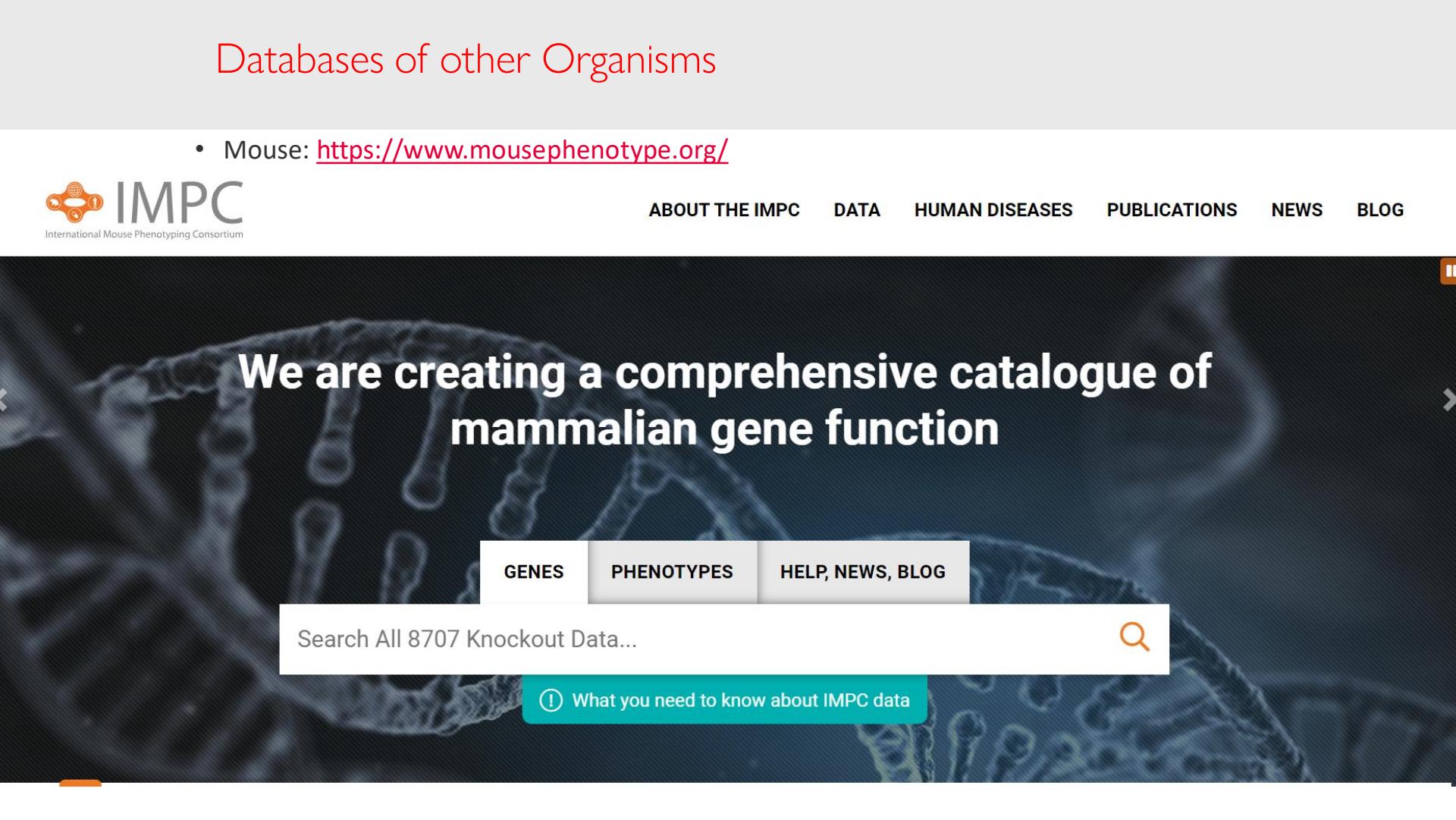
The screenshot shows the homepage of the Mouse Genome Informatics (MGI) database. At the top left is the MGI logo with a mouse icon. The main title "Mouse Genome Informatics" is centered above a dark blue navigation bar. The navigation bar includes links for "Search", "Download", "More Resources", "Submit Data", "Find Mice (IMSR)", "Analysis Tools", "Contact Us", and "Browsers". To the right of the navigation bar is the "ALLIANCE of GENOME RESOURCES" logo. The main content area features a search bar with a "Quick Search" button. Below the search bar is a sidebar with links to various databases and tools: Genes, Phenotypes & Mutant Alleles, Human-Mouse: Disease Connection, Gene Expression Database (GXD), Recombinase (cre), Function, Strains, SNPs & Polymorphisms, Vertebrate Homology, Mouse Models of Human Cancer, Batch Data and Analysis Tools, and Nomenclature. A "Getting Started:" section provides links to "Introduction to mouse genetics", "How to use MGI (Text & Video)", and "Cre Portal Tutorial". To the right of the sidebar is a box titled "/*NEW: MOUSE RESOURCES FOR COVID-19 RESEARCH__*/" which contains text about MGI's role in supporting COVID-19 research. Below this is a large banner featuring a mouse and the word "HTTPS" in large blue letters, with the text "MGI is now supporting the more secure HTTPS protocol". At the bottom of the page is a "What's new at MGI" section with a list of recent updates, including improvements to the Disease Connection search, enhanced QTL representation, and the naming of MGD as a Global Core Biodata Resource by the Global Biodata Coalition. The URL https://www.informatics.jax.org/humanDisease.shtml is visible at the bottom left.

Databases of other Organisms

- Mouse: <https://www.mousephenotype.org/>



ABOUT THE IMPC DATA HUMAN DISEASES PUBLICATIONS NEWS BLOG



A faint, grayscale background image of a mouse skeleton, showing its bones against a dark blue gradient.

We are creating a comprehensive catalogue of mammalian gene function

GENES

PHENOTYPES

HELP, NEWS, BLOG

Search All 8707 Knockout Data...



(!) What you need to know about IMPC data

Databases of other Organisms

- Zebrafish: <http://zfin.org/>

Search expert curated zebrafish data

Any ▾ heart contraction abnormal

Search

Fig. 1 of Monroe et al., 2016

Genes
Search for genes, transcripts, clones, and other markers

Expression
Search for gene expression data, and annotated images

Mutants/Tg
Search for mutants, knockdowns, transgenics, and affected phenotypes

Antibodies
Search for antibodies by gene, labeled anatomy, and other attributes

BLAST
Align nucleotide and protein sequences with zebrafish datasets

Publications
Search for zebrafish research publications and scientific literature

About ZFIN

The Zebrafish Information Network (ZFIN) is the database of genetic and genomic data for the zebrafish (*Danio rerio*) as a model organism. ZFIN provides a wide array of expertly curated, organized and cross-referenced zebrafish research data.

[Learn More](#)

Additional Resources

Data Mining
ZebrafishMine BioMart

Databases of other Organisms

- Drosophila: <http://flybase.org/>

The screenshot shows the FlyBase website homepage. At the top, there is a navigation bar with links for Home, Tools, Downloads, Links, Community, Species, About, Help, and Archives. Below the navigation bar, there are several search and browse options: BLAST, GBrowse, JBrowse, Resources, RNA-Seq, Vocabularies, ImageBrowse, and Batch Download. A banner at the top right indicates the version is FB2020_05, released on Oct 14, 2020. The main content area features a "QuickSearch" bar with various filters like Human Disease, Protein Domains, Gene Groups, Pathways, GO, Data Class, and specific search fields for FlyBase, Homologs, GAL4 etc., Expression, Phenotype, and References. Below the search bar, there is a "Everything" search input field and a "Search" button. To the left of the search bar, there is a video thumbnail titled "Using JBrowse on FlyBase". On the right side of the search bar, there is a note about using wild cards (*). The bottom half of the page displays a grid of 12 images representing different fly tissues and organs: Adipose, Circulatory, Excretory, Muscle, Imaginal Precursor, Integumentary, Tracheal, Digestive, Nervous, and Reproductive.

Databases of other Organisms

- Ensembl : >300 vertebrate species (<https://www.ensembl.org/info/about/species.html>) &
>45000 genomes from non-vertebrate species (<http://ensemblgenomes.org/>)

The screenshot shows the homepage of Ensembl Genomes. At the top, there's a grid of small images representing different organisms. Below this is the main header: "e! EnsemblGenomes Providing genome data for non-vertebrate species, with tools for the manipulation, analysis and visualisation of that data". To the right is a "Contact us" link. The page features several sections:

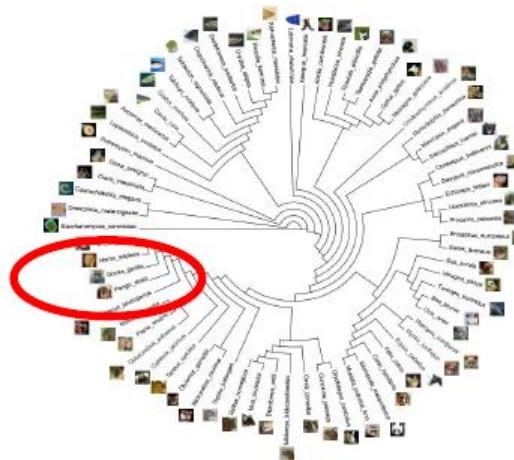
- Ensembl**: COVID-19, SARS-CoV-2 Genome sequence & annotation data.
- Ensembl**: Rapid Release, 2 weekly releases of new assemblies with gene & protein feature annotation.
- EnsemblPlants**: Includes *Triticum aestivum* IWGSC, *Oryza sativa* Japonica Group IRGSP1.0, *Arabidopsis thaliana* TAIR10, and a "Go to Ensembl Plants" button.
- EnsemblMetazoa**: Includes *Cenorhabditis elegans* WBcel235, *Drosophila melanogaster* BDGP6.2B, and *Bombus terrestris* ASMT16v1, with a "Go to Ensembl Metazoa" button.
- EnsemblProtists**: Includes *Plasmodium falciparum* 3D7 ASM270v2, *Dichotomium discoideum* dicty_2.7, and *Phytophthora infestans* ASM1429v1, with a "Go to Ensembl Protists" button.
- EnsemblFungi**: Includes *Magnaporthe oryzae* MG8, *Saccharomyces cerevisiae* R64-1-1, and *Aspergillus nidulans* ASM1142v1, with a "Go to Ensembl Fungi" button.
- EnsemblBacteria**: Includes *Streptococcus pneumoniae* Spn42298_v1.0, *Escherichia coli* AL505-MS, and *Bacillus subtilis* ASM73511v1, with a "Go to Ensembl Bacteria" button.

At the bottom left, there's a logo for EMBL-EBI. In the bottom right corner, there's a logo for ELIXIR with the text "Europe's life science research infrastructure".

Databases of other Organisms ...

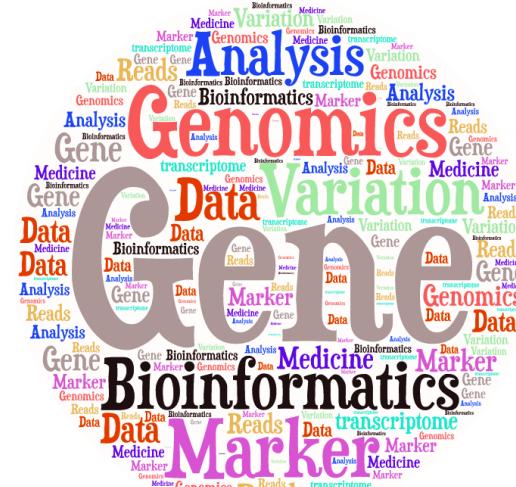
Exercise 4

- Explore rs2075650 in the databases of other organisms.
 - Hint: you can search by rsID or (mapped) gene id or phenotype.*



Publicly available bioinformatics resources

- Genome Browsers
 - Nucleotide Sequence Databases
 - Protein Sequence Databases
 - Database Searching by Sequence Similarity
 - Protein Domains: Databases and Search Tools
 - Human Traits & Diseases Databases
 - Phylogeny & Taxonomy
 - Databases of other Organisms
 - Gene Prediction
 - Gene Expression Databases
 - Gene Regulation
 - Metabolic, Gene Regulatory & Signal Transduction Network Databases
 - Publications Database



Gene Expression Databases

- Genotype-Tissue Expression (GTEx) : Correlations between genotype and tissue-specific gene expression (<https://www.gtexportal.org/home/>).

The screenshot shows the GTEx Portal homepage. At the top, there's a navigation bar with links for Home, Downloads, Expression, Single Cell, QTL, IGV Browser, Tissues & Histology, Documentation, About GTEx, Publications, Access Biospecimens, FAQs, and Contact. A search bar and a Google Sign In button are also at the top.

A banner at the top left announces the "snRNA-Seq Data released" on 2021-07-20, stating they have released snRNA-Seq data using 8 tissues and 16 GTEx donors (25 frozen tissue samples total). It links to the Single Cell Overview page.

The main content area has two main sections:

- Resource Overview**: Includes links to Current Release (V8), Tissue & Sample Statistics, Tissue Sampling Info (Anatomogram), Access & Download Data, Release History, and How to cite GTEx. It also provides a detailed description of the GTEx project's goal and data collection.
- Explore GTEx**: This section is divided into several categories:
 - Browse**: By gene ID, By variant or rs ID, By Tissue, Histology Viewer.
 - Single Cell**: Data Overview, Multi-Gene Single Cell Query.
 - Expression**: Multi-Gene Query, Transcript Browser.
 - QTL**: Locus Browser (Gene-centric), Locus Browser (Variant-centric).

At the bottom left, there's a section for Developmental GTEx with a brief description of its goals and a link to the main GTEx project page.

Gene Expression Databases

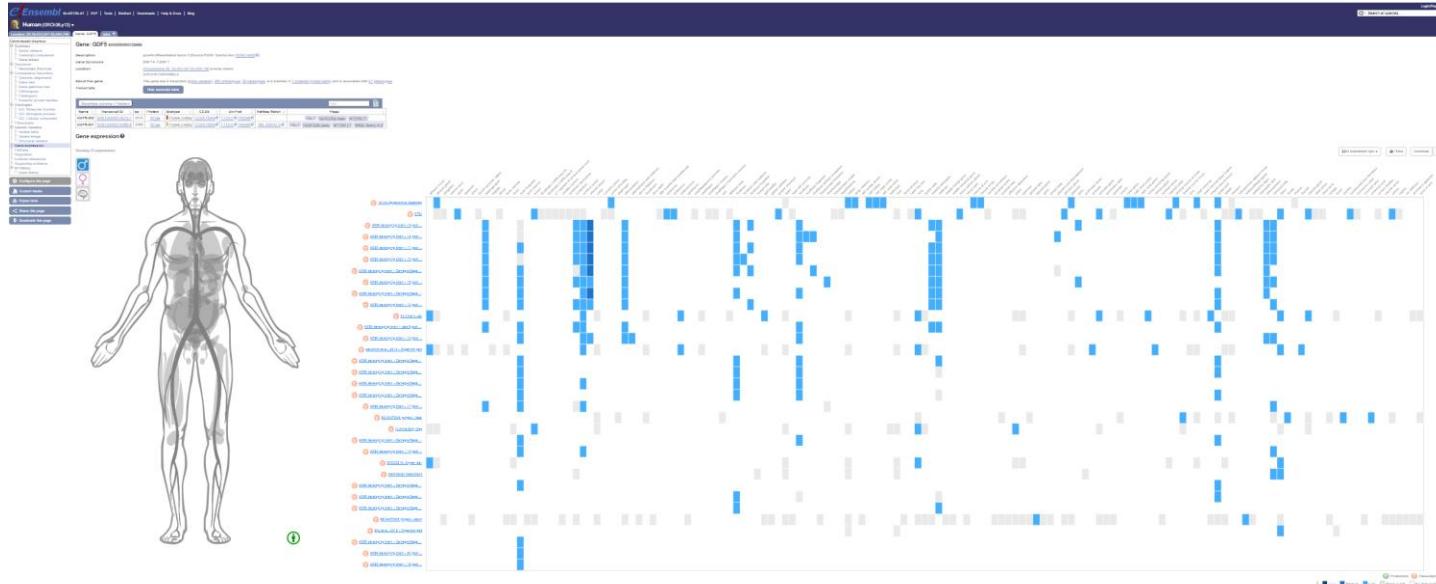
- Expression Atlas: Differential and Baseline Expression (<http://www.ebi.ac.uk/gxa/home> or through Ensembl).

The screenshot shows the Expression Atlas homepage. At the top, there's a navigation bar with links to EMBL-EBI, Services, Research, Training, About us, and a search icon. A green banner on the right says "Query single cell expression" and has a link to "To Single Cell Expression Atlas". Below the banner, the main title "Expression Atlas" is displayed next to a logo of a magnifying glass over a blue circle. The subtext "Gene expression across species and biological conditions" is also present. The main search area includes a search bar, a dropdown for "Species" set to "Any", and a dropdown for "Biological conditions". Below this, there's a section for "Gene / Gene properties" with a search input and examples like "REG1B, zinc finger, O14777 (UniProt), GO:0010468 (regulation of gene expression)". There are "Search" and "Clear" buttons. The footer of the main search area displays the text "Ensembl 99, Ensembl Genomes 46, WormBase ParaSite 14, EFO 3.10.0". Below the search area, there's a navigation bar with tabs for "Animals", "Plants", and "Fungi". Under the "Animals" tab, there are cards for six model organisms: Homo sapiens, Mus musculus, Rattus norvegicus, Drosophila melanogaster, Gallus gallus, and Caenorhabditis elegans. Each card shows a small icon of the organism, its name, the number of experiments (e.g., 1449 for Homo sapiens), the baseline value (e.g., 59 for Homo sapiens), and the differential value (e.g., 1390 for Homo sapiens). A red decorative bar is at the bottom of the page.

Organism	Experiments	Baseline	Differential
Homo sapiens	1449	59	1390
Mus musculus	1153	46	1107
Rattus norvegicus	152	3	149
Drosophila melanogaster	140	4	136
Gallus gallus	36	3	33
Caenorhabditis elegans	29	1	28

Gene Expression Databases

- Expression Atlas: Differential and Baseline Expression (<http://www.ebi.ac.uk/gxa/home> or through Ensembl).



Gene Expression Databases ...

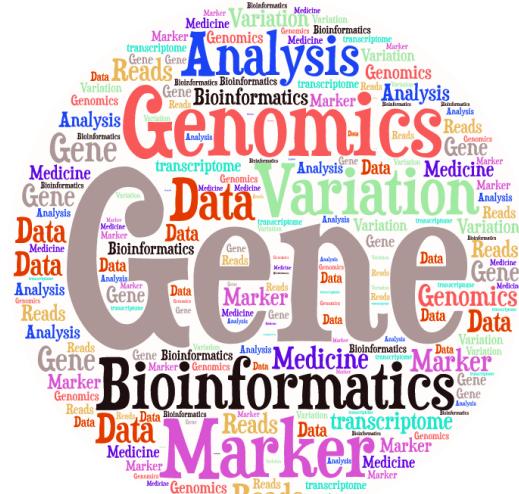
Exercise 5

- Does rs2075650 affect the expression of the gene?
 - Hint: Use GTEx portal
- In which tissue *TOMM40* is expressed? Any connections with Alzheimer disease?
 - Hint: Use Expression Atlas



Publications Database

- Genome Browsers
 - Nucleotide Sequence Databases
 - Protein Sequence Databases
 - Database Searching by Sequence Similarity
 - Protein Domains: Databases and Search Tools
 - Human Traits & Diseases Databases
 - Phylogeny & Taxonomy
 - Databases of other Organisms
 - Gene Prediction
 - Gene Expression Databases
 - Gene Regulation
 - Metabolic, Gene Regulatory & Signal Transduction Network Databases
 - Publications Database



Publications Database

- PubMed (<https://www.ncbi.nlm.nih.gov/pubmed>) comprises over 34 million citations.
- How do I search PubMed?
 - Identify the key concepts for your search.
 - Enter the terms* in the search box.
 - Keywords
 - Author name
 - Journal name
 -
 - Suggestions will display as you type your search terms.
 - Click Search.



Publications Database

- Anatomy of the summary results:

- [Policy Issues in the Development and Adoption of Biomarkers for Molecularly](#)

- [1. Targeted Cancer Therapies: Workshop Summary.](#)

National Cancer Policy Forum, Board on Health Care Services, Institute of Medicine.
Washington (DC): National Academies Press (US); 2015.

PMID: 25855848 [Free Books & Documents](#)

[Similar articles](#)

[journal title](#)
[abbreviation](#)

[authors](#)

- [Four-wave mixing experiments with extreme ultraviolet transient gratings.](#)

- Bencivenga F, Cucini R, Capotondi F, Battistoni A, Mincigrucci R, Giangrisostomi E, Gessini A, Manfredda M, Nikolov IP, Pedersoli E, Principi E, Svetina C, Parisse P, Casolari F, Danailov MB, Kiskinova M, Masciovecchio C. *Nature*. 2015 Apr 9;520(7546):205-8. doi: 10.1038/nature14341.

PMID: 25855456

[Similar articles](#)

[volume & issue](#)

[e-pagination](#)

- [Molecular imaging of angiogenesis after myocardial infarction by \(111\)In-](#)

- [3. DTPA-cNGR and \(99m\)Tc-sestamibi dual-isotope myocardial SPECT.](#)

Hendrikx G, De Saint-Hubert M, Dijkgraaf I, Bauwens M, Douma K, Wiertz R, Pooters I, Van den Akker NM, Hackeng TM, Post MJ, Mottaghy FM. *EJNMMI Res*. 2015 Jan 28;5:2. doi: 10.1186/s13550-015-0081-7. eCollection 2015.

PMID: 25853008 [Free PMC Article](#)

[Similar articles](#)

[publicaton date](#)

Publications Database ... Exercise 6

- Try to find more information about rs2075650 and the gene that is located.
- Can you find a paper for which:
 - “Lopes” is one of the authors
 - Dealing with “osteoarthritis”
 - The name of the journal is “Lancet”



Pipeline

Variant:

Ensembl:

- ✓ position,
- ✓ consequences (transcript and regulatory region)
- ✓ 1kG frequencies,
- ✓ GWAS signals around the variant,
- ✓ regulatory marks around the variant
- ✓ nearby genes.

ExAC: allele frequencies

GTEx: associated gene.

Pubmed: papers where the variant is cited.

Gene:

Ensembl:

- ✓ Position
- ✓ Associated phenotypes
- ✓ Gene ontology annotations

Uniprot:

- ✓ Function, Tissue, Localization, Disease

OMIM:

- ✓ gene annotation
- ✓ associated diseases

GWAS catalog:

- ✓ Associated variants and association details.

Gene Expression Atlas:

- ✓ Tissues in which expression of the gene was observed

GTEx:

- ✓ List of variants that affects the expression of the gene.

Mouse Genomics Informatics:

- ✓ Mouse phenotype of the gene.



Dr Daniel Sugees
Senior Bioinformatician

Team144 pipeline

Variant details	
General information:	
rsID:	rs143384
Chromosome:start-end:	20:34025756-34025756
Allele string:	A/G
MAF:	0.438898
Consequence:	5_prime_UTR_variant
Variation type:	SNP
gerp (average gerp):	5.04 (3.497)
GWAVA score:	0.79
Ancestral allele:	G
Minor allele:	A
Synonyms:	rs431839, rs61433024, rs765106, rs3748435, rs17422934
Phenotypes (risk allele):	Height(A), Infant length(G), Height(G)

GWAS signals					
GWAS signals within 1Mbp of the variant:					
rsID	SNPID	Distance	Trait	p-value	PMID
rs17310467		chr20:33545616 -481kbp	Hemostatic factors and hematological phenotypes	4E-34	22443383
rs11906160		chr20:33565755 -461kbp	Anticoagulant levels	1E-6	22216198
rs1535466		chr20:33718706 -308kbp	Height	1.8E-29	25282103
rs2295888		chr20:33722863 -303kbp	Prothrombin time	5E-13	22703881
rs6120849		chr20:33730387 -296kbp	Protein C levels	7E-37	20802025
rs6088735		chr20:33745676 -281kbp	Hemostatic factors and hematological phenotypes	4E-34	22443383
rs6060278		chr20:33753262 -273kbp	Hemostatic factors and hematological phenotypes	4E-34	22443383
rs867186		chr20:33764554 -262kbp	Anticoagulant levels	4E-9	22216198
rs867186		chr20:33764554 -262kbp	Coagulation factor levels	6E-37	20231535
rs867186		chr20:33764554 -262kbp	D-dimer levels	4E-6	21502573
rs867186		chr20:33764554 -262kbp	Hemostatic factors and hematological phenotypes	2E-6	22443383
rs867186		chr20:33764554 -262kbp	Protein C levels	1E-64	25376901
rs11167260		chr20:33775200 -251kbp	Amyotrophic lateral sclerosis	4E-6	24529757



Dr Daniel Sugees
Senior Bioinformatician

HelmholtzZentrum münchen
German Research Center for Environmental Health

Thank you!

HELMHOLTZ RESEARCH FOR
GRAND CHALLENGES

What is a genome assembly?

Sequence reads

CGGCCTTGGGCTCCGCCTTCAGCTCAAGA		
CAGCTGTCCCAGATGAC	ACTTAACCTCCCTCCCAGCTGTCC	
GGGCTCCGCCTTCAGCTC		TCCCAGCTGTCCCAGATGACGCCATC
	AACTTCCCTCCCAGCT	
CGGCCTTGGGCTCC		TCCGCCTTCAGCTCAAGACTTAACCTTC
	CAGATGACGCC	

Match up overlaps

CGGCCTTGGGCTCCGCCTTCAGCTCAAGA	AACTTCCCTCCCAGCT	CAGATGACGCC
TCCGCCTTCAGCTCAAGACTTAACCTTC	TCCCAGCTGTCCCAGATGACGCCATC	
GGGCTCCGCCTTCAGCTC	ACTTAACCTCCCTCCCAGCTGTCC	
CGGCCTTGGGCTCC		CAGCTGTCCCAGATGAC

Genome assembly

CGGCCTTGGGCTCCGCCTTCAGCTCAAGACTTAACCTCCCTCCCAGCTGTCCCAGATGACGCCAT

Ensembl ... the front page ... Exercise 1



1. Go to the species homepage for **Giant Panda**. What is the name of the genome assembly for Panda?
 - ASM200744v2, INSDC Assembly [GCA_002007445.2](#), Apr 2020
2. How long is the Panda genome (in bp)? How many coding genes have been annotated?
 - 2,444,060,653 & 20,857
3. Repeat for **Human**.
 - GRCh38.p13 (Genome Reference Consortium Human Build 38), INSDC Assembly GCA_000001405.28, Dec 2013
 - 3,096,649,726
 - 20,471 (incl 662 readthrough)



Ensembl ... Exploring variants ... Exercise 2

Explore rs2075650 (build 37).

1. What type of variants is? **SNP**
2. Where is this variant located (chr - position - strand)? **Chromosome 19:44892362 (forward strand)**
3. Are there big differences in allele frequencies between populations? **Not really. Max 8% in some sub-African pop and 10% in som AMR sub-pop too.**
4. What is the ancestral allele frequency in the Japanese in Tokyo (JPT) population from the 1000G set? **12%**
5. What is the least frequent genotype for this variant in the KHV population from the 1000G set? **G|G**
6. In how many transcripts is this variant found? **5**
7. Are all transcripts from the same gene? Yes, **TOMM40**
8. How many and which consequence type are predicted for this variant? **1, Intron**
9. How many phenotypes are associated with this variant? **67**
10. How many phenotypes are associated with the gene that this variant is located in? **1**
11. How many publications refer to rs2075650? **313**