

マイクロアレイ染色体検査普及のための産学連携コンソーシアム主催
マイクロアレイ染色体検査解釈ハンズオンウェビナー 2023.9.19

マイクロアレイ染色体検査解釈 ハンズオンウェビナー

初級編 解説資料

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UCSC genome browser の活用



Genomes

Genome Browser

Tools

Mirrors

Downloads

My Data

View

Help

About Us

ゲノムバージョンが表示されている



Human GRCh38/hg38

Human GRCh37/hg19

Human T2T-CHM13/hs1

Mouse GRCm39/mm39

Mouse GRCm38/mm10

Genome Archive GenArk

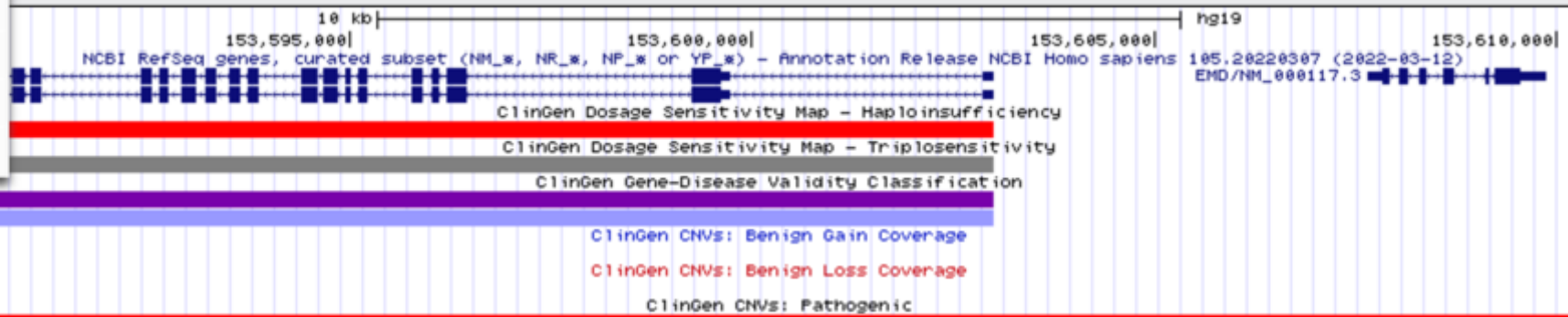
SARS-CoV-2 (COVID-19)

Other

UCSC Genome Browser on Human (GRCh37/hg19)

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chrX:153,587,471-153,613,200 25,730 bp. gene, chromosome range, search terms, help pages, see examples go examples



FLNA/NM_001173333.1
nodular heterotopia and aortic dissection

- nssv578369_unk
- nssv579153_unk
- nssv579158_unk
- nssv579162_unk
- nssv578371_unk
- nssv578385_unk
- nssv579178_unk
- nssv579183_unk
- nssv578388_unk
- nssv578389_unk
- nssv578391_unk
- nssv578394_unk
- nssv13653771_unk
- nssv13652896_unk
- nssv13654877_unk
- nssv13638892_unk
- nssv13645188_unk
- nssv13651626_unk
- nssv13644938_unk
- nssv13653549_unk
- nssv13639848_unk
- nssv13639971_unk
- nssv13640283_unk
- nssv13640952_unk
- nssv13646405_unk
- nssv13648154_unk
- nssv13653114_unk

left or right to new position. Press "?" for keyboard shortcuts. Use drop-down controls below and press refresh to alter tracks displayed.

collapse all

track search

hide all

add custom tracks

configure

reverse

resize

expand all

Mapping and Sequencing refresh

[Base Position](#)

dense

[P13 Fix Patches](#)

hide

[P13 Alt Haplotypes](#)

hide

[Assembly](#)

hide

[BAC End Pairs](#)

hide

[BU ORChID](#)

hide

[Chromosome Band](#)

dense

[18 deCODE Recomb](#)
[No data-chrX]

hide

[ENCODE Pilot](#)

hide

[Exome Probesets](#)

hide

[18 FISH Clones](#)

hide

[18 Fosmid End Pairs](#)

hide

[Gap](#)

hide

[GC Percent](#)

hide

[GRC Incident](#)

hide

[GRC Map Contigs](#)

hide

[Hg18 Diff](#)

hide

[Hg38 Diff](#)

hide

[Hi Seq Depth](#)

hide

[INSDC](#)

hide

[liftOver & ReMap](#)

hide

[LRG Regions](#)

hide

[Map Contigs](#)

hide

[Mappability](#)

hide

[Problematic Regions](#)

hide

[Recomb Rate](#)

hide

[RefSeq Acc](#)

hide

[Restr Enzymes](#)

hide

[Short Match](#)

hide

[STS Markers](#)

hide

Genes and Gene Predictions refresh

領域内の遺伝子

[UCSC Genes](#)

pack

[NCBI RefSeq](#)

pack

[CCDS](#)

hide

[CRISPR Targets](#)

hide

[Ensembl Genes](#)

hide

[17 EvoFold](#)

hide

[Exoniphy](#)

hide

[Updated GENCODE](#)

hide

[H-Inv 7.0](#)

hide

[New HGNC](#)

hide

[IKMC Genes Mapped](#)

hide

[lincRNAs](#)

hide

[LRG Transcripts](#)

hide

[MGC Genes](#)

hide

[Old UCSC Genes](#)

hide

[ORFeome Clones](#)

hide

[Other RefSeq](#)

hide

[Pfam in UCSC Gene](#)

hide

[Prediction Archive](#)

hide

[Retroposed Genes sno/miRNA](#)

hide

[Yale Pseudo60](#)

hide

[TransMap V5](#)

hide

[tRNA Genes](#)

hide

[UCSC Alt Events](#)

hide

[UniProt](#)

[Vega Genes](#)

[Yale Pseudo60](#)

Phenotype and Literature

病原性のあるCNV

refresh

[Publications](#)

hide

[CADD](#)

hide

[ClinGen](#)

pack



[ClinGen
CNVs](#)

pack

[ClinVar Variants](#)

hide

Updated [Constraint
scores](#)

hide

[Coriell CNVs](#)

hide

[COSMIC Regions](#)

hide

[DECIPHER CNVs](#)

pack

[DECIPHER
SNVs](#)

hide

[Development Delay](#)

pack

[GAD View](#)

hide

[GenCC](#)

hide

[Gene Interactions](#)

hide

[GeneReviews](#)

hide

[GWAS Catalog](#)

hide

[Haploinsufficiency](#)

pack

[HGMD Variants](#)

hide

[Lens Patents](#)

hide

[LOVD Variants](#)

hide

18 [MGI Mouse QTL](#)

hide

[OMIM Alleles](#)

hide

[OMIM Cyto Loci](#)

hide

[OMIM Genes](#)

pack

[Orphanet](#)

hide

New [PanelApp](#)

hide

[REVEL Scores](#)

hide

18 [RGD Human
QTL](#)

hide

18 [RGD Rat QTL](#)

hide

[SNPedia](#)

hide

[UniProt Variants](#)

hide

[Variants in
Papers](#)

hide

[Web Sequences](#)

hide

(黄色矢印) クリックすると項目の詳細
や細かい設定ができる

COVID-19

refresh

[COVID GWAS
v4](#)

[No data-chrX]

[COVID GWAS
v3](#)

[No data-chrX]

[Rare Harmful Vars](#)

hide

mRNA and EST

refresh

18 [CGAP SAGE](#)

hide

[Gene Bounds](#)

hide

18 [H-Inv](#)

hide

[Human ESTs](#)

hide

[Human mRNAs](#)

hide

[Human RNA Editing](#)

hide

[Other ESTs](#)

[Other mRNAs](#)

18 [Poly\(A\)](#)

[PolyA-Seq](#)

[SIB Alt-Splicing](#)

[Spliced ESTs](#)





Select subtracks by evidence and class:

<input type="checkbox"/> <input type="checkbox"/> All	<i>Evidence</i>	Curated	Submitted
<i>Class</i>		<input type="checkbox"/> <input type="checkbox"/>	<input type="checkbox"/> <input type="checkbox"/>
Pathogenic <input type="checkbox"/> <input type="checkbox"/>		<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Likely Pathogenic <input type="checkbox"/> <input type="checkbox"/>			<input checked="" type="checkbox"/>
Uncertain <input type="checkbox"/> <input type="checkbox"/>			<input checked="" type="checkbox"/>
Likely Benign <input type="checkbox"/> <input type="checkbox"/>			<input checked="" type="checkbox"/>
Benign <input type="checkbox"/> <input type="checkbox"/>		<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

ClinGen CNVs

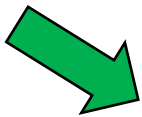
Defaultだとpathogenicしか表示されないようになっているのでbenign, uncertainを表示させたいならpackに変更を

List subtracks: only selected/visible all (11 of 11 selected)

<input type="checkbox"/>		Class ↓ ¹	Evidence ↓ ²	views ↓ ³	Track Name ↓ ⁴	
<input checked="" type="checkbox"/>	pack	Benign	Curated	CNVs	ClinGen CNVs: Curated Benign	Schema
<input checked="" type="checkbox"/>	pack	Benign	Submitted	CNVs	ClinGen CNVs: Benign	Schema
<input checked="" type="checkbox"/>	pack  Configure	Benign	Submitted	Coverage	ClinGen CNVs: Benign Gain Coverage	Schema
<input checked="" type="checkbox"/>	pack  Configure	Benign	Submitted	Coverage	ClinGen CNVs: Benign Loss Coverage	Schema
<input checked="" type="checkbox"/>	pack	Likely Benign	Submitted	CNVs	ClinGen CNVs: Uncertain: Likely Benign	Schema
<input checked="" type="checkbox"/>	pack	Likely Pathogenic	Submitted	CNVs	ClinGen CNVs: Uncertain: Likely Pathogenic	Schema
<input checked="" type="checkbox"/>	pack	Pathogenic	Curated	CNVs	ClinGen CNVs: Curated Pathogenic	Schema
<input checked="" type="checkbox"/>	pack	Pathogenic	Submitted	CNVs	ClinGen CNVs: Pathogenic	Schema
<input checked="" type="checkbox"/>	pack  Configure	Pathogenic	Submitted	Coverage	ClinGen CNVs: Pathogenic Gain Coverage	Schema
<input checked="" type="checkbox"/>	pack  Configure	Pathogenic	Submitted	Coverage	ClinGen CNVs: Pathogenic Loss Coverage	Schema
<input checked="" type="checkbox"/>	pack	Uncertain	Submitted	CNVs	ClinGen CNVs: Uncertain	Schema

11 of 11 selected

Submit



- +
COVID-19
refresh
- +
mRNA and EST
refresh
- +
Expression
refresh
- +
Regulation
refresh
- +
Comparative Genomics
refresh
- +
Neandertal Assembly and Analysis
refresh
- +
Denisova Assembly and Analysis
refresh
- Variation
refresh

病原性のないCNV (コントロール)

dbSNP 155 <input type="button" value="hide"/>	1000G Archive <input type="button" value="hide"/>	Array Probesets <input type="button" value="hide"/>	dbSNP Archive <input type="button" value="hide"/>	dbVar Common Struct Var <input type="button" value="show"/>	DGV Struct Var <input type="button" value="pack"/>
EVS Variants <input type="button" value="hide"/>	ExAC <input type="button" value="hide"/>	Genome In a Bottle <input type="button" value="hide"/>	18 Genome Variants <input type="button" value="hide"/>	GIS DNA PET <input type="button" value="hide"/>	gnomAD <input type="button" value="hide"/>
HAIB Genotype <input type="button" value="hide"/>	18 HapMap SNPs <input type="button" value="hide"/>	HGDP Allele Freq <input type="button" value="hide"/>	Platinum Genomes <input type="button" value="hide"/>		

-
Repeats
refresh

RepeatMasker <input type="button" value="dense"/>	Interrupted Rpts <input type="button" value="hide"/>	Microsatellite <input type="button" value="hide"/>	NumtS Sequence <input type="button" value="hide"/>	Segmental Dups <input type="button" value="dense"/>	Self Chain <input type="button" value="hide"/>
Simple Repeats <input type="button" value="hide"/>	WM + SDust <input type="button" value="hide"/>				

設定を更新