

```
##   CHR      MB
## 1    1 2.882119
## 2    2 3.409471
## 3    3 3.362215
## 4    4 3.144614
## 5    5 3.282147
## 6    6 3.385661
## 7    7 3.328516
## 8    8 2.940057
## 9    9 3.630920
## 10  10 3.009317
## 11  11 3.332975
## 12  12 2.803641
## 13  13 3.056790
## 14  14 3.880058
## 15  15 3.012148
## 16  16 3.025738
## 17  17 2.933941
## 18  18 2.827001
## 19  19 3.183279
## 20  20 3.612372
## 21  21 3.099087
## 22  22 3.161019
## 23  23 3.209078
## 24  24 2.883651
## 25  25 3.377691
## 26  26 3.258615
## 27  27 3.095501
## 28  28 4.078299
## 29  29 3.245302
```

```
# Se for usar e quiser salvar esse arquivo, tirar o # da linha de comando abaixo.
write.table(size_CHR, "Resultado_tamanho_ROH_por_CHR.txt", quote=F, row.names=F, colnames=T)

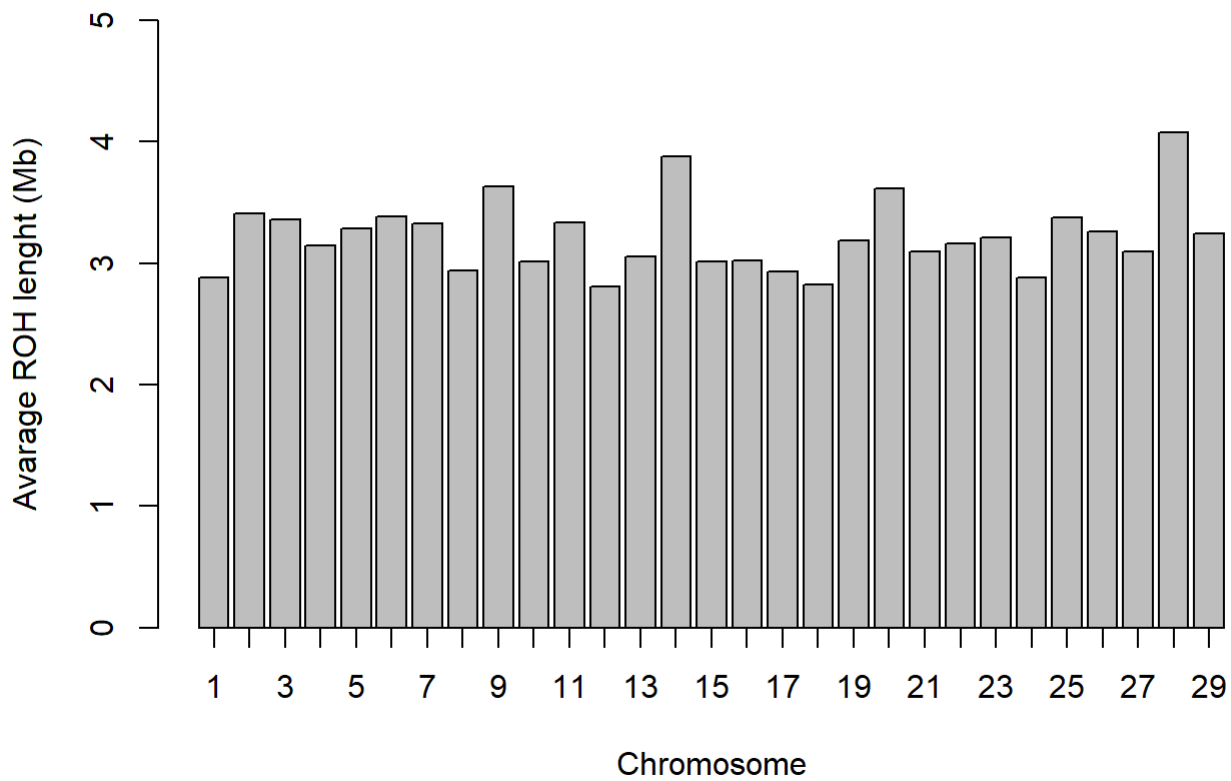
#### Grafico do comprimento medio de ROHs por cromossomo (Mb) ####
# Tamanho medio de ROHs por cromossomo
max(size_CHR$MB)
```

```
## [1] 4.078299
```

```
y<-barplot(size_CHR$MB,ylim=c(0,5),ylab="Avarage ROH lenght (Mb)",xlab="Chromosome")
y
```

```
##      [,1]
## [1,] 0.7
## [2,] 1.9
## [3,] 3.1
## [4,] 4.3
## [5,] 5.5
## [6,] 6.7
## [7,] 7.9
## [8,] 9.1
## [9,] 10.3
## [10,] 11.5
## [11,] 12.7
## [12,] 13.9
## [13,] 15.1
## [14,] 16.3
## [15,] 17.5
## [16,] 18.7
## [17,] 19.9
## [18,] 21.1
## [19,] 22.3
## [20,] 23.5
## [21,] 24.7
## [22,] 25.9
## [23,] 27.1
## [24,] 28.3
## [25,] 29.5
## [26,] 30.7
## [27,] 31.9
## [28,] 33.1
## [29,] 34.3
```

```
axis(1, at=y, labels=1:29)
```



# Se for usar esse grafico, SALVAR!

```
#####  
#### Proporcao de ROHs por tamanho ####  
#### ROH de 1 a 2 Mb, 2 a 4 Mb, ... ####  
#####
```

```
#### Separando as ROHs de acordo com o tamanho  
head(saida_hom)
```

##	FID	IID	PHE	CHR	SNP1	SNP2	POS1	POS2	KB	NSNP
	DENSITY	PHOM	PHET	MB						
## 1	0	102916029440	-9	1	BovineHD0100006914	BovineHD0100012022	23381349	42095937	18714.589	2816
	6.646	1.000	0.000	18.714589						
## 2	0	102916029440	-9	1	BovineHD0100047134	BovineHD0100029888	102458103	105162097	2703.995	377
	7.172	0.995	0.005	2.703995						
## 3	0	102916029440	-9	1	BovineHD0100041142	BovineHD0100043043	143141556	148784184	5642.629	975
	5.787	0.998	0.002	5.642629						
## 4	0	102916029440	-9	1	BovineHD0100043081	BovineHD0100044197	148857503	152070453	3212.951	397
	8.093	0.997	0.003	3.212951						
## 5	0	102916029440	-9	1	BovineHD0100044217	BovineHD0100045574	152126033	156040374	3914.342	685
	5.714	0.999	0.001	3.914342						
## 6	0	102916029440	-9	2	BovineHD0200019851	BovineHD0200020565	68732542	71627667	2895.126	181
	15.995	1.000	0.000	2.895126						

```

mb_1_2<-saida_hom[saida_hom$MB<2,] # Arquivo com ROHs de 1 a 2 Mb
Porc1_2Mb<-(nrow(mb_1_2)*100)/nrow(saida_hom) # Proporcao de ROHs de 1 a 2 Mb
mb_2_4<-saida_hom[saida_hom$MB>2 & saida_hom$MB<4,] # Arquivo com ROHs de 2 a 4 Mb
Porc2_4Mb<-(nrow(mb_2_4)*100)/nrow(saida_hom) # Proporcao de ROHs de 2 a 4 Mb
mb_4_8<-saida_hom[saida_hom$MB>4 & saida_hom$MB<8,] # Arquivo com ROHs de 4 a 8 Mb
Porc4_8Mb<-(nrow(mb_4_8)*100)/nrow(saida_hom) # Proporcao de ROHs de 4 a 8 Mb
mb_8_16<-saida_hom[saida_hom$MB>8 & saida_hom$MB<16,] # Arquivo com ROHs de 8 a 16 Mb
Porc8_16Mb<-(nrow(mb_8_16)*100)/nrow(saida_hom) # Proporcao de ROHs de 8 a 16 Mb
mb_16<-saida_hom[saida_hom$MB>16,] # Arquivo com ROHs acima de 16 Mb
Porc16Mb<-(nrow(mb_16)*100)/nrow(saida_hom) # Proporcao de ROHs acima de 16 Mb

##### CRIANDO AS COLUNAS DA TABELA #####

# Nomes das classes
classes<-rbind("ROH1-2 Mb","ROH2-4 Mb","ROH4-8 Mb","ROH8-16 Mb","ROH>16 Mb")
# Numero de ROHs total por classe
N_ROH<-rbind(nrow(mb_1_2),nrow(mb_2_4),nrow(mb_4_8),nrow(mb_8_16),nrow(mb_16))
# Proporcao dos ROHs nas classes
Porc_Mb<-rbind(Porc1_2Mb,Porc2_4Mb,Porc4_8Mb,Porc8_16Mb,Porc16Mb)
# Tamanho das ROHs por classe (em Megabases)
size<-rbind(mean(mb_1_2$MB),mean(mb_2_4$MB),mean(mb_4_8$MB),mean(mb_8_16$MB),mean(mb_16$MB))
# Numero de animais que tem estas classes
N_IID<-rbind(nrow(as.data.frame(table(mb_1_2$IID))),nrow(as.data.frame(table(mb_2_4$IID))),
             nrow(as.data.frame(table(mb_4_8$IID))),nrow(as.data.frame(table(mb_8_16$IID))),
             nrow(as.data.frame(table(mb_16$IID))))
# Numero medio de ROHs por individuo
N_ROH_IID<-rbind(mean(as.data.frame(table(mb_1_2$IID))[,2]),
                 mean(as.data.frame(table(mb_2_4$IID))[,2]),
                 mean(as.data.frame(table(mb_4_8$IID))[,2]),
                 mean(as.data.frame(table(mb_8_16$IID))[,2]),
                 mean(as.data.frame(table(mb_16$IID))[,2]))

##### CRIANDO A TABELA #####
# Tutorial - Tabela 1. Exemplo de parametros avaliados por classe de ROH
tabela_ROH<-cbind(classes,N_ROH,Porc_Mb,size,N_IID,N_ROH_IID)
tabela_ROH

```

##	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]
## Porc1_2Mb	"ROH1-2 Mb"	"61269"	"58.1702697314079"	"1.34880904263167"	"2093"	"29.2732919254658"
## Porc2_4Mb	"ROH2-4 Mb"	"23949"	"22.7377595488336"	"2.77562034448202"	"2093"	"11.4424271380793"
## Porc4_8Mb	"ROH4-8 Mb"	"11942"	"11.3380234887541"	"5.52765317082566"	"2081"	"5.73858721768381"
## Porc8_16Mb	"ROH8-16 Mb"	"5805"	"5.51140733145347"	"11.0534292037898"	"1847"	"3.1429344883595"
## Porc16Mb	"ROH>16 Mb"	"2362"	"2.24253989955092"	"24.6646769665538"	"1132"	"2.08657243816254"

2\_Genome\_Coverage\_xlsx

# Dados

## Exemplo para calcular a proporção do genoma coberta por ROH em cada cromossomo

Cromossomo	Tamanho do Cromossomo em Mb	Tamanho médio das ROHs	Fórmula <sup>1</sup>	Proporção <sup>2</sup>
BTA1	158,53	2,88	(Tamanho médio das ROHs *100) / Tamanho do Cromossomo em Mb	1,82
BTA2	136,23	3,41		2,50
BTA3	121,01	3,36		2,78
BTA4	120	3,14		2,62
BTA5	120,09	3,28		2,73
BTA6	117,81	3,39		2,87
BTA7	110,68	3,33		3,01
BTA8	113,32	2,94		2,59
BTA9	105,45	3,63		3,44
BTA10	103,31	3,01		2,91
BTA11	106,98	3,33		3,12
.	.	.	.	.
.	.	.	.	.
.	.	.	.	.
BTA29	51,1	3,25	6,35	6,35

<sup>1</sup>A coluna "fórmula" contém a fórmula para calcular a proporção do cromossomo que é coberta por ROHs

<sup>2</sup>A coluna "Proporção" contém os valores sem a fórmula. Assim essa coluna pode ser usada para montar o gráfico

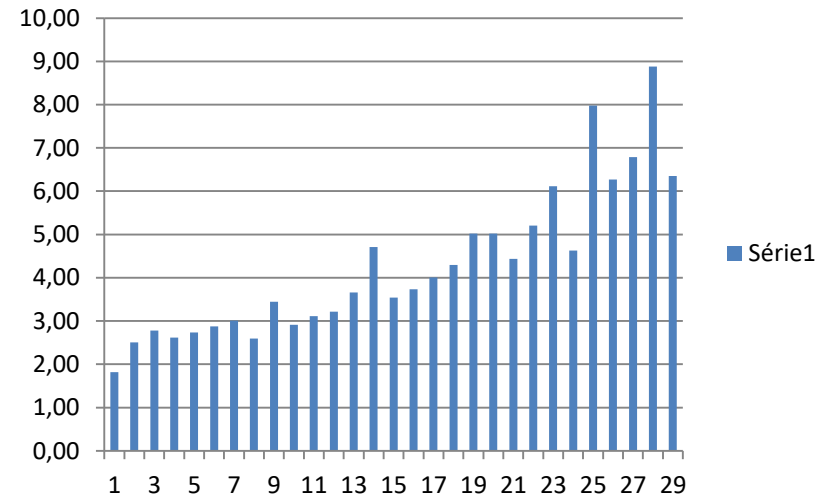
# No Excel

Exemplo para calcular a proporção do genoma coberta por ROH em cada cromossomo				
Cromossomo	Tamanho do Cromossomo em Mb	Tamanho médio das ROHs	Fórmula <sup>1</sup>	Proporção <sup>2</sup>
BTA1	158,53	2,88	1,82	1,82
BTA2	136,23	3,41	2,50	2,50
BTA3	121,01	3,36	2,78	2,78
BTA4	120	3,14	2,62	2,62
BTA5	120,09	3,28	2,73	2,73
BTA6	117,81	3,39	2,87	2,87
BTA7	110,68	3,33	3,01	3,01
BTA8	113,32	2,94	2,59	2,59
BTA9	105,45	3,63	3,44	3,44
BTA10	103,31	3,01	2,91	2,91
BTA11	106,98	3,33	3,12	3,12
BTA12	87,22	2,80	3,21	3,21
BTA13	83,47	3,06	3,66	3,66
BTA14	82,4	3,88	4,71	4,71
BTA15	85,01	3,01	3,54	3,54
BTA16	81,01	3,03	3,74	3,74
BTA17	73,17	2,93	4,01	4,01
BTA18	65,82	2,83	4,30	4,30
BTA19	63,45	3,18	5,02	5,02
BTA20	71,97	3,61	5,02	5,02
BTA21	69,86	3,10	4,44	4,44
BTA22	60,77	3,16	5,20	5,20
BTA23	52,5	3,21	6,11	6,11
BTA24	62,32	2,88	4,63	4,63
BTA25	42,35	3,38	7,98	7,98
BTA26	51,99	3,26	6,27	6,27
BTA27	45,61	3,10	6,79	6,79
BTA28	45,94	4,08	8,88	8,88
BTA29	51,1	3,25	6,35	6,35

- Selecionar a coluna de proporção

- Guia 'Inserir'

- Selecionar 'Gráfico de colunas'



Demais edições podem ser feitas na guia de Ferramentas de Gráfico

# *Como saber o tamanho de cada cromossomo?*

Caso não tenha a informação do tamanho de cada cromossomo da espécie com a qual está trabalhando, isso pode ser pesquisado no site NCBI



- Digitar NCBI na guia de pesquisa do google
- Clicar no primeiro link

The image shows a Google search interface with the search term "NCBI". The search results page displays approximately 94,000,000 results in 1.09 seconds. The top result is the "National Center for Biotechnology Information" website, with a URL of <https://www.ncbi.nlm.nih.gov>. Below the main result, there are links to "PubMed", "BLAST", "Nucleotide", and "Gene". A knowledge panel on the right side of the page provides additional information about the National Center for Biotechnology Information, including its location in Bethesda, Maryland, its founding year (1988), and its founder, Claude Pepper.

Google

NCBI

Todas Imagens Livros Videos Shopping Mais Ferramentas

Aproximadamente 94.000.000 resultados (1,09 segundos)

<https://www.ncbi.nlm.nih.gov> Traduzir esta página

**National Center for Biotechnology Information**  
Welcome to NCBI. The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.

**PubMed**  
PubMed® comprises more than 33 million citations for biomedical ...

**BLAST**  
The Basic Local Alignment Search Tool (BLAST) finds regions of ...

**Nucleotide**  
The Nucleotide database is a collection of sequences from ...

**Gene**  
The .gov means it's official. Federal government websites often end ...

Mais resultados de nih.gov »

**National Center for Biotechnology Information**  
Empresa

National Center for Biotechnology Information é uma secção da United States National Library of Medicine, um ramo dos National Institutes of Health, com sede em Bethesda, Maryland. A instituição foi fundada em 1988 em resultado de legislação proposta pelo senador Claude Pepper. [Wikipédia](#)

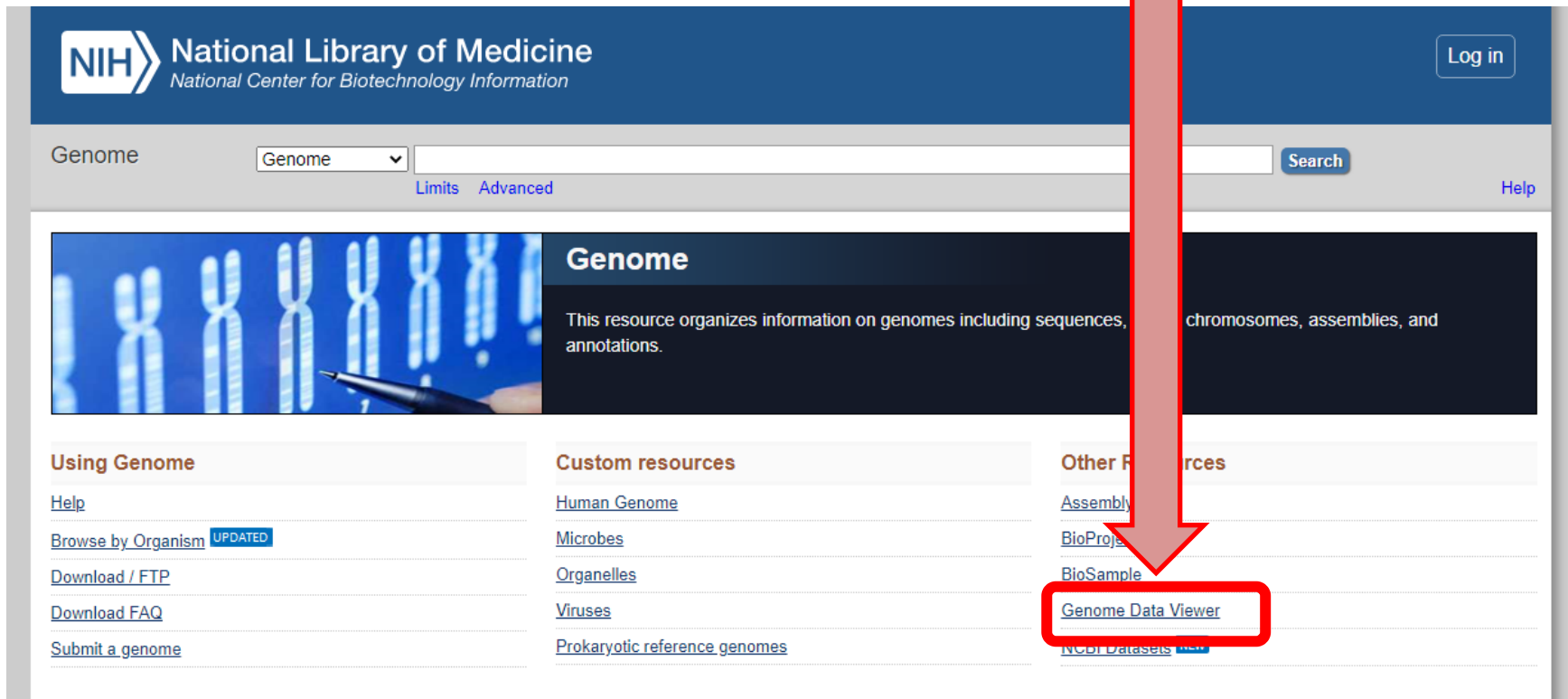
**Fundador:** Claude Pepper

**Fundação:** 4 de novembro de 1988

- Clicar em Genome no menu no canto direito

The image shows a screenshot of the National Center for Biotechnology Information (NCBI) website. At the top left, the NIH logo and the text "National Library of Medicine National Center for Biotechnology Information" are visible. A "Log in" button is in the top right. Below the header is a search bar with a dropdown menu set to "All Databases" and a "Search" button. On the left side, there is a vertical navigation menu with items like "NCBI Home", "Resource List (A-Z)", "All Resources", "Chemicals & Bioassays", "Data & Software", "DNA & RNA", "Domains & Structures", "Genes & Expression", "Genetics & Medicine", "Genomes & Maps", "Homology", "Literature", and "Proteins". The main content area features a "Welcome to NCBI" message, a description of the center's mission, and links for "About the NCBI", "Mission", "Organization", and "NCBI News & Blog". Below this are three columns: "Submit" (Deposit data or manuscripts into NCBI databases), "Download" (Transfer NCBI data to your computer), and "Learn" (Find help documents, attend a class or watch a tutorial). On the right side, there is a "Popular Resources" section with a list of links: "Genome" (highlighted with a red box and a red arrow pointing to it), "SNP", "Gene", "Protein", and "PubChem". At the bottom right, there is a link for "NCBI News & Blog".

# - Clicar em Genome Data Viewer



The image shows a screenshot of the National Library of Medicine (NIH) website. At the top left, the NIH logo is displayed next to the text "National Library of Medicine" and "National Center for Biotechnology Information". A "Log in" button is located in the top right corner. Below the header, there is a search bar with the word "Genome" on the left, a dropdown menu set to "Genome", and a "Search" button. Links for "Limits" and "Advanced" are also present. A "Help" link is in the top right of the main content area. The main content area features a large banner with a blue background and white chromosome illustrations. The banner is titled "Genome" and contains the text: "This resource organizes information on genomes including sequences, chromosomes, assemblies, and annotations." Below the banner, there are three columns of links. The first column, titled "Using Genome", includes links for "Help", "Browse by Organism" (with an "UPDATED" badge), "Download / FTP", "Download FAQ", and "Submit a genome". The second column, titled "Custom resources", includes links for "Human Genome", "Microbes", "Organelles", "Viruses", and "Prokaryotic reference genomes". The third column, titled "Other Resources", includes links for "Assembly", "BioProject", "BioSample", "Genome Data Viewer" (which is circled in red), and "NCBI Datasets". A large red arrow points downwards from the top of the page towards the "Genome Data Viewer" link.

NIH National Library of Medicine  
National Center for Biotechnology Information

Log in

Genome Genome [dropdown] Search

Limits Advanced Help

## Genome

This resource organizes information on genomes including sequences, chromosomes, assemblies, and annotations.

### Using Genome

- Help
- Browse by Organism **UPDATED**
- Download / FTP
- Download FAQ
- Submit a genome

### Custom resources

- Human Genome
- Microbes
- Organelles
- Viruses
- Prokaryotic reference genomes

### Other Resources

- Assembly
- BioProject
- BioSample
- Genome Data Viewer**
- NCBI Datasets

- Selecionar a espécie de interesse (neste caso foi a espécie *Bos taurus*)
- Caso a espécie da sua pesquisa não esteja visível, clique nos “+” no diagrama para ver mais espécies

Switch view

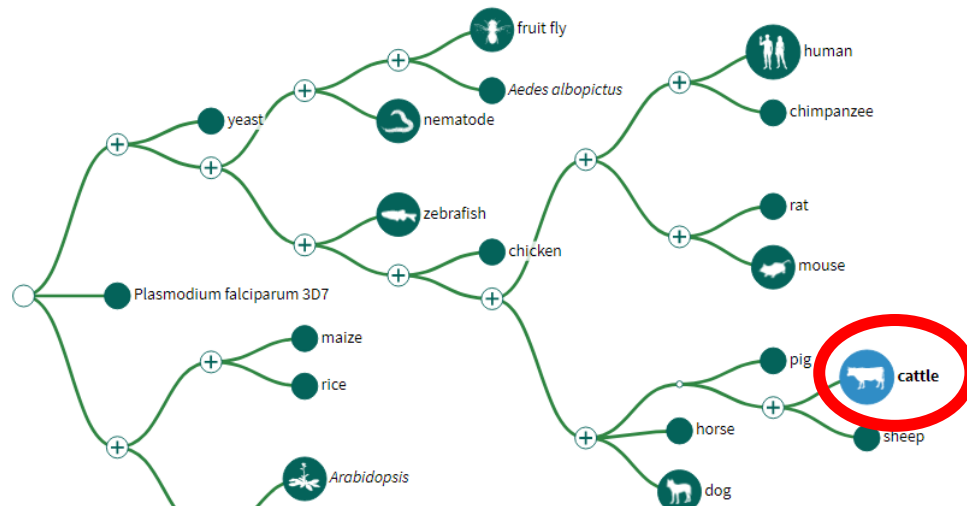


Search organisms

Bos taurus (cattle)

To view more organisms in the tree, click on nodes that have '+' signs. Press and hold the '+' to expand and reveal all the subgroups. Or, search for an organism using the search box above.

New! Click on Switch view at the top to see another way of navigating genomes.



Bos taurus (cattle)



Search in genome

Location, gene or phenotype



Examples: RHO, chr22:56224000-56233000, DNA repair

Assembly

ARS-UCD1.2

Browse genome

BLAST genome

Download via NCBI Datasets

Assembly details

Name	ARS-UCD1.2
RefSeq accession	GCF_002263795.1
GenBank accession	GCA_002263795.2
Submitter	USDA ARS
Level	Chromosome
Category	Representative genome

Annotation details

# No menu à direita, é importante selecionar corretamente a Assembly

Search in genome

Location, gene or phenotype

Examples: [RHO](#), [chr22:56224000-56233000](#), [DNA repair](#)

Assembly

- ARS-UCD1.2
- ARS-UCD1.2**
- Btau\_5.0.1
- Bos\_taurus\_UMD\_3.1.1
- Btau\_4.6.1

[Download via NCBI Datasets](#)

**Assembly details**

Name	ARS-UCD1.2
RefSeq accession	<a href="#">GCF_002263795.1</a>
GenBank accession	<a href="#">GCA_002263795.2</a>
Submitter	USDA ARS
Level	Chromosome
Category	Representative genome

**Annotation details**

Annotation Release 106 [i](#)

Release date May 10, 2018

MT 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21

- Se você estiver trabalhando com animais genotipados, a fazenda/empresa que genotipou os animais pode te passar essa informação.
- Neste caso, a opção é ARS-UCD1.2

# Ainda no menu à direita

Search in genome

Location, gene or phenotype

Examples: [RHO](#), [chr22:56224000-56233000](#), [DNA repair](#)

Assembly

ARS-UCD1.2

**ARS-UCD1.2**

Btau\_5.0.1

Bos\_taurus\_UMD\_3.1.1

Btau\_4.6.1

[Download via NCBI Datasets](#)

**Assembly details**

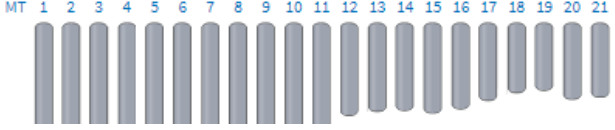
Name	ARS-UCD1.2
RefSeq accession	<a href="#">GCF_002263795.1</a>
GenBank accession	<a href="#">GCA_002263795.2</a>
Submitter	USDA ARS
Level	Chromosome
Category	Representative genome

**Annotation details**

Annotation Release 106

Release date May 19, 2010

MT 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21



- Os cromossomos da espécie estarão listados abaixo
- Clicar no Cromossomo 1
- Vai carregar uma nova página

- Na nova página, encontre a opção da lupa e deixe a opção de zoom em 0%

Genome Data Viewer

Home Share this page Reset All More Info

Bos taurus (cattle)

Assembly: ARS-UCD1.2 (GCF\_002263795.1) Chr 1 (NC\_037328.1)

Search assembly: chr17:29546210 30576098

Pick Assembly

Ideogram View

Unplaced/unlocalized scaffolds: 2,180

NC\_037328.1

Exon Navigator: There are no genes in the region.

NC\_037328.1

NCBI Bos taurus Annotation Release 106, 2018-05-11

Ensembl release 106

RNA-seq exon coverage, aggregate (filtered), NCBI Bos taurus Annotation Release 106 - log base 2 scaled

RNA-seq intron-spanning reads, aggregate (filtered), NCBI Bos taurus Annotation Release 106 - log base 2 scaled

RNA-seq intron features, aggregate (filtered), NCBI Bos taurus Annotation Release 106

Filtered (read count from min to max)

NC\_037328.1: 123M...123M (20,001 nt)

Tracks shown: 7/842

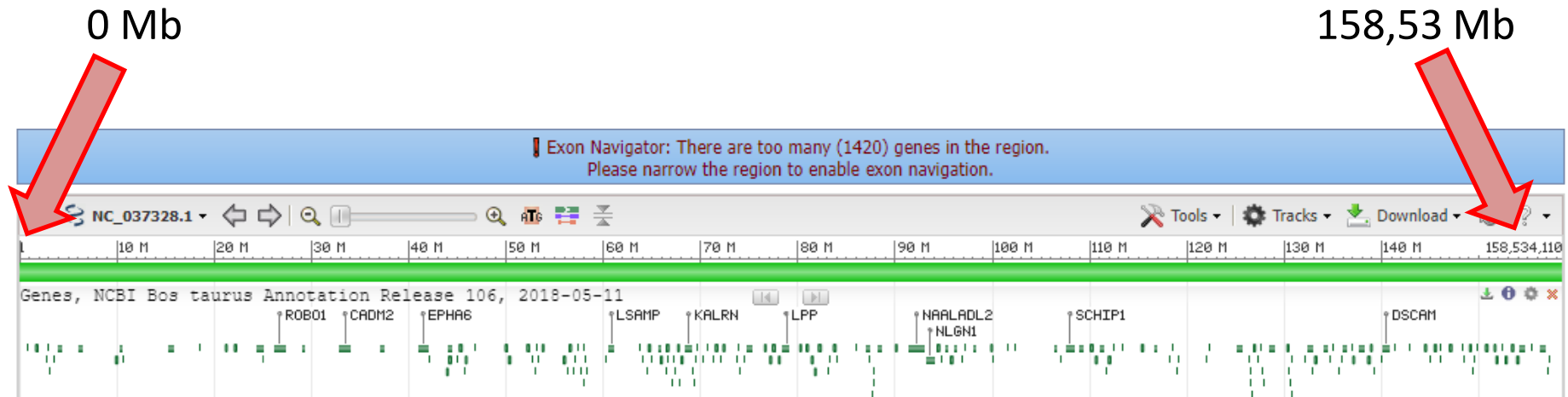
Exon Navigator: There are too many (14) Please narrow the region to enable

0%

NC\_037328.1

20 M 40 M 60 M 80 M

- Assim, o cromossomo será mostrado em toda a sua extensão, de 0 até seu tamanho final em Mb



Então, o tamanho/comprimento do cromossomo 1 dos bovinos (BTA1), na montagem ARS-UCD1.2 é de 158,534,110 Megabases (Mb)

BTA: *Bos taurus* autosome

(Os cromossomos autossômicos da espécie *Bos taurus* são identificados pela sigla BTA)



- No canto esquerdo clicar nos outros cromossomos para ver e anotar os tamanhos

The image shows a genomic browser interface for *Bos taurus* (cattle). The top header displays the species name and the assembly used, ARS-L. A search bar contains the coordinates "chr17:29546210 30576098". Below the search bar, there are tabs for "Pick Assembly" and "Ideogram View". The "Ideogram View" section shows a set of chromosome ideograms labeled MT, 1 through 13, 14 through 27, and 28 through X. Chromosome 2 is highlighted with a green box. To the right of the ideograms, there are tracks for "Unplaced/unlocalized scaffolds" (2,180 scaffolds) and "NC\_037329.1". The tracks show gene annotations from NCBI and Ensembl, with a scale bar indicating 10 M.

<b>Cromossomo</b>	<b>Tamanho do Cromossomo (Mb)</b>
BTA1	158,53
BTA2	136,23
BTA3	121,01
BTA4	120
BTA5	120,09
BTA6	117,81
BTA7	110,68
BTA8	113,32
BTA9	105,45
BTA10	103,31
BTA11	106,98
BTA12	87,22
BTA13	83,47
BTA14	82,4
BTA15	85,01
BTA16	81,01
BTA17	73,17
BTA18	65,82
BTA19	63,45
BTA20	71,97
BTA21	69,86
BTA22	60,77
BTA23	52,5
BTA24	62,32
BTA25	42,35
BTA26	51,99
BTA27	45,61
BTA28	45,94
BTA29	51,1