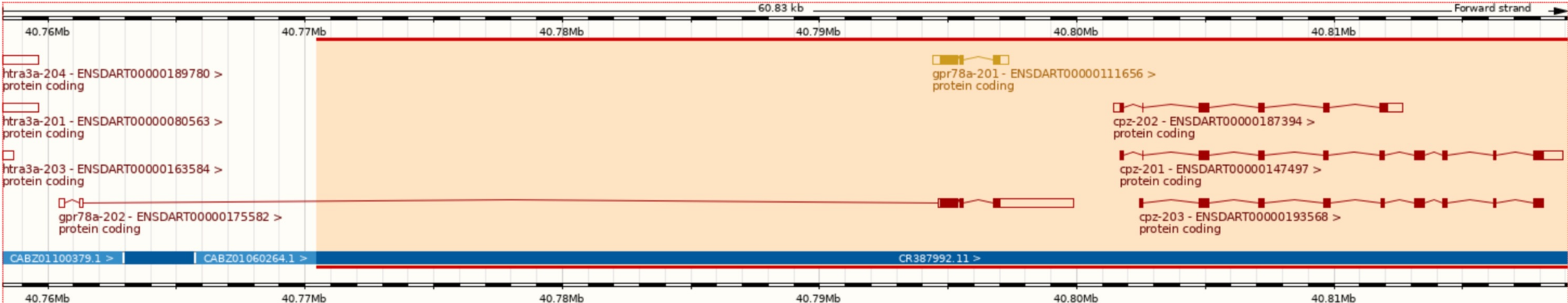
Extra Ensembl

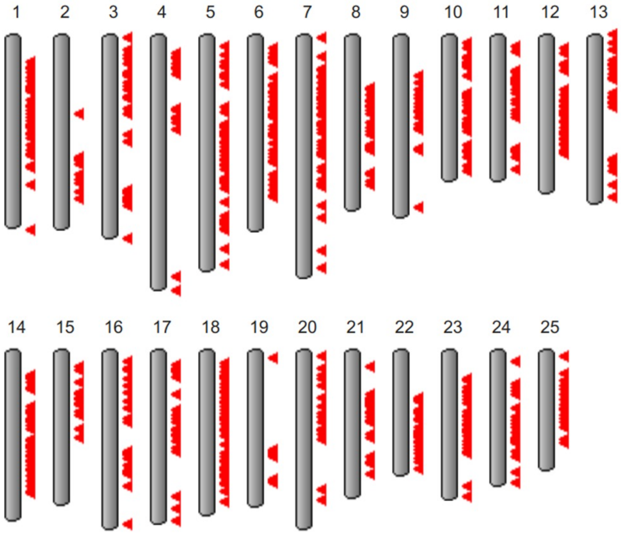
Zebrafish Genome

- **GRCz11** (danRer11) - latest assembly, released in 2017
- Sequencing strategy:
  - 90% clone by clone sequencing
    - **High quality**
  - 10% whole genome shotgun sequencing
    - **Lower quality**
    - Fills gaps between clones
    - Identified by accessions beginning with **CABZ**



Zebrafish Genome History

- Genome project started in **2001** at Sanger Institute
- Initially sequenced pool of **Tübingen** zebrafish
- But zebrafish **very polymorphic** compared to humans
- Too much variation to join clones, so lots of **gaps**
- + same region represented by 2+ clones, leading to **artificial duplication**
- Later used **double haploid** Tübingen fish for some clones and most WGS
- Only **925 gaps** between scaffolds and **N50 > 7 Mbp**
- GRCz11 contains **alternative** scaffolds



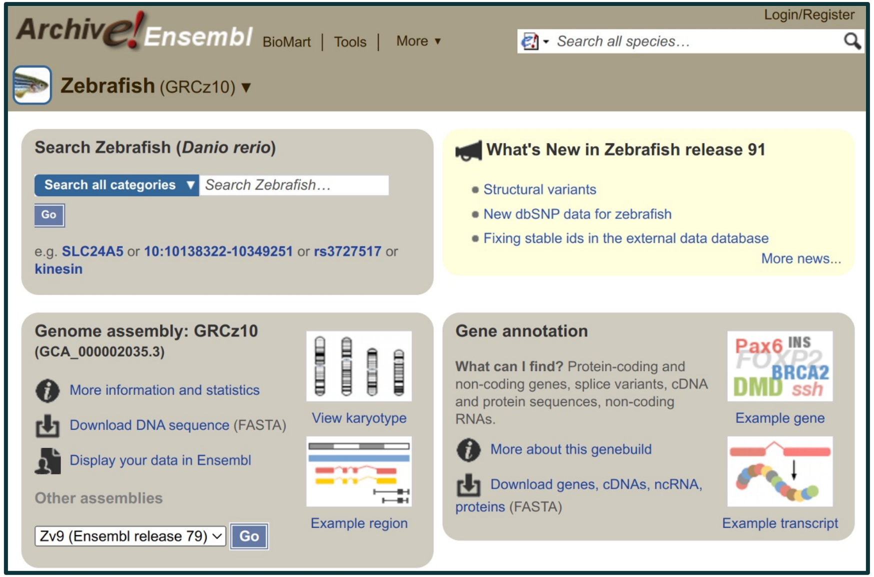
From https://www.ncbi.nlm.nih.gov/grc/zebrafish

- When downloading sequence from Ensembl FTP site, "`toplevel`" includes alternative sequence, but "`primary_assembly`" doesn't and is probably what you want

Older Assemblies

- Previous assemblies available in Ensembl **archives**: www.ensembl.org/info/website/archives/assembly.html
  - GRCz10 / danRer10: http://e91.ensembl.org/
  - Zv9 / danRer7: http://e77.ensembl.org/
  - Zv8 / danRer6: http://e54.ensembl.org/

- Even **older** assemblies available in UCSC
- Numbering coordinated when **GRC** (Genome Reference Consortium) took over managing zebrafish assembly from Sanger Institute



Search Zebrafish (*Danio rerio*)

Search all categories ▾ Search Zebrafish… Go

e.g. SLC24A5 or 10:10138322-10349251 or rs3727517 or kinesin

What's New in Zebrafish release 91

- Structural variants
- New dbSNP data for zebrafish
- Fixing stable ids in the external data database

More news...

Genome assembly: GRCz10 (GCA_000002035.3)

More information and statistics

Download DNA sequence (FASTA)

Display your data in Ensembl

Other assemblies

Zv9 (Ensembl release 79) Go

View karyotype

Example region

Gene annotation

What can I find? Protein-coding and non-coding genes, splice variants, cDNA and protein sequences, non-coding RNAs.

More about this genebuild

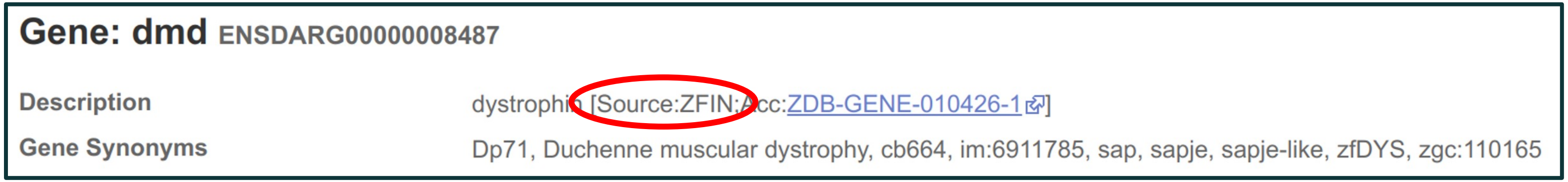
Download genes, cDNAs, ncRNA, proteins (FASTA)

Example gene

Example transcript

Gene Names

- Names assigned to Ensembl genes automatically based on **sequence similarity**
  - Mistakes are possible
  - Names can change
- **ZFIN gene symbols** (i.e. the name assigned by ZFIN) are preferred (>23,000 genes), but other databases are also used, e.g. HGNC for ~150 genes, miRBase for ~300 genes
- Description indicates source of name
- Genes without a match are given a name based on the sequence used to identify them, e.g AL645792.1 (clone) or **CABZ**01052570.1 (WGS)



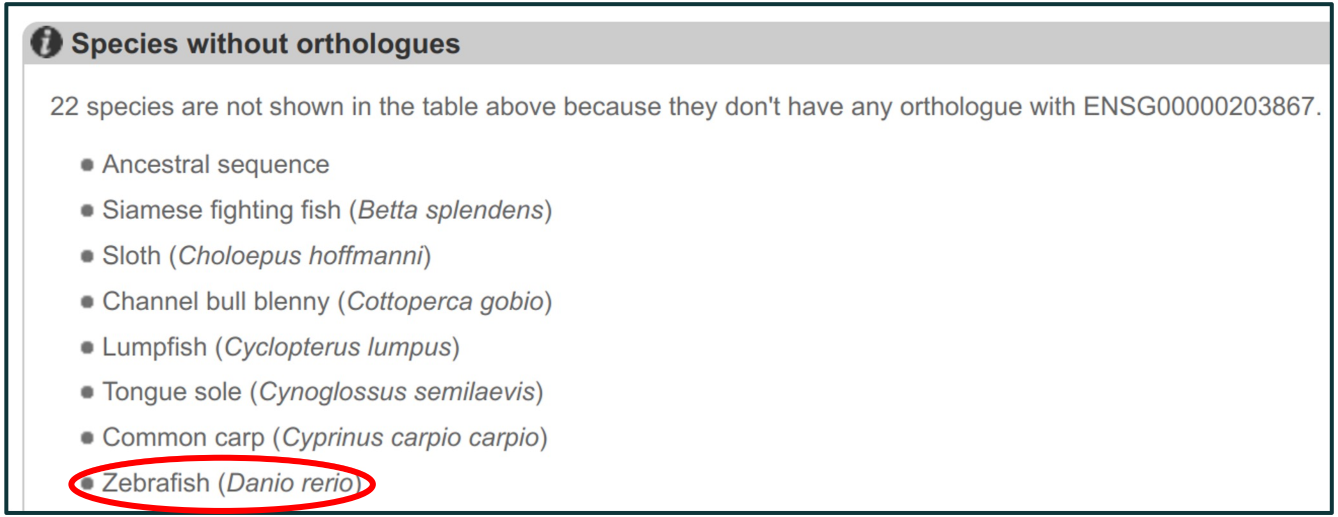
Gene: dmd ENSDARG00000008487

Description dystrophin [Source:ZFIN;Acc:ZDB-GENE-010426-1]

Gene Synonyms Dp71, Duchenne muscular dystrophy, cb664, im:6911785, sap, sapje, sapje-like, zfDYS, zgc:110165

Synteny Example

- No zebrafish orthologue listed for human RBM20 gene (ENSG00000203867)



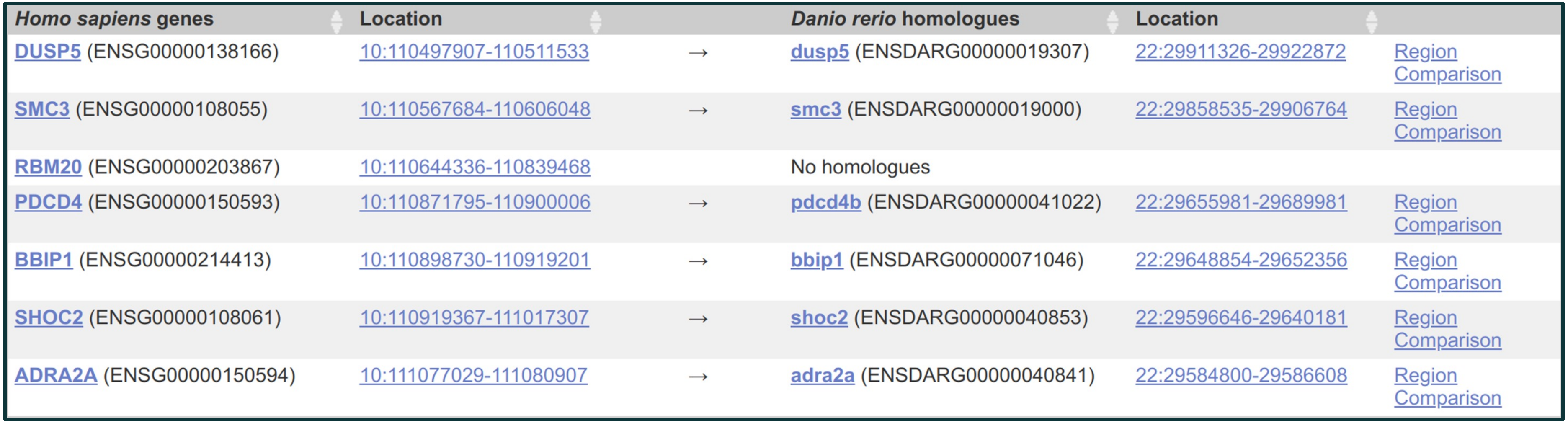
Species without orthologues

22 species are not shown in the table above because they don't have any orthologue with ENSG00000203867.

- Ancestral sequence
- Siamese fighting fish (*Betta splendens*)
- Sloth (*Choloepus hoffmanni*)
- Channel bull blenny (*Cottoperca gobio*)
- Lumpfish (*Cyclopterus lumpus*)
- Tongue sole (*Cynoglossus semilaevis*)
- Common carp (*Cyprinus carpio carpio*)
- Zebrafish (*Danio rerio*)

Synteny Example

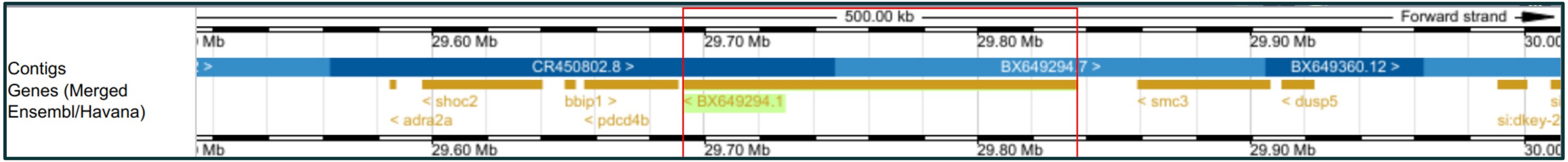
- If we look at the region around RBM20 in human and then click on **Synteny** we see conservation of synteny with zebrafish chr22

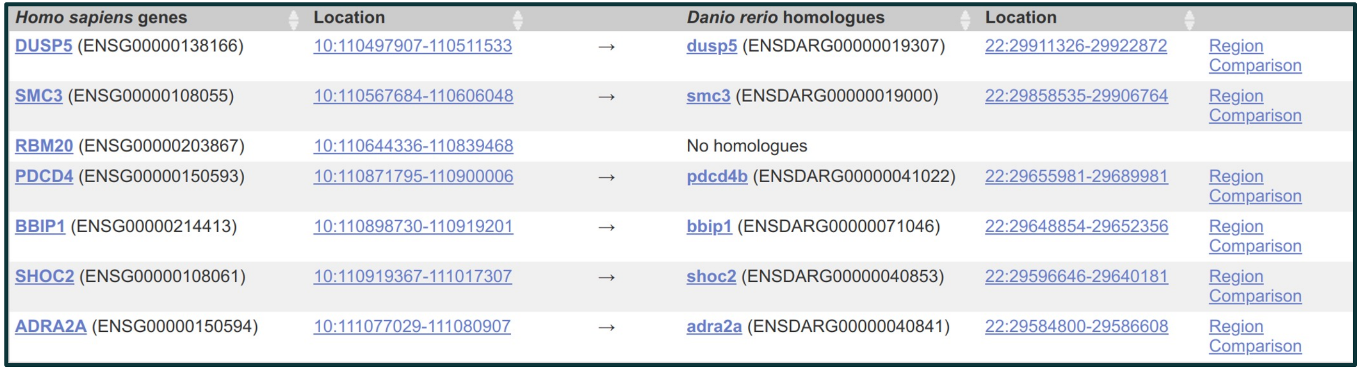


Homo sapiens genes	Location		*Danio rerio* homologues	Location	
DUSP5 (ENSG00000138166)	10:110497907-110511533	→	dusp5 (ENSDARG00000019307)	22:29911326-29922872	Region Comparison
SMC3 (ENSG00000108055)	10:110567684-110606048	→	smc3 (ENSDARG00000019000)	22:29858535-29906764	Region Comparison
RBM20 (ENSG00000203867)	10:110644336-110839468		No homologues		
PDCD4 (ENSG00000150593)	10:110871795-110900006	→	pdcd4b (ENSDARG00000041022)	22:29655981-29689981	Region Comparison
BBIP1 (ENSG00000214413)	10:110898730-110919201	→	bbip1 (ENSDARG00000071046)	22:29648854-29652356	Region Comparison
SHOC2 (ENSG00000108061)	10:110919367-111017307	→	shoc2 (ENSDARG00000040853)	22:29596646-29640181	Region Comparison
ADRA2A (ENSG00000150594)	10:111077029-111080907	→	adra2a (ENSDARG00000040841)	22:29584800-29586608	Region Comparison

Synteny Example

- If we look at the chr22 region in zebrafish then all the surrounding genes are the same and RBM20 is likely to be BX649294.1





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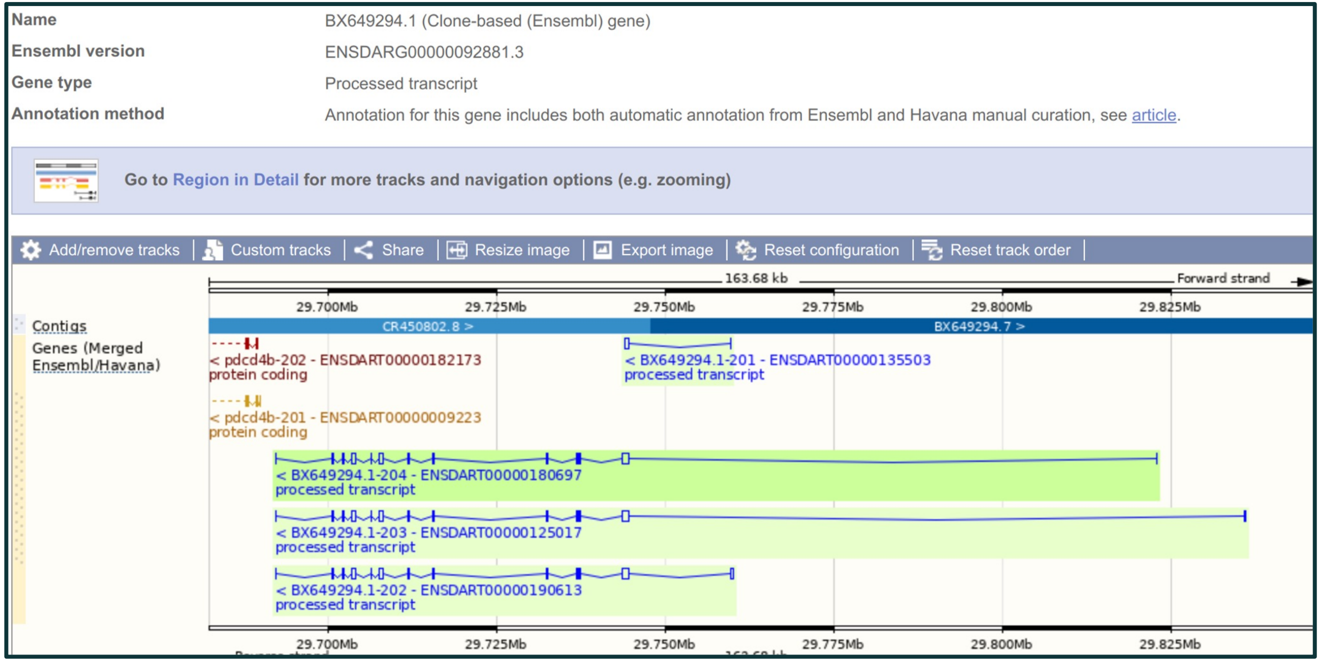
ADRA2A (ENSG00000150594)	10:111077029-111080907	→	adra2a (ENSDARG00000040841)	22:29584800-29586608	Region Comparison

Synteny Example

- Erroneously labelled as processed transcript and so not in protein gene tree, so not labelled as orthologue or named by orthology

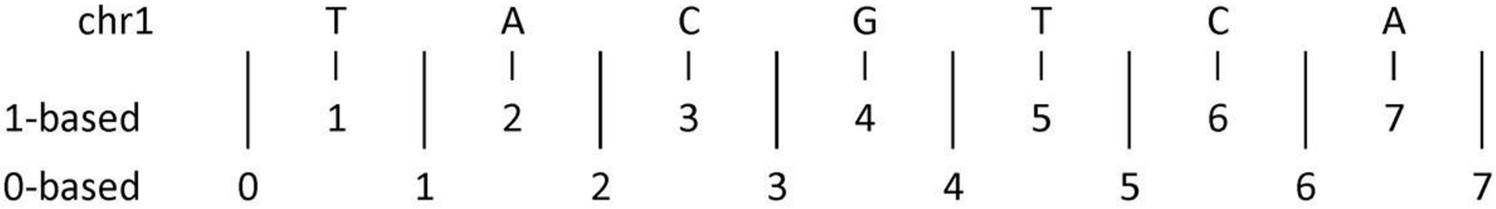


Name	BX649294.1 (Clone-based (Ensembl) gene)
Ensembl version	ENSDARG00000092881.3
Gene type	Processed transcript
Annotation method	Annotation for this gene includes both automatic annotation from Ensembl and Havana manual curation, see article.

Go to Region in Detail for more tracks and navigation options (e.g. zooming)

UCSC & Ensembl Differences

- **Ensembl:** 1
  UCSC: chr1
- **Ensembl:** 1-based coordinates (bases numbered)
  UCSC: 0-based coordinates (numbers between bases)



- The **G** is **1:4-4** in Ensembl coordinates but **1:3-4** in UCSC

Thank You!

Any questions?