

- Move from a gene to a location display with tabs

- BLAST a sequence
- Mine data with BioMart
- Read our FAQs
- Try our SNP Effect Predictor

- Alternate haplotypes are available

- Current location is indicated

- Search for a gene, location, variation, clone, probeset, or phenotype

- View whole genome alignments

- Configure this page to customise your view

- Conserved sequence from analysis of multi-species alignments

- Browse **invertebrates** at [www.ensemblgenomes.org](http://www.ensemblgenomes.org)

- Browse genes & annotation for over 50 species in our chordate site

- Genes and transcripts in the GENCODE set. Click on them to learn more

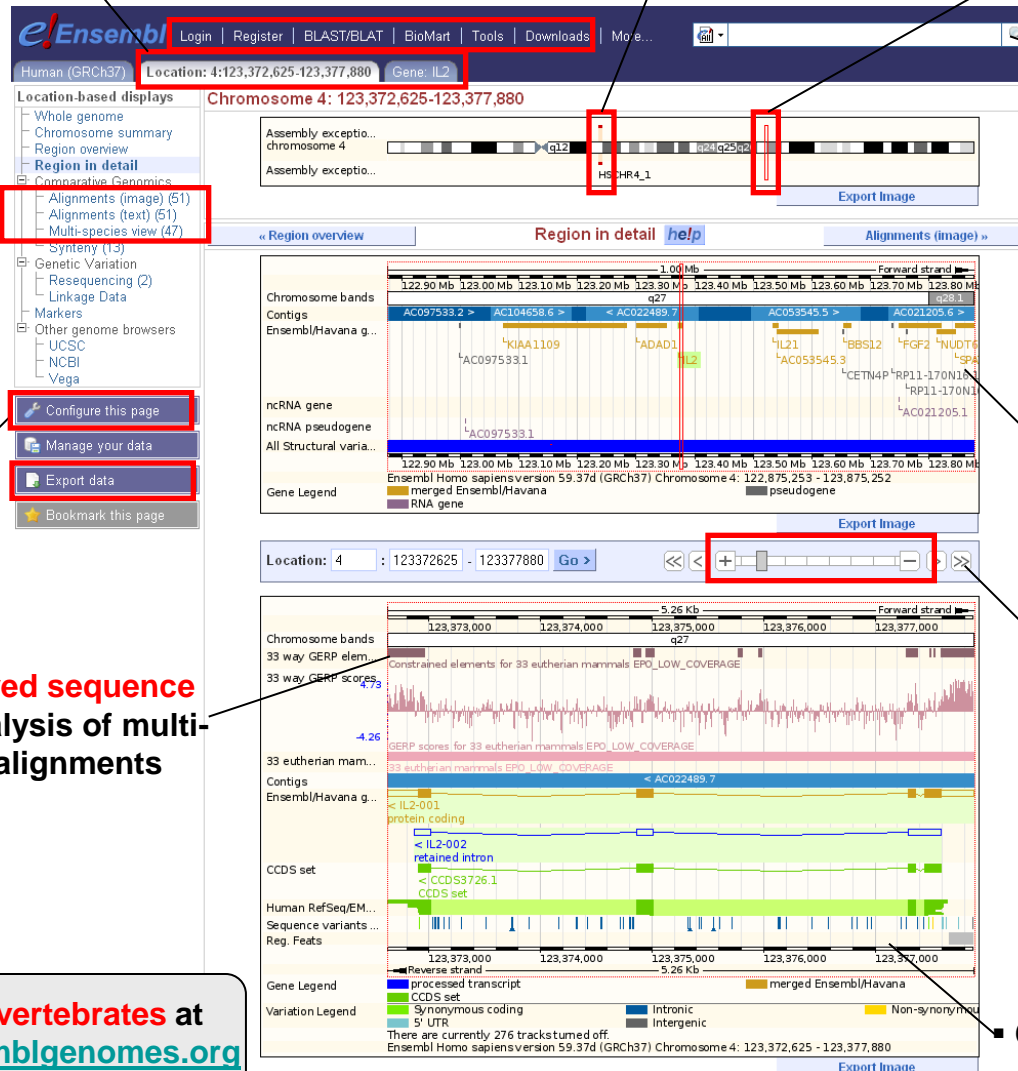
- Zoom** into a region

Variation: rs3087209

**Variation Properties**

bp	123377483
Status	cluster, freq, hapmap
Class	snp
Ambiguity	M
code	
Mapweight	1
Alleles	A/C
Source	dbSNP, Illumina_Human1M-duoV3
Type	NON_SYNONYMOUS_CODING

- Click a colour-coded sequence variant for a pop-up box of information



- Comparative and variation displays are available

- The **transcript table** lists splice variants and has **sortable columns**

## Navigate using buttons

- **Gold**  
transcripts are protein coding and are agreed on by Ensembl and Vega/Havana

- **Red** transcripts are protein coding and are from Ensembl or VEGA/Havana

- **Blue, Grey, or Pink** transcripts are non-coding

- **Export**  
sequence

## The Transcript Tab: Exons View

# Protein / signatures

### Colour key for variations

- Click a variation for population frequencies, phenotypes, and risk alleles

Download  
to open  
in Word

Upstream  
sequence

## Intron

## Coding sequence

Comparison image

Protein information

Protein summary

Domains & features (13)

Variations (3)

External Data

Personal annotation

ID History

Transcript history

Protein history

Configure this page

Manage your data

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Download view as RTF

« Supporting evidence »

Exons

help

cDNA sequence »

Key

Colour key for variations

Variations

5' UTR

Downstream

Intronic

Non-synonymous coding

Regulatory region

Synonymous coding

Upstream

Show/hide columns

Search:

No.	Exon / Intron	Start	End	Start Phase	End Phase	Length	Sequence
	5' upstream sequence						.....GgacaaagaaaatttctgagttactttgtgtatcCGCACcccttaaaagaaaggagaaagaaactgtcttcatcacgaaggcgcttaattgtgaagaattagag
1	ENSE000001293064	123,377,449	123,377,880	0	432		CTATCACCTTAAGTGTGGGCTTAATGTAAACAAGAGGGAGTTTCACCTACATCCATTAAGTCAATGTCCTTTGGGGGTTTAAAGAAATTTCCAAAGAGTGATCATCAAGAGAGGAAAAATGAAGGTAATGTCTTTTTCAGACGGTAAAGACCTCTTTGAAAATATGTGTAATATGTGAACACATTTTGTACACCCCTAATAATTTTTCAGAAATTAACAGTATAAATGTCATCTCTGTTTCAAGAGTTCCCTATCACTCTTTTAACTCACTCTCAAGTAACTCAACCTGCGGACAAAGTATACAGGATGCAACTCTCTGCTTGCAATGCTCACTAAGCTTTGACCTTGTCACCAAGAGCGACACTTCTTAAGTCTGAAAGAAACACAGCTACACTGAGCACTTACCTGCGGATTTACCTGGAATTAAT
	Intron 1-2	123,377,369	123,377,448		90		gaagtatatctcttcttactaaaaattattacatttagtaactagctggagatcatttcttaacacaaagatcataacttctttag
2	ENSE00000935280	123,377,299	123,377,368	0	60		AATTCAAGAATCCCAACTCACCAGGATGCTCACATTTAAAGTTTACATGCCCAAGAA

UTR

Coding sequence

Click a variation population frequency phenotypes, and