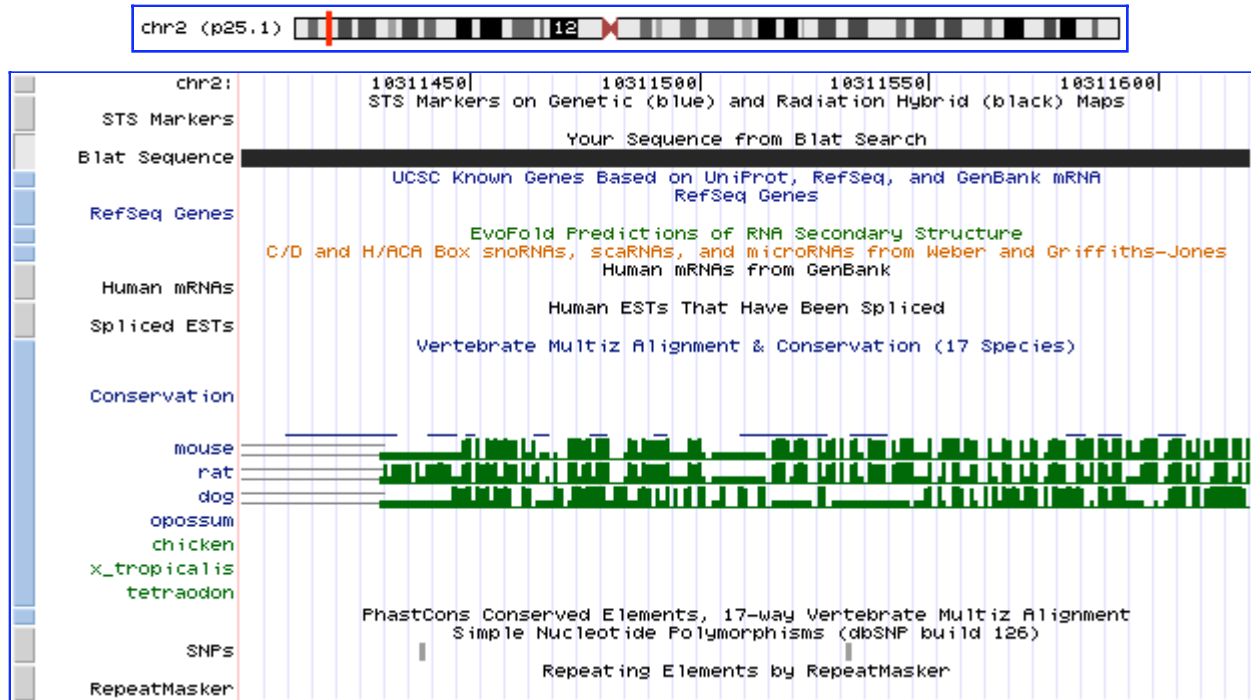


Home Genomes Blat Tables Gene Sorter PCR DNA Convert PDF/PS Help

# UCSC Genome Browser on Human Mar. 2006 Assembly

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

position/search  jump clear size 220 bp.



move start < 2.0 > Click on a feature for details. Click on base position to zoom in around cursor. Click on left mini-buttons for track-specific options. move end < 2.0 >

Use drop down controls below and press refresh to alter tracks displayed. Tracks with lots of items will automatically be displayed in more compact modes.

### Mapping and Sequencing Tracks

<a href="#">Base Position</a> <input type="text" value="dense"/>	<a href="#">Chromosome Band</a> <input type="text" value="hide"/>	<a href="#">STS Markers</a> <input type="text" value="dense"/>	<a href="#">FISH Clones</a> <input type="text" value="hide"/>	<a href="#">Recomb Rate</a> <input type="text" value="hide"/>
<a href="#">Map Contigs</a> <input type="text" value="hide"/>	<a href="#">Assembly</a> <input type="text" value="hide"/>	<a href="#">Gap</a> <input type="text" value="hide"/>	<a href="#">Coverage</a> <input type="text" value="hide"/>	<a href="#">BAC End Pairs</a> <input type="text" value="hide"/>
<a href="#">Fosmid End Pairs</a> <input type="text" value="hide"/>	<a href="#">GC Percent</a> <input type="text" value="hide"/>	<a href="#">Short Match</a> <input type="text" value="hide"/>	<a href="#">Restr Enzymes</a> <input type="text" value="hide"/>	Blat Sequence <input type="text" value="dense"/>

### Genes and Gene Prediction Tracks

<a href="#">Known Genes</a> <input type="text" value="pack"/>	<a href="#">RefSeq Genes</a> <input type="text" value="dense"/>	<a href="#">Other RefSeq</a> <input type="text" value="hide"/>	<a href="#">MGC Genes</a> <input type="text" value="hide"/>	<a href="#">Ensembl Genes</a> <input type="text" value="hide"/>
<a href="#">N-SCAN</a> <input type="text" value="hide"/>	<a href="#">SGP Genes</a> <input type="text" value="hide"/>	<a href="#">Geneid Genes</a> <input type="text" value="hide"/>	<a href="#">Genscan Genes</a> <input type="text" value="hide"/>	<a href="#">Superfamily</a> <input type="text" value="hide"/>
<a href="#">EvoFold</a> <input type="text" value="full"/>	<a href="#">sno/miRNA</a> <input type="text" value="full"/>			

**mRNA and EST Tracks**

<a href="#">Human mRNAs</a> <input type="text" value="dense"/>	<a href="#">Spliced ESTs</a> <input type="text" value="dense"/>	<a href="#">Human ESTs</a> <input type="text" value="hide"/>	<a href="#">Other mRNAs</a> <input type="text" value="hide"/>	<a href="#">Other ESTs</a> <input type="text" value="hide"/>
<a href="#">H-Inv</a> <input type="text" value="hide"/>				

**Expression and Regulation**

<a href="#">Allen Brain</a> <input type="text" value="hide"/>	<a href="#">GNF Atlas 2</a> <input type="text" value="hide"/>	<a href="#">GNF Ratio</a> <input type="text" value="hide"/>	<a href="#">Affy U133</a> <input type="text" value="hide"/>	<a href="#">Affy GNF1H</a> <input type="text" value="hide"/>
<a href="#">Affy U133Plus2</a> <input type="text" value="hide"/>	<a href="#">Affy U95</a> <input type="text" value="hide"/>	<a href="#">CpG Islands</a> <input type="text" value="hide"/>	<a href="#">FirstEF</a> <input type="text" value="hide"/>	<a href="#">Reg Potential 7 species</a> <input type="text" value="hide"/>

**Comparative Genomics**

<a href="#">Conservation</a> <input type="text" value="full"/>	<a href="#">Most Conserved</a> <input type="text" value="full"/>	<a href="#">Fugu Chain</a> <input type="text" value="hide"/>	<a href="#">Fugu Net</a> <input type="text" value="hide"/>	<a href="#">Tetraodon Chain</a> <input type="text" value="hide"/>
<a href="#">Tetraodon Net</a> <input type="text" value="hide"/>	<a href="#">Tetraodon Ecores</a> <input type="text" value="hide"/>	<a href="#">Zebrafish chain</a> <input type="text" value="hide"/>	<a href="#">Zebrafish Net</a> <input type="text" value="hide"/>	<a href="#">X. tropicalis Chain</a> <input type="text" value="hide"/>
<a href="#">X. tropicalis Net</a> <input type="text" value="hide"/>	<a href="#">Chicken Chain</a> <input type="text" value="hide"/>	<a href="#">Chicken Net</a> <input type="text" value="hide"/>	<a href="#">Cow Chain</a> <input type="text" value="hide"/>	<a href="#">Cow Net</a> <input type="text" value="hide"/>
<a href="#">Dog Chain</a> <input type="text" value="hide"/>	<a href="#">Dog Net</a> <input type="text" value="hide"/>	<a href="#">Rat Chain</a> <input type="text" value="hide"/>	<a href="#">Rat Net</a> <input type="text" value="hide"/>	<a href="#">Mouse Chain</a> <input type="text" value="hide"/>
<a href="#">Mouse Net</a> <input type="text" value="hide"/>	<a href="#">Rhesus Chain</a> <input type="text" value="hide"/>	<a href="#">Rhesus Net</a> <input type="text" value="hide"/>	<a href="#">Chimp Chain</a> <input type="text" value="hide"/>	<a href="#">Chimp Net</a> <input type="text" value="hide"/>

**Variation and Repeats**

<a href="#">SNPs</a> <input type="text" value="dense"/>	<a href="#">RepeatMasker</a> <input type="text" value="dense"/>	<a href="#">Simple Repeats</a> <input type="text" value="hide"/>	<a href="#">Self Chain</a> <input type="text" value="hide"/>
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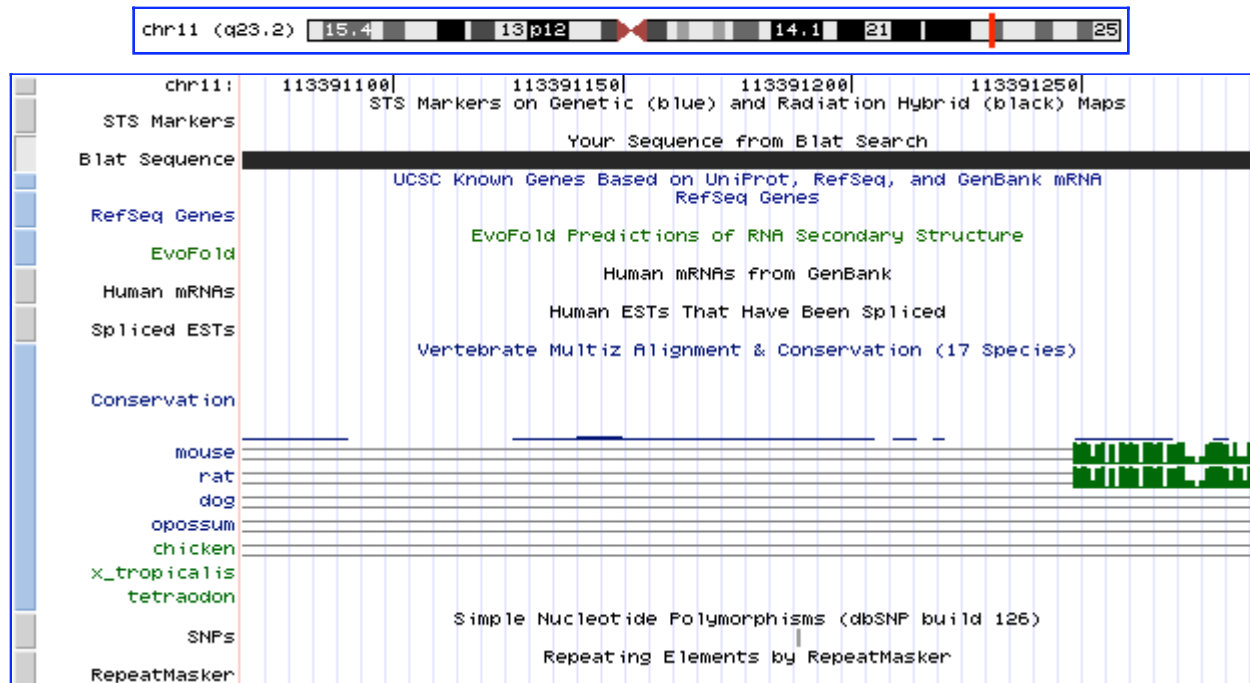
## UCSC Genome Browser on Human Mar. 2006 Assembly

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

zoom out 1.5x 3x 10x

position/search  jump clear size 220 bp.

configure



move start

< 2.0 >

Click on a feature for details. Click on base position to zoom in around cursor. Click on left mini-buttons for track-specific options.

move end

< 2.0 >

default tracks

hide all

custom tracks

configure

refresh

Use drop down controls below and press refresh to alter tracks displayed. Tracks with lots of items will automatically be displayed in more compact modes.

### Mapping and Sequencing Tracks

[Base Position](#)

dense ▾

[Chromosome Band](#)

hide ▾

[STS Markers](#)

dense ▾

[FISH Clones](#)

hide ▾

[Recomb Rate](#)

hide ▾

[Map Contigs](#)

hide ▾

[Assembly](#)

hide ▾

[Gap](#)

hide ▾

[Coverage](#)

hide ▾

[BAC End Pairs](#)

hide ▾

[Fosmid End Pairs](#)

hide ▾

[GC Percent](#)

hide ▾

[Short Match](#)

hide ▾

[Restr Enzymes](#)

hide ▾

[Blat Sequence](#)

dense ▾

### Genes and Gene Prediction Tracks

[Known Genes](#)

pack ▾

[RefSeq Genes](#)

dense ▾

[Other RefSeq](#)

hide ▾

[MGC Genes](#)

hide ▾

[Ensembl Genes](#)

hide ▾

<a href="#">N-SCAN</a> <input type="text" value="hide"/>	<a href="#">SGP Genes</a> <input type="text" value="hide"/>	<a href="#">Geneid Genes</a> <input type="text" value="hide"/>	<a href="#">Genscan Genes</a> <input type="text" value="hide"/>	<a href="#">Superfamily</a> <input type="text" value="hide"/>
<a href="#">EvoFold</a> <input type="text" value="dense"/>	<a href="#">sno/miRNA</a> <input type="text" value="hide"/>			

**mRNA and EST Tracks**

<a href="#">Human mRNAs</a> <input type="text" value="dense"/>	<a href="#">Spliced ESTs</a> <input type="text" value="dense"/>	<a href="#">Human ESTs</a> <input type="text" value="hide"/>	<a href="#">Other mRNAs</a> <input type="text" value="hide"/>	<a href="#">Other ESTs</a> <input type="text" value="hide"/>
<a href="#">H-Inv</a> <input type="text" value="hide"/>				

**Expression and Regulation**

<a href="#">Allen Brain</a> <input type="text" value="hide"/>	<a href="#">GNF Atlas 2</a> <input type="text" value="hide"/>	<a href="#">GNF Ratio</a> <input type="text" value="hide"/>	<a href="#">Affy U133</a> <input type="text" value="hide"/>	<a href="#">Affy GNF1H</a> <input type="text" value="hide"/>
<a href="#">Affy U133Plus2</a> <input type="text" value="hide"/>	<a href="#">Affy U95</a> <input type="text" value="hide"/>	<a href="#">CpG Islands</a> <input type="text" value="hide"/>	<a href="#">FirstEF</a> <input type="text" value="hide"/>	<a href="#">Reg Potential 7 species</a> <input type="text" value="hide"/>

**Comparative Genomics**

<a href="#">Conservation</a> <input type="text" value="full"/>	<a href="#">Most Conserved</a> <input type="text" value="hide"/>	<a href="#">Fugu Chain</a> <input type="text" value="hide"/>	<a href="#">Fugu Net</a> <input type="text" value="hide"/>	<a href="#">Tetraodon Chain</a> <input type="text" value="hide"/>
<a href="#">Tetraodon Net</a> <input type="text" value="hide"/>	<a href="#">Tetraodon Ecores</a> <input type="text" value="hide"/>	<a href="#">Zebrafish chain</a> <input type="text" value="hide"/>	<a href="#">Zebrafish Net</a> <input type="text" value="hide"/>	<a href="#">X. tropicalis Chain</a> <input type="text" value="hide"/>
<a href="#">X. tropicalis Net</a> <input type="text" value="hide"/>	<a href="#">Chicken Chain</a> <input type="text" value="hide"/>	<a href="#">Chicken Net</a> <input type="text" value="hide"/>	<a href="#">Cow Chain</a> <input type="text" value="hide"/>	<a href="#">Cow Net</a> <input type="text" value="hide"/>
<a href="#">Dog Chain</a> <input type="text" value="hide"/>	<a href="#">Dog Net</a> <input type="text" value="hide"/>	<a href="#">Rat Chain</a> <input type="text" value="hide"/>	<a href="#">Rat Net</a> <input type="text" value="hide"/>	<a href="#">Mouse Chain</a> <input type="text" value="hide"/>
<a href="#">Mouse Net</a> <input type="text" value="hide"/>	<a href="#">Rhesus Chain</a> <input type="text" value="hide"/>	<a href="#">Rhesus Net</a> <input type="text" value="hide"/>	<a href="#">Chimp Chain</a> <input type="text" value="hide"/>	<a href="#">Chimp Net</a> <input type="text" value="hide"/>

**Variation and Repeats**

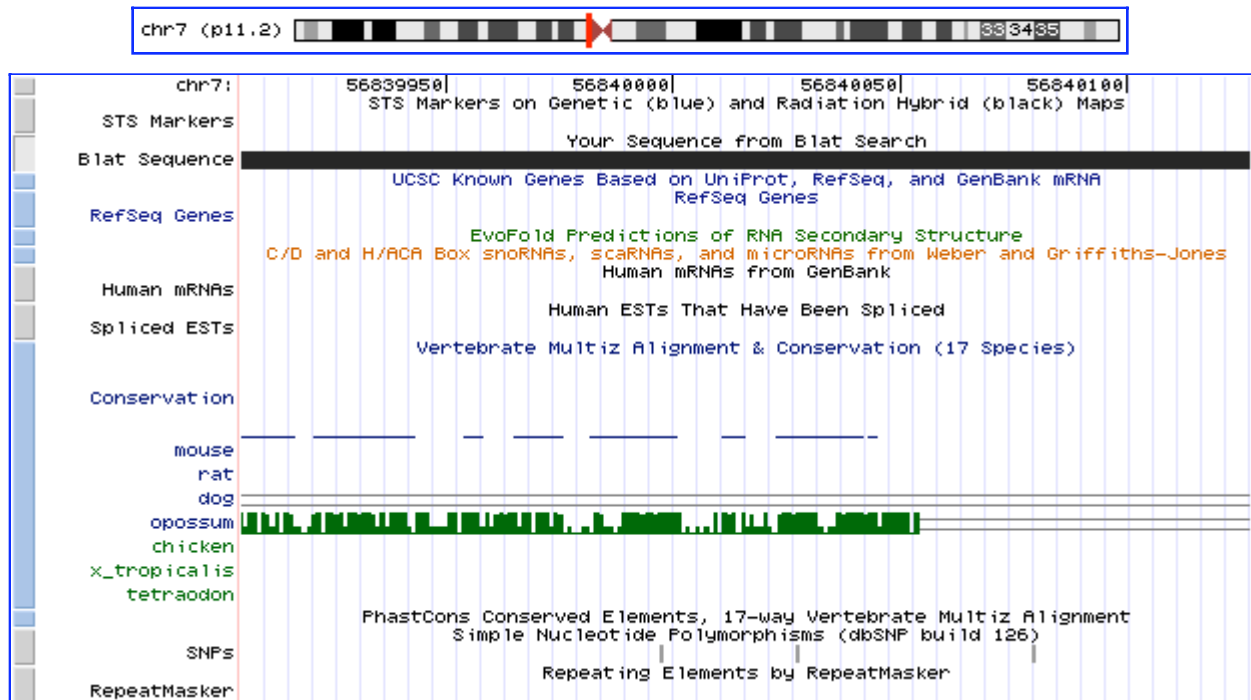
<a href="#">SNPs</a> <input type="text" value="dense"/>	<a href="#">RepeatMasker</a> <input type="text" value="dense"/>	<a href="#">Simple Repeats</a> <input type="text" value="hide"/>	<a href="#">Self Chain</a> <input type="text" value="hide"/>
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# UCSC Genome Browser on Human Mar. 2006 Assembly

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

position/search  jump clear size 222 bp.



move start < 2.0 > Click on a feature for details. Click on base position to zoom in around cursor. Click on left mini-buttons for track-specific options. move end < 2.0 >

Use drop down controls below and press refresh to alter tracks displayed. Tracks with lots of items will automatically be displayed in more compact modes.

### Mapping and Sequencing Tracks

<a href="#">Base Position</a> <input type="button" value="dense"/>	<a href="#">Chromosome Band</a> <input type="button" value="hide"/>	<a href="#">STS Markers</a> <input type="button" value="dense"/>	<a href="#">FISH Clones</a> <input type="button" value="hide"/>	<a href="#">Recomb Rate</a> <input type="button" value="hide"/>
<a href="#">Map Contigs</a> <input type="button" value="hide"/>	<a href="#">Assembly</a> <input type="button" value="hide"/>	<a href="#">Gap</a> <input type="button" value="hide"/>	<a href="#">Coverage</a> <input type="button" value="hide"/>	<a href="#">BAC End Pairs</a> <input type="button" value="hide"/>
<a href="#">Fosmid End Pairs</a> <input type="button" value="hide"/>	<a href="#">GC Percent</a> <input type="button" value="hide"/>	<a href="#">Short Match</a> <input type="button" value="hide"/>	<a href="#">Restr Enzymes</a> <input type="button" value="hide"/>	Blat Sequence <input type="button" value="dense"/>

### Genes and Gene Prediction Tracks

[Known Genes](#)

pack ▾

[N-SCAN](#)

hide ▾

[EvoFold](#)

full ▾

[RefSeq Genes](#)

dense ▾

[SGP Genes](#)

hide ▾

[sno/miRNA](#)

full ▾

[Other RefSeq](#)

hide ▾

[Geneid Genes](#)

hide ▾

[MGC Genes](#)

hide ▾

[Genscan Genes](#)

hide ▾

[Ensembl Genes](#)

hide ▾

[Superfamily](#)

hide ▾

**mRNA and EST Tracks**[Human mRNAs](#)

dense ▾

[H-Inv](#)

hide ▾

[Spliced ESTs](#)

dense ▾

[Human ESTs](#)

hide ▾

[Other mRNAs](#)

hide ▾

[Other ESTs](#)

hide ▾

**Expression and Regulation**[Allen Brain](#)

hide ▾

[Affy U133Plus2](#)

hide ▾

[GNF Atlas 2](#)

hide ▾

[Affy U95](#)

hide ▾

[GNF Ratio](#)

hide ▾

[CpG Islands](#)

hide ▾

[Affy U133](#)

hide ▾

[FirstEF](#)

hide ▾

[Affy GNF1H](#)

hide ▾

[Reg Potential 7 species](#)

hide ▾

**Comparative Genomics**[Conservation](#)

full ▾

[Tetraodon Net](#)

hide ▾

[X. tropicalis Net](#)

hide ▾

[Dog Chain](#)

hide ▾

[Mouse Net](#)

hide ▾

[Most Conserved](#)

full ▾

[Tetraodon Ecores](#)

hide ▾

[Chicken Chain](#)

hide ▾

[Dog Net](#)

hide ▾

[Rhesus Chain](#)

hide ▾

[Fugu Chain](#)

hide ▾

[Zebrafish chain](#)

hide ▾

[Chicken Net](#)

hide ▾

[Rat Chain](#)

hide ▾

[Rhesus Net](#)

hide ▾

[Fugu Net](#)

hide ▾

[Zebrafish Net](#)

hide ▾

[Cow Chain](#)

hide ▾

[Rat Net](#)

hide ▾

[Chimp Chain](#)

hide ▾

[Tetraodon Chain](#)

hide ▾

[X. tropicalis Chain](#)

hide ▾

[Cow Net](#)

hide ▾

[Mouse Chain](#)

hide ▾

[Chimp Net](#)

hide ▾

**Variation and Repeats**[SNPs](#)

dense ▾

[RepeatMasker](#)

dense ▾

[Simple Repeats](#)

hide ▾

[Self Chain](#)

hide ▾

refresh