

# Generating oligo coordinate file for captureC analyser

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We have our own UCSC server – here  
<https://genome.molbiol.ox.ac.uk/>

When clicking that, you should see following :

## UCSC Genome Bioinformatics

[Genomes](#) - [Blat](#) - [Tables](#) - [Gene Sorter](#) - [PCR](#) - [VisiGene](#) - [Session](#) - [FAQ](#) - [Help](#)

1) Go to the Genomes,  
And select the genome, and the gene you want to look at

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### Mouse (*Mus musculus*) Genome Browser Gateway

The UCSC Genome Browser was created by the [Genome Bioinformatics Group of UC Santa Cruz](#).  
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group	genome	assembly	position	search term	
<input type="text" value="Mammal"/>	<input type="text" value="Mouse"/>	<input type="text" value="July 2007 (NCBI37/mm9)"/>	<input type="text" value="chr11:32,144,213-32,192,922"/>	<input type="text" value="Npri3"/>	<input type="button" value="submit"/>

2) Press “submit”

Scroll down a little – click on “Restr Enzymes” :

The image shows a software interface titled "Mapping and Sequencing" with a "refresh" button in the top right corner. Below the title bar, there are six columns of track names, each with a "hide" dropdown menu below it. The tracks are: Base Position, STS Markers, Assembly, BAC End Pairs, Chromosome Band, and Gap. The second row contains: GC Percent, GRC Incident, Map Contigs, Mappability (with a crossed-out 'X' icon), MGI QTL, and Short Match. The third row contains: Restr Enzymes. The "Restr Enzymes" text and its "hide" dropdown are circled in red. To the right of this circle, red text reads: "Click the track name 'Restr Enzymes'".

Mapping and Sequencing						refresh
<a href="#">Base Position</a>	<a href="#">STS Markers</a>	<a href="#">Assembly</a>	<a href="#">BAC End Pairs</a>	<a href="#">Chromosome Band</a>	<a href="#">Gap</a>	
hide ▼	hide ▼	hide ▼	hide ▼	hide ▼	hide ▼	
<a href="#">GC Percent</a>	<a href="#">GRC Incident</a>	<a href="#">Map Contigs</a>	<del>X</del> <a href="#">Mappability</a>	<a href="#">MGI QTL</a>	<a href="#">Short Match</a>	
hide ▼	hide ▼	hide ▼	hide ▼	hide ▼	hide ▼	
<a href="#">Restr Enzymes</a>						
hide ▼						

Click the track name "Restr Enzymes"

Genomes Genome Browser Tools Mirrors Downloads

### Restr Enzymes Track Settings

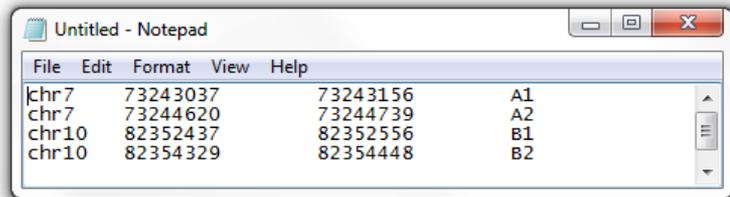
## Restriction Enzymes from REBASE

Display mode:   3.

Filter display by enzymes (separate with commas):

1.

1. Write your restriction enzyme name here
2. Select "pack" as the display mode
3. Press "Submit"



**Write a file of your BIOTINYLATED CAPTURE OLIGO coordinates.**

**col1   col2   col3   col4**  
**chr   start   stop   name**

Copypaste your coordinates to custom track field :

[Home](#)
[Genomes](#)
[Genome Browser](#)
[Tools](#)
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### Add Custom Tracks

clade 
 genome 
 assembly

Display your own data as custom annotation tracks in the browser. Data must be formatted in [BED](#), [bigBed](#), [bedGraph](#), [GFF](#), [GTF](#), [WIG](#), [bigWig](#), [MAE](#), [BAM](#), set [track](#) and [browser](#) line attributes as described in the [User's Guide](#). Data in the bigBed, bigWig, BAM and VCF formats must be provided via a URL embed

Paste URLs or data:      Or upload:  No file chosen     

<a href="#">chr7</a>	73243037	73243156	<a href="#">A1</a>
<a href="#">chr7</a>	73244620	73244739	<a href="#">A2</a>
<a href="#">chr10</a>	82352437	82352556	<a href="#">B1</a>
<a href="#">chr10</a>	82354329	82354448	<a href="#">B2</a>

Untitled - Notepad

File	Edit	Format	View	Help
chr7	73244620	73244739	A2	
chr10	82352437	82352556	B1	
chr10	82354329	82354448	B2	

### Manage Custom Tracks

genome: Mouse assembly: July 2007 (NCBI37/mm9) [mm9]

Name	Description	Type	Doc	Items	Pos	delete
User Track	User Supplied Track	bed		4	chr7:	<input type="checkbox"/>

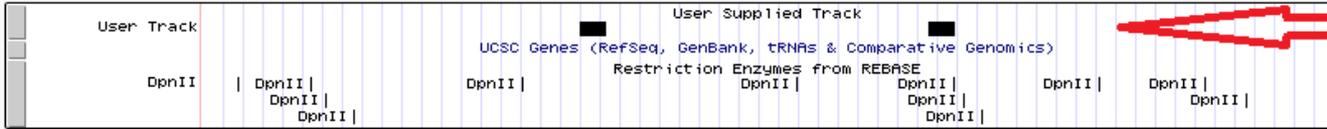
- add custom tracks
- go to genome browser
- go to table browser
- go to variant annotation integrator

## UCSC Genome Browser on Mouse July 2007 (NCBI37/mm9) Assembly

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

chr7:73,241,334-73,246,442 5,109 bp.  go

chr7 (qC) 7qA1 7qA2 7qA3 7qB1B2 7qB3 7qB4 7qB5 7qC 7qD1 D2 7qD3 7qE1 7qE3 7qF1 qF2 7qF3 F4 qF5



"User track" = your biotinylated oligos !

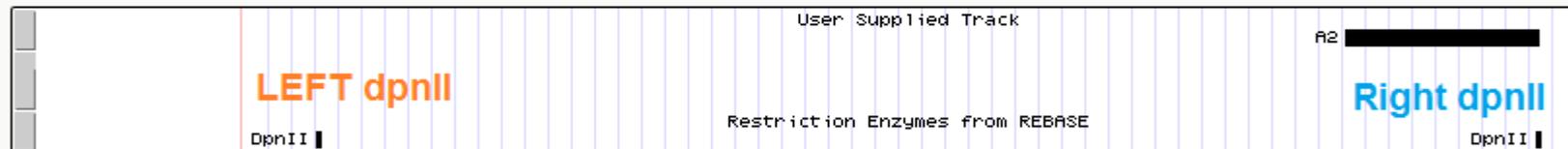
DpnII cut sites !

## UCSC Genome Browser on Mouse July 2007 (NCBI37/mm9) Assembly

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

chr7:73,243,976-73,244,753 778 bp.

chr7 (qC) 7qA1 A2 7qA3 7qB1B2 7qB3 7qB4 7qB5 7qC 7qD1 D2 7qD3 7qE1 7qE3 7qF1 qF2 7qF3 F4 qF5



**Zoom in so, that you can see in which DpnII fragment your oligo is !**

chr7:73,244,732-73,244,737 6 bp.  go

chr7 (qC) 7qA1 A2 7qA3 7qB1B2 7qB3 7qB4 7qB5 7qC | qD1 D2 7qD3 7qE1 7qE3 7qF1 qF2 7qF3 F4qF5



Right side coordinate  
( in this case  
chr7 73 244 736 )

chr7:73,244,016-73,244,021 6 bp.  go

chr7 (qC) 7qA1 A2 7qA3 7qB1B2 7qB3 7qB4 7qB5 7qC | qD1 D2 7qD3 7qE1 7qE3 7qF1 qF2 7qF3 F4qF5



Left side coordinate  
( in this case  
chr7 73 244 017 )

**Left side coordinate**

chr7 73 244 017

**Right side coordinate**

chr7 73 244 736

**The 9-column line for this oligo in the oligo-coordinate file will now be :**

<b>A1</b>	<b>7</b>	<b>73244017</b>	<b>73244736</b>	<b>7</b>	<b>73243017</b>	<b>73245736</b>	<b>1</b>	<b>A</b>
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**Coordinates of the DpnII fragment**

**Exclusion fragment coordinates**

**(DpnII flanked by 1000bases both directions)**

"A1" is the name of the oligo capture (first column)

Last two columns are "SNP position" and "SNP base"

- 1 and A are good defaults to state "I don't have a SNP defined"

**To define SNP, the same line would look like this :**

<b>A1</b>	<b>7</b>	<b>73244017</b>	<b>73244736</b>	<b>7</b>	<b>73243017</b>	<b>73245736</b>	<b>73244516</b>	<b>C</b>
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