

# Meg3在小鼠骨骼肌发育中作用的研究

## Research on the function of meg3 in mouse skeletal muscle development

汇报人：王子帅

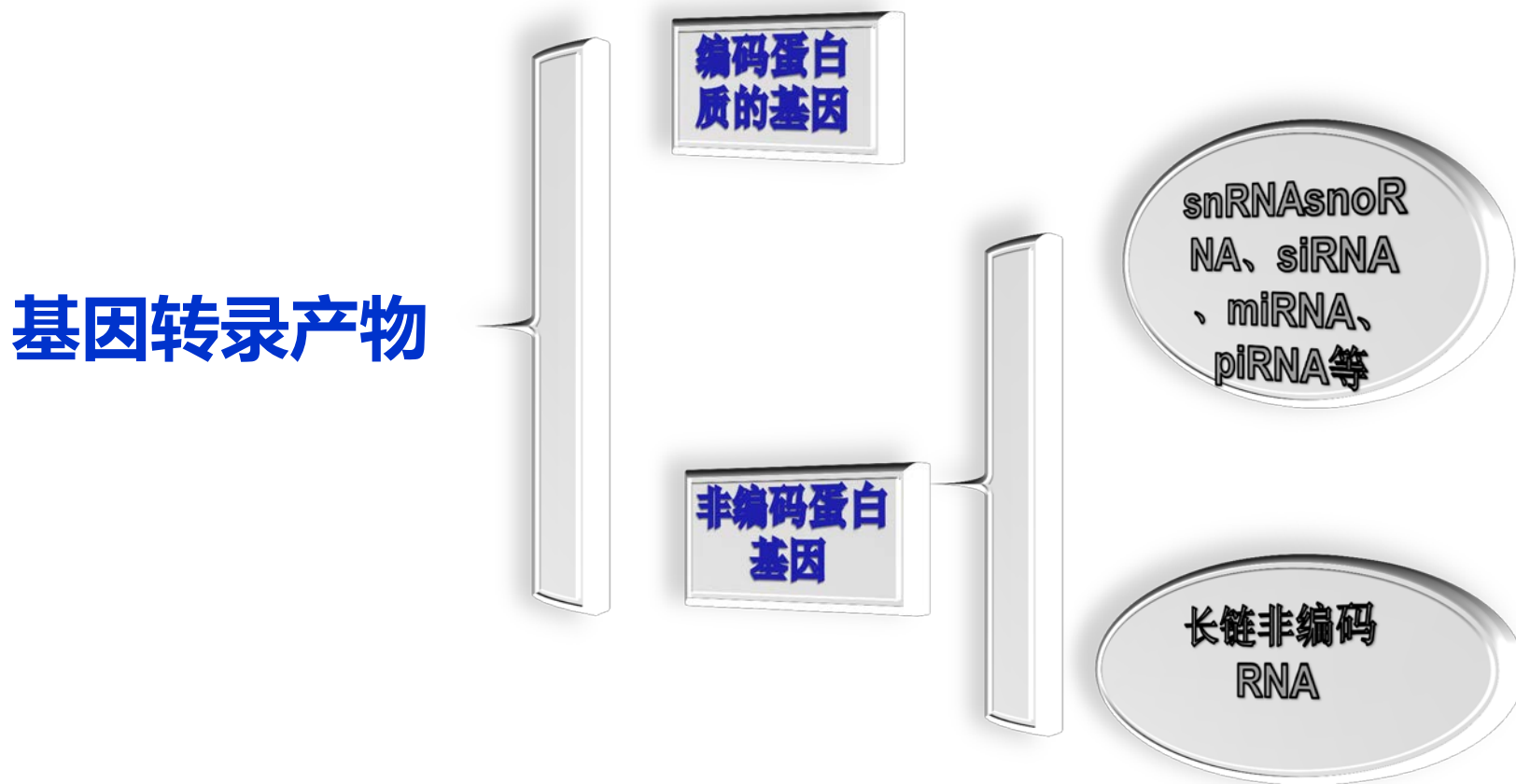
组员：李聪、王红杨、范金

# 汇报内容

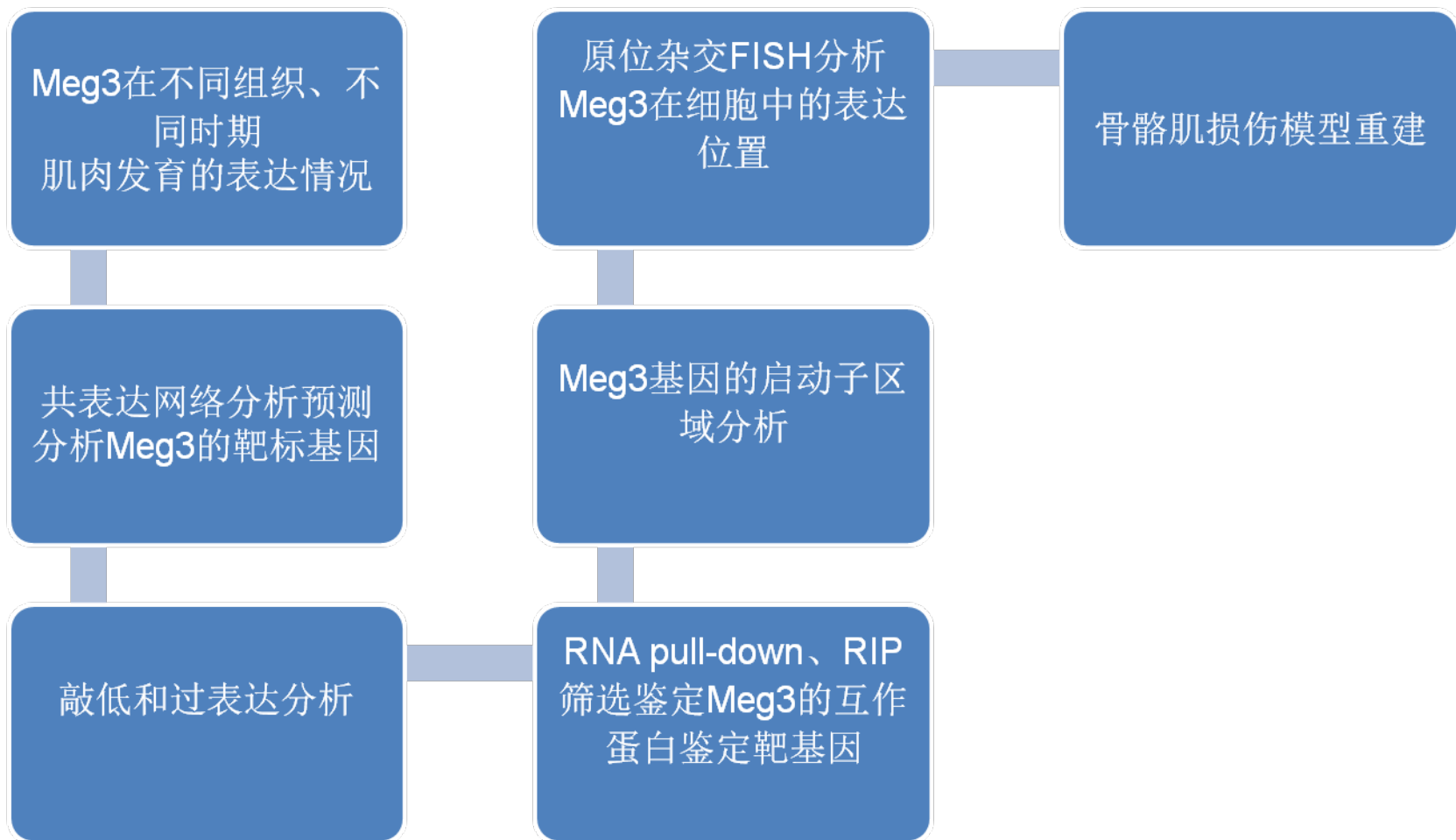
- 研究背景
- 研究内容
- 方法与结果
  - Meg3的筛选
  - 转录本的确定



# 一、研究背景



# 二、研究内容



# 三、方法和结果

0天和65天ICR系小鼠各四只，取背肌，  
通过芯片筛选差异表达lncRNA和mRNA共6000多个

	A	B	C	D	E	F	G	H	I	J	K	L	M
1	ProbeName	p	FC (abs)	Regulation	type	seqname	GeneSymbol	source	RNAlength	chrom	strand	txStart	txEnd
2	ASMM9PART	2.509E-07	215.05664	up	noncoding	uc007pgs.1	V00821	UCSC_kg	473	chr12	-	114656769	114659220
3	ASMM9PART	0.0001984	44.385597	up	noncoding	ENSMUST1	Amd-ps1	Ensembl	994	chrX	+	151589737	151590731
4	MM9LINC RNA	0.0005128	14.58157	up	noncoding	MM9LINC1	mouse1incR	lincRNA	843	chr16	+	23994502	23995345
5	ASMM9PART	0.0013966	37.32185	up	noncoding	uc008feg.1	S60130	UCSC_kg	329	chr18	-	64609340	64609669
6	ASMM9PART	0.0141759	10.218201	up	noncoding	uc009efh.1	AK009064	UCSC_kg	656	chr6	-	129182643	129188000
7	ASMM9PART	0.0001424	12.930533	up	noncoding	ENSMUST1	Gm9115	Ensembl	1348	chrX	-	99919740	99921088
8	CUST_32_PI42	0.0015541	30.827337	up	noncoding	uc008sno.1	Cell9	UCSC_kg	701	chr4	+	42643256	42645246
9	ASMM9PART	0.0002441	13.524063	up	noncoding	ENSMUST1	Gm15470	Ensembl	1371	chr7	+	48745720	48747091
10	ASMM9PART	0.0007357	23.600565	up	noncoding	ENSMUST1	Cell9-ps1	Ensembl	327	chr4	+	41792005	41793621
11	ASMM9PART	0.0050958	11.745033	up	noncoding	ENSMUST1	2310001H17	Ensembl	656	chr6	-	129182643	129188000


# Meg3 的筛选

倍数 (个) RNA (个)	Fold-change (>10)	Fold-change (>50)
Noncoding RNA up 总数: (1640) 去掉重复	>10 = 75 比例: 4.5731%	>50 = 13 比例: 0.7926%
Noncoding RNA down 总数: (1099) 去掉重复	>10 = 80 比例: 7.2793%	>50 = 15 比例: 1.3648%
Coding RNA up 总数: (1438)	>10 = 65 比例: 4.5201%	>50 = 3 比例: 0.2086%
Coding RNA down 总数: (1470)	>10 = 110 比例: 7.4829%	>50 = 10 比例: 0.6802%



# Meg3 的筛选

<http://david.abcc.ncifcrf.gov/summary.jsp>



**Functional Annotation Tool**  
DAVID Bioinformatics Resources 6.7, NIAID/NIH

[Home](#) [Start Analysis](#) [Shortcut to DAVID Tools](#) [Technical Center](#) [Downloads & APIs](#) [Term of Service](#) [Why DAVID?](#) [About Us](#)

[Upload](#) [List](#) [Background](#)

## Upload Gene List

[Demolist 1](#) [Demolist 2](#)

[Upload Help](#)

Step 1: Enter Gene List


A: Paste a list

Or

B: Choose From a File

Multi-List File [?](#)

## Functional Annotation Tool

 Submit your gene list to start the tool!

[Tell us how you like the tool](#)  
[Read technical notes of the tool](#)  
[Contact us for questions](#)

### Key Concepts:

#### The DAVID Gene Concept

DAVID 6.7 is designed around the "DAVID Gene Concept", a graph theory evidence-based method to agglomerate species-specific gene/protein identifiers from a variety of public genomic resources including NCBI, PIR and Uniprot/SwissProt. The DAVID Gene Concept method groups tens of million of identifiers from over 65,000 species into 1.5 million unique protein/gene records. [More](#)

#### Term/Gene Co-Occurrence Probability

Ranking functional categories based on co-occurrence with sets of genes in a gene list can rapidly aid in unraveling new biological processes associated with cellular functions and pathways. DAVID 6.7 allows investigators to sort gene categories from dozens of annotation systems. Sorting can be based either the number of genes within each category or by the EASE-score. [More](#)

# Meg3 的筛选

<http://www.genecards.org/cgi-bin/BatchQueries/Batch.pl>

 **BETA**  
GeneCards Batch Queries

an academic web site of the

 **מכון ויצמן למדע**  
WEIZMANN INSTITUTE OF SCIENCE

in association with

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**LifeMap**  
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Welcome, 787532491@qq.com

You have 100 more genes to retrieve today (of maximum allowed 100 per day).

If you require a larger quota, please [contact us](#)

GeneALaCart generates a file of [GeneCards](#) annotations for your list of genes. You can use any white space separator. [About GeneAlaCart](#)

Query by:

Output file order:

Output file name:

Upload a file with up to 500 genes

Or type/paste here up to 500 genes

View examples of [input gene identifiers](#), [output file examples \(txt, Excel\)](#), and [output file format](#)

Please choose the fields to be included in the output file from the list below:

email (for uploaded file or > 250 genes)

**Symbol**  
 **Category**  
 **GIFtS**  
 **GC ID**

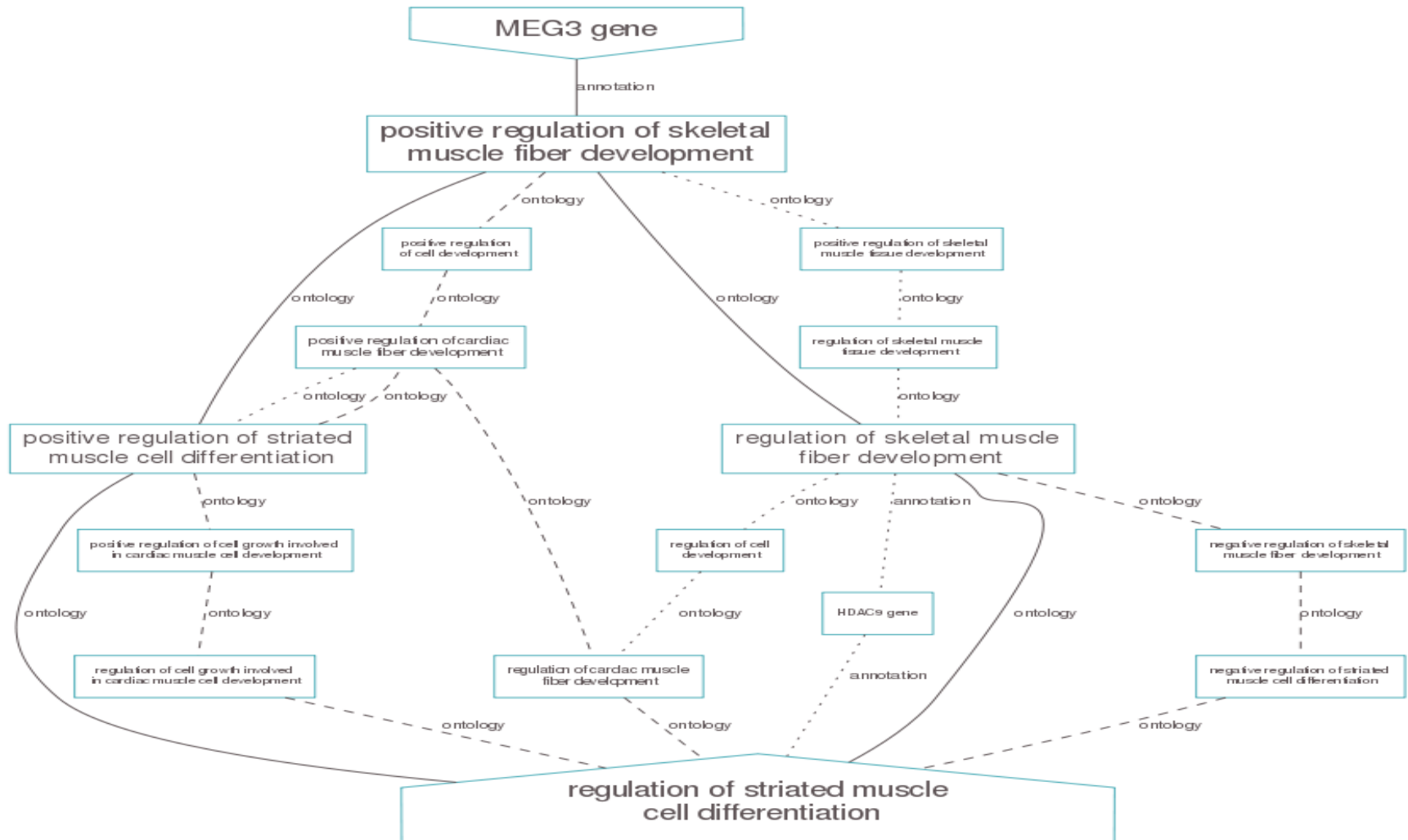
**Gene Name**

[approved / not approved]  **Source**



# Meg3 的筛选

<http://biograph.be/concept/graph/C1422767/C1523177>



<http://biograph.be/concept/graph/C1422767/C1523177>

## 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	
Mammal	Mouse	Dec. 2011 (GRCm38/mm10)	chr12:109,542,023-109,568,594	meg3	submit
				Meg3 (Mus musculus maternally expressed 3 (Meg3), transcript variant 2, non-coding RNA.)	

[Click here to reset](#) the browser user interface settings to their defaults.

## Mouse Genome Browser – mm10 assembly ([sequences](#))

The Dec. 2011 *Mus musculus* assembly (Genome Reference Consortium Mouse Build 38 (GCA\_000001635.2)) was produced by the [Mouse Genome Reference Consortium](#). For more information about this assembly, see [GRCm38](#) in the NCBI Assembly database.

### Sample position queries

A genome position can be specified by the accession number of a sequenced genomic region, an mRNA or EST, a chromosomal coordinate range, or keywords from the GenBank description of an mRNA. The following list shows examples of valid position queries for the Mouse genome. See the [User's Guide](#) for more information.

Request:	Genome Browser Response:
chr16	Displays all of chromosome 16
chr16:1-5000000	Displays first 5 million bases of chr 16



*Mus musculus*  
(Photo courtesy of [The Jackson Laboratory](#))

## UCSC Genes

[Meg3 \(uc029rxy.1\) at chr12:109542023-109568594](#) - Mus musculus maternally expressed 3 (Meg3), transcript variant 2, non-coding RNA.  
[Meg3 \(uc011ysb.1\) at chr12:109546430-109571729](#) - Mus musculus maternally expressed 3 (Meg3), transcript variant 3, non-coding RNA.  
[Meg3 \(uc007pav.2\) at chr12:109549157-109571729](#) - Mus musculus maternally expressed 3 (Meg3), transcript variant 3, non-coding RNA.  
[Meg3 \(uc007pau.2\) at chr12:109545398-109568594](#) - Mus musculus maternally expressed 3 (Meg3), transcript variant 1, non-coding RNA.  
[Meg3 \(uc007pat.2\) at chr12:109544027-109571729](#) - Mus musculus maternally expressed 3 (Meg3), transcript variant 4, non-coding RNA.  
[Meg3 \(uc007par.2\) at chr12:109540996-109571729](#) - Mus musculus maternally expressed 3 (Meg3), transcript variant 3, non-coding RNA.  
[Meg3 \(uc007paq.2\) at chr12:109540996-109568594](#) - Mus musculus maternally expressed 3 (Meg3), transcript variant 2, non-coding RNA.  
[Meg3 \(uc007pap.2\) at chr12:109540996-109545319](#) - Mus musculus maternally expressed 3 (Meg3), transcript variant 3, non-coding RNA.

## RefSeq Genes

[Meg3 at chr12:109545398-109568600](#) - (NR\_003633)  
[Meg3 at chr12:109540996-109568600](#) - (NR\_027651)  
[Meg3 at chr12:109540996-109571729](#) - (NR\_027652)  
[Meg3 at chr12:109540996-109571729](#) - (NR\_046475)

## Non-Mouse RefSeq Genes

[MEG3 at chr12:109543703-109559344](#) - (NR\_037685)  
[MEG3 at chr12:109543703-109559344](#) - (NR\_037686)

## Non-Mouse Aligned mRNA Search Results

[AF151783](#) - Homo sapiens, MEG3

## Ensembl Genes

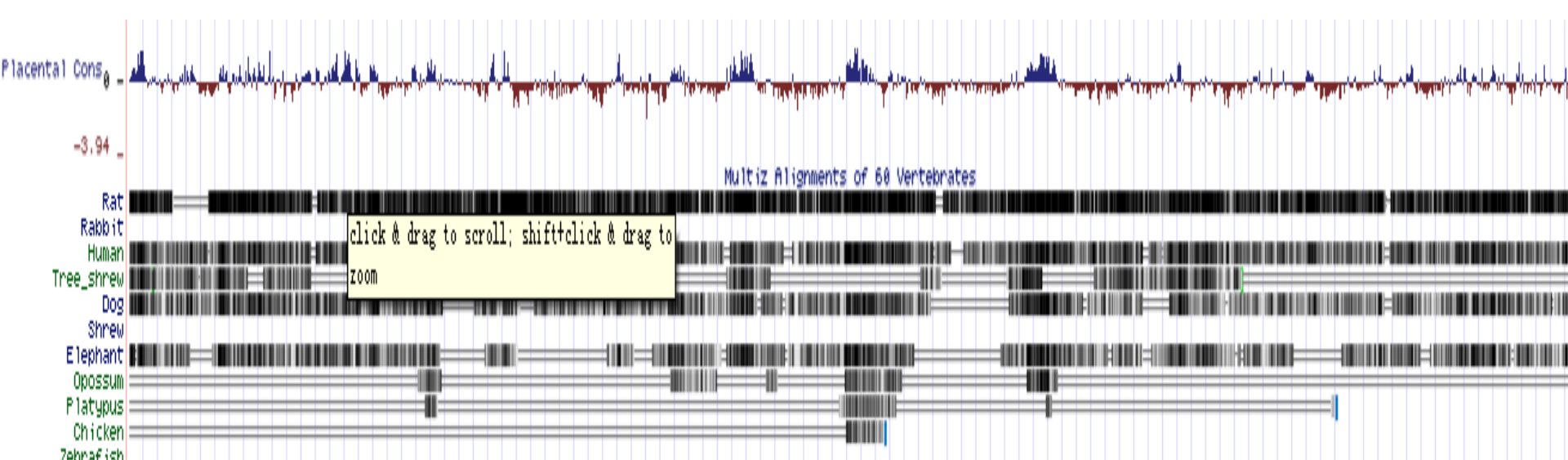
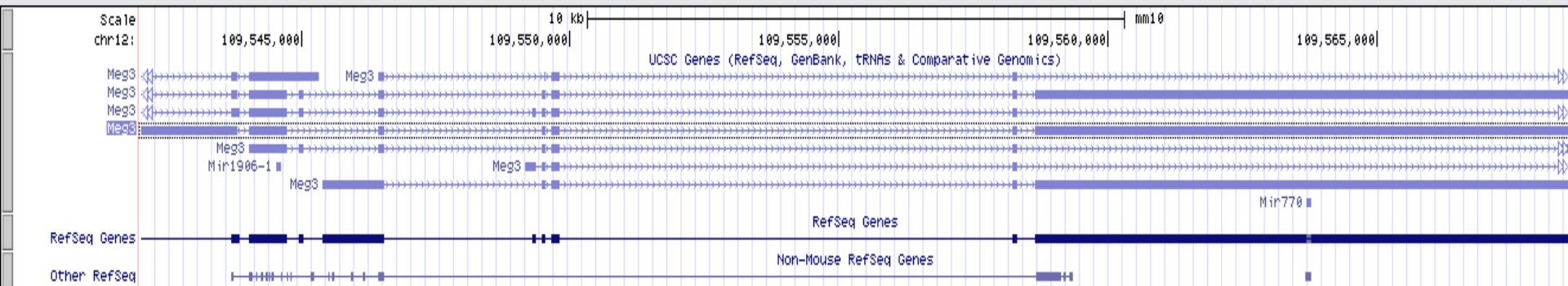
[Meg3 at chr12:109549157-109558803](#) - (ENSMUST000000128458)  
[Meg3 at chr12:109546391-109571719](#) - (ENSMUST000000166636)  
[Meg3 at chr12:109544498-109558320](#) - (ENSMUST000000126289)  
[Meg3 at chr12:109542023-109561682](#) - (ENSMUST000000143272)  
[Meg3 at chr12:109541005-109571721](#) - (ENSMUST000000143836)  
[Meg3 at chr12:109541001-109545319](#) - (ENSMUST000000129245)  
[Meg3 at chr12:109541007-109559189](#) - (ENSMUST000000124106)  
[Meg3 at chr12:109542268-109544307](#) - (ENSMUST000000128178)  
[Meg3 at chr12:109545398-109571726](#) - (ENSMUST000000146701)  
[Meg3 at chr12:109546445-109571722](#) - (ENSMUST000000143847)  
[Meg3 at chr12:109549255-109549775](#) - (ENSMUST000000150851)

# UCSC Genome Browser on Mouse Dec. 2011 (GRCm38/mm10) Assembly

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

chr12:109,542,023-109,568,594 26,572 bp.

chr12 (qF1) 12qA1.1 A1.2 qA1.3 12qA2 12qA3 12qB1 12qB3 12qC1 12qC2 12qC3 12qD1 qD2 12qD3 12qE 12qF1 12qF2



RepeatMasker

## Mouse Gene Meg3 (uc029rxy.1) Description and Page Index

**Description:** Mus musculus maternally expressed 3 (Meg3), transcript variant 2, non-coding RNA.

**RefSeq Summary (NR\_027651):** This gene encodes several alternatively spliced, non-protein-coding transcripts, and appears to function as an RNA. It is an imprinted gene, with preferential expression from the maternal allele. It is closely linked to, and co-expressed with reciprocally imprinted, paternally expressed Dlk1 gene. This co-regulation suggests a causative role in the pathologies found in uniparental disomy animals, characterized by defects in skeletal muscle maturation, bone formation, placenta size and organization and prenatal lethality.[provided by RefSeq, Nov 2010].

### Transcript (Including UTRs)

**Position:** chr12:109,542,023-109,568,594 **Size:** 26,572 **Total Exon Count:** 7 **Strand:** +

<b>Page Index</b>	Sequence and Links	Other Species	mRNA Descriptions	Other Names	Model Information
Methods					

Data last updated: 2012-09-13

### - Sequence and Links to Tools and Databases

<a href="#">Genomic Sequence (chr12:109.542.023-109.568.594)</a>		mRNA (may differ from genome)		No protein	
<a href="#">Gene Sorter</a>	<a href="#">Genome Browser</a>	<a href="#">Protein FASTA</a>	<a href="#">Table Schema</a>	<a href="#">BioGPS</a>	<a href="#">CGAP</a>
<a href="#">Ensembl</a>	<a href="#">ExonPrimer</a>	<a href="#">GeneCards</a>	<a href="#">Gepis Tissue</a>	<a href="#">PubMed</a>	<a href="#">Stanford SOURCE</a>
<a href="#">Wikipedia</a>					

### + Orthologous Genes in Other Species

### - Descriptions from all associated GenBank mRNAs

[AK145456](#) - Mus musculus 5 days embryo whole body cDNA, RIKEN full-length enriched library, clone:10C0047O18 product:unclassifiable, full insert sequence.

[AK155982](#) - Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830003A04 product:unclassifiable, full insert sequence.

[AK157178](#) - Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830206C10 product:unclassifiable, full insert sequence.

[Y13832](#) - Mus musculus mRNA for GT12 protein.

[BC094421](#) - Mus musculus cDNA clone IMAGE:6413494.

[AK147321](#) - Mus musculus adult male brain UNDEFINED\_CELL\_LINE cDNA, RIKEN full-length enriched library, clone:M5C1012O18 product:GTL2, imprinted maternally expressed untranslated mRNA, full insert sequence.

[BC024818](#) - Mus musculus maternally expressed 3, mRNA (cDNA clone IMAGE:5357967), with apparent retained intron.

[AK018105](#) - Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330403F08 product:Mus musculus GTL2, imprinted maternally expressed untranslated mRNA (Gtl2), mRNA., full insert sequence.

[BC048191](#) - Mus musculus maternally expressed 3, mRNA (cDNA clone IMAGE:6831921).

[AK032931](#) - Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330548N14 product:maternally expressed gene 3, full insert sequence.

## Genomic Sequence Near Gene

### Get Genomic Sequence Near Gene

Note: if you would prefer to get DNA for more than one feature of this track at a time, try the [Table Browser](#) using the output format sequence.

#### Sequence Retrieval Region Options:

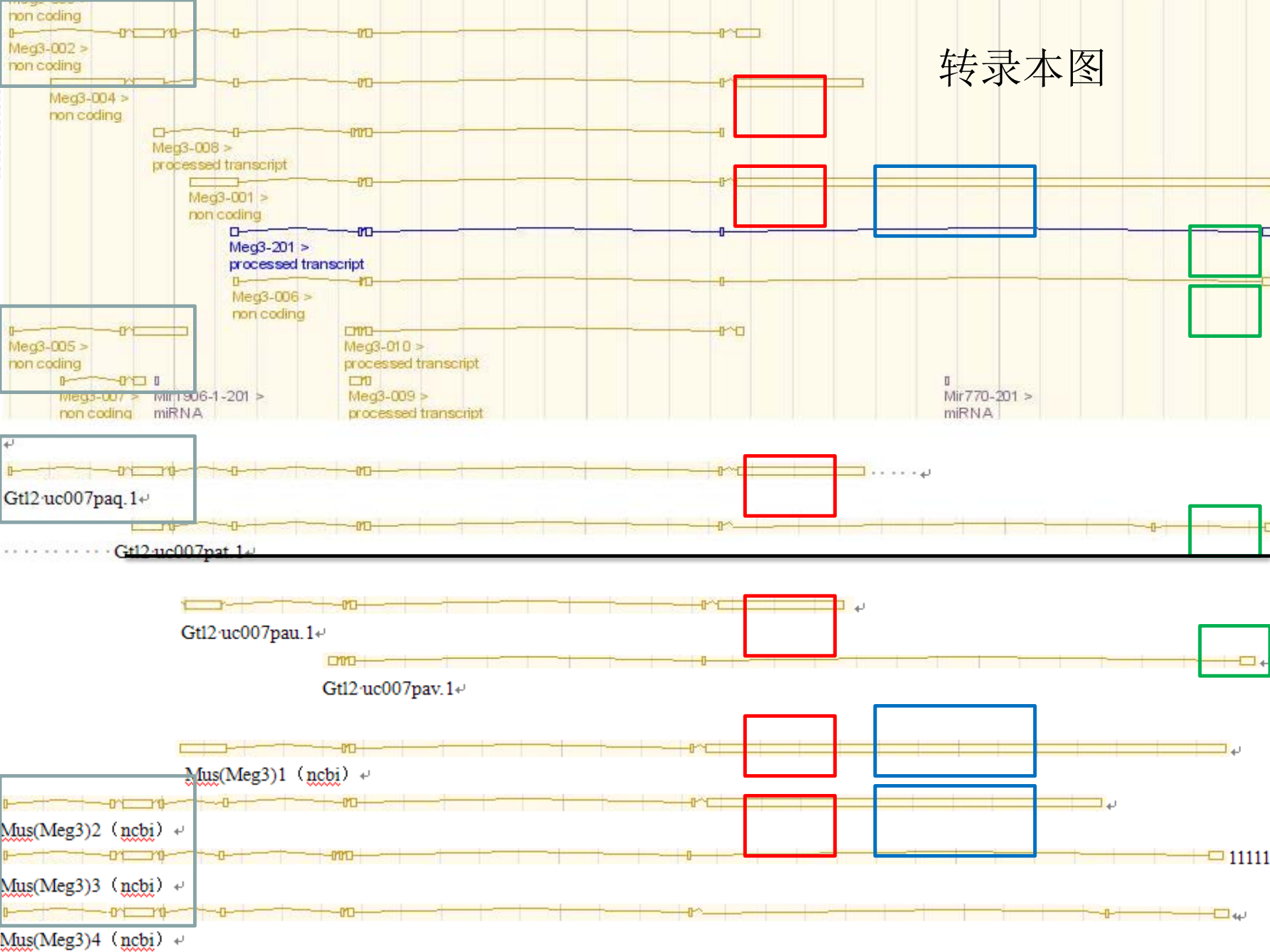
- Promoter/Upstream by  bases
- 5' UTR Exons
- CDS Exons
- 3' UTR Exons
- Introns
- Downstream by  bases
- One FASTA record per gene.
- One FASTA record per region (exon, intron, etc.) with  extra bases upstream (5') and  extra downstream (3')
  - Split UTR and CDS parts of an exon into separate FASTA records

Note: if a feature is close to the beginning or end of a chromosome and upstream/downstream bases are added, they may be truncated in order to avoid extending past the edge of the chromosome.

#### Sequence Formatting Options:

- Exons in upper case, everything else in lower case.
- CDS in upper case, UTR in lower case.
- All upper case.
- All lower case.
- Mask repeats:  to lower case  to N

# 转录本图



请老师和同学批评指正！

谢 谢！