

**A**

UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

move: <<< << < > >> >>> zoom in: 1.5x 3x 10x base zoom out: 1.5x 3x 10x 100x

chr3:108,475,647-108,476,324 678 bp

enter position, gene symbol or search terms go

chr3 (q13.13)

Scale 200 bases hg19

chr3: 108,475,800 108,475,900 108,476,000 108,476,100 108,476,200 108,476,300

RefSeq Genes

RETNLB

Your Sequence from Blast Search

Blast Sequence



HNF4 $\alpha$  consensus: AGGTCAaAGGTCA  
SVM score: 2.51

C

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

move: <<< << < > >> >>> zoom in: 1.5x 3x 10x base zoom out: 1.5x 3x 10x 100x

chr16:48,814,340-48,819,718 5,379 bp enter position, gene symbol or search terms go

chr16 (qB5) 16qA1 16qB1 16qB2 16qB3 16qB4 16qB5 C1.1 16qC1.3 qC2 16qC3.1 16qC3.5 16qC4

Scale 2 kb mm10

chr16: 48,815,000 48,815,500 48,816,000 48,816,500 48,817,000 48,817,500 48,818,000 48,818,500 48,819,000 48,819,500

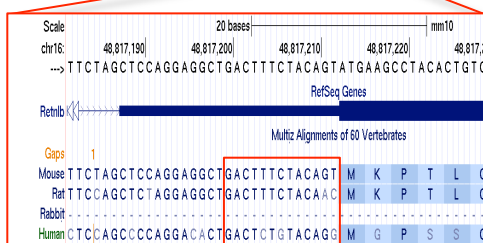
RefSeq Genes

Multiz Alignments of 60 Vertebrates

Rat

Rabbit

Human




# B

UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

move <<< << < > >> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x


chr3:108,475,879-108,476,894 1,016 bp  go

chr3 (q13.13)  24 29


Scale 500 bases hg19

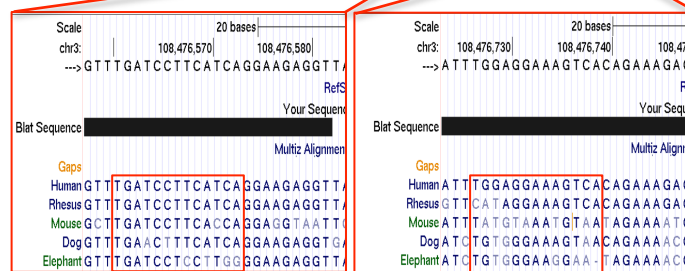
chr3: 108,476,000 108,476,500

RefSeq Genes

RETNLB 

Your Sequence from Blat Search

Blat Sequence 

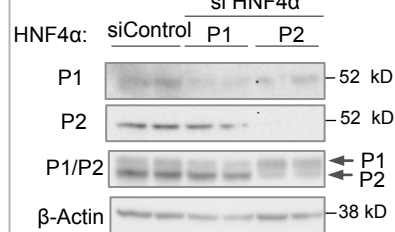
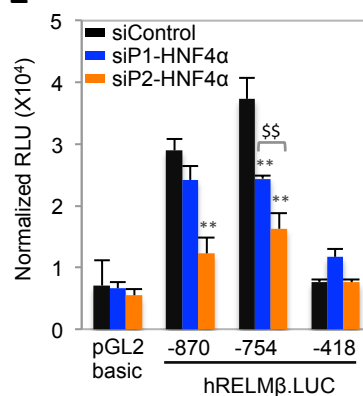


SVM score:  
Human 1.23  
Mouse 1.08

D

HNF4α SVM sites STAT6 NF-κB CDX2 KLF4

# E



**F**

Condition	Normalized RLU (x10 <sup>4</sup> )
Vector	~0.5
HNF4a2	~18
HNF4a8	~8

