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Genome Browser Gateway

Home Genomes Genome Browser Tools Mirrors Downloads My Data Help About Us

- Human GRCh38/hg38
- Human GRCh37/hg19**
- Mouse GRCm38/mm10
- Mouse NCBI37/mm9
- Mouse: 16 strains
- Other

You might want to navigate to your nearest mirror - genome-asia.ucsc.edu

- User settings (sessions and custom tracks) will differ between sites.
- Take me to genome-asia.ucsc.edu
- Let me stay here genome.ucsc.edu

选择点击HG19

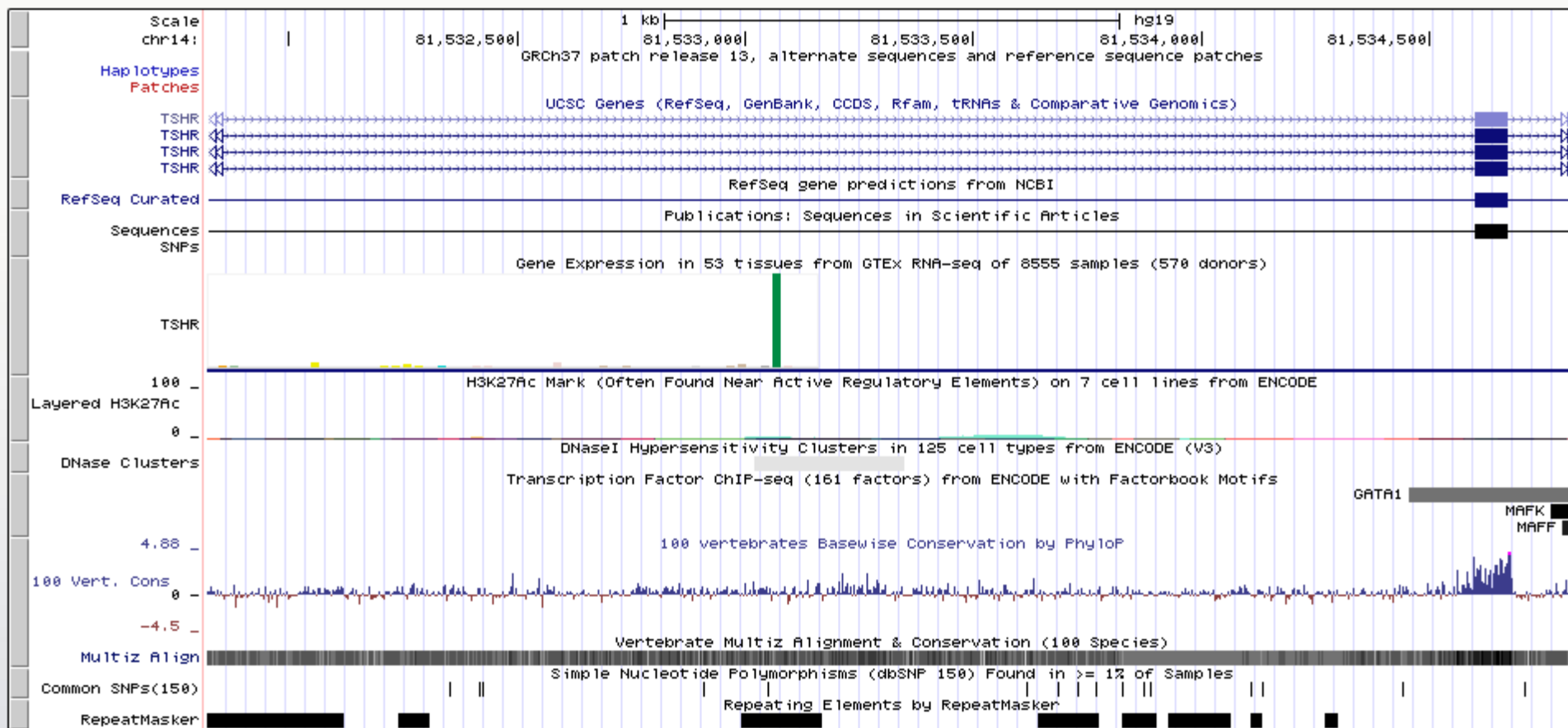
UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

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

chr14:81,531,822-81,534,822 3,001 bp

chr14 (q31.1) p13 p12 14p11.2 q11.2 14q12 q21.1 21.2 23.1 q24.3 31.1 q31.3 q32.2

键入包含CG位点的位置信息，
范围可尽量大一些

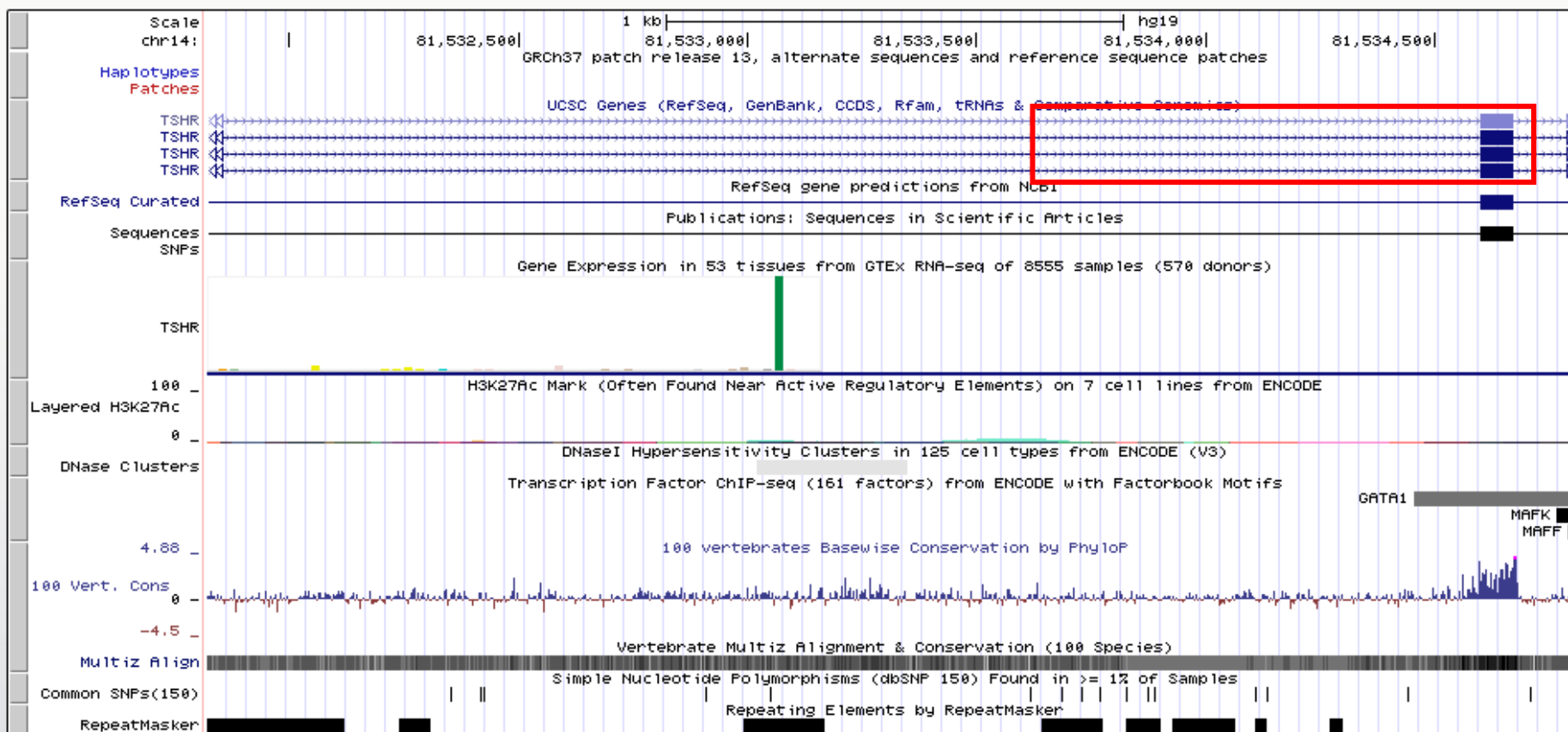


UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

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

chr14:81,531,822-81,534,822 3,001 bp. chr14:81,531,822-81,534,822 go

chr14 (q31.1) p13 p12 14p11.2 q11.2 14q12 q21.1 21.2 23.1 q24.3 31.1 q31.3 q32.2



点击方块



Human Gene TSHR (uc001xvb.1) Description and Page Index

Description: Homo sapiens thyroid stimulating hormone receptor (TSHR), transcript variant 2, mRNA.

RefSeq Summary (NM_001018036): The protein encoded by this gene is a membrane protein and a major controller of thyroid cell. Defects in this gene are a cause of several types of hyperthyroidism. Three transcript variants encoding different isoforms have been identified.

Transcript (Including UTRs)

Position: hg19 chr14:81,421,869-81,574,828 **Size:** 152,960 **Total Exon Count:** 8 **Strand:** +

Coding Region

Position: hg19 chr14:81,422,025-81,574,800 **Size:** 152,776 **Coding Exon Count:** 8

Page Index	Sequence and Links	Genetic Associations	MalaCards	CTD	Gene Alleles
RNA-Seq Expression	Microarray Expression	RNA Structure	Protein Structure	Other Species	GO Annotations
mRNA Descriptions	Pathways	Other Names	Model Information	Methods	

Data last updated: 2013-06-14

Sequence and Links to Tools and Databases [点击此处](#)

Genomic Sequence (chr14:81,421,869-81,574,828)		mRNA (may differ from genome)		Protein (231 aa)	
Gene Sorter	Genome Browser	Other Species FASTA	VisiGene	Gene interactions	Table Schema
BioGPS	CGAP	Ensembl	Entrez Gene	ExonPrimer	GeneCards
GeneNetwork	Gepis Tissue	H-INV	HGNC	Lynx	MGI
MOPED	OMIM	PubMed	Stanford SOURCE	Treefam	UniProtKB
Wikipedia					



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

submit

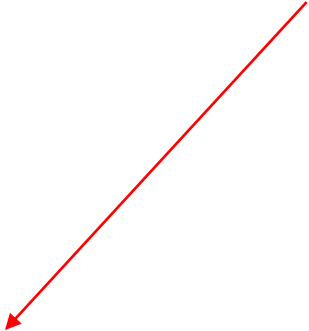
提交，可结合实际情况修改信息

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>hg19_knownGene_uc001xvb.1 range=chr14:81420369-81574828 5'pad=0 3'pad=0 strand=+ repeatMasking=none
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x

快捷键ctrl+F，输入SourceSeq序列进行搜索



U	P	U	R	S	I
Color_	Forward	Genome	CHR	MAPINFO	SourceSeq
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第 1 个, 共 1 个 | TCCAACCCCACT ^ v x

最终结果如图所示