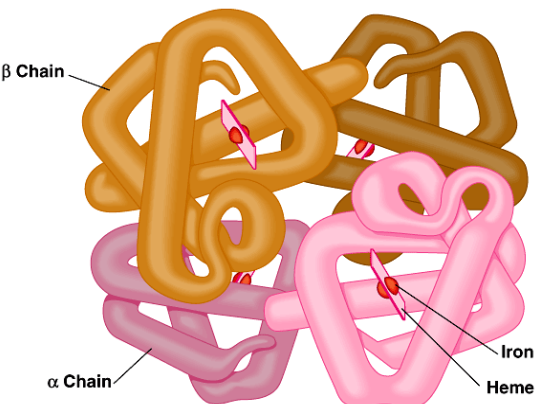


Using Bioinformatics in Medicine

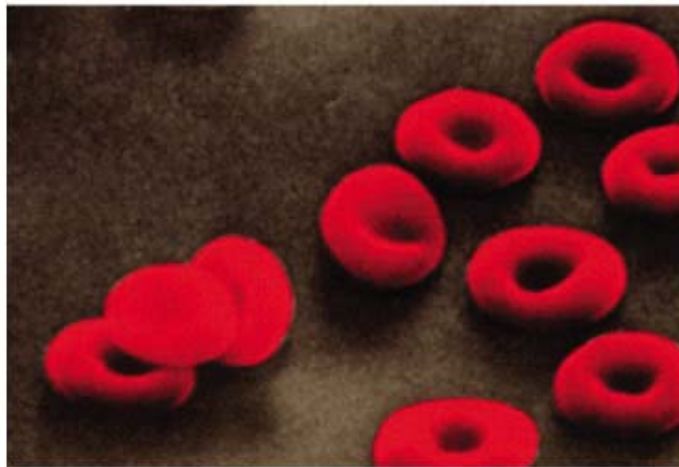


Sickle Cell Anemia & the **Hemoglobin** Gene



Sickle Cell Anemia

- **Most common genetic disease in US**
 - ◆ high incidence in African-Americans
 - ◆ affects red blood cells
 - ◆ potentially lethal



10 μ m

Val	His	Leu	Thr	Pro	Glu	Glu	...
1	2	3	4	5	6	7	

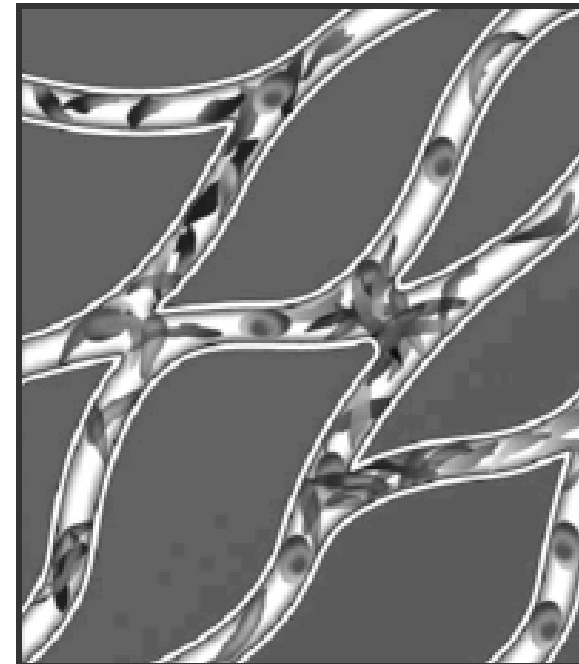


10 μ m

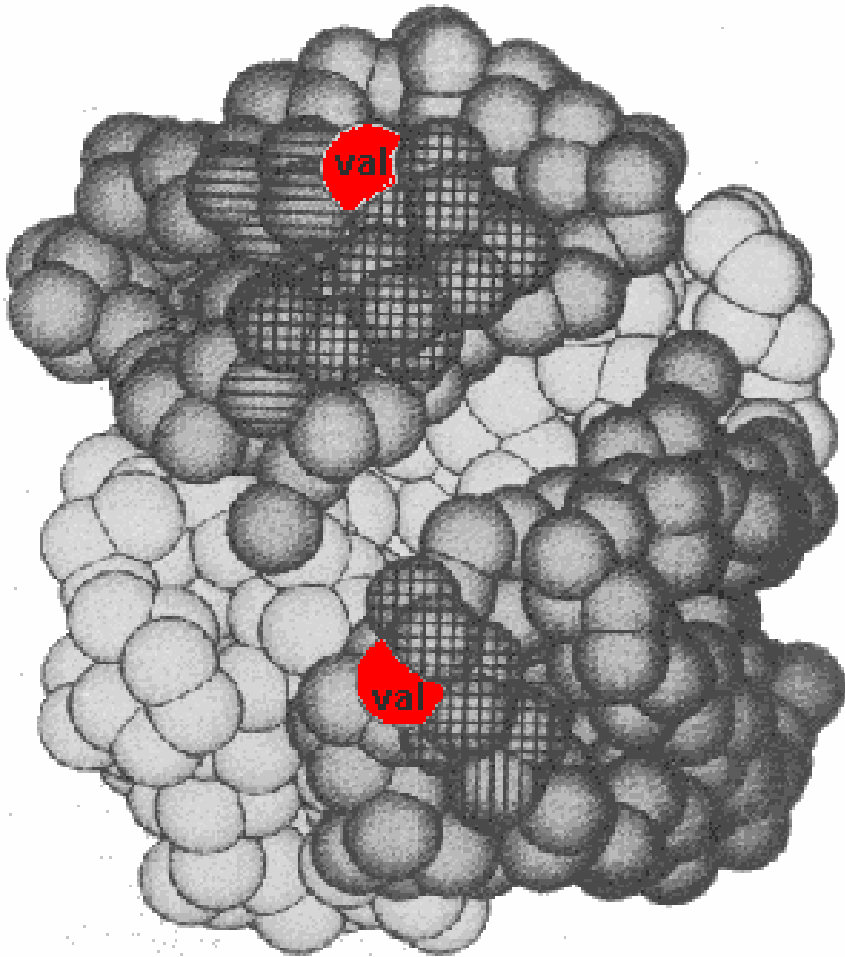
Val	His	Leu	Thr	Pro	Val	Glu	...
1	2	3	4	5	6	7	

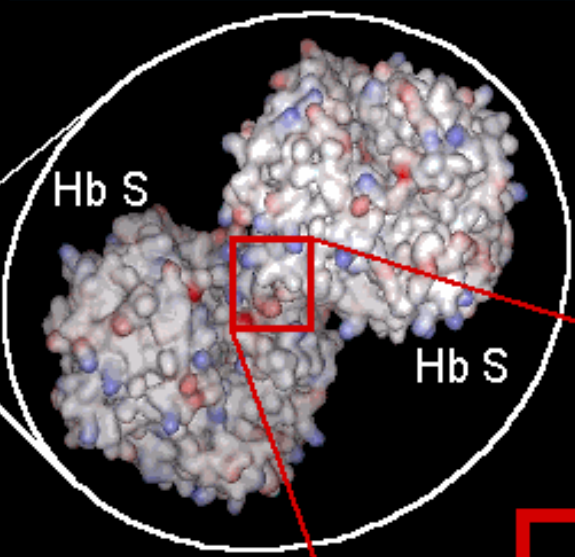
Symptoms

- **Anemia**
 - ◆ jaundice, fatigue, paleness, shortness of breath
- **Hypoxia (low oxygen) & capillary damage**
 - ◆ severe pain in organs & joints
 - ◆ retinal damage (blindness)
- **Delayed growth**
 - ◆ delayed puberty, stunted growth
- **Infections**
 - ◆ more susceptible
 - ◆ depressed immune
 - ◆ death from bacterial infections
- **Stroke**
 - ◆ blocked small blood vessels in brain
 - ◆ primarily in children

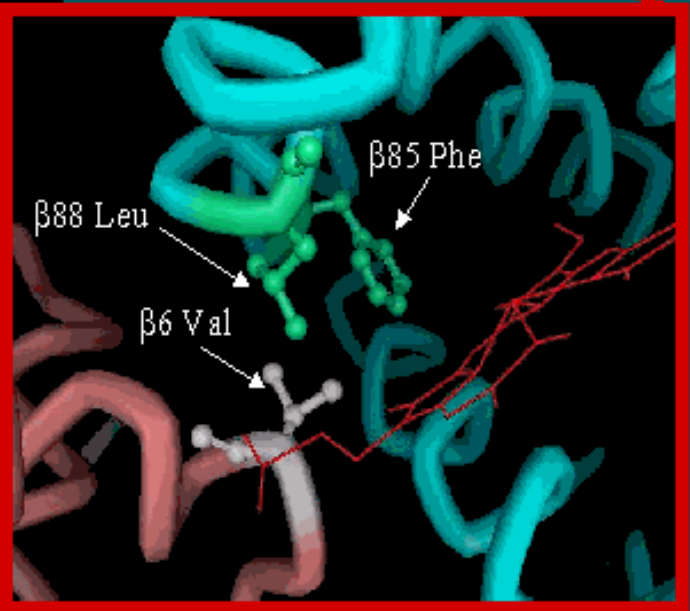


Sickle cell hemoglobin





Hemoglobin S: $\beta 6 \text{ Glu} \rightarrow \text{Val}$



Cell biology

- **Hb S molecules stick together**
 - ◆ form fibers
 - ◆ under low blood oxygen levels
 - ◆ distortion of cells from normal round to sickle shape







Genetics

▪ Sickle cell mutation

- ◆ Hb S
- ◆ changes 6th amino acid of β hemoglobin chain
- ◆ normal glutamic acid \rightarrow valine

▪ Recessive allele

- ◆ heterozygote
 - Hb AS, normal, but carrier
- ◆ homozygote recessive
 - Hb SS, sickle cell disease
- ◆ 2 sickle cell carriers mate...
 - each child has 1/4 chance of having the disease

	Hb A	Hb S
Hb A	 HbAA	 HbAS
Hb S	 HbAS	 HbSS

Prevalence in U.S.

■ Carriers

- ◆ ~2 million Americans carry sickle cell trait
- ◆ 1 in 14 African-Americans

■ Disease

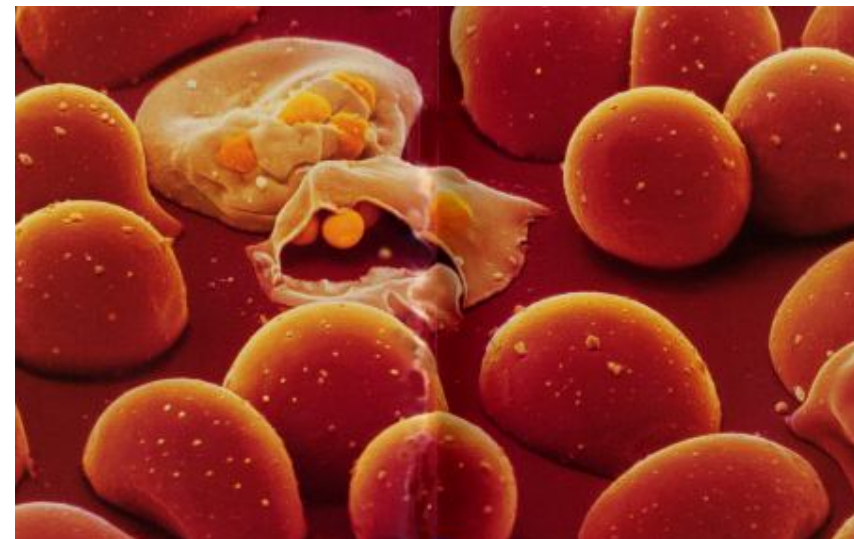
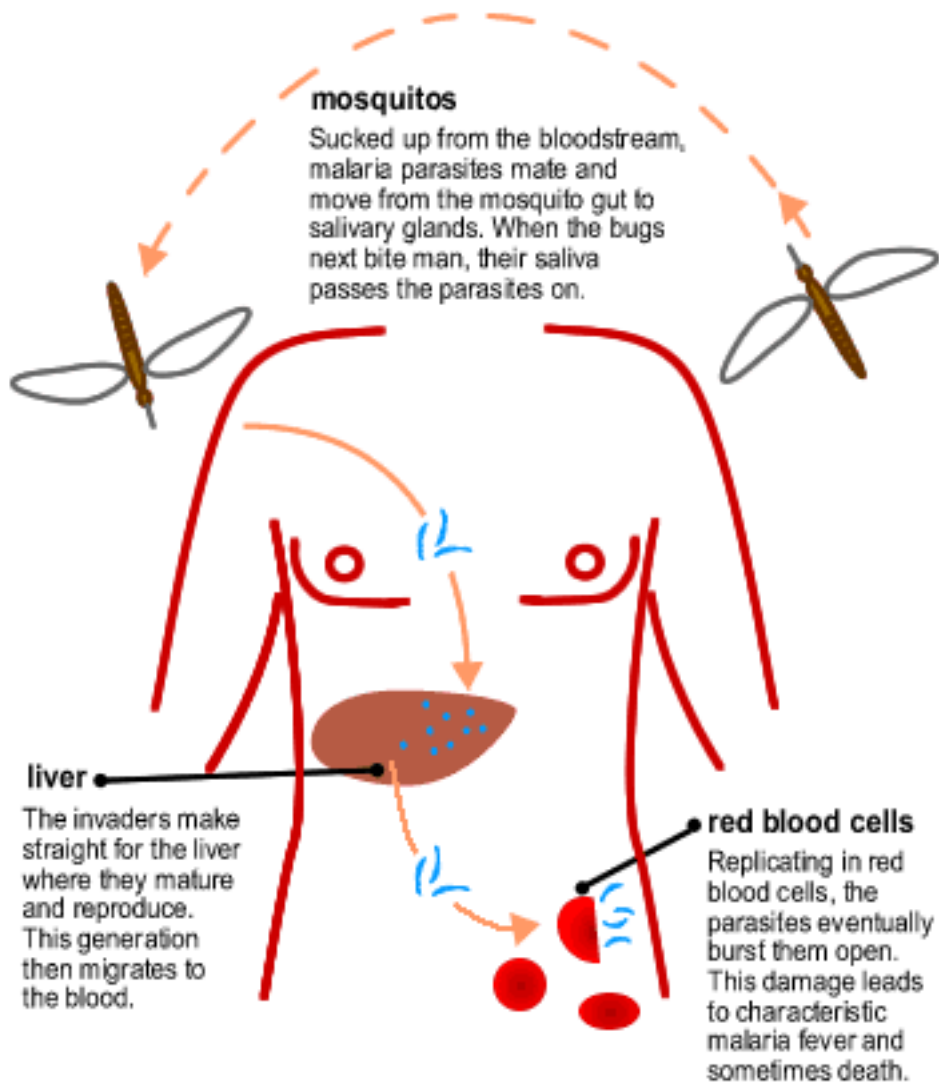
- ◆ ~72,000 Americans have disease
- ◆ ~1 in every 700 African-American babies born in U.S. has sickle cell disease

The Malaria Connection

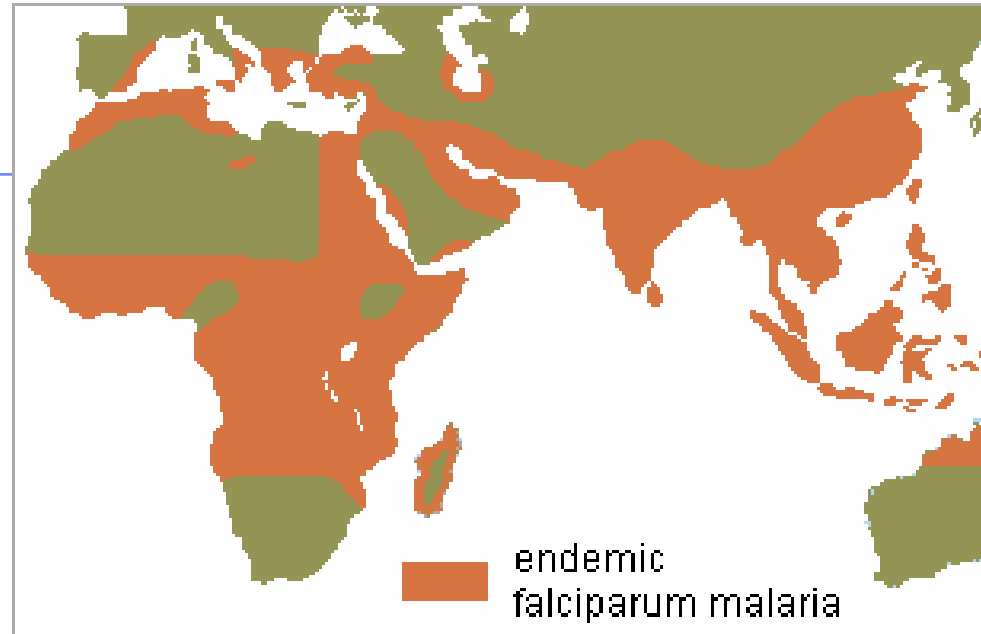
- Sickle cell disease is surprisingly common for a potentially lethal genetic disease
- Heterozygote advantage
 - ◆ heterozygotes are tolerant of malaria infection & do not suffer symptoms of sickle cell disease



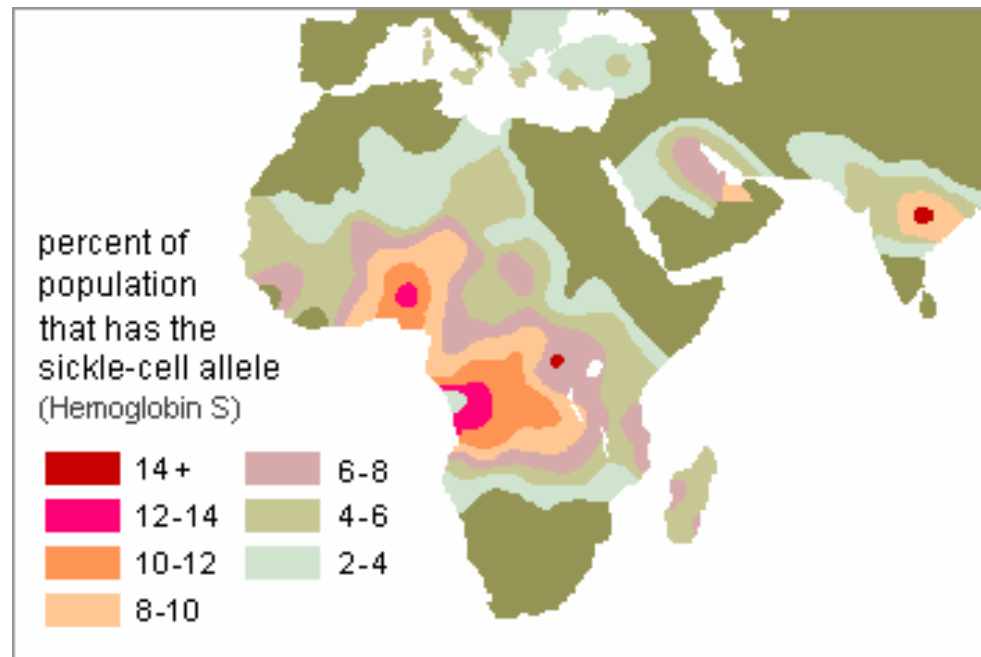
Malaria



Prevalence of Malaria



Prevalence of Sickle Cell Anemia



[~sickle cell movie~](#)

Public health

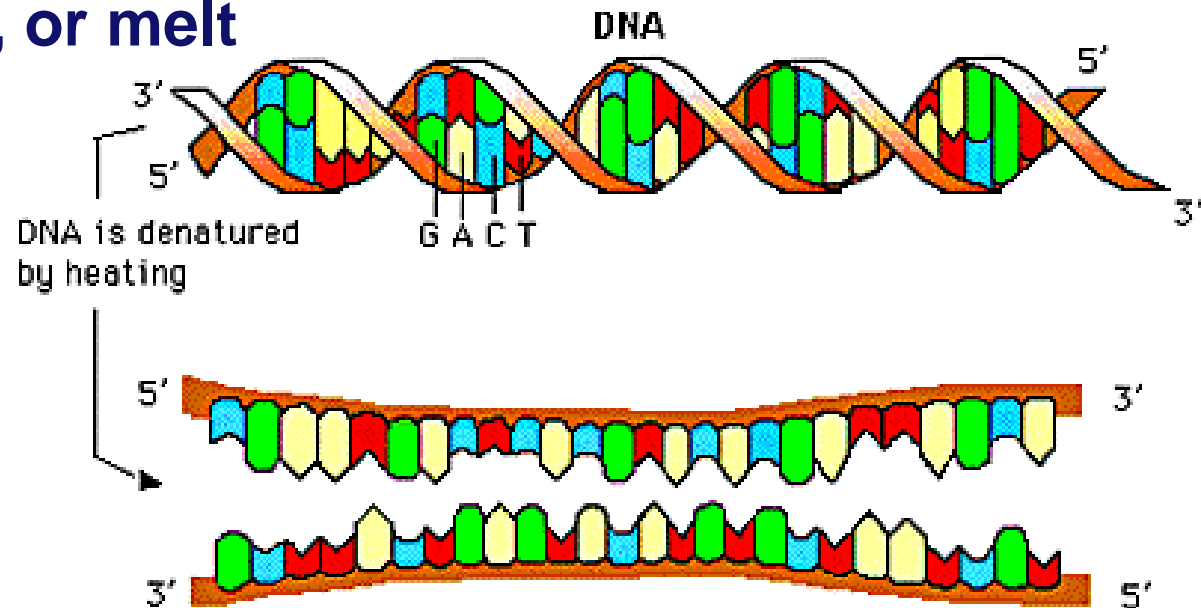
- **Many carriers of this mutant allele are not aware that they have it**
 - ◆ at risk of having children with the disease
- **DNA test for sickle cell allele would benefit public health**
 - ◆ genetic counseling
 - ◆ pre-natal testing

Your Assignment

- **Develop a simple inexpensive DNA test for sickle cell allele**
 - ◆ **develop DNA probe**
 - **test for presence of sickle cell mutation**
 - ◆ **use bioinformatics tools**
 - **online databases of DNA sequences**
 - ◆ **UCSC Genome Browser**
 - **probe design tool**
 - ◆ **Primer3**

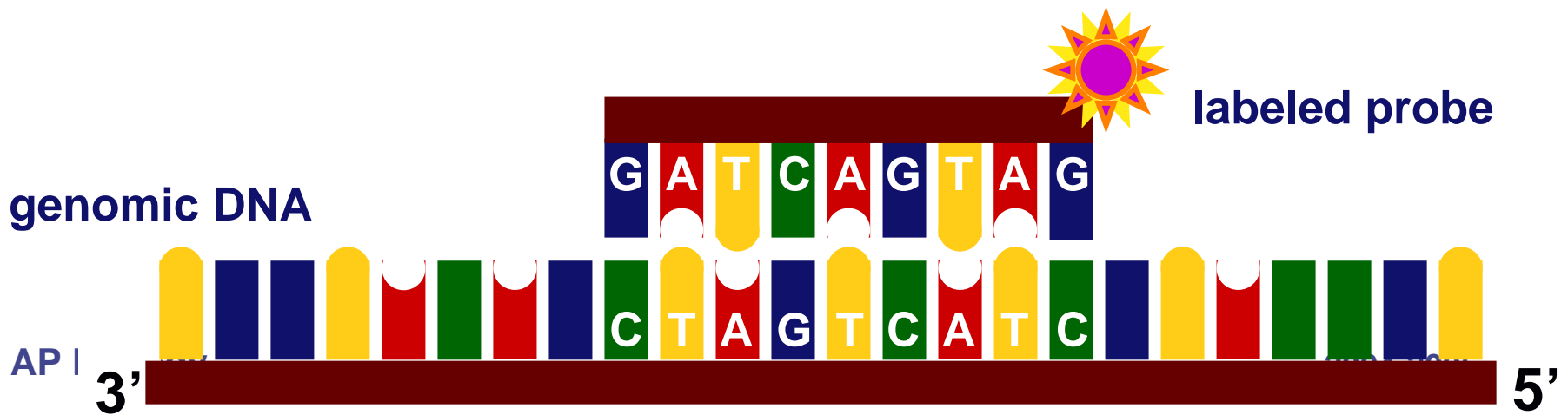
DNA review

- DNA double helix
 - ◆ A–T, C–G
 - ◆ base pair bonds can be broken by heating to 100°C
 - separate strands
 - denature, or melt



DNA probes

- **Probe**
 - ◆ short, single stranded DNA molecule
 - ◆ mix with denatured DNA
- **DNA Hybridization**
 - ◆ probe bonds to complementary DNA sequence
- **Label**
 - ◆ probe is labeled for easy detection



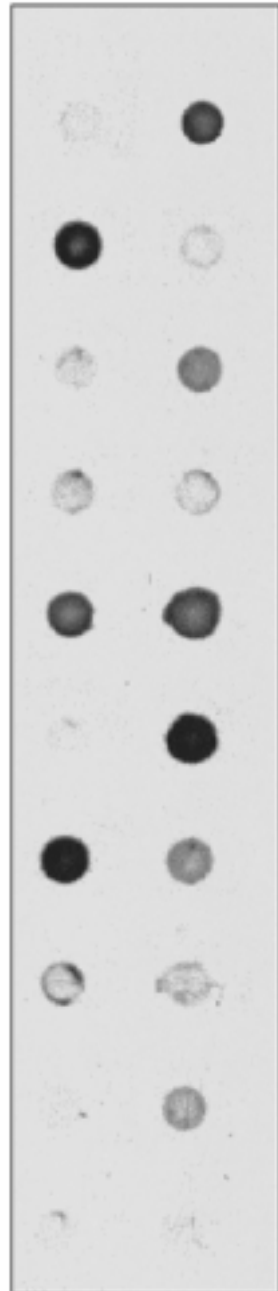
Designing Probes

- **Allele specific probes**
 - ◆ probes require matched sequences
 - ◆ can detect single base differences in alleles
 - ◆ single mis-matched base near middle of probe greatly reduces hybridization efficiency



Dot blot

- **Genomic DNA**
 - ◆ denature DNA
 - ◆ bind DNA from cells on filter paper
- **DNA hybridization**
 - ◆ wash probe over filter paper
 - ◆ if complementary sequence present, probe binds to genomic DNA
 - ◆ expose on X-ray film
 - dark spots show bound probe



Get hemoglobin sequence

- UCSC Genome Browser
 - ◆ human genome database
 - ◆ <http://genome.ucsc.edu/>
 - UCSC Genome Browser home page
 - click on link to Genome Browser
 - in genome pulldown menu, choose “Human”
 - for position text box, type “HBB” (hemoglobin β)
 - hit “submit”

Human Genome Browser Gateway

The UCSC Genome Browser was created by the [Genome Bioinformatics Group of UC Santa Cruz](#).
Software Copyright (c) The Regents of the University of California. All rights reserved.

genome	assembly	position	image width	
Human	July 2003	HBB	620	<input type="button" value="Submit"/>

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

Genome Browser Results

- Listing of genes & sequences in database
 - ◆ Click on “RefSeq” gene for HBB (NM_000518)

Known Genes

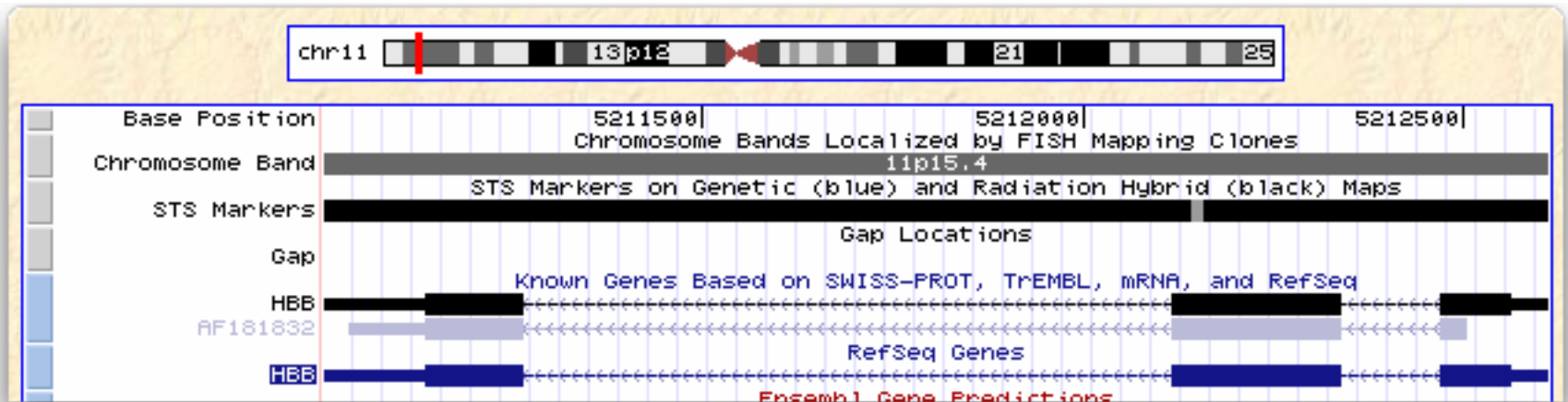
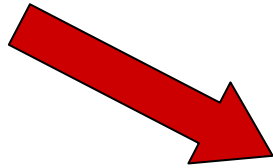
[HBB at chr11:5203302-5204770](#) - (AF181832) Hemoglobin beta subunit variant (Fragment).
[HBB at chr11:5203270-5204877](#) - (BC007075) hemoglobin, beta
[HBBP at chr3:45240961-45242758](#) - (AF438313) Ras-induced senescence 1 (P40BBp).

RefSeq Genes

[HBB at chr11:5203271-5204877](#) - (NM_000518) beta globin



Chromosome view

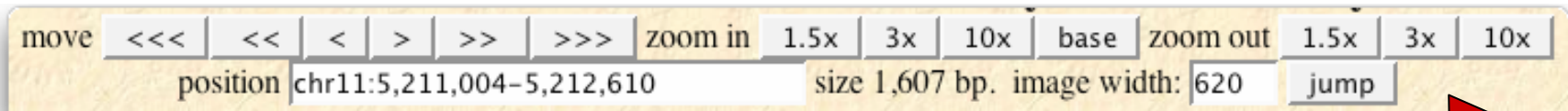


- Position of HBB in genome
 - ◆ at base 5.2 million on chromosome 11

Change view of chromosome

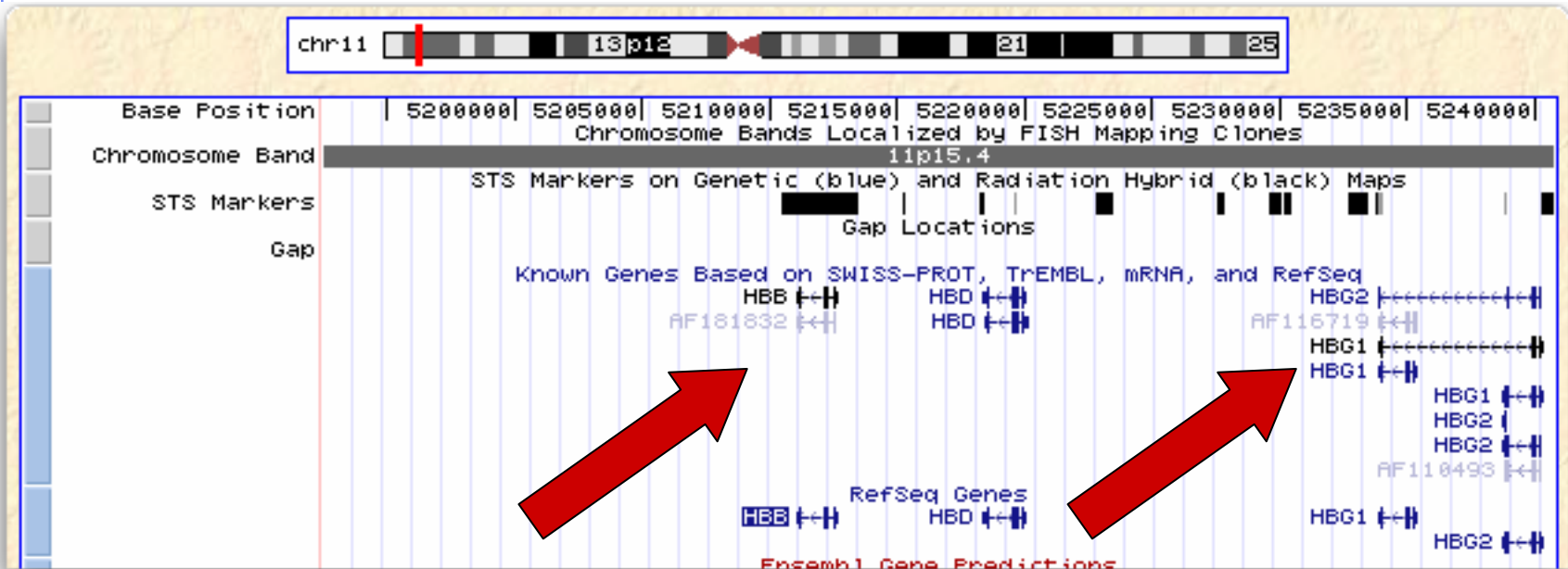
- **Move & zoom tools**

- ◆ zoom out ~30x to see more of chromosome 11

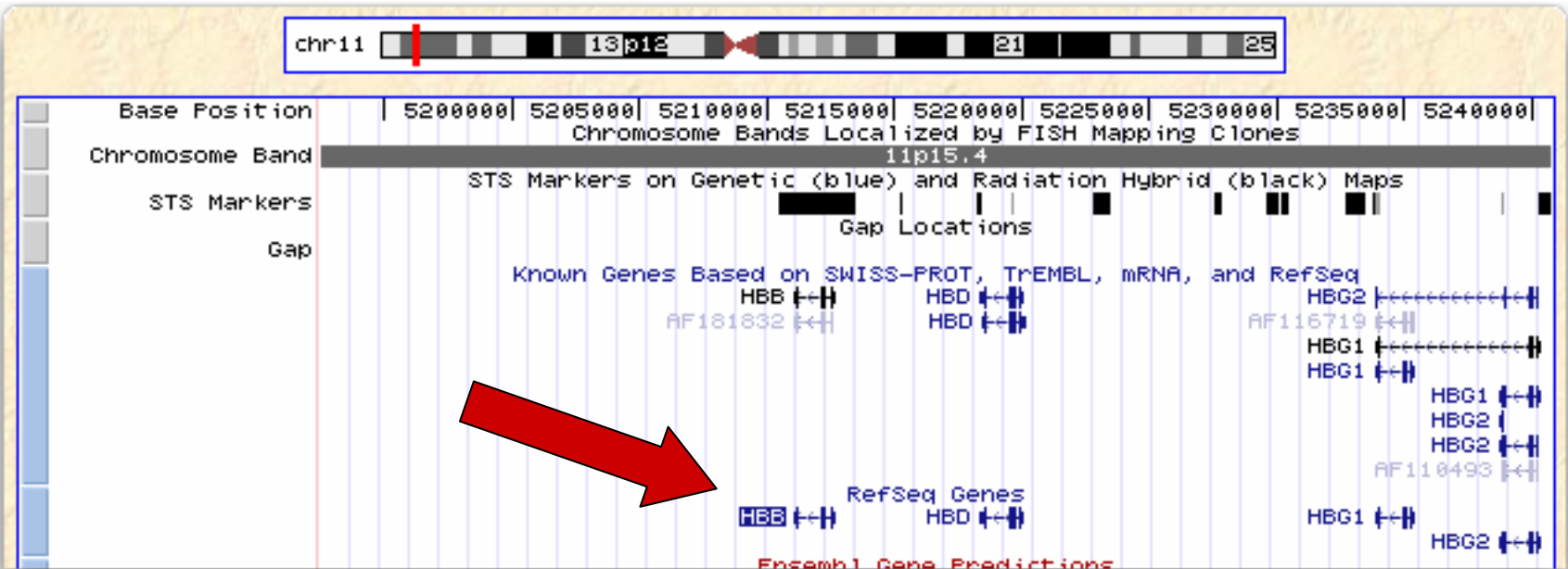


More Hb genes

- Cluster of hemoglobin genes on chromosome 11
 - HBD, HBG1, HBG2 & HBE1
 - what are these genes?



Get the DNA sequence



- Click on the HBB RefSeq gene
 - ◆ HBB RefSeq summary page

HBB RefSeq gene summary page

Position: [chr11:5211005-5212610](#)

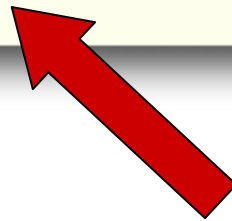
Band: 11p15.4

Genomic Size: 1606

Strand: -

Links to sequence:

- [Predicted Protein](#)
- [mRNA Sequence](#) may be different from the genomic sequence.
- [Genomic Sequence](#) from assembly



- Click on “Genomic Sequence from assembly”

Formatting the sequence

- **Sequence Formatting Options**
 - ◆ “exons in upper case, everything else in lower case”
 - ◆ hit “submit”
- **Genomic DNA**
 - ◆ lower case = introns
 - spliced out of mRNA before translation
 - ◆ upper case = exons
 - translated into polypeptide chain

HBB DNA sequence

>hg16_refGene_NM_000518 range=chr11:5211005-5212610 5'pad=0 3'pad=0 revComp=TRUE

ACATTTGCTTCTGACACAACCTGTGTTCACTAGCAACCTCAAACAGACACC

ATGGTGCATCTGACTCCTGAGGAGAAGTCTGCCGTTACTGCCCTGTGGGG

CAAGGTGAACGTGGATGAAGTTGGTGGTGAGGCCCTGGGCAGgttggtat

caaggttacaagacaggtttaaggagaccaatagaaactgggcatgtgga

gacagagaagactccttgggtttctgataggcactgactctctctgcctat

tggctctatccccacccttagGCTGCTGGTGGTCTACCCTTGGACCCAG

AGGTTCTTTGAGTCCTTTGGGGATCTGTCCACTCCTGATGCTGTTATGGG

CAACCCTAAGGTGAAGGCTCATGGCAAGAAAGTGCTCGGTGCCTTTAGTG

ATGGCCTGGCTCACCTGGACAACCTCAAGGGCACCTTTGCCCACTGAGT

GAGCTGCACTGTGACAAGCTGCACGTGGATCCTGAGAACTTCAGGgtgag

tctatgggacgcttgatgttttctttccccttcttttctatggttaagtt

catgtcataggaaggggataagtaacaggggtacagtttagaatgggaaac

agacgaatgattgcatcagtggtgaagtctcaggatcgtttttagtttctt

ttatgtgctgttcataacaattgttttcttttgtttaattcttgctttct

tttttttcttctccgcaattttactattatacttaatgccttaacatt

gtgtataacaaaaggaaatatctctgagatacattaagtaacttaaaaa

aaactttacacagtctgcctagtagtactatgtggaatatatgtgtgc

ttatgtgcatattcataatctccctactttattttcttttatttttaatt

gatacataatcattatacatatttatgggttaaagtgtaatgttttaata

tgtgtacacatattgaccaaatacagggttaattttgcatttgtaattttaa

aaaatgctttcttcttttaataacttttttgttatcttattttctaata

ctttccctaactcttttctttcagggcaataatgatacaatgtatcatgc

ctctttgcaccattctaaagaataacagtgataatctctgggttaaggca

atagcaatatctctgcatataaatatctctgcatataaatgtaactgat

- first 50 bases are untranslated “leader” sequence
- actual protein coding sequence starts at base 51
 - ◆ starting with letters **ATG**

Get the mutant sequence

- **Sickle cell mutation**
 - ◆ single base mutation
 - ◆ 6th amino acid: **glutamic acid** → **valine**
 - ◆ need DNA sequence to design probe
- **SNPs**
 - ◆ single nucleotide polymorphisms
 - ◆ “variations and repeats” section: **pack**

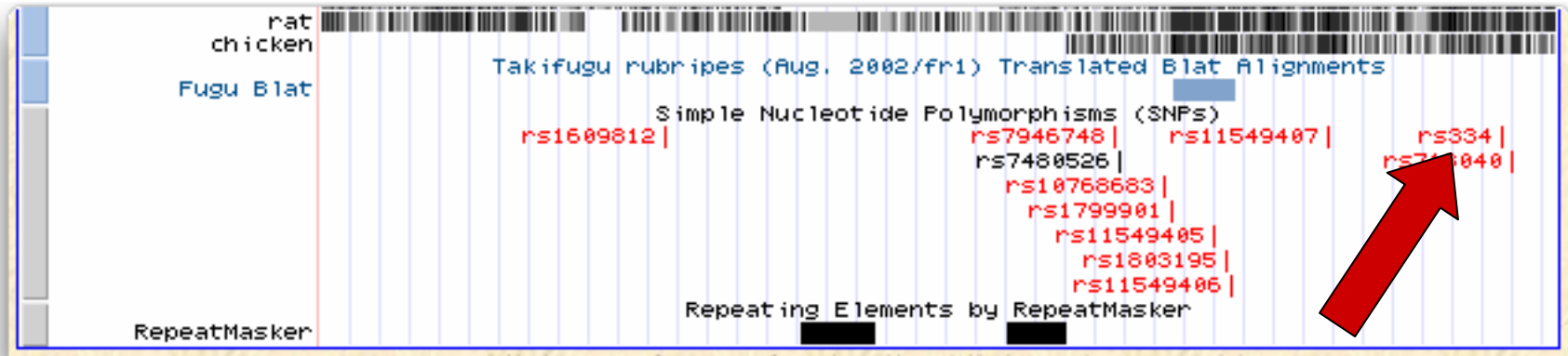


Variation and Repeats

SNPs pack ▾	Perlegen Haplotypes [No data-chr11]	Haplotype Blocks [No data-chr11]	Segmental Dups hide ▾	RepeatMasker dense ▾
Simple Repeats hide ▾	Microsatellites hide ▾	Self Chain hide ▾		

refresh

SNPs of HBB gene



- several SNPs of HBB gene
 - ◆ need mutation in exon
 - ◆ near beginning of HBB protein
 - ◆ **rs334 = Hb S** mutation

rs334 Hb S sickle cell mutation

- “Sequence in Assembly” = normal sequence
- “Alternate Sequence” = sickle cell sequence

Simple Nucleotide Polymorphism (SNP) rs334

Position: [chr11:5212541-5212541](#)

Band: 11p15.4

Genomic Size: 1

[View DNA for this feature](#)

[Average Heterozygosity](#): Not Known

[Standard Error of Avg. Het.](#): Not Known

Functional Status: coding-nonsynon, reference

[Validation Status](#): no-information

Allele1: A

Allele2: T

Sequence in Assembly: catggtgcacctgactcctgAggagaagtctgccgttactg

Alternate Sequence: catggtgcacctgactcctgTggagaagtctgccgttactg

[Variant Source](#): OTHER

[Variant Type](#): SNP



Align Hb A & Hb S sequences

- Line up sequences

Normal: catggtgcacctgactcctgA ggagaagtctgccgttactg

HBB:

ATGGTGCATCTGACTCCTGAGGAGAAGTCTGCCGTTACTGCCCTGTGGGG

Mutant: catggtgcacctgactcctgTggagaagtctgccgttactg

- ◆ sequence fragment is enough to design DNA probes for normal & mutant sequences

Designing the probe

■ Primer3

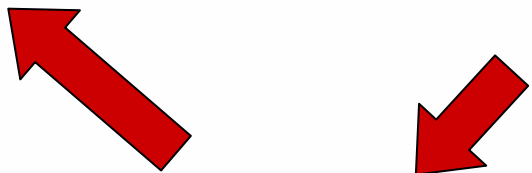
◆ free on Web from MIT

http://frodo.wi.mit.edu/cgi-bin/primer3/primer3_www.cgi

◆ powerful tool for primer design

■ paste in sequence fragment

Primer3	disclaimer	source code
pick primers from a DNA sequence	cautions	FAQ
Paste source sequence below (5'->3', string of ACGTNacgtn -- other letters treated as N -- numbers and blanks ignored). FA format ok. Please N-out undesirable sequence (vector, ALUs, LINEs, etc.) or use a Mispriming Library (repeat library) :		
NONE <input type="button" value="v"/>		
<code>catggtgcacc{tgactcctgTggagaagtc}tgccgttactg</code>		
<input type="checkbox"/> Pick left primer or use left primer below.	<input checked="" type="checkbox"/> Pick hybridization probe (internal oligo) or use oligo below.	<input type="checkbox"/> Pick right primer or use right primer below (5'->3' on opposite strand).



Allele specific probes

- Need 2 probes
 - ◆ normal allele probe
 - ◆ sickle cell allele probe
 - ◆ choose hybridization probes
- Customize probes
 - ◆ 12-16 bases
 - ◆ 40°-60°C

Hyb Oligo (Internal Oligo) General Conditions

<u>Hyb Oligo Size:</u>	Min	<input type="text" value="12"/>	Opt	<input type="text" value="14"/>	Max	<input type="text" value="16"/>
<u>Hyb Oligo Tm:</u>	Min	<input type="text" value="40.0"/>	Opt	<input type="text" value="50.0"/>	Max	<input type="text" value="60.0"/>
<u>Hyb Oligo GC%</u>	Min:	<input type="text" value="20.0"/>	Opt:	<input type="text"/>	Max:	<input type="text" value="80.0"/>

longer probes are stable
at higher temperatures

Your probes...

- Ready to order!

Primer3 Output

Using 1-based sequence positions

OLIGO	<u>start</u>	<u>len</u>	<u>tm</u>	<u>gc%</u>	<u>any</u>	<u>3'</u>	<u>seq</u>
INTERNAL_OLIGO	15	20	59.99	60.00	5.00	4.00	ctcctgTggagaagtctgcc

SEQUENCE SIZE: 41
INCLUDED REGION SIZE: 41

```
1 catggtgcacctgactcctgTggagaagtctgccgttactg
      ^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^
```



- Place an order at your local DNA lab!