Mapping a *simple* genetic trait relative to genetic markers in a cross

We can use HapMap markers like Drosophila mutations to map simple diseases!

- Score offspring of **ABC/abc x abc/abc**
  - "**A**" and "**B**" can be SNPs with known locations
  - "**C**" is the disease gene (cc = diseased)

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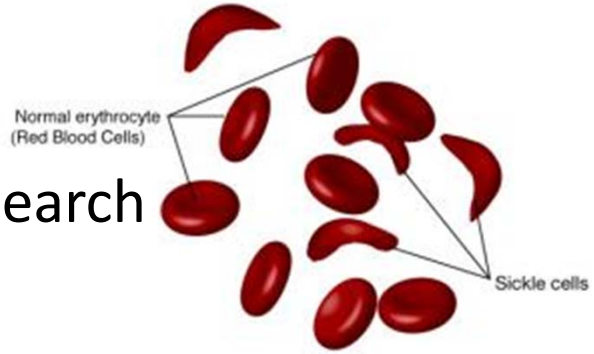
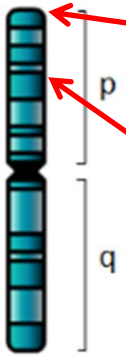
- Determine whether C is between A and B, and approximately how far away
  - Tells relative location of disease gene!

Hypothetical example : sickle cell anemia (recessive)

- Have multiple cases of carriers having kids with affected individuals
  - Have genotypes for parents and offspring
- Know it's on chromosome 11 from past research
- Have two genetic markers:
  - "A" marker is a known C/T SNP
    - Location: 11p15.6
    - AA = C/C, Aa = C/T, aa = T/T
  - "B" marker is a known A/C SNP
    - Location: 11p12.3
    - BB = A/A, Bb = A/C, bb = C/C





Hypothetical example : sickle cell anemia

- Offspring of **AB/ab(carrier) x ab/ab(diseased)**
  - AB/ab: 416 healthy; 1 diseased
  - ab/ab: 0 healthy; 426 diseased
  - Ab/ab: 72 healthy; 3 diseased
  - aB/ab: 4 healthy; 78 diseased

- **Speculate about which marker (A or B) is closer to the disease-causing gene.**

Hypothetical example : sickle cell anemia

- Offspring of **AB/ab(carrier) x ab/ab(diseased)**
  - AB/ab: 416 healthy; 1 diseased
    - Another gene (C) causes disease, so split row above:
      - ABC/abc: 416 healthy
      - ABc/abc: 1 diseased
  - ab/ab: 0 healthy; 426 diseased
  - Ab/ab: 72 healthy; 3 diseased
  - aB/ab: 4 healthy; 78 diseased

- **Speculate about which marker (A or B) is closer to the disease-causing gene.**

Hypothetical example : sickle cell anemia

- Score offspring of **ABC/abc x abc/abc**
  - ABC/abc: 416 — Healthy (Cc)
  - abc/abc: 426 — Diseased (cc)
  - AbC/abc: 72 — Healthy
  - aBc/abc: 78 — Diseased
  - Abc/abc: 3 — Diseased
  - aBC/abc: 4 — Healthy
  - abC/abc: 0 — Healthy
  - ABc/abc: 1 — Diseased

Cc = healthy
cc = diseased

Hypothetical example : sickle cell anemia

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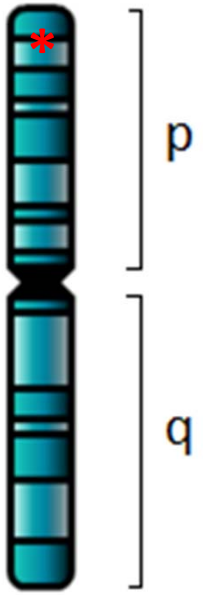
  - ABC/abc: 416 — Healthy (Cc)
  - abc/abc: 426 — Diseased (cc)
  - AbC/abc: 72 — Healthy
  - aBc/abc: 78 — Diseased
  - Abc/abc: 3 — Diseased
  - aBC/abc: 4 — Healthy
  - abC/abc: 0 — Healthy
  - ABc/abc: 1 — Diseased

Without doing ANY math, tell me the order of the genes:

A) ABC
B) ACB
C) CAB

Hypothetical example : sickle cell anemia



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  - AB/ab: 416 healthy; 1 diseased
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  - Ab/ab: 72 healthy; 3 diseased
  - aB/ab: 4 healthy; 78 diseased
- **A – C – B order**
  - **A-C : 0.8% rec; C-B : 15.1% rec**
  - **A** is at 11p15.6
  - **B** is at 11p12.3 *__C__ is near 11p15.5!*

A goal of “mapping” is to localize alleles at genes causing disease

- Some markers will be associated with the disease – these are likely “near” the associated gene
- Some markers will **not** be associated (or will be “more weakly associated”) with the disease – these are likely further away

Image Credits, Unit 5-2

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