CONCEPT: QTL MAPPING

● **Quantitative trait loci (QTL)** are locations of genes that control variation in complex (quantitative) ______________

□ **Quantitative traits** are any traits that can be measured (usually continuous)

□ **QTL Mapping** is the method for determining QTLs in the genome

□ The method of QTL ___________________ is as follows:

1. Mate two inbred lines with different traits (Ex: Tomato weight of 230g x tomato weight of 10g)

   - Produces intermediate F_1 generation

2. Backcross F_1 to the large tomato parents (230g)

   - Produces **back-cross 1** generation (BC_1)

3. Take DNA samples and determine genotype of BC_1 and Parental strains

   - Divide the genome into SNP markers

4. Calculate weight for each BC_1 tomato

   - Calculate mean for all BC tomatoes

   - Calculate mean for all BC tomatoes with the same markers

5. Determine if QTL is affecting fruit weight

   - If no QTL is affecting fruit weight then the overall mean will equal the “marker mean”

   - If QTL is affecting fruit weight then overall mean will not equal the “marker mean”

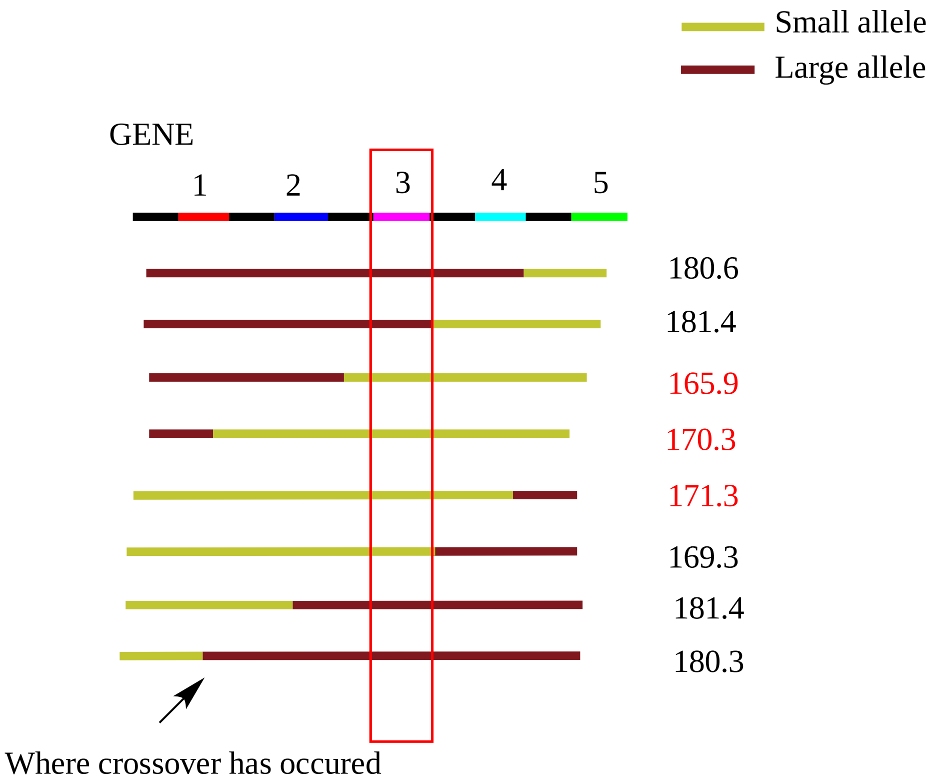
6. Use **lod scores** to statistically confirm your hypothesis

EXAMPLE: Example data from QTL Mapping

Plant	**Fruit Weight**	**Marker 1**	**Marker 2**	**Marker 3**	**Marker 4**
Overall mean weight	176.3	-	-	-	-
Weight of L/L		176.5	178.6	182.1	175.9
Weight of L/S		174.5	173.4	168.4	172.3

- Once the QTL is identified, the gene that causes the variation will need to be ____________________________
    - There can be 100+ genes in between two genomic markers used for sequencing
    - **Fine-mapping** is the method used to determine the gene from the QTL
        - Use **congenic stocks (nearly-isogenic):** are identical, but contain crossovers near QTLs

EXAMPLE:



QTL Mapping in Random-Mating Populations

- **Association mapping** can identify QTLs in genomes based on *linkage disequilibrium* between marker and QTL
    - □ **Linkage disequilibrium** is the nonrandom association of alleles at two loci (so alleles are not independent)
    - □ This method can be done in ____________________, as it tests many alleles at once & does not need crosses
        - It also does not require fine-mapping as it directly identifies the responsible gene at the QTL
    - □ The method of mapping using **genome-wide association studies** is as follows:
        1. Sequence genome of 2000 individuals with a disease and 2000 without a disease
            - Identify all SNPs in the genomes (HUGE amount of data)
        2. Statisticians determine if one SNP is more frequently associated with disease than other

EXAMPLE: