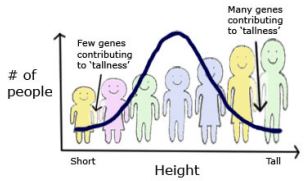
Module – Complex Trait (Quantitative) Genetics



Student Assessment Exercise starts at 08h55

202 Lecture 14 — Heritability and tools for finding the genes underlying complex traits

1. QTL analysis wrap-up (Ch19 Section 5) 2. Genome-Wide Association Studies (GWAS) (Ch19 Section 6)
• Note: We do not have time to cover narrow sense heritability
PRIMERs—Quantitative Genetics Reading: **Ch 19: 19.5, 19.6** **Textbook Questions : See myCourses.**

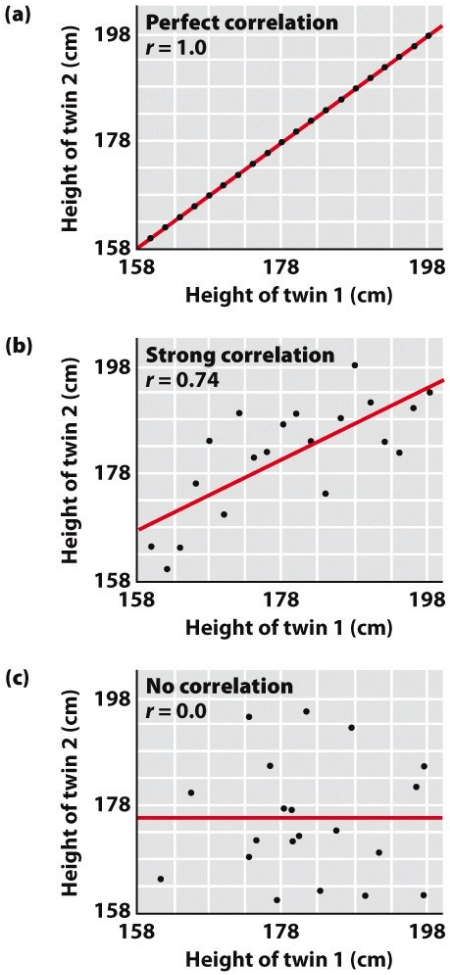
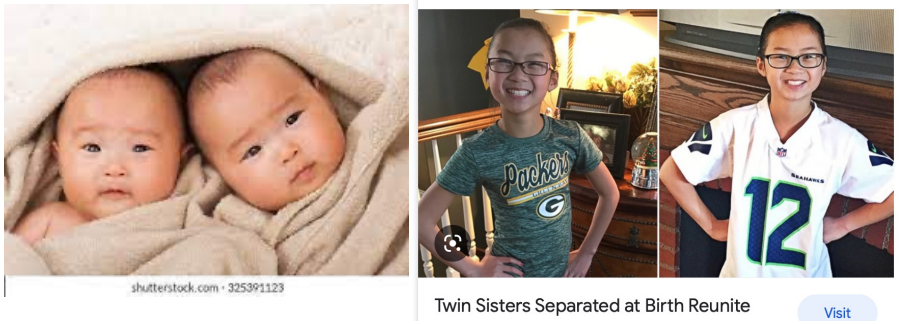


Figure 19-4
Introduction to Genetic Analysis, Tenth Edition

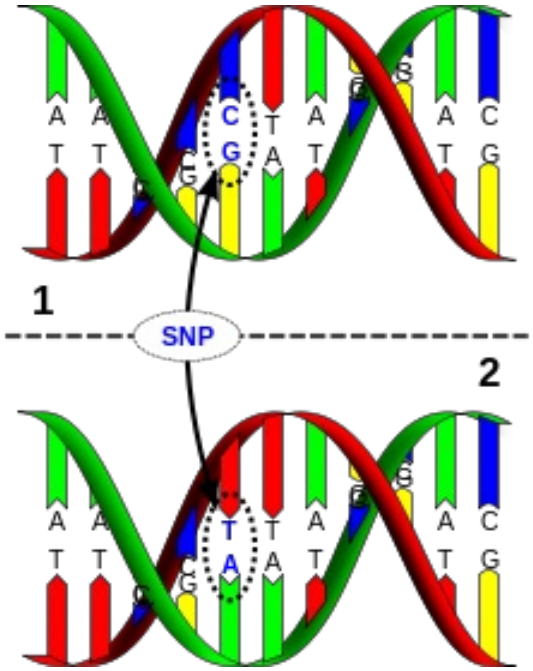


TWIN STUDIES:

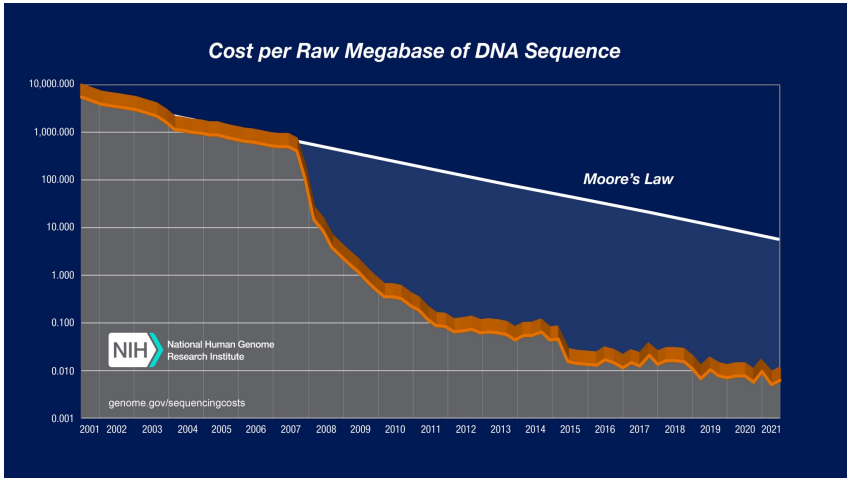
r = Correlation =

Broad Sense Heritability (H^2)

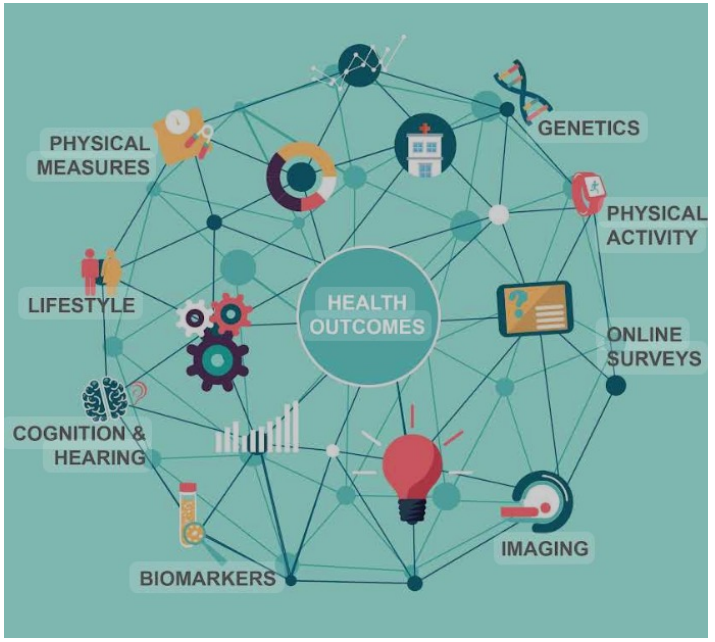
Quantitative Trait Locus mapping (QTLs and the genetic architecture of complex traits)



Genome-Wide Association Approach to Common and Complex Diseases



Low sequencing costs



Lots of data in "Biobanks" including sequence data

Genetic architecture of complex traits. Two basic approaches:

- **QTL mapping**…resembles classical mapping approaches (controlled crosses used to locate genes that influence the quantitative trait)
- **Association mapping** or **genome-wide association studies (GWAS**)…relies on population surveys (controlled crosses *not* used) to locate genes that influence the quantitative trait

Genetic architecture of complex traits. Two basic approaches:

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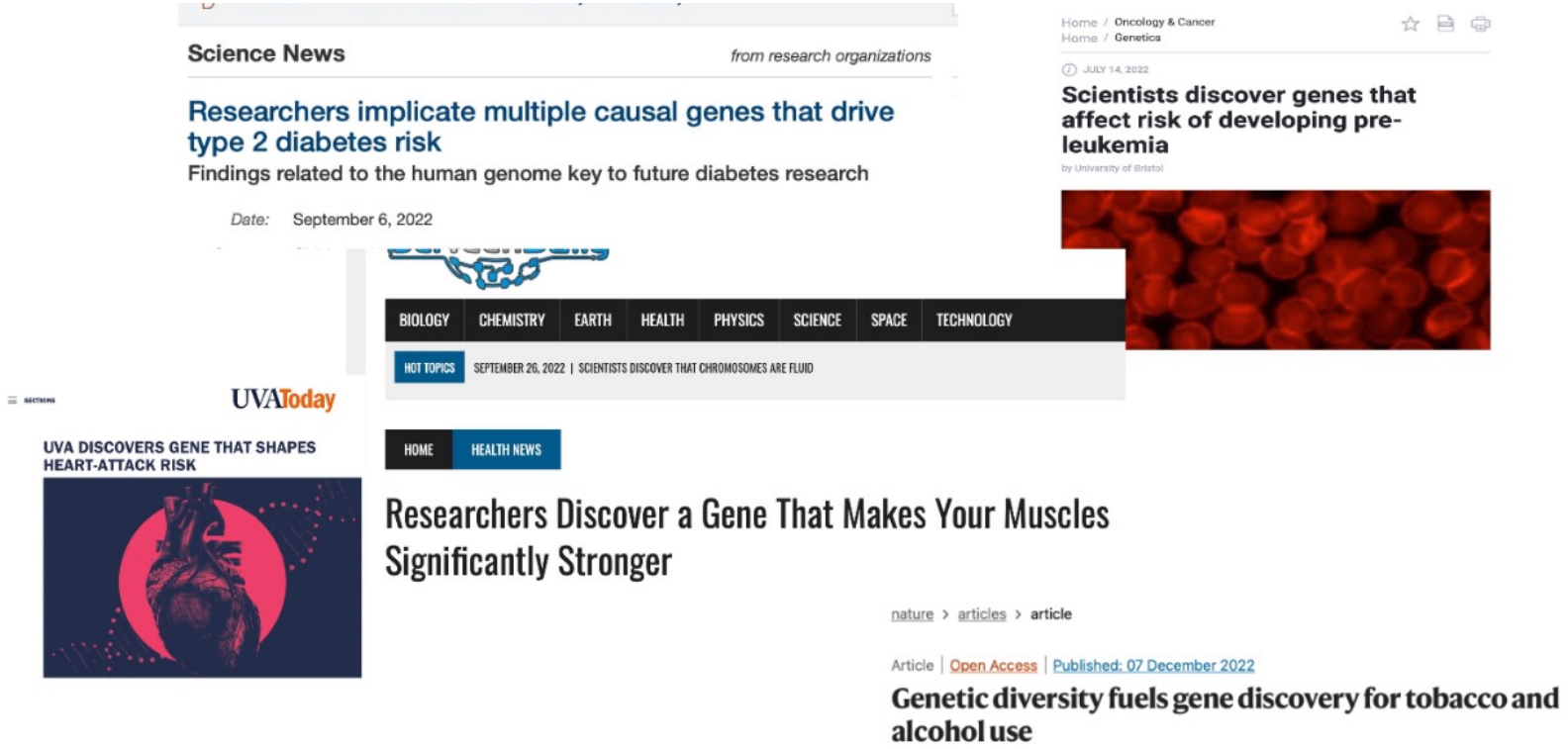
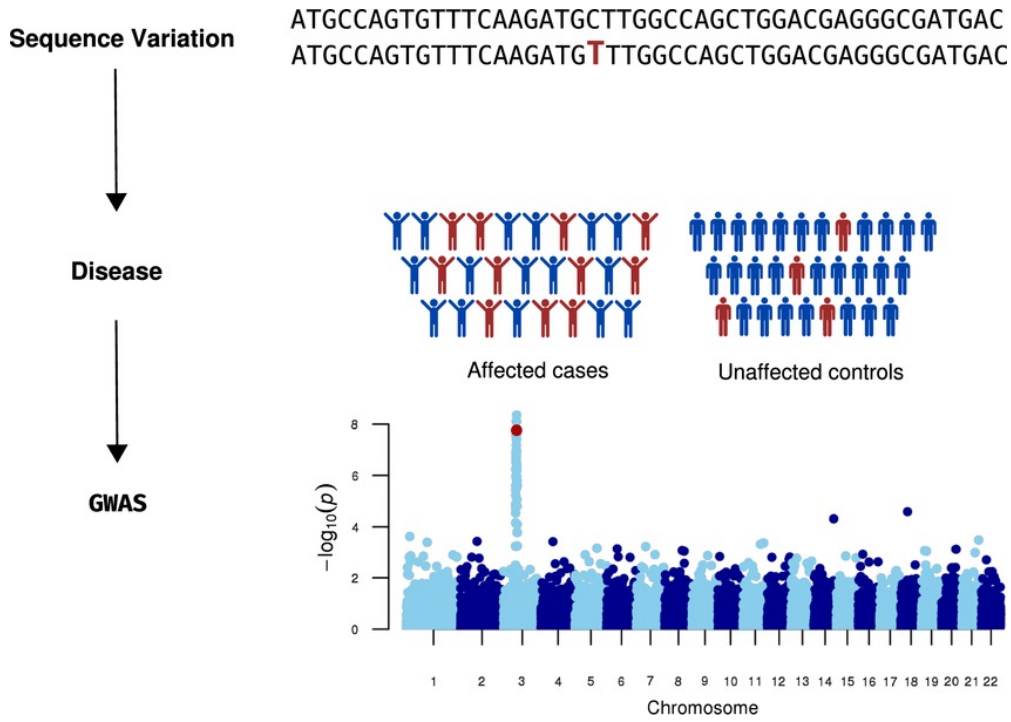
GWAS had been important in finding genetic risk factors for major diseases and other complex traits



Using SNPs to Track Predisposition to Disease and other Genetic Traits



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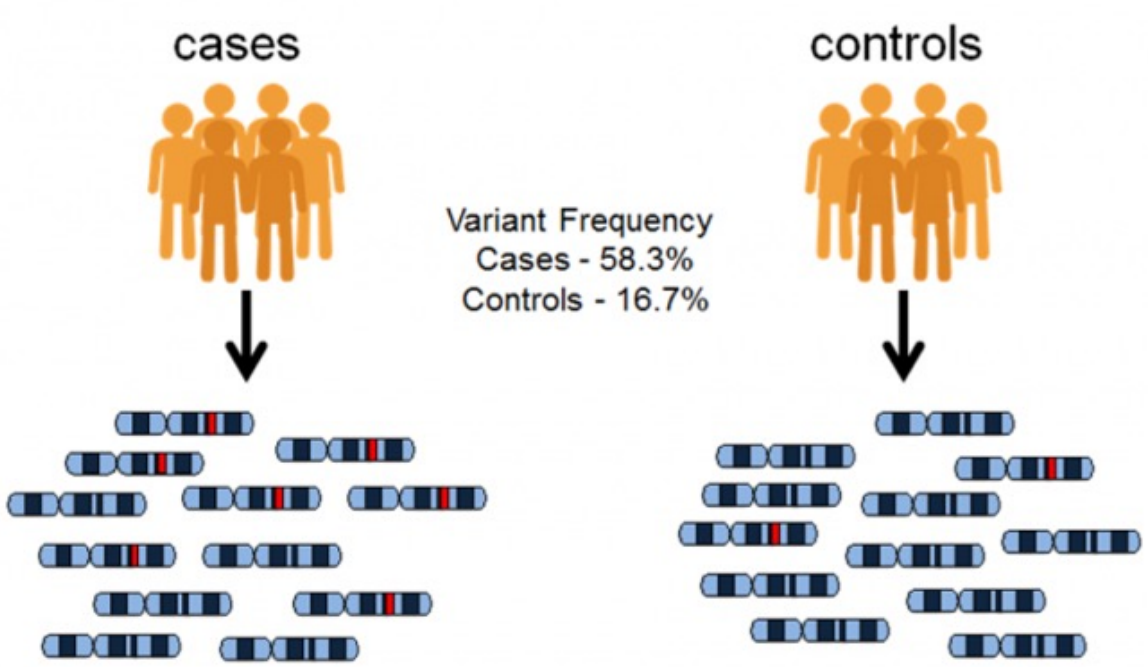
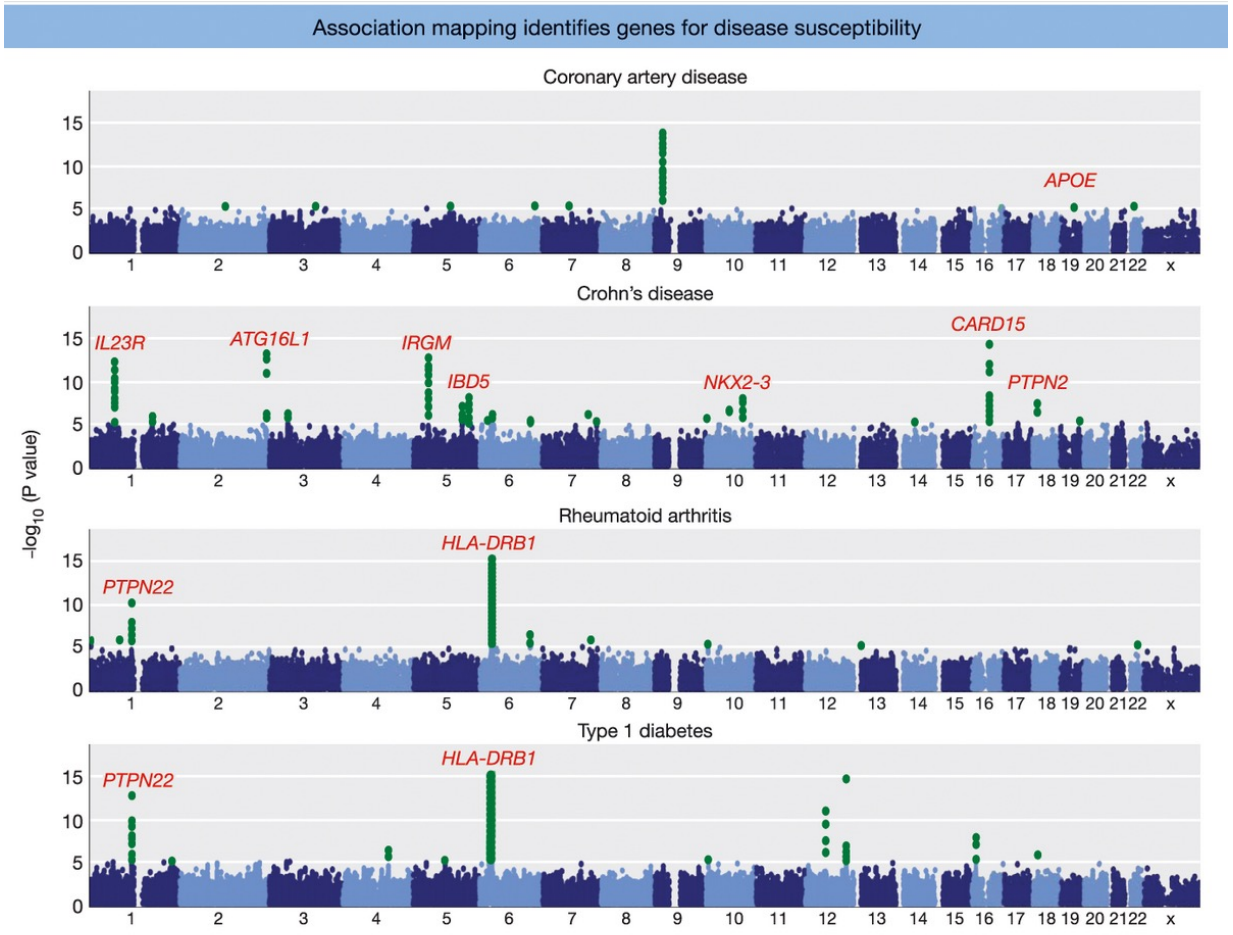
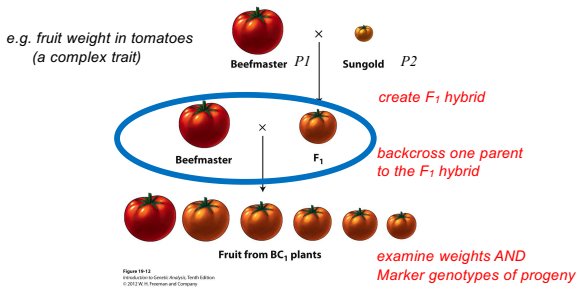
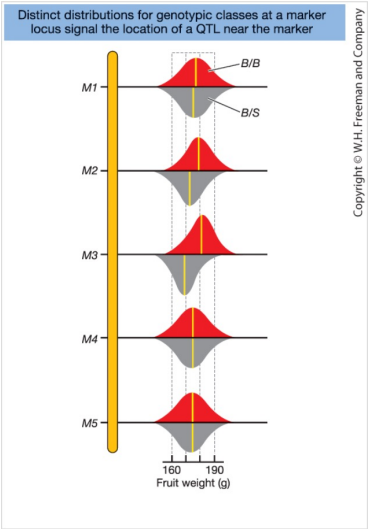



Association mapping identifies genes for disease susceptibility
Coronary artery disease
APOE
Crohn's disease
IL23R
ATG16L1
IRGM
IBD5
NKX2-3
CARD15
PTPN2
Rheumatoid arthritis
HLA-DRB1
PTPN22
Type 1 diabetes
HLA-DRB1
PTPN22
−log10 (P value)
0
5
10
15
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 x

Clinical Genetic Testing Direct to Consumer

QTL mapping begins with crosses of two inbred lines
(that differ in the trait of interest and their molecular marker genotypes)

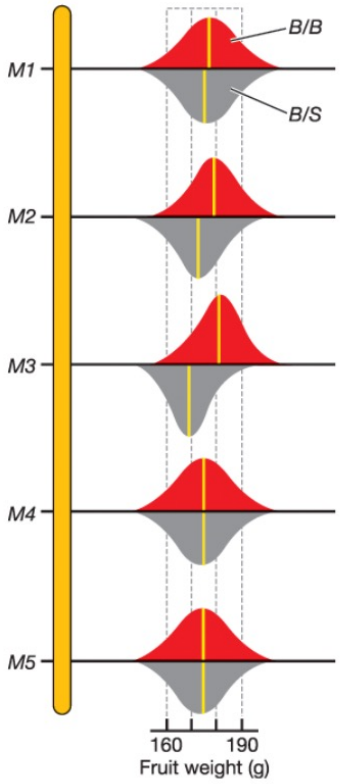




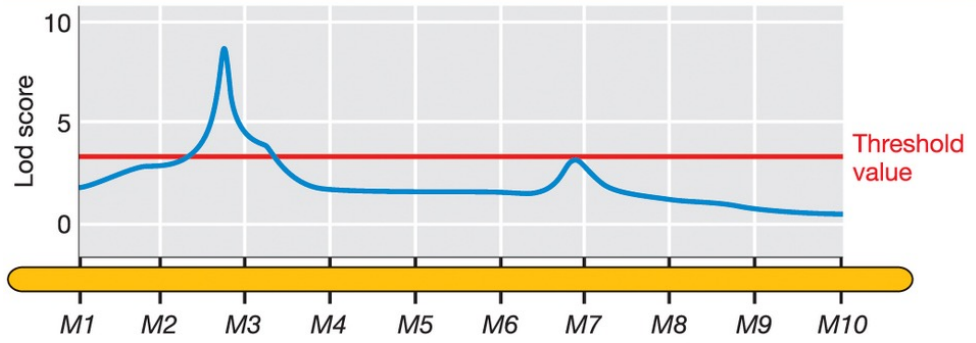
Population between Two Inbred Tomato Lines—Beefmaster and Sungold

		Markers				
Plant	**Fruit wt. (g)**	**M1**	***M2***	***M3***	***M4***	***M5***
Beefmaster	230	B/B	B/B	B/B	B/B	B/B
Sungold	10	S/S	S/S	S/S	S/S	S/S
BC_1–001	183	B/B	B/B	B/B	B/S	B/S
BC_1–002	176	B/S	B/S	B/B	B/B	B/B
BC_1–003	170	B/B	B/S	B/S	B/S	B/S
BC_1–004	185	B/B	B/B	B/B	B/S	B/S
BC_1–005	182	B/B	B/B	B/B	B/B	B/B
BC_1–006	170	B/S	B/S	B/S	B/S	B/B
BC_1–007	170	B/B	B/S	B/S	B/S	B/S
BC_1–008	174	B/S	B/S	B/S	B/S	B/S
BC_1–009	171	B/S	B/S	B/S	B/B	B/B
BC_1–010	180	B/S	B/S	B/B	B/B	B/B
BC_1–011	185	B/S	B/B	B/B	B/S	B/S
BC_1–012	169	B/S	B/S	B/S	B/S	B/S
BC_1–013	165	B/B	B/B	B/S	B/S	B/S
BC_1–014	181	B/S	B/S	B/B	B/B	B/S
BC_1–015	169	B/S	B/S	B/S	B/B	B/B
BC_1–016	182	B/B	B/B	B/B	B/S	B/S
BC_1–017	179	B/S	B/S	B/B	B/B	B/B
BC_1–018	182	B/S	B/B	B/B	B/B	B/B
BC_1–019	168	B/S	B/S	B/S	B/B	B/B
BC_1–020	173	B/B	B/B	B/B	B/B	B/B
Mean of B/B	—	176.3	179.6	180.7	176.1	175.0
Mean of B/S	—	175.3	173.1	169.6	175.3	176.4

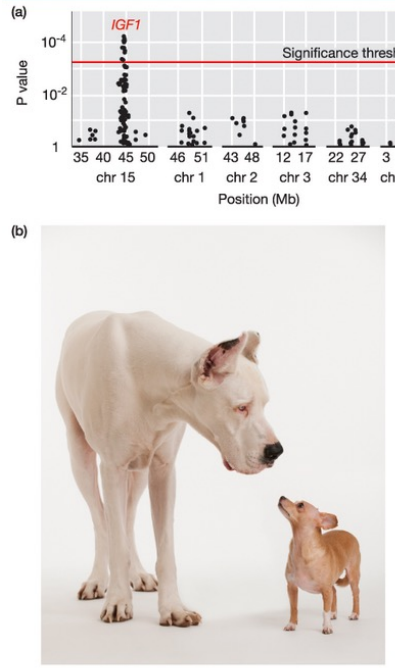
Distinct distributions for genotypic classes at a marker locus signal the location of a QTL near the marker



Lod scores provide statistical evidence for QTL



Association mapping finds a gene for body size in dogs



Wrap-up

Midterm questions to be selected from the following topics:

Hardy-Weinberg theory
Inbreeding (including calculation of *F* from pedigrees)
Forces that change allele frequencies in populations (mutation, migration, drift, selection)
Quantitative genetic variation, heritability, response to selection.
Tools for mapping the genes underlying complex traits (GWAS)