

Chromosomal inheritance and gene location

Chromosomal theory of heredity

- 1865- Mendel's research was published. But no evidence
- 1900- recognition of Mendel's research
- 1902- Sutton & Boveri – (Microscope, gene & chromosome)
- Hunt Morgan – eye gene - fruit fly

Mendel's theory	Sutton
Factors are in pairs (alleles)	Chromosomes have their genes Homologous pair
Factors separate at the time of gamete formation	Homologous pair are separate during gamete formation
Alleles on factors assort independently	Chromosome assort themselves independently

Chromosomal Theory of Inheritance

- Chromosomes contain the units of heredity (genes)
- Pair chromosomes segregate during meiosis, each sex cell has half of the number of chromosomes found in a somatic cell. (Mendel's law of segregation)
- Chromosomes assort independently during meiosis (Mendel's law of independent assortment)
- Each chromosome contain many different genes

Modes of Inheritance

Autosomal recessive alleles [silent carriers]
albinism, cystic fibrosis, certain types of
hemophilia, Tay-Sachs disease, PKU, blue
eyes.

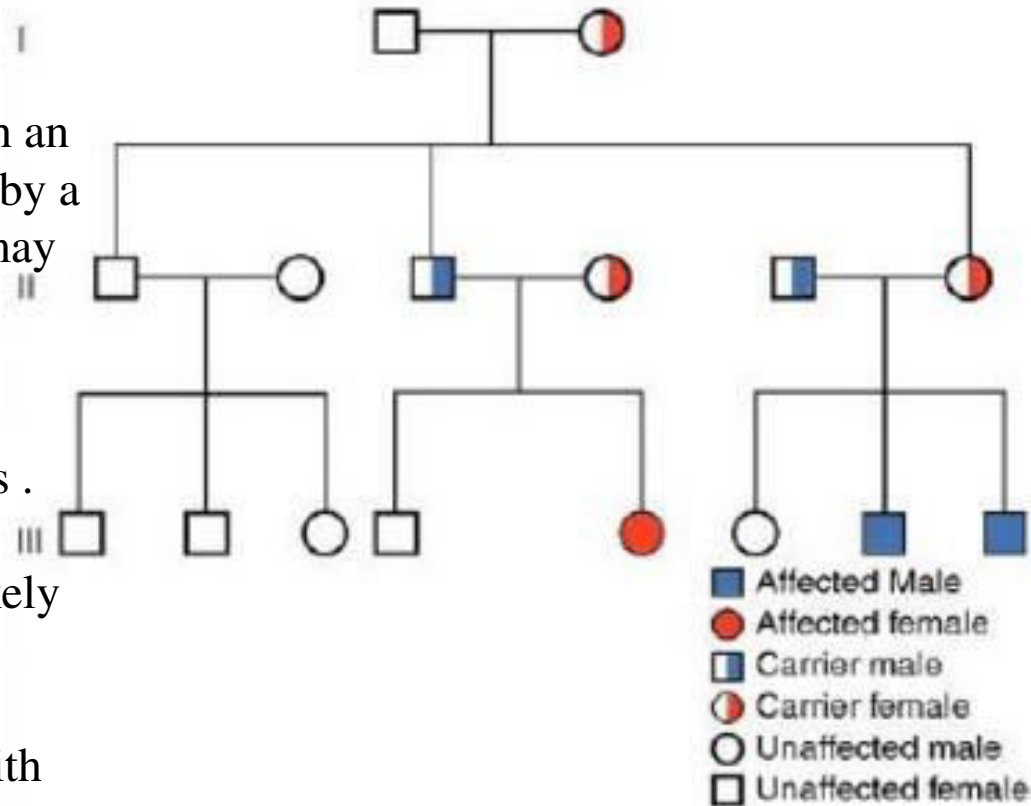
A pedigree following a trait associated with an
autosomal recessive allele is often marked by a
skipping of generations. That is, children may
express a trait which their parents do not.

In such a situation, both parents are
heterozygotes, also known as silent carriers .

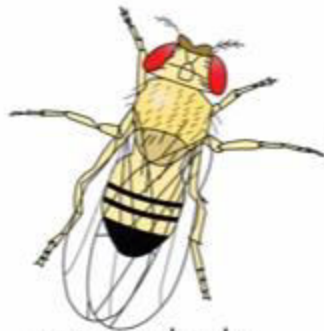
Close relatives who reproduce are more likely
to have affected children.

Both males and females will be affected with
equal frequency

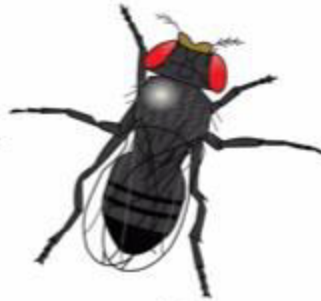
A low number of individuals normal affected



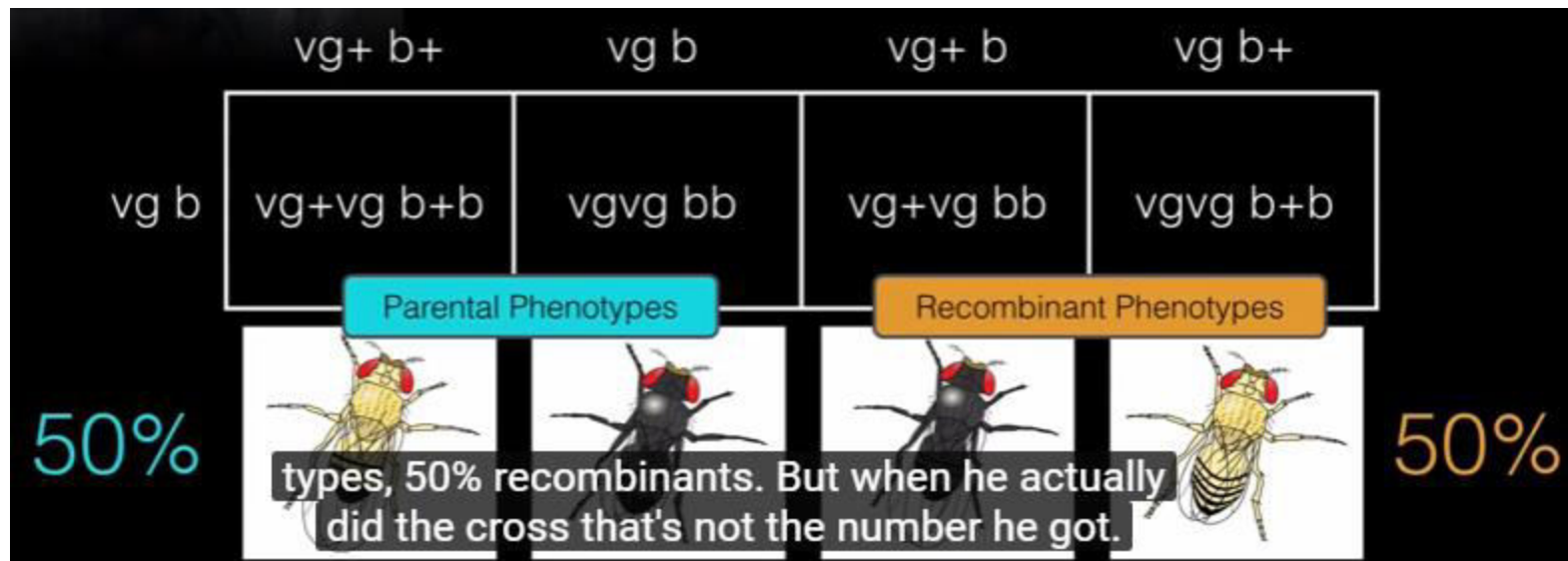
Thomas Hunt Morgan genetic law



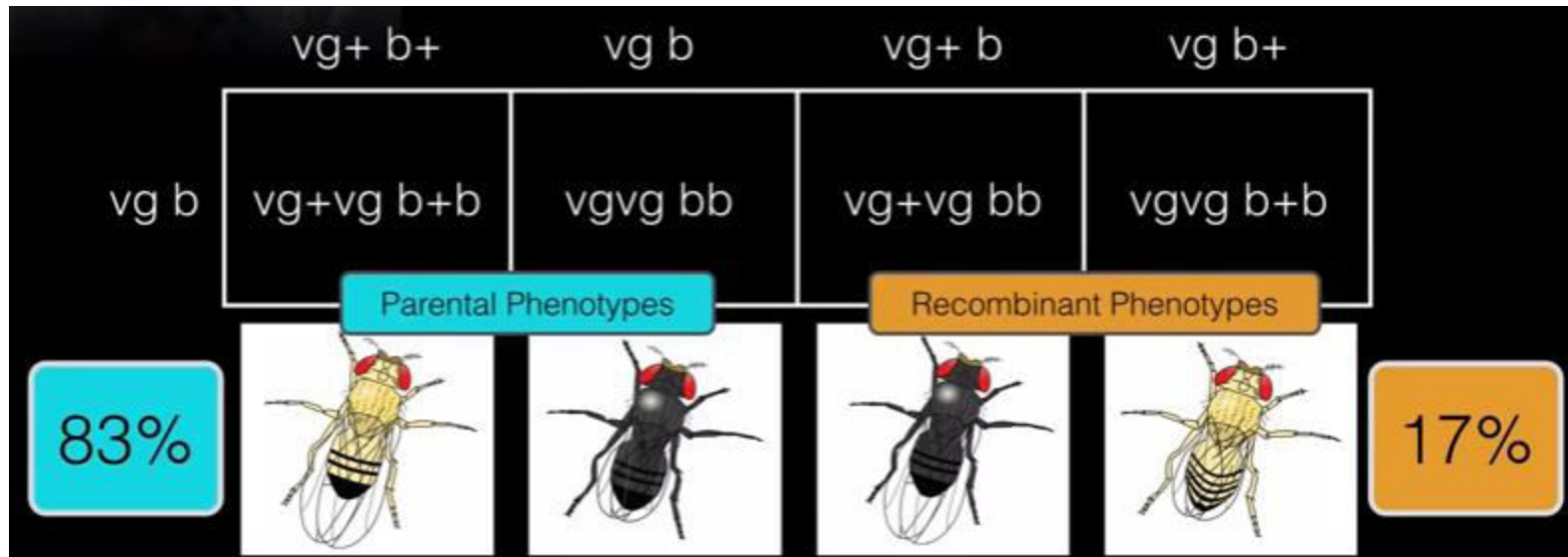
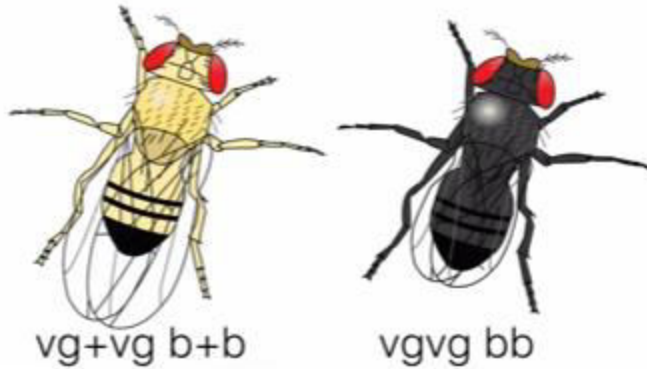
vg+vg b+b



vgvg bb

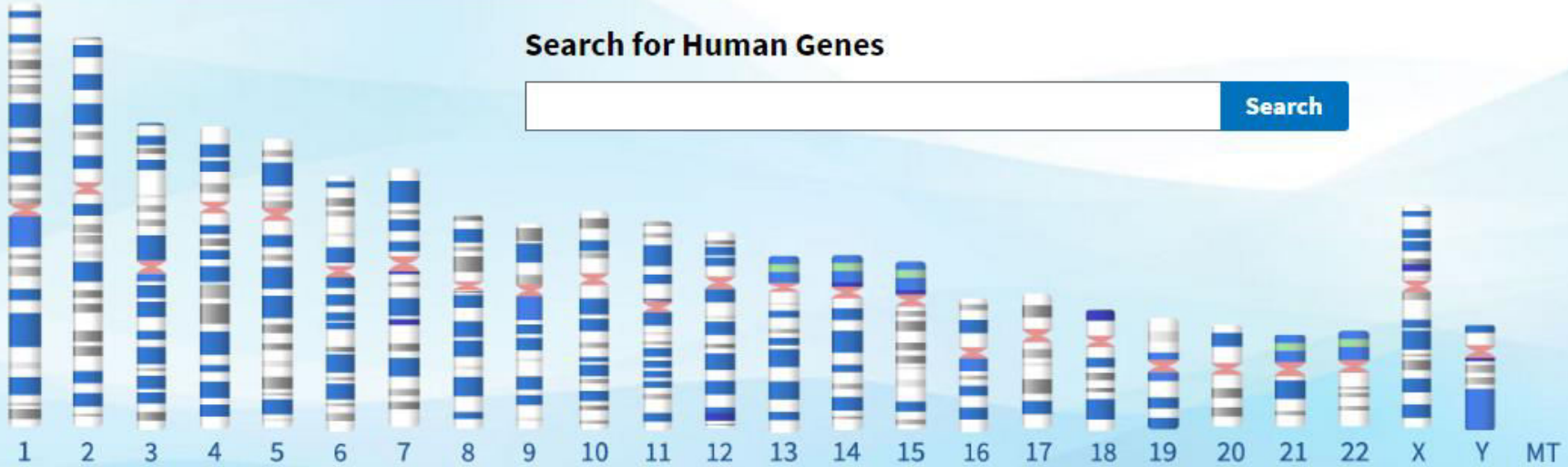


Thomas Hunt Morgan - recombination genetic law



Genome data viewer

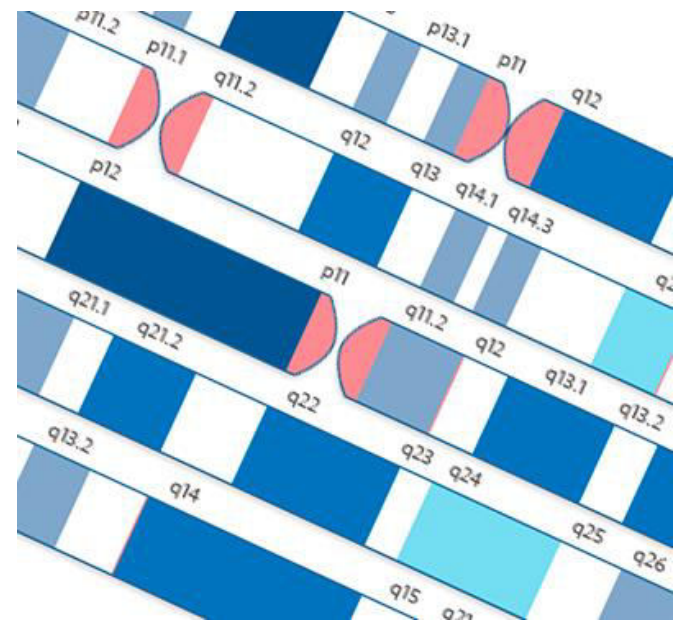
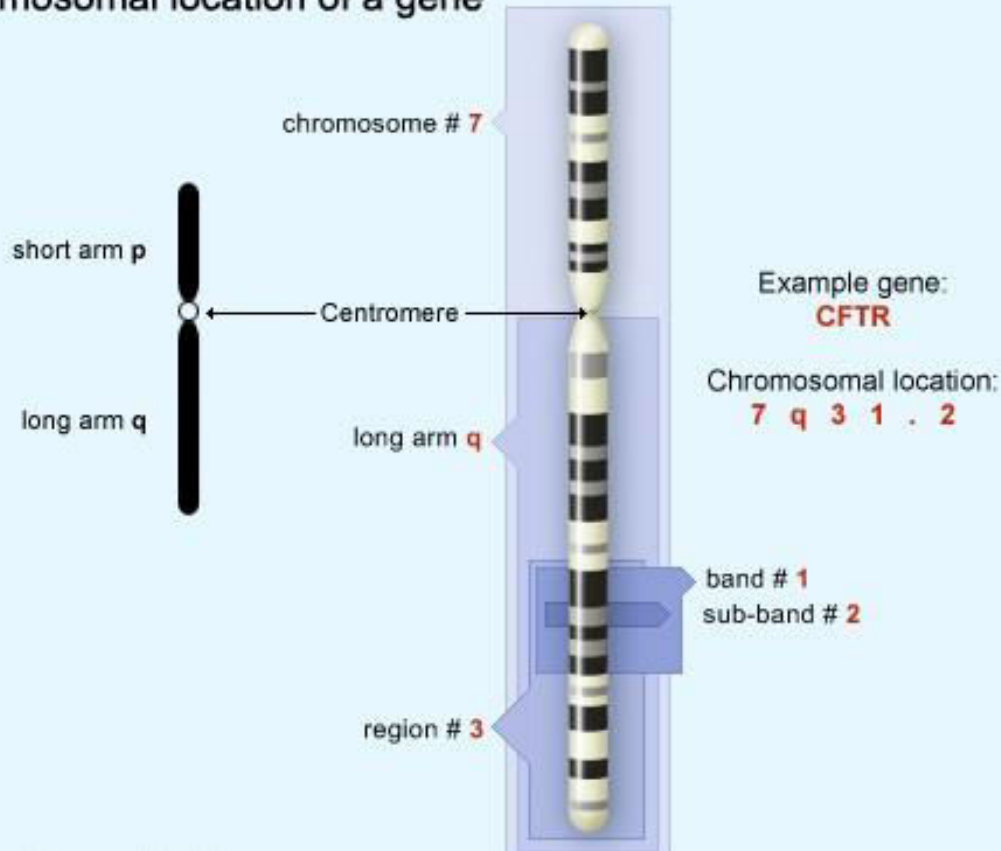
Search for Human Genes



Select a chromosome to access the genome data viewer

Cytogenetic location

Chromosomal location of a gene



GENOME data viewer

Genome Data Viewer Homo sapiens: GRCh38.p10 (GCF_000001405.36) Chr 10 (NC_000010.11): 1 - 133.8M

Reset All Share this page FAQ Help Version 4.1

▼ Pick Assembly
GCF_000001405.36 (GRCh38.p10)
Locations for Gene COX1
Sequence Location
NC_012920.1 5,904 - 7,445
Select an assembly to change view

▼ Ideogram View
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
16 17 18 19 20 21 22 X Y MT

▼ Search
Location, gene or phenotype
Enter a location, gene name or phenotype

▼ Your Data
▼ Add Tracks
▼ Design Details

NC_000010.11: 1..134M (134Mbp)

Genes, NCBI Homo sapiens Annotation Release 108, 2016-06-07
ITGB1 RET CXCL12 MBL2 SIRT1 PTEN FRS CYP2C19 CYP2C9 MGMT

Genes, Ensembl release 87
ENSG00000151474 ENSG00000120549 ENSG00000185532 ENSG00000150275 ENSG00000183230 ENSG00000148655 ENSG00000156113 ENSG00000185737 ENSG00000172987 ENSG00000107518

dbSNP Build 149 (Homo sapiens Annotation Release 108) all data

ClinVar Short Variations based on dbSNP Build 149 (Homo sapiens Annotation Release 108), 2016-11-28

Cited Variants, dbSNP Build 149 (Homo sapiens Annotation Release 108)

RNA-seq exon coverage, aggregate (filtered), NCBI Homo sapiens Annotation Release 108 - log base 2 scaled

RNA-seq intron-spanning reads, aggregate (filtered), NCBI Homo sapiens Annotation Release 108 - log base 2 scaled

RNA-seq intron features, aggregate (filtered), NCBI Homo sapiens Annotation Release 108

The image displays a genome browser interface for Chromosome 10 of Homo sapiens. The top navigation bar shows the assembly (GRCh38.p10) and the specific region (NC_000010.11: 1..134M). The main area contains several tracks: 1) Gene annotations from NCBI (Release 108) and Ensembl (Release 87), showing genes like ITGB1, RET, CXCL12, MBL2, SIRT1, PTEN, FRS, CYP2C19, CYP2C9, and MGMT. 2) dbSNP Build 149 variants. 3) ClinVar short variations. 4) Cited variants. 5) RNA-seq exon coverage (log base 2 scaled). 6) RNA-seq intron-spanning reads (log base 2 scaled). 7) RNA-seq intron features (log base 2 scaled). The left sidebar provides options to pick an assembly, view ideograms, and search for locations or genes. The bottom sidebar shows options for 'Your Data', 'Add Tracks', and 'Design Details'.

Gene location

[Homo sapiens \(human\) Annotation Release 108 \(Current\)](#)

[BLAST human sequences](#)

Chromosome: [1] 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y MT

Master Map: Genes On Sequence

[Summary of Maps](#)

[Maps & Options](#)

Region Displayed: 0-250M bp

[Download/View Sequence/Evidence](#)

Ideogram	Contig	Regions	Genes_seq	Symbol	O	Links	E	Cyto	Description
	NT_077402.3 NT_187170.1 NT_077912.2	REGION108		TP73	+	OMIM HGNC sv pr dl hm sts SNP	best RefSeq	1p36.32	tumor protein p73
		PRAME_REG.. REGION200		TARDBP	+	OMIM HGNC sv pr dl hm sts SNP	best RefSeq	1p36.22	TAR DNA binding protein
		REGION228 REGION189 REGION109		MTOR	+	OMIM HGNC sv pr dl hm sts SNP	best RefSeq	1p36.22	mechanistic target of rapamycin
		FOXO6		MTHFR	+	OMIM HGNC sv pr dl hm sts SNP	best RefSeq	1p36.22	OTTHUMP00000002368
				NPPB	+	OMIM HGNC sv pr dl hm sts SNP	best RefSeq	1p36.22	natriuretic peptide B
	NT_032977..			HDAC1	+	OMIM HGNC sv pr dl hm sts SNP	best RefSeq	1p35.2-p35.1	histone deacetylase 1
				JUN	+	OMIM HGNC sv pr dl hm sts SNP	best RefSeq	1p32.1	Jun proto-oncogene, AP-1 transcription factor sub
				LEPR	+	OMIM HGNC sv pr dl hm sts SNP	best RefSeq	1p31.3	leptin receptor
		REGION229		F3	+	OMIM HGNC sv pr dl hm sts SNP	best RefSeq	1p21.3	coagulation factor III, tissue factor
		REGION190		GSTM1	+	OMIM HGNC sv pr dl hm sts SNP	best RefSeq	1p13.3	glutathione S-transferase mu 1
	NT_187174.1 NT_187172.1 NT_187175.1 NT_187174.1 NT_187175.1 NT_187176.1	CEN1		MUC1	+	OMIM HGNC sv pr dl hm sts SNP	best RefSeq	1q22	mucin 1, cell surface associated
		1q21		LMNA	+	OMIM HGNC sv pr dl hm sts SNP	best RefSeq	1q22	lamin A/C
		REGION2 MTX1		CRP	+	OMIM HGNC sv pr dl hm sts SNP	best RefSeq	1q23.2	C-reactive protein OTTHUMP00000033307 pentr
				F5	+	OMIM HGNC sv pr dl hm sts SNP	best RefSeq	1q24.2	coagulation factor V
	NT_004487..			FASLG	+	OMIM HGNC sv pr dl hm sts SNP	best RefSeq	1q24.3	Fas ligand
				PTGS2	+	OMIM HGNC sv pr dl hm sts SNP	best RefSeq	1q31.1	PGH synthase 2 PHS II cyclooxygenase 2 prosta
		REGION3		CFH	+	OMIM HGNC sv pr dl hm sts SNP	best RefSeq	1q31.3	complement factor H
		REGION199		IL10	+	OMIM HGNC sv pr dl hm sts SNP	best RefSeq	1q32.1	interleukin 10
				PARP1	+	OMIM HGNC sv pr dl hm sts SNP	best RefSeq	1q42.12	poly(ADP-ribose) polymerase 1
	NT_167186.2	REGION110 TBCE REGION111 REGION112 OLFACTORY..		AGT	+	OMIM HGNC sv pr dl hm sts SNP	best RefSeq	1q42.2	OTTHUMP00000035878