1. Problem 1
    - Mate a M1(♀) fly with a Wildtype Male (♂)

	M	WT
♀	0	13
♂	0	11

    - ➔ The mutation is recessive

    - Mate a M1 (♀) fly with a F1 (♂)

	M	WT
♀	13	13
♂	8	14

    - ➔ The trait is autosomal

    - Mate a M2(♀) fly with a Wildtype Male (♂)

	M	WT
♀	14	0
♂	10	0

    - ➔ The mutation is dominant

    - Mate a F1 (♀) fly with a WT (♂)

	M	WT
♀	60	49
♂	58	52

    - ➔ The trait is autosomal

    - Mate a Homozygote Mutant ($\frac{M1}{M1}$) (♀) fly with an F1 Heterozygote ($\frac{M2}{+}$) Male (♂)

	M	WT
♀	4	7
♂	8	5

    - Mate a resultant Heterozygote Mutant ($\frac{M1}{+}$) ($\frac{+}{M2}$) (♀) fly with an M1 Mutant ($\frac{M1}{M1}$) ($\frac{+}{+}$) (♂) 10x (240 offspring)

	M	WT
♀	120	5
♂	112	3

P	($\frac{M1}{M1}$) ($\frac{+}{+}$)	M

P	$(\frac{+}{M1})(\frac{M2+}{+})$	M
R	$(\frac{M1}{M1})(\frac{M2}{+})$	M
R	$(\frac{+}{M1})(\frac{+}{+})$	WT

- We can only recognize (see) one class or recombinants = 8.
- Total Recombinants = 8*2=`16
- Distance = 6cM ± 2.4

2. Problem 2
   - Mate a Mutant Female (♀) fly with a Wildtype Male (♂)
     F1= All Heterozygous $(\frac{M}{+})$
   - Mate an F1 Heterozygous Male with a Mutant Female

	M	WT
♀	47	48
♂	53	52

   - When looking at the DNA Marker Summary, it is clear that Markers 1,2,3 are linked with the chromosome which carries the wingless. This is apparent because the wingless phenotypes (mutants) show a homozygous genetype for markers 1,2,3 whereas the winged heterozygotes show a heterozygous genotype for markers 1,2,3. Further, about half of the wingless mutants show a heterozygous genotype for markers 4,5,6 and the other half do not. We expect a complete linkage between the markers on the gene and the wingless because there is no recombination in the heterozygous male. Thus, we can determine that the wingless gene is on the same chromosome as markers 1,2, and 3, which is chromosome 2.
   - To determine map distances, we must now allow for meiotic crossing over. Thus we must use a heterozygous female with a mutant male.

	M	WT
♀	57	50
♂	54	39

   - Marker 1

P	85	wg-	One band
P	66	wg+	Two bands
R	26	wg-	Two bands
R	23	wg+	One band

     i. $\frac{49}{200} = 24.5cM \pm 7$

   - Marker 2

P	108	wg-	One band

P	86	wg+	Two bands
R	3	wg-	Two bands
R	3	wg+	One band

i. $\frac{6}{200} = 3cM \pm 1.7$

- Marker 3

P	97	wg-	One band
P	77	wg+	Two bands
R	14	wg-	Two bands
R	12	wg+	One band

i. $\frac{26}{200} = 13cM \pm 3.6$

- Marker 1,3

			M1	M3
DR	4	wg-	Two bands	Two bands
DR	2	wg+	One band	One band

i. Order ➔ M1, wg-, M3

- Marker 2,3 (increased total offspring number to 400)

			M1	M3
DR	1	wg-	Two bands	Two bands
DR	1	wg+	One band	One band

i. Order ➔ M3, wg-, M2

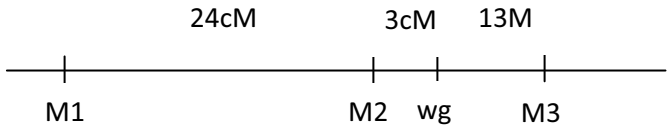
- Marker 1,2 (increased total offspring number to 400)

			M1	M2
DR	1	wg-	one bands	Two bands
DR	1	wg+	two band	One band

i. Order ➔ wg-, M2, M1

- Overall Order ➔ M3, wg-, M2, M1

Map



3

Strains 1-4 x MATa on -Lys -Leu

none grow

Strains 1-4 x MATα on -Lys -Leu

all grow

Strains 1-4 are MATa ✓

Strains 1-4 x MATα on -Lys -Leu 37°

Strains 1, 3, 4 grow

1, 3, 4 are recessive
2 is dominant ✓

To find Strains 1, 3, 4 MATα

Cross Strain x MATα

↓

Tetrads → Haploid on -Leu does not grow

x MATa on -Leu-Lys 37°C grows ✓

↓

Strain MATα

Also - plate haploid on YPD 37 deg to ensure strains 1,3,4 Matalpha are temp sensitive.

To find Strain 2 MATα

Cross Strain x MATα

↓

Tetrads → Haploid on -Leu does not grow

x MATa on -Leu-Lys grows

x MATa on -Leu-Lys 37° does not grow ✓ ✓

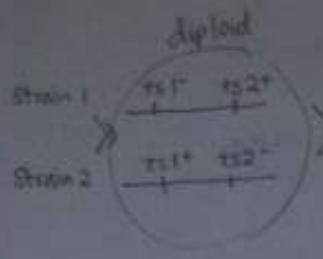
	MATα 1	2	3	4
1	-	-	+	+
2	-	-	-	-
3	+	-	-	-
4	+	-	-	-

3, 4 in same group ✓

1

2 can be in any group (dominant, can't tell)

on YPD 37°C



PD
ts1⁻ ts2⁺
ts1⁻ ts2⁺
ts1⁺ ts2⁻
ts1⁺ ts2⁻
4 ts⁻

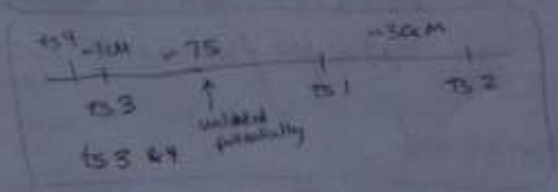
T
ts1⁻ ts2⁺
ts1⁻ ts2⁻
ts1⁺ ts2⁺
ts1⁺ ts2⁻
1 ts⁺
3 ts⁻

doesn't matter → if dominant/recessive (haploids!)

NPD
ts1⁻ ts2⁻
ts1⁻ ts2⁻
ts1⁺ ts2⁺
ts1⁺ ts2⁺
2 ts⁺
2 ts⁻

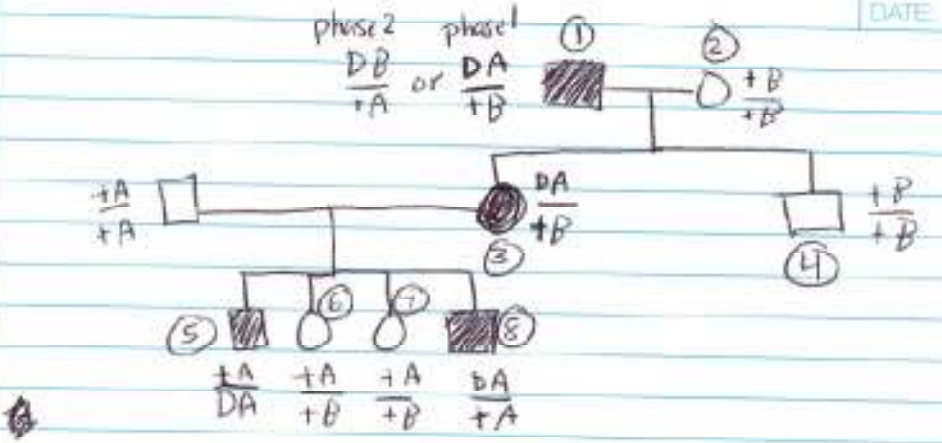
Similarly for all ts1/2/3/4 crosses

cross	PD	T	NPD	Total	Linkage
linked ✓ ts1/ts2	86	59	5	150	$100 \times \frac{59+6(5)}{2(150)} = 29.6$cM
~~linked~~ ts1/ts3 or unlinked	29	100	21	150	$100 \times \frac{100+6(21)}{2(150)} = 75.3$cM
~~linked~~ or unlinked ts1/ts4	34	92	24	150	$100 \times \frac{92+6(24)}{2(150)} = 78.7$cM
unlinked ts2/ts3	20	105	25	150	$100 \times \frac{105+20(20)}{2(150)} > 100$cM
unlinked ts2/ts4	21	94	35	150	$100 \times \frac{94+6(35)}{2(150)} > 100$cM
~~totally~~ linked ✓ ts3/ts4	148	2	0	150	$100 \times \frac{2}{2(150)} = 0.6$cM



great

4.



$$LOD = \log_{10} \frac{P(\text{observed segregation} \mid \text{loci completely linked})}{P(\text{observed segregation} \mid \text{loci unlinked})}$$

individuals 5, 6, 7, 8, 3, & 4 are all informative

individual 5

$$\frac{+A}{+A} \times \frac{DA}{+B} \rightarrow \frac{+A}{DA}$$

P(obtaining this genotype | complete linkage) = 1 * 1/2 = 1/2

P(obtaining this genotype | unlinked) = 1 × 1/4 = 1/4

individual 5 LOD score = $\log_{10} \frac{1/2}{1/4} = \log_{10} 2 = .3$

individual 6 = $\log_{10} \left(\frac{1/2}{1/4}\right) = .3$

individual 6 $\frac{+A}{+A} \times \frac{DA}{+B} \rightarrow \frac{+A}{+B}$

individual 7

$\frac{+A}{+A} \times \frac{DA}{+B} \rightarrow \frac{+A}{+B}$ LOD score = .3

individual 8

$\frac{+A}{+A} \times \frac{DA}{+B} \rightarrow \frac{DA}{+A}$ LOD score = $\log_{10}\left(\frac{1/2}{1/4}\right) = .3$

4 continued

Individual 3 and Individual 4 parents

If phase 1 $\frac{DA}{+B}$ X $\frac{+B}{+B}$

If phase 2 $\frac{DB}{+A}$ X $\frac{+B}{+B}$

P (data given that completely linked) = ½ (Probability of phase 1 for 3 &4) + ½ (probability of phase 2)

P = ½*1/2*1/2

P=1/8

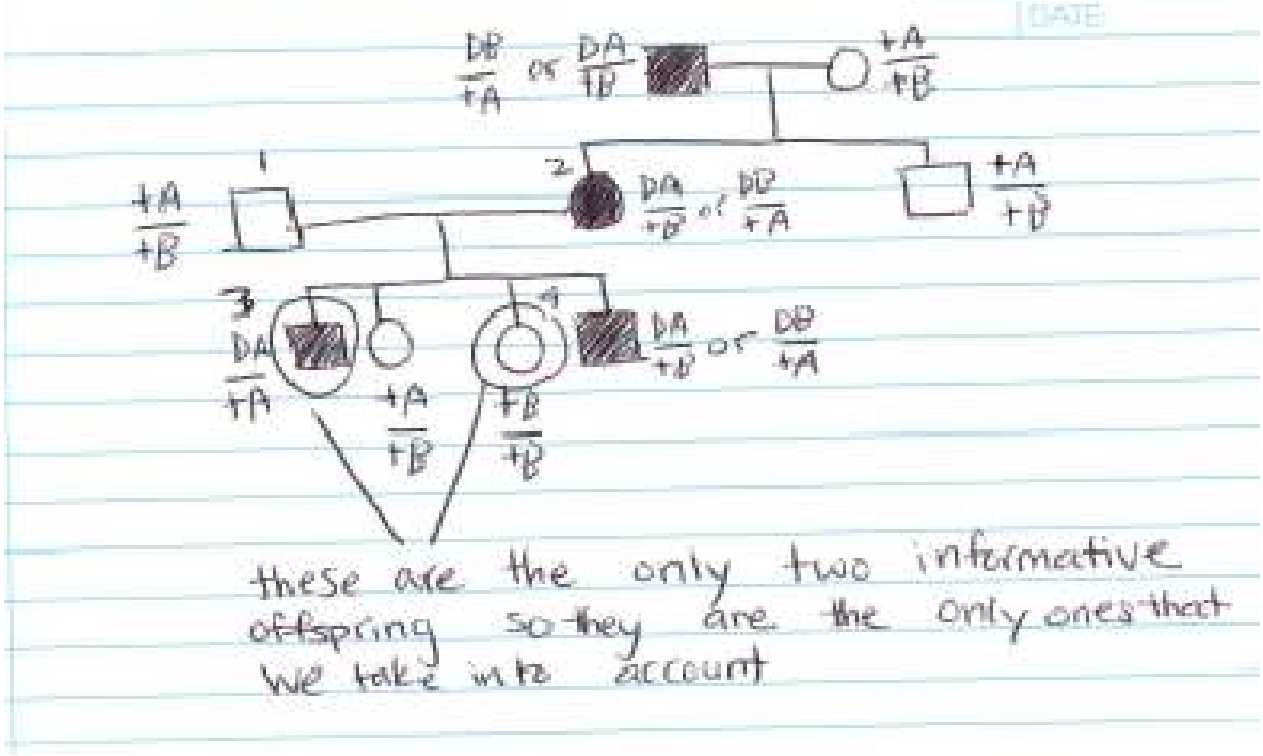
P (data given unlinkage) = ¼ * ¼

P= [(1/8)/(1/16)] = 2

LOD 2 = .3

Overall answer for part a = 1.2+.3 = 1.5

4b.



Individual 3 and Individual 4 parents

If phase 1 $\frac{+A}{+B}$ X $\frac{DA}{+B}$

If phase 2 $\frac{+A}{+B}$ X $\frac{DB}{+A}$

P (data given that completely linked) = ½ (Probability of phase 1 for 3 &4) + ½ (probability of phase 2)

P = ½*1/4*1/4 + 0

P=1/16

P (data given unlinkage) = ½*1/4

P= [(1/16)/(1/8)] = 2

LOD 2 = .3

Overall Answer for Part B = .3