Setting up you mapping cross

P$_0$

♀ **EG1000** (chromosome: I: $\frac{dpy}{dpy}$; II: $\frac{rol}{rol}$; III: $\frac{lon}{lon}$)

or

♀ **EG1020** (chromosome: VI: $\frac{bli}{bli}$; V: $\frac{dpy}{dpy}$; X: $\frac{lon}{lon}$)

X

♂ **mutant** (chromosome: ? : $\frac{mut}{+}$)

- Generate the above cross for each of the mapping strains provided.

F$_1$

- All animals will be heterozygous for the appropriate mapping alleles and therefore phenotypically “wild-type” in this generation.
- If your mutant allele is dominant the phenotype will be present in 1/2 of the offspring in this generation.
- Clone out at least 10 hermaphrodites from this mating for analysis in the F_2 generation.
- Remember that only 1/2 of all worms in this generation will harbor your mutation of interest.

F$_2$

- In this generation you will be scoring the diversity of phenotypes you observe from each hermaphrodite clone that was isolated from the previous generation.
- Look for worms that exhibit the phenotype associated with your mutation of interest and for each of these worms score the additional phenotypes you see (those associated with the mapping strain).
- Remember that we are mapping by exclusion, so identifying a mapping phenotype that is never observed in the mutant animal suggests that both genes are on the same chromosome. An example of this is provided below.

Example 1.

chromosome		?	VI
	allele	*mut*	*bli*
?	*mut*	$\frac{mut}{mut}$	$\frac{bli}{mut}$
VI	*bli*	$\frac{bli}{mut}$	$\frac{bli}{bli}$

- In example 1 we will use blister (*bli),* a marker on chromosome VI, to determine whether our mutant of interest is located on that chromosome. The punnett square outlines the theoretic genotypic outcomes for this cross, which are similar to the outcome you expect to see in your F_2 generation. However, if your mutation of interest and *bli* are on the same chromosome, you will never observe the blister phenotype in a mutant worm.

- Use the worksheets on the following page to map your mutant of interest.