## Flow Chart for a Cross

Set up a bulk pair mating
(7-10 $\sigma^{\text {T }}$ and 3-5 ${ }^{\text {th }}$ )


Set up a bulk pair mating
(7-10 $\sigma^{7}$ from first mating and 3-5 ${ }_{q}^{a}$ from strain with the background you want to maintain)


Set up single-pair matings
(set up using $\delta^{7}$ from cross plates and ${ }_{\phi}^{\lambda}$ from the strain with the background you want to maintain; set up at least 8 and it might be best to set them up at different times through out the day)


Set up the next set of singlepair matings using $\sigma^{7}$ from that positive plate and ơ from the strain with the background you want to maintain

Go back the the last plate with positive $\sigma^{\top}$, chunk that
plate and set up a new round of single-pair matings using $\sigma^{7}$ from that chunk.

- Continue with the above for a minimum of six rounds of outcrossing. This ensures that your newly built strain has as much of the ${ }_{\phi}^{1}$ strain background as possible.
- After the strain has been outcrossed, the genome needs to be homozygosed.
- Pick single hermaphrodites to eight different plates.
- Genotype the offspring from each plate.
- Ideally, you want to genotype for both the allele you want and the allele you don't want.
- If you get an offspring that is homozygous for the allele you want, you are done!

Freeze the strain!

- If you don't, continue putting single ơ on eight plates and genotyping the offspring until you get a plate that shows offspring that are homozygous for your allele.
- If you are not able to genotype both alleles, genotype for the allele you want. Go through enough rounds of homozygosing (putting eight single ờ on plates from a plate shown to have positive animals) such that each plate shows animals with the allele you want. This process will probably take 6-8 rounds of homozygosing.

