You need to identify the dominant mutation.

**If the mutated phenotype is dominant, then the wild-type phenotype is recessive**.

I**f you cross a wild-type individual with a mutated individual, you will see the mutated phenotype in the F1.** This is because **the progeny will be carrying at least one dominant mutated allele that will hide the expression of the recessive form.** So even if the progeny is heterozygous for the trait, they will express the mutation.

**If the mutation is not dominant, then the whole progeny will be wild-type.**

Let us analyze an example.

- wild-type trait → yellow eyes, rr
- mutated trait → red eyes, RR or Rr

Cross: a mutated individual with wild-type individual

**Option 1:**

Parentals) RR x rr

Gametes) R R r r

Punnett square) R R

r Rr Rr

r Rr Rr

F1) 100% Rr, heterozygous mutated individuals with red eyes.

**Option 2:**

Parentals) Rr x rr

Gametes) R r r r

Punnett square) R r

r Rr rr

r Rr rr

F1) 50% Rr, heterozygous mutated individuals with red eyes.

50% rr, homozygous recessive expressing the wild-type phenotype

In both options, **the mutated phenotypes appear in the F1. You do not need to perform another cross to make it appear in F2.**

**If the mutation were recessive, it would probably appear in the F2.**