# User Guidelines

## Information required from user prior to TILLING

- The genomic and coding/amino acid sequence of the gene of interest
- Any domains or region of interest to be included in TILLING
- Any information of homologues of the gene of interest

## Information sent to users

On completion of TILLING the following information will be sent to the user

- Plant line number, sequencing trace files, the nucleotide/amino acid change, position and flanking sequence of each mutation
- M3 seed

Users are responsible for sowing, genotyping and phenotypic analysis of mutant lines however please contact us for any advice.

***Note that for publication purposes it is recommended that mutant lines are backcrossed at least three times.***