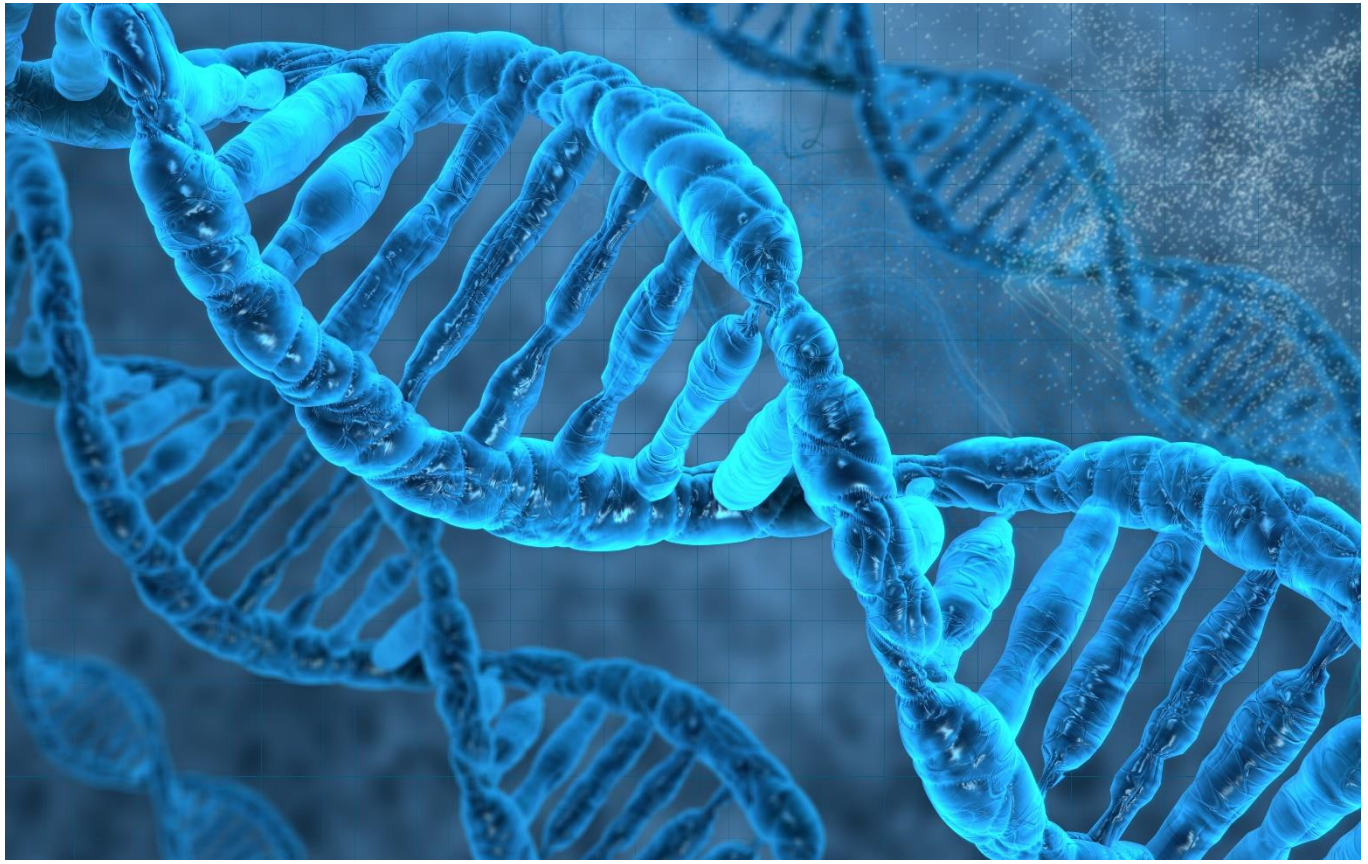
CD Genomics
The Genomics Services Company



# VARIANT CALLING

## Whole Genome Sequencing



# Whole Genome Sequencing

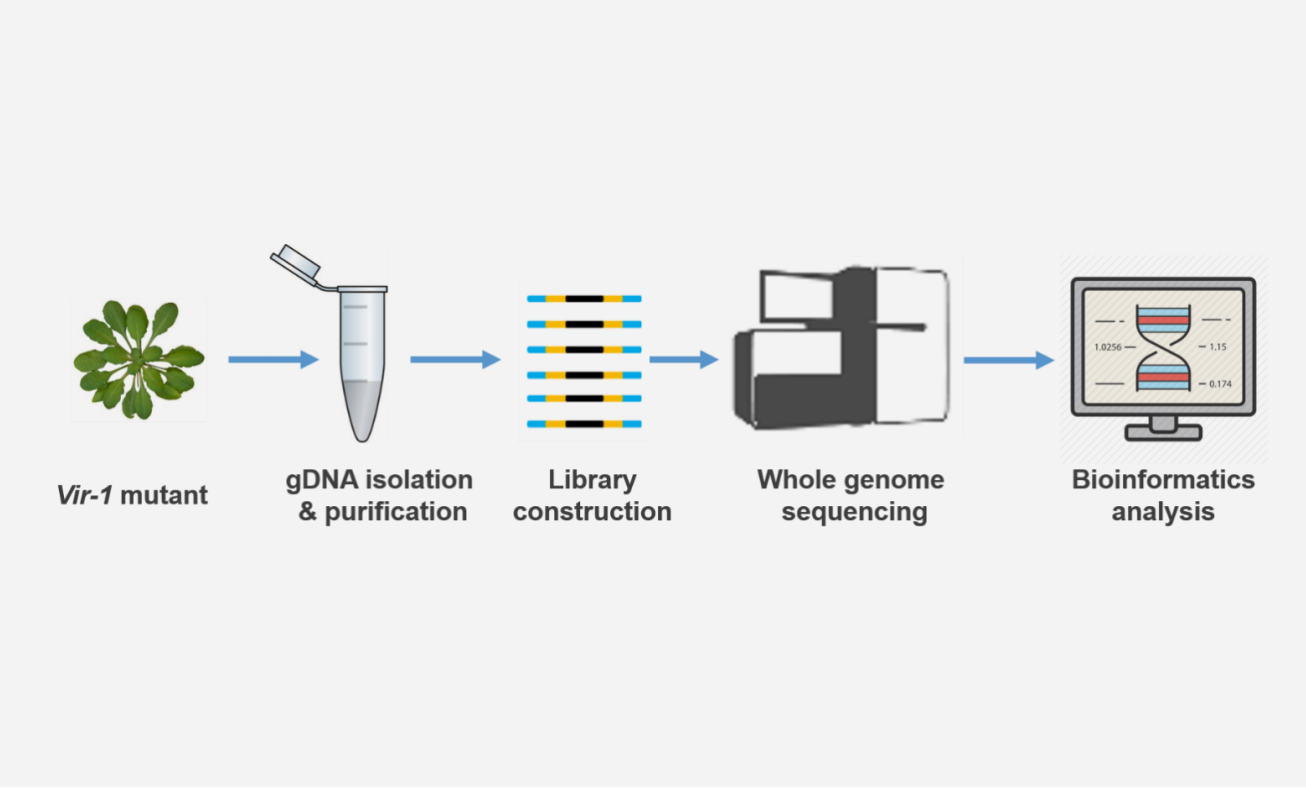
Virilizer (Vir), first isolated from *Drosophila melanogaster*, plays a role in sex determination. In humans, its homologue and METTL3 are involved in N6-adenosine methylation ($m^6A$) writing. As $m^6A$ of mRNA is an important process in most eukaryotes, it is very important to understand its role and the status of factors accompanying this modification. Whole genome sequencing enables the genome-wide mutation profiling in the *vir-1* mutant of *Arbidopsis*.

## Features

- Single base-pair resolution
- Genome-wide variation profiling (SNPs, InDels, CNVs, SVs)
- *De novo* assembly or reference-based assembly

## Applications

- Create a reference genome
- Population evolution and phylogenetic studies
- Disease research, drug discovery and development, and personalized medicine

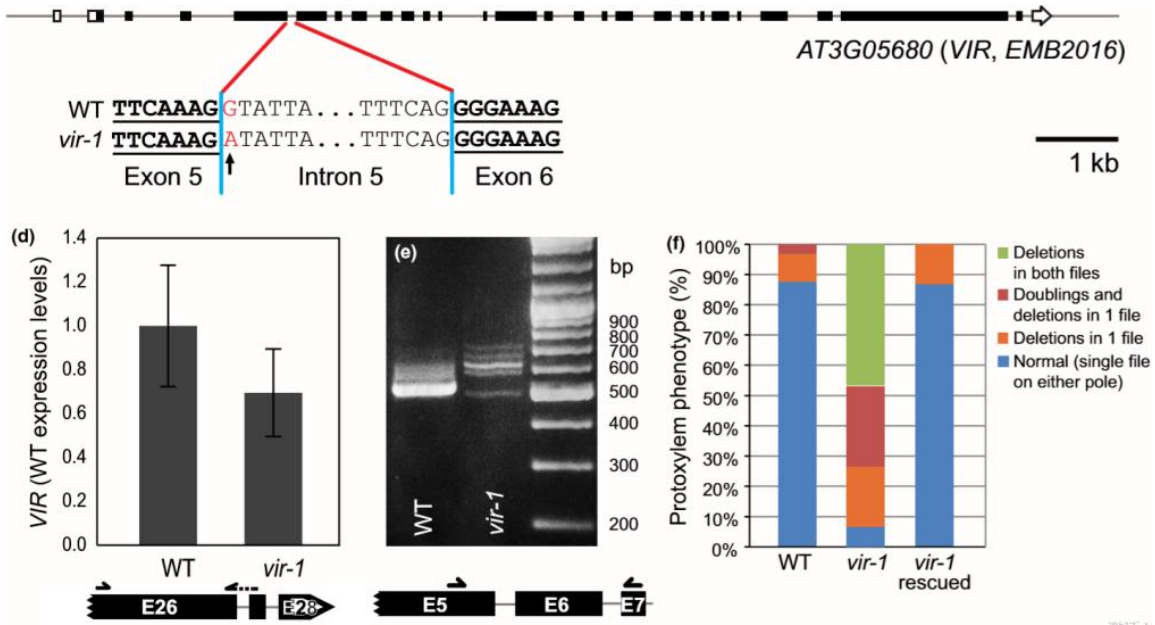


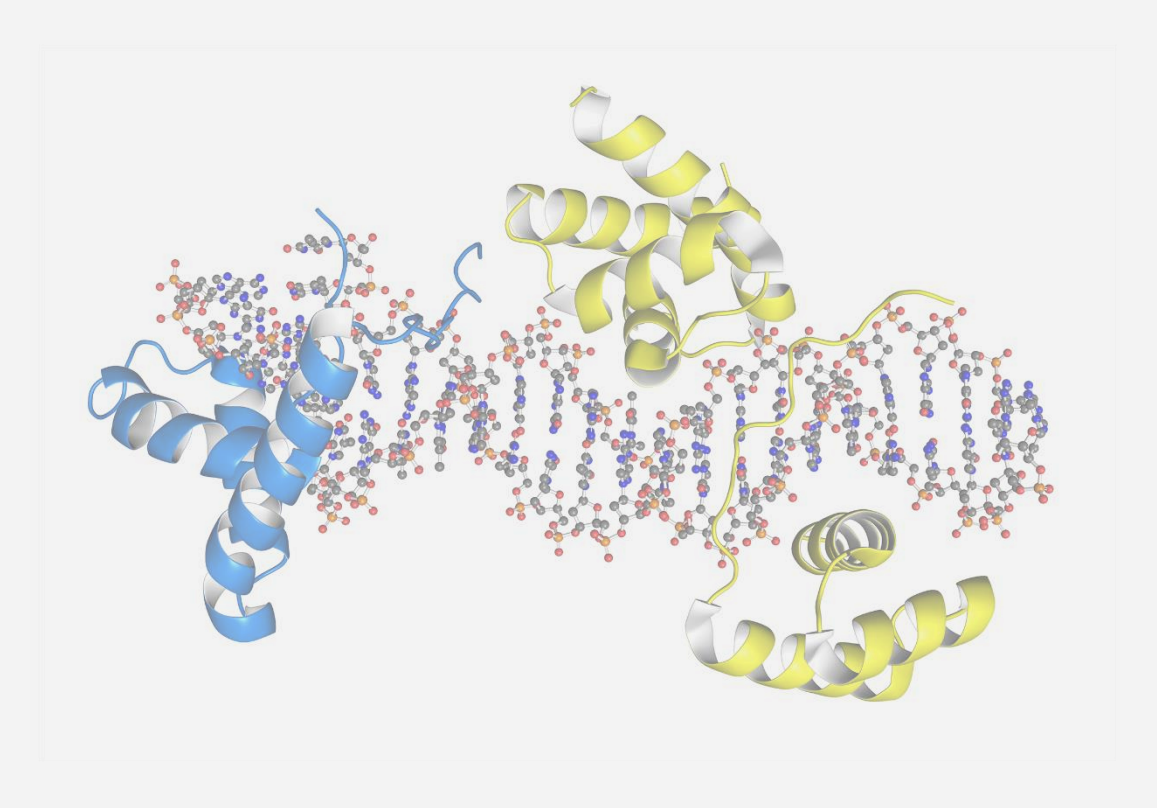

# Assay Overview

The *vir-1* mutant was isolated in an ethyl methanesulfonate (EMS) mutagenesis screening for reduced and irregular *AHP6prom:GFP* expression (AHP6 is a factor required for protoxylem formation in *Arabidopsis*). Total DNA was extracted and subjected to whole genome sequencing on Illumina instruments, so as to identify the mutations and functions of Virilizer in *Arabidopsis*.

# Data Overview

The *vir-1* mutation (orthologous to the splicing regulator/m6A writer protein Virilizer) is caused by a G-to-A conversion at the first nucleotide of the 5th intron of the VIR gene. Although the *vir-1* mutation does not significantly change VIR expression levels at a0.05, it leads to numerous predominantly wrongly spliced VIR transcripts as detected by RT-PCR.





# Conclusions

Researchers use combined methods of genetics, proteomics and RNA biochemistry to investigate a core set of m$^6$A write proteins in *A. thaliana*, which includes MTA, MTB, FIP37, Virilizer and the E3 ubiquitin ligase HAKAI.

**Reference:**

Růžička K, Zhang M, Campilho A, et al. Identification of factors required for m6A mRNA methylation in Arabidopsis reveals a role for the conserved E3 ubiquitin ligase HAKAI. New Phytologist, 2017, 215(1): 157-172.