Template for DL's Project

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Report Date: 07-03-2021
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SUMMARY Here, the summary will be described with necessary information. Like total sample number: 188, NGS plateform Illumina, the reference genome the *Zea mays* AGVRV2 reference genome.

WORKFLOW

The background information: who Delin Liprovided 188 Maize samples for what purpose: construct a genetic mapÁnd the analysis workflow: Figure 1.
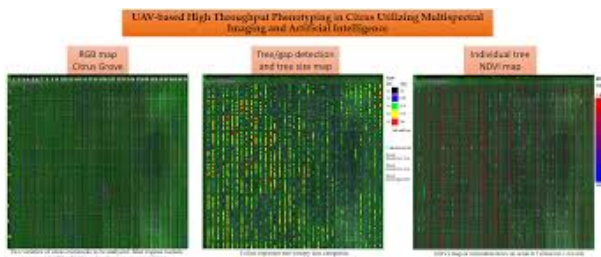

Figure 1 A generalized workflow

SECTION SUMMARY I

Necessary information for the first section I with table and/or figure2.

Figure 2 Maize

NOTE: Results will be stored for up to 12 weeks after delivery of the report. If you would like your results purged sooner, please send your request via email to *delin.bio@xxx.com*.

SECTION SUMMARY II

Subsection
Give detail Criteria like SNPs filtering:

- Requre how many or percentage samples covered.
- The MAF $\leqslant 1\%$
- The Heter

SECTION SUMMARY III

Summary in section III with tables and/or figure 3.

Figure 3 Caption: Wheat

SECTION SUMMARY IV

Summary in section IV with tables and/or figure.

OUTPUTS

Give a list of files will deliver.

- **Maize.vcf**: The genotype in vcf format.
- **Maize.geneticmap.txt**: The constructed genetic map.

METHODS

Give the methods and citations.