

## Technical Specifications:

### Service 1: 6K SNP Genotyping in Soybean using Genotyping Array (96 Array Format)

We are seeking proposals from qualified service providers for the Soybean SNP Genotyping Array and with over 6,000 genetic markers for Soybean samples. We will supply DNA samples, and the selected service provider will be responsible for Sample QC and genotyping on the Gene Titan platform.

1. The Soybean Genotyping Array, encompassing more than 6,000 genetic markers should be used for Genotyping of 96 soybean samples.
2. Service provider should do QC of DNA samples by Qubit, Nanodrop, and Agarose Gel and DNA QC report should be provided.
3. Service provider should do the Incubation based DNA Amplification which includes Denaturation, Neutralization and Amplification as per the standard protocol of Genotyping.
4. Service provider should do the Fragmentation & Precipitation as per standard protocol and leave it at -20 degrees for 24 hours as per the standard protocol of Genotyping.
5. Service provider should do the Drying, Resuspension Fragment Quantification using the multimode detector as per standard Protocol of Genotyping.
6. After Resuspension service provider should do QC by Agarose Gel Electrophoresis.
7. Service provider should do the Denaturation in the PCR machine, and Hybridization with Array in the Gene titan machine for 24 hours as per standard protocol of Genotyping.
8. Service provider should prepare the Ligation, Staining, Stabilization reagent trays for Gene Titan MC as per standard protocol of Genotyping.
9. Service provides to ensure that samples should be genotyped using the Axiom Soybean Genotyping Array with 6K Markers on the Gene Titan platform.
10. Bioinformatics Analysis by DrSeq pipeline: Raw data QC, Genotyping Table, Flexible and fast identification and classification of germplasm, Identification of high-yield variants, gene mapping, and tracking of disease genes and genetic variation analysis.
11. The service provider should provide the Sample QC report, Raw data should be provided in .cel format, Genotyping call for each sample should be provided in a .vcf / .txt format file.
12. The samples should not be sent out side of India and technology should not be changed.
13. Service provider should provide the per sample and total costing.

**Service 2: Whole Genome Sequencing with Standard Analysis in soybean:**

1. Whole Genome Sequencing should be performed using Illumina NovaSeq 6000
2. Total number of Samples: 04
3. The DNA sample QC should be done by Qubit, Nanodrop, and Agarose Gel and DNA QC report should be provided.
4. Libraries should be prepared by the Roche Kapa Hyper plus kit.
5. Library quality check should be done by the Qubit and Bioanalyzer.
6. Prepared libraries should be sequenced on S4 flow cell of Illumina NovaSeq 6000 using sequencing chemistry 2\*150 bp.
7. Service provider should provide 33 GB high quality data per sample.
8. Standard Bioinformatics Analysis: Data QC and pre-processing, Mapping to the reference genome, SNP, InDel using GATK, FreeBayes or Bcftools, Variant annotation, gene calling.
9. The service provider should provide the DNA QC, Library QC, Raw data, bioinformatics analysis report.