

Title	ddRAD-Seq Analysis (ddRAD-Seq Library Preparation, Sequencing, and Bioinformatics)	
Samples	● DNA (192 samples) □ Plant Tissues ()	
DNA Extraction	● No	□ Yes (□ magnetic beads □ spin column)
Bioinformatics	□ No (Read Data Only) ● Yes (SNP Detection)	
Method	1. DNA Quality Check 2. ddRAD-Seq Library Preparation (PstI and MspI) 3. Sequencing DNBSEQ-G400RS; 100bp pair-end; 1 lanes Total 560M reads (2.9M reads per sample) ※ The number of reads is only an estimate 4. Bioinformatics <ul style="list-style-type: none"> • Read QC and Trimming • Read mapping to a Reference Genome (We use reference sequences provided by our clients to conduct the analysis.) • Variant Call <Option> GWAS, Phylogenetic Analysis, Primer Design, etc.	
Deliverables	<ul style="list-style-type: none"> • Report • Sequence Data (Fastq files) • Mapping Data (bam files) • Result of Variant Call (a VCF file) • DNA solution 	
Reference Price	842,600 JPY	Sequencing: 475,600 JPY
		Bioinformatics: 385,000 JPY
Days Required	70 Business Days	Sequencing: 40 Business Days
		Bioinformatics: 30 Business Days

Supplemental information on restriction enzymes:

We confirmed the variants identified through ddRAD-Seq across various plant species by employing different combinations of restriction enzymes. When restriction enzymes like PstI, MspI, and EcoRI are used to recognize and cut numerous different sites in the genome, there is no notable variance in the number of variants obtained or their distribution across the genome. Hence, unless specified otherwise, we suggest employing the "PstI and MspI" combination for all plant species.