Service: Norway spruce 50K array genotyping

Estimated number of samples: (up to) 3072 samples of DNA samples of Norway spruce, i.e. up to 32 x 96-well plates.

Description

Genotyping service using 50K array for Norway spruce, expected output ~45K high-quality SNPs, distributed over 40 000 scaffolds and 19 000 unique gene models, evenly covering the twelve linkage groups
-There should be no batch-to-batch variation in SNP content of the array.
- The array technology should be able to guarantee that 100% identical SNP content with every order (i.e. all data should be 100% comparable and compatible)
-Photolithographic manufacturing technology must be used for manufacturing of the arrays.
- The assay should guarantee inclusion of all candidate SNPs with a neighbouring SNP as close as 20 bases from the candidate SNP.

The client provides relevant information about the submitted samples, including the species, sample origin, ploidy, tissue, known (or assumed) level of inbreeding, plate design (sample ID/well) and DNA quantification method and DNA concentration.

If more than 10% of the samples on a given 96-well plate fail the ultrasensitive fluorescent nucleic acid stain threshold based on Contractor's readings, client will be notified and will have the option to re-submit failing samples. If Client would like to resubmit, must notify the contractor within 5 business days. If not, contractor reserves the right to move forward with processing all samples on that plate. Client may resubmit samples only once. After the resubmission, every sample received will be processed, regardless of passing Contractors QC requirements.

Data pre-processing

All samples undergo quality check (QC) upon reception (with fluorochrome selectively binding dsDNA such as PicoGreen or SYBR-Green).
Raw data from the array, including the preliminary QC information, array annotation files and hybridization results/files, are pre-processed using the appropriate software.

The following preliminary results are provided:

- A list of high-quality individuals
- A list of high-quality SNPs
- Summary statistics on samples and SNPs
- Genotype matrix