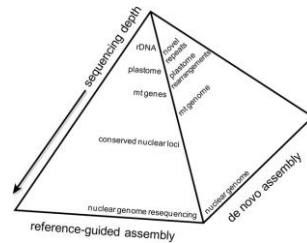


Computation - Applications

- Genome Survey Sequencing (GSS) / Genome skimming
- SSR discovery
- SNP discovery / genetic mapping
- Genome assembly
- Transcriptomics

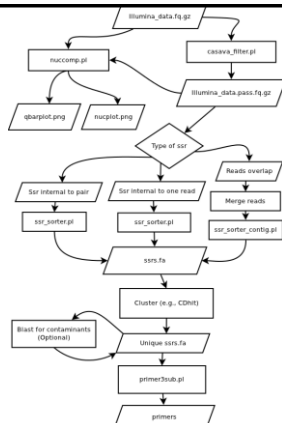
Genome Survey Sequencing / Genome Skimming



Straub et al. 2012. American Journal of Botany 99(2):349-364.

SSR Discovery

- Paired-end reads.
- Overlap or not.
- Ssr_sorter.pl.
- Cluster.
- Blast (optional).
- Primer3.



Ssr_sorter.pl

- Paired-end reads
- Find internal repeats
- Complexity filter

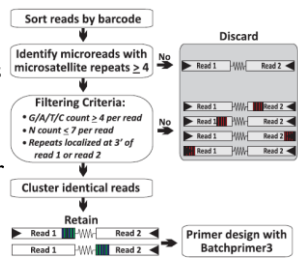
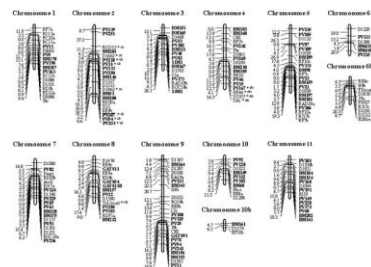


Fig. 1 Flow chart for informatic microsatellite identification by microread-based multiplexed massively parallel sequencing. Green vertical hashes indicate the location of targeted microsatellites, while red vertical hashes indicate microsatellites that did not fit selection criteria.

SNP Discovery / Genetic Mapping

- 10s to 100s of thousands of SNPs can be surveyed on an Illumina Infinium SNP chip.
- Align reads (bowtie, BWA) -> SAMTools
- Genome Wide Association Study
- Genomic selection

SNP Discovery / Genetic Mapping



Genome Assembly

- De novo assembly
- Paired-end insert sizes

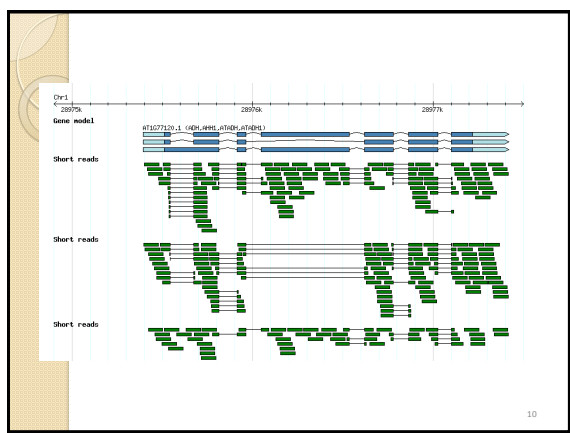


Transcriptomics

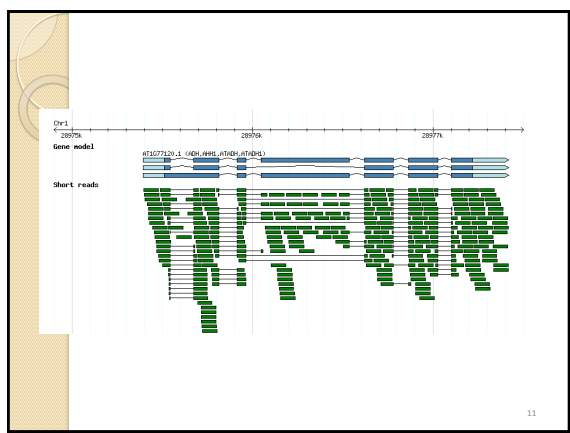
- Reduce genome complexity
- SNP discovery (but note: RNA editing)
- Differential expression

Transcriptomics

- Alternative splicing
- Multi-maps
- Other



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