A) Barcoded library $n_1$

Barcoded library $n_2$

... Barcoded library $n_i$

Barcoded library $n_i$

B) Illumina or 454 Sequencing

C) De novo assembly

Assembly to reference

D) SAMtools & BWA

- Generate .sam and .bam files
- Produce .vcf report

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iMSAT

E) Filter .vcf report
- Remove all sites that have a polymorphism within $n$ bp
- Remove all SNPs

F) Identify STR motifs
- Count repeat lengths

G) Write output file
- Include 300 bp of leading and trailing sequence to aid in primer design

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Primer design & genetic analyses

User defines number ($n$) of bp for filtering

Filter non SSR indels

Output tab delimited files

.fasta files for import into primer software packages