Text S1. Information about main software parameters and command lines used in the sections *2.3. SNP calling and genotyping: defining a SNP panel for all locations studied* and *2.5. Multiplex MassARRAY design and implementation*.

Main options used for reads alignment and SNP genotyping:

Step	Software/module	Main options
Reference genome indexing and reads alignment	**Bowtie 1.3.0**	
	bowtie-build	—
	bowtie	--best --strata -m 1 -v 3
SNP calling and genotyping	**Stacks 2.41**	
	gstacks	--model marukilow --var-alpha 0.05 --gt-alpha 0.05 --max-clipped 0 --max-insert-len 0
	populations	—

Command lines:

2.3. SNP calling and genotyping: defining a SNP panel for all locations studied.

Bowtie 1.3.0

bowtie-build to index reference genomes

bowtie-build -f ReferenceGenome.fna Basename of the Bowtie index --threads 7 -q

Reads alignment against index (one command per sample)

bowtie --best --strata -m 1 -v 3 -p 7 --chunkmbs 20000 --sam -q --no-unal -x /Basename of the Bowtie index /sample.fq /sample.sam 2> /sample.log

Stacks 2.41

SNPs calling and genotyping

gstacks -t 7 -I /bams/ -O /gstacks/ -M /popmap.txt --model marukilow --var-alpha 0.05 --gt-alpha 0.05 --max-clipped 0 --max-insert-len 0

populations -t 7 -P /input/ -M /popmap.txt -O /output/ --vcf –genepop

2.5. Multiplex MassARRAY design and implementation.

Extract adjacent sequences to target position from reference genome (sequence length = 201 nucleotides)

perl FlankingRegions.pl -p /targetpositions.txt -g /ReferenceGenome.fna -o /output.fasta -s 100

Github link: https://github.com/adriancasanovachiclana/Genomic-scripts

Online manuals

Bowtie

http://bowtie-bio.sourceforge.net/manual.shtml

Stacks

http://catchenlab.life.illinois.edu/stacks/

References

Bowtie

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