Fast and cost-effective genetic mapping in apple using next-generation sequencing

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INPUT

1x .fastq

↓ barcode_splitter.py

96x .fastq

↓ bwa

96x .sam

→ SAMtools

File size

large → small

OUTPUT

1x .bed
1x .fam
1x .bim

↑ PLINK

1x .map
1x .ped

↑ vcftools
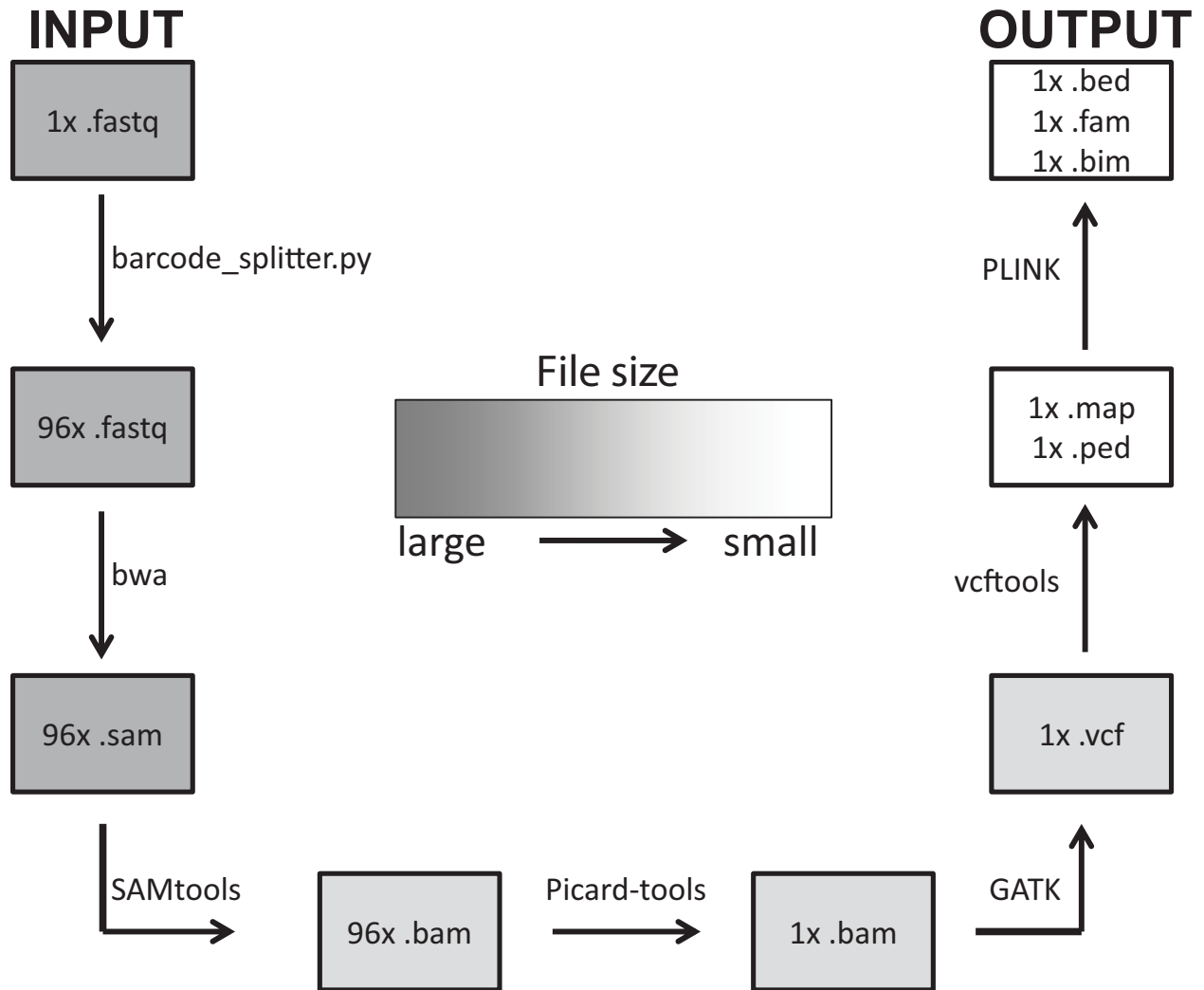
1x .vcf

↑ GATK

96x .bam → Picard-tools → 1x .bam

Figure S1 A custom GBS analysis pipeline. Each box represents a file type, indicated by its file extension, within the pipeline. Starting with a single .fastq file from the Illumina HiSeq 2000 sequencing machine and ending with a single set of PLINK files, the software packages and custom scripts used to move from one file type to another are indicated beside each arrow. Details of each step of the pipeline are provided in the Materials and Methods.
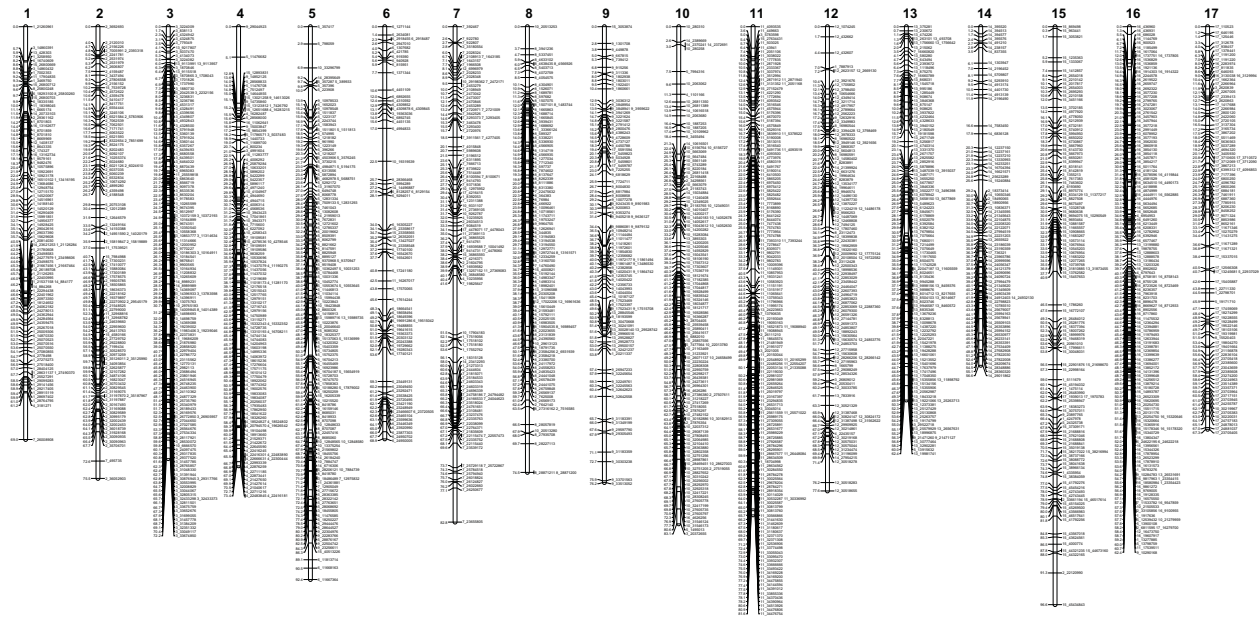
Figure S2 A composite genetic linkage map of the *Malus x domestica* genome. The map was constructed from 1994 SNPs discovered and genotyped using GBS, including SNPs from all three pseudo-testcross segregation types, in a Golden Delicious x Scarlet Spur F1 population.
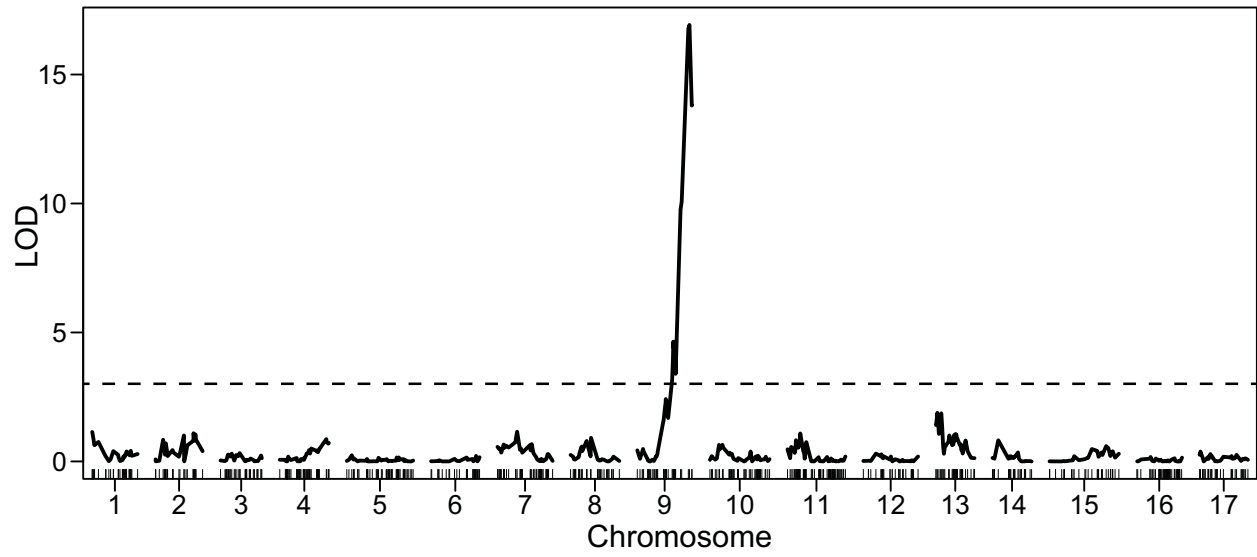
Figure S3 Genome-wide LOD scores for apple fruit skin color. Each SNP is represented by a single vertical line at the bottom of the plot. Only a single peak associated with skin color was identified on linkage group 9 and this peak overlaps with the known apple skin color locus. The horizontal dashed line represents the significance threshold determined by permutation.