WebPanel 3. SNP selection and Fluidigm genotyping validation

Fourteen hundred selected SNPs were successfully mapped to the ABFT reference genome, 929 remained after removing duplicates (those matching to the same contig on the same position), and 423 of the 929 fulfilled Fluidigm specifications. Genotyping of 15 SNPs of the 230 selected for validation in 184 samples was not successful, and one sample failed for more than 20% of the SNPs. The genotyping rate of remaining SNPs and individuals was 99%. Genotyping technical reproducibility, assessed by comparing the Fluidigm and RAD-seq derived genotypes for the 32 repeated samples, was 98%. Most of the mismatches between RAD-seq and Fluidigm derived genotypes were due to homozygous calls in RAD-seq that are heterozygous in Fluidigm (see below).

Genotyping technique		*Catalog from which SNPs originate*	
RAD-seq	*Fluidigm*	*With clones*	*Without clones*
AA	AB	85.24	76.04
	BB	0.02	0
AB	AA or BB	0.41	0.3
% of mismatches		2.85	1.25

Notes: From the average percent of mismatching genotypes between RAD-seq and Fluidigm for each catalog with and without clones, percentage of homozygote (AA) RAD-seq genotypes coded as heterozygotes (AB) or as homozygotes for an alternative allele (BB) in Fluidigm, and percentage of heterozygote (AB) RAD-seq genotypes coded as homozygotes (AA/BB) in Fluidigm.