

Tables

Table 1. Forward genetics screens developed in *Arabidopsis thaliana*, the lines involved in the crossing and the technologies used to identify the causative mutation in each case. The chromosome where the mutation was found and the mutated gene location are also specified.

Sample	Mutant		Wild-type	Method	Chr	Gene
OCF2	Col-0	x	Ler-0	SHOREmap	2	SOC1 (~18.8 Mb)
BCF2	Col-0	x	Col-0	NGM, SHOREmap, GATK and SAMtools	3	HASTY (~14.05 Mb)
mob1/ mob2	Col-0	x	Col-0	CandiSNP	5	CPK28 (~26.45 Mb)
sup#1	Ws-0	x	Col-0	Ratio of homozygous to heterozygous SNPs	4	SGT1b (~6.85 Mb)

Table 2. Measurement of the homozygous SNP density correlation to a theoretical normal distribution in several out-cross and back-cross experiments. Analysis of variance and distribution shape (kurtosis and skewness).

Sample	SNPs	Chr	r2	SD (Mb)	Kurtosis	Skewness
OCF2	151	2	0.949	6.01	1.85	-0.392
BCF2	15	3	0.959	3.20	2.02	0.201
mob1	25	5	0.944	7.20	2.69	-0.240
mob2	41	5	0.894	3.71	2.37	0.445
sup#1	4633	4	0.976	3.66	3.50	0.370

Table 3. SDM mutant identification success when using an automatic filtering approach to discard contigs. 3 different contig sizes analysed, the percentages of the maximum ratio used as threshold are specified. In brackets, the number of contigs discarded out of the total number of contigs.

Sample	Contig size (kb)	Threshold	Identification
OCF2	2-4	5% (230/6568)	Unsucessful
	5-10	3% (189/2634)	Sucessful
	10-20	3% (186/1328)	Sucessful
BCF2	2-4	35% (7807/7821)	Sucessful
	5-10	21% (108/3130)	Sucessful
	10-20	21% (95/1562)	Sucessful
mob1	2-4	17% (254/8992)	Unsucessful
	5-10	15% (239/3603)	Sucessful
	10-20	15% (220/1805)	Sucessful
mob2	2-4	35% (8950/8994)	Sucessful
	5-10	21% (195/3582)	Sucessful
	10-20	21% (189/1804)	Sucessful
sup#1	2-4	3% (228/6201)	Sucessful
	5-10	3% (153/2491)	Sucessful
	10-20	3% (93/1240)	Sucessful