

**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.

Study	Sample	Mutant		Wild-type	SNP caller
Galvão et al. 2012	OCF2	Col-0	x	Ler-0	SHOREmap
Allen et al. 2013	BCF2	Col-0	x	Col-0	NGM, SHOREmap, GATK and samtools
Monaghan et al. 2014	bak1-5 mob1 and mob2	Col-0	x	Col-0	CandiSNP
Uchida et al. 2014	sup#1	Ws-0	x	Col-0	Ratios of homozygous to heterozygous SNPs

**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.** Hypothetical candidate mutations obtained by SDM in out-cross and back-cross experiments and real mutation positions. (For simplicity, the 151 candidate positions predicted for sup#1 were not itemised here).

Sample	Cross	Chr	Mutated gene	Candidates	Position
					9773, 2
					55086,
					119055

Sample	Cross	Chr	Mutated gene	Candidates	Position
OCF2	Out-cross	2	SOC1 (~18.8 Mb)	28	119587 173637 174359 <b>188089</b> 189464 193083
BCF2	Back-cross	3	HASTY (~14.05 Mb)	4	<b>140508</b> 101637
mob1	Back-cross	5 (~26.45 Mb)	CPK28	9 11218614, 18036595, 18155812	111867 <b>264578</b>
mob2	Back-cross	5 (~26.45 Mb)	CPK28	10 <b>26560691, 26626055, 26710709,</b>	181433 182611 <b>267168</b>
sup#1	Out-cross	4	SGT1b (~6.85 Mb)	151	791043

**Table 4.**SDM mutation identification success when using different percentages of the maximum ratio as threshold to discard contigs. Four percentages were analysed for each sample.

	OCF2	BCF2	mob1	mob2	sup#1
1%	yes	yes	yes	no	yes
5%	yes	no	yes	no	yes
10%	yes	yes	yes	yes	no
20%	yes	yes	no	no	no