

Table S3 Reliable mutant directionality even when *Gl,Sb* marker pair is not used.

Mutant	<i>R,D</i>	<i>Gl,+</i>	<i>+,Sb</i>	<i>+,+</i>	<i>Sb,H</i>	<i>H,Pr</i>
psg19	→	10	7	2	←	←
psg3	→	14	3	0		
psg27	→	6	1	0	←	←
psg21		12	2	1	←	←
psg22	→	1	2	4	←	←
psg10	→	5	21	11	←	←
psg14	→	12	4	0	←	←
psg15	→	11	13	0		←
psg9	→	7	1	0	←	←
psg20	→	4	1	2	←	←

Direction of recombination “splits” in the *R,D*, *Sb,H*, and *H,Pr* pairs accurately locate mutations to the *Gl,Sb* interval.