


















Model	Chr.	3	6	6	5	8	4	4 and 6	10	9	3 and 9	pLOD	
	Position (cM)	136.5~138.5	25.6~33.6	99.6~105.6	118.6~120.6	49.6~63.6	75.1		1.1	72.7			
	Validated QTL	<i>qATL3</i>	<i>qATL6.1</i>	<i>qATL6.2</i>	<i>qATL5</i>								
	Effect	Main	Main	Main	Main	Main	Main	Interaction	Main	Main	Interaction		
1		1	0	0	0	0	0	0	0	0	0	1.75	
2		1	1	0	0	0	0	0	0	0	0	4.22	
3		1	1	1	0	0	0	0	0	0	0	5.35	
4		1	1	1	1	0	0	0	0	0	0	8.05	
5		1	1	1	1	1	0	0	0	0	0	7.96	
6		1	1	1	1	1	1	0	0	0	0	7.90	
7		1	1	1	1	1	1	1	0	0	0	7.62	
8		1	1	1	1	1	1	1	1	0	0	7.03	
9		1	1	1	1	1	1	1	1	1	1	6.40	
10		1	1	1	1	1	1	1	1	0	0	7.03	
11		1	1	1	1	1	1	1	0	0	0	7.73	
12		1	1	1	1	1	1	0	0	0	0	7.90	
13		1	1	1	1	1	0	0	0	0	0	7.96	
14		1	1	1	1	0	0	0	0	0	0	8.05	
15		1	0	1	1	0	0	0	0	0	0	5.61	
16		0	0	1	1	0	0	0	0	0	0	3.37	
17		0	1	0	0	0	0	0	0	0	0	1.55	

**Figure S2.** Model selections in multiple QTL mapping including main and interaction effects for anther length.

0 and 1 represent excluding and including QTL to models, respectively. Model 4 and 14 showed the highest penalty LOD score, suggesting that the model including *qQTL3*, *qATL5*, *qATL6.1*, and *qATL6.2* was the best model explaining anther length in the BC<sub>3</sub>F<sub>1</sub> population.