

**Additional File 7.** Results of positive selection using site models

Branches	Models	$\ln L$	Parameters	PSS <sup>3</sup>
Large <sup>1</sup>	M0	-13826.6585	$\omega = 0.1777$	-
	M3	-13511.5122	$p_0 = 0.2974, p_1 = 0.4798, p_2 = 0.2228$	n.d. <sup>4</sup>
			$\omega_0 = 0.0151, \omega_1 = 0.1715, \omega_2 = 0.5014$	
	M1a	-13681.8672	$p_0 = 0.8422, p_1 = 0.1578$	-
			$\omega_0 = 0.1451, \omega_1 = 1.0000$	
	M2a	-13681.8672	$p_0 = 0.8422, p_1 = 0.1578, p_2 = 0.00000$	n.d.
			$\omega_0 = 0.1451, \omega_1 = 1.0000, \omega_2 = 27.2532$	
	M7	-13509.8118	$\beta(0.6711, 2.6316)$	-
M8	-13509.8124	$\beta(0.6711, 2.6317)$	n.d.	
		$p_1 = 0.0000, \omega = 1.0000$		
Small <sup>2</sup>	M0	-10086.6556	$\omega = 0.1903$	-
	M3	-9892.8530	$p_0 = 0.4314, p_1 = 0.3686, p_2 = 0.2000$	n.d.
			$\omega_0 = 0.0210, \omega_1 = 0.2345, \omega_2 = 0.5702$	
	M1a	-9981.9712	$p_0 = 0.7960, p_1 = 0.2040$	-
			$\omega_0 = 0.1255, \omega_1 = 1.0000$	
	M2a	-9981.9712	$p_0 = 0.7960, p_1 = 0.2040, p_2 = 0.0000$	n.d.
			$\omega_0 = 0.1255, \omega_1 = 1.0000, \omega_2 = 36.8437$	
	M7	-9894.3065	$\beta(0.5060, 1.8960)$	-
$\beta(0.5099, 1.8960)$				
M8	-9894.3098	$p_1 = 0.0000, \omega = 3.8696$	n.d.	

<sup>1</sup>, The sequences used in the large data include the Brassicaceae-specific gene copies (sequences used in the phylogenetic analysis in Figure 2) and their original copies (sequences used in the

phylogenetic analysis in Figure 1).

<sup>2</sup>, The sequences used in the small data include the Brassicaceae-specific gene copies and the two parasitic plant gene copies (sequences used in the phylogenetic analysis in Figure 2).

<sup>3</sup>, Sites undergone positive selection calculated by Bayes Empirical Bayes (BEB) analysis.

<sup>4</sup>, not detected.