

Supporting Information

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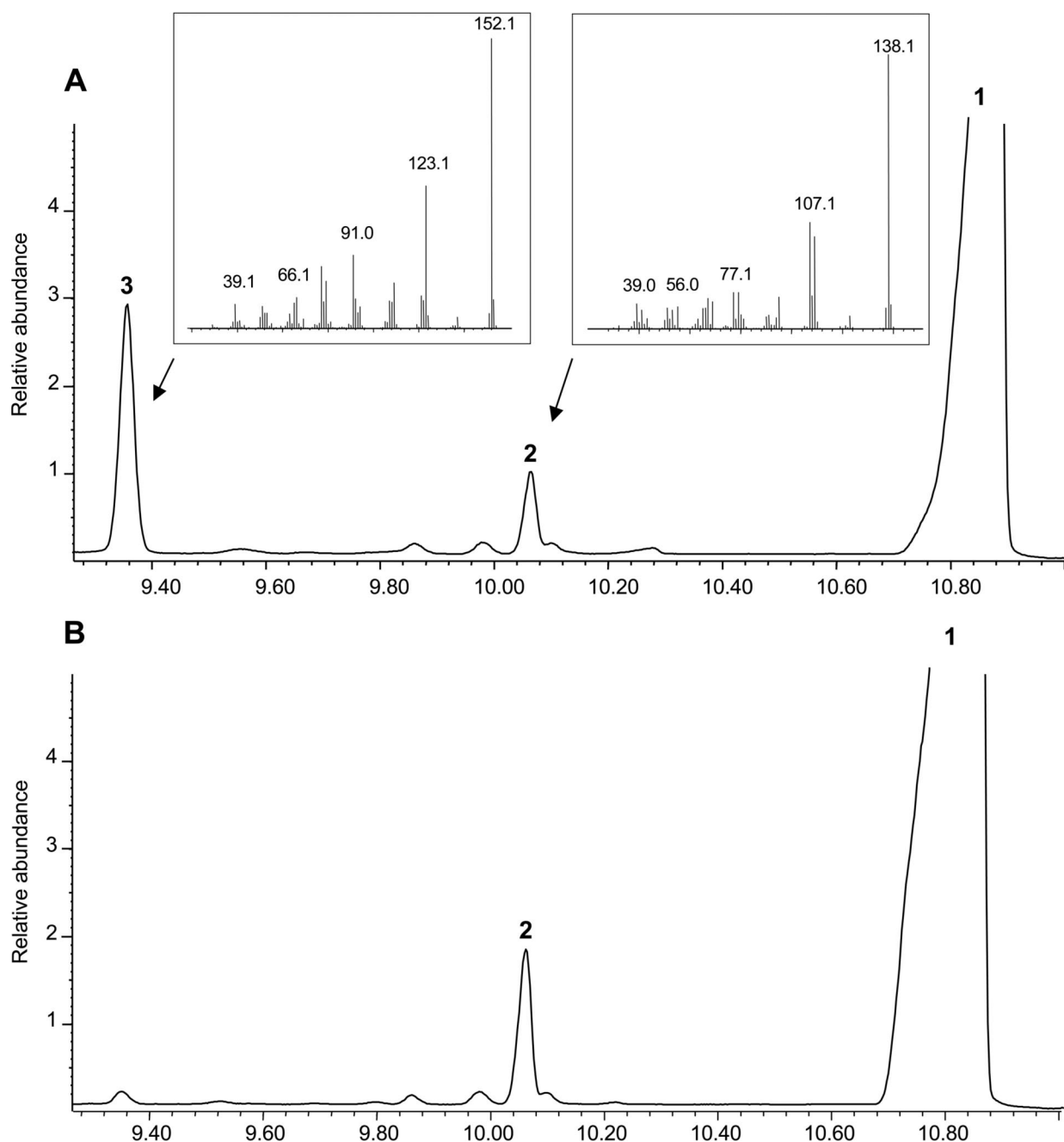


Fig. S1. Gas chromatography-mass spectrometry (GC-MS) analysis of mutant OOMTs reaction products. (A) Incubation of OOMT1 Y127F with orcinol (500 μ M) in the presence of *S*-adenosyl-L-methionine (1 mM). (B) Incubation of OOMT2 F126Y with orcinol (500 μ M) in the presence of *S*-adenosyl-L-methionine (1 mM). Peak 1, orcinol; peak 2, MHT; peak 3, DMT. Total ion chromatograms are shown, and mass spectra of the peaks matched those of the corresponding authentic standards. Reactions were carried out in a total volume of 200 μ l with 2 μ g of purified protein and were allowed to proceed for 60 min. GC-MS analyses were performed according to Lavid *et al.* [Lavid N, *et al.* (2002) *Plant Physiol* 129:1899–1907]. Reaction products of native OOMT1 and OOMT2 were characterized previously by Lavid *et al.*

Table S1. Kinetic parameters of OOMTs with orcinol and MHT

Gene name	ORCINOL				MHT			
	K_m , μM	$K_{cat} \cdot 10^{-3}$, s^{-1}	K_{cat}/K_m $(\text{M}^{-1} \cdot \text{s}^{-1})$	Specific activity, $\text{pkat} \cdot \text{mg}^{-1}$	K_m (μM)	$K_{cat} \cdot 10^{-3}$, s^{-1}	K_{cat}/K_m , $\text{M}^{-1} \cdot \text{s}^{-1}$	Specific activity, $\text{pkat} \cdot \text{mg}^{-1}$
Old Blush OOMT1	69 (7)	174 (4)	2,538 (202)	2,200 (49)	50 (4)	19 (2.5)	386 (16)	241 (30)
Old Blush OOMT2	127 (24)	37 (2)	304 (56)	460 (18)	11 (1)	52 (3)	4,797 (349)	657 (38)
Old Blush OOMT1 Y127F	170 (9)	27 (3)	158 (24)	333 (32)	31 (5)	53 (2)	1,739 (259)	665 (22)
Old Blush OOMT2 F126Y	93 (4)	22 (2)	242 (3)	280 (14)	90 (9)	3.7 (0.3)	42 (7)	47 (3)
<i>R. chinensis</i> B (OOMT1-like)	56 (8)	183 (9)	3,083 (453)	2,296 (122)	60 (8)	28 (1.4)	593 (99)	352 (17)
<i>R. gigantea</i> E (OOMT1-like)	106 (9)	171 (10)	1,618 (240)	2,140 (134)	58 (10)	22 (2)	370 (13)	277 (37)
<i>R. roxburghii</i> A (OOMT2-like)	52 (3)	15 (1.5)	303 (16)	189 (6)	9.5 (1.5)	30 (1)	3,060 (361)	379 (9)
<i>R. rugosa</i> A (OOMT2-like)	72 (5)	10 (0.4)	140 (4)	126 (5)	8 (1.4)	24 (0.5)	3017 (437)	297 (4)

Data are expressed as the means of triplicates assays and standard errors are indicated in parentheses.

Section	Species	Gene	Size, bp	Accession	OOMT Type	
<i>Indicae</i>	<i>R. chinensis</i> cv. Old Blush	OOMT1	1324	AJ786302	1	
		OOMT2	1321	AJ786303	2	
	A	1302	AM182763	1		
	B	1305	AM182764	2		
	C	1305	AM182765	2		
	D	1333	AM182766	1		
	E	1324	AM182767	1		
	F	1337	AM182768	2		
		pseudogene A	668	AM182834	2	
	<i>R. chinensis</i> <i>spontanea</i>	A	1305	AM182780	2	
		B	1324	AM182781	1	
		C	1324	AM182782	1	
		D	1321	AM182783	2	
		E	1324	AM182784	1	
		F	1305	AM182785	2	
		G	1305	AM182786	2	
		H	1305	AM182787	2	
	<i>R. gigantea</i>	A	1324	AM182794	1	
		B	1324	AM182795	2	
		C	1324	AM182796	1	
		D	1324	AM182797	2	
		E	1324	AM182798	1	
		F	1324	AM182799	2	
		G	1324	AM182800	2	
		H	1321	AM182801	2	
		I	1324	AM182802	2	
		J	1324	AM182803	1	
		K	1309	AM182804	2	
			pseudogene A	1261	AM182842	2
		<i>R. odorata</i> cv. Hume's Blush	A	1324	AM182823	2
			B	1321	AM182824	2
			C	1324	AM182825	2
	D		1324	AM182826	1	
	E		1321	AM182827	2	
	F		1337	AM182828	2	
	A		1324	AM182829	1	
	<i>R. odorata</i> <i>ochroleuca</i> cv. Parks Yellow	B	1324	AM182830	2	
		C	1324	AM182831	2	
		D	1337	AM182832	2	
		E	1324	AM182833	1	
		A	1278	AM182805	2	
	<i>Pimpinellifoliae</i>	<i>R. hugonis</i>	B	1278	AM182806	2
			A	1330	AM182811	2
<i>Synstylae</i>	<i>R. phoenicia</i>	A	1328	AM182817	2	
		B	1328	AM182818	2	
	<i>R. wichuraiana</i>	C	1328	AM182819	2	
		D	1328	AM182820	2	
		E	1328	AM182821	2	
		F	1328	AM182822	2	
Subgenus <i>Platyrhodon</i>	<i>R. roxburghii</i>	A	1324	AM182812	2	
		pseudogene A	1309	AM182849	2	
		pseudogene B	1298	AM182850	2	

OOMT1-like genes (based on the presence of a tyrosine residue at the position corresponding to residue 127 in Old Blush 1) are indicated in bold.