

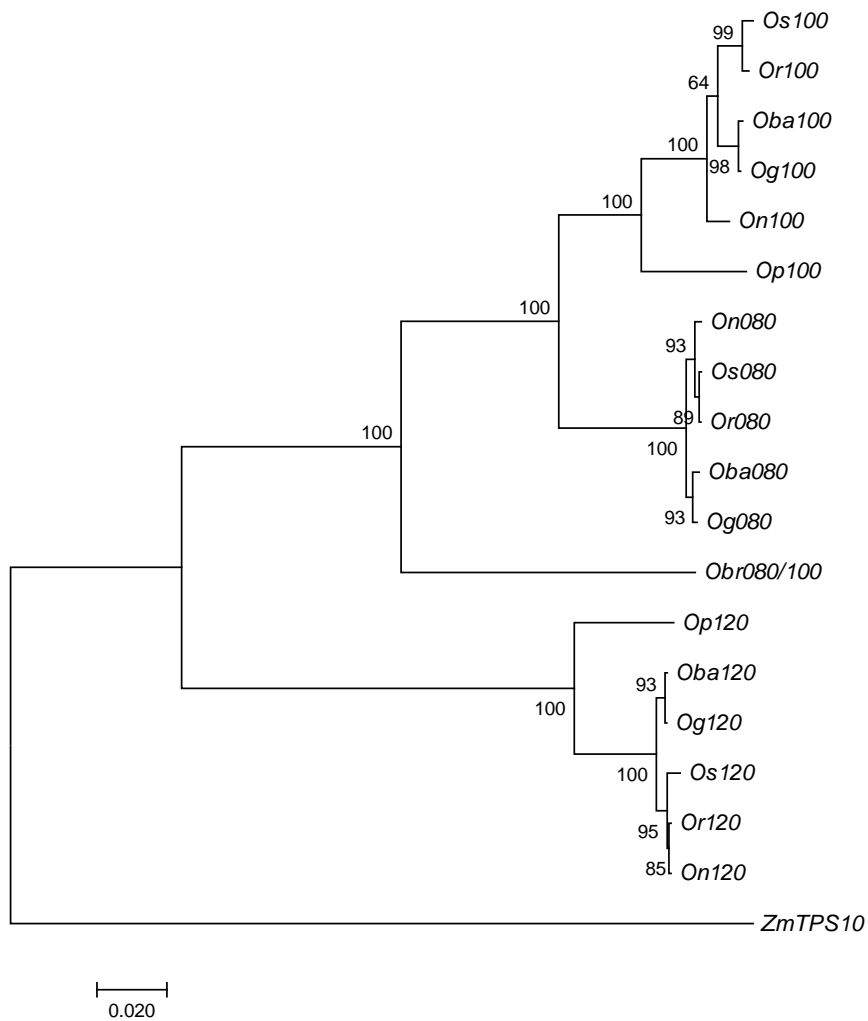
Supplemental Table S1. Sequence identities of terpene synthase (*TPS*) genes. The respective *TPS* genes from the six *Oryza* species were compared to the three *TPS* genes *Os08g07080*, *Os08g07100*, and *Os08g07120* from *O. sativa*. The comparison was based on genomic sequences.

Species	ID	New name	Os08g07080	Os08g07100	Os08g07120
<i>O. rufipogon</i>	ORUFI08G04560	Or080	100.0%	73.0%	50.1%
		Or100	73.0%	100.0%	47.5%
		Or120	49.8%	47.8%	99.8%
<i>O. nivara</i>	ONIVA06G22070	On080	98.2%	73.2%	49.8%
		On100	73.0%	99.4%	48.3%
		On120	50.3%	47.9%	98.5%
<i>O. glaberrima</i>	ORGLA08G0035100	Og080	97.5%	73.1%	50.1%
	ORGLA08G0035300	Og100	71.1%	92.4%	50.1%
	ORGLA08G0035500	Og120	48.1%	48.9%	87.2%
<i>O. barthii</i>	OBART08G04100	Oba080	97.4%	73.0%	50.2%
	OBART08G04130	Oba100	71.1%	92.3%	50.1%
	OBART08G04130	Oba120	46.2%	47.3%	85.8%
<i>O. punctata</i>	OPUNC08G04040	Op100	76.8%	81.0%	49.0%
	OPUNC08G04060	Op120	51.1%	49.6%	76.1%
<i>O. brachyantha</i>		Obr080/100	58.9%	60.1%	47.6%

Supplemental Table S2. Primers used for gene expression analysis by RT-qPCR.

Primer name	Sequence (5' to 3')
<i>080TPS</i> FP	GTTATATGCTCCAACATGGTG
<i>080TPS</i> RP	TTCATCATATCCTTCCATGAG
<i>100TPS</i> FP	TCATCGACACCTGCAGCTAA
<i>100TPS</i> RP	TTCTTCTTTTAGCACTTCAG
<i>120TPS</i> FP	CCTTACACTACCAACAGAAC
<i>120TPS</i> RP	GCTGTTCGTGCAAGATCAAC
<i>OsUBQ5</i> FP	ACCACTTCGACCGCCACTACT
<i>OsUBQ5</i> RP	ACGCCTAAGCCTGCTGGTT

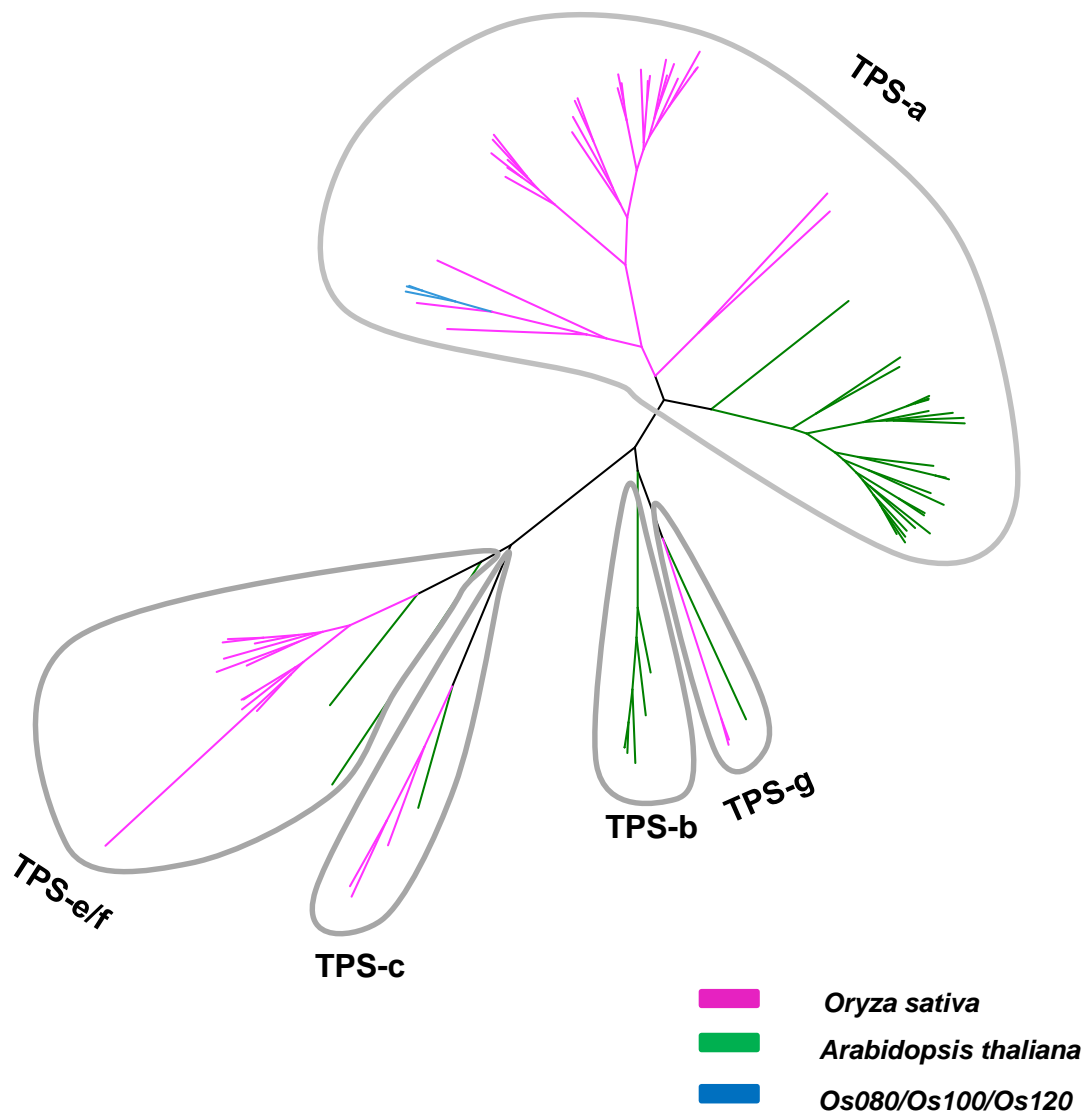
FP: forward primer; RP: reverse primer



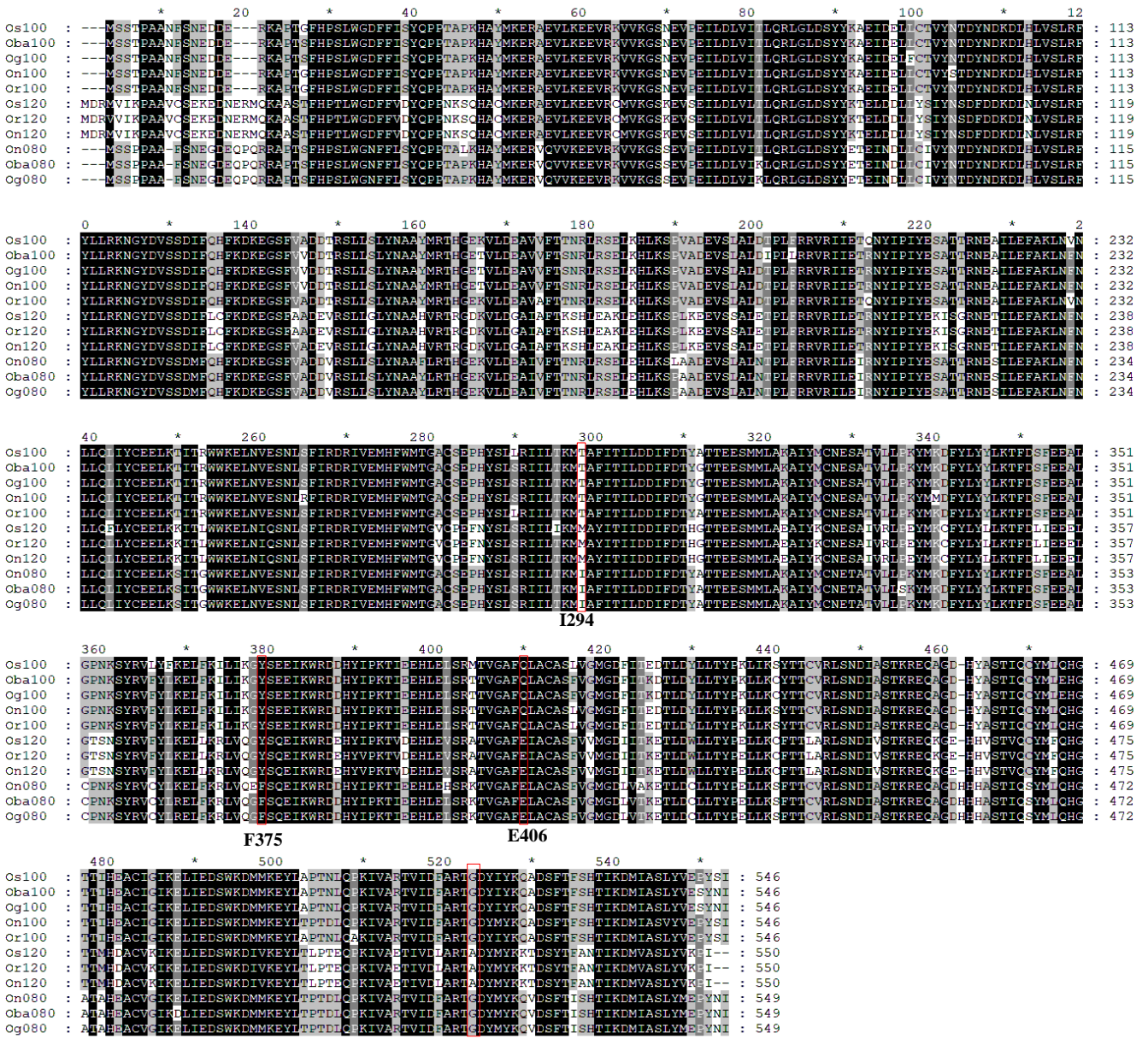
Supplemental Figure S1. Phylogenetic tree of *TPS*s based on cDNA sequences. The *TPS* genes are from the seven *Oryza* species. A maize *ZmTPS10* was used as outgroup.

<i>Or120</i>	TCTTTATTGTGAGGAGCTAAAAAAG	750
<i>On120</i>	TCTTTATTGTGAGGAGCTAAAAAAG	750
<i>Os120</i>	TCTTTATTGTGAGGAGCTAAAAAAG	750
<i>Oba120</i> & <i>Og120</i>	TCTTTATTGTGAGTAGCTAAAAAAG	750
	*	
<i>Or120</i>	ATCACATTATGGTGGGAGGAGCTTA	775
<i>On120</i>	ATCACATTATGGTGGGAGGAGCTTA	775
<i>Os120</i>	ATCACATTATGGTGGGAGGAGCTTA	775
<i>Oba120</i> & <i>Og120</i>	ATCACATTATGGTGGGAGGAGCTTA	775
	*	
<i>Or120</i>	GTTCAAGGATACTCACAGGAGATTA	1150
<i>On120</i>	GTTCAAGGATACTCACAGGAGATTA	1150
<i>Os120</i>	GTTCAAGGATACTCACAGGAGATTA	1150
<i>Oba120</i> & <i>Og120</i>	GTTCAAGGATACTAACAGGAGATTA	1150
	*	

Supplemental Figure S2. *Oba120* and *Og120* as pseudogenes. There are two mutation “G” to “T”, G” to “T” and “C” to “A”. The outcome of these mutations is the creation of three stop codons: TAG, TAG and TAA.



Supplemental Figure S3. Phylogenetic tree of all terpene synthase (*TPS*) genes from *Oryza sativa* and *Arabidopsis thaliana*. The phylogenetic tree was conducted using cDNA sequences. The *TPS* genes from the two species are color-coded. Also indicated are *TPS* subfamilies and the three tandemly arrayed *TPS* genes from *O. sativa* (*Os080*, *Os100* and *Os120*) within the *TPS-a* subfamily.



Supplemental Figure S4. Multiple sequenced alignment of *Oryza* TPSs. Indicated are four amino acids in the active sites that are implicated in determining product specificity.