## Table S1. Media recipes

Media	Composition per litre of media		
Water agar (1%)	10 g Agar		
Potato Dextrose Agar (PDA)	PDA: 39 g Difco <sup>™</sup> dehydrated PDA		
Fries (pH 6)	30.0 g sucrose		
	5.0 g yeast extract		
	5.0 g ammonium tartrate		
	1.0 g NH <sub>4</sub> NO <sub>3</sub>		
	1.0 g KH <sub>2</sub> PO <sub>4</sub>		
	0.5 g MgSO₄·7H₂O		
	0.13 g CaCl		
	0.1 g NaCl		
	If solid media add 15.0 g Agar		
Lysogeny Broth (LB)	10.0 g NaCl		
	10.0 g triptone		
	5.0 g yeast extract		
	If solid media add 15.0 g Agar		
YPD	10 g yeast extract		
	20.0 g triptone		
	After autoclaving add:		
	20.0 g glucose		
Synthetic dropout media lacking uracil	I 6.7 g Yeast base media (no amino acids)		
(pH 5.8)	1.6 g amino acid mix lacking uracil		
	After autoclaving add 30 g glucose		
	If solid media add 15.0 g Bacto Agar		

## Table S2. List of primers

Name	forward	reverse	
Phl	ccctcgttgaccaagaatc	aagttcgtggacacgacct	
Leo	gacgtgaccctgttcatca	gagcattcactaggcaacca	
Sts01_5flank	ttctggttcggaataagctctt	gagcattcactaggcaa- atttattgtgcgcgttcg	
Sts01_3flank	ctaagaaccagttgctccc- tctttgcacctacgatttttcc	c- cattcctgattcctcttgtttg	
Sts02_5flank	gcgcggaatggtgtaaagt	gagcattcactaggcaa- aaagatgatctcgcctgcc	
Sts02_3flank	ctaagaaccagttgctcccc- tgaaccggcgtaccagttta	accaacacgtcagtgacgac	
XW_STS01	atcaactatcaactattaactatatcgtaatacca-	tgtcatttaaattagtgatggtgatggtgatgcac-	
	atgtcccattcccgccacga	cacctccacggcagtgacct	
XW_STS02_exon1	atcaactatcaactattaactatatcgtaatacca-	gacccatggagaagcacatgactccggacatga	
	atggctccgatagatgcatca	agcctttaccaagatcggcatgtc	
XW_STS02_exon2	tactttgagtaccgacatgccgatcttggtaaa	tgtcatttaaattagtgatggtgatggtgatgcac-	
	ggcttcatgtccggagtcatgtg	accccaaatccttccttcattg	
Phleo_qPCR	ggaagttcgtggacacga	gacgtgaccctgttcatca	
Elng.f_qPCR	atgatcgacgtttccacc	tcaatagcctcgaggagg	
Actin_qPCR	agtcgaagcgtggtatcct	acttggggttgatgggag	
SnToxA_qPCR	gtccgtctgtcaacaacatcg	tcagttcccacgagcctatagc	

## **Table S3.** NMR data for eudesma-4,11-diene (**1**) (300MHz, CDCl<sub>3</sub>). Chemical shifts ( $\delta$ ) for C (C<sup>13</sup> NMR) and H (H<sup>1</sup> NMR) and C $\rightarrow$ H correlation at 2-4 bonds distance (HMBC) are presented.

Carbon	Сδ	$H\delta_a$	$H\delta_{b}$	HMBC
number	(ppm)	(ppm)	(ppm)	с→н
1#	40.45	1.32	1.5	14
2	19.26	1.57		
3	33.32	1.89	1.99	15
4	124.69	-	-	15
5	135.04	-	-	14, 15
6	30.91	2.54		
7	46.98	1.87	-	13
8	27.83	1.59		
9#	42.44	1.29	1.51	14
10	34.64	-	-	14
11	151.01	-	-	13
12	108.19	4.70	4.72	13
13	21.03	1.75	-	12
14	24.8	1.04	-	
15	19.44	1.61	_	

<sup>#</sup> Data insufficient to distinguish between C1 and C9

## Table S4. NMR data for acora-4,9-diene (4) (300MHz, CDCl<sub>3</sub>).

Chemical shifts ( $\delta$ ) for C (C<sup>13</sup> NMR) and H (H<sup>1</sup> NMR) and C $\rightarrow$  H correlation at 2-4 bonds distance (HMBC) are presented.

Carbon	Сδ	$H\delta_a$	$H\delta_b$	HMBC
number	(ppm)	(ppm)	(ppm)	с→н
1	47.94	-	-	2a, 2b⁺
2	26.78	1.58*	1.67	3b
3	34.77	1.78	2.09	2a
4	149.09	-	-	2b⁺, 15
5	123.97	5.27	-	15
6	29.22	1.98*		2a, 2b <sup>+</sup> , 14 <sup>+</sup>
7	28.4	1.83	-	12, 13
8	32.63	1.97	2.18	7 <i>,</i> 14 <sup>+</sup>
9	121.6	5.38	-	14+
10	134.4	-	-	2a, 2b $^{+}$ , 14 $^{+}$
11	55.49	1.65*	-	12, 13
12	21.48	0.81	-	7 <i>,</i> 11 <sup>+</sup> , 13
13	23.29	0.93	-	12
14	23.99	1.66*	-	
15	15.29	1.6*	-	

\*Signals not clear on H NMR, values obtained from HSQC

<sup>+</sup>HMBC correlations with H 2b, H11 and H14 are tentative because signals are too close



Figure S1. Organisms that showed low or no sensitivity to *P. nodorum* VOCs emitted *in vitro*.

Split plate assay of the effect of VOCs produced by wild type *P. nodorum* (SN15). The top row of plates show effect (or lack of effect) caused by SN15 VOCs over *Cytospora sp., Fusarium oxysporum, Eutiarosporella tritici-australis, Pseudomonas syringae, Flavobacterium sp.* and *Bacillus cereus*. The bottom row of plates presents each test organism next to the control, media only: non-inoculated Fries agar.



Figure S2. GC-MS from the isolated sesquiterpenes produced by STS1 expressed in yeast.

The peak corresponding to **4** is marked with its number. The presented structures correspond to the best match within the NIST library. The numbers are the score given by the NIST library (the score could go up to 1000). The proposed structure for **4** is isosativene but did not show a good spectral match to the NIST library as the lower score indicates.



Figure S3. GC-MS from the isolated sesquiterpenes produced by STS2 expressed in yeast.

The peaks corresponding to **1** and **2** are marked with their number. The presented structures correspond to the best match within the NIST library. The numbers are the score given by the NIST library (the score could go up to 1000).



Figure S4. MSMS Identification of  $\beta$ -elemene.

Figure shows the MS chromatogram (A), MS spectrum (B) and  $MS^2$  spectra of ion 93<sup>+</sup> (C), 107<sup>+</sup> (D), 147<sup>+</sup> (E) and 189<sup>+</sup> (F). All panels compare acquired data from the spectra (above), and the *P. nodorum* sample (below).





Figure shows the MS chromatogram (A), MS spectrum (B) and MS/MS spectra of ion  $119^+$  (C),  $133^+$  (D),  $147^+$  (E) and  $161^+$  (F). All panels compare acquired data from the spectra (above), and the purified sample from *P. nodorum* (below).



Figure S6. Eudesma-4,11-diene (1) H NMR (300MHz, CDCl3)



Figure S7. Eudesma-4,11-diene (1) C NMR (300MHz, CDCl<sub>3</sub>)



Figure S8. Eudesma-4,11-diene (1) HSQC (300MHz, CDCl<sub>3</sub>)



Figure S9. Eudesma-4,11-diene (1) HMBC (300MHz, CDCl<sub>3</sub>)



Figure S10. Acora-4,9-diene (4) H NMR (300MHz, CDCl<sub>3</sub>)



Figure S11. Acora-4,9-diene (4) C NMR (300MHz, CDCl<sub>3</sub>)



Figure S12. Acora-4,9-diene (4) HSQC (300MHz, CDCl<sub>3</sub>)



Figure S13. Acora-4,9-diene (4) HMBC (300MHz, CDCl<sub>3</sub>)



**Figure S14.** Pathogenicity test of sts1 and sts2 on wheat 5 days post inoculation. Two *sts1*, two *sts2* strains and two ectopic mutants were inoculated on wheat cv. Axe. SN15 was used as a positive control and 0.02% tween 20 solution as negative control.



**Figure S15**. Neighbour joining phylogenetic tree of fungal terpene synthases (plant sesquiterpene synthases as outliers). Red arrow indicates *P. nodorum* Sts1, blue arrow indicates *P. nodorum* Sts2, red asterisk indicates a characterised trichodiene synthase, and blue asterisks indicate characterised aristolochene synthases. The presented chemical structures correspond to some of the reported products of the terpene synthases of each group.