

**Table S1** The results of eQTLs

Year	eQTL1	Position1 (cM)	eQTL2	Position2 (cM)	LOD	PVE (%)	ADDby ADD
2019	<i>eQKnps.sau-2D</i>	280	<i>eQKnps.sau-4D.1</i>	215	5.08	6.33	-2.83
2019	<i>eQKnps.sau-2B</i>	175	<i>eQKnps.sau-4D.2</i>	220	5.65	8.73	-3.27
2019	<i>eQKnps.sau-3B</i>	15	<i>eQKnps.sau-5A</i>	0	5.29	5.90	-2.10
Mean	<i>eQKnps.sau-1D</i>	165	<i>eQKnps.sau-5D</i>	85	5.02	8.04	1.40

**Table S2** Kompetitive allele-specific PCR (KASP) markers *for QKnps.sau-2D.1*

Marker	Sequences (5' to 3')
<i>KASP-AX-111462389-FAM</i>	<b>GAAGGTGACCAAGTTCATGCTACCACAAGTGTTTTCGTTTTGT</b>
<i>KASP-AX-111462389-HEX</i>	<b>GAAGGTCGGAGTCAACGGATTACCACAAGTGTTTTCGTTTTGG</b>
<i>KASP-AX-111462389-R</i>	<b>GACAAAGCACGAAAAGTCC</b>

Note: The FAM probe sequence of the forward primer was GAAGGTGACCAAGTTCATGCT, and the HEX probe sequence of the reverse primer was GAAGGTCGGAGTCAACGGATT

**Table S3** The re-mapping results of *QKnps.sau-2D.1*

QTL	Environment	Interval (cM)	Left Marker	Right Marker	LOD	PVE (%)	Add
<i>QKnps.sau-2D.1</i>	2016	76.5-77.5	<i>AX-109283238</i>	<i>AX-111606890</i>	15.19	16.13	2.21
	2019	76.5-77.5	<i>AX-109283238</i>	<i>AX-111606890</i>	7.99	10.24	2.54
	2021	76.5-77.5	<i>AX-109283238</i>	<i>AX-111606890</i>	9.87	11.77	2.63
	Mean	76.5-77.5	<i>AX-109283238</i>	<i>AX-111606890</i>	12.72	15.90	2.01

**Table S4** The results of phenotyping and genotyping by *KASP-AX-111462389* in the CN18 x T1208 RIL population

QTL	Environment	Genotype <i>aa</i>	Genotype <i>AA</i>	Difference	<i>P</i> value
<i>QKnps.sau-2D.1</i>	2016	37.36(n=148)	43.29(n=175)	5.92	$P<0.001$
	2019	62.53(n=148)	68.64(n=175)	6.11	$P<0.001$
	2021	57.80(n=148)	63.56(n=175)	5.76	$P<0.001$
	mean	52.54(n=148)	58.41(n=175)	5.87	$P<0.001$

**Table S5** The results of phenotyping and genotyping by *KASP-AX-111462389* in the CN17 x CN11 RIL population

QTL	Genotype <i>aa</i>	Genotype <i>AA</i>	Difference	<i>P</i> value
<i>QKnps.sau-2D.1</i>	41.45 (n=60)	46.93(n=42)	5.48	$P < 0.05$

**Table S6** The 15 genes in the interval of the QTL

Gene ID name	Annotation
<i>TraesCS2D02G138100</i>	Hepatoma-derived growth factor-related protein 2
<i>TraesCS2D02G138200</i>	Transmembrane protein 115
<i>TraesCS2D02G138300</i>	BTB-POZ and MATH domain protein
<i>TraesCS2D02G138400</i>	Terpene synthase
<i>TraesCS2D02G138500</i>	Terpene synthase
<i>TraesCS2D02G138600</i>	Terpene synthase
<i>TraesCS2D02G138700</i>	carboxyl-terminal peptidase, putative (DUF239)
<i>TraesCS2D02G138800</i>	Lipase
<i>TraesCS2D02G138900</i>	ARM repeat superfamily protein
<i>TraesCS2D02G139000</i>	cDNA, clone: J075123K08, full insert sequence
<i>TraesCS2D02G139100</i>	Terpene synthase
<i>TraesCS2D02G139200</i>	Cysteine desulfurase
<i>TraesCS2D02G139300</i>	Microtubule-actin cross-linking factor 1
<i>TraesCS2D02G139400</i>	Chaperone protein dnaJ-related
<i>TraesCS2D02G139500</i>	Chaperone protein dnaJ-related