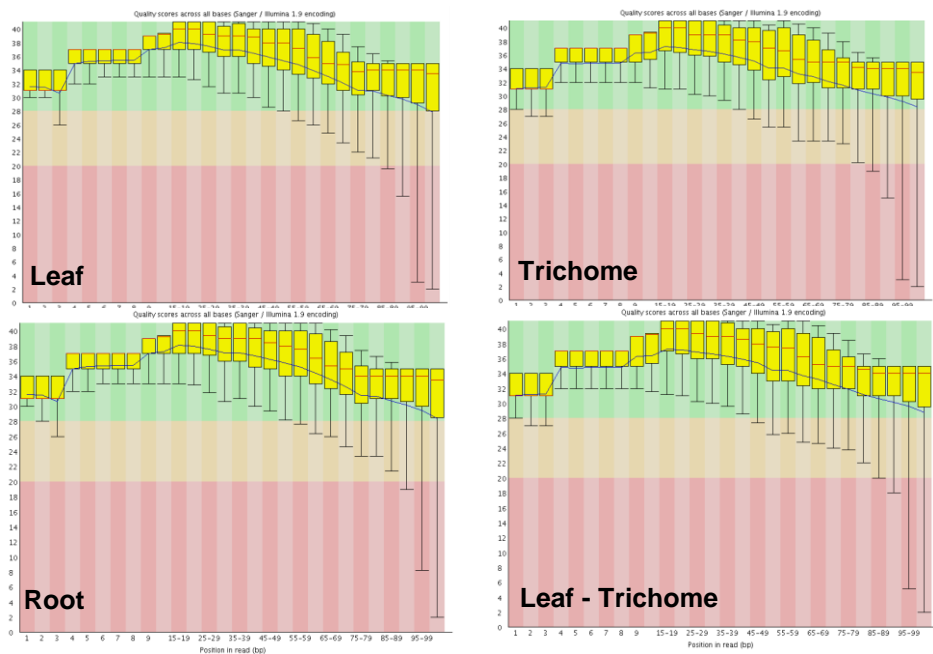


**Supplementary Figure 1. Trichomes on sweet basil leaf surface and composition of sweet basil essential oil.** (A) Scanning electron microscope image of sweet basil leaf showing three types of trichomes, a, Non glandular hairy trichome; b, Peltate glandular trichome (PGT); c, Capitate glandular trichome. (B) Isolated PGT of sweet basil stained with DAPI. (C) Process of secretion by PGT, a, presecretory stage; b, formation of storage cavity; c, secretion into the storage cavity. (D) GC-MS analysis of sweet basil leaf showing the presence of monoterpenes, 1, α-pinene, 2, β-pinene, 3, Eucalyptol, 4, linalyl acetate, phenylpropene 5, Eugenol, and sesquiterpene, 6, α-bergamotene, 7, germacrene-D, 8, γ-muurolene, 9, β-copaene.

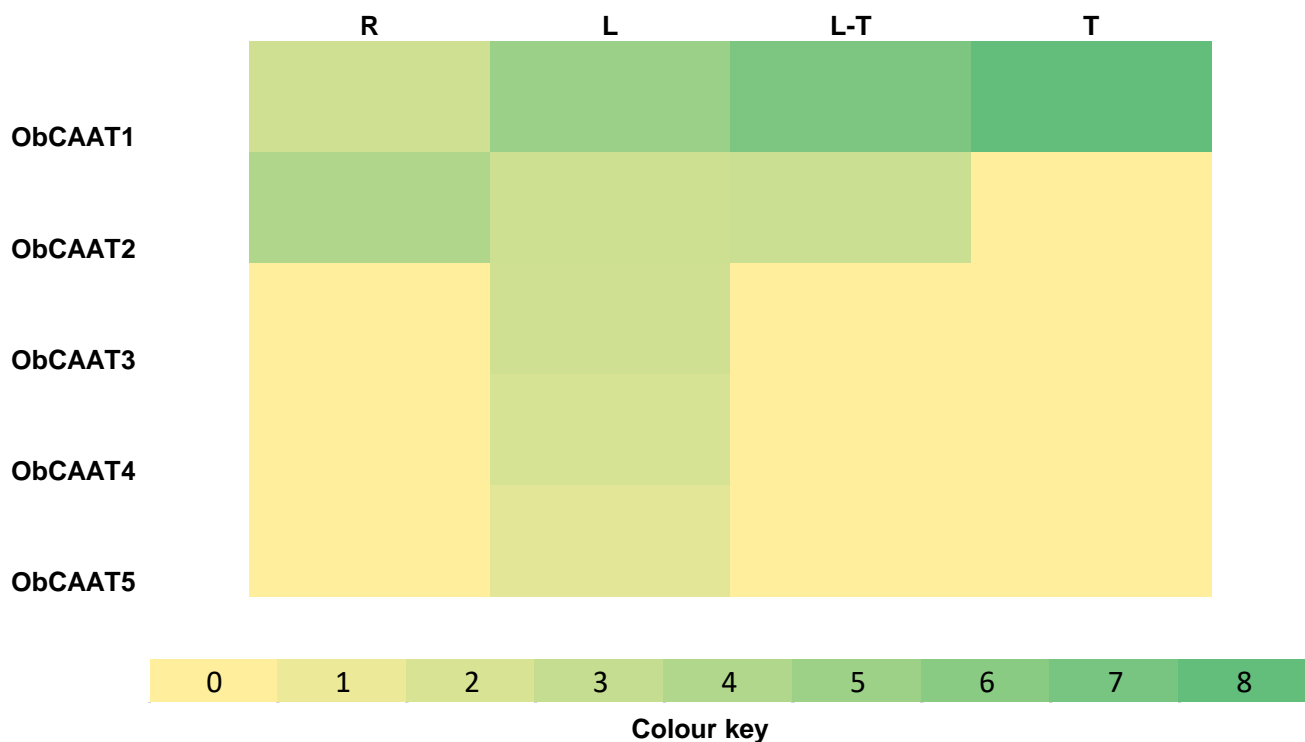


Overview of quality of deep sequencing

Sample	Total Bases	Read Count	N (%)	GC (%)	Q20 (%)	Q30 (%)
Leaf	18,449,677,272	182,670,072	0.007	48.3	93.99	85.84
Root	19,013,829,942	188,255,742	0.007	46.46	94.38	86.62
Trichome	17,198,322,218	170,280,418	0.030	44.18	96.11	89.85
Leaf-Trichome	20,491,806,170	202,889,170	0.029	48.17	95.18	87.96

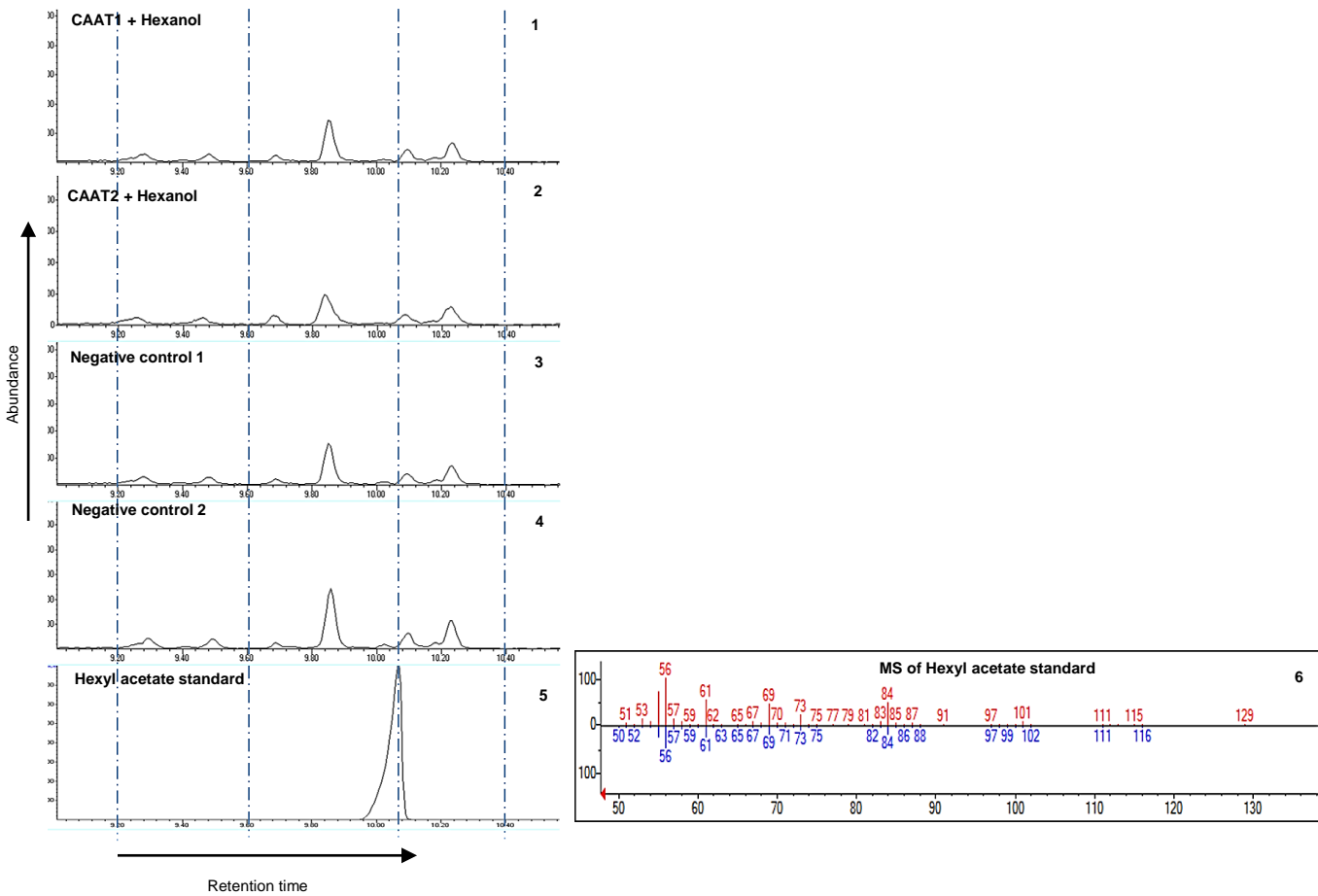
Statistics of deep sequencing

**Supplementary Figure 2. Quality of reads and statistics of sequencing**

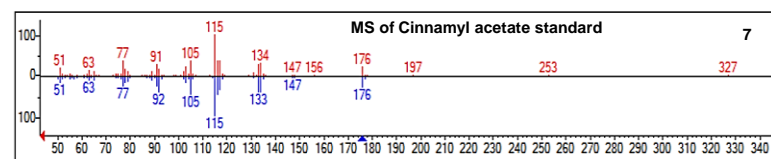
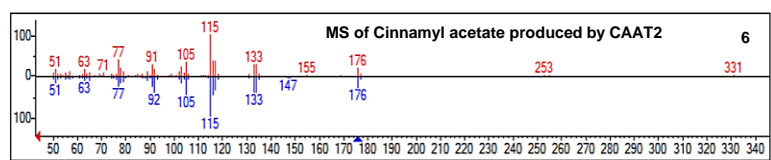
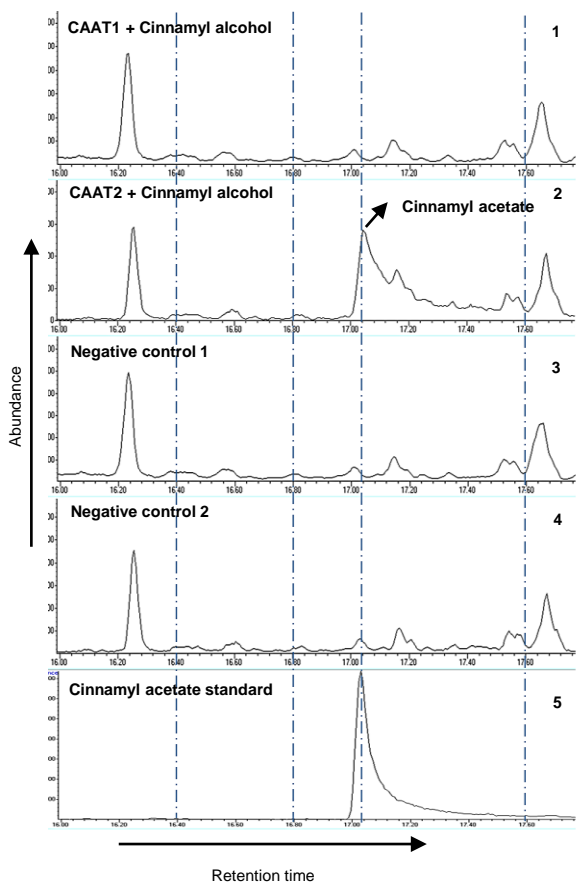


**Supplementary Figure 3. Heat map representing differential expression pattern of five BAHD acyltransferases along various tissues [root (R), leaf (L), leaf stripped of PGTs (L-T) and PGTs (T)]**

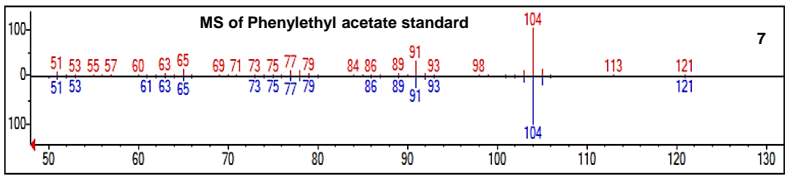
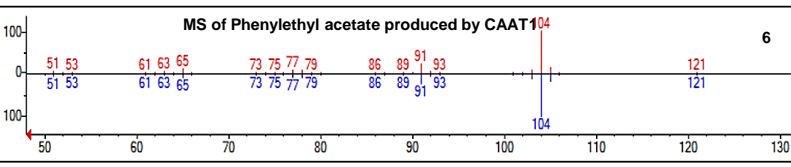
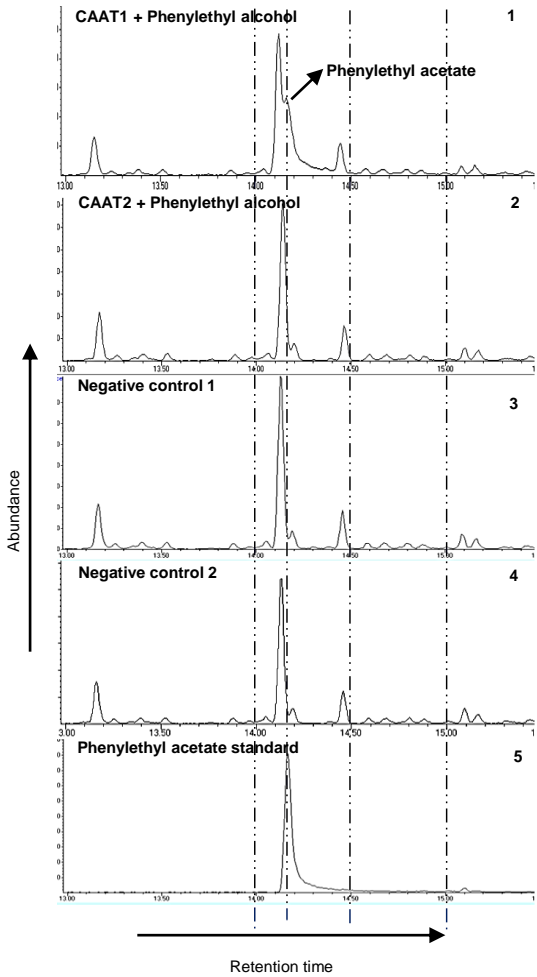
A



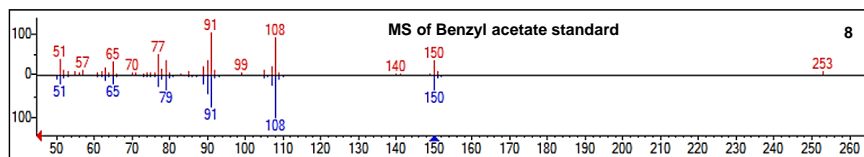
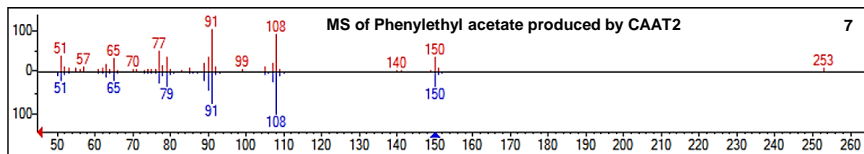
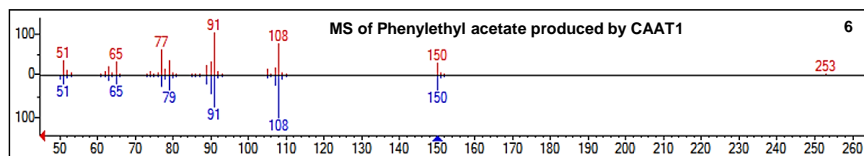
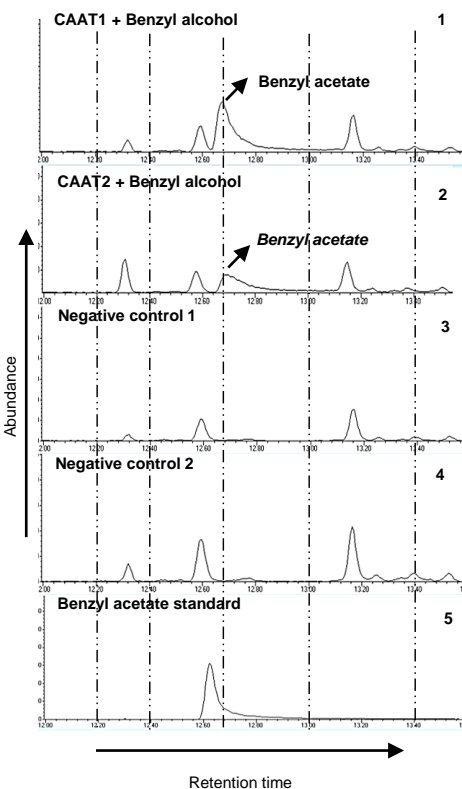
B



C

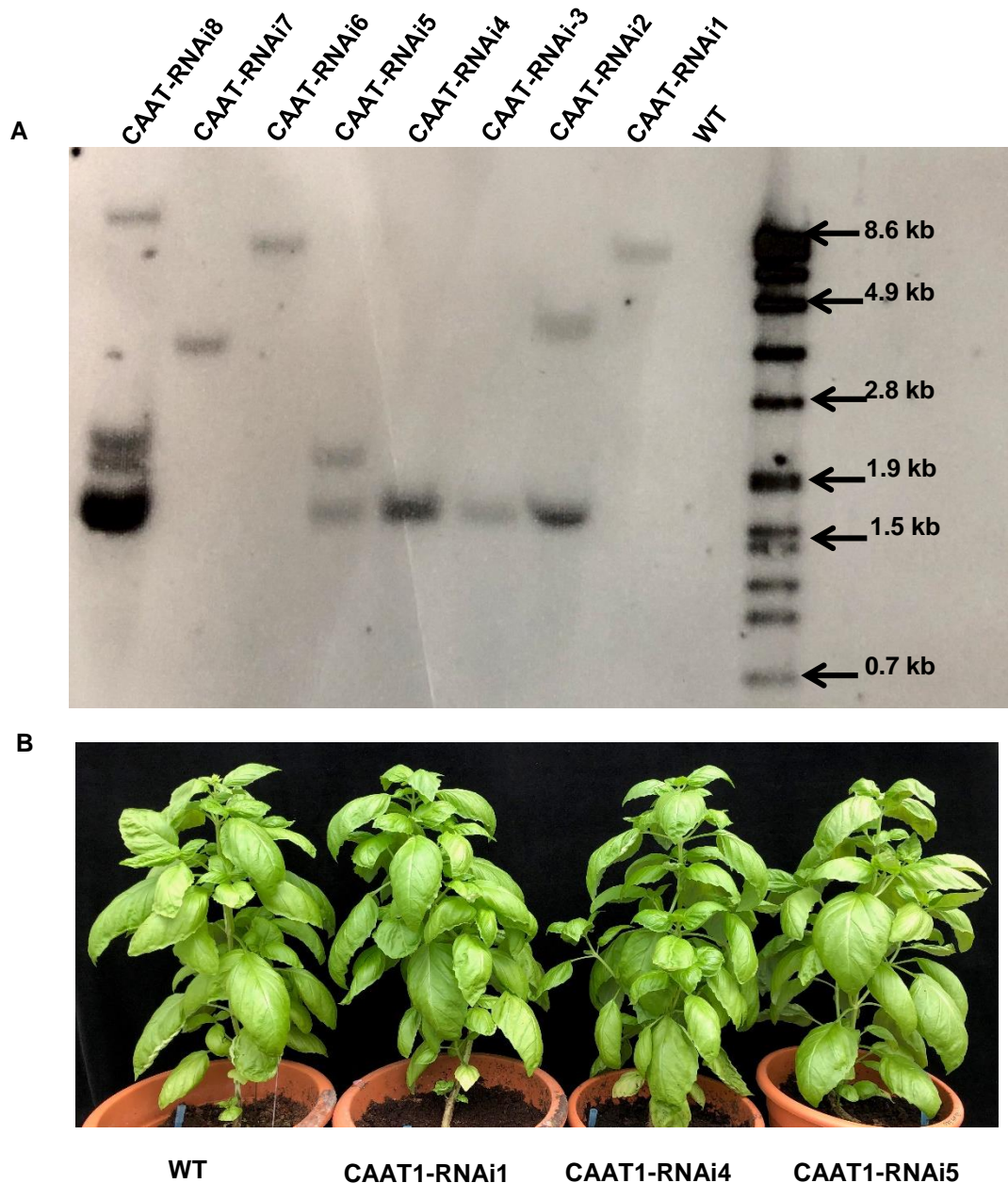


D

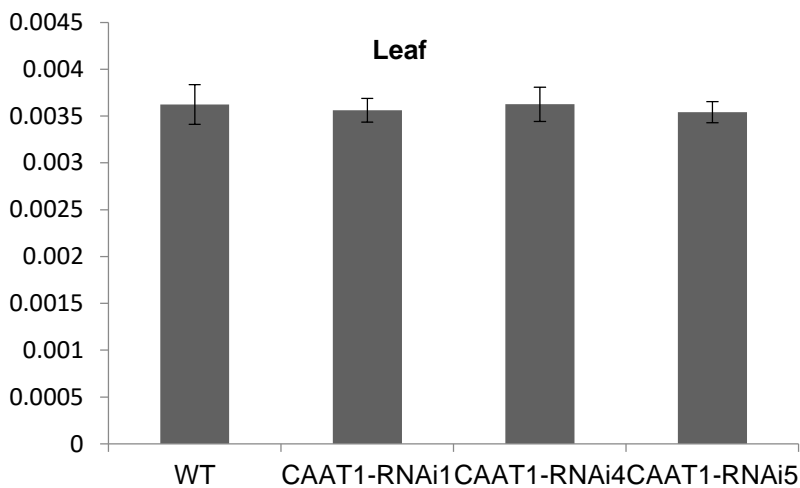
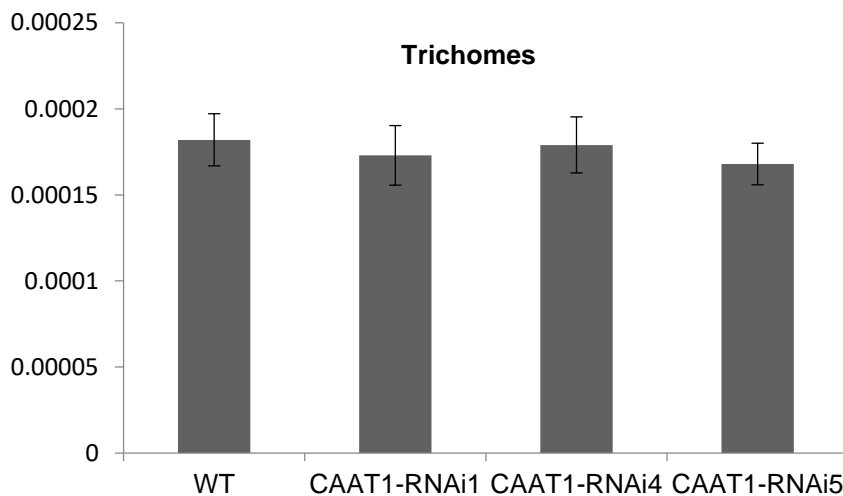


**Supplementary Figure 4 A: *In planta* functional characterization of ObCAAT1 and ObCAAT2.** GC-MS analysis of products formed by ObCAAT1 and ObCAAT2 in-planta in *N.benthamiana* leaves. **A** (1, 2) Hexyl acetate was not observed in hexanol and ObCAAT1 and ObCAAT2 infiltrated *N. benthamiana* respectively (3) Hexyl acetate was not observed in ObCAAT1 and ObCAAT2 infiltrated *N. benthamiana* (4) Hexyl acetate was not observed in hexanol infiltrated *N. benthamiana* (5) Hexyl acetate standard, (6) Mass spectrogram of hexyl acetate standard. **B** (1) Cinnamyl acetate was not observed in cinnamyl alcohol and ObCAAT1 infiltrated *N. benthamiana* leaves, (2) Cinnamyl acetate was observed in cinnamyl alcohol and ObCAAT2 infiltrated *N. benthamiana* leaves (3) Cinnamyl acetate was not observed in ObCAAT1 and ObCAAT2 infiltrated *N. benthamiana*, (4) Cinnamyl acetate was not observed in cinnamyl alcohol infiltrated *N. benthamiana*, (5) Cinnamyl acetate standard, (6) Mass spectrogram of cinnamyl acetate produced by ObCAAT2 in *N. benthamiana*, (7) Mass spectrogram of cinnamyl acetate standard. **C** (1) Phenylethyl acetate was observed in phenylethyl alcohol and ObCAAT1 infiltrated *N. benthamiana* leaves, (2) Phenylethyl acetate in phenylethyl alcohol and ObCAAT2 infiltrated *N. benthamiana* leaves (3) Phenylethyl acetate was not observed in ObCAAT1 and ObCAAT2 infiltrated *N. benthamiana*, (4) Phenylethyl acetate was not observed in phenylethyl alcohol infiltrated *N. benthamiana*, (5) Phenylethyl acetate standard, (6) Mass spectrogram of phenylethyl acetate produced by ObCAAT1 in *N. benthamiana*, (7) Mass spectrogram of phenylethyl acetate standard. **D** (1) Benzyl acetate was observed in benzyl alcohol and ObCAAT1 infiltrated *N. benthamiana* leaves, (2) Benzyl acetate was observed in benzyl alcohol and ObCAAT2 infiltrated *N. benthamiana* leaves (3) Benzyl acetate was not observed in ObCAAT1 and ObCAAT2 infiltrated *N. benthamiana*, (4) Benzyl acetate was not observed in benzyl alcohol infiltrated *N. benthamiana*, (5) Benzyl acetate standard, (6) Mass spectrogram of benzyl acetate produced by ObCAAT1 in *N. benthamiana*, (7) Mass spectrogram of benzyl acetate produced by ObCAAT2 in *N. benthamiana*, (8) Mass spectrogram of benzyl acetate standard.

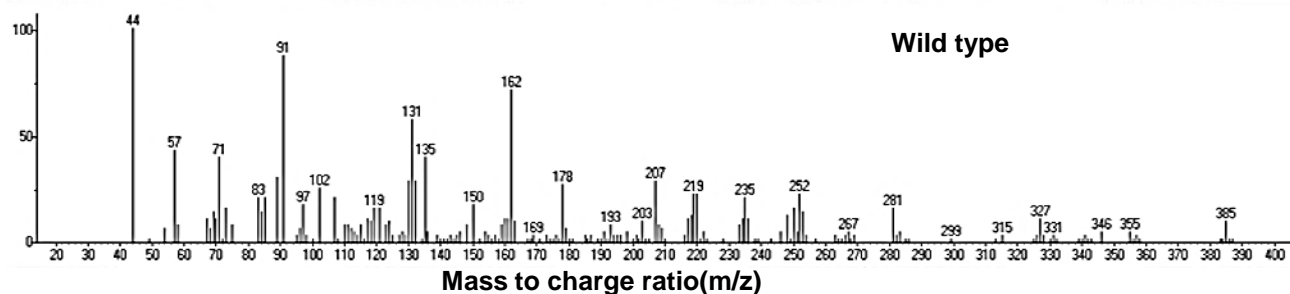
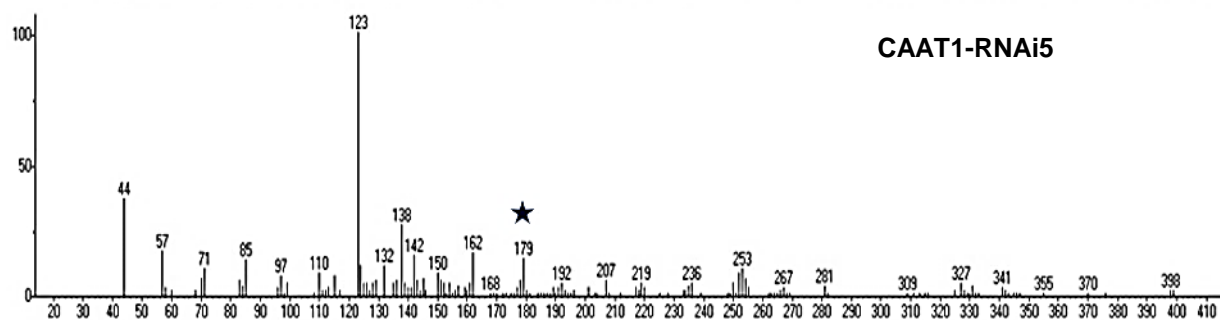
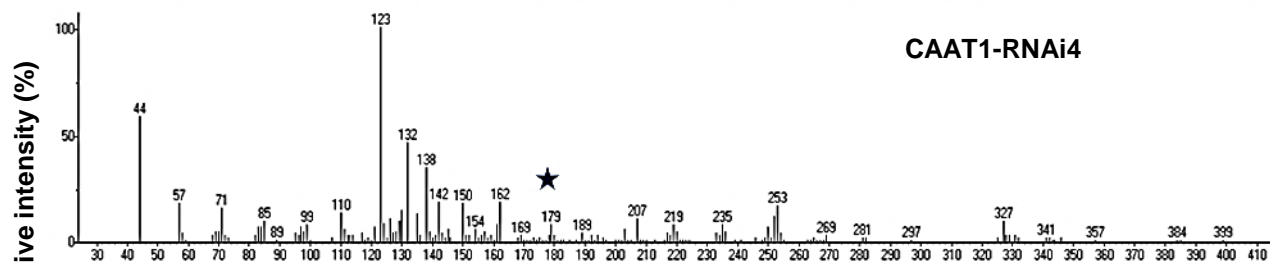
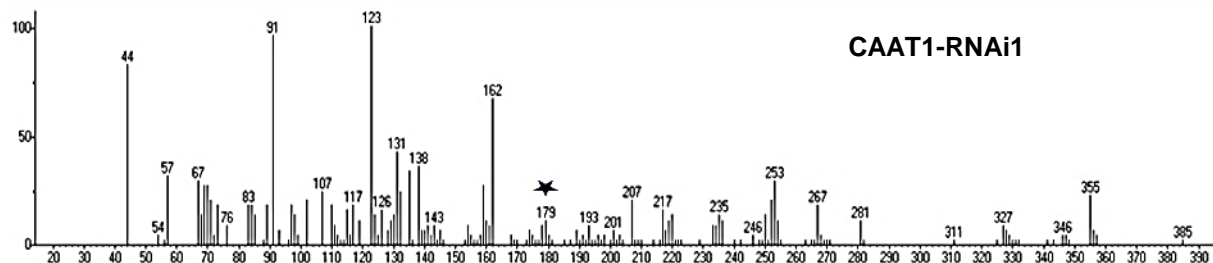
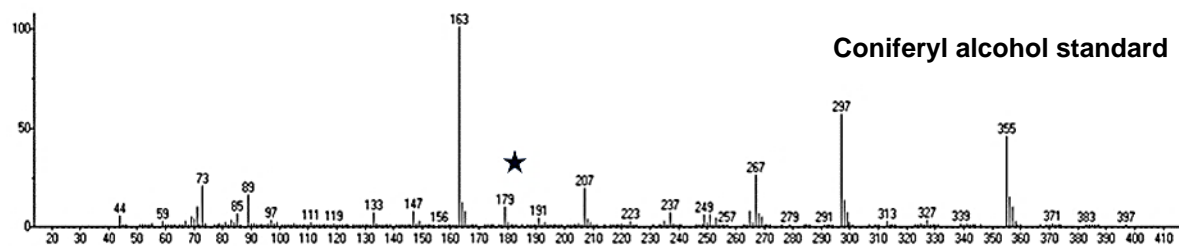




**Supplementary Figure 5. Southern blot and phenotypic analysis of *ObCAAT1*-RNAi sweet basil lines.** (A) Southern blot of *ObCAAT1*-RNAi sweet basil lines showing different T-DNA insertions. 20µg of DNA was digested with *NdeI* enzyme. (B) No phenotypic change was observed in *ObCAAT*-RNAi lines with respect to wild type.

**A****B**

**Supplementary Figure 6. Total lignin quantification of *ObCAAT*-RNAi sweet basil lines by thioglycolic acid method.** Unaltered lignin content in (A) leaf and (B) trichomes of *ObCAAT1*-RNAi lines when compared to WT. Values are mean  $\pm$  SE (n = 6).



**Supplementary Figure 7. MS spectrum with fragmentation peak at m/z 179 for coniferyl alcohol.** Fragmentation peak at m/z 179 for coniferyl alcohol was present in (A) coniferyl alcohol standard, (B) CAAT1-RNAi1, (C) CAAT1-RNAi4, (D) CAAT1-RNAi5 and absent in (E) wild type. (Reference: Predicted GCMS spectrum (non-derivatized) of coniferyl alcohol from Pubchem Database).

**Supplementary Table 1. List of primers used in present study**

Name	Sequence (5'-3')	Purpose
<i>ObCAAT1_F</i>	<b>CACCATGGGCGAAGTAGCAAAAGATGA</b>	Full length primer
<i>ObCAAT1_R</i>	TCAAGCCTCCATCAAGAAGTCCTT	Full length primer
<i>ObCAAT2_F</i>	<b>CACCATGTATATTTTCCACCTCCACTCCT</b>	Full length primer
<i>ObCAAT2_R</i>	CTAAGGTAGGTTGAAAGAGTGAAATGA	Full length primer
<i>ObCAAT1_q_F</i>	AAGATGAGAAGAAATTAGTT	qPCR
<i>ObCAAT1_q_R</i>	TCAAAATCGTGGCCTCCTTTGT	qPCR
<i>ObCAAT2_q_F</i>	AGGAATATAATCCAGCTGTCGG	qPCR
<i>ObCAAT2_q_R</i>	AGGAACAAGTCTGGCATGAACAGA	qPCR
<i>ObEF1<math>\alpha</math>-F</i>	AATGGCAAAAAGCTCGAAGA	qPCR
<i>ObEF1<math>\alpha</math>-R</i>	TCGCAGACATGACAGACACA	qPCR
<i>ObEGS1_F</i>	<b>CACCATGGAGGAAAATGGGATGAAAAG</b>	Full length primer
<i>ObEGS1_R</i>	TTAAAATGCTGCTGAAGCCGGCGGTGGA	Full length primer
<i>ObCAAT1_LOC_F</i>	<b>CACCATGGGCGAAGTAGCAAAAGATGA</b>	Subcellular localization
<i>ObCAAT1_LOC_R</i>	AGCCTCCATCAAGAAGTCCTTGTCTT	Subcellular localization
<i>ObCAAT2_LOC_F</i>	<b>CACCATGTATATTTTCCACCTCCACTCCT</b>	Subcellular localization
<i>ObCAAT2_LOC_R</i>	AGGTAGGTTGAAAGAGTGAAATGA	Subcellular localization
<i>35S(591)-F</i>	CTCAGAAGACCAAAGGGCTATT	Southern blot probe
<i>35S(-34)-R</i>	TGTTTGTTTTGTTGTGGTATTG	Southern blot probe
<i>ObCAAT1_SphI</i>	<u>CGCATGC</u> ACAAAGGAGGCCACGATT	RNAi
<i>ObCAAT1_NotI</i>	<u>CGCGGCCGCTTGGT</u> GCGCTCCAGGAAT	RNAi
<i>ObCAAT1_NdeI</i>	<u>CCATATG</u> ACAAAGGAGGCCACGATT	RNAi
<i>ObCAAT1_XbaI</i>	<u>CTCTAGATTGGT</u> GCGCTCCAGGAAT	RNAi

