

## ***New Phytologist* Supporting Information**

Article title: **Regulation of metabolic gene clusters in *Arabidopsis thaliana***

Authors: Hans-Wilhelm Nützmann and Anne Osbourn

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The following Supporting Information is available for this article:

**Fig. S1** Relative transcript level of the thalianol and marneral cluster genes in RNA preparations from leaf and root tissue of the Col-0 wild type.

**Fig. S2** GC-MS analysis of Col-0 and *arp6* root extracts.

**Fig. S3** Relative transcript levels of the thalianol and marneral cluster genes in *Ler* wild type and corresponding *arp6* mutant line.

**Fig. S4** ChIP analysis of H2A.Z abundance at the marneral gene cluster and control loci.

**Tables S1** *A. thaliana* mutant lines

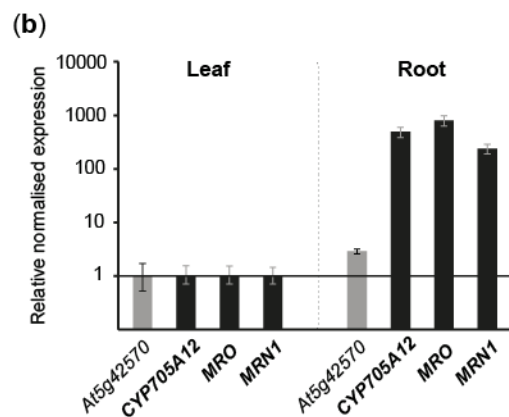
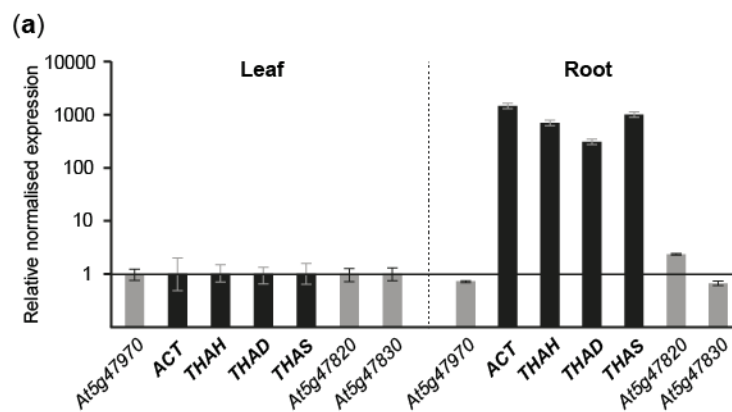
**Tables S2** Oligonucleotides

**Fig. S1** Relative transcript level of the thalianol and marneral cluster genes in RNA preparations from leaf and root tissue of the Col-0 wild type.

(a) Thalianol gene cluster

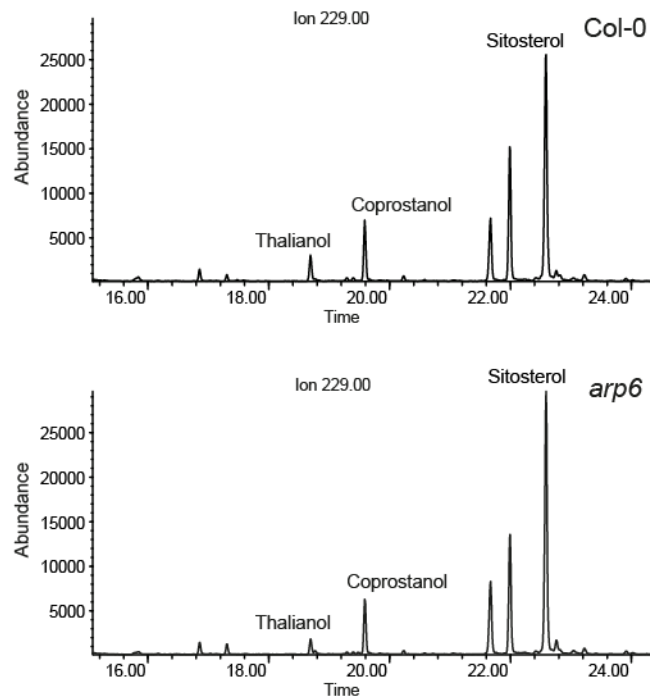
(b) Marneral gene cluster

Black bars indicate cluster genes and grey bars indicate flanking genes. Gene expression level was measured by qRT-PCR and leaf transcript level rate was set as 1. *PP2AA3* (*At1g13320*) was used as internal control (Hong *et al.*, 2010). Error bars indicate standard deviation of three biological replicates.



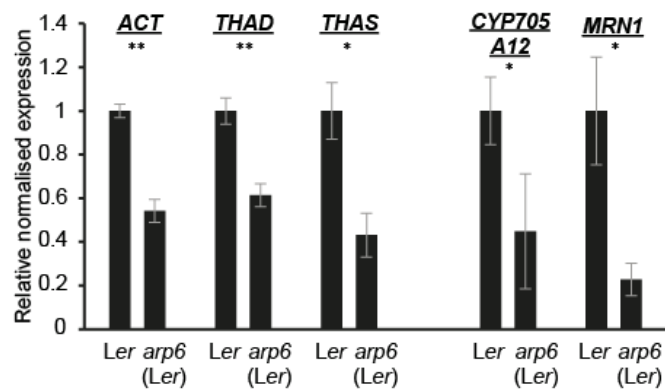
**Fig. S2** GC-MS analysis of Col-0 and *arp6* root extracts.

Extracted ion chromatograms ( $m/z$  229) for Col-0 and *arp6* root extracts are shown. The thalianol, coprostanol and sitosterol peaks are indicated.



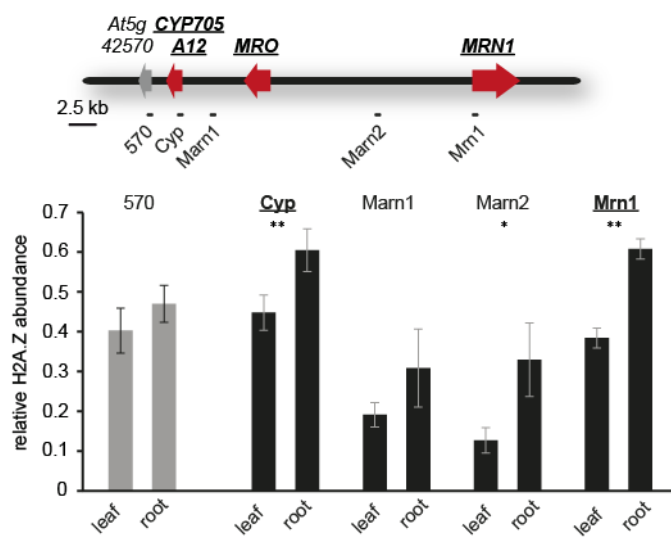
**Fig. S3** Relative transcript levels of the thalianol and marneral cluster genes in *Ler* wild type and corresponding *arp6* mutant line.

Transcript levels were measured by qRT-PCR and wild type transcript rate was set as 1. *PP2AA3* (*At1g13320*) was used as internal control (Hong *et al.*, 2010). Error bars indicate standard deviation of three biological replicates.



**Fig. S4** ChIP analysis of H2A.Z abundance at the marneral gene cluster and control loci.

H2A.Z abundance within the marneral gene cluster was measured in chromatin preparations from root and leaf tissue of *A. thaliana* by ChIP coupled to qRT-PCR. The cluster is transcribed in the roots and silent in the leaves. H2A.Z abundance was quantified relative to *FLC*. The probes used for this analysis are indicated in the map of the marneral cluster. Error bars indicate standard deviation of three biological replicates. Asterisks indicate statistical significance (*t*-test; \*,  $P < 0.05$ ; \*\*,  $P < 0.01$ ).



**Table S1** *A. thaliana* mutant lines

The *A. thaliana* mutant lines were chosen based on described chromatin regulatory function of the disrupted genes. Special emphasis was given to lines that are affected in their histone modifications and structure.

<b>Line</b>	<b>Gene function</b>	<b>Reference</b>
<i>atxr7</i>	histone methyltransferase	Tamada <i>et al.</i> , 2009
<i>suvh2</i>	histone methyltransferase	Naumann <i>et al.</i> , 2005
<i>atx1</i>	histone methyltransferase	Pien <i>et al.</i> , 2008
<i>ref6</i>	histone demethylase	Noh <i>et al.</i> , 2004; Lu <i>et al.</i> , 2011
<i>atjmj4</i>	histone demethylase	Noh <i>et al.</i> , 2004
<i>elf6</i>	histone demethylase	Noh <i>et al.</i> , 2004; Jeong <i>et al.</i> , 2009
<i>hda6</i>	histone deacetylase	Murfett <i>et al.</i> , 2001; Probst <i>et al.</i> , 2004
<i>vim1</i>	binds to methylated DNA	Woo <i>et al.</i> , 2007
<i>prmt5</i>	histone arginine methyltransferase	Pei <i>et al.</i> , 2007
<i>prmt10</i>	histone arginine methyltransferase	Niu <i>et al.</i> , 2007
<i>otld1</i>	histone deubiquitinase	Krichevsky <i>et al.</i> , 2011
<i>vin3-8</i>	subunit of the polycomb response complex	Sung & Amasino, 2004; Bond <i>et al.</i> , 2009
<i>arp6</i> (Col-0)	subunit of SWR1 complex	Deal <i>et al.</i> , 2007
<i>haf1</i>	histone acetyltransferase	Crane & Gelvin, 2007
<i>hda18</i>	histone deacetylase	Xu <i>et al.</i> , 2005

**Table S2** Oligonucleotides

## qRT-PCR

Oligo	Forward	Reverse
AT1G13320	GTTGTGGAGAACATGATACGG	GCTAGACATCATCACATTGTC
AT5G42570	GGTTTCTTATGGAGTATGATAGGTT	TTCTTTCCCTCAGGACT
CYP705A12	CCACAAACTACTCCGACCAC	CTTCTTCTTCGCCTTACCTTG
MRO	ATCACGAAATCTGCCATAAA	CTTCCAGCGTCTCCATCAATA
MRN	ATGCTTGCTTGTGGGTAGAA	TTTGCGGCTAACATAACTTGG
AT5G47970	GGATACCAACGAGACCTGTG	CATCACATCTTTGTAGCTGCATG
ACT	CGGCCATACTAACACTACT	TGCCTACCCATACTTCAACAG
THAD	ATCCTGATTTCTGGGAAGACC	TGTTGCACCATCATTCCAATT
THAH	TGGTGTTTGGAGGTGGAGTGA	GGGAAATCTTGATAGGCAGTC
THAS	CTTCAATCCACTATGGCACTC	TAAAATAATCACTCTTAGGGTCTT C
AT5G48020	TTACAACGAGGAAGGGACGAT	ACCGGAACCTTAACCGCAACC
AT5G48030	GACAGCGTGAAGTCTTGAG	CACTGGGAAGATCCAGTTGC

## ChIP

Oligo	Forward	Reverse
AT5G42570	GACCGACACAACAAACAACAC	GAAGGATCAGTGCCATTTCCG
AT5G42580	GCAGAACTCATCATCGTTGAC	GACCGATGATTGGTAGAGAAG
MRO	CGATACACCCAAAATCAAATC	GTTAGGAAAGTGGTTAAGCAC
MRN	CACGTTAACCAGTTAGCAGATTG	GTTGGCATCAAACCTCCAGATC
AT5G47970	GAGGCGATAGAAATGACTTAGTTG	GACCCACTTTCGTTGGTGTTT
ACT	TCAAGCTTAACCAATATCACGTG	CGATGACTGATAGTTGAAGGC
THAD	GAAAAGTCTTCATCTTCTCC	GATTGGTAATGAAGGAGGGCTC
THAH	TAAGAGAAGTGTACTTGATATTCGG	CGACTGCTTAACCTACCTTTG
THAS	GTCCAAGTAAACTTAGAGCAACC	CTGCGTTGGCATCAAATTCC

AT5G48020	CAATGATGAATGAACAATGGAG	CAGTAGTGACCAGTTCTGTAG
AT5G48030	CTAGGGTTTTAACTTTGGCTGC	CCATTGGAAGGGACCATTTTC
Thal1	GATGAAGAGTGGCATGAGGC	CGAAAGGCATGTCTTCGCTC
Thal2	GTTATCCGACTCATGCAATGC	GCATAGTGAAGACAGAGAGTTG
Thal3	CATGATTACCTGTTAGAGGAG	GTCAACGCAACAGAGAATTC
Thal4	CAACGTGATTTTATTCTTATGG	GTATTGAAAACACCCGTTAAG
Thah2	GAAGTATTTTCAATGGGGCAATAC	GTTGGAAGTTTCATCTTTGAATAC C
Thal5	GATACCTAGAAGGATTCCACG	CTTTTGCCTTCCAACCTATAG
Thal6	CATCTTTTGGCAAGTTTCACTCTC	GATTCATGAAGCACATGGTCG
Thas2	CACATGTTCTCAGAGAGTATC	CACAACGACTACCTTTGGCAG
Thas3	CCTGGATAAGAGAACAAGTGC	CTTGTACTCTTTGAACACATTCAAC

#### Nucleosome Positioning

Oligo	Forward	Reverse
THASnupo1	GATGACAATGCGAAACGTAGTTG	CACGATGCATGTGAGAAACGG
THASnupo2	CGTTAAGGAATAAAATTATTTG	CCACAAAATACGTAGAAAAG
<b>THASnupo3</b>	<b>CACACCCGTTTCTCACATGC</b>	<b>CATCAACCACAAAATACGTAG</b>
THASnupo4	CTTTTCTACGTATTTTTGTGG	AACAATGTGTTAGTTTTGAG
THASnupo5	GGTTGATGTTTAAAATTTTAC	TGGTTTGTGTTGAGTTATAATAG
THASnupo6	CTCAAACTAACACATTGTT	GTTTTCAAATTTTAATACAAACC
THASnupo7	CTATTATAACTCAAACAAACCA	CTTGCAATTAATATGTTTTCA
THASnupo8	CATTTACATAATAGAAATCATC	CGCTTCGTATTTTTTATAGTCG
THASnupo9	GGTTTGTATTAAAATTTGAAAAC	GGACAAGGAGGACACATTAT
THASnupo10	CCTAAAACATCGACTATAAAA	CAGCCTCCACATTTTGTAAGG
THASnupo11	GTATAATGTGTCCTCCTTGTC	GTTGGTGGTGAACAGGTGAG
<b>THASnupo12</b>	<b>CCTTACAAAATGTGGAGGCTG</b>	<b>GCATCAAATTCCTCAAATCTGC</b>
THASnupo13	GGAGAGGATACTCACCTGTTC	GAATTTGTGCCGAGCATCCTC



THASnupo14	CTATGCAGGGAGGCAGATTTG	GTAGTCTTGAAACGTGACGTG
THASnupo15	CACAAGAAATTGCCGAGGTAG	CAAAGTATTTACCTGCATGC
47970nupo1	CTGAACTCGTTTCTTGAAAACC	GCAATTTCAATCAGAAGATAG
47970nupo2	CGATCAAGACTACCTTGAACAC	CCTCTAAAATCTATAAGCTTGTG
47970nupo3	CTGAAATTTTGACATCGTTCAC	CTCCTCTTCTTATTACATCAGAG
47970nupo4	GAGGCGATAGAAATGACTTAGTTG	GATGCTTCACAAGTCGCAAC
<b>47970nupo5</b>	<b>GAGGAGAGATCTAAAAGATGAAA G</b>	<b>GACCCACTTTCGTTGGTGTTC</b>
47970nupo6	CTTGTGAAGCATCGGGAGAC	GAATGACGTCAAAAAGGAATG
47970nupo7	GTCCCGCCTTTTGTTTCCTT	GACGAGAGAGGGTGAAATTGG
47970nupo8	GCAAATCTCAGCGACCACAA	GACGAATACAGGCAGCTATAG
<b>47970nupo9</b>	<b>GTGTTCTTGTCTGAAACTCG</b>	<b>GTTGGTAAATCTCAGCTTCTC</b>
47970nupo10	GACCAGCAGTGTCCCATATC	CAGTATCGAATCTAAAGCAACG
47970nupo11	CTAAAACAAGGATCTACGATGG	CAAGAACACTTGAAATCGATCG
47970nupo12	GCGACTGCCAAGCGAAATTC	GACACTGCTGGTCAAGAACG
THADnupo1	CATTGATCAATGCATGGGATC	GATCATTGATGCCATTGTTGC
THADnupo2	GGCTACTCTGTGTCATTTGC	CATAAGAGGAGGAAGATGAAG
THADnupo3	CAATGGCATCAATGATCACTG	CTGAAGAAAAGATCGTAAGAG
<b>THADnupo4</b>	<b>CATCTTCCTCCTCTTATGTC</b>	<b>GAGCACAGCCAGCTCGTGAG</b>
THADnupo5	CTTACGATCTTTTCTTCAGG	GGTGAAGATGACCAATGATTG
<b>THADnupo6</b>	<b>GAGAAAACATATTATATTTAGG</b>	<b>GCAAATGACACAGAGTAGCC</b>
THADnupo7	CTTAAAAAGTAATGACGTCAGC	CATGCATTGATCAATGATCAG
THADnupo8	GTGCTTGTCCCAGAGAACAAC	GATCAGGCTTTGTTTATTACC
THADnupo9	CCAATGTGAATGCTATAACG	GAAAGCTGACGTCATTACT
THADnupo10	GACACTCTTTATTTTATTATC	CTGGGACAAGCACAATCGAG
THADnupo11	CAGATGTTTAAAATGTCTCT	CATTGGTTAATTTTGAAGG
THADnupo12	GGTGTCTTTAGTATAAATTAG	GATAATAAAATAAAGAGTGTC
THADnupo13	CCAATAAGTCCCAACATCCAC	AGAGACATTTTAAACATCTG

THADnupo14	GTAAGTTGAAACCTCTATAGC	CTAATTTATACTAAAGACACC
THADnupo15	GACATTCACAACCTTCTACAG	GGACTTATTGGTTTGAGTGG
THADnupo16	CAATTTTAACATAATTTATATTC	GATTAGTAACTAAAACTGTAG
THADnupo17	TTGTTACTATGTTGCAAC	CTGTAGAAGTTGTGAATGTC
THAL6nupo2	GAATAGGAATATGAAAAAAGTG	GATAGGTAGAGATGATCATACC
THAL6nupo3	CACAGTAGAATCCATACTCAC	GTGAAACTTGCCAAAAGATG
THAL6nupo4	CGTTGCAACTTACAACCATAC	CCTATTCACCTTACGATGATG
<b>THAL6nupo5</b>	<b>GACTAGAAAAACGTGGGACC</b>	<b>GACTTCTAAGAGGTAAAGAGG</b>
THAL6nupo6	CAAATATTCAAGTTTCCCGGAC	GTTGTAAGTTGCAACGCCATG
THAL6nupo7	GCAATCACTTGAGTGAAAAC	GTCTTTCGATGATTAGTACG
THAL6nupo8	CAATTAGTGATGCTTGAGCTAG	CCACAATATTTTTATGTTTTG
THAL1nupo1	CTTTCAAAGATGCATCTGTTGC	GACGCAACTGATTTTTTTGTAGC
THAL1nupo2	GAGATGAAGAGTGGCATGAGG	CAGAGTTAGCTAATAATATGGC
THAL1nupo3	GCTACAAAAAATCAGTTGCGTC	GCTCAGATCTTTCCAATGTG
THAL1nupo4	CTAACTCTGAAGTTACAAATCC	GTAACTTCCTATGCTCGAAAG
THAL1nupo5	CACATTGGAAAGATCTGAGCG	CTCCATTACACTATAACACTGC
THAL1nupo6	GGAAGTTAACTAATTTAAATG	GTTGGAATAATCAACAAATGAC
THAL1nupo7	GTGTAATGGAGTTCGAGTC	CTTGGTTGATAAACTGTAGC
<b>THAL1nupo8</b>	<b>GTTGATTATTCCAACATGCC</b>	<b>CTTCATGCAATCGAACTTTATC</b>
THAL1nupo9	CCAAGTTATATAACCCAATG	CATCGTTTATGTTCTCCACTTC
THAHnupo1	CAAAGGTGTTTACAACCTTC	CCTCTTCATTTTCAAATGT
THAHnupo2	TTGAAACTATATAGTATCATG	CTTGGTAAGTACTGGAACCTC
THAHnupo3	ACATTTTGAAAATGAAGAGG	CACCCCACTTTTGACAAATC
THAHnupo4	GTACTIONACCAAGTTTTAAAAC	GAAAAGTTGTGTCTCACAAAG
THAHnupo5	GATTTGTCAAAGTGGGGTGC	GGTTAATATATTTCTTCAGG
THAHnupo6	GAGACACAACCTTTTCTTCATAG	CAAGTACACTTCTCTTATAACC
THAHnupo7	TGAGTAACACTATCCTGAAG	CAAATTATACCTAGTTTTTGG

THAHnupo8	GTATAGGTTATAAGAGAAGTG	CACCTCAACTTAGACCTAG
THAHnupo9	CCAAAACTAGGTATAATTTG	CAAATAACTTTTATACTAGACC
THAHnupo10	CTAGGTCTAAGTTGAGGTG	CAACGACTGCTTAACCTACC
THAHnupo11	GGTCTAGTATAAAGTTATTTG	GTCATTACAAACAAACAACCTC
THAHnupo12	CCAAAGGTAGGTTAAGCAGTC	GAATAATCTTAACCTACCTATG
THAHnupo13	GTCTGCACTCTGCAAAAAAC	TAGTTTCATGAAGAAGGTTG
THAHnupo14	GTATACTATACATGTTAACG	GTAAACACCTTTTGTAATTGC
THAHnupo15	GTGAGCTTCTAACCTAAAATC	GATAATATATGTTTTTTGCAG
THAHnupo16	GGTTGAGTATGTGCGGATCG	CGTTAACATGTATAGTATAC
THAHnupo17	GTTATATTGAGTTGTTTGTTTG	GACCACACGAAGCTCATTTG
THAHnupo18	CATAGGTAGGTTAAGATTATTC	CAACAGCGGCTACAGCTATG
<b>THAHnupo19</b>	<b>CAAATGAGCTTCGTGTGGTC</b>	<b>CATTGCACTTCGGGTTTCGAC</b>
<b>THAHnupo20</b>	<b>GTTTGGGCATGGATCGACG</b>	<b>CTCTAATATGGTATCAGAGCC</b>
07700nupo -1	CACATTCCTCAGCCGTTGATG	CTATCTCCCAGCTAGCAACC

Bold, oligos used for stably positioned nucleosomes in thalianol gene cluster.

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