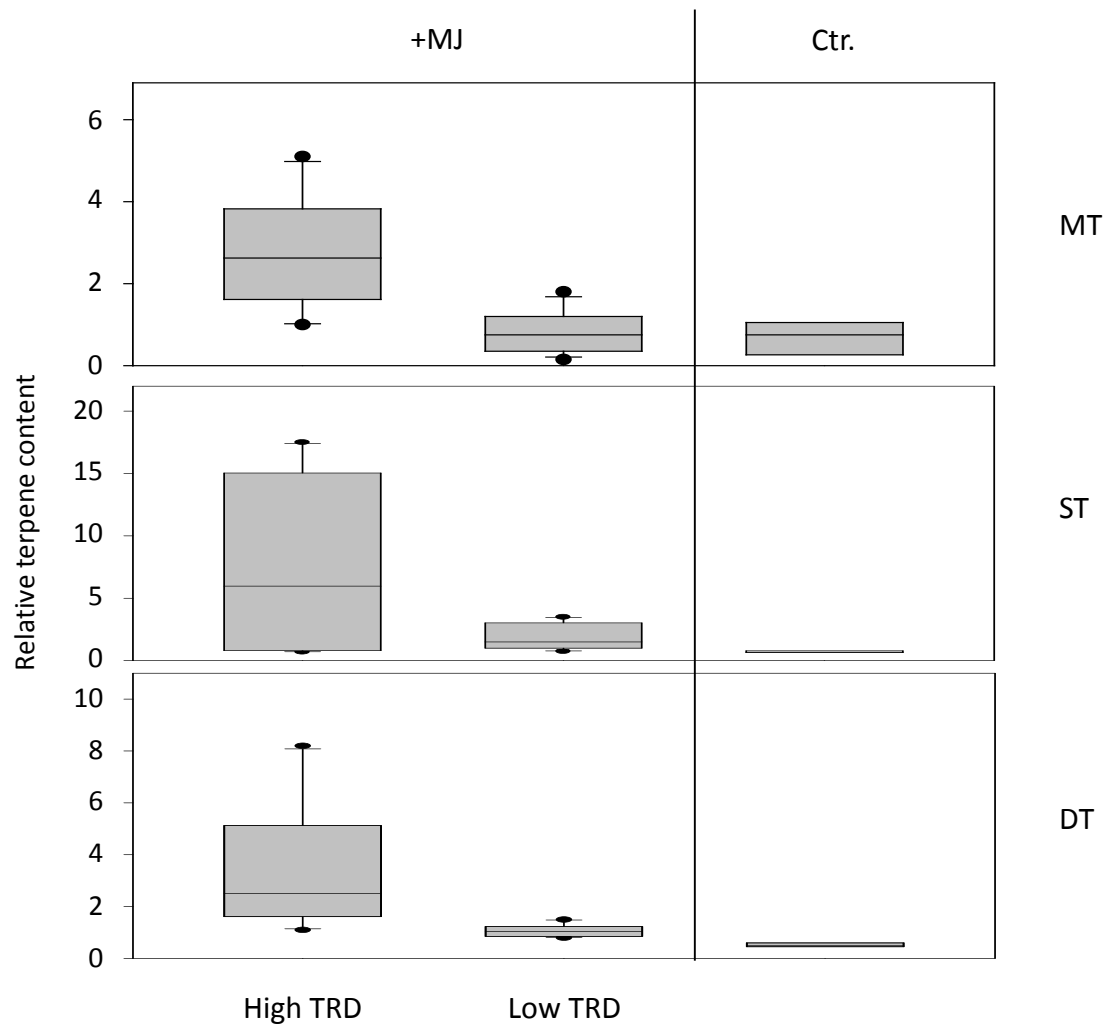


**Figure S1.**

Box plot of the relative amounts of major monoterpenes (MT), sesquiterpenes (ST), and diterpenes (DT) in Norway spruce sapwood after methyl jasmonate (MJ) treatment in high and low traumatic resin duct (TRD) trees and in unsprayed control trees (Ctr.). Sapwood was collected at various distances above the treatment site ~4 weeks after treatment. The mean terpene content at the MJ treatment site in low TRD trees was set to 1.0. Data from the different distances per treatment were pooled.



**S1.** Nucleotide sequence of the 13-LOX cDNA fragment

GGAGCCCTATATCATTGCAGCACATAGGCATCTAAGTGCTATGCACCCTATACTCAAATT  
GCTTCATCCACACATGCGCTACACCATGGAAATCAATGCATTAGCCCGACCAAGTTTGAT  
CAATGCAGAGGGTGTTATTGAATCCTTCTTTACACCAGACAAGTACTCCATGG

**Figure S2a.**

Box plot of the relative abundance of mRNA transcripts of *PaIDS1*, *PaIDS2*, and *PaIDS5* genes in Norway spruce sapwood (a) and bark (b) after methyl jasmonate (MJ) treatment in high and low traumatic resin duct (TRD) trees and in unsprayed control trees (Ctr.). Samples were collected at various distances above the MJ treatment site 4 weeks after treatment. Transcript abundance of each *IDS* gene was measured by quantitative real-time PCR using SYBR-Green for detection and normalized against ubiquitin. The mean transcript abundance at the MJ treatment site in low TRD trees was set to 1.0. Data from the different distances per treatment were pooled.

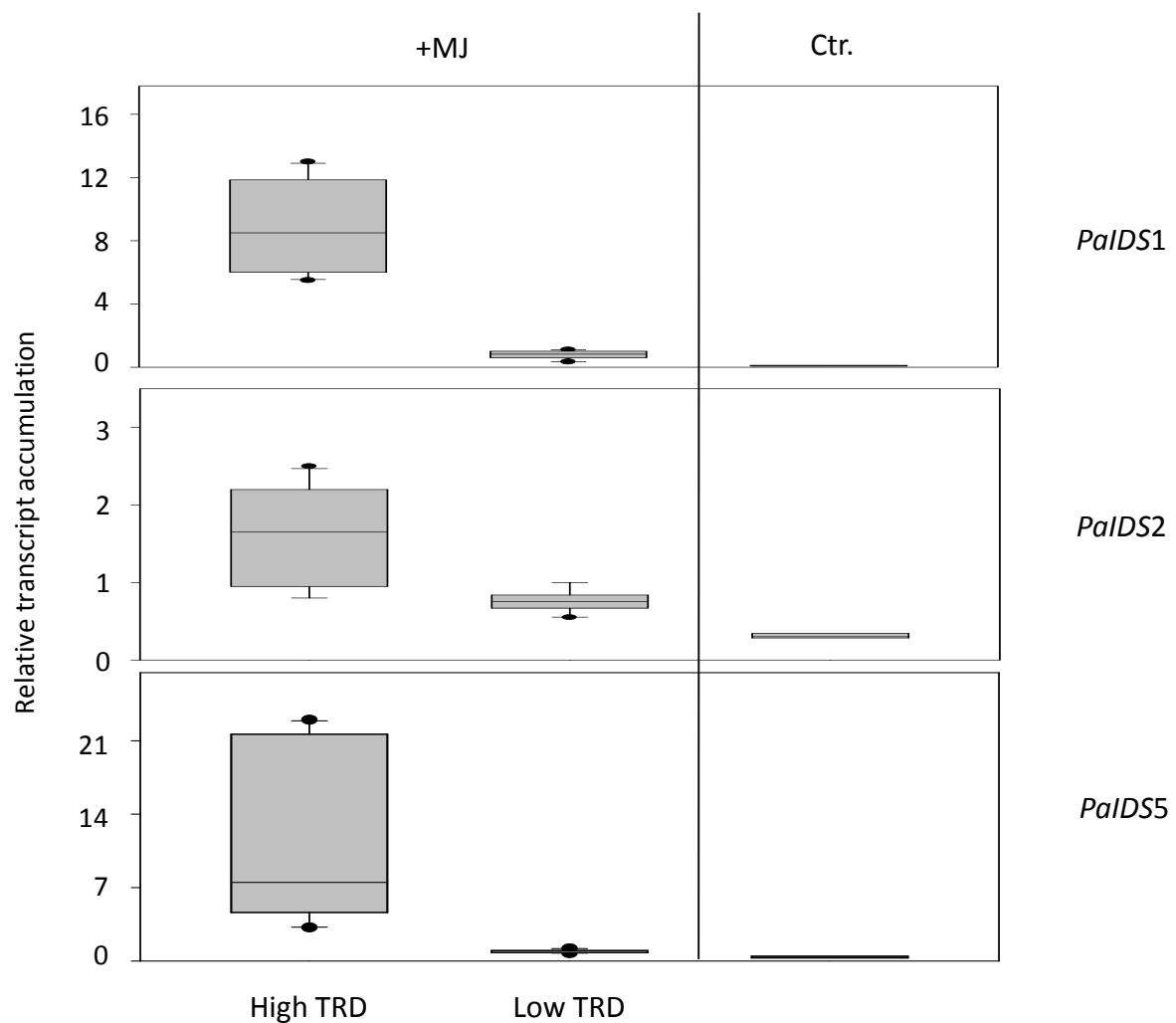
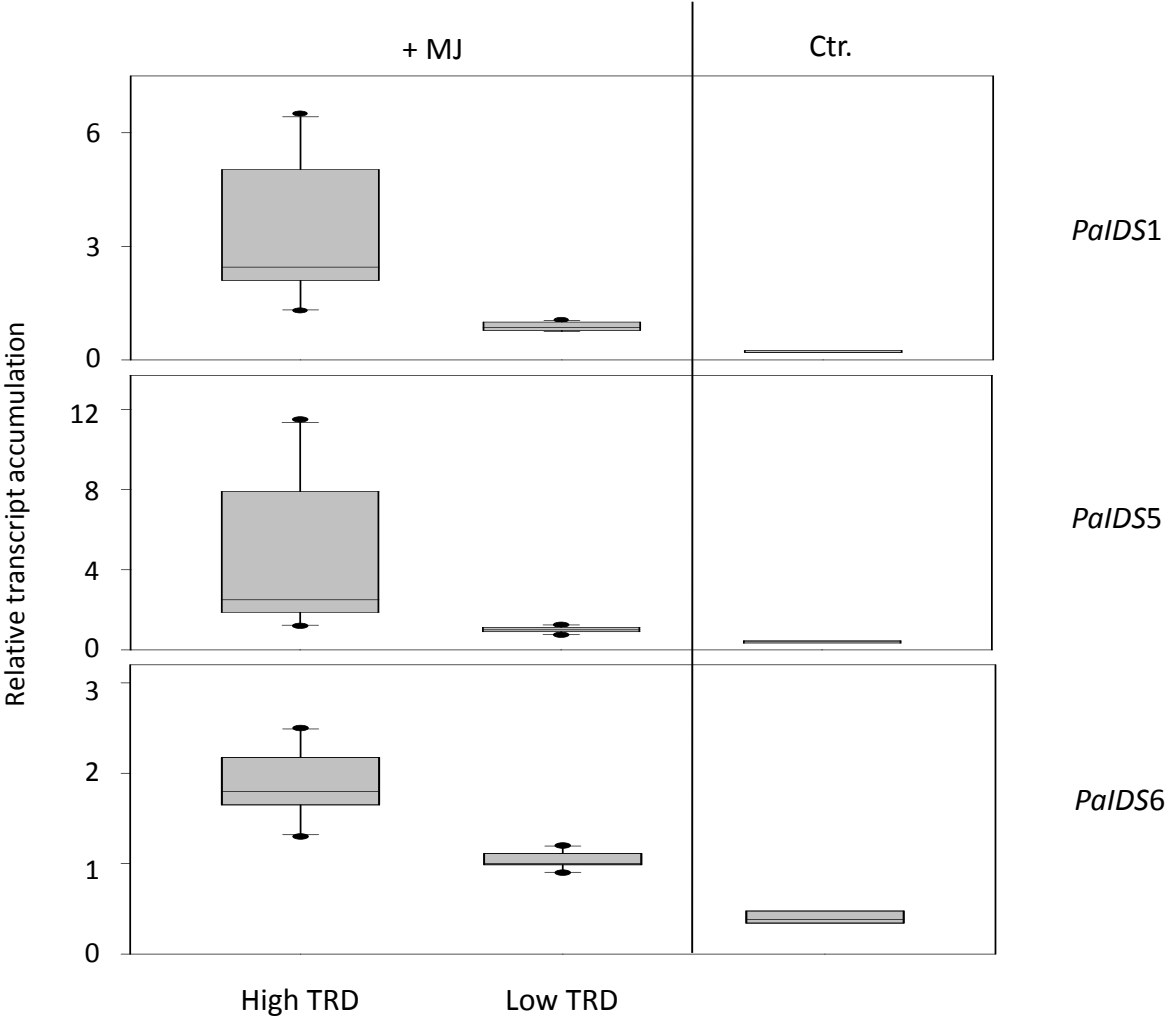


Figure S2b.



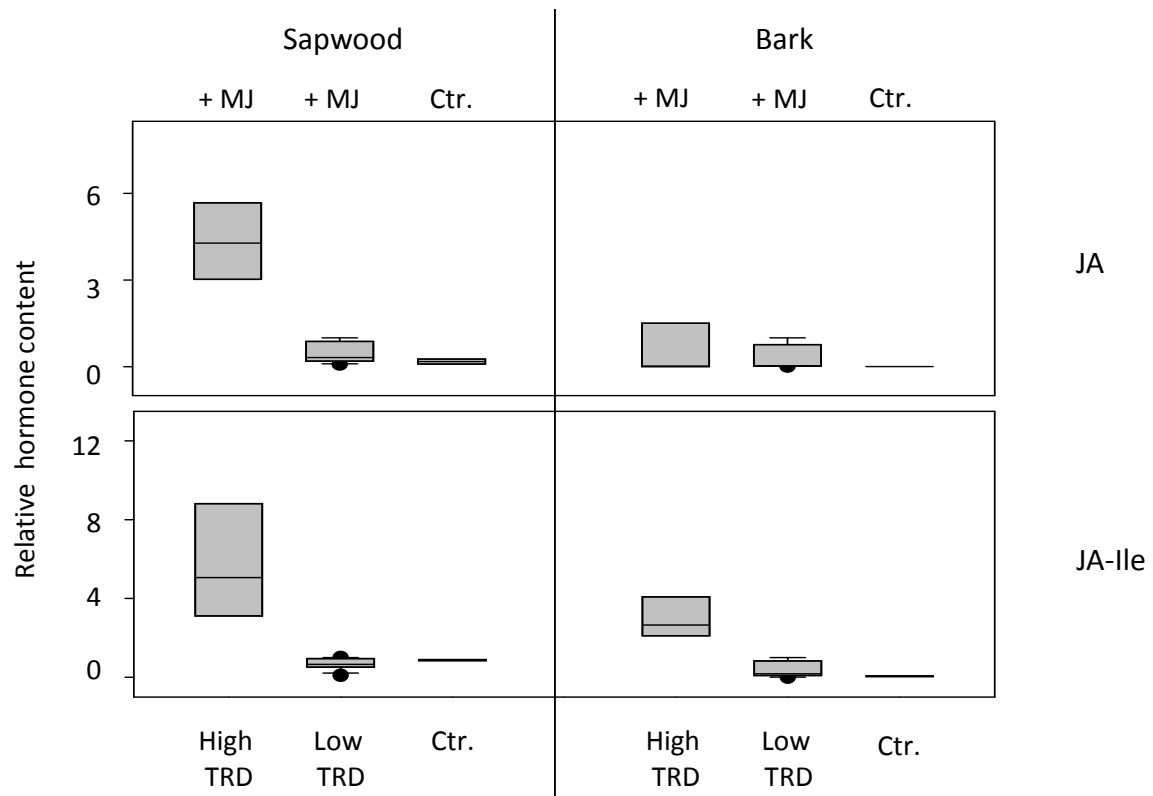
**Table S2.** Primer sequences used in this study

Gene	Purpose	Forward Primer	Reverse primer
<i>NPR1</i>	screening	CCTTGCACTATGCTGCAGC	CCTGCTCCAGTATCTCAATGC
	qRT-PCR	TATGCTGCAGCATACTGTGATC	CTCATCAGAAGTCAAATCAGAAGG
<i>13-LOX</i>	screening	GGAGCCCTATATCATTGCAGC	CCATGGAGTACTTGTCTGGTG
	qRT-PCR	CAGCACATAGGCATCTAAGTGC	CATGCTCTGTCATATGCAGATGC
<i>MPK3</i>	screening	CTCGCTGGTATCGTGACA	GGGTGACTCAAGGCTTCTTG
	qRT-PCR	AGCTATTGATATCTGGTCAGTGG	TTGCCTGATGTATCTTCTAGCATTG
<i>ACO</i>	qRT-PCR	GCCATGTCCAAGACCAGAGC	GTGGTGCATCGATCCAACGG

All primer sequences are listed in 5'- 3' orientation. Primers used in quantitative real time PCR analysis were HPLC purified.

**Figure S3.**

Box plot of the relative amounts of jasmonate (JA), and jasmonate-isoleucine conjugate (JA-Ile) in Norway spruce sapwood and bark after methyl jasmonate (MJ) treatment in high and low traumatic resin duct (TRD) trees and in unsprayed control trees (Ctr.). Sapwood and bark was collected at various distances above the treatment site ~4 weeks after treatment. The mean JA/JA-Ile level at the MJ treatment site in low TRD trees was set to 1.0. Data from the different distances per treatment were pooled.



**Table S3.** Number and size of TRD (in %) of traumatic resin ducts (TRD) at different sampling position of trees that were selected for analysis of terpene content, hormone quantity and transcript level.

Family	Tree number	Distance from MJ treatment (in cm)	Number of TRD	Coverage of TRD (in %)
15	3	0	1	18
		15	0	0
		30	0	0
		45	0	0
		60	0	0
15	7	0	1	18
		15	0	0
		30	0	0
		45	0	0
		60	0	0
24	2	0	0	0
		15	0	0
		30	0	0
		45	0	0
		60	0	0
24	7	0	4	71
		15	5	71
		30	6	59
		45	2	35
		60	0	0
24	9	0	2	71
		15	3	47
		30	4	53
		45	2	24
		60	3	53

Coverage of TRD (in %) was determined as percent coverage of resin ducts (including the epithelial cells lining the ducts) across 870  $\mu\text{m}$  in the tangential direction on sapwood cross-sections.

**Figure S4.**

Box plot of the relative abundance of mRNA transcripts of *NPR1*, *MPK3*, *13-LOX*, and *ACO* genes in Norway spruce sapwood and bark after methyl jasmonate (MJ) treatment in high and low traumatic resin duct (TRD) trees and in unsprayed control trees (Ctr.). Transcript abundance of each gene was measured by quantitative real-time PCR using SYBR-Green for detection and normalized against ubiquitin. Sapwood and bark was collected at various distances above the treatment site ~4 weeks after treatment. The mean transcript abundance at the MJ treatment site in low TRD trees was set to 1.0. Data from the different distances per treatment were pooled.

