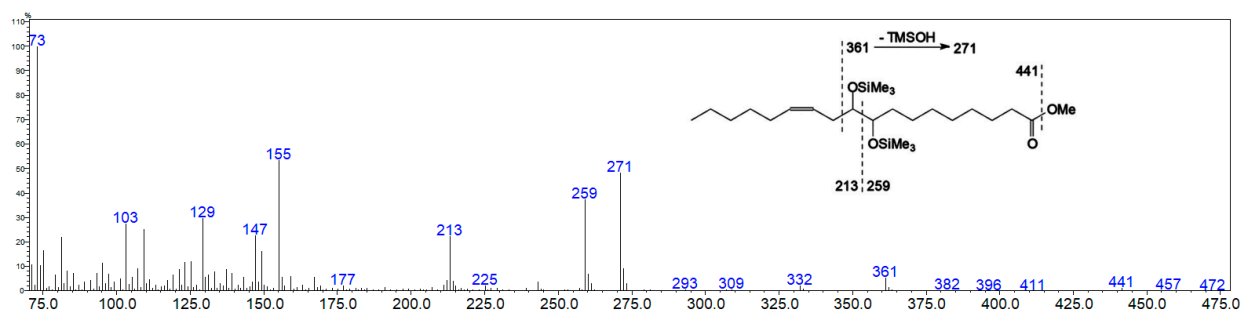
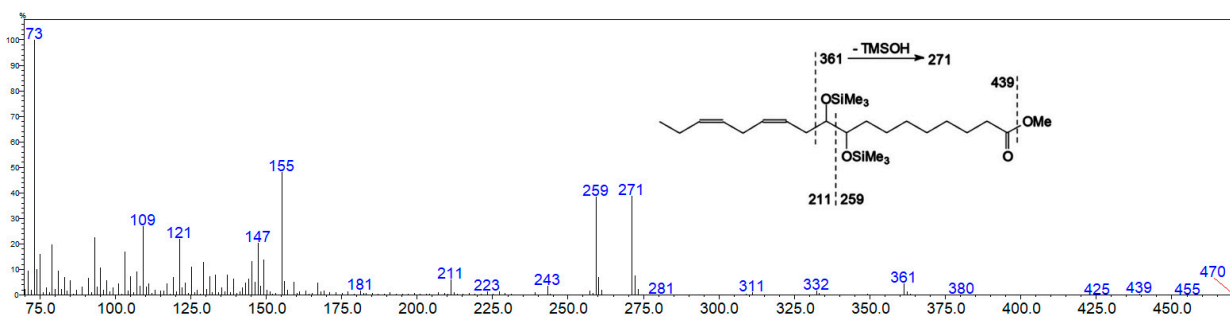


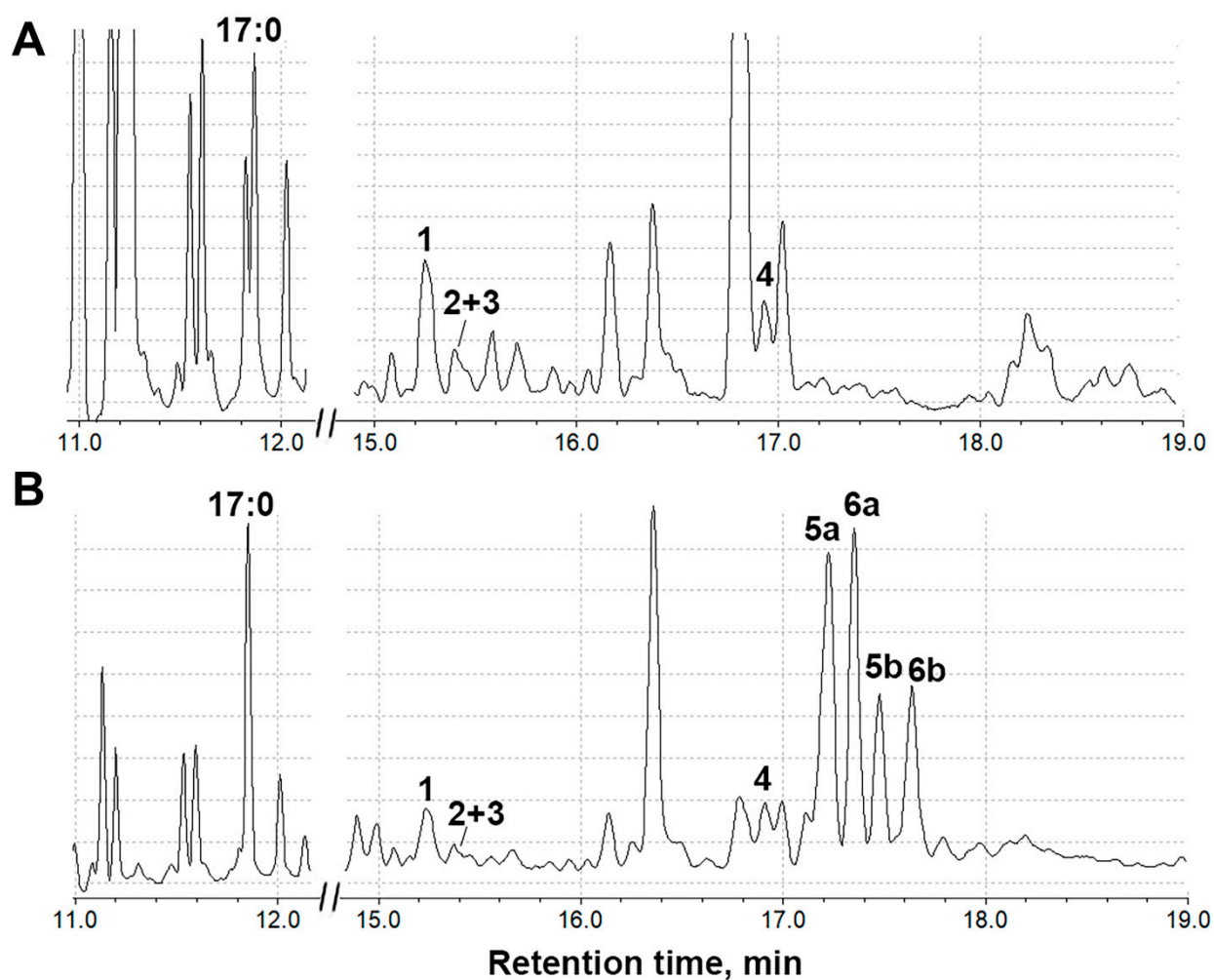
Supplementary Figure S1. Changes in marker genes expression of other signaling pathways in response to treatment with NaCl 25 mM (red) and 50 mM (blue) in shoots and roots. Abbreviations: ICS (isochorismate synthase), PR1 (pathogenesis-related protein 1), ERF (ethylene-inducible transcription factor), EBF (EIN3 (ETHYLENE-INSENSITIVE3) BINDING F-BOX1), WIN (wound-induced (WIN) protein), NCED (9-cis-epoxycarotenoid dioxygenase), CYP707A (ABA-8'-hydroxylases), ABF2 (ABRE-binding bZIP proteins), PP2C (serine/threonine phosphatase 2C), LTP (lipid transfer protein), GA20ox (gibberellin (GA) 20-oxidase), GA3ox (GA3 oxidase), EXP (expansins), AMI (indole-3-acetamide hydrolase), TIR (transport inhibitor response), IAA (indole-3-acetic acid inducible 28 (IAA28)).



Supplementary Figure S2. The electron impact mass spectrum of compounds 5a (vic-diol) and the corresponding mass fragmentation scheme. Compound 5b has the identical spectrum.



Supplementary Figure S3. The electron impact mass spectrum of compounds 6a (vic-diol) and the corresponding mass fragmentation scheme. Compound 6b has the identical spectrum.



Supplementary Figure S4. The total ion current (TIC) GC-MS chromatograms of lipxygenase cascade products (Me/TMS) in *S. tuberosum* shoots extracts after incubation with linoleic and α -linolenic acids: (A) shoots after NaCl treatment; (B) roots after NaCl treatment. **1** – 9-HOD (derivative of 9-LOX product); **2** – 9-HOT (derivative of 9-LOX product); **3** – 13-HOD + 13-HOT, **4** – 9,10-epoxy-11-hydroxy-12-octadecenoic acid (9-EAS product); **5a** and **5b** – *threo* and *erythro* isomers of 9,10-dihydroxy-12-octadecenoic acid (*vic*-diols formed the NaBH₄ reduction of alpha-ketol, 9-AOS product of 9-HPOD conversion), **6a** and **6b** – *threo* and *erythro* isomers of 9,10-dihydroxy-12,15-octadecadienoic acid (*vic*-diols formed the NaBH₄ reduction of alpha-ketol, 9-AOS product of 9-HPOT conversion).

Supplementary Table S1. Primers for qRT-PCR amplification.

	Gene name	Forward primer	Reverse primer
LOX pathway	<i>StLOX</i>	GTAGACCACCAACACGAACAGATCC	CAGGGCATGTAATTCAGGGAGG
	<i>StAOS1</i>	CCATCGCCACCTGTAAACAAG	CCGCCTGTGAGATCAGTGGAG
	<i>StAOS2</i>	CCCAAATTCCATGAACTTATACAGAG	GACCGAGAGTGAGTACAGGATGAAGC
	<i>StAOS3</i>	CCTATTTTCGATTGTTTTGTGAGGGG	CTCCAAGTTTCTCCGCTTCATC
	<i>StHPL</i>	CTGAACCTAAACATGCCCAGATTAAG	GCCGAGGAGAGTGAGGGAGAAG
	<i>StDES</i>	CCCTCATCTCTTCAGGTTTGTGG	GGTGGGCGAAGTCTCAATGTCTC
	<i>StHPL/EAS</i>	CTTGCAGGATTCAACGCTTATGG	CACCTTCCTCCTTGATGATCGTC
	<i>StJaz</i>	CAAGTGATTTCATCGTCGTCATCGTC	GAAAATCATCAAAAACAATGACTTGTCC
	<i>StAOC</i>	GCTCAATGAACGTGACCGTGAAG	CGATCTCCTTTCTTCTTCTTCTCGTG
SA	<i>StICS</i>	GGTACTTGCTCGTAGCACCAGAGTTG	GCTGAGGCGGTCCCAGTAAATAG
	<i>StPR1</i>	CATCTCATTGTTACTCACTTGTCTCATGG	GAATTGGCATAATTTTGTGCTCGGGATG
Ethylene	<i>StERF</i>	GGATGGTCGCCGTTTAGTTTCAC	CCGCTGTCTAACGCCTCTATAATGTC
	<i>StEBF</i>	GCCGTGACTGACATAGTCCTTATTGG	CAGAACAGCTTCAAGTTTGGACAACC
	<i>StWIN</i>	GCCGTGACTGACATAGTCCTTATTGG	CAGAACAGCTTCAAGTTTGGACAACC
ABA	<i>StABF2</i>	GACCACAGCAACTGCAACAGAAC	CTGCCCAACTGCCACTATTTG
	<i>StNCED2</i>	GCGAACTACAAAACCTCTTCC	CCCCGTTAATGCAATTAGGG
	<i>StPP2C</i>	CGAGGTGGAGAAGGAAGAACTC	CACTGTGGAGTCTGAAGCTCGC
	<i>StC707A</i>	GTGTTTAAGCTCTTTGATTGTGGTG	CTGGGGTTTTGTGAGTAAAGCTG
	<i>StLtp1</i>	GTCCTCTCGGAGGCTGTTGTG	GGGAGACTAGCAGCTTTGCC
GA			
	<i>StGA3ox</i>	GCCCTACAATAAATTCTTACCCG	GGTACAACCCGTTTGACAATATGTG
	<i>StGA20ox</i>	CAAAGCTACCTTGGAAGAGACACTC	GAAGTGGCTCTTCTCTACGCCTAG
	<i>StEXP7</i>	GCCTAATGATAATGGTGGTTGGTG	CATAACCTTCGTAATGTCACCTGC
Auxin, IAA	<i>StAMI</i>	GAGTACCTGGAGGATCTTCAAGTGG	CATCCAAGTATCAAACTTTGTGC
	<i>StTIR1</i>	GAAGTGGAGGACCTTAGTGGGC	GCACGATTTATCCGAAGAGTTCTC
	<i>StIAA28</i>	GGGTCTTTTCAGAACTGTTGATTTG	CTTCCTGAATGATCTCACTGGTGG
Housekeeping genes	<i>STTub</i>	GTTACTTGCTGTTTGAGATTCCCTG	CTGTGAGGTAACGTCCATGACG
	<i>STEF</i>	CTTCCTACCTCAAGAAGGTTGGTTAC	CTTGCTGTTGGTCTCTTGGGC
	<i>STGAP</i>	GGTTAAGGATGAGAAGACCTTC	GCGGAGATCACAACCTTCTTG
	<i>STUbi</i>	GACAATGTAAAGGCTAAGATTCAAGAC	GTGGACTCCTTCTGGATGTTGTAG
	<i>STAct</i>	GTGAGTCACACTGTCCCTATCTATG	CAGTGGTGGTGAACATATAACCTCT
	<i>STATP</i>	GGTAAAGGAGGAGTTGGAAGAC	CAAGGGCAAATAATGGAGAATAC

Supplementary Table S2. List of marker genes for different hormonal systems, the expression of which was analyzed in the present study.

	Gene designation in the article (in the figures)	Gene name	Function/Role
SA	ICS	Isochorismate synthase	SA biosynthesis
	PR1	Pathogenesis-related protein 1	Defense reaction
Ethylene	ERF	Ethylene-inducible transcription factor	Activation of the expression of ethylene-induced genes
	EBF	EIN3 (ETHYLENE-INSENSITIVE3) BINDING F-BOX1	Negative regulator of ethylene-dependent signaling
	Win	Wound-induced (Win) protein	Defense reaction
ABA	NCED	9-cis-epoxycarotenoid dioxygenase	ABA biosynthesis
	C707A3	ABA-8'-hydroxylases	ABA degradation
	ABF2	ABRE-binding bZIP proteins (transcription factor)	ABA signal transmission
	PP2C	serine/threonine phosphatase 2C	Negative regulator of ABA signal transmission
	LTP	Lipid Transfer Protein	Lipid Transfer, membrane stabilization
GA	GA20ox	GA20-oxidases	Gibberelin biosynthesis
	GA3ox	GA3 oxidase	Gibberelin biosynthesis
	EXP	Expansins	Loosening of the cell wall
Auxin (IAA)	AMI	Indole-3-acetamide hydrolase	Auxin biosynthesis
	TIR	Transport inhibitor response	Auxin signal transmission
	IAA	Indole-3-acetic acid inducible 28 (IAA28)	Repressor of IAA signaling

Supplementary Table S3. Identified lipoxygenase (StLOX) in underground potato organs. The matched peptides in the protein sequence are highlighted in red.

Organ	Protein	Score	Protein sequence
roots and tuber	Q43190 (LOX14_SOLTU) Lipoxygenase Mr 96909 pI 5.50	597	<p>1 MLGQIVGGLI GGHHDSKKVK GTVVMKKNA LDFTDLAGSL TDKIFEALGQ 51 KVSFQLISSV QSDPANGLOQ KHSNPAYLEN FLFTLTPLAA GETAFGVTFD 101 WNEEFGVPGA FIIKNTHINE FFLKSLTLED VPNHGKVHFV CNSWVYPSFR 151 YKSDRIFFAN QPYLPSETPE LLRKYRENEL LTLRGDGTGK REAWDRIYDY 201 DVYNDLGNDP QGKENVRTTL GGSADYPYPR RGRTGRPPTR TDPKSESIP 251 LILSLDIYVP RDERFGHLKM SDFLTYALKS IVQFILPELH ALFDGTPNEF 301 DSFEDVLRLY EGGIRLPQGP LFKALTDAIP LEMIRELLRT DGEGLRFPT 351 PLVIKDSKTA WRTDEEFARE MLAGVNPHI SRLQEFPPKS KLDPEAYGNQ 401 NSTITAEHIE DKLDGLTVDE AMNNNKLFIL NHHDVLIPYL RRINTTTTKT 451 YASRTLLFLQ DNGSLKPLAI ELSLPHPDGD QFGVTSKVYT PSDQGVESSI 501 WQLAKAYVAV NDSGVHQLIS HWLNTHAVIE PFVIATNRQL SVLHPIHKLL 551 YPHFRDTMNI NAMARQILIN AGGVLESTVF PSKFAMEMSA VVYKDWVFDP 601 QALPADLVKR GVAVEDSSSP HGVRLLIEDY PYAVDGLEIW SAIKSWVTDY 651 CSFYYSDEE ILKDNELQAW WKELREVGHG DKKNEPWWPE METPQELIDS 701 CTTIIWIASA LHA AVNFGQY PYAGYLPNRP TVSRRFMPPEP GTPEYEELKK 751 NPDKAFLKTI TAQLQTLLGV SLIEILSRHT TDEIYLGQRE SPEWTKDKEP 801 LAAFDKFGKK LTDIEKQIIQ RINGDNILINR SGPVNAPYTL LFPTSEGGLT 851 GKGIPNSVSI</p>
tuber	Q43190_SOLTU Lipoxygenase Mr 96909 pI 5.50	303	<p>1 MLGQIVGGLI GGHHDSKKVK GTVVMKKNA LDFTDLAGSL TDKIFEALGQ 51 KVSFQLISSV QSDPANGLOQ KHSNPAYLEN FLFTLTPLAA GETAFGVTFD 101 WNEEFGVPGA FIIKNTHINE FFLKSLTLED VPNHGKVHFV CNSWVYPSFR 151 YKSDRIFFAN QPYLPSETPE LLRKYRENEL LTLRGDGTGK REAWDRIYDY 201 DVYNDLGNDP QGKENVRTTTL GGSADYPYPR RGRTGRPPTR TDPKSESIP 251 LILSLDIYVP RDERFGHLKM SDFLTYALKS IVQFILPELH ALFDGTPNEF 301 DSFEDVLRLY EGGIRLPQGP LFKALTDAIP LEMIRELLRT DGEGLRFPT 351 PLVIKDSKTA WRTDEEFARE MLAGVNPHI SRLQEFPPKS KLDPEAYGNQ 401 NSTITAEHIE DKLDGLTVDE AMNNNKLFIL NHHDVLIPYL RRINTTTTKT 451 YASRTLLFLQ DNGSLKPLAI ELSLPHPDGD QFGVTSKVYT PSDQGVESSI 501 WQLAKAYVAV NDSGVHQLIS HWLNTHAVIE PFVIATNRQL SVLHPIHKLL 551 YPHFRDTMNI NAMARQILIN AGGVLESTVF PSKFAMEMSA VVYKDWVFDP 601 QALPADLVKR GVAVEDSSSP HGVRLLIEDY PYAVDGLEIW SAIKSWVTDY 651 CSFYYSDEE ILKDNELQAW WKELREVGHG DKKNEPWWPE METPQELIDS 701 CTTIIWIASA LHA AVNFGQY PYAGYLPNRP TVSRRFMPPEP GTPEYEELKK 751 NPDKAFLKTI TAQLQTLLGV SLIEILSRHT TDEIYLGQRE SPEWTKDKEP 801 LAAFDKFGKK LTDIEKQIIQ RINGDNILINR SGPVNAPYTL LFPTSEGGLT 851 GKGIPNSVSI</p>