

Supplementary information

The transcriptome of potato tuber phellogen reveals cellular functions of cork cambium and genes involved in periderm formation and maturation

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Table S2 List of meristem-related genes found in the phellogen transcriptome

Gene name	Sol genomics ID	TAIR ID	Reference
Cambium			
<i>ACA8</i>	Sotub07g009770.1.1	AT5G57110.2	1
<i>AGO4</i>	Sotub01g009760.1.1	AT2G27040.2	1
<i>APH3</i>	Sotub01g022470.1.1	AT3G21510.1	1
<i>Aquaporin</i>	Sotub03g036560.1.1	AT3G16260.1	2
<i>Aquaporin</i>	Sotub01g014220.1.1	AT3G56950.2	2
<i>Aquaporin</i>	Sotub06g009110.1.1	AT4G00430.1	2
<i>Aquaporin</i>	Sotub01g032080.1.1	AT4G23400.1	2
<i>Aquaporin</i>	Sotub01g049070.1.1	AT4G35100.2	2
<i>ARF3</i>	Sotub02g020520.1.1	AT2G33860.1	3
<i>ARF4</i>	Sotub01g036930.1.1	AT1G54990.1	3
<i>ATHB-15 [HD-ZipIII]</i>	Sotub03g036370.1.1	AT1G79840.2	3
<i>ATHB9</i>	Sotub01g030790.1.1	AT4G00730.1	3
<i>CDK</i>	Sotub01g029100.1.1	AT2G44740.1	2
<i>CDK</i>	Sotub01g029950.1.1	AT3G60550.1	2
<i>CDK inhibitor</i>	Sotub12g030040.1.1	AT2G32710.2	2
<i>CDK inhibitor</i>	Sotub09g017820.1.1	AT5G48820.1	2
<i>Cyclin</i>	Sotub01g025990.1.1	AT5G21080.1	2
<i>Cyclin A</i>	Sotub03g029000.1.1	AT2G18540.1	2
<i>Cyclin B</i>	Sotub02g026170.1.1	AT1G20610.1	2
<i>Cyclin D3</i>	Sotub02g031650.1.1	AT4G34090.1	4
<i>Cyclin D3:1</i>	Sotub02g031450.1.1	AT5G67260.1	4
<i>Cyclin D3:2</i>	Sotub01g044850.1.1	AT5G67260.1	4
<i>DNA methyltransferase-associated protein (DMAP1)</i>	Sotub01g023480.1.1	AT2G47210.1	5
<i>DRM-type DNA-methyltransferase</i>	Sotub02g010360.1.1	AT5G14620.1	5
<i>Expansin</i>	Sotub02g034760.1.1	AT1G26770.2	2
<i>Expansin</i>	Sotub02g024320.1.1	AT3G03220.1	2
<i>Expansin</i>	Sotub01g049420.1.1	AT3G45970.1	2
<i>GSK3</i>	Sotub01g040370.1.1	AT1G09840.6	6
<i>GSK3</i>	Sotub01g030780.1.1	AT4G00720.1	6
<i>GSK3</i>	Sotub02g018890.1.1	AT4G18710.1	6
<i>GSK3</i>	Sotub02g036240.1.1	AT5G14640.1	6
<i>H2B</i>	Sotub03g016600.1.1	AT2G28720.1	2
<i>H2B</i>	Sotub02g018820.1.1	AT4G18740.1	2
<i>H4</i>	Sotub11g029670.1.1	AT5G59970.1	2
<i>PXY</i>	Sotub02g030330.1.1	AT5G65700.2	1
<i>REVERSION-TO-ETHYLENE SENSITIVITY1 (RTE1)</i>	Sotub02g010060.1.1	AT3G51040.3	1
<i>RUL1</i>	Sotub03g018340.1.1	AT5G58300.2	1

<i>SCRAMBLED (SCM)</i>	Sotub02g021640.1.1	AT2G20850.1	1
<i>VASCULAR TISSUE SIZE (VAS)</i>	Sotub01g040060.1.1	AT5G13900.1	7
<i>VASCULAR TISSUE SIZE (VAS)</i>	Sotub01g042060.1.1	AT5G64080.1	7
<i>XET/XTH</i>	Sotub03g008310.1.1	AT1G11545.1	2
<i>XET/XTH</i>	Sotub01g028070.1.1	AT1G32170.1	2
<i>XET/XTH</i>	Sotub12g019260.1.1	AT4G25810.1	2
<i>XET/XTH</i>	Sotub12g019250.1.1	AT4G25810.1	2
<i>XET/XTH</i>	Sotub01g037390.1.1	AT5G13870.1	2
Shoot apical meristem			
<i>HD2 (HD2B)</i>	Sotub11g024650.1.1	AT3G44750.2	8
<i>MRG 1</i>	Sotub02g031380.1.1	AT4G37280.1	9
<i>No Apical Meristem (NAM)</i>	Sotub03g017140.1.1	AT3G49530.1	10
<i>No Apical Meristem (NAM)</i>	Sotub03g029340.1.1	AT5G61430.1	10
<i>No Apical Meristem (NAM)</i>	Sotub04g009390.1.1	AT1G01720.1	10
<i>PHAVOLUTA-like HD-AIPIII protein</i>	Sotub02g016070.1.1	AT2G34710.1	11
<i>RING1B</i>	Sotub02g020780.1.1	AT5G44280.1	12
<i>RINGLET2 (RTL2)</i>	Sotub02g020390.1.1	AT1G28420.1	13
<i>TOPLESS (TPL)</i>	Sotub03g030200.1.1	AT3G15880.1	14
<i>Topless-Related 2 (TPR2)</i>	Sotub01g037850.1.1	AT5G27030.1	15
Floral meristem			
<i>CONSTANS</i>	Sotub01g025960.1.1	AT3G63500.2	16
<i>CONSTANS</i>	Sotub01g047820.1.1	AT4G38960.1	16
<i>CONSTANS</i>	Sotub02g022400.1.1	AT5G54470.1	16
<i>CYCLING DOF FACTOR 2 (CDF2)</i>	Sotub02g034790.1.1	AT5G39660.2	17
<i>Jumonji</i>	Sotub04g018130.1.1	AT5G04240.1	18
<i>RED AND FAR-RED INSENSITIVE 2 (RF12)</i>	Sotub01g037570.1.1	AT3G05545.1	19
<i>SCM</i>	Sotub02g021640.1.1	AT2G20850.1	1
<i>SFH12</i>	Sotub01g047280.1.1	AT2G21540.2	20
<i>StJMJ16</i>	Sotub04g009950.1.1	AT1G08620.2	21
<i>TFL2</i>	Sotub01g027600.1.1	AT5G17690.1	22
Root meristem			
<i>ACAR FAMILY PROTEIN 4 (AtSCAR4)</i>	Sotub02g019430.1.1	AT2G34150.2	23
<i>CYTOCHROME C-2 (CYTC-2)</i>	Sotub01g040200.1.1	AT4G10040.1	24
<i>HAWAIIAN SKIRT (HS/HWS)</i>	Sotub01g032770.1.1	AT3G61590.2	25
<i>MPK6</i>	Sotub05g022310.1.1	AT4G01370.1	26
<i>RanGap 1</i>	Sotub01g023990.1.1	AT5G19320.1	26
<i>TONNEAU 1</i>	Sotub04g009490.1.1	AT3G55000.1	26
<i>TONNEAU 2/FASS</i>	Sotub01g021510.1.1	AT5G18580.1	26

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Table S3 Functional protein association networks within the phellogen transcriptome. Analysis was performed using STRING program (<https://string-db.org/>) based on Arabidopsis orthologs of phellogen-selected genes. Table lists interactomes based on Fig S5

Phellogen query	Query annotation	Members of interactome	TAIR ID	Interacted protein function
H2B (AT2G28720.1)	Histone H2B; core component of nucleosome	H2AXA (histone H2AXa)	AT1G08880.1	Chromatin remodeling
		HTA6 (Histone H2A 6)	AT5G59870.1	Chromatin remodeling
H3 (AT5G65360.1)	Histone H3; core component of nucleosome	Histone H4	AT5G59970.1	Chromatin remodeling
		HTA6	AT5G59870.1	Chromatin remodeling
H4 (AT5G59970.1)	Histone H4; core component of nucleosome	Histone H3	AT5G65360.1	Chromatin remodeling
		HMG (High mobility group)	AT3G28730.1	Chromatin remodeling
GPAT3/GPAT4 (AT1G01610.1)	Glycerol-3-phosphate acyltransferase; cutin biosynthesis	GPDHp (Glycerol-3-phosphate dehydrogenase)	AT5G40610.1	Glycerolipid metabolism
		LPAT2 (Lysophosphatidyl acyltransferase 2)	AT3G57650.1	Glycerolipid metabolism
ACT7 (AT5G09810.1)	Actin 7; cytoskeleton array	transducin/WD40 domain-containing protein	AT3G18060.1	Actin filaments elongation during cell divisions
		CPA (Capping protein A)	AT3G05520.2	Actin filaments elongation during cell divisions
BTH4/MED15 (AT1G15780.1)	Uncharacterized protein	NA	NA	NA
POD (AT5G66390.1)	Peroxidase 72; lignin/suberin biosynthesis	CAD5 (Cinnamyl alcohol dehydrogenase 5)	AT4G34230.1	Lignin biosynthesis
		OMT1 (<i>O</i> -Methyltransferase 1)	AT5G54160.1	Lignin biosynthesis
APK1/ATH8 (AT2G39190)	Transport and beta-oxidation of fatty acids	ABCA1 (ATP-binding cassette A1)	AT2G41700.1	Transport and beta-oxidation of fatty acids

Table S4 Primers used in this study

Gene Name	Sol genomics ID	NCBI ID	TAIR ID	Forward primer	Reverse primer	Amplicon size (bp)
CDS						
<i>ACT7</i>	Sotub03g020330	XM_006355076	AT5G09810	<u>CACCGATTA</u> AAAAATGGCCGACGG	CAAACAACCTAAAAGAGACAC	1420
<i>BTH4</i>	Sotub04g009440	XM_006359266	AT1G15780	<u>CACCGAGATGAATGGGAATAATTG</u>	CACTAGGAACTTGACAATC	832
<i>CCoAOMT1</i>	Sotub02g031720	XM_006339817	AT4G34050	<u>CACCGCAGTTATCAATGACAAGC</u>	CTTGAACCTAATAGGTACATG	951
<i>CFT</i>	Sotub01g036860	XM_006367783	AT1G28590	<u>CACCAATGGCGTTGACAGTTAGC</u>	CGATGATTTATGTTGTTATTTG	1303
<i>GPAT3</i>	Sotub01g032090	XM_006339523	AT1G01610	<u>CACCAAAATGTCACCTTCCAAAATCC</u>	GACCTTAACAAGCCCGAGGG	1823
<i>H2B</i>	Sotub03g016600	XM_006364383	AT2G28720	<u>CACCGCAAACAATGGCACCAAAGG</u>	CATTCAAGGAATAGCTATG	583
<i>H3</i>	Sotub10g009520	XM_006360980	AT5G65360	<u>CACCCCAAATGGCTCGTACCAAG</u>	GAATCGAGTAAATTCTGAATC	517
<i>H4</i>	Sotub11g029670	XM_006363280	AT5G59970	<u>CACCCAAAATGTCTGGCCGTGG</u>	CAGAAACATAACCAATTACATC	390
<i>MTN</i>	Sotub06g010040	XM_006361145	AT5G02380	<u>CACCTTATAATGTCTGGTTGTGGTTC</u>	GTCCATATAGTTGAAGCAC	284
<i>OSP</i>	Sotub07g011080	XM_006344513	AT2G48030	<u>CACCGCATATGAATTGTACCTCTC</u>	CAGGGAGGGAGTTAACAAG	560
<i>PED3</i>	Sotub04g020700	XM_006355290	AT4G39850	<u>CACCGTTAGTTCATCGCCATCCTCTG</u>	GTACACCATTTAATTTTTGG	1127
<i>PhDZnP</i>	Sotub01g044570	XM_006346280	AT3G19510	<u>CACCTGAGATGTCAACTCTTGAAAC</u>	CAATCTCAACCATTCCCG	2502
<i>POD</i>	Sotub02g027930	XM_015304568	AT5G66390	<u>CACCTAAATCATGCCACAAGCACAAG</u>	CAGATGGAACAAGCGATG	1019
<i>VAS</i>	Sotub01g040060	XM_006349221	AT5G13900	<u>CACCATTAATGGAGATGAAATAT</u>	GATAGATCATAACAAGGGAG	508
qPCR						
<i>qACT7*</i>				GGAGAAGTTAGGTGGTGG	CAAACAACCTAAAAGAGACAC	181
<i>qBTH4*</i>				GAAGAAGATAGGAAGGTGG	GGACATAAGAATCAACAAGCC	115
<i>qCCoAOMT1*</i>				CTTGAACCTAATAGGTACATG	CTGCTTTAGAGGATTTATTATC	168
<i>qCFT*</i>				CGATGATTTATGTTGTTATTTG	GATGTATACTGCTTTCTTCTC	147
<i>qGPAT3*</i>				GGTGGGGTTCTTGGATTTG	TAACAGAATCCCTCAAAGC	160
<i>qH2B*</i>				CAGCTCTTAATCAGTTTTAG	CATTCAAGGAATAGCTATG	156
<i>qH3*</i>				GTTACTATCATGCCTAAGG	GAATCGAGTAAATTCTGAATC	158
<i>qH4*</i>				GGAAGACTGTTACTGCTATG	CTACTAATACCCAATAACC	109
<i>qMTN*</i>				CCATCATCGAAGGAGTTGC	GTCCATATAGTTGAAGCAC	172
<i>qOSP*</i>				CATCATTTACTAAAGATTTTG	CAGGGAGGGAGTTAACAAG	173
<i>qPED3*</i>				GTACACCATTTAATTTTTGG	CATAATCTTTCCGGTCAGC	138

<i>qPhDZnP</i>				GACTCTCCCAAAGTAAGAC	CAATCTCAACCATTCACCG	198
<i>qPOD*</i>				CAGATGGAACAAGCGATG	GCCAAGTCTATGGTTAAGATGG	217
<i>qVAS*</i>				GTCTTAAAGGTGCATCAAATTC	CAACAATTAATACACAAAGG	145
Reference gene						
<i>qNAC</i>	Sotub10g027110	XM_006339185	AT3G12390	ATATAGAGCTGGTGATGACT	TCCATGATAGCAGAGACTA	97
<i>qUbq</i>	Sotub12g030900	Y10024.1	AT2G47110	GTTTTACAAGGTTGATGATTC	GAGCAAATCTAAGATAAAGC	202
<i>qACT</i>	Sotub10g022240	XM_006351284	AT3G12110	GAGTTGATTGTTGGGTTATG	GTGAAATGATTTAATGATGTG	179

Underlined CCAC was required for pENTER cloning

*Primers designed based on phellogen transcriptome sequences