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Supplement Figures and tables for

Intracellular Consequences of SOS1 Deficiency during Salt Stress

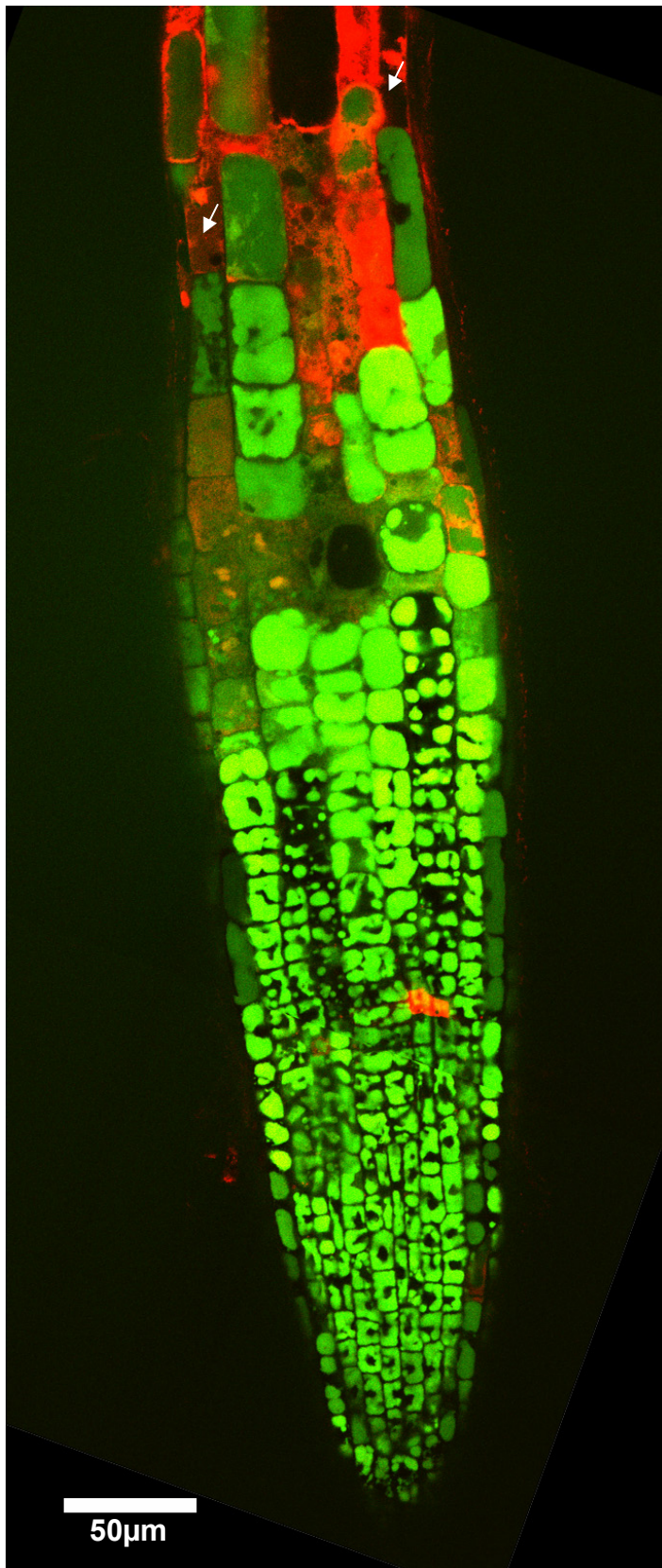
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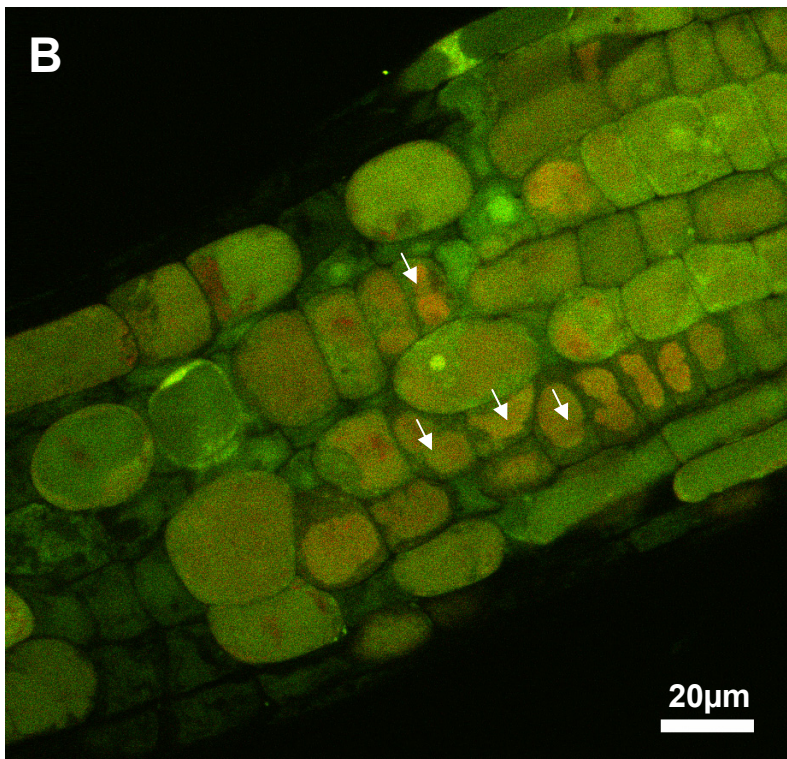
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Supplementary Figure 1

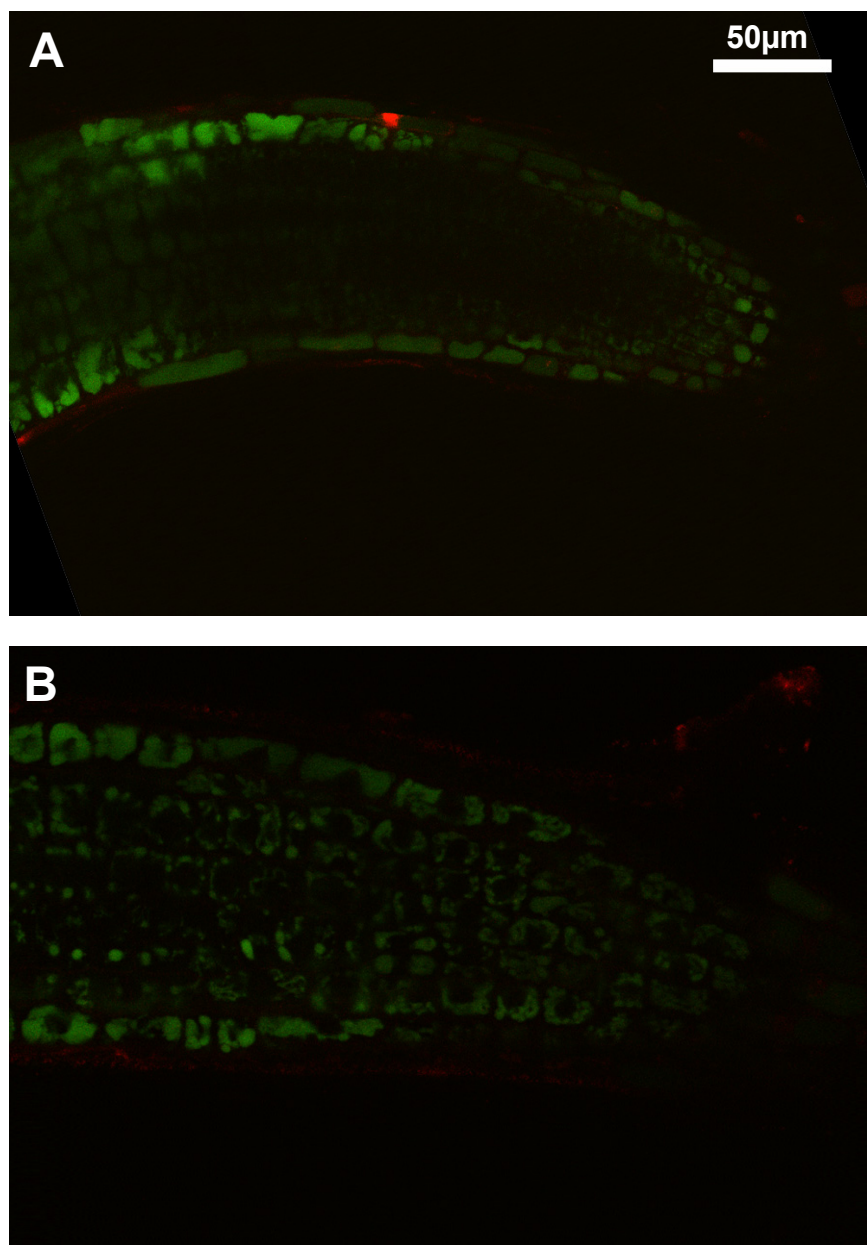
Col3 root at higher sodium concentration

Col3 roots were incubated at 200mM NaCl for 12 hrs and stained with CoroNa Green and propidium iodide. Arrows indicate dead cells. The CoroNa green intensities were recorded with 10% weaker sensitivity than that used in Figure 1 and 2, to avoid severe saturation of the fluorescence signal.



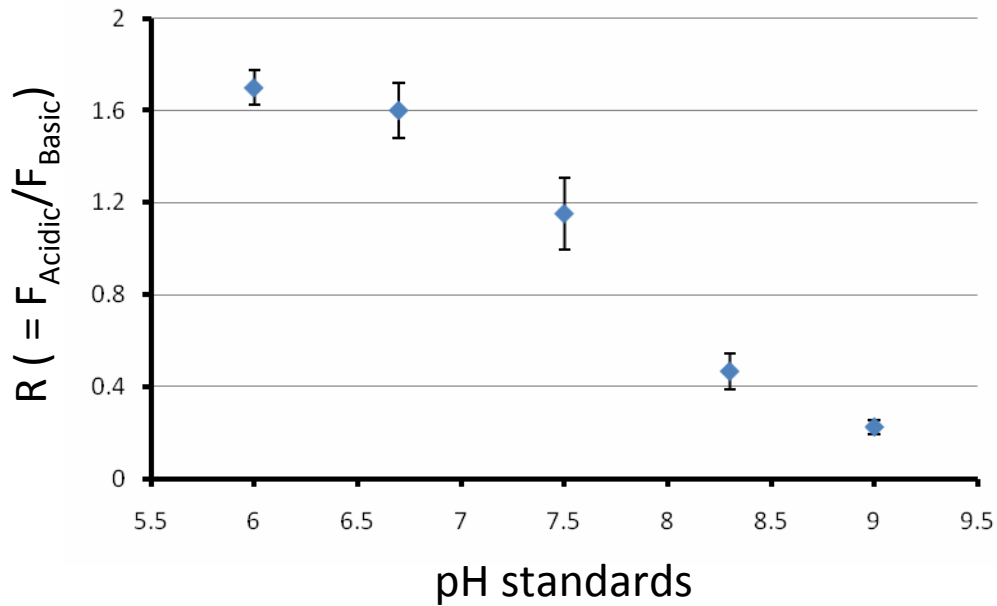
Supplementary Figure 2. Intracellular pH of Col3 root cells under higher sodium concentration

A. Col3 root were incubated at 200mM NaCl for 12 h and stained with carboxyl SNARF pH indicator. **B.** Magnification of A. Arrows indicate alkalized vacuoles.



Supplementary Figure 3. CoroNa Green negative controls.

Col3 (A) and sos1-1 (B) root cells stained with CoroNa Green with no NaCl added in the media. Confocal planes showing epidermis and cortex cells of the root tip region were shown with the microscope setting the same as used in Figure 2A-D.



Supplementary Figure 4. Determination of pH with carboxy SNARF pH indicator

The ratios of fluorescence intensities from acidic and basic channels were indicated for standard pHs of 6.0, 6.7, 7.5, 8.3 and 9.0. Error bars are standard deviation (n=12). The formula to calculate the pH was generated using the ratios from standard pHs 6.0 and 9.0 as the acidic and basic endpoints, respectively, following the supplier's manual (Invitrogen, MP01270): $\text{pH} = 7.5 - \text{Log}(0.52(R-0.22)/(1.70-R))$

Supplementary table 1: Complete list of qRT-PCR results

	Col3			<i>atsos1-1</i>		
100mM NaCl (hrs)	0	2	8	0	2	8
NHXs						
NHX1 (At5g27150)	1.00 ±0.02	1.33 ±0.17	1.05 ±0.13	0.99 ±0.11	1.31 ±0.21	0.88 ±0.08
NHX2 (At3g05030)	1.00 ±0.09	1.41 ±0.49	1.14 ±0.23	0.93 ±0.12	1.17 ±0.27	0.45 ±0.03
NHX3 (At5g55470)	1.00 ±0.07	1.03 ±0.12	1.13 ±0.42	0.83 ±0.23	4.25 ±1.58	1.24 ±0.19
NHX4 (At3g06370)	1.00 ±0.09	1.02 ±0.18	0.70 ±0.10	0.71 ±0.34	1.69 ±0.32	2.46 ±0.67
NHX5 (At1g54370)	1.00 ±0.02	0.76 ±0.15	0.68 ±0.14	1.06 ±0.06	0.94 ±0.17	0.70 ±0.31
NHX6 (At1g79610)	1.00 ±0.04	1.25 ±0.15	1.18 ±0.10	0.98 ±0.11	1.37 ±0.05	1.39 ±0.30
NHX8 (At1g14660)	1.00 ±0.11	0.81 ±0.19	0.76 ±0.25	1.03 ±0.19	1.25 ±0.07	1.73 ±0.28
Ca2+ transporters						
CAX1 (At2g38170)	1.00 ±0.06	0.66 ±0.11	0.86 ±0.22	0.76 ±0.13	0.72 ±0.07	2.12 ±0.12
CAX2 (At3g13320)	1.00 ±0.07	1.12 ±0.07	0.96 ±0.08	0.90 ±0.10	2.09 ±0.28	1.45 ±0.19
CAX4 (At5g01490)	1.00 ±0.06	1.17 ±0.36	1.30 ±0.25	0.99 ±0.19	6.71 ±1.01	56.73 ±13.19
ACA1 (At1g27770)	1.00 ±0.08	1.13 ±0.57	0.96 ±0.31	1.15 ±0.29	6.49 ±0.37	10.32 ±2.79
CNGC19 (At3g17690)	1.00 ±0.04	5.00 ±2.57	1.92 ±1.65	0.87 ±0.32	26.75 ±8.18	22.76 ±12.49
CNGC14 (At2g24610)	1.00 ±0.06	1.01 ±0.18	0.94 ±0.15	0.83 ±0.08	1.08 ±0.22	1.54 ±0.33
5PTase2 (At4g18010)	1.00 ±0.03	1.53 ±0.51	0.95 ±0.19	0.74 ±0.13	2.64 ±0.29	3.29 ±0.28
Regulation of PH						
AHA1 (At2g18960)	1.00 ±0.05	0.99 ±0.05	1.10 ±0.06	1.06 ±0.06	0.80 ±0.09	0.35 ±0.04
AHA2 (At4g30190)	1.00 ±0.05	0.84 ±0.16	1.09 ±0.09	1.11 ±0.27	0.49 ±0.24	0.19 ±0.05
VHA-A (At1g78900)	1.00 ±0.02	0.95 ±0.12	0.86 ±0.07	1.02 ±0.05	0.94 ±0.08	0.72 ±0.10
AVA-P4 (At1g75630)	1.00 ±0.05	0.89 ±0.23	0.78 ±0.13	1.02 ±0.08	0.78 ±0.20	0.25 ±0.07
AVP1 (At1g15690)	1.00 ±0.04	1.03 ±0.05	0.98 ±0.06	0.93 ±0.08	0.80 ±0.04	0.30 ±0.03
AVP2 (At1g78920)	1.00 ±0.05	1.08 ±0.11	1.15 ±0.07	1.24 ±0.18	1.29 ±0.08	0.81 ±0.08
K+ transporters						
HKT1 (At4g10310)	1.00 ±0.04	0.63 ±0.23	0.24 ±0.02	0.27 ±0.12	0.13 ±0.03	0.01 ±0.00
AKT1 (At2g26650)	1.00 ±0.04	0.96 ±0.09	0.87 ±0.04	0.97 ±0.16	0.87 ±0.09	0.81 ±0.32
KC1 (At4g32650)	1.00 ±0.04	0.97 ±0.26	1.23 ±0.17	0.98 ±0.40	1.10 ±0.16	1.00 ±0.06
CNGC5 (At4g32650)	1.00 ±0.07	0.93 ±0.21	0.83 ±0.17	1.00 ±0.03	0.87 ±0.09	0.51 ±0.14
KUP1 (At2g30070)	1.00 ±0.05	1.16 ±0.14	1.43 ±0.20	1.11 ±0.07	2.25 ±0.91	1.99 ±0.40
TRH1 (At4g23640)	1.00 ±0.06	1.01 ±0.15	0.91 ±0.18	0.83 ±0.24	0.98 ±0.14	0.68 ±0.20
TPK1 (At5g55630)	1.00 ±0.02	1.04 ±0.00	0.80 ±0.09	1.10 ±0.07	0.87 ±0.03	0.46 ±0.01
KEA2 (At4g00630)	1.00 ±0.04	0.80 ±0.04	1.05 ±0.10	1.10 ±0.11	0.91 ±0.20	0.40 ±0.01

Supplementary table 1 (continued)

100mM NaCl (hrs)	Col3			<i>atsos1-1</i>		
	0	2	8	0	2	8
Membrane trafficking						
ACT2 (At3g18780)	1.00 ±0.02	0.82 ±0.15	0.64 ±0.06	1.06 ±0.15	0.70 ±0.09	0.40 ±0.09
GNOM (At1g13980)	1.00 ±0.03	1.03 ±0.08	0.88 ±0.11	0.80 ±0.06	0.87 ±0.07	0.23 ±0.03
SYP111 (At1g08560)	1.00 ±0.04	0.59 ±0.10	0.69 ±0.05	0.90 ±0.10	0.55 ±0.14	0.11 ±0.02
SYP121 (At3g11820)	1.00 ±0.06	1.34 ±0.20	1.03 ±0.32	1.03 ±0.18	8.61 ±0.71	12.91 ±6.70
SYP122 (At3g11820)	1.00 ±0.10	1.29 ±0.10	0.78 ±0.18	0.93 ±0.36	7.78 ±2.31	14.13 ±2.15
EXO70B1 (At5g58430)	1.00 ±0.02	1.05 ±0.04	0.82 ±0.13	0.79 ±0.16	4.19 ±1.06	1.89 ±0.16
EXO70C1 (At5g13150)	1.00 ±0.08	0.95 ±0.11	0.97 ±0.17	0.72 ±0.18	0.60 ±0.06	0.45 ±0.07
EXO70H7 (At5g59730)	1.00 ±0.14	1.35 ±0.46	0.62 ±0.19	1.12 ±0.20	11.59 ±3.74	6.72 ±0.82
Chlathrin Adaptor (At1g60970)	1.00 ±0.11	1.32 ±0.72	1.35 ±0.46	1.22 ±0.20	2.86 ±2.16	7.31 ±4.35
PIN1 (At1g73590)	1.00 ±0.03	1.09 ±0.78	1.18 ±0.33	0.96 ±0.09	1.32 ±0.39	1.59 ±0.27
Aquaporins						
PIP1;1 (At3g61430)	1.00 ±0.03	0.94 ±0.59	0.51 ±0.16	1.00 ±0.15	0.98 ±0.68	0.18 ±0.14
PIP2;1 (At3g53420)	1.00 ±0.04	1.21 ±0.80	0.64 ±0.18	0.95 ±0.13	1.45 ±1.08	0.13 ±0.10
TIP1 (At2g36830)	1.00 ±0.04	1.19 ±0.69	0.61 ±0.18	0.88 ±0.25	0.95 ±0.50	0.18 ±0.13
TIP2 (At3g26520)	1.00 ±0.01	0.63 ±0.27	0.53 ±0.05	0.83 ±0.13	0.62 ±0.13	0.11 ±0.06

Supplementary table 2: List of qRT-PCR primers

AtCytB(690F)	AGGCACGTCAACAATGGCCAAAA	HKT1(577F)	ACGGCGAGAGATGTTCTTAGTTCCAA
AtCytB(785R)	TGTAGTGTAGCCCTCTCTGATCGAA	HKT1(687R)	CATGTTCTCATTCTGTTGGGACAAAT
AtNHX1(1279F)	CAGCACAGTGGTGTGGTATGCTG	AKT1(638F)	TCTTCGAGAGTCGGTGCCTTGTT
AtNHX1(1387R)	GTATGGATTTTGGGGTGTGTCATCA	AKT1(741R)	GCAGCACAATGAACCGCAAAAA
AtNHX2(1131F)	CAGCATCAAGCAGCAAGTTGTGATC	AKT1(1031R)	CCGACTTGTTCCATGGACTACCAAA
AtNHX2(1239R)	GCGCAATTCTGTGTGCCCTGAT	AtKC1(929F)	TGCTTTTCAACATTGGCCTCA
AtNHX3(1012F)	CACTTCCAGGCATGTATTGCAATG	AtKC1(1028R)	TTGATCGCACTCCTCATGGC
AtNHX3(1130R)	CCCCAAAGCTTAAGCTGCTTGCTT	AtCNGC5(1471F)	GCTTTAGTGCGAAGGGTTCCA
AtNHX4(1110F)	TGCTGCAATGTCAATTTCTAGCTGAGAT	AtCNGC5(1560R)	TGTGAACAAGCATGGTTTCAGC
AtNHX4(1214R)	GACTGACCAGGACTGTTGCGTACAAC	AtCNGC12(1163F)	CCAAGGGAACCGAAGAGGAA
AtNHX5(746F)	GCAGGATTGGACACCGAGAATCTT	AtCNGC12(1268R)	AGCCATGGAACACGCTTTAACA
AtNHX5(856R)	AGAAACAATGCCGGAGAGACCAAC	AtKUP1(1006F)	GCGATACCCGAGCCTGTGTT
AtNHX6(1222F)	TGGCAGGACCTGCTCATAGGAAA	AtKUP1(1099R)	TCGAAAACGTTGCGGATATGA
AtNHX6(1327R)	TGAACAGATTGCAGAGCAAGAGCAA	AtTRH1(1044F)	TGCCACGTTCTCGATTGTCA
AtNHX8(1180F)	TGGTCTGGATTAAGGGGTGCTGTTT	AtTRH1(1135R)	TCTGGCCAAGGACCCATCTT
AtNHX8(1285R)	GGAATAGAAACCTTGTTCCCGTATCTGAA	AtKEA2(657F)	TGCAGAAAACCGAAATGCTGA
AtCAX1(781F)	TGTTTTGTCCGACATGCAACTGAGTA	AtKEA2(749R)	ATGGAAAGTCCCGCCTAGC
AtCAX1(1317R)	AATGTGAACGCTGTGATGATTATGGAA	ACT2(1730F)	CAAGCAGCATGAAGATTAAGGTCGTT
AtCAX2(1007F)	AGACCAAGTCTTTGACAAAGGAATTGCTA	ACT2(1842R)	CTTGAGATCCACATCTGCTGGAAT
AtCAX2(1610R)	AAAAAGCTGGAAGTTAAGGTCCATCTGTT	At1g13980(1621F)	CTCGATTGTGATATAACTTGCAGCA
At5g01490(1194F)	AATGGGAATAGAAATGGACCTTAACCTCAA	At1g13980(1720R)	TGTGCATTGCAGACAAAGGACAGT
At5g01490(1293R)	CGAAGTCCCATCCTGTAATACTAAGGAAGTA	AtSYP121(718F)	GGGAGCTTATCTCGTCCGAGTATAGAGA
At1G27770(2171F)	CTGGCATCACTGTCAGAATGGTGA	AtSYP121(836R)	TCTCTCACTCTCTCCAGTGGAATCAGT
At1G27770(2270R)	TCGATAGCTATGCCATCATCAGTCAATAT	AtSYP111(475F)	AAGGCTCTCTGGGACTCCGGTTT
At3g17690(1152F)	TTCCGAGGAAAGTTTCTCCTTGACAT	AtSYP111(582R)	ATCTTTTGCCTCAGCCCTGAAA
At3g17690(1251R)	CTTCCCTGCGTGTGCCTAAGTGTA	EXO70C1(1099F)	ATTAACTGGCTCAGACGCGGCTA
At2g24610(1508F)	GTTGACGAGGAAACCATTCTTCATTCA	EXO70C1(1199R)	CTCGGTACCGGAGTTCGTCCATTAT
At2g24610(1607R)	CAAATAGCGGTACACGACGAACAAGAT	EXO70H7(1354F)	GCCGTTGCCGGATTCTTTATACAT
At4g18010(544F)	CATTATCGGGTTTCAAGAAGTGGT	EXO70H7(1459R)	CGTGAGTAAAATCACCAAGCGATAC
At4g18010(643R)	TCTACGAATTATCGATTCCCATTTTCG	AtTIP1(376F)	GGTGGCTTGGCTGTGCC
AtAHA1(2730F)	GACATTTTGAAGTTTGCCATTCGGTAT	AtTIP1(466R)	CAAGCCCGAATGTATCACG
AtAHA1(2840R)	CTTTCTCCAATACCGTAATCTTTCTTGTT	AtPIP1_1(679F)	ATCCCAATCACTGGCACAGG
AtAHA2(2425F)	CATTAGTCAAGCTCTGATCTTCGTCACAA	AtPIP1_1(778R)	CCCCAACACCCAGTGGTCA
AtAHA2(2516R)	CAATGAGGAAAGCAATCATCAGCAAT	AtPIP2_1(656F)	CCATTCCCATTACCGGAACC
AtAVA_P4(158F)	CGGCGAAGAGTGGAGTTGGAGTT	AtPIP2_1(760R)	CAACCCAAAATATCCAGTGGTCA
AtAVA_P4(275R)	GCGATGATCAAACATAAATACCTAACACA	AtTIP2(378F)	CGGTGGCGAGCCAATTC
AtAVP1(1734F)	GGAACACCACTGCTGCTATTGGAA	AtTIP2(477R)	GGTGTAGACGAGCCCGAAGG
AtAVP1(1854R)	GGGTCAAACATCTACGGTGTGGAT		
AtAVP2(1949F)	TCGGGTCTAGTGGACGAAAATGGTAT		
AtAVP2(2051R)	CCATAGTAAGGACATAAGCTGCAGTGCTT		