Supplemental data

Table S1. List of primers used in this study.

Purpose	Primer	Primer sequence (5'-3')
Amplification of *SLAC7* artificial miRNA	SM7-1	AGTCTAATAGGATATATGGCCTGCAGGAGATTCAGTTTGA
	SM7-2	TGCAGGCCATATATCCTATTAGACTGCTGCTGCTACAGCC
	SM7-3	CTCAGGCGATAAATCCTATTAGATTCCTGCTGCTAGGCTG
	SM7-4	AATCTAATAGGATTTATCGCCTGAGAGAGGCAAAAGTGAA
Identification of *slac7*	NTLB5	AATCCAGATCCCCCGAATTA
	FHU78F	TTATTGTTGCTTCCCTTGCC
	FHU78R	ATCACTCACCACCCTTCAGG
Amplification of *SLAC7* promoter	SP7F	TTGTCGACTGTCGTCAAGGCGGAGGG
	SP7R	GCTCTAGATCGTCGCATGTGACTATCC
SLAC7 overexpression constructs	SO7F	TTGGTACCGCAGTGAAAGAAGCATCC
	SO7R	TTGGATCCACATGTTGTACTGAGCGTGT
Subcellular location constructs	SB7F	TTGAATTCGCAGTGAAAGAAGCATCC
	SB7R	TTTCTAGAACATGTTGTACTGAGCGTGT
	SLAC7-F	GGGCAAGGGAAGCAACAATA
	SLAC7-R	GGCTGCGACCGGAACAC
	ubiqutin-F	AACCAGCTGAGGCCCAAGA
	ubiqutin-R	AACCAGCTGAGGCCGCCGA
	AR320-F	GATTTCCTCGTTTCGGGAGAT
	AR320-R	TTTCGGGATGCTCAAATCG
	AR350-F	ATCAAGGGCGAGGAAAGAATC
	AR350-R	CATCCACTGCAAAGCGGCT
	AR440-F	GGACAGCGGAAGTTTTAACCAT
	AR440-R	ATTTGCGGAAGTATTGACG
	AR500-F	CATTAGTCCGCGTACGAGGT
	AR500-R	CAAGTGAGCATGGACCAATC
	IP240-F	GATCGCGTTTGATTAGAGTGA
	IP240-R	CCACTTATAGTGACTGGATGA
	IP350-F	GGTTCCGCAACGAGAAGA
	IP350-R	CGCAATGGCGTCGAAAG
	IP570-F	GGTAACTGGTTGACTCCT
	IP570-R	CGCGCAATTCATCAATCT
	IP760-F	GCATGAGTGGGAGCAACACA
	IP760-R	CTAGCCTTCTGTTTCAAACGT
	IP840-F	GCCGCCAATTTTCCAGTGT
	IP840-R	GCCGCCAATTTTCCAGTGT
	CK040-F	GTTTTCTACCTGGTGGCATTCC
	CK040-R	GTTTTCTACCTGGTGGCATTCC
	CK110-F	TGGCCGGGATAGCCTACAA
	CK110-R	TGCCGCTTCTGCCACTCT

	CK230-F	CCTTCACCAAAGACCAGGAGTT
	CK230-R	CACGATGAAACCTTCCACATAGTC
	CK810-F	CACCGGCCAGGGAATCTT
	CK810-R	GCCATCATCTTGTTCGTCGAT
RT-qPCR	*CK860*-F	CACGCACACGAGCTGCTAAT
	CK860-R	CCGGGTCCCACCTGTCA
	PORA-F	TGTACTGGAGCTGGAACAACAA
	PORA-R	GAGCACAGCAAAATCCTAGACG
	YGL1-F	CCTTTTCAGTTCAGGCAAGC
	YGL1-R	CCTTTTCAGTTCAGGCAAGC
	NYC1-F	GCCATGAATGTCATGCAACACC
	NYC1-R	ATCCTCGGAACCAATGTCCTTGC
	NYC3-F	TGCTGCATCCTGTCCACACCTTG
	NYC3-R	TGCTGCATCCTGTCCACACCTTG
	PAO-F	TCCGATGTTACCGAAGGAGT
	PAO-R	CTGGAAAAAGTTCCGAGCAC
	SGR-F	CGGTGTCGCACACCATCAACC
	SGR-R	GGAGTGGAAGTAGACCCACAC
	RCCR-F	TGGTGCTTCTGGACCTTCTC
	RCCR-R	CGGCAAATTTGAAGTCAGGT
	NOL-F	GCCAGCACAAGAGGATGATTG
	NOL-R	GGTAACTCCTTGTTGGCTGCAT
	RBCS-F	TCCGCTGAGTTTTGGCTATTT
	RBCS-R	GGACTTGAGCCCTGGAAGG
	RBCL-F	CTTGGCAGCATTCCGAGTAA
	RBCL-R	ACAACGGGCTCGATGTGATA
	CAB1-F	AGATGGGTTTAGTGCGACGAG
	CAB1-R	AGATGGGTTTAGTGCGACGAG
	CAB2-F	TGTTCTCCATGTTCGGCTTCT
	CAB2-R	GCTACGGTCCCCACTTCACT
	HEMA1-F	CGCTATTTCTGATGCTATGGGT
	HEMA1-R	TCTTGGGTGATGATTGTTTGG
	OsDOS-F	ATGATGATGATGGGGGAAGG
	OsDOS-R	CTCACGGGGAGGTGAGACC
	Osh69-F	GGCCTTGTGAACCCTGACA
	Osh69-R	GGCCTTGTGAACCCTGACA

Table S2. Up-regulated genes in *slac7* leaves.

ProbeSet ID	OsGI	Fold
Os.7991.1.S1_at	LOC_Os04g41620	57.3793
OsAffx.3920.1.S1_s_at	LOC_Os04g27670	35.1909
Os.13965.1.S1_at	LOC_Os01g28500	23.1269
Os.53239.1.S1_at	LOC_Os12g30550	20.7827
OsAffx.3920.1.S1_at	LOC_Os04g27670	20.1257
Os.51063.1.S1_at	LOC_Os09g28210	19.7996
Os.38856.1.A1_s_at	LOC_Os01g67950	17.4152
OsAffx.32170.1.S1_at	LOC_Os12g43450	14.8086
Os.1385.1.S1_at	LOC_Os01g71670	14.4199
Os.12201.1.S1_at	LOC_Os09g27750	12.3757
Os.2677.1.S1_at	LOC_Os07g48830	12.1314
Os.28200.1.S1_x_at	LOC_Os03g61160	11.7676
Os.22312.3.A1_a_at	LOC_Os05g28740	11.7144
Os.20206.1.S1_at	LOC_Os02g41840	9.6125
Os.27232.1.S1_at	LOC_Os01g68650	9.5219
Os.27793.1.S1_at	LOC_Os02g14430	9.0977
Os.49536.1.S1_at	LOC_Os08g09950	7.9776
Os.10166.1.S1_at	LOC_Os04g41680	7.4858
Os.12633.1.S1_at	LOC_Os11g26790	7.397
Os.12633.1.S1_s_at	LOC_Os11g26790	7.3705
Os.27638.1.S1_at	LOC_Os05g48200	6.933
Os.6786.1.S1_a_at	LOC_Os10g40720	6.807
Os.11897.1.S1_at	LOC_Os03g61150	6.7942
Os.11323.1.S1_at	LOC_Os03g20120	6.7567
Os.1385.2.S1_x_at	LOC_Os01g71670	6.7122
Os.27793.1.S1_x_at	LOC_Os02g14430	6.6596
Os.12241.1.S1_at	LOC_Os03g14050	6.5453
Os.26687.1.S1_at	LOC_Os04g40990	6.3434
Os.50846.1.S1_s_at	LOC_Os01g10490	6.2441
Os.42285.1.S1_x_at	LOC_Os01g58550	6.1799
Os.46941.1.S1_s_at	LOC_Os06g48500	5.6994
Os.49023.1.S1_x_at	LOC_Os03g22680	5.5996
Os.12415.1.S1_at	LOC_Os09g02180	5.5436
Os.12551.1.S1_s_at	LOC_Os05g46480	5.5001
Os.37834.1.S1_a_at	LOC_Os04g58280	5.4875
Os.8098.1.S1_at	LOC_Os11g18570	5.4413
Os.5147.1.S1_at	LOC_Os03g49440	5.2053
Os.8850.1.S1_x_at	LOC_Os09g04160	5.1817
Os.51595.1.S1_at	LOC_Os01g46370	5.1141
Os.37822.2.S1_at	LOC_Os01g12020	5.1089
Os.11179.1.S1_at	LOC_Os03g16780	5.0423
Os.50825.1.S1_s_at	LOC_Os05g39990	5.0421

Os.11546.1.S1_at	LOC_Os06g35520	5.0232
Os.32022.1.S1_x_at	LOC_Os07g37620	5.0211
Os.4644.1.S1_at	LOC_Os01g60770	4.9483
Os.4683.2.S1_at	LOC_Os01g42520	4.8672
Os.25734.2.S1_a_at	LOC_Os04g34170	4.85
Os.43596.1.S1_at	LOC_Os01g10110	4.8407
Os.10933.1.S1_at	LOC_Os01g50910	4.8172
Os.10379.1.S1_at	LOC_Os02g49860	4.8136
Os.10497.1.S1_s_at	LOC_Os07g23640	4.8132
Os.6042.1.S1_at	LOC_Os07g25810	4.7688
Os.9086.1.S1_at	LOC_Os03g10210	4.6762
Os.51718.1.S1_at	LOC_Os11g26780	4.6389
Os.17405.1.S1_a_at	LOC_Os12g31860	4.5591
Os.27244.1.A1_s_at	LOC_Os04g32850	4.5191
Os.11169.1.S1_a_at	LOC_Os06g49190	4.5122
Os.27795.1.S1_at	LOC_Os11g06980	4.4895
Os.39066.1.S1_at	LOC_Os05g31140	4.431
Os.11795.1.S1_s_at	LOC_Os03g63950	4.3221
Os.18633.1.S1_at	LOC_Os04g43710	4.3207
Os.38638.1.S1_at	LOC_Os06g04990	4.2548
Os.23219.1.S1_at	LOC_Os01g52690	4.2362
Os.7771.1.S1_at	LOC_Os06g43600	4.2352
Os.12234.1.S1_s_at	LOC_Os10g40730	4.1476
Os.11795.1.S1_a_at	LOC_Os03g63950	4.1143
Os.8385.2.S1_at	LOC_Os10g06000	4.1034
Os.6363.1.S1_at	LOC_Os10g38080	4.0862
Os.28139.1.S1_at	LOC_Os01g62260	4.0736
Os.11513.1.S1_at	LOC_Os12g38140	4.058
Os.11287.1.S1_at	LOC_Os06g50930	4.0115
Os.14366.1.S1_at	LOC_Os08g37830	4.0069
Os.10006.1.S1_at	LOC_Os01g47400	4.002
Os.2404.1.S1_at	LOC_Os10g40700	3.9615
Os.55380.1.S1_at	LOC_Os06g46740	3.9597
Os.49245.1.S1_at	LOC_Os02g43330	3.9513
Os.4980.1.S1_at	LOC_Os03g59300	3.9441
Os.12735.1.S1_at	LOC_Os11g44810	3.9305
Os.12201.2.S1_at	LOC_Os09g27820	3.9227
Os.14830.1.S1_a_at	LOC_Os01g63190	3.9201
Os.14372.1.S1_at	LOC_Os03g04220	3.9085
Os.50843.1.S1_at	LOC_Os01g46340	3.9063
Os.37729.1.S1_s_at	LOC_Os01g03360	3.8852
Os.49225.1.S2_at	LOC_Os08g42700	3.864
Os.17356.1.A1_a_at	LOC_Os11g15060	3.8531
Os.14318.1.S1_at	LOC_Os08g42470	3.8312

Os.6242.1.S1_s_at	LOC_Os07g41600	3.7979
Os.18450.1.S1_s_at	LOC_Os05g34700	3.7872
Os.12198.1.S1_a_at	LOC_Os06g20370	3.7814
Os.20936.1.S1_a_at	LOC_Os07g05360	3.7751
Os.33604.1.S1_a_at	LOC_Os07g33480	3.7701
Os.37909.1.S1_at	LOC_Os05g27780	3.7617
Os.10733.1.S1_at	LOC_Os07g38130	3.76
Os.7947.1.S1_a_at	LOC_Os05g31140	3.7348
Os.18388.3.S1_at	LOC_Os01g49650	3.7227
Os.38848.1.S1_at	LOC_Os06g15330	3.715
Os.18395.1.S1_s_at	LOC_Os06g15620	3.7085
Os.57456.1.S1_x_at	LOC_Os01g24710	3.6747
Os.7753.1.S1_at	LOC_Os01g18170	3.6697
Os.2368.1.S1_at	LOC_Os03g60720	3.6517
OsAffx.3463.1.S1_at	LOC_Os03g40770	3.6489
Os.45916.1.S1_x_at	LOC_Os01g14850	3.6412
Os.264.1.S1_at	LOC_Os04g59260	3.6404
Os.50483.1.S1_at	LOC_Os04g42860	3.6376
Os.8827.1.S1_at	LOC_Os01g60740	3.6273
Os.12822.1.S1_at	LOC_Os05g44120	3.6221
Os.14366.1.S1_s_at	LOC_Os08g37840	3.6181
Os.6275.1.S1_at	LOC_Os01g67110	3.6109
Os.28462.1.S1_s_at	LOC_Os12g02290	3.6108
Os.24972.1.S1_at	LOC_Os02g09930	3.6048
Os.54579.1.S1_x_at	LOC_Os07g23640	3.5872
Os.49519.1.S1_at	LOC_Os07g46480	3.5856
Os.9962.1.S1_s_at	LOC_Os01g14850	3.5791
Os.23412.1.S1_at	LOC_Os12g41180	3.5714
Os.10635.1.S1_s_at	LOC_Os04g51880	3.5698
Os.10678.1.S1_at	LOC_Os10g05990	3.5535
Os.9488.1.S1_at	LOC_Os08g01220	3.5498
Os.4613.1.S1_at	LOC_Os02g51040	3.5417
Os.37876.1.S1_at	LOC_Os10g39920	3.516
Os.7578.1.S1_at	LOC_Os03g14140	3.5111
Os.28030.1.S1_s_at	LOC_Os06g48160	3.5015
Os.6417.1.S1_at	LOC_Os07g37850	3.4919
Os.28406.1.S1_at	LOC_Os09g11480	3.4912
Os.53726.1.S1_at	LOC_Os07g05370	3.487
Os.12838.1.S1_at	LOC_Os06g49760	3.4724
Os.49627.1.S1_at	LOC_Os06g37150	3.4356
Os.45916.1.S1_s_at	LOC_Os01g14850	3.4337
Os.22594.1.S1_at	LOC_Os01g03390	3.4275
Os.8385.1.S1_s_at	LOC_Os10g05970	3.3937
Os.6442.1.S1_at	LOC_Os03g08790	3.393

Os.37890.1.S1_s_at	LOC_Os11g24070	3.387
Os.5299.2.S1_a_at	LOC_Os05g37970	3.3845
Os.9312.1.S1_at	LOC_Os03g01270	3.3825
Os.22839.1.S2_at	LOC_Os06g48200	3.3785
Os.18406.1.S1_at	LOC_Os07g40220	3.3758
Os.20617.2.S1_s_at	LOC_Os03g20710	3.3685
Os.37820.1.S1_x_at	LOC_Os10g06000	3.3657
Os.37890.1.S1_at	LOC_Os11g24070	3.3579
OsAffx.14465.1.S1_s_at	LOC_Os04g58120	3.3551
Os.46021.1.S1_at	LOC_Os01g46600	3.3304
OsAffx.26492.1.S1_s_at	LOC_Os04g46830	3.3119
OsAffx.27219.1.S1_at	LOC_Os05g38290	3.2998
Os.21524.1.S1_at	LOC_Os10g05820	3.2852
Os.7566.1.S1_at	LOC_Os04g53950	3.2801
Os.43929.1.S1_s_at	LOC_Os06g15430	3.2759
Os.12286.1.S1_at	LOC_Os03g52690	3.2752
Os.32141.1.S1_at	LOC_Os03g49610	3.2617
Os.7938.1.S1_at	LOC_Os04g59190	3.2575
Os.7947.1.S1_x_at	LOC_Os05g31140	3.2568
Os.27474.1.S1_at	LOC_Os05g16430	3.2504
Os.54579.1.S1_s_at	LOC_Os07g23640	3.2469
Os.19843.1.S1_at	LOC_Os01g55100	3.2336
Os.9551.1.S1_at	LOC_Os05g43690	3.2134
Os.5297.1.S1_at	LOC_Os10g22590	3.1866
Os.10578.1.A1_at	LOC_Os03g20410	3.1825
Os.53609.1.S1_s_at	LOC_Os01g10490	3.1822
Os.9172.2.S1_at	LOC_Os02g02400	3.1771
Os.28032.1.A1_at	LOC_Os01g21070	3.168
Os.12387.1.S1_at	LOC_Os04g39150	3.1656
Os.10109.1.S1_at	LOC_Os12g40890	3.165
Os.4893.1.S1_at	LOC_Os05g29810	3.1466
Os.20617.2.S1_x_at	LOC_Os07g46280	3.1423
Os.48829.1.A1_at	LOC_Os03g04660	3.1388
Os.38378.1.S1_a_at	LOC_Os01g01340	3.1333
Os.8385.2.S1_x_at	LOC_Os10g06000	3.1323
Os.12452.1.S1_s_at	LOC_Os08g36910	3.113
Os.8263.1.S1_s_at	LOC_Os04g32030	3.1115
Os.13559.1.S1_at	LOC_Os03g06940	3.109
Os.55270.1.S1_s_at	LOC_Os04g54210	3.1003
Os.26971.1.S1_at	LOC_Os01g66600	3.0864
OsAffx.12022.1.S1_s_at	LOC_Os02g13600	3.0632
Os.4380.1.S1_at	LOC_Os11g02350	3.0617
Os.49654.1.S1_at	LOC_Os03g18970	3.0586
Os.32022.1.S1_at	LOC_Os07g37620	3.0449

Os.27140.1.S1_a_at	LOC_Os03g61910	3.0436
Os.9782.1.S1_at	LOC_Os09g19930	3.0409
Os.20617.1.S1_at	LOC_Os07g46280	3.031
Os.38309.1.S1_at	LOC_Os06g36390	3.0274
Os.10620.1.S1_at	LOC_Os05g07940	3.0239
Os.14153.2.S1_x_at	LOC_Os08g44840	3.021
OsAffx.27459.3.S1_x_at	LOC_Os06g05010	3.0201
Os.46435.1.S1_s_at	LOC_Os04g39110	3.014
Os.15191.1.S1_s_at	LOC_Os05g41220	3.0113
Os.6423.1.S1_at	LOC_Os08g39330	3.0079
Os.35123.1.S1_at	LOC_Os01g22230	2.9788
Os.30886.1.S1_at	LOC_Os03g61360	2.9633
Os.22839.1.S1_at	LOC_Os06g48200	2.9553
Os.34387.1.S1_at	LOC_Os01g24790	2.9519
Os.9836.1.S1_at	LOC_Os11g10590	2.9486
Os.52136.1.S1_at	LOC_Os03g59430	2.9425
Os.14139.1.S1_at	LOC_Os04g31340	2.9409
Os.38985.1.S1_at	LOC_Os07g02060	2.9387
Os.17294.1.S1_a_at	LOC_Os03g29540	2.938
Os.52605.1.S1_at	LOC_Os12g38120	2.9282
Os.12244.1.S1_at	LOC_Os03g15960	2.9178
Os.49209.1.S1_at	LOC_Os05g43140	2.9147
Os.5831.1.S1_at	LOC_Os01g55220	2.9139
Os.53973.1.S1_at	LOC_Os02g50040	2.9054
Os.11534.1.S1_at	LOC_Os05g10670	2.8936
Os.6542.1.S1_at	LOC_Os03g08630	2.8926
Os.12170.1.S1_at	LOC_Os03g47940	2.8917
Os.7126.1.S1_at	LOC_Os01g18050	2.8837
Os.9080.1.S1_at	LOC_Os03g08550	2.8693
Os.5045.1.S1_at	LOC_Os01g03680	2.8577
Os.46881.1.S1_at	LOC_Os10g39770	2.856
Os.27506.1.A1_at	LOC_Os11g15340	2.8554
Os.23971.1.S1_a_at	LOC_Os01g14050	2.8521
Os.22197.1.S1_at	LOC_Os06g20200	2.8474
Os.623.3.S1_x_at	LOC_Os01g09640	2.8429
Os.26705.1.S1_at	LOC_Os07g38590	2.8415
OsAffx.12645.1.S1_s_at	LOC_Os02g54870	2.8394
Os.12835.1.S1_at	LOC_Os09g35700	2.8383
Os.962.1.S1_at	LOC_Os01g03490	2.8262
Os.313.1.S1_a_at	LOC_Os02g49720	2.8261
Os.12186.1.S1_at	LOC_Os03g21040	2.825
Os.6318.1.S1_at	LOC_Os05g45020	2.822
Os.5117.1.S1_at	LOC_Os06g46350	2.8215
Os.43963.1.S1_at	LOC_Os07g33580	2.8168

Os.12823.1.S1_at	LOC_Os04g16450	2.8156
Os.12326.1.S1_s_at	LOC_Os07g42160	2.8152
Os.4671.1.S1_a_at	LOC_Os01g24710	2.8114
Os.50062.1.S1_at	LOC_Os03g21730	2.8085
Os.12198.1.S1_at	LOC_Os06g20370	2.8049
Os.15914.1.S1_at	LOC_Os09g23350	2.804
Os.4653.1.S1_at	LOC_Os01g03340	2.8003
Os.29377.1.S1_at	LOC_Os06g22290	2.7988
Os.10839.1.S1_at	LOC_Os03g16350	2.7981
Os.10403.1.S1_at	LOC_Os03g55350	2.7912
Os.37860.1.S1_at	LOC_Os11g02330	2.7889
OsAffx.12740.1.S1_s_at	LOC_Os03g05520	2.7846
Os.8916.1.S1_at	LOC_Os02g50820	2.7845
Os.26511.1.S1_at	LOC_Os04g49370	2.7836
Os.151.1.S1_x_at	LOC_Os03g51690	2.7769
Os.1818.1.S1_at	LOC_Os01g45640	2.7695
Os.7727.1.S1_at	LOC_Os05g11910	2.7676
Os.10651.1.S1_at	LOC_Os02g41910	2.7662
Os.46582.1.S1_at	LOC_Os10g36180	2.7662
Os.51775.1.S1_at	LOC_Os12g05210	2.745
Os.7348.1.S1_at	LOC_Os08g38910	2.7434
Os.15076.1.S1_at	LOC_Os04g02900	2.7417
Os.32248.1.S1_at	LOC_Os01g09860	2.7416
Os.11398.1.S1_at	LOC_Os10g05980	2.7335
Os.9797.1.S1_at	LOC_Os11g32260	2.73
Os.9172.2.S1_x_at	LOC_Os02g02400	2.7297
Os.38408.1.S1_a_at	LOC_Os09g21230	2.7242
OsAffx.14326.1.S1_s_at	LOC_Os04g48490	2.713
Os.31975.1.S1_x_at	LOC_Os05g10670	2.7094
Os.8458.1.S1_s_at	LOC_Os04g05050	2.707
Os.2367.1.S1_at	LOC_Os03g21820	2.7048
Os.38346.1.S1_x_at	LOC_Os01g36350	2.6988
Os.25599.1.A1_at	LOC_Os08g42440	2.6966
Os.46540.1.S1_at	LOC_Os10g41060	2.6925
Os.4281.1.S1_x_at	LOC_Os06g03830	2.6919
Os.34515.1.A1_at	LOC_Os12g23780	2.6817
Os.12560.1.S1_s_at	LOC_Os01g02060	2.6771
Os.23971.2.S1_x_at	LOC_Os01g14050	2.6751
Os.11327.1.S1_at	LOC_Os03g18130	2.6694
Os.52857.1.S1_at	LOC_Os05g13650	2.666
Os.4149.2.S1_x_at	LOC_Os03g50810	2.6618
Os.12252.1.S1_at	LOC_Os03g41060	2.6606
OsAffx.27815.1.S1_s_at	LOC_Os06g24990	2.6604
Os.14539.1.S1_at	LOC_Os07g01600	2.6565

Os.8367.1.S1_at	LOC_Os08g02490	2.6487
Os.12812.1.S1_at	LOC_Os05g28210	2.6472
Os.25952.1.S1_at	LOC_Os05g27780	2.6471
Os.4614.1.S1_a_at	LOC_Os02g40260	2.6451
Os.623.2.S1_x_at	LOC_Os01g09640	2.645
Os.10736.1.S1_at	LOC_Os06g05440	2.6396
Os.52593.1.S1_s_at	LOC_Os09g21230	2.6364
Os.37692.1.S1_at	LOC_Os07g44070	2.6223
Os.43963.1.S1_x_at	LOC_Os07g33580	2.6179
Os.51775.1.S1_x_at	LOC_Os12g05210	2.6064
Os.32478.1.S1_at	LOC_Os01g46400	2.6004
Os.17446.1.S1_at	LOC_Os04g48270	2.5974
OsAffx.30538.1.S1_x_at	LOC_Os10g26150	2.593
Os.6219.1.S1_at	LOC_Os04g45330	2.587
Os.19480.1.S1_at	LOC_Os03g20870	2.5844
Os.23145.1.S1_at	LOC_Os08g03310	2.5828
Os.32292.1.S1_at	LOC_Os01g36240	2.5826
Os.12400.2.S1_x_at	LOC_Os08g30020	2.5771
Os.5913.1.S1_at	LOC_Os04g57970	2.5764
Os.21231.1.S1_at	LOC_Os01g38610	2.5699
Os.32078.1.S1_at	LOC_Os01g51140	2.5698
Os.17136.1.S1_at	LOC_Os03g51920	2.5681
Os.2750.2.S1_a_at	LOC_Os10g42230	2.5671
Os.51029.1.S1_at	LOC_Os09g02770	2.5644
OsAffx.25285.1.S1_at	LOC_Os03g29770	2.564
Os.27247.1.S1_at	LOC_Os06g50950	2.5588
Os.27331.1.S1_at	LOC_Os05g36930	2.5552
Os.10785.3.S1_at	LOC_Os10g34480	2.5522
Os.51106.1.S1_at	LOC_Os06g14540	2.5473
Os.11831.1.S1_at	LOC_Os06g13560	2.5436
Os.9172.1.S1_x_at	LOC_Os02g02400	2.5431
Os.21634.1.S1_at	LOC_Os01g55240	2.5424
Os.12400.4.S1_at	LOC_Os08g30020	2.5393
Os.35020.1.S1_at	LOC_Os11g03300	2.5391
Os.26698.1.S1_a_at	LOC_Os01g19820	2.5371
Os.56528.1.S1_at	LOC_Os05g42210	2.5349
Os.36264.1.S1_x_at	LOC_Os01g53750	2.534
Os.8353.1.S1_at	LOC_Os01g68770	2.5242
Os.10784.1.S1_at	LOC_Os02g26700	2.522
Os.14078.1.S1_s_at	LOC_Os10g07210	2.5178
OsAffx.4277.1.S1_s_at	LOC_Os05g08750	2.5146
Os.54530.1.S1_at	LOC_Os06g49100	2.5143
Os.15841.1.S1_a_at	LOC_Os11g05290	2.5091
Os.12077.1.S1_at	LOC_Os08g44270	2.5066

Os.22907.1.S1_at	LOC_Os05g50190	2.501
Os.21574.1.S1_a_at	LOC_Os03g46660	2.479
Os.27974.1.S1_at	LOC_Os01g55000	2.478
Os.54793.1.S1_at	LOC_Os02g42950	2.4766
Os.5095.1.S1_at	LOC_Os07g40130	2.4747
OsAffx.12986.1.S1_at	LOC_Os03g22200	2.4746
Os.7611.1.S1_at	LOC_Os03g06670	2.4627
Os.50239.1.S1_a_at	LOC_Os05g30220	2.4616
Os.57465.1.S1_x_at	LOC_Os03g28330	2.459
Os.7649.1.S1_at	LOC_Os12g05040	2.4576
Os.17149.1.S1_at	LOC_Os03g60910	2.4509
OsAffx.21790.1.S1_at	LOC_Os01g67540	2.4469
Os.10675.1.A1_at	LOC_Os01g68140	2.4458
Os.26082.1.S1_s_at	LOC_Os02g15810	2.4438
Os.10797.1.S1_at	LOC_Os02g01380	2.4438
OsAffx.22469.1.S1_x_at	LOC_Os07g07040	2.4392
Os.12994.1.S1_at	LOC_Os12g38400	2.431
Os.10300.1.S1_x_at	LOC_Os01g01840	2.43
Os.5577.1.S1_at	LOC_Os11g08300	2.4232
Os.7916.1.S1_at	LOC_Os01g59150	2.42
Os.2225.1.S1_at	LOC_Os04g44870	2.4132
OsAffx.28387.1.S1_s_at	LOC_Os07g10420	2.4089
Os.17584.1.S1_at	LOC_Os02g56860	2.4084
Os.37213.1.S1_at	LOC_Os07g29310	2.3995
Os.53458.1.S1_at	LOC_Os09g17560	2.3993
Os.48101.1.S1_at	LOC_Os04g54810	2.3929
Os.5500.1.S1_s_at	LOC_Os08g23180	2.3884
Os.6656.1.S1_at	LOC_Os02g18410	2.385
Os.5467.1.S1_at	LOC_Os04g43990	2.3835
Os.2344.1.S1_at	LOC_Os10g28230	2.381
Os.53396.1.S1_at	LOC_Os07g08390	2.3747
Os.16088.1.S1_x_at	LOC_Os07g48420	2.3733
Os.15269.1.S1_at	LOC_Os03g04240	2.3719
Os.49826.1.S1_at	LOC_Os04g31790	2.3662
Os.46187.1.S1_at	LOC_Os07g40940	2.363
Os.49708.1.S1_at	LOC_Os06g46680	2.3546
Os.24471.1.S1_at	LOC_Os07g30760	2.3536
OsAffx.17970.1.S1_at	LOC_Os09g31080	2.3508
Os.20548.1.S1_at	LOC_Os04g51680	2.3496
Os.38249.2.S1_at	LOC_Os01g38530	2.3478
Os.45997.1.S1_x_at	LOC_Os01g45640	2.3442
Os.26811.1.A1_at	LOC_Os06g39780	2.3429
Os.5594.1.S1_at	LOC_Os05g48340	2.3302
Os.26957.1.A1_a_at	LOC_Os08g10080	2.3277

Os.18257.1.S1_at	LOC_Os07g10840	2.3245
Os.855.1.S1_at	LOC_Os01g03730	2.3244
Os.5318.1.S1_a_at	LOC_Os10g42610	2.3223
Os.14092.1.S1_at	LOC_Os02g44710	2.3204
Os.11331.1.S1_at	LOC_Os08g10500	2.3154
Os.31975.1.S1_at	LOC_Os05g10670	2.3107
Os.12735.1.S1_s_at	LOC_Os11g44810	2.3101
Os.1564.1.S1_at	LOC_Os01g22380	2.3095
Os.19849.1.S1_at	LOC_Os01g56930	2.3048
Os.11252.1.S1_at	LOC_Os02g37160	2.3038
Os.49690.1.S1_s_at	LOC_Os07g04190	2.3029
Os.27379.1.S1_at	LOC_Os08g44360	2.2989
Os.48287.1.S1_at	LOC_Os04g38570	2.2973
Os.27509.1.S1_at	LOC_Os01g53790	2.2963
Os.25677.1.S1_at	LOC_Os03g28330	2.2932
OsAffx.10845.1.S1_s_at	LOC_Os06g11860	2.2894
Os.23125.1.S1_at	LOC_Os03g19780	2.2888
Os.15199.1.S1_at	LOC_Os08g14860	2.2884
Os.53766.1.S1_at	LOC_Os08g37690	2.283
Os.20306.1.S1_at	LOC_Os04g44600	2.2769
Os.7705.1.S1_at	LOC_Os04g54300	2.2704
Os.32021.1.S1_at	LOC_Os05g13620	2.2671
OsAffx.14380.1.S1_s_at	LOC_Os04g52670	2.2661
Os.18511.1.S1_at	LOC_Os10g07210	2.261
Os.623.1.S1_x_at	LOC_Os05g10690	2.2578
Os.8403.1.S1_s_at	LOC_Os12g03470	2.2531
Os.51241.1.S1_at	LOC_Os11g35310	2.2528
Os.15580.1.S1_at	LOC_Os03g42600	2.2503
Os.29966.1.S1_at	LOC_Os06g04760	2.2499
Os.6335.1.S1_at	LOC_Os11g13670	2.249
Os.15713.1.S1_a_at	LOC_Os04g42620	2.2488
Os.30886.1.S1_x_at	LOC_Os03g61360	2.2479
Os.2678.1.S1_at	LOC_Os02g13870	2.2393
Os.9220.2.S1_x_at	LOC_Os04g54930	2.2374
Os.15008.1.S1_at	LOC_Os05g35460	2.2368
Os.22360.1.S1_at	LOC_Os03g15020	2.2366
Os.7610.1.S1_a_at	LOC_Os08g04780	2.2358
Os.11762.1.S2_x_at	LOC_Os08g45030	2.2341
Os.15938.1.S1_at	LOC_Os03g17790	2.2328
Os.52202.1.S1_at	LOC_Os03g22450	2.2323
Os.21335.1.A1_at	LOC_Os12g42420	2.2316
Os.18249.1.S1_at	LOC_Os04g45720	2.2282
Os.14289.1.S1_at	LOC_Os04g45750	2.225
Os.9546.1.S1_x_at	LOC_Os06g41120	2.217

Os.9303.1.S1_at	LOC_Os02g46460	2.2161
Os.51757.1.S1_at	LOC_Os06g26270	2.2126
Os.37689.1.S1_at	LOC_Os12g38440	2.1961
Os.10196.1.S1_at	LOC_Os01g58320	2.1949
Os.4223.1.S1_s_at	LOC_Os06g07220	2.1937
Os.4671.2.S1_a_at	LOC_Os04g42470	2.1912
Os.55554.1.S1_at	LOC_Os08g38270	2.1909
Os.8403.1.S1_a_at	LOC_Os12g03470	2.1904
Os.5087.1.S1_at	LOC_Os11g03780	2.1884
Os.27483.1.S1_at	LOC_Os08g13440	2.1859
Os.11476.1.S1_at	LOC_Os06g10230	2.1855
Os.12110.1.S1_at	LOC_Os12g02530	2.1788
Os.55420.1.A1_x_at	LOC_Os11g38440	2.171
Os.32736.1.S1_at	LOC_Os03g56820	2.1688
Os.12286.1.S2_a_at	LOC_Os03g52690	2.168
Os.20775.1.S1_at	LOC_Os09g32510	2.1652
Os.17271.1.S1_at	LOC_Os12g07310	2.1644
OsAffx.25290.1.S1_at	LOC_Os03g29970	2.1638
Os.7699.1.S1_at	LOC_Os10g22050	2.1603
Os.3396.1.S1_at	LOC_Os06g49880	2.1583
Os.5812.1.S1_at	LOC_Os03g20500	2.1492
Os.20079.1.S2_at	LOC_Os11g25170	2.1461
Os.55800.1.S1_at	LOC_Os04g37980	2.1452
Os.27279.1.A1_at	LOC_Os03g26870	2.145
Os.32267.1.S1_at	LOC_Os01g56330	2.1429
Os.9975.1.S1_at	LOC_Os03g17200	2.1422
Os.9031.1.S1_a_at	LOC_Os08g30730	2.1392
Os.49751.1.S1_at	LOC_Os03g51970	2.1371
Os.7348.1.S1_a_at	LOC_Os08g38910	2.135
Os.6210.1.S1_at	LOC_Os03g56270	2.1348
Os.54829.1.S1_at	LOC_Os08g02220	2.1347
Os.18503.1.S1_s_at	LOC_Os09g22410	2.1291
Os.10544.1.S1_at	LOC_Os03g53630	2.1286
Os.7272.1.S1_at	LOC_Os10g06720	2.1275
Os.27712.2.S1_x_at	LOC_Os06g48510	2.1224
Os.23158.1.S1_at	LOC_Os05g02820	2.1184
Os.57477.1.S1_x_at	LOC_Os11g47760	2.1165
Os.14561.1.S1_at	LOC_Os12g42760	2.113
Os.27688.1.A1_at	LOC_Os04g21350	2.1125
OsAffx.2920.1.S1_s_at	LOC_Os02g39720	2.1109
OsAffx.12379.1.S1_at	LOC_Os02g36850	2.1088
Os.54934.1.S1_at	LOC_Os05g37060	2.1081
Os.52394.2.S1_at	LOC_Os12g39440	2.1059
Os.35495.1.S1_at	LOC_Os01g16030	2.1052

Os.27395.1.S1_a_at	LOC_Os04g57760	2.1007
Os.55444.1.S1_at	LOC_Os03g47270	2.0968
OsAffx.3970.1.S1_at	LOC_Os04g31760	2.089
Os.10246.3.S1_at	LOC_Os06g06460	2.0882
Os.36960.1.S1_at	LOC_Os01g49230	2.0856
OsAffx.20681.1.S1_at	LOC_Os10g09710	2.0833
Os.54443.1.S1_at	LOC_Os07g42610	2.0831
Os.21243.1.S1_at	LOC_Os02g36490	2.082
Os.18057.1.A1_at	LOC_Os02g50640	2.0768
Os.17916.1.S1_at	LOC_Os05g12630	2.0765
Os.51616.1.S1_at	LOC_Os03g16600	2.0753
Os.52428.1.S1_x_at	LOC_Os06g43510	2.0751
Os.12363.1.S1_at	LOC_Os04g58200	2.0746
Os.11286.1.A1_at	LOC_Os04g13140	2.0738
Os.21812.2.S1_a_at	LOC_Os03g12250	2.0721
Os.8178.1.S1_at	LOC_Os11g37970	2.0698
Os.53969.1.S1_at	LOC_Os03g22700	2.067
Os.39943.2.A1_at	LOC_Os10g05680	2.0661
Os.1475.1.S1_at	LOC_Os01g09540	2.0644
Os.12787.1.S1_at	LOC_Os10g18340	2.064
Os.7216.1.S1_at	LOC_Os10g25780	2.0593
Os.8456.1.S1_at	LOC_Os05g10210	2.0563
Os.14381.2.S1_x_at	LOC_Os03g28300	2.0539
Os.51228.2.A1_at	LOC_Os03g14130	2.0539
Os.14232.1.S1_at	LOC_Os01g46120	2.0529
Os.11785.1.S1_at	LOC_Os06g47700	2.0474
Os.11432.1.S1_s_at	LOC_Os01g62360	2.0468
Os.13708.1.S1_at	LOC_Os03g14250	2.0466
Os.10880.1.S1_at	LOC_Os04g45270	2.0461
Os.9546.1.S1_at	LOC_Os06g41120	2.0445
Os.38604.1.S1_s_at	LOC_Os11g14220	2.0442
Os.11604.1.S1_at	LOC_Os10g42190	2.0434
Os.21886.1.S1_at	LOC_Os03g59750	2.0406
Os.49042.1.A1_s_at	LOC_Os01g09620	2.0399
Os.33534.1.S1_s_at	LOC_Os07g06620	2.0373
OsAffx.17937.1.S1_at	LOC_Os09g27670	2.0373
Os.6291.1.S1_x_at	LOC_Os06g47600	2.0357
OsAffx.6446.1.S1_at	LOC_Os09g29960	2.0355
Os.6592.1.S1_a_at	LOC_Os05g04380	2.0343
Os.53679.1.S1_s_at	LOC_Os09g31080	2.034
Os.11997.1.S1_at	LOC_Os07g48510	2.0331
Os.24851.1.S1_at	LOC_Os02g33420	2.0328
Os.14122.1.S1_at	LOC_Os01g13210	2.0316
Os.315.1.S1_at	LOC_Os03g39710	2.0313

Os.14567.1.S1_at	LOC_Os02g39580	2.0256
Os.19401.1.S1_at	LOC_Os03g04100	2.0225
Os.12767.1.S1_a_at	LOC_Os07g34570	2.0195
Os.12391.1.S1_a_at	LOC_Os02g54820	2.0143
Os.39943.2.A1_x_at	LOC_Os10g05680	2.0141
Os.16999.1.A1_at	LOC_Os03g24950	2.0117
Os.4958.1.A1_at	LOC_Os01g68830	2.0062
Os.39828.1.A1_s_at	LOC_Os03g52690	2.0005
Os.37717.1.A1_s_at	LOC_Os05g15770	2.0001

Table S3. Down-regulated genes in *slac7* leaves.

ProbeSet ID	OsGI	Fold
Os.16025.1.S1_s_at	LOC_Os06g39960	0.4958
Os.51098.1.S1_at	LOC_Os12g05890	0.4948
Os.15283.1.S1_at	LOC_Os04g57310	0.4941
Os.4773.1.S1_at	LOC_Os06g04240	0.4935
Os.28798.1.S1_at	LOC_Os01g58310	0.4905
Os.35510.1.S1_at	LOC_Os02g01220	0.4881
Os.17108.1.S1_at	LOC_Os12g38170	0.4826
Os.20627.2.S1_at	LOC_Os07g33620	0.4819
Os.51226.1.S1_at	LOC_Os03g52910	0.4816
Os.4940.1.S1_at	LOC_Os06g46970	0.4812
Os.51753.1.A1_at	LOC_Os12g35340	0.4806
Os.32263.1.S1_at	LOC_Os01g55310	0.4794
Os.6864.1.S1_at	LOC_Os01g61070	0.4748
Os.10305.1.S1_at	LOC_Os08g41880	0.4733
OsAffx.28017.1.S1_at	LOC_Os06g39960	0.4695
Os.51546.1.S1_at	LOC_Os03g08520	0.4628
Os.54420.1.S1_at	LOC_Os01g16980	0.4577
Os.2245.1.S1_at	LOC_Os05g43040	0.4574
Os.54420.1.S1_x_at	LOC_Os01g16980	0.4571
Os.15856.1.S1_at	LOC_Os10g06630	0.4524
Os.51227.1.S1_x_at	LOC_Os04g27790	0.4497
Os.28649.1.S1_at	LOC_Os01g37460	0.4488
Os.606.1.S1_at	LOC_Os06g04220	0.4437
Os.15281.1.S1_x_at	LOC_Os07g46930	0.4436
OsAffx.7250.1.S1_at	LOC_Os11g29740	0.4406
Os.46397.1.S1_x_at	LOC_Os10g35490	0.4387
Os.20183.1.S1_at	LOC_Os07g19320	0.4386
Os.4604.1.S1_at	LOC_Os03g15460	0.4307
OsAffx.12052.1.S1_at	LOC_Os02g15280	0.4302
Os.12713.1.S2_a_at	LOC_Os01g03320	0.424
Os.50587.1.S1_at	LOC_Os05g03960	0.4221
Os.49761.1.S1_at	LOC_Os03g54170	0.4164
Os.20230.1.S1_at	LOC_Os11g37950	0.4129
Os.46151.1.S1_at	LOC_Os10g36200	0.3972
OsAffx.26230.1.S1_at	LOC_Os04g29550	0.3969
Os.6776.1.S1_at	LOC_Os07g35480	0.3835
Os.1479.1.S1_at	LOC_Os07g48980	0.3825
OsAffx.4953.1.S1_at	LOC_Os06g28630	0.3721
Os.10583.1.S1_at	LOC_Os06g04920	0.369
Os.12092.1.S1_at	LOC_Os09g25810	0.3622
Os.52678.1.S1_at	LOC_Os04g41130	0.3542
Os.7507.1.S1_at	LOC_Os10g02880	0.3398

Os.48986.1.S1_s_at	LOC_Os05g04000	0.3326
Os.9417.1.S1_at	LOC_Os09g36680	0.1463
Os.12922.1.S1_at	LOC_Os09g36700	0.0918
Os.20851.1.A1_x_at	LOC_Os04g48650	0.0465

Table S4. Gene ontology analysis of differentially expressed genes.

GO Term	Count[a]	p-Value[b]
(a) Biological process		
GO:0005975 carbohydrate metabolic process	45	2.37E-13
GO:0005488 binding	201	4.99E-12
GO:0055114 oxidation-reduction process	52	1.47E-10
GO:0008152 metabolic process	158	1.81E-10
GO:0006869 lipid transport	13	2.90E-09
GO:0010876 lipid localization	13	2.90E-09
GO:0007047 cellular cell wall organization	16	4.04E-09
GO:0045229 external encapsulating structure organization	16	4.04E-09
GO:0071554 cell wall organization or biogenesis	20	1.24E-08
GO:0070882 cellular cell wall organization or biogenesis	16	3.66E-08
GO:0071555 cell wall organization	16	1.34E-07
GO:0071702 organic substance transport	14	7.63E-07
GO:0071840 cellular component organization or biogenesis	28	1.39E-06
GO:0016043 cellular component organization	24	3.61E-06
GO:0005976 polysaccharide metabolic process	15	5.25E-06
GO:0071841 cellular component organization or biogenesis at cellular level	23	2.46E-05
GO:0044262 cellular carbohydrate metabolic process	13	6.25E-05
GO:0019566 arabinose metabolic process	4	6.25E-05
GO:0046373 L-arabinose metabolic process	4	6.25E-05
GO:0046556 alpha-N-arabinofuranosidase activity	4	6.25E-05
GO:0000003 reproduction	11	7.54E-05
GO:0006950 response to stress	31	9.18E-05
GO:0000272 polysaccharide catabolic process	9	0.000105
GO:0019953 sexual reproduction	5	0.000105
GO:0044042 glucan metabolic process	11	0.000286
GO:0044238 primary metabolic process	101	0.000432
GO:0006979 response to oxidative stress	11	0.000613
GO:0050896 response to stimulus	37	0.0016
GO:0009251 glucan catabolic process	5	0.00275
GO:0009056 catabolic process	19	0.00327
(b) Molecular function		
GO:0003824 catalytic activity	194	5.58E-17
GO:0016798 hydrolase activity, acting on glycosyl bonds	37	5.58E-17
GO:0004553 hydrolase activity, hydrolyzing O-glycosyl compounds	36	7.05E-17
GO:0043167 ion binding	90	7.36E-12
GO:0043169 cation binding	90	7.36E-12
GO:0016787 hydrolase activity	82	3.63E-11
GO:0016491 oxidoreductase activity	53	2.39E-09
GO:0046872 metal ion binding	74	2.43E-07
GO:0020037 heme binding	23	3.12E-06

GO:0046906 tetrapyrrole binding	23	4.04E-06
GO:0015923 mannosidase activity	6	1.41E-05
GO:0004567 beta-mannosidase activity	5	3.05E-05
GO:0004338 glucan exo-1,3-beta-glucosidase activity	4	3.21E-05
GO:0080079 cellobiose glucosidase activity	4	3.21E-05
GO:0004565 beta-galactosidase activity	6	4.94E-05
GO:0015925 galactosidase activity	6	6.13E-05
GO:0047701 beta-L-arabinosidase activity	4	6.25E-05
GO:0033907 beta-D-fucosidase activity	4	0.000111
GO:0046914 transition metal ion binding	48	0.000178
GO:0008289 lipid binding	8	0.000428
GO:0004867 serine-type endopeptidase inhibitor activity	6	0.000645
GO:0005506 iron ion binding	18	0.000657
GO:0004601 peroxidase activity	11	0.000781
GO:0016684 oxidoreductase activity, acting on peroxide as acceptor	11	0.000781
GO:0016762 xyloglucan:xyloglucosyl transferase activity	5	0.00139
GO:0004866 endopeptidase inhibitor activity	6	0.00176
GO:0030414 peptidase inhibitor activity	6	0.00176
GO:0061134 peptidase regulator activity	6	0.00176
GO:0061135 endopeptidase regulator activity	6	0.00176
GO:0016209 antioxidant activity	11	2.54E-03
GO:0033897 ribonuclease T2 activity	3	0.00745
GO:0004096 catalase activity	3	0.00992
(c) Cellular component		
GO:0005576 extracellular region	39	2.81E-26
GO:0005618 cell wall	15	1.47E-08
GO:0030312 external encapsulating structure	15	1.09E-07
GO:0048046 apoplast	11	4.48E-06
GO:0071944 cell periphery	16	0.000139
GO:0009514 glyoxysome	3	0.00992

Note: The listed terms is top ten overrepresented GO terms according to the low p-value. [a] Count of GO terms in the differential expressed genes in the *slac7* and wild-type. [b] The p-value was calculated using the molecule annotation system (MAS) 3.0 (CapitalBio).

Table S5. RT-qPCR verified differential expression of the genes initially identified by microarray analysis.

Gene category	LOC NO.	Fold	Gene Function Annotation
Malate metabolism	LOC_Os04g40990	12.7	Malate synthase, glyoxysomal, putative, expressed
	LOC_Os04g43710	8.6	Phosphoenolpyruvate carboxylase kinase 4, putative, expressed
	LOC_Os05g48200	13.9	Glutamate synthase, chloroplast precursor, putative, expressed
Development related	LOC_Os04g48650	0.2	Retrotransposon protein, putative, unclassified
	LOC_Os06g13390	0.1	SAM dependent carboxyl methyltransferase family protein
	LOC_Os11g15060	7.7	SAM dependent carboxyl methyltransferase family protein
	LOC_Os01g10110	9.7	Cytokinin dehydrogenase 1 precursor, putative, expressed
	LOC_Os12g40890	6.3	Auxin-induced protein AUX28, putative, expressed
Transcription factors	LOC_Os01g09640	5.7	Myb-like DNA-binding domain, SHAQKYF class family protein expressed
	LOC_Os12g38400	4.9	Myb-like DNA-binding domain containing protein, expressed
	LOC_Os03g10210	9.4	Homeobox domain containing protein, expressed
	LOC_Os02g43330	7.9	Homeobox domain containing protein, expressed
	LOC_Os03g51690	5.6	Homeobox protein OSH1, putative, expressed
	LOC_Os03g22680	11.2	CHY zinc finger family protein, expressed
	LOC_Os03g54170	0.2	MADS-box protein CMB1, putative, expressed
	LOC_Os06g39960	0.2	bZIP transcription factor family protein, expressed
	LOC_Os08g10080	4.7	NAC-domain containing protein 21/22, putative, expressed
	LOC_Os11g03300	5.1	NAC domain transcription factor, putative, expressed
	LOC_Os08g42470	7.7	bHLH transcription factor GBOF-1, putative, expressed
Oxidation stress related	LOC_Os02g14430	8.2	Peroxidase 52 precursor, putative, expressed
	LOC_Os04g59190	6.5	Peroxidase family protein, expressed
	LOC_Os04g59260	7.3	Peroxidase family protein, expressed
	LOC_Os06g35520	10	Peroxidase 52 precursor, putative, expressed
	LOC_Os03g48780	0.1	Oxalate oxidase 2 precursor, putative, expressed
	LOC_Os06g50930	8	Senescence-associated protein DIN1, putative, expressed
	LOC_Os02g02400	6.4	Catalase isozyme A, putative, expressed
	LOC_Os03g28330	4.8	sucrose synthase, putative, expressed
	LOC_Os08g36910	6.6	alpha-amylase precursor, putative, expressed

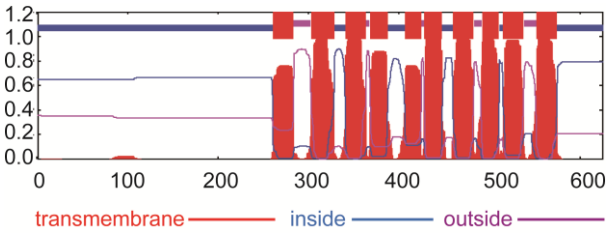

Figure S1 10 predicted transmembrane regions of SLAC7 protein.

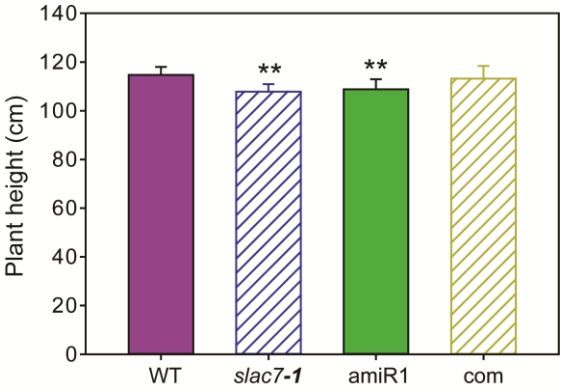

Figure S2 Plant height of different transgenic plants (*slac7*-1, amiR1 and com). Data represent mean values ±SD of three independent experiments conducted with 60 different plants. Double asterisks denote a highly significant difference using Student's *t*-test ($P < 0.01$).

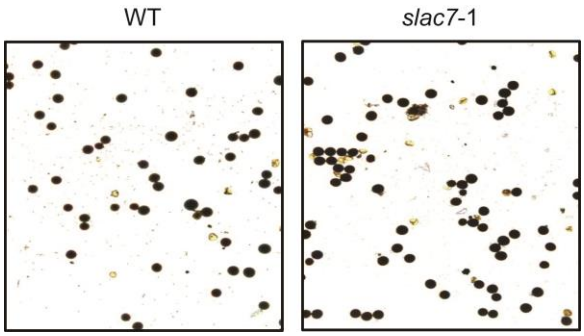

Figure S3 Pollen starch staining shows normal *slac7*-1 fertility.

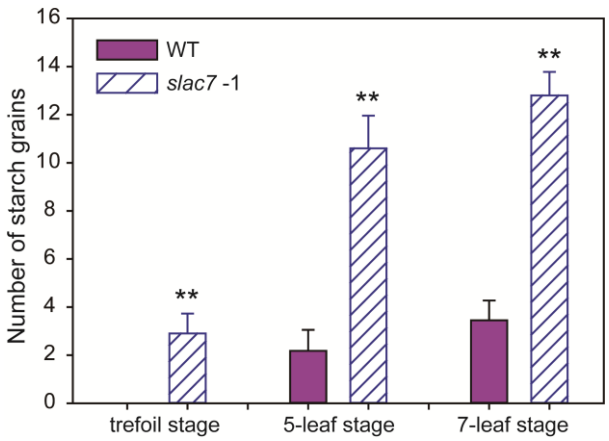

Figure S4 Starch grain number of each chloroplast of *slac7*-1 and wild-type leaves at different development stages. Data represent the mean values ±SD of 15 independent experiments conducted with different samples. Double asterisks denote a highly significant difference between *slac7*-1 and wild-type plants using Student's *t*-test ($P < 0.01$).

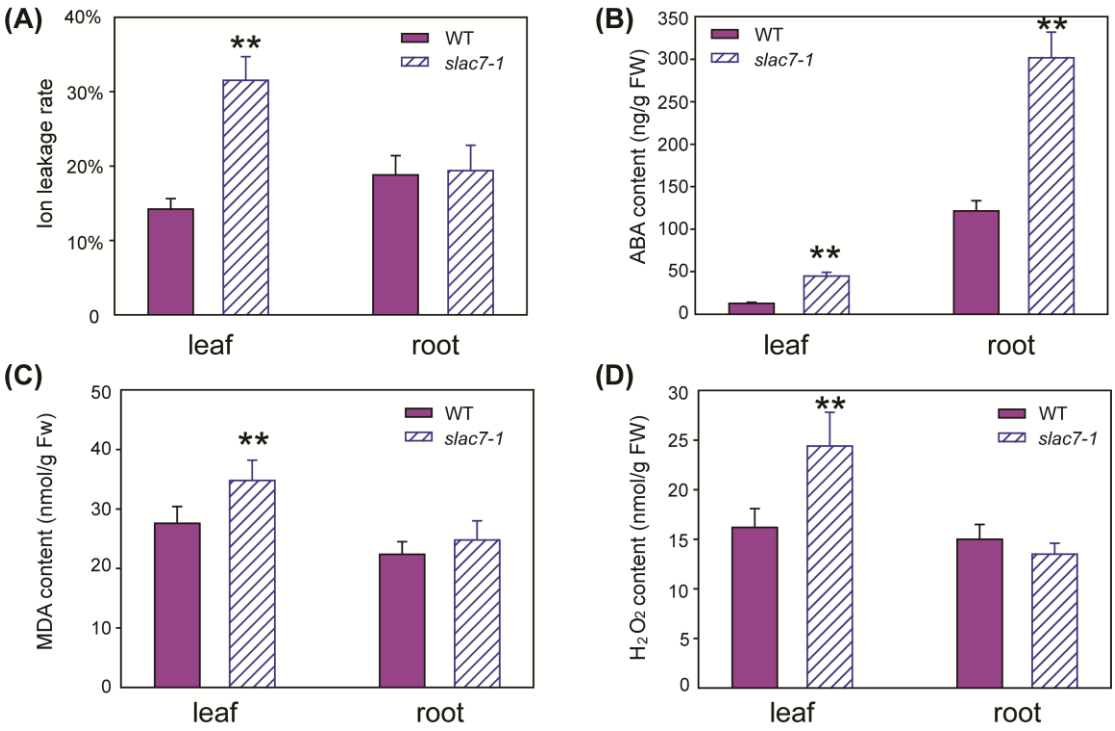

Figure S5 *slac7*-1 leaves were severely damaged.

(A) Ion leakage rate of *slac7*-1 under normal growth condition. **(B)** ABA content in *slac7*-1 leaves and roots. **(C)** MDA content in *slac7*-1 leaves and roots. **(D)** H_2O_2 content in *slac7*-1 leaves and roots. Data represent the mean values ±SD of three independent experiments conducted with different plants at 12-leaf stage. Double asterisks denote a highly significant difference between *slac7*-1 and wild-type plants using Student's *t*-test ($P < 0.01$).

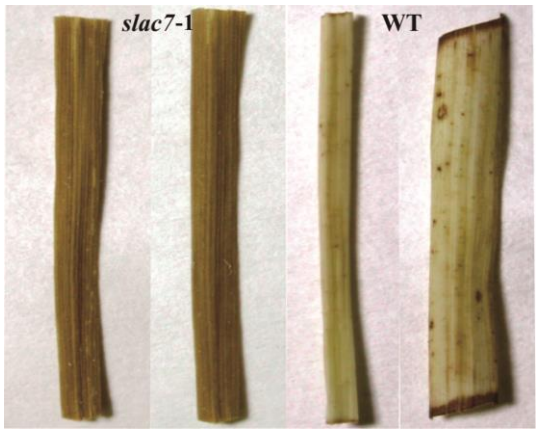

Figure S6 Leaves of *slac7*-1 and wild-type plants stained with DAB solution.

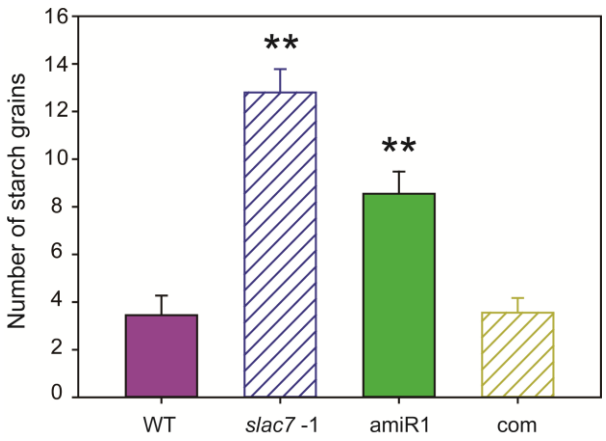

Figure S7 Starch grain number of each chloroplast of different transgenic plants at 7-leaf stage. Data represent the mean values ±SD of 15 independent experiments conducted with different samples. Double asterisks denote a highly significant difference using Student's *t*-test ($P < 0.01$).

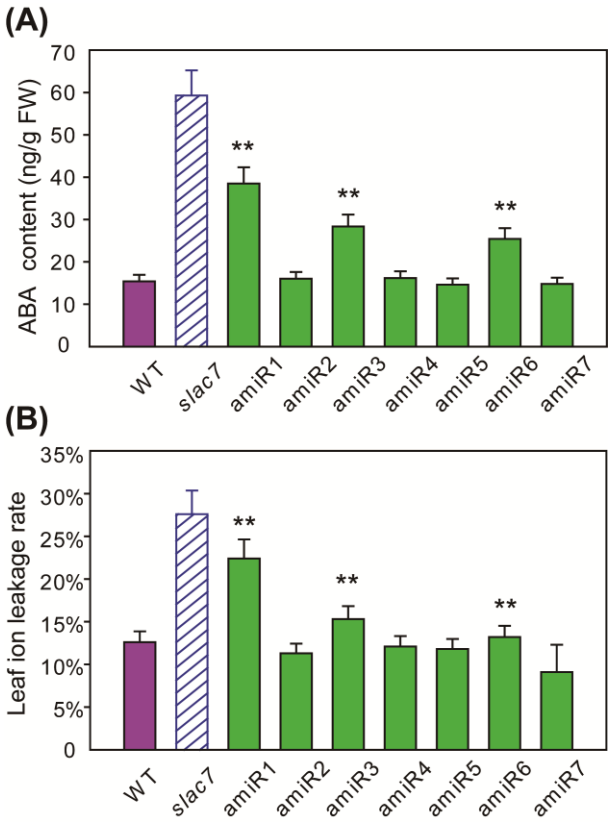

Figure S8 Leaves of *SLAC7* amiRNA transgenic plants were severely damaged.

(A) ABA content in SLAC7 amiRNA transgenic plants. **(B)** Leaf ion leakage rate in SLAC7 amiRNA transgenic plants. Data represent the mean values ±SD of three independent experiments conducted with different plants at 12-leaf stage. Double asterisks denote a highly significant difference between plants using Student's *t*-test ($P < 0.01$)

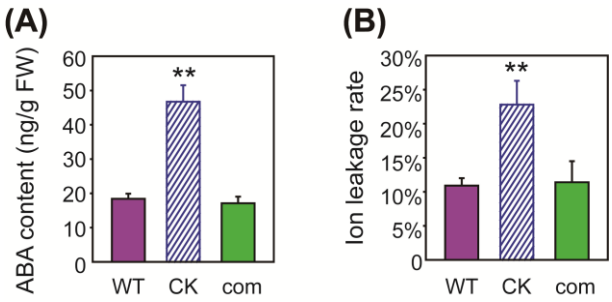

Figure S9 Complementation of *slac7*-1.

(A) ABA content in pC2301+*SLAC7* (com) and *slac7*-1 (CK) leaves. **(B)** Leaf ion leakage rate in pC2301+*SLAC7* (com) and *slac7*-1 (CK) leaves. Data represent the mean values ±SD of three independent experiments conducted with different plants at 12-leaf stage. Double asterisks denote a highly significant difference using Student's *t*-test ($P < 0.01$).

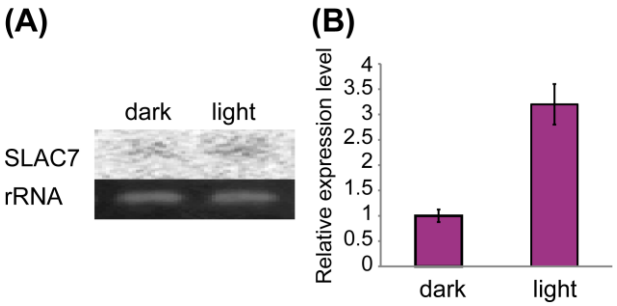

Figure S10. Expression level of *SLAC7* tested by (A) Northern blot and (B) RT-qPCR.

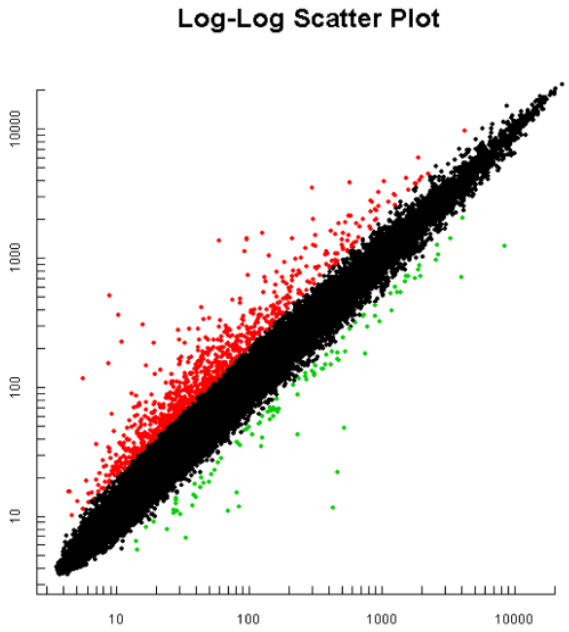

Figure S11 Log-Log scatter plot of significant differentially expressed genes in *slac7*-1 plants.

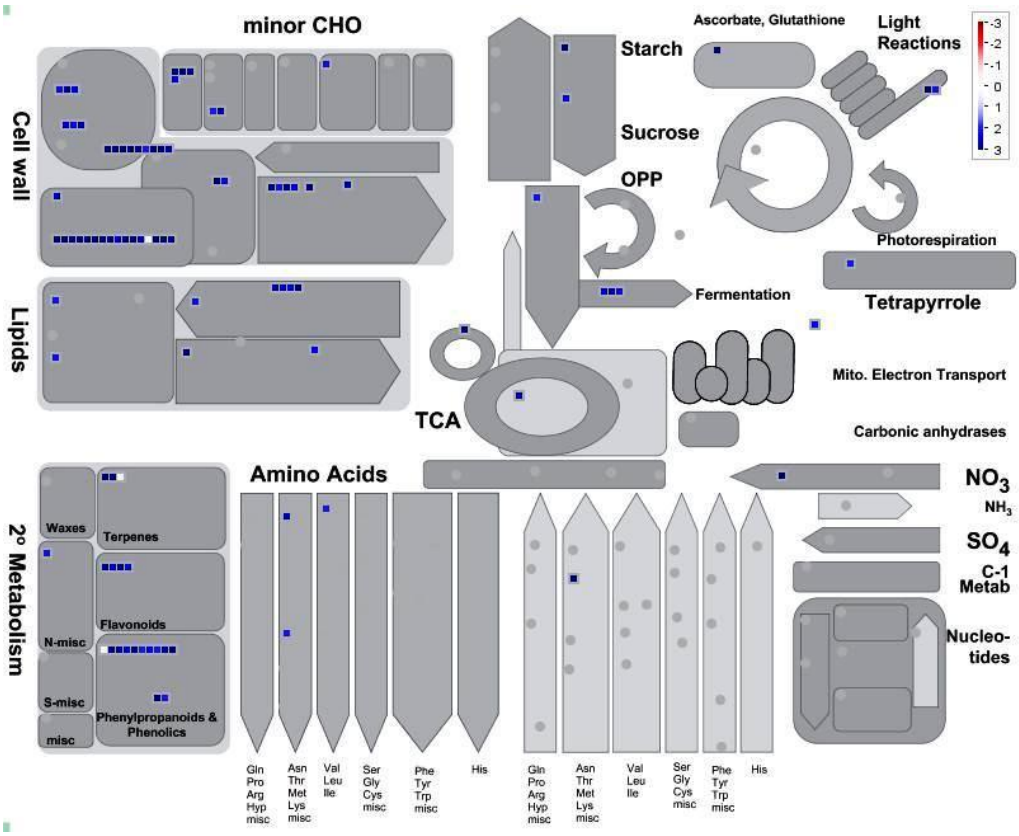

Figure S12 Microarray analysis of the differential expression genes in whole metabolism using MapMan softwoare (version 3.6.0RC1).

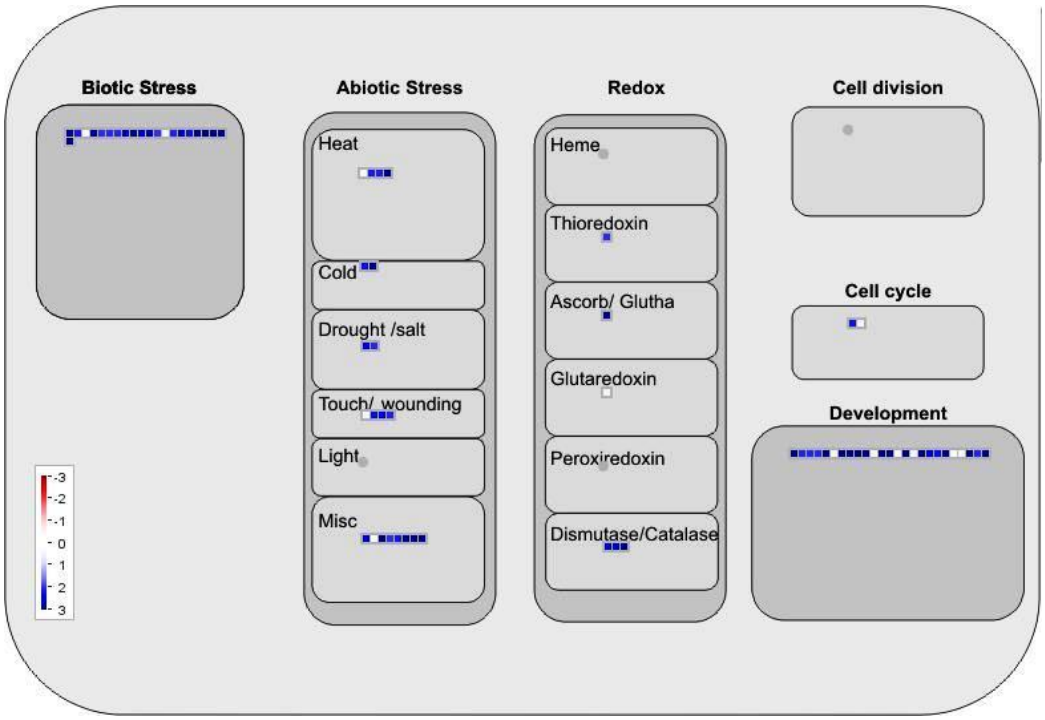

Figure S13 Microarray analysis of the differential expression genes in cellular response using MapMan softwoare (version 3.6.0RC1).

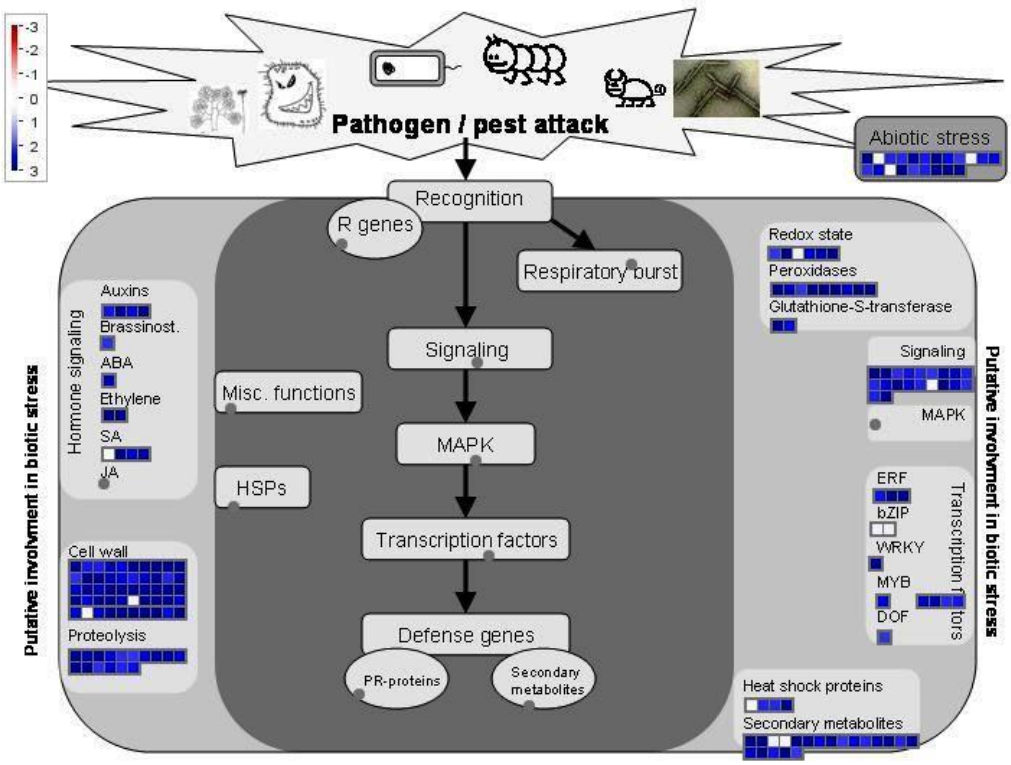

Figure S14 Microarray analysis of the differential expression genes in stress response using MapMan softwoare (version 3.6.0RC1).

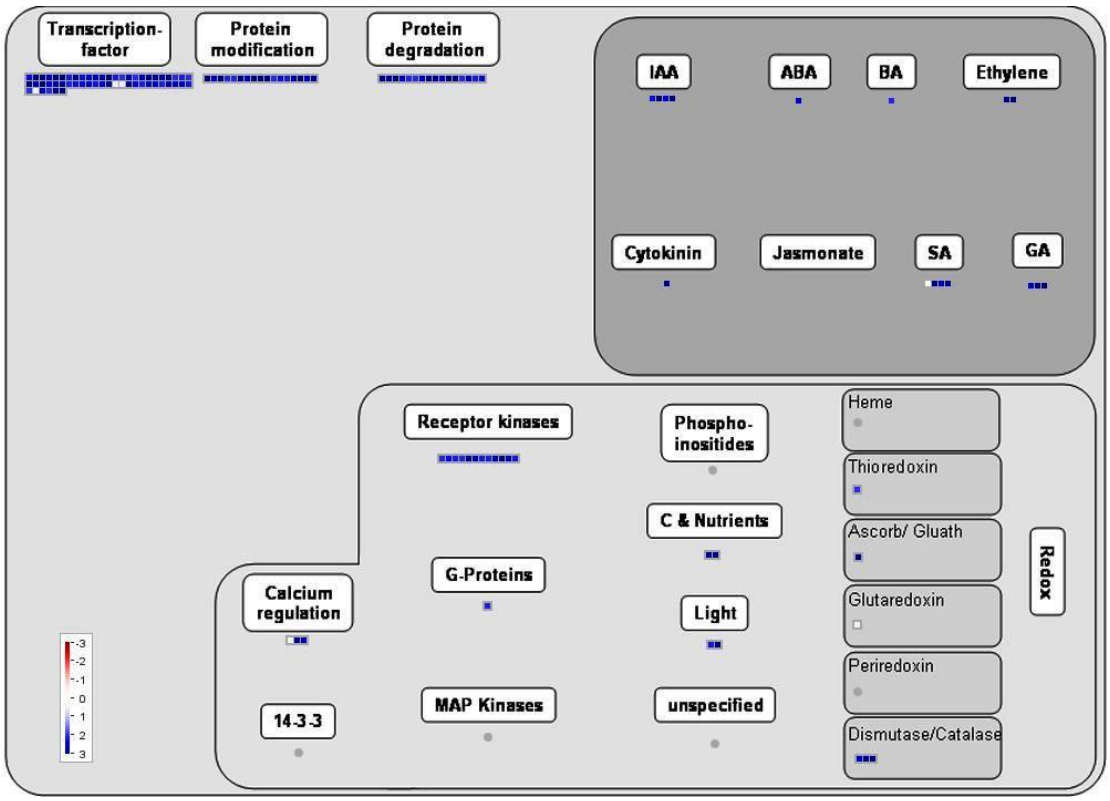

Figure S15 Microarray analysis of the differential expression genes in regulation network using MapMan softwoare (version 3.6.0RC1).

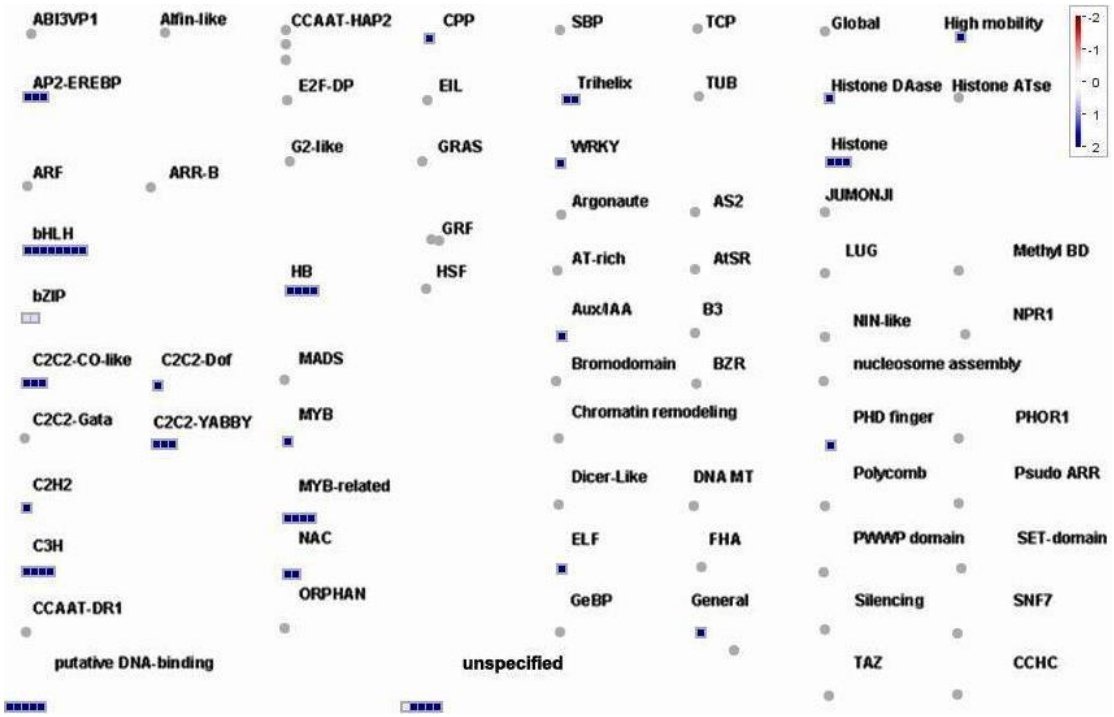

Figure S16 Microarray analysis of the differential expression genes in transcription network using MapMan softwoare (version 3.6.0RC1).

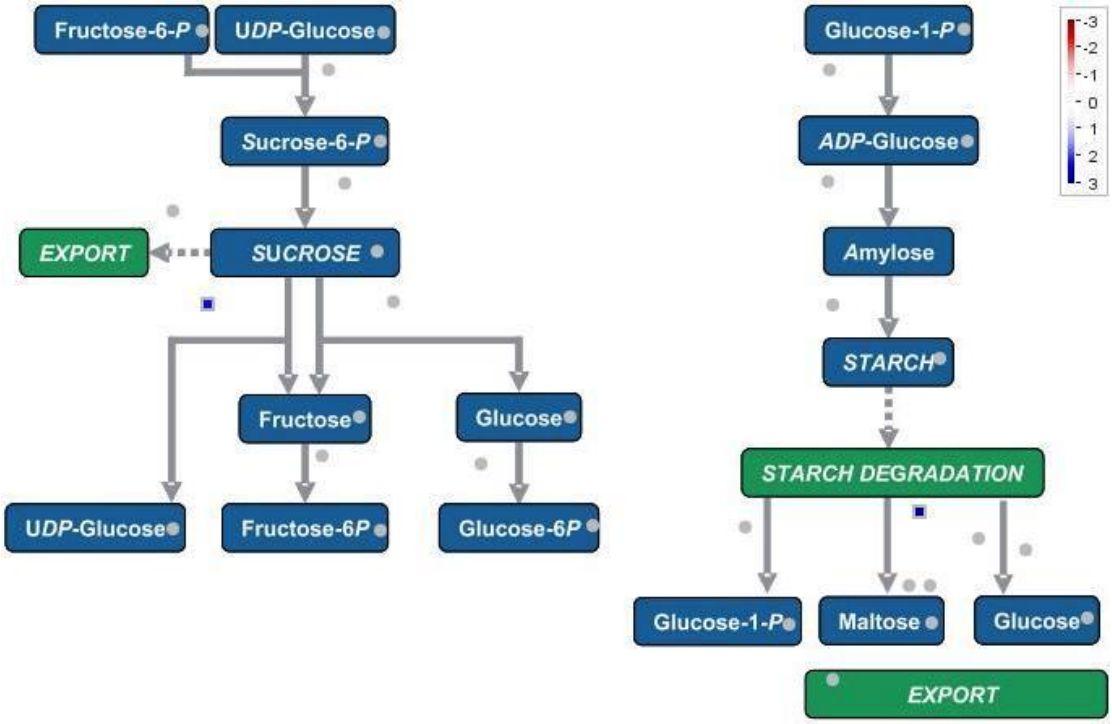

Figure S17 Microarray analysis of the differential expression genes in the metabolism of sucrose and starch using MapMan softwoare (version 3.6.0RC1).

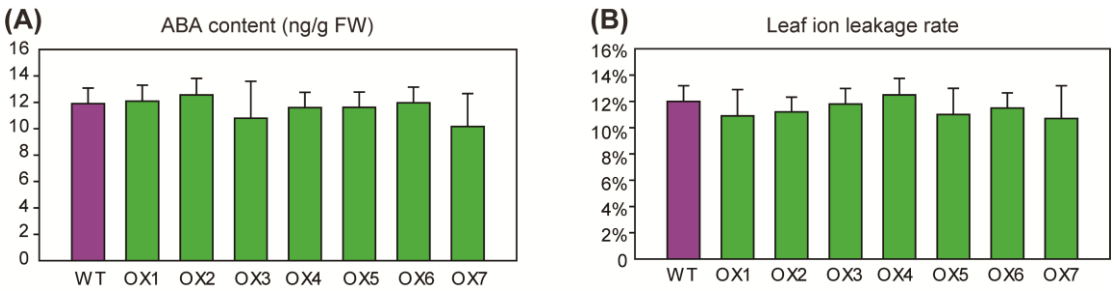

Figure S18 ABA level and leaf ion leakage rate of *SLAC7* overexpression transgenic plants.

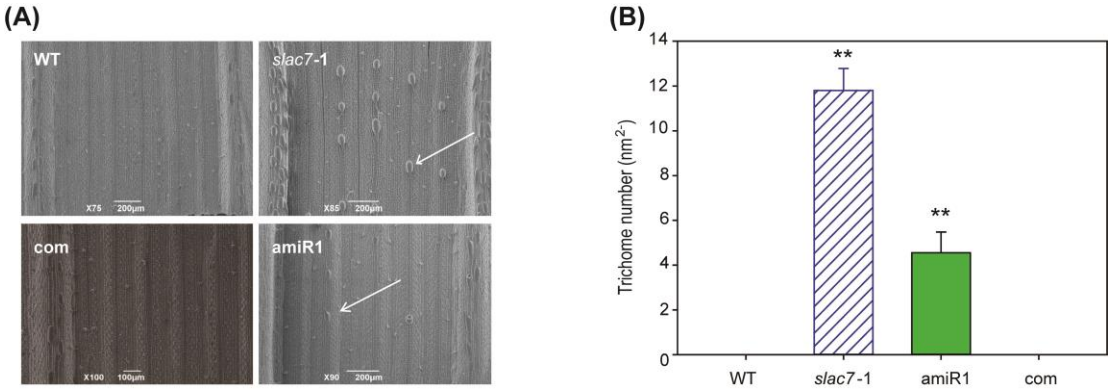

Figure S19 The leaf trichome numbers of different transgenic plants. **(A)** Leaf trichomes of *slac7*-1 and amiR1 observed by scanning electron microscope. (B) The trichome numbers of *slac7*-1 and amiR1 leaves were significantly more than that of wild type. Data represent the mean values ±SD of six independent experiments conducted with 7-leaf stage plants. Double asterisks denote a highly significant difference using Student's *t*-test ($P < 0.01$)

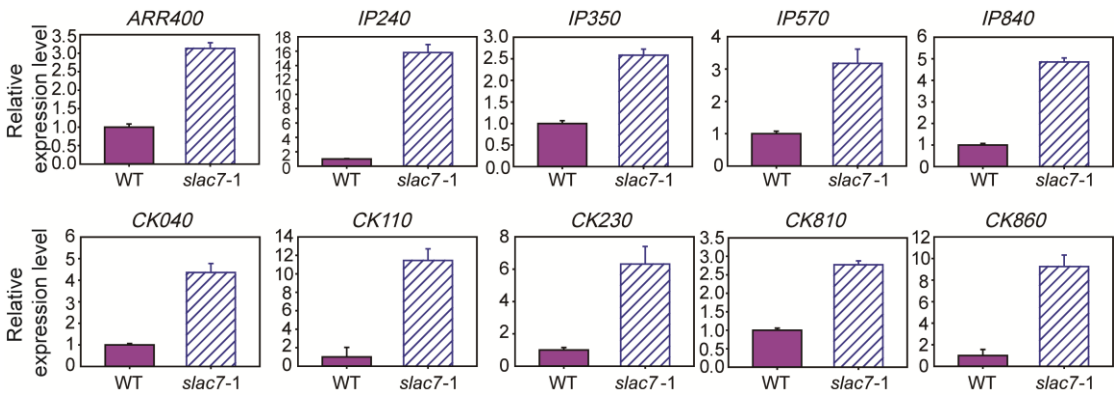

Figure S20 Relative expression level of cytokinin metabolism related genes in *slac7*-1 leaves.

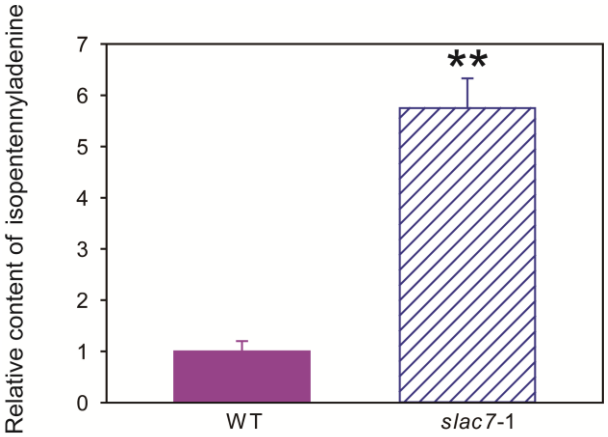

Figure S21 Relavtive content of isopentennyladenine in *slac7*-1 and wild-type leaves. Data represent mean values ±SD of three independent experiments conducted with different plants. Double asterisks denote a highly significant difference using Student's *t*-test ($P < 0.01$).