

Supporting Information Appendix



Mean JA (A), JA-Ile (B), OH-JA (C), OH-JA-Ile (D), COOH-JA-Ile (E) and JA-Val (F) levels (\pm SE, n=5) in flowers of EV, ir-*aoc* and ir-*coi1* plants. Samples from three different floral stages were analyzed. Asterisks indicate significant differences in ir-*aoc* or ir-*coi1* compared with control plants (*, p < 0.05; **, p < 0.01; Student's t-test).



Fig. S2. Phylogenetic analysis and sequence alignment of JAZ genes in different species.

(A) Phylogenetic analysis of JAZ gene family from *N. attenuata* (Na), *Oryza sativa*,
(Os), *N. tabacum* (Nt), *Vitis vinfera* (Vv), *Solanum lycopersicum* (Sl) and Arabidopsis
(At). (B) Sequence alignment of JAZ genes from different species. EAR motif was highlighted in red box. TIFY domain was highlighted in green box. Jas motif was highlighted in yellow box.



Fig. S3. Subcellular localization of JAZi and JAZ homo-/hetero dimerization. (A) Subcellular localization of NaJAZi. YFP and JAZi-YFP were transiently expressed in *N. attenuata* leaves. After incubation for 48 h, transformed cells were observed under a confocal microscope. The photographs were taken in UV light, visible light, and in combination (merged), respectively. Scale bar, 20 µm. (B) NaJAZb homo- and heterodimerization assay by yeast two-hybrid. BD-JAZs and AD-JAZb were co-transformed into yeast strain Y2Hgold. BD and AD-JAZb co-transformed yeast were used as control. (C) NaJAZi homo- and heterodimerization assays. BD-JAZs and AD-JAZi were co-transformed into yeast two-hybrid assays. BD-JAZs and AD-JAZi were co-transformed into yeast strain Y2Hgold. The transformants were grown on QDO (SD/-Ade/-His/-Leu/-Trp/) plate with 40mg/L X-α-gal. (D) Immunoblot analysis of JAZ proteins in yeast strains used for Y2H assays shown in (C). BD-JAZi fusion protein was detected with anti-myc antibody.



Fig. S4. Interactions between NaCO1 and NaJAZs and *in vitro* NaJAZ degradation assay.

(A) Interactions between NaCOI1 and NaJAZ proteins by yeast two-hybrid assays. GAL4 DNA-binding domain (BD) and activation domain (AD) fusions were cotransformed into yeast strain Y2Hgold. The transformants were grown on QDO (SD/-Ade/-His/-Leu/-Trp/+40mg/L X- α -gal) plates in the presence of coronatine (COR) or JA-Ile or a solvent control. (B) *In vitro* JAZb degradation assays. Purified HIS-JAZb was incubated with total crude extracts from EV and total crude extracts from EV plus MG132. HIS-JAZb was detected using anti-HIS antibody at the indicated incubation time points. The Coomassie Brilliant Blue (CBB) staining is shown as a protein loading control. (C) Mean relative abundance (±SE, n=3) of HIS-JAZi protein levels in different treatments. The relative protein abundance was analyzed by ImageJ software.





Fig. S5. Silencing of *NaJAZi* does not affect leaf resistance to *M. sexta* larvae.

(A) Mean transcripts levels (\pm SE, n=5) of NaJAZi in *N. attenuata* leaves after W+R or wounding control (W+H₂O). Transcripts levels were analyzed by RT-qPCR. (B) Growth phenotype of *NaJAZi*-silencing plants. (C) Mean transcript levels (\pm SE, n=7) of *NaJAZi* in leaves of VIGS control and JAZi VIGS plants after W+R treatment. Transcripts levels were analyzed by RT-qPCR. Mean JA (D) and JA-IIe (E) levels (\pm SE, n=7) in leaves of VIGS control and JAZi VIGS plants after W+R treatments. Samples were harvested before or 1 h after treatments. Mean nicotine (F), 17hydroxygeranyllinalool diterpene glycosides (DTGs) (G), caffeoyputrescine (H) and dicaffeoylspermidine (I) levels (\pm SE, n=7) in leaves of VIGS control and JAZi VIGS plants after W+R treatments. (J) *M. sexta* performance on VIGS control and JAZi VIGS plants. *M. sexta* larva mass (\pm SE, n=30) was measured at 9, 13 and 16 d after feeding on indicated plants. Asterisks indicate significant differences in JAZi VIGS plants compared with VIGS EV control plants (**, p < 0.01; Student's t-test).



Fig. S6. Transcript abundance of JAZ genes in *NaJAZi*-silenced plants. Mean transcript levels (±SE, n=5) of *JAZi* (A), *JAZa* (B), *JAZb* (C), *JAZc* (D), *JAZd* (E), *JAZe* (F), *JAZh* (G) and *JAZj* (H) in the flowers of VIGS control and JAZi VIGS plants. Transcripts levels were analyzed by RT-qPCR. Asterisks indicate significant differences in JAZi VIGS plants compared with control plants (*, p < 0.05; **, p < 0.01; Student's t-test).



Fig. S7. Up- and down-regulated genes in *NaJAZi*-silenced plants. Heatmap shows up- and down-regulated genes in JAZi-silencing flowers. The color gradient refers to relative signal abundance. Mean transcript levels (\pm SE, n=5) of *NaTPS38* (B), *NaPI* (C), *NaMYB8* (D), *NaDEF1* (E) and *NaDEF2* (F) in flowers of VIGS control and JAZi VIGS plants. Transcripts levels were analyzed by RT-qPCR. Asterisks indicate significant differences in JAZi VIGS plants compared with control plants (**, p < 0.01; Student's t-test).



Fig. S8. Silencing of *NaJAZi* does not affect nicotine and DTG levels in developing flowers.

Mean 17-hydroxygeranyllinalool diterpene glycosides (DTGs) (A) and nicotine (B) relative abundance (±SE, n=5) in the flowers of VIGS control and JAZi VIGS plants.





Fig. S9. Relative defensin protein levels in different genotypes.

(A) Mean defensin protein levels (\pm SE, n=3) in flowers of ir-*aoc*, ir-*coi1* and EV plants (*, p < 0.05; **, p < 0.01; Student's t-test). (B) Mean defensin protein levels (\pm SE, n=5) in flowers of VIGS control and JAZi VIGS plants (*, p < 0.05; Student's t-test). (C) Mean defensin protein levels (\pm SE, n=5) in flowers of VIGS control and MYC2 VIGS plants (*, p < 0.05; Student's t-test). The relative protein abundance was analyzed by ImageJ software.

Α		
	NaDEF1	MARSLCFMAFAVL-AMMLFVAYEVQAKSTCKAESNTFEGFCVTKPPCRRACLKEKFTDGK
	NaDEF2	MARSLCFMAFAIL-AMMLFVAYEVQAR-ECKTESNTFPGICITKPPCRKACISEKFTDGH
	NaD1	MARSLCFMAFAIL-AMMLFVAYEVQAR-ECKTESNTFPGICITKPPCRKACISEKFTDGH
	VrD1	MERKTFSFLFSLLLVLASDVAVERGEARTCMIKKE-GWGKCLIDTTCAHSCKNRGYIGGD
	NaDEF1	C <mark>SKILRRC</mark> ICYKPCVFDGKMINTGAETLAEEANTLAEALLEEEMMDN
	NaDEF2	C <mark>SKILRR</mark> CLCTKPCVFDEKMTKTGAEILAEEAKTLAAALLEEEIMDN
	NaD1	C <mark>SKILRR</mark> CLCTKPCVFDEKMTKTGAEILAEEAKTLAAALLEEEIMDN
	VrD1	CKGMTRTCYCLVNC



Fig. S10. Ectopic expression of *NaDEF2* in leaves enhances resistance to *M. sexta* larvae.

(A) Alignment analysis of *N. attenuata* NaDEF1, NaDEF2, *N. alata* NaD1 and *V.radiata* VrD1. The putative α -amylase inhibitory activity region is highlighted in red. (B) Southern blot analysis for the determination of T-DNA copy numbers of four independend ov*DEF2* lines. Genomic DNA was isolated from seedlings homozygous to the hygromycin resistance marker and digested in separate reactions with *Xba*I and *Eco*RV. A radiolabeled fragment of the hygromycin resistance marker (*hpt*II) served as probe. (C) *M. sexta* performance on leaves of rosette-stage wild type (WT) and ov*DEF2* plants in the glasshouse. *M. sexta* larval mass was determined 3, 6, 9, 11 and 13 days after infestation (±SE, n = 12 plants). Asterisks indicate statistically significant differences between control and transgenic plants (*, p < 0.05; **, p < 0.01; Student's t-test). (D) Pictures depict *M. sexta* caterpillars after 13 days of feeding from WT and ov*DEF2* plants.



Fig. S11. Silencing of *NaJAZj* does not affect the expression of floral defense-related genes.

Mean transcript levels (±SE, n=5) of *NaJAZj* in different tissues of *N. attenuata*. Transcripts levels were analyzed by RT-qPCR. (B) Mean transcripts levels (±SE, n=4-5) of *NaJAZj* (B), *NaDEF1* (C) and *NaTPS38* (D) in the flowers of VIGS control and JAZj VIGS plants. Transcripts levels were analyzed by RT-qPCR. Asterisks indicate significant differences in NINJA-like VIGS plants compared with control plants (**, p < 0.01; Student's t-test).



Fig. S12. Alignment analysis of NINJA and NINJA-like.

EAR motif is highlighted in the red box. B domain is highlighted in the yellow box and the C domain is highlighted in the green box.



Fig. S13. Transcript accumulations of the *NaNINJA* gene.Mean transcripts levels (±SE, n=5) of *NaNINJA* in different tissues of *N. attenuata*.Transcripts levels were analyzed by RT-qPCR.

Gene name	Leaf control	Leaf treated	Stem treated	Root treated	Flower bud	Corolla early	Corolla late	Opening flower	Pedicel	Stigma	Nectary	Anther	Ovary
NaJAZa	43.95	1634.56	800.62	344.79	216.39	274.45	104.7	70.56	152.9	138.37	105.83	114.17	108.3
NaJAZb	71.67	431.55	251.72	5.02	24.27	43.09	43.13	20.06	15.24	19.48	2.2	12.91	13.61
NaJAZc	24.4	114.45	69.67	78.99	89.16	67.87	63.8	51.38	72.59	102.1	66.49	21.04	84.32
NaJAZd	7.74	736.5	359.93	78.29	37.15	38.95	47.38	34.15	17.65	47.27	67.33	50.82	53.3
NaJAZe	4.47	9.56	8.46	77.91	23.47	14.52	5.9	8.06	8.31	10.99	12.37	20.86	17.33
NaJAZf	0	151.31	3.5	1.09	1.11	2.59	0.3	0	0	0	0	0.75	0
NaJAZg	0	0	0	51.52	0	0.08	0	0	0.1	0.12	0	0	0
NaJAZh	42.29	740.37	551.18	48.82	74.2	54.96	28.27	17.65	33.64	47.41	30.33	31.28	33.9
NaJAZi	0	0.53	0.29	0.07	157.91	248.72	0.57	1.08	0.25	151.92	8.93	61.48	16.27
NaJAZj	0.59	690.1	219.95	11.69	35.08	35.65	20.26	12.43	3.14	12.08	13.81	40.8	7.78
NaJAZk	1.1	1.74	3.6	2.56	2.21	2.52	4.22	1.72	3.35	2.21	2.63	0.84	3.21
NaJAZI	0	0.17	0.2	0.23	0	0.18	0	0.24	0	0	0	0	0.24
NaJAm	3.71	2.73	9.33	10.93	9.01	7.67	8.58	15.1	6.58	10.5	16.14	6.4	26.73

Table S1. The transcripts per million (TPM) values of JAZs from the RNA-seqanalysis.

 Table S2. DNA primers used in this study.

Gene	Sequence (5'-3')	Purpose
JAZi-RT-F	TCATTCTGTGGCATGTTCGT	RT-qPCR
JAZi-RT-R	TGAAACTGCAGAGATGGTGC	RT-qPCR
AD/BD-NaJAZi-F	GCCAGCATATGATGAAGCACAGAATTGGCCT	Y2H
AD/BD-NaJAZi-R	TCCATCCCGGGTGGTATGGATTAGCTGCTTGAA	Y2H
AD/BD-NaJAZb-F	GCCAGCATATGATGGATTCAAGTATTATTGA	Y2H
AD/BD-NaJAZb-R	TCAATCCCGGGTGGCTTTCCCAATGAACGCTTG	Y2H
BD-COI1-F	TTCATCATATGATGGAGGAGCGTAGCTCCAC	Y2H
BD-COI1-R	TCCATCCCGGGAATTCAGCGAGAAGGGAATTTG	Y2H
AD-MYC2a-F	CCCAGCATATGATGACGGACTATAGAATACC	Y2H
AD-MYC2a-R	TACAGATCGATGTCGCGATTCAGCAATTCTGG	Y2H
AD-MYC2b-F	CCCAGCATATGATGAATTTGTGGAATACTAG	Y2H
AD-MYC2b-R	TACAGATCGATGGCGTGTTTCAGCAACTCTGG	Y2H
AD/BD-NINJA-F	GCGCGCATATGATGGATGAAAACGATCTTGA	Y2H
AD/BD-NINJA-R	TAAATCCCGGGAAGCTTTGGGCAGAGGCAGCCG	Y2H
AD-NaJAZa-F	GCCAGCATATGATGGCATCATCGGAGATTGT	Y2H
AD-NaJAZa-R	TCCATCCCGGGTGGACGAATTGAATACCTACAC	Y2H
AD-NaJAZc-F	TCAGTCCCGGGTATGGAGAGAGATTTTATGGG	Y2H
AD-NaJAZc-R	TCAATCTCGAGCGGTCTCCTTACCGGCTATCA	Y2H

BD-NaJAZc-F	TCAGTCCATGGAGAGAGAGAGAGATTTTATGGG	Y2H
BD-NaJAZc-R	TCAATGTCGAC G GGTCTCCTTACCGGCTATCA	Y2H
AD/BD-NaJAZd-F	GCCAGCATATGATGGGGGTTATCGGAGATTGT	Y2H
AD/BD-NaJAZd-R	TCGATCCCGGGTGAAAGAACTGCTCAGTTTTCA	Y2H
AD/BD-NaJAZe-F	GCCAGCATATGATGGGTTTGACTCATCATGT	Y2H
AD/BD-NaJAZe-R	TCAATCCCGGGTGCGTCTCCTTGACCAAATTGA	Y2H
AD/BD-NaJAZf-F	GCCAGCATATGATGAGAAGAAACTGTAACTTG	Y2H
AD/BD-NaJAZf-R	TCGATCCCGGGTGGTGATGATATGGAGAAGTTT	Y2H
AD/BD-NaJAZg-F	GCCAGCATATGATGGAGAGAGAGATTTCATGGG	Y2H
AD/BD-NaJAZg-R	TCGATCCCGGGTGTATAGTAGCAGGAAGAACAG	Y2H
AD/BD-NaJAZh-F	GCCCGCATATGATGTCAAATTCGCAAAATTC	Y2H
AD/BD-NaJAZh-R	TCGGTCCCGGGTGTAACTTGAAATTGAGATCGA	Y2H
AD/BD-NaJAZj-F	GCCCGCATATGATGAGAAAAAACTGTAACTT	Y2H
AD/BD-NaJAZj-R	TCATTCCCGGGTGGCGATGATAAGGAGAAGTTG	Y2H
AD/BD-NaJAZk-F	GACAGCATATGATGCCGCCGGAAGAATCAGT	Y2H
AD/BD-NaJAZk-R	TAGGTCCCGGGTGCCTGTCTTTTCGCTTCTCAA	Y2H
AD/BD-NaJAZI-F	GCCCGCATATGATGTATTGCAGCTCCAAAGT	Y2H
AD/BD-NaJAZI-R	CAGGTCCCGGGTGACTATTCTTTTCCTTCAAAC	Y2H
AD/BD-NaJAZm-F	GCCAGCATATGATGGCGCCGGAAGAAACAGT	Y2H
AD/BD-NaJAZm-R	TCCATCCCGGGTGCTCTTTGGCATCTTTGTCAT	Y2H
AD-TOPLESS-F	CCGCAGAATTCATGTCATCTCTCAGCAGAGA	Y2H
AD-TOPLESS-R	AATCAGGATCCCTCTTGGTGCTTGTTCGGAGC	Y2H
AD/BD-NINJA-like-F	CCGCAGAATTCATGTTTACTGTGTTAATGGC	Y2H
AD/BD-NINJA-like-R	AATCAGGATCCCAGAACAAGGGGGGGATTACAG	Y2H
TOPO-NINJA-like-F	CACCATGTTTACTGTGTTAATGGC	pENTR
TOPO-NINJA-like-R	AGAACAAGGGGGGGATTACAG	pENTR
TOPO-JAZi-F	CACCATGGGCTGTCCCTAAGAAAA	pENTR
TOPO-JAZi-R	ACAGGTGATCCAACCTTCCA	pENTR
NINJA-like-RT-F	GCTCAGAATGCTGGGAAAAG	RT-qPCR
NINJA-like-RT-R	CATCTTTCCGGTGAACCACT	RT-qPCR
TPS38-RT-F	ATGGGCTGTTGGTTTCACT	RT-qPCR
TPS38-RT-R	TGCATTGATGTCCCATCTGT	RT-qPCR
PI-RT-F	ACACGAGACTTGGGAAATGG	RT-qPCR
PI-RT-R	GTGTCCCTGGAAAACCTTCA	RT-qPCR
MYB8-RT-F	ACCGGGACGAACAGATAATG	RT-qPCR
MYB8-RT-R	CGACGAAGAATTTGGGTGTT	RT-qPCR
DEF2-RT-F	TGCATTACCAAACCACCTTG	RT-qPCR
DEF2-RT-R	CAGCCAAAGTTTTTGCTTCC	RT-qPCR
DEF1-RT-F	ACATTCGAGGGATTCTGCGT	RT-qPCR

DEF1-RT-R	TCCTCGGCTAAAGTTTCAGCT	RT-qPCR
NINJA-RT-F	ATCTACCGTGGGTCTCAACG	RT-qPCR
NINJA-RT-R	AGTTTGCTCTTCGCTTGCAT	RT-qPCR
JAZa-RT-F	ATGACGATATTCTACGGCGG	RT-qPCR
JAZa-RT-R	TAAGTGAAGCTCGTCTCGCA	RT-qPCR
JAZb-RT-F	ACACCAAATGCATCCACAAA	RT-qPCR
JAZb-RT-R	GACGCCGTTTCTTCTTCTTG	RT-qPCR
JAZc-RT-F3	TACCTGCCTCAGGTCATTCC	RT-qPCR
JAZc-RT-R3	GGAACCGCTGCTGACATTAT	RT-qPCR
JAZd-RT-F	ACCGCAGTTTTGAACCAACT	RT-qPCR
JAZd-RT-R	ATTTGCCTTAGCTGCTGGAA	RT-qPCR
JAZe-RT-F	CGCACTACACGTCGACAACT	RT-qPCR
JAZe-RT-R	CAGCGCTGTTAGTTGGAACA	RT-qPCR
JAZh-RT-F	TCGAATTTCGTGCAGACTTG	RT-qPCR
JAZh-RT-R	TACAGCACTCTGACGAACGG	RT-qPCR
JAZj-RT-F	AGCTCAGGCTTATGCCTCCT	RT-qPCR
JAZj-RT-R	TCTGAAATTGGTGACCGGAT	RT-qPCR
MYC2a-RT-F	GGCCCGGAACAACTACTACA	RT-qPCR
MYC2a-RT-R	CCCCGTCGATTAAAGTCTGA	RT-qPCR
MYC2b-RT-F	TCTGGTGCGATGAAGTCAAG	RT-qPCR
MYC2b-RT-R	CTGCTTCGACGTGATTCAAA	RT-qPCR
JAZj-VIGS-F	TCATCACTAGTCCACAGCAGCTAACAATATT	VIGS
JAZj-VIGS-R	ATCTCCCCGGGCAAAATATATGTACAAATGG	VIGS
MYC2a-VIGS-F	CCAGCACTAGTATCAAGAGGTAGCAACGATG	VIGS
MYC2a-VIGS-R	ACTTTCCCGGGGACACATTTGGTACAACAGC	VIGS
MYC2b-VIGS-F	CCAGCACTAGTATGAATTTGTGGAATACTAG	VIGS
MYC2b-VIGS-R	ACTTTCCCGGGGGGCATAGGTCCATGTCTCGC	VIGS
JAZi-VIGS-F	TCATCACTAGTATCACAATTTTCTACAACG	VIGS
JAZi-VIGS-R	ATCTCCCCGGGGAAGTATCCGCATATCGCAAA	VIGS
NINJA-like-VIGS-F	CACGCGGATCCATGTTTACTGTGTTAATGGC	VIGS
NINJA-like-VIGS-R	CCCGCATCGATTTGATTCAAAGAAAGATTCA	VIGS

 Table S3. Gene accession numbers used in this study

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Name	Species	Accession number

AtAFP1	Arabidopsis	AT1G69260
AtAFP2	Arabidopsis	AT1G13740
AtAFP3	Arabidopsis	AT3G29575
AtAFP4	Arabidopsis	AT3G02140
AtNINJA	Arabidopsis	AT4G28910
AtJAZ1	Arabidopsis	AT1G19180
AtJAZ2	Arabidopsis	AT1G74950
AtJAZ3	Arabidopsis	AT3G17860
AtJAZ4	Arabidopsis	AT1G48500
AtJAZ5	Arabidopsis	AT1G17380
AtJAZ6	Arabidopsis	AT1G72450
AtJAZ7	Arabidopsis	AT2G34600
AtJAZ8	Arabidopsis	AT1G30135
AtJAZ9	Arabidopsis	AT1G70700
AtJAZ10	Arabidopsis	AT5G13220
AtJAZ11	Arabidopsis	AT3G43440
AtJAZ12	Arabidopsis	AT5G20900
AtJAZ13	Arabidopsis	AT3G22275
OsJAZ1	Oryza sativa	Os04g55920
OsJAZ2	Oryza sativa	Os07g05830
OsJAZ3	Oryza sativa	Os08g33160
OsJAZ4	Oryza sativa	Os09g23660
OsJAZ5	Oryza sativa	Os04g32480
OsJAZ6	Oryza sativa	Os03g28940
OsJAZ7	Oryza sativa	Os07g42370
OsJAZ8	Oryza sativa	Os09g26780
OsJAZ9	Oryza sativa	Os03g08310
OsJAZ10	Oryza sativa	Os03g08330
OsJAZ11	Oryza sativa	Os03g08320
OsJAZ12	Oryza sativa	Os10g25290
OsJAZ13	Oryza sativa	Os10g25230
OsJAZ14	Oryza sativa	Os10g25250
OsJAZ15	Oryza sativa	Os03g27900
NtJAZ2b	N. tabacum	KC246550
NtJAZ2b-2	N. tabacum	KC246551
NtJAZ3b	N. tabacum	KC246552
NtJAZ4	N. tabacum	KC246553
NtJAZ5	N. tabacum	KC246554
NtJAZ6	N. tabacum	KC246555
NtJAZ7a	N. tabacum	KC246556

NtJAZ7b	N. tabacum	KC246557
NtJAZ8	N. tabacum	KC246558
NtJAZ9	N. tabacum	KC246559
NtJAZ10	N. tabacum	KC246560
NtJAZ11a	N. tabacum	KC246561
NtJAZ11b	N. tabacum	KC246562
NtJAZ12a	N. tabacum	KC246563
NtJAZ12b	N. tabacum	KC246564
VvJAZ1	Vitis vinfera	XM-002284819
VvJAZ2	Vitis vinfera	XM-002262714
VvJAZ3	Vitis vinfera	XM-003634778
VvJAZ4	Vitis vinfera	XM-002272327
VvJAZ5	Vitis vinfera	XM-002277733
VvJAZ6	Vitis vinfera	XM-002277769
VvJAZ7	Vitis vinfera	XM-002277916
VvJAZ8	Vitis vinfera	CBI30922
VvJAZ9	Vitis vinfera	XM-002277121
VvJAZ10	Vitis vinfera	XM-002263220
VvJAZ11	Vitis vinfera	XM-002282652
SIJAZ1	Solanum lycopersicum	Solyc07g042170
SIJAZ2	Solanum lycopersicum	Solyc12g009220
SIJAZ3	Solanum lycopersicum	Solyc03g122190
SIJAZ4	Solanum lycopersicum	Solyc12g049400
SIJAZ5	Solanum lycopersicum	Solyc03g118540
SIJAZ6	Solanum lycopersicum	Solyc01g005440
SIJAZ7	Solanum lycopersicum	Solyc11g011030
SIJAZ8	Solanum lycopersicum	Solyc06g068930
SIJAZ9	Solanum lycopersicum	Solyc08g036640
SIJAZ10	Solanum lycopersicum	Solyc08g036620
SIJAZ11	Solanum lycopersicum	Solyc08g036660
SIJAZ12	Solanum lycopersicum	Solyc01g009740
SIJAZ13	Solanum lycopersicum	LOC104649733