WT scions were grafted on WT and iaaM rootstock, seperately. Scion and rootstock tissues were harvested at 0 hour, 24 hours and 96 hours, seperately.
Note: changes of gene expression level in WT scions on WT rootstock were presented in balck; while WT scions on iaaM rootstock in red.
Similarly, changes of gene expression level in WT rootstock were presented in black, while in iaaM rootstock in red

Tissues	**Gene name**	**Gene ID**	**Changes in expression level in fold**						**Gene function**
			0 hr		24 hrs		96 hrs		
Callus formation related genes									
WT sicons on WT or iaaM rootstocks	WIND1	Nitab4.5_0004997g0010.1	1.0	1.0	20.5	31.1	7.7	23.9	wound indcued; callus formation
	LBD18	Nitab4.5_0007537g0010.1	1.0	1.0	2.3	2.9	1.7	1.6	auxin and lateral root development
	LBD17	Nitab4.5_0004192g0020.1	1.0	1.0	3.3	28.2	14.2	80.7	auxin and lateral root development
	LBD16	Nitab4.5_0000086g0170.1	1.0	1.0	6.5	22.8	13.4	65.4	auxin and lateral root development
	Histone H4	Nitab4.5_0000270g0260.1	1.0	1.0	1.9	1.3	1.2	1.7	cell division
	Cyclin-A1-1	Nitab4.5_0006720g0060.1	1.0	1.0	1.2	1.2	1.9	2.4	cell division
	Cyclin-A2-2	Nitab4.5_0007182g0040.1	1.0	1.0	2.1	1.6	1.5	2.1	cell division
	Cyclin-B2-3	Nitab4.5_0010763g0020.1	1.0	1.0	1.2	1.1	1.7	2.4	cell division
	Cyclin-B2-4	Nitab4.5_0000588g0060.1	1.0	1.0	1.3	1.3	1.8	2.6	cell division
	Cyclin-D3-1	Nitab4.5_0006486g0030.1	1.0	1.0	0.9	2.0	2.0	3.4	cell division
	G2/mitotic-specific cyclin-1	Nitab4.5_0002967g0030.1	1.0	1.0	1.0	1.1	2.0	2.8	cell division
	G2/mitotic-specific cyclin-2	Nitab4.5_0008332g0040.1	1.0	1.0	2.6	2.4	3.2	4.4	cell division
	G2/mitotic-specific cyclin S13-6	Nitab4.5_0000428g0070.1	1.0	1.0	1.1	1.0	1.5	2.0	cell division
	Cyclin-P3-1	Nitab4.5_0006928g0020.1	1.0	1.0	3.0	2.3	4.7	1.9	cell division
WT or iaaM rootstocks with WT scions	WIND1	Nitab4.5_0004997g0010.1	1.0	4.2	7.9	12.9	16.2	22.5	wound indcued; callus formation
	LBD18	Nitab4.5_0007537g0010.1	1.0	1.9	0.6	1.6	0.3	1.1	auxin and lateral root development
	LBD17	Nitab4.5_0004192g0020.1	1.0	2.2	0.1	0.9	0	2.2	auxin and lateral root development
	LBD16	Nitab4.5_0000086g0170.1	1.0	1.2	0.1	0.1	0	2.0	auxin and lateral root development
	Histone H4	Nitab4.5_0000270g0260.1	1.0	2.3	3.2	9.3	2.5	6.3	cell division
	Cyclin-A1-1	Nitab4.5_0006720g0060.1	1.0	1.3	1.4	4.7	5.5	6.0	cell division
	Cyclin-A2-2	Nitab4.5_0007182g0040.1	1.0	1.2	2.0	8.2	5.6	7.0	cell division
	Cyclin-B2-3	Nitab4.5_0010763g0020.1	1.0	1.4	0.7	3.2	2.8	4.7	cell division
	Cyclin-B2-4	Nitab4.5_0000588g0060.1	1.0	1.1	0.8	3.2	2.7	4.1	cell division
	Cyclin-D3-1	Nitab4.5_0006486g0030.1	1.0	1.7	3.0	3.7	3.0	7.3	cell division
	G2/mitotic-specific cyclin-1	Nitab4.5_0002967g0030.1	1.0	0.5	0.6	3.3	2.6	3.5	cell division
	G2/mitotic-specific cyclin-2	Nitab4.5_0008332g0040.1	1.0	1.6	2.0	6.2	5.8	7.2	cell division
	G2/mitotic-specific cyclin S13-6	Nitab4.5_0000428g0070.1	1.0	1.3	1.1	3.8	3.0	3.7	cell division
	Cyclin-P3-1	Nitab4.5_0006928g0020.1	1.0	0.5	1.5	1.2	2.3	2.0	cell division
Vascular development related genes									
WT sicons on WT or iaaM rootstocks	Expansin-A15	Nitab4.5_0000141g0090.1	1.0	1.0	36.5	17.5	10.6	11.6	cell wall looseing
	Expansin-like B1	Nitab4.5_0000500g0210.1	1.0	1.0	123.1	315.0	42.1	219.9	cell wall looseing
	Expansin-like A1	Nitab4.5_0001274g0040.1	1.0	1.0	1.7	3.4	3.9	3.0	cell wall looseing
	Expansin-like B1	Nitab4.5_0003567g0050.1	1.0	1.0	124.4	253.9	57.2	176.9	cell wall looseing
	Expansin-A15	Nitab4.5_0005766g0020.1	1.0	1.0	32.2	15.4	9.9	3.0	cell wall looseing
	Cellulose synthase-like protein E1	Nitab4.5_0007779g0010.1	1.0	1.0	3.8	14.5	5.2	14.6	cell wall construction
	Caffeoyl-CoA O-methyltransferase 1	Nitab4.5_0002694g0030.1	1.0	1.0	2.2	3.5	1.1	3.8	cell wall reinforcement
	Caffeoyl-CoA O-methyltransferase 3	Nitab4.5_0002765g0010.1	1.0	1.0	1.0	2.0	0.8	2.0	cell wall reinforcement
	Laccase-4	Nitab4.5_0000119g0250.1	1.0	1.0	1.5	0.4	1.3	0.7	secondary xylem cell wall lignification.
	HCA2	Nitab4.5_0000003g0600.1	1.0	1.0	1.6	2.5	1.5	1.3	phloem formation
	NAC096	Nitab4.5_0003100g0030.1	1.0	1.0	23.9	71.6	25.9	21.8	vascularreconnection
	NAC071	Nitab4.5_0014378g0010.1	1.0	1.0	22.9	59.6	37.4	23.7	vascularreconnection
	VAN3-binding protein	Nitab4.5_0000678g0030.1	1.0	1.0	1.1	1.7	2.2	1.4	xylem formation
	TMO6	Nitab4.5_0000533g0150.1	1.0	1.0	2.3	5.6	7.1	4.5	provasculature formation
	Peroxidase 12	Nitab4.5_0000099g0090.1	1.0	1.0	3.8	13.5	2.3	22.5	second cell wall thickening
WT or iaaM rootstocks with WT scions	Expansin-A15	Nitab4.5_0000141g0090.1	1.0	64.0	126.6	5.7	30.2	15.0	cell wall looseing
	Expansin-like B1	Nitab4.5_0000500g0210.1	1.0	15.2	37.6	2.1	1.7	4.5	cell wall looseing
	Expansin-like A1	Nitab4.5_0001274g0040.1	1.0	1.1	1.0	1.7	1.4	1.5	cell wall looseing
	Expansin-like B1	Nitab4.5_0003567g0050.1	1.0	175.1	205.6	20.8	62.0	72.7	cell wall looseing
	Expansin-A15	Nitab4.5_0005766g0020.1	1.0	13.7	3.7	6.1	3.7	13.2	cell wall looseing
	Cellulose synthase-like protein E1	Nitab4.5_0007779g0010.1	1.0	4.5	1.4	3.5	2.5	5.4	cell wall construction
	Caffeoyl-CoA O-methyltransferase 1	Nitab4.5_0002694g0030.1	1.0	6.2	4.2	8.2	1.3	7.2	cell wall reinforcement
	Caffeoyl-CoA O-methyltransferase 3	Nitab4.5_0002765g0010.1	1.0	1.9	1.5	2.2	0.6	2.2	cell wall reinforcement
	Laccase-4	Nitab4.5_0000119g0250.1	1.0	0.1	0.4	0.1	0.0	0.1	secondary xylem cell wall lignification.
	HCA2	Nitab4.5_0000003g0600.1	1.0	0.8	3.3	8.2	2.2	7.1	phloem formation
	NAC096	Nitab4.5_0003100g0030.1	1.0	0.8	3.6	11.7	1.2	11.9	vascularreconnection
	NAC071	Nitab4.5_0014378g0010.1	1.0	1.0	8.6	13.6	2.6	8.3	vascularreconnection
	VAN3-binding protein	Nitab4.5_0000678g0030.1	1.0	0.5	0.9	1.2	2.0	1.9	xylem formation
	TMO6	Nitab4.5_0000533g0150.1	1.0	0.9	0.3	1.2	1.2	2.2	provasculature formation
	Peroxidase 12	Nitab4.5_0000099g0090.1	1.0	3.1	7.3	37.8	1.2	24.3	second cell wall thickening
Ethylene biosynthesis and responsive genes									
WT sicons on WT or iaaM rootstocks	ACCH	Nitab4.5_0002916g0060.1	1.0	1.0	2.1	15.7	24.3	72.1	ethylene synthesis
	NAC71	Nitab4.5_0014378g0010.1	1.0	1.0	22.9	59.6	37.4	23.7	ethylene signaling pathway
	WRKY transcription factor 33	Nitab4.5_0001226g0020.1	1.0	1.0	13.0	33.4	14.3	34.2	ethylene signaling pathway
	ERF92	Nitab4.5_0000777g0080.1	1.0	1.0	15.1	35.1	12.1	17.2	ethylene signaling pathway
	TIR1	Nitab4.5_0008145g0010.1	1.0	1.0	0.4	0.9	0.9	1.1	ethylene signaling
	Ethylene receptor 2	Nitab4.5_0004443g0040.1	1.0	1.0	1.1	2.5	2.3	3.6	ethylene receptor
	WRKY transcription factor 33	Nitab4.5_0000047g0140.1	1.0	1.0	23.8	50.1	27.3	65.9	ethylene signaling pathway
	ACS	Nitab4.5_0000915g0150.1	-	-	-	-	-	-	ethylene synthesis
	ACS	Nitab4.5_0000373g0240.1	1.0	1.0	3.0	7.9	5.9	4.5	ethylene synthesis
	ERF5	Nitab4.5_0007739g0010.1	1.0	1.0	1.9	4.5	0.9	3.3	ethylene signaling pathway
WT or iaaM rootstocks with WT scions	ACCH	Nitab4.5_0002916g0060.1	1.0	2.6	7.4	9.8	24.3	26.9	ethylene synthesis
	NAC71	Nitab4.5_0014378g0010.1	1.0	1.0	8.6	13.6	2.6	8.3	ethylene signaling pathway
	WRKY transcription factor 33	Nitab4.5_0001226g0020.1	1.0	1.3	7.3	11.3	5.4	11.7	ethylene signaling pathway
	ERF92	Nitab4.5_0000777g0080.1	1.0	1.9	10.9	8.7	6.8	5.6	ethylene signaling pathway
	TIR1	Nitab4.5_0008145g0010.1	1.0	0.7	0.2	0.2	0.2	0.5	ethylene signaling

Ethylene receptor 2	Nitab4.5_0004443g0040.1	1.0	0.5	1.1	1.5	1.5	1.9	ethylene receptor
WRKY transcription factor 33	Nitab4.5_0000047g0140.1	1.0	15.5	100.6	110.4	72.7	153.6	ethylene signaling pathway
ACS	Nitab4.5_0000915g0150.1	1.0	0.0	115.9	386.9	0.0	134.0	ethylene synthesis
ACS	Nitab4.5_0000373g0240.1	1.0	0.9	1.1	2.4	0.8	3.5	ethylene synthesis
ERF5	Nitab4.5_0007739g0010.1	1.0	1.1	2.6	5.1	2.1	3.8	ethylene signaling pathway