

Supplementary

Table S1. Statistics of SNP detection in samples

Sample	Total SNPs	Homozygous ¹	Heterozygous ²	Other ³
Control	1,185,693	2,893	767,018	415,782
Yein-early	1,583,458	304,513	772,143	506,80

¹ The same SNP type showed in 90% of sample reads mapped to the reference genome

² The same SNP type showed in 40%~60% of sample reads mapped to the reference genome

³ Not applicable as homozygous/heterozygous

Table S2. Statistics of SNP classification by genome annotation

Sample	Total SNPs	Annotated SNPs ¹	IGR ² & Gene Structure	Total	Homozygous	Heterozygous	Other ³
WT	1,185,693	1,080,086	intergenic region	745,808	1,720	454,333	259,755
			genic region	364,278	486	454,333	107,075
			exon	161,724	308	112,512	48,904
			intron	212,199	192	150,771	61,236
Yein-early	1,193,106	1,078,912	intergenic region	994,979	195,825	472,230	326,924
			genic region	456,272	78,296	249,768	45,701
			exon	203,235	35,194	109,730	58,311
			intron	265,470	45,261	146,653	73,556

¹ Loci where genes are organized in a reference gene annotation (gff) file and can be classified as genic/intergenic

² Intergenic region

³ Not applicable as homozygous/heterozygous

Table S3. Statistics of InDel detection in samples

Sample	Total		Homozygous ¹		Heterozygous ²		Other ³	
	Total	Insertions/Deletions	Total	Insertions/Deletions	Total	Insertions/Deletions	Total	Insertions/Deletions
WT	282,178	136,488 / 145,690	12,427	4,259/8,168	126,723	61,006/65,717	143,028	71,223/71,805
Yein-early	385,594	185,496 / 200,098	40,890	17,426/23,464	147,033	70,097/76,936	197,671	97,973/99,698

¹ The same InDel type showed in 90% of sample reads mapped to the reference genome

² The same InDel type showed in 40%~60% of sample reads mapped to the reference genome

³ No applicable as the homozygous/heterozygous

Table S4. Statistics of InDel classification by genome annotation

Sample	Total InDels	Annotated InDels ¹	IGR ² & Gene Structure	Total	Homozygous	Heterozygous	Other ³
WT	282,178	256,036	intergenic region	195,814	8,459	87,186	100,169
			genic region	60,222	1,429	30,148	28,645
			CDS	4,928	359	2,048	2,521
			exon	14,809	570	7,222	7,017
			intron	47,003	922	23,775	22,306
Yein-early	385,594	352,308	intergenic region	273,340	28,455	103,746	141,139
			genic region	78,968	7209	33,516	38,243
			CDS	6,528	717	2,309	3,502
			exon	19,444	1943	8,030	9,471
			intron	61,643	5494	26,416	29,733

¹ Loci where genes are organized in a reference gene annotation (gff) file and can be classified as genic/intergenic

² Intergenic region

³ Not applicable as the homozygous/heterozygous

※ If the reference gene position overlaps or due to the anti-sense form of the gene, the number of exons and introns may be counted as duplicates.

Table S5. Transcription factors with homozygous SNPs and InDels

Type	ID	Position	WT	Yein-early	Description
SNP	scaffold00430	109464	A	G	protein FAR1-RELATED SEQUENCE 5
SNP	scaffold00194	37085	T	C	L10-interacting MYB domain-containing protein
SNP	scaffold00899	8530	A	G	protein FAR1-RELATED SEQUENCE 5-like
InDel	scaffold00072	742016	*	+1G	wall-associated receptor kinase-like 10 isoform X3
InDel	scaffold00072	745918	*	++1T	wall-associated receptor kinase-like 22

Table S6. SNP primer sequences used in this study

Primer name	Sequence(5'-3')	Length	Tm	GC contents
Yein-SNP1 F	5- CGGAGGAAACGATGTA ACTACTG -3	23bp	60.1°C	47.8%
Con-SNP1 R	5- TCCATCCTGCAAAGTCAACA -3	20bp	60.2°C	45.0%
Yein-SNP2 F	5-CCGCGTACTGTTGACTGATAAT-3	22bp	59.2°C	45.5%
Con-SNP2 R	5-TCATAATTGAACTAGGGGCAAAA-3	23bp	59.9°C	34.8%
Yein-SNP3 F	5- AGAGCTAAGAGGAAAAC CAGAAATT-3	25bp	59.4°C	36.0%
Con-SNP3 R	5- ATCACCAACGCAACTTCCTC -3	20bp	60.1°C	50.0%
Yein-SNP4 F	5- GTTTGGAGATGTCTTGTAGAAGGAC -3	25bp	59.6°C	44.0%
Con-SNP4 R	5- TCCCCGATAGTGTCTTGAATG -3	21bp	59.9°C	47.6%
Con-SNP5 F	5- GCTGAAAGGCAACAAATGAACT-3	22bp	60.7°C	40.90%
Yein-SNP5 F	5- CTGAAAGGCAACAAATGAACC-3	21bp	59.6°C	42.90%
Con-SNP5 R	5- TCGCCCATTAAGTCTCCAC -3	20bp	60.1°C	50.00%
Yein-SNP6 F	5- CATAAAAATGGTCTGTTGCACAG-3	23bp	59.6°C	39.1%
Con-SNP6 R	5- TAGGACCACTTTTGGCAAGC -3	20bp	60.2°C	50.0%
Yein-SNP7 F	5- AGGCTTCAAGCTTGATTGTCA-3	21bp	60.0°C	42.9%
Con-SNP7 R	5- TTTCGGTCGCTGAATGTGTA-3	20bp	60.3°C	45.0%
Yein-SNP8 F	5- CGAGTACACATTCAGCGATCA -3	21bp	59.9°C	47.6%
Con-SNP8 R	5- CATGGCCCGTGGTCTATAAT -3	20bp	59.7°C	50.0%
Yein-SNP9 F	5- GGAGAAAGTTGAGCTTGATCTGATT -3	25bp	61.4°C	40.0%
Con-SNP9 R	5- TGCTGTTTAGCTTGGTAGGC -3	20bp	58.2°C	50.0%
Yein-SNP10 F	5- CCCAATAGATTTGTCCATGCAG-3	22bp	61.6°C	45.5%
Con-SNP10 R	5- CCAACATAATTCGGGAGGTG -3	20bp	60.2°C	50.0%

			20		40		60	
C.unshiu	MPFAPFVG	VN	HHGHSILFGC	GLISNEDIET	FTWLFRTWLS	CMSNSAPIGI	ITDQDKAMKA	AIENVFPNTR 70
Yein-early	MPFAPFVG	VN	HHGHSILFGC	GLISNEDIET	FTWLFRTWLS	CMSNSAPIGI	ITDQDKAMKA	AIENVFPNTR 70
	80			100		120		140
C.unshiu	HRWCLWHILK	KIPEKLG	GGYK	EYRDISNVLH	CAVYDSQSSA	KFEETWHHMI	VEFELGGNEW	LRGLYNERHR 140
Yein-early	HRWCLWHILK	KIPEKLG	GGYK	EYRDISNVLH	CAVYDSQSSA	KFEETWHHMI	VEFELGGNEW	LRGLYNERHR 140
	160			180		200		
C.unshiu	WVPCYLKNSF	WAGMSTTQ	RS	ESMNAFFDGY	VNSKTTLKQF	VEQYSNALKN	KAQKEVEEDA	RCSSHQLPCV 210
Yein-early	WVPCYLKNSF	WAGMSTTQ	RS	ESMNAFFDGY	VNSKTTLKQF	VEQYSNALKN	KAQKEVEEDA	RCSSHQLPCV 210
	220			240		260		280
C.unshiu	TSYAMEKQIR	DVYTISK	FQE	FQQELVGKMY	CEFVN	SMGCE	YIVREDVKVD	TWKKRTFFEY YCDKENGEIH 280
Yein-early	TSYAMEKQIR	DVYTISK	FQE	FQQELVGKMY	CEFVN	SMGCE	YIVREDVKVD	TWKKRTFFEY YCDKENGEIH 280
	300			320		340		
C.unshiu	CSCSRFQFRG	ILYRHAITIM	IRNDMEVLPE	KFILRRWRKD	VWRCHSRVKT	SHELHSCTDE	QKRYEKM CVS 350	
Yein-early	CSCSRFQFRG	ILYRHAITIM	IRNDMEVLPE	KFILRRWRKD	VWRCHSRVKT	SHELHSCTDE	QKRYEKM CVS 350	
	360			380		400		420
C.unshiu	FAEVANVAAK	DVESYNLVLN	WIEKVRIDLP	ETIQCGGNDV	TIVTGQGS	CS	NSVGIEMHDV	ETVRDPVVKR 420
Yein-early	FAEVANVAAK	DVESYNLVLN	WIEKVRIDLP	ETIQCGGNDV	TIITGQGS	CS	NSVGIEMHDV	ETVRDPVVKR 420
	440			460		480		
C.unshiu	RKCRPPCQRK	KSTKSSKSAR	SNAKDGHVSD	QVATMIPTFQ	NLQQSSVDRN	MYPHGVMDYS	NGLMNLHHIT 490	
Yein-early	RKCRPPCQRK	KSTKSSKSAR	SNAKDGHVSD	QVATMIPTFQ	NLQQSSVDRN	MYPHGVMDYS	NGLMNLHHIT 490	
	500			520		540		
C.unshiu	GDNVYPTATQ	NSSTHPQLQP	QVHGHFQQLL	FHQNNEYGVN	REFGSDFEE*		540	
Yein-early	GDNVYPTATQ	NSSTHPQLQP	QVHGHFQQLL	FHQNNEYGVN	REFGSDFEE*		540	

Figure S1. Comparison of the amino acid sequences of FAR1-RELATED SEQUENCE 5 between WT and Yein-early.