

**Table S1.** Up-regulated genes in irJAZd plants compared to WT plants determined by microarrays

<b>Classification</b>	<b>Fold Change</b>	<b>Bincode (TAIR)</b>	<b>Annotation</b>	<b>Gene ID</b>	<b>ACC number</b>
<b>TCA / org. transformation.</b>	4.30	8.3	Carbonate dehydratase	Na_454_18630	P27141
<b>Miscellaneous enzyme families</b>	4.39	26.12	Peroxidase	Na_454_32590	Q9XIV8
<b>RNA.regulation of transcription</b>	4.11	27.3.5	ARR17 (ARABIDOPSIS RESPONSE REGULATOR 17)	Na_454_26424	NP_567037
	3.49	27.3.99	Leucine zipper factor-related	Na_454_15857	NP_563798
<b>DNA.synthesis/chromatin structure</b>	3.72	28.1.3	Histone H1	Na_454_08010	AAC41651
<b>Protein.targeting.nucleus</b>	3.02	29.3.1	IMPORTIN ALPHA ISOFORM 2	Na_454_15992	ABM05488
<b>Protein.postranslational modification</b>	3.05	29.4	Protein kinase	Na_454_34744	CAA50374
<b>Signalling.receptor kinases</b>	3.50	30.2.26	CCR1 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 1)	Na_454_31246	NP_187589

**Table S1.** (continued)

Classification	Fold Change	Bincode (TAIR)	Annotation	Gene ID	ACC number
Not assigned	26.28	35.1	Carbon-nitrogen hydrolase family protein	Na_454_20897	NP_196765
	4.85	35.1	Carbon-nitrogen hydrolase family protein	Na_454_17587	NP_196765
	3.00	35.1	Glycosyl transferase family 1 protein	Na_454_37011	NP_173105

\* Microarray data is processed by SAM after 75% percentile normalization (FDR=2.09).

\* Up-regulated genes were determined by a greater than 3-fold induction of normalized signals in their expression ratio (irJAZd / WT) of 2h-WOS treated leaves. The values are the average ratio of 3 biological replicates of the microarrays.

\* All changes in gene expression were statistically significant by t-test ( $P < 0.05$ )

\* Gene annotation is processed by Blast X (E-value  $< 1e-5$ )

\* Classification of genes is based on GO classification from TAIR (<http://www.arabidopsis.org>).