

Table S3 Information of DEGs in the comparison of F-I-S vs I-F-R.

gene_id	log2FoldChange	gene_description
103344802	7.007206425	microRNA MIR397b
114824758	5.118160333	auxin-responsive protein SAUR20-like
114820172	5.083560147	uncharacterized LOC114820172
103438138	4.932543092	spermidine synthase 1-like
103442953	4.883473905	glycine-rich cell wall structural protein 1.0-like
103436235	4.643487298	proline-rich protein 4
103431109	4.326668216	uncharacterized LOC103431109
103447316	4.2019432	UDP-glycosyltransferase 87A1-like
103452054	4.166557526	protein terminal ear1
103445556	4.151068871	glycine-rich protein 23-like
103429376	4.085918901	thaumatin-like protein 1b
103452136	3.906048963	flavonoid 3'-O-methyltransferase-like transcript variant X2
103409872	3.884896012	primary amine oxidase 2-like
103412509	3.825818982	bromo and FHA domain-containing protein DDB_G0267958-like
103435474	3.639806906	glycine-rich protein DOT1
103428632	3.549177131	salicylate carboxymethyltransferase-like
103445531	3.505931844	ninja-family protein 1-like
103455627	3.49095605	phosphoethanolamine N-methyltransferase 1 transcript variant X2
103451594	3.381703578	glycine-rich cell wall structural protein
103411271	3.30848148	PF02362:B3 DNA binding domain
103431549	3.246001569	uncharacterized protein DDB_G0282077
103423993	3.230736627	putative phyto-sulfokines 6 transcript variant X1
103450652	3.222380536	WAT1-related protein At1g21890
103405958	3.202583653	uncharacterized LOC103405958
103440379	3.090078179	salicylate carboxymethyltransferase-like
103450780	3.047819387	acid phosphatase 1 transcript variant X2
114827083	3.019964612	uncharacterized LOC114827083
103425818	2.894076948	carbonic anhydrase chloroplastic-like transcript variant X1
103438567	2.785102112	probable trehalose-phosphate phosphatase D
114826857	2.765183124	cytochrome P450 94B3-like
103442672	2.718354281	GDSL esterase/lipase At2g42990-like
103430060	2.692621002	sec14 cytosolic factor-like transcript variant X1
103441610	2.686645698	probable glycerol-3-phosphate acyltransferase 3
103407182	2.658414837	EG45-like domain containing protein 2 transcript variant X1
103420753	2.63750889	superoxide dismutase [Fe] chloroplastic transcript variant X1
103454095	2.624329451	WAT1-related protein At1g21890-like
103427570	2.550283913	short-chain dehydrogenase TIC 32 chloroplastic-like transcript variant X1
103447381	2.494426854	acyl-lipid omega-3 desaturase (cytochrome b5) endoplasmic reticulum-like
103424673	2.425729946	probable isoaspartyl peptidase/L-asparaginase 2
103451024	2.37415737	protein ECERIFERUM 26-like
103427864	2.356005182	GDSL esterase/lipase At1g28610-like
103425704	2.281425616	2-methyl-6-phytyl-1,4-hydroquinone methyltransferase chloroplastic-like
103437493	2.270012859	transcription factor bHLH137
103428757	2.245045936	uncharacterized protein At2g23090-like
114819193	2.240469815	indole-3-acetic acid-amido synthetase GH3.10-like
103448410	2.203293231	transcription factor bHLH63-like transcript variant X5
103408523	2.201624381	uncharacterized LOC103408523
103437865	2.183819574	uncharacterized LOC103437865
103427603	2.171077877	zinc transporter 2-like
103415195	2.159378921	WUSCHEL-related homeobox 7-like
103402702	2.141476816	CLAVATA3/ESR (CLE)-related protein 43
103450886	2.042605551	ABC transporter G family member 11
114827640	-2.012672573	probable protein ABIL5
103452898	-2.04127348	putative E3 ubiquitin-protein ligase LIN-1 transcript variant X3
103403196	-2.048768238	auxin-responsive protein SAUR32-like
103448346	-2.07810196	putative lipid-transfer protein DIR1
103443267	-2.082131537	ABC transporter G family member 4
103405695	-2.135353249	uncharacterized protein At4g06744-like
103405656	-2.153257374	uncharacterized LOC103405656
114819126	-2.167409627	glycosyl hydrolase 5 family protein-like

103455679	-2.198129357	germin-like protein subfamily 1 member 13
103413130	-2.41245403	2-alkenal reductase (NADP(+)-dependent)-like%2C transcript variant X2
103433975	-2.43241071	transcription factor bHLH96-like
103453302	-2.586135796	UDP-glycosyltransferase 76E4-like%2C transcript variant X3
114824793	-2.626173896	LOB domain-containing protein 12-like
103451986	-2.648470978	polygalacturonase At1g48100
103450960	-2.662136648	transcription factor bHLH94-like
103403327	-2.750576472	cytochrome P450 71B37-like
103453283	-2.817707786	UDP-glycosyltransferase 76B1-like
103446853	-2.864776643	putative receptor-like protein kinase At4g00960
114821588	-2.94436952	aspartyl protease AED3
103436283	-3.212442697	basic form of pathogenesis-related protein 1-like
103455103	-3.258894183	uncharacterized acetyltransferase At3g50280
103414217	-3.319917815	MLP-like protein 34
103404101	-3.780861151	pathogenesis-related protein PR-1-like
103439877	-3.823644548	putative RING-H2 finger protein ATL21B
103452507	-4.509997503	potassium transporter 5-like%2C transcript variant X2