

Table S2. Transcripts that are upregulated in R junglerice plants.

Transcript	Pfam Description	Fold Change R/S
TR12349 c0_g1		5.72
TR14367 c1_g1		4.79
TR14485 c0_g2		30.44
TR1644 c0_g1		4.79
TR18025 c0_g3		8.64
TR18672 c0_g1		4.58
TR18672 c0_g3		3.82
TR19020 c0_g1		15.27
TR19421 c0_g1		6.64
TR19466 c0_g4		12.49
TR19629 c0_g1		108.88
TR19962 c0_g3		9.46
TR20241 c0_g1		4.95
TR20812 c2_g2		6.55
TR21019 c0_g2		14.43
TR21114 c2_g6		7.21
TR21448 c0_g1	PPR repeat family : PPR repeat : Pentatricopeptide repeat domain	13.59
TR21477 c0_g2	Trypsin-like peptidase domain	4.81
TR21768 c2_g3		21.70
TR22895 c0_g5		5.16
TR22999 c0_g5		100.90
TR23397 c0_g2		647.93
TR23438 c0_g1		22.35
TR23501 c0_g6		25.53
TR23670 c0_g1		30.90
TR23741 c0_g3		6.95
TR23900 c0_g2	Cytochrome P450	5.13
TR23959 c2_g3		20.91
TR23991 c1_g2		4.38
TR24104 c0_g2	Kelch motif : Galactose oxidase, central domain	4.69
TR24160 c1_g2		7.53
TR24185 c6_g3	MuDR family transposase	13.55
TR24204 c3_g6		25.56
TR24229 c0_g3		31.78
TR24268 c0_g2		33.25
TR24342 c4_g1		8.18
TR24367 c5_g3		45.72
TR24647 c0_g2		12.43
TR24853 c2_g1		6.98
TR25452 c5_g5		21.55
TR25458 c1_g1		20.41
TR25675 c1_g4		12.99
TR25862 c0_g5	Phosphatidylserine decarboxylase	5.38
TR25970 c1_g1		9.06
TR26066 c0_g3		23.00

TR26252 c1_g2		14.09
TR26255 c0_g1		19.69
TR26431 c1_g1		3.63
TR26674 c0_g1		5.87
TR26728 c2_g5		5.14
TR26934 c1_g1		23.40
TR26963 c1_g6	Leucine Rich repeats (2 copies) : Leucine rich repeat	1036.75
TR26964 c1_g1		57.47
TR27484 c1_g1		10.13
TR28196 c0_g1		8.35
TR28196 c0_g2		4.63
TR28485 c3_g2		10.77
TR28737 c0_g5		11.46
TR29090 c1_g2		3.93
TR29124 c0_g1		4.17
TR29170 c0_g3	Domain of unknown function (DUF3372)	3.93
TR29191 c1_g2		23.06
TR29284 c0_g1		11.57
TR29490 c4_g3		10.00
TR29667 c2_g1	Leucine Rich repeats (2 copies) : Leucine rich repeat	8.55
TR29667 c2_g3	Leucine Rich repeats (2 copies) : Leucine rich repeat	6.70
TR29667 c4_g3		7.28
TR29667 c6_g1	Leucine Rich repeats (2 copies) : Leucine rich repeat	7.47
TR29681 c3_g7		5.03
TR29902 c2_g1		8.34
TR29934 c0_g2		7.95
TR30171 c0_g4		10.19
TR30193 c0_g1		5.43
TR30196 c1_g1	Domain of unknown function (DUF1979)	33.43
TR30443 c3_g1		7.45
TR30462 c3_g6		21.06
TR30465 c0_g2		18.78
TR30609 c1_g2		498.04
TR30640 c7_g1		4.44
	Hsp90 protein : Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase : Basic region leucine zipper : bZIP transcription factor : Protein of unknown function (DUF3348)	214.50
TR30665 c3_g1	Endonuclease/Exonuclease/phosphatase family : Endonuclease-reverse transcriptase	17.21
TR44218 c0_g2		7.93
TR57584 c0_g2		7.62
TR58416 c0_g2		50.20
TR58468 c2_g1		5.59
TR58919 c0_g1	Dimerisation domain	5.21
TR58919 c0_g2	Dimerisation domain	6.08
TR58919 c0_g3	O-methyltransferase : Dimerisation domain : Methyltransferase domain	6.87
TR59654 c1_g1		

TR59775 c0_g1		7.78
TR60352 c0_g1		7.93
TR60979 c0_g4		4.47
TR61158 c0_g2		10.25
TR61934 c0_g3		4.18
TR62991 c0_g2	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase : CW-type Zinc Finger	22.86
TR63298 c0_g1	Plant invertase/pectin methylesterase inhibitor : Putative RNase-like toxin	13.06
TR6355 c0_g1		19.27
TR64772 c0_g2		30.05
TR65058 c0_g3		14.15
TR65289 c1_g8		5.11
TR65289 c1_g9		17.00
TR65290 c4_g3		15.64
TR65309 c2_g1		12.31
TR65588 c1_g2	Alpha-L-arabinofuranosidase C-terminus : Protein of unknown function (DUF1574)	7.40
TR65766 c2_g9		99.81
TR66292 c2_g2	tify domain : Divergent CCT motif	4.93
TR66330 c1_g1		11.83
TR66528 c1_g1		8.09
TR66795 c2_g1		10.97
TR66804 c0_g1		5.73
TR66814 c0_g2		6.60
TR66913 c2_g1		47.10
TR67082 c0_g1		9.98
TR67610 c0_g4		8.76
TR67781 c0_g1		232.00
TR67946 c2_g3		15.26
TR68264 c1_g1		7.29
TR68436 c2_g5		9.42
TR68804 c3_g1		10.76
TR68804 c4_g2		31.98
TR68853 c3_g5		4.64
TR68899 c0_g1		6.57
TR68923 c0_g2		5.86
TR69104 c2_g2	zinc-binding in reverse transcriptase : Reverse transcriptase-like : Histidine carboxylase PI chain	9.45
TR69122 c0_g1		15.86
TR69469 c0_g1		8.39
TR69469 c0_g2		7.32
TR69519 c1_g1		12.89
TR69702 c1_g2		4.55
TR69702 c2_g3		8.31
TR69733 c2_g2	DDE superfamily endonuclease : Plant transposon protein	6.51
TR69753 c1_g1		3.87

TR69753 c1_g2		8.60
TR69768 c0_g2	Indole-3-glycerol phosphate synthase	4.37
TR69943 c3_g2		123.04
	Myb/SANT-like DNA-binding domain : Plant transposon protein : DDE	
TR70024 c2_g2	superfamily endonuclease	76.81
TR70069 c0_g1		7.97
TR70426 c2_g1		29.11
TR70468 c0_g1		8.32
TR70621 c0_g2		61.71
	Reverse transcriptase (RNA-dependent DNA polymerase) : Integrase core	
TR70739 c1_g1	domain	59.24
TR70853 c1_g1		12.74
TR70867 c0_g1	Protein kinase domain : Protein tyrosine kinase : Kinase-like	4.34
TR70944 c0_g3		9.59
TR71065 c1_g1		9.43
TR71074 c1_g2		6.67
TR71117 c1_g3		7.09
TR71138 c4_g1		11.87
TR71371 c0_g7		4.27
TR71663 c0_g4		64.80
TR71815 c1_g6		19.31
TR71950 c0_g1		50.08
TR72166 c0_g1		46.90
TR72334 c4_g7		12.20
TR72549 c0_g3	GATA zinc finger	26.29
	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) : RNA recognition	
TR72795 c1_g1	motif (a.k.a. RRM, RBD, or RNP domain)	5.10
TR72828 c2_g1		66.74
TR72828 c2_g2		56.13
TR72894 c0_g1		21.05
TR72930 c2_g3		11.30
TR72974 c1_g2		5.62
	DAHPh synthetase I family : NUDIX domain : Iron-sulfur binding domain of	
TR73296 c1_g1	endonuclease III	260.70
TR73545 c2_g1		11.02
TR73642 c3_g2		8.88
TR73822 c1_g2		89.25
TR73970 c1_g2		21.59
TR74131 c2_g1		10.96
	Retroviral aspartyl protease : Reverse transcriptase (RNA-dependent DNA	
	polymerase) : Integrase core domain : Retrotransposon gag protein :	
	Chromo (CHRromatin Organisation MODifier) domain : Aspartyl protease :	
TR74436 c4_g1	Zinc knuckle	12.84
TR74457 c2_g1		31.91
TR74457 c3_g2		25.43
TR8613 c0_g3		44.75