

Table S1. Transcripts upregulated in S junglerice plants

Transcript	Pfam description	Fold Change S/R
TR12523 c0_g2		4.51
TR13246 c0_g1	NB-ARC domain : Leucine rich repeat : Leucine Rich repeats (2 copies)	15.39
TR14485 c0_g1		25.47
TR14775 c0_g1		62.11
TR15547 c0_g1		7.86
TR16084 c0_g1		8.45
TR17997 c0_g1	Protein of unknown function (DUF1258)	22.99
TR18497 c0_g1		12.35
TR20362 c0_g1		25.10
TR20629 c0_g3		4.95
TR21382 c5_g5	Response regulator receiver domain	31.13
TR21600 c0_g1	F-box domain : F-box-like	17.59
TR21797 c0_g5	Ankyrin repeats (3 copies) : Ankyrin repeat : Ankyrin repeats (many copies)	4.45
TR22189 c0_g1	Protein of unknown function (DUF1668) : Syntaxin	16.68
TR22604 c1_g4		23.53
TR22887 c2_g3	non-haem dioxygenase in morphine synthesis N-terminal : 2OG-Fe(II) oxygenase superfamily	6.48
TR22987 c0_g1	Ribonuclease T2 family	4.16
TR23126 c0_g4		16.47
TR23429 c3_g1		14.31
TR23467 c1_g3		7.60
TR23569 c0_g1	Leucine rich repeat : Leucine Rich repeats (2 copies) : Leucine rich repeat N-terminal domain : Protein kinase domain : Protein tyrosine kinase	271.73
TR23741 c1_g5		6.31
TR23977 c0_g2		5.41
TR23996 c1_g5		6.26
TR24204 c3_g5		4.75
TR24278 c1_g6		4.56
TR24620 c1_g4		8.84
TR24647 c2_g2		8.93
TR24895 c0_g1		3.87
TR25472 c1_g5	CRAL/TRIO domain	9.21
TR25488 c0_g4	Endonuclease/Exonuclease/phosphatase family	37.01
TR25694 c1_g3		10.20
TR25970 c2_g3	JmjC domain, hydroxylase	12.81
TR26039 c3_g6		5.70
TR26068 c1_g2		9.98
TR26099 c2_g1		11.30
TR26193 c5_g3	Thioesterase domain : Lipase (class 3) : Alpha/beta hydrolase family	11.32

TR26350 c2_g1	X-domain of DnaJ-containing	22.16
TR26583 c1_g3		28.65
TR26590 c1_g1		11.09
TR26685 c0_g1		26.71
TR26706 c1_g2	RNA polymerase III RPC4	3.51
TR26856 c0_g1		22.52
TR26963 c1_g10	Leucine Rich repeats (2 copies) : Leucine Rich Repeat : Leucine rich repeat	7.27
TR26982 c3_g1		5.31
	Ankyrin repeat : Ankyrin repeats (3 copies) : Ankyrin repeats (many copies)	
TR27357 c2_g2		4.43
TR27391 c0_g2		7.92
TR27471 c3_g2		6.10
TR27506 c2_g1		10.85
TR27743 c0_g2		5.02
TR27921 c1_g1		8.93
TR28075 c1_g2		16.07
TR28085 c0_g3		7.23
TR28134 c1_g2		25.21
TR28240 c0_g1		15.93
	NAD dependent epimerase/dehydratase family : 3-beta hydroxysteroid dehydrogenase/isomerase family : NADH(P)-binding : Male sterility protein : short chain dehydrogenase : KR domain : Polysaccharide biosynthesis protein : NmrA-like family : RmlD substrate binding domain	
TR28305 c1_g2		9.23
TR28465 c0_g3	Terpene synthase family, metal binding domain	6.83
TR28492 c6_g2		15.52
TR28522 c2_g2		4.84
TR28642 c1_g4		23.86
TR28642 c1_g5	Ubiquitin family : Ubiquitin-2 like Rad60 SUMO-like	3.79
TR29061 c2_g2		9.82
TR29144 c4_g1		5.20
TR29271 c0_g1		9.49
TR29392 c0_g5		13.77
TR29824 c1_g2		11.42
TR29974 c1_g1		4.83
TR30111 c0_g2		6.00
TR30123 c1_g3		5.90
TR30142 c3_g3		4.17
	Leucine Rich repeats (2 copies) : Leucine rich repeat : Leucine Rich Repeat : Leucine rich repeat N-terminal domain : Protein kinase domain : Protein tyrosine kinase	
TR30386 c1_g2		18.67
TR30518 c1_g2		1216.91
TR30538 c3_g2		142.81
TR30626 c2_g3	Leucine Rich Repeat	4.15
TR30687 c6_g5		32.93
TR30690 c4_g7		3.53

TR30719 c3_g2		11.75
	Leucine Rich repeats (2 copies) : Leucine rich repeat : Protein kinase domain : Protein tyrosine kinase : Leucine rich repeat N-terminal domain :	
TR347 c0_g1	Phosphotransferase enzyme family	6.96
TR54478 c0_g1	Zinc knuckle	37.67
TR57584 c0_g1		11.83
TR58416 c0_g1		17.31
TR58827 c0_g1		60.48
TR59452 c0_g1		14.19
TR59455 c0_g1		4.23
TR59464 c0_g1		18.09
TR60420 c0_g2	Domain of unknown function (DUF4218)	6.44
TR62832 c0_g1		36.59
TR62968 c0_g1	Alpha/beta hydrolase family	4.26
TR63845 c0_g1		3.64
TR63951 c0_g1	GYF domain	105.79
TR64380 c0_g1		11.51
TR64538 c0_g1		7.07
TR64889 c4_g3		4.57
TR65135 c3_g11		6.47
TR65158 c3_g3		3.74
TR65403 c0_g1		12.15
TR65581 c4_g1		22.92
TR65820 c2_g6	Alpha amylase, catalytic domain	3.63
TR65929 c0_g1		5.37
	Reverse transcriptase (RNA-dependent DNA polymerase) : Integrase core domain : gag-polyprotein of LTR copia-type : GAG-pre-integrase domain : Retrotransposon gag protein : NB-ARC domain : Protein of unknown function (DUF2946)	
TR66340 c2_g2		55.18
TR66489 c0_g1		118.76
TR66509 c4_g1		12.83
TR66516 c2_g10		117.52
	zinc-binding in reverse transcriptase : Reverse transcriptase (RNA-dependent DNA polymerase)	
TR66518 c6_g2		4.78
TR66639 c1_g1		8.51
TR66970 c1_g4		3.90
TR67294 c0_g1	NB-ARC domain : Leucine rich repeat : Leucine Rich repeats (2 copies)	16.97
TR67377 c2_g4	2OG-Fe(II) oxygenase superfamily	19.20
TR67437 c1_g1		4.45
TR67599 c0_g1		8.49
TR67725 c0_g4		6.11
TR67966 c0_g1	Plant transposon protein : DDE superfamily endonuclease	9.45
TR68188 c1_g2		6.26
TR68272 c3_g5	Mo25-like	6.59
TR68598 c3_g1		4.93
TR68651 c0_g3		11.58

TR68681 c1_g1		75.38
TR68939 c0_g3		10.41
TR69164 c0_g1		7.19
	NB-ARC domain : Leucine Rich repeats (2 copies) : Leucine rich repeat :	
TR69374 c1_g4	AAA domain : AAA ATPase domain	3.44
TR69376 c1_g2	hAT family C-terminal dimerisation region	13.80
TR69600 c1_g2		5.56
	Leucine Rich repeats (2 copies) : Leucine rich repeat : Protein kinase	
TR69705 c0_g1	domain : Protein tyrosine kinase	7.51
	Terpene synthase family, metal binding domain : Terpene synthase, N-	
TR69785 c2_g1	terminal domain	4.86
TR69855 c1_g9		18.97
TR69897 c0_g1		3.92
	NB-ARC domain : AAA ATPase domain : AAA domain : Archaeal ATPase :	
	Protein of unknown function (DUF815) : ATPase family associated with	
TR70101 c2_g3	various cellular activities (AAA)	4.86
TR70217 c5_g4		75.28
TR70305 c2_g1		26.27
	Terpene synthase family, metal binding domain : Terpene synthase, N-	
TR70441 c0_g2	terminal domain	5.47
TR70690 c4_g6		4.32
TR70869 c2_g3		3.61
TR71322 c2_g2	MuDR family transposase	11.58
	Leucine rich repeat : Leucine Rich repeats (2 copies) : Leucine Rich Repeat	
	: Leucine rich repeat N-terminal domain : gag-polypeptide of LTR copia-	
TR71925 c1_g5	type : Domain of unknown function (DUF4219) : Zinc knuckle	6.82
TR72109 c0_g1		9.19
TR72167 c2_g4		6.59
TR72367 c2_g4		6.71
TR72419 c1_g1		5.43
TR72440 c3_g4	Acetyltransferase (GNAT) domain	15.56
TR72668 c0_g1		7.47
TR72676 c0_g1		3.29
TR72702 c6_g3		64.67
TR72783 c0_g5		12.39
	zinc-RING finger domain : Zinc finger, C3HC4 type (RING finger) : RING-	
	type zinc-finger : zinc finger of C3HC4-type, RING : Ring finger domain :	
TR72796 c3_g1	RING/Ubox like zinc-binding domain	6.43
TR73129 c1_g1		9.48
TR73157 c0_g1		11.61
TR73718 c5_g3		5.91
TR73752 c1_g3		8.55
TR73752 c2_g3		8.80
TR73839 c1_g3		3.86
TR73992 c4_g6		3.95
TR74320 c2_g4		10.32

TR74364 c3_g1		34.39
TR74369 c2_g1		11.95
TR74390 c1_g1	Leucine rich repeat : Leucine Rich repeats (2 copies)	44.87
TR74390 c2_g1		46.47
	NB-ARC domain : AAA domain : NACHT domain : Archaeal ATPase :	
TR74390 c2_g2	Poxvirus A32 protein : AAA ATPase domain	8.42
TR74484 c1_g1	NAF domain	22.99
TR74499 c2_g1		8.29
TR8613 c0_g1		7.20
