

TABLE S4

Sequence annotation and comparison between orthologous coding sequences in the *O. glaberrima* cv. CG14 BAC OG-BBa0049I08 and *O. sativa* cv. Nipponbare

<i>O. glaberrima</i> Gene Name	Best BLASTN homology	Best BLASTN EST homology	Best BLASTX homology (swiss prot)	Protein domain	Putative Function	Putative <i>O. sativa</i> (Nipponbare) orthologous gene	% of nucleotide identity	% of protein identity	% of similarity	Length (bp)	Ka (dN)	Ks (dS)	Ka/Ks
OG-BBa0049I08.1 ^P	NM_001063292 <i>O. sativa</i> Os06g0141100 (0.0)	CB618108 <i>O. sativa</i> (0.0)	Q94A82 <i>A. thaliana</i> NADH pyrophosphatase NUDT19 (8c-69)	pfam09296, NUDIX-like; cd03429, NADH pyrophosphatase	Putative NADH pyrophosphatase protein	LOC_Os06g04910	99	98.4	98.4	1224	0.0025	0.0000	99
OG-BBa0049I08.2	CT830197 <i>O. sativa</i> flcDNA (0.0)	CT850081 <i>O. sativa</i> (0.0)	O13801 <i>Schizosaccharomyces pombe</i> RNA-binding protein (2c-9)	pfam00641, Zn-finger	Putative Zinc finger protein	LOC_Os06g04920	99.3	99.3	100	438	0.0028	0.0266	0.1063
OG-BBa0049I08.3	AK121184 <i>O. sativa</i> flcDNA (2c-131)	EE592322 <i>O. sativa</i> (5c-169)	Q02921 <i>G. max</i> Early nodulin 93 (2c-11)	pfam03386, Early nodulin 93 ENOD93 protein	Putative ENOD93 protein	LOC_Os06g04930	61.3	60.9	62.2	/	/	/	/
OG-BBa0049I08.4	AC136219 <i>O. sativa</i> BAC (0.0)	CT843513 <i>O. sativa</i> (1c-92)	P73714 <i>Synechocystis</i> Zinc metalloprotease (1c-9)	cd06163 zinc metalloproteases	Hypothetical protein	no orthologous gene	/	/	/	/	/	/	/
OG-BBa0049I08.45*	/	/	/	/	Hypothetical protein	no orthologous gene	/	/	/	/	/	/	/
OG-BBa0049I08.5	AK122162 <i>O. sativa</i> flcDNA (2c-148)	EL586675 <i>O. sativa</i> (2c-162)	Q02921 <i>G. max</i> Early nodulin 93 (8c-20)	pfam03386, Early nodulin 93 ENOD93 protein	Putative ENOD93 protein	LOC_Os06g04940	65	54.1	59.5	/	/	/	/
OG-BBa0049I08.6	AK121791 <i>O. sativa</i> flcDNA (1c-157)	CI240527 <i>O. sativa</i> (1c-158)	Q02921 <i>G. max</i> Early nodulin 93 (4c-14)	pfam03386, Early nodulin 93 ENOD93 protein	Putative ENOD93 protein	LOC_Os06g04950	89.1	76.8	78.4	/	/	/	/
OG-BBa0049I08.7	/	/	/	/	Hypothetical protein	no orthologous gene	/	/	/	/	/	/	/
OG-BBa0049I08.75	/	/	/	/	Hypothetical protein	no orthologous gene	/	/	/	/	/	/	/
OG-BBa0049I08.8	NM_001063299 <i>O. sativa</i> Os06g0142000 (0.0)	CB622551 <i>O. sativa</i> (0.0)	Q9SH88 <i>A. thaliana</i> Ribosome biogenesis regulatory protein (3c-48)	/	Putative protein	LOC_Os06g04970	98.6	97.7	98.4	2073	0.0112	0.0237	0.4728
OG-BBa0049I08.85*	AP002838 <i>O. sativa</i> BAC (2c-156)	CT858525 <i>O. sativa</i> (8c-67)	/	/	Hypothetical protein	no orthologous gene	/	/	/	/	/	/	/
OG-BBa0049I08.9*	AP004090 <i>O. sativa</i> BAC (8c-69)	CT844843 <i>O. sativa</i> (3c-68)	/	/	Hypothetical protein	no orthologous gene	/	/	/	/	/	/	/
OG-BBa0049I08.10*	AC121363 <i>O. sativa</i> BAC (3c-128)	CB649669 <i>O. sativa</i> (1c-57)	P47927 <i>A. thaliana</i> Floral homeotic protein APETALA 2 (4c-8)	/	Hypothetical protein	no orthologous gene	/	/	/	/	/	/	/

OG-BBa0049I08.11	AK073027 <i>O. sativa</i> flcDNA (0.0)	CB658549 <i>O. sativa</i> (0.0)	Q9FJT2 <i>A. thaliana</i> F- box/FBD/LRR-repeat (5e-4)	/	Putative F-box protein	LOC_Os06g04980	98.1	96.5	97.7	1542	0.0173	0.0198	0.8715
OG-BBa0049I08.12	AK122162 <i>O. sativa</i> flcDNA (2e-175)	CI252819 <i>O. sativa</i> (2e-175)	Q02921 <i>G. max</i> Early nodulin 93 (1e-17)	pfam03386, Early nodulin 93 ENOD93 protein	Putative ENOD93 protein	LOC_Os06g04990	99.7	100	100	348	0.0000	0.0142	0.001
OG-BBa0049I08.13	CT837557 <i>O. sativa</i> flcDNA (4e-177)	CT856080 <i>O. sativa</i> (4e-177)	Q02921 <i>G. max</i> Early nodulin 93 (1e-14)	pfam03386, Early nodulin 93 ENOD93 protein	Putative ENOD93 protein	LOC_Os06g05000	100	100	100	348	0.0000	0.0000	99
OG-BBa0049I08.14	CT827995 <i>O. sativa</i> flcDNA (1e-158)	EE592204 <i>O. sativa</i> (5e-176)	Q02921 <i>G. max</i> Early nodulin 93 (1e-17)	pfam03386, Early nodulin 93 ENOD93 protein	Putative ENOD93 protein	LOC_Os06g05010	99.4	100	100	351	0.00002	0.0260	0.001
OG-BBa0049I08.15	CT827995 <i>O. sativa</i> flcDNA (9e-173)	CI050172 <i>O. sativa</i> (1e-176)	Q02921 <i>G. max</i> Early nodulin 93 (1e-17)	pfam03386, Early nodulin 93 ENOD93 protein	Putative ENOD93 protein	LOC_Os06g05020	99.1	98.3	99.1	348	0.0074	0.0143	0.5175
OG-BBa0049I08.16	NM_001063304 <i>O. sativa</i> Os06g0142500 (0.0)	CB617832 <i>O. sativa</i> (0.0)	Q9LMN7 <i>A. thaliana</i> Wall- associated receptor kinase 5 (5e- 130)	cd00180, Serine/Threonine protein kinases	Putative Serine/Threonine protein kinases	LOC_Os06g05050	92	87.8	92.1	2291	0.0447	0.0571	0.7828
OG-BBa0049I08.17	NM_001063305 <i>O. sativa</i> Os06g0142600 (0.0)	CB635675 <i>O. sativa</i> (0.0)	O82804 <i>A. thaliana</i> Protein Early flowering 3 (1e-55)	/	Putative Early flowering protein	LOC_Os06g05060	99.2	98.8	99.1	2283	0.0057	0.0155	0.3669
OG-BBa0049I08.18	AP000399 <i>O. sativa</i> BAC (0.0)	CT860562 <i>O. sativa</i> (0.0)	O23081 <i>A. thaliana</i> Cysteine-rich receptor-like protein kinase 41 (2e- 57)	cd00180, Serine/Threonine protein kinases	Putative Serine/Threonine protein kinases	LOC_Os06g05070	97.6	97.6	98.5	1386	0.0081	0.1700	0.0465
OG-BBa0049I08.19	CT834467 <i>O. sativa</i> flcDNA (0.0)	CT848007 <i>O. sativa</i> (0.0)	P00428 <i>Bos taurus</i> Cytochrome c oxidase subunit 5B, mitochondrial (6e-14)	cd00924, Cytochrome c oxidase subunit Vb	Putative cytochrome oxidase	LOC_Os06g05080	99.8	99.4	99.4	465	0.0032	0.0000	99
OG-BBa0049I08.20	AK103971 <i>O. sativa</i> flcDNA (0.0)	CA998930 <i>O. sativa</i> (0.0)	Q9SNQ2 <i>O. sativa</i> protein arginine N-methyltransferase (0.0)	cd02440, S- adenosylmethionine- dependent methyltransferases	Putative methyltransferase protein	LOC_Os06g05090	98.8	98.4	99	1143	0.0071	0.0299	0.2366
OG-BBa0049I08.21	AK121920 <i>O. sativa</i> flcDNA (0.0)	EC366141 <i>O. sativa</i> (0.0)	Q38854 <i>A. thaliana</i> 1-deoxy-D- xylulose-5-phosphate synthase, chloroplastic (0.0)	cd02007, Thiamine pyrophosphate (TPP) family, DXS subfamily, TPP-binding module	Putative 1-deoxy-D- xylulose-5-phosphate synthase	LOC_Os06g05100	99.9	99.6	99.7	2169	0.0018	0.0000	99
OG-BBa0049I08.22	AK071301 <i>O. sativa</i> flcDNA (0.0)	CB672512 <i>O. sativa</i> (0.0)	P22302 <i>Nicotiana plumbaginifolia</i> Superoxide dismutase chloroplastic (5e-60)	PRK10543, superoxide dismutase; pfam02777, Iron/manganese superoxide dismutases	Putative Superoxide dismutase	LOC_Os06g05110	99.9	99.6	100	768	0.0016	0.0000	99
OG-BBa0049I08.23	AK061597 <i>O. sativa</i> flcDNA (9e-80)	CI020918 <i>O. sativa</i> (9e-80)	/	/	Putative protein	LOC_Os06g05120	/	/	/	/	/	/	/

OG-BBa0049I08.24	AK120946 <i>O. sativa</i> flcDNA (0.0)	CX101001 <i>O. sativa</i> (0.0)	Q9SQJ3 <i>Gossypium hirsutum</i> Myristoyl-acyl carrier protein thioesterase, chloroplastic (6c-146)	cd00586, 4-hydroxybenzoyl- CoA thioesterase (4HBT)	Putative Myristoyl- acyl carrier protein thioesterase	LOC_Os06g05130	97.4	99	99	1284	0.0044	0.0300	0.1457
OG-BBa0049I08.25	AP003487 <i>O. sativa</i> BAC (0.0)	CA083999 <i>Saccharum officinarum</i> (1e-99)	O49287 <i>A. thaliana</i> Putative pentatricopeptide repeat- containing protein (2e-93)	pfam01535, PPR repeat	Putative PPR protein	LOC_Os06g05140	99.8	99.6	99.6	2292	0.0018	0.0037	0.4789
OG-BBa0049I08.26	AP003487 <i>O. sativa</i> BAC (0.0)	CF326731 <i>O. sativa</i> (0.0)	Q80SY5 <i>M. musculus</i> Pre-mRNA- splicing factor 38B (2e-40)	pfam03371, PRP38 family	Putative protein	LOC_Os06g05150	98	97.2	97.5	1296	0.0070	0.0048	1.471
OG-BBa0049I08.27 ^P	AK067270 <i>O. sativa</i> flcDNA (0.0)	FL869738 <i>Panicum</i> <i>vulgatum</i> (0.0)	Q9LW86 <i>A. thaliana</i> Probable sulfate transporter (1e-141)	pfam00916, Sulfate transporter family	Putative sulfate transporter	LOC_Os06g05160	/	/	/	/	/	/	/

p: Partial gene; *****: Pseudogene; **C:** Nipponbare genes manually corrected. Genes in grey are located in the *S_I* locus.