



Erratum

Early and multiple *Ac* transpositions in rice suitable for efficient insertional mutagenesis

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Table 2 of this article should be as follows:

Table 2. Insertion Tagged Sites with similarity to sequences in public databases.

Plant	ITS ^a	Blast homology	Organism	Accession	Insertion	Identity (bp) / Similarity (aa)
2A-8	8	Genomic clone ^b Genomic clone	O. sativa O. sativa	AQ325528 AQ796410	- -	46/51 bp [90%] 304/319 bp [95%]
2A-9	8	Ferredoxin NADP-reductase ^c Nodulin N21-like protein ^{b,e} Nodulin N21-like protein ^c Hypothetical protein ^c Genomic clone ^b	O. sativa O. sativa O. sativa O. sativa O. sativa	BAA85425 BAA85439 ^e BAA85440 BAA85435 AQ325528	ORF 5 th intron ORF ORF -	13/13 aa [100%] 46/46 bp [100%] 51/57 aa [89%] 25/25 aa [100%] 46/51 bp [90%]
2A-10	4	Genomic clone ^b Genomic clone Genomic clone	O. sativa O. sativa O. sativa	AQ325528 AQ861699 AP002883	- - -	46/51 bp [90%] 217/220 bp [98%] 128/139 bp [92%]
2A-11	7	EST / Nodulin N21-like protein ^{c,e} EST / Putative harpin-induced protein ^f EST Genomic clone ^b Genomic clone ^c Genomic clone	O. sativa / A. thaliana O. sativa / A. thaliana O. sativa O. sativa O. sativa O. sativa	AU078645 / BAA85424 ^e BF430546 / AAD21461 ^f AU69979 AQ325528 AP000616 AP002069	3' UTR 5' UTR - - - -	112/112 bp [99%] 186/187 bp [99%] 42/43 bp [97%] 46/51 bp [90%] 166/181 bp [91%] 356/373 bp [95%]
5-1	6	RPR1 / EST Genomic clone / Hypothetical protein ^g	O. sativa O. sativa	BAA75812 / AW070066 AP002537 / BAB16867 ^g	ORF 5' UTR	33/44 aa [74%] 245/270 bp [94%]
5-7	3	Unknown protein / Genomic clone S-adenosyl-L-methionine:salicylic methyltransferase	A. thaliana / O. sativa A. thaliana	AAC77868 / AQ074191 BAB08594	ORF ORF	66/97 aa [67%] 71/90 aa [78%]
5-11	3	Genomic clone / Ribosome apurinic lyase ^h	O. sativa / T. aestivum	AQ691029 / BAA87875 ^h	3' UTR	268/280 bp [95%]
5-12	3	EF-hand cont. protein / EST EST	A. thaliana / O. sativa O. sativa	BAB02809 / C98851 C99498	ORF -	122/140 aa [88%] 171/176 bp [97%]
7-1	6	Cyt-5 DNA methyltransferase (MET1) / EST EST / Ribosomal protein ^{d,i} Hypothetical protein Genomic clone	Z. mays / T. aestivum O. sativa / A. thaliana O. sativa O. sativa	AAG15406 / BE400695 AU031084 / AAB71459 ⁱ BAA81761 AP002901	ORF 3' UTR ORF -	42/42 aa [100%] 62/63 bp [98%] 47/59 aa [78%] 34/36 bp [94%]
7-2	4	EST / Ribosomal protein ^{d,i} Genomic clone / Hypothetical protein ^l Genomic clone / Hypothetical protein ^m	O. sativa / A. thaliana O. sativa / A. thaliana O. sativa	AU031084 / AAB71459 ⁱ AQ688452 / AAD32789 ⁱ AP002843 / BAB17166 ^m	3' UTR ORF ORF	62/63 bp [98%] 59/59 bp [100%] 52/52 bp [100%]
7-3	6	Hypothetical protein / Genomic clone	O. sativa	BAB17166 / AP002843	ORF	14/16 aa [87%] - 65 / 68 bp [95%]
7-5	4	Genomic clone	O. sativa	AZ046446	-	229/266 bp [86%]

^a Number of different ITSs.

^{b,d} Same Ac insertion.

^c Ac insertions located on the same PAC clone P0514G12 on chromosome 6 (accession AP000616).

^{e,g,m} Homology derived from AP000616 (chr. 6), AP002537 (chr. 1), AP002843 (chr. 1) respectively.

^f Homology derived from BlastX of BF430546 (79/161 aa - 48%).

^h Homology derived from BlastX of AQ691029 (67/109 aa - 60%).

ⁱ Homology derived from BlastX of AU031084 (32/33 aa - 96%).

^l Homology derived from BlastX of AQ688452 (40/76 aa - 52%).