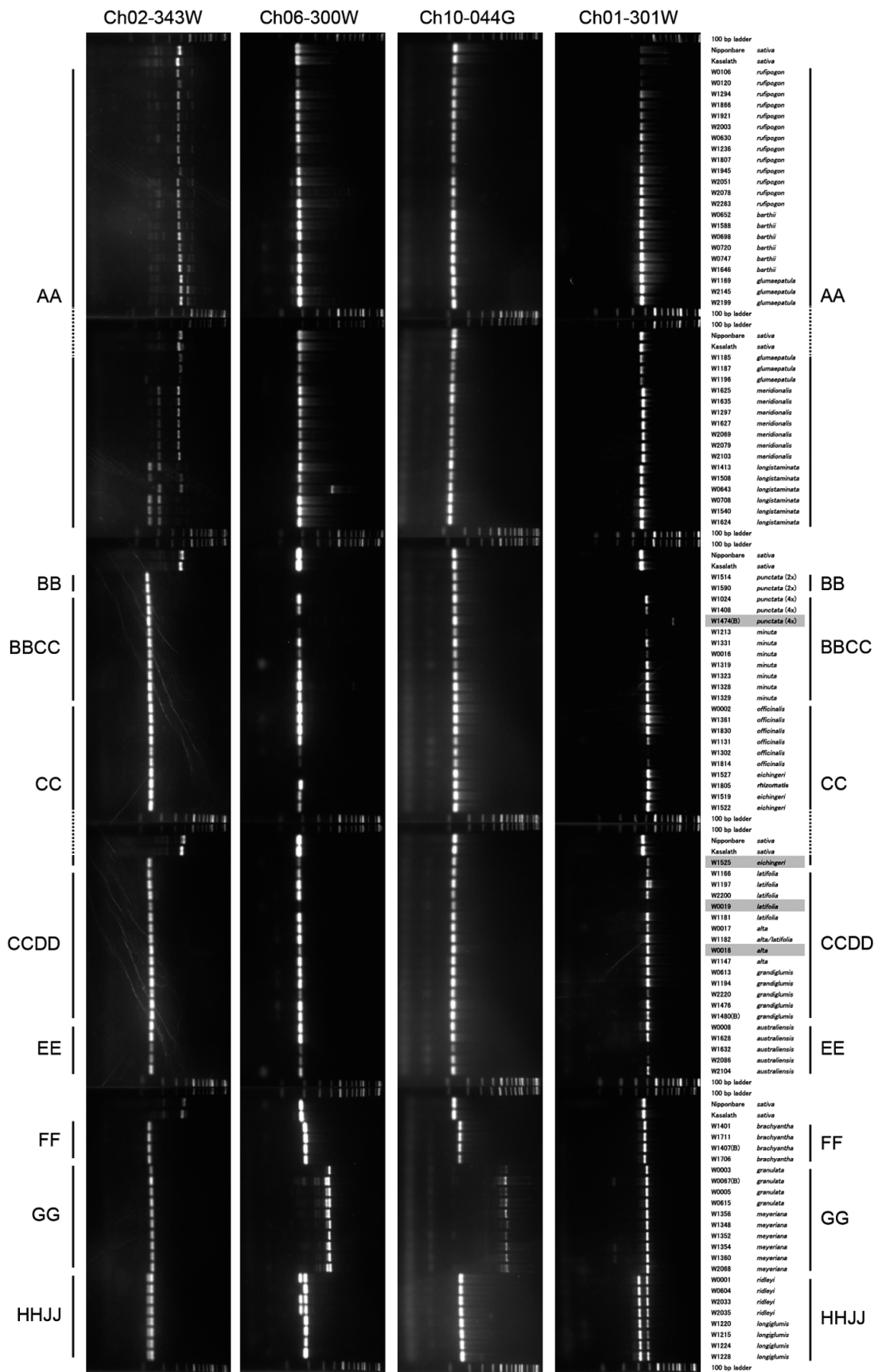
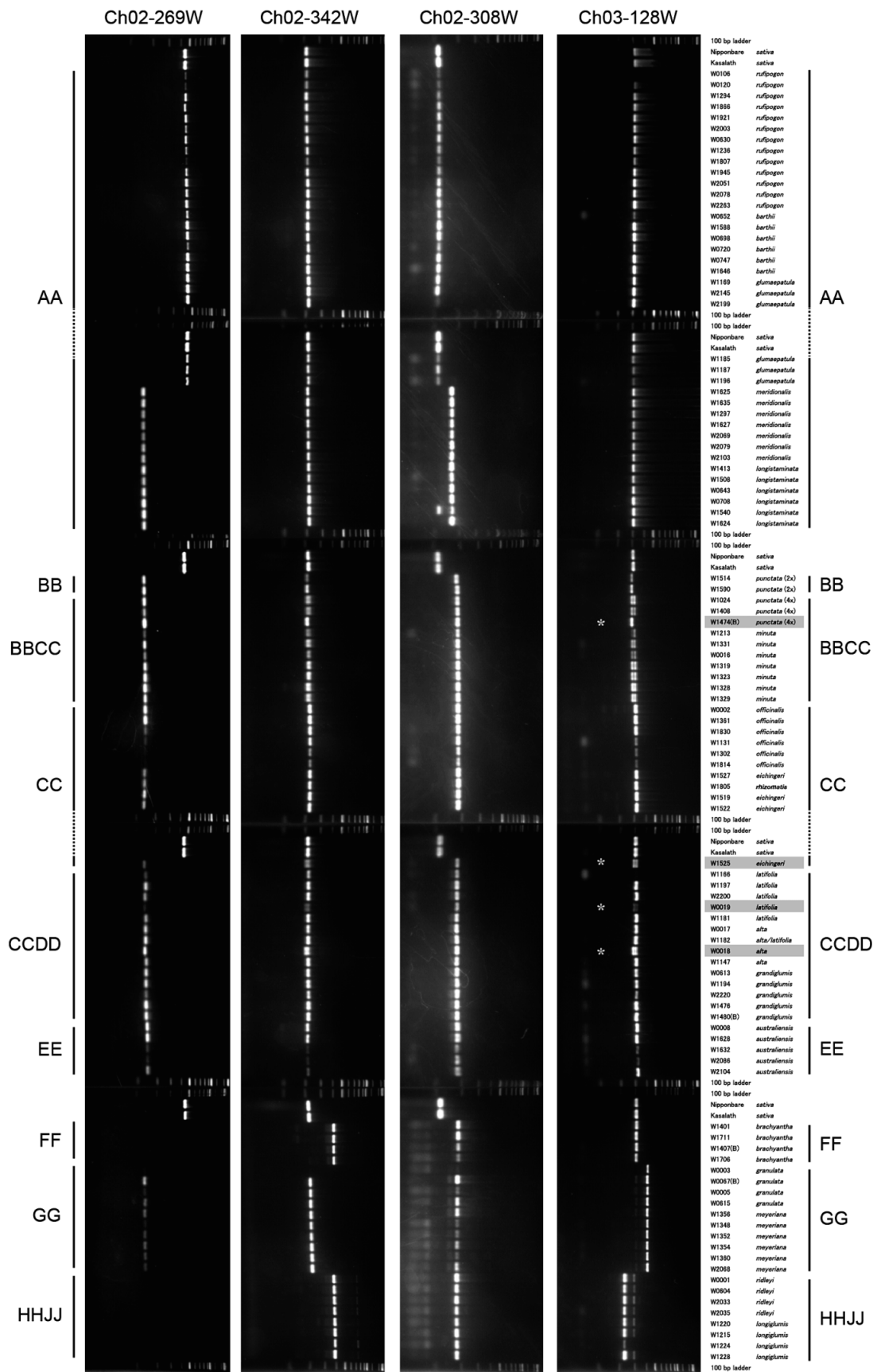


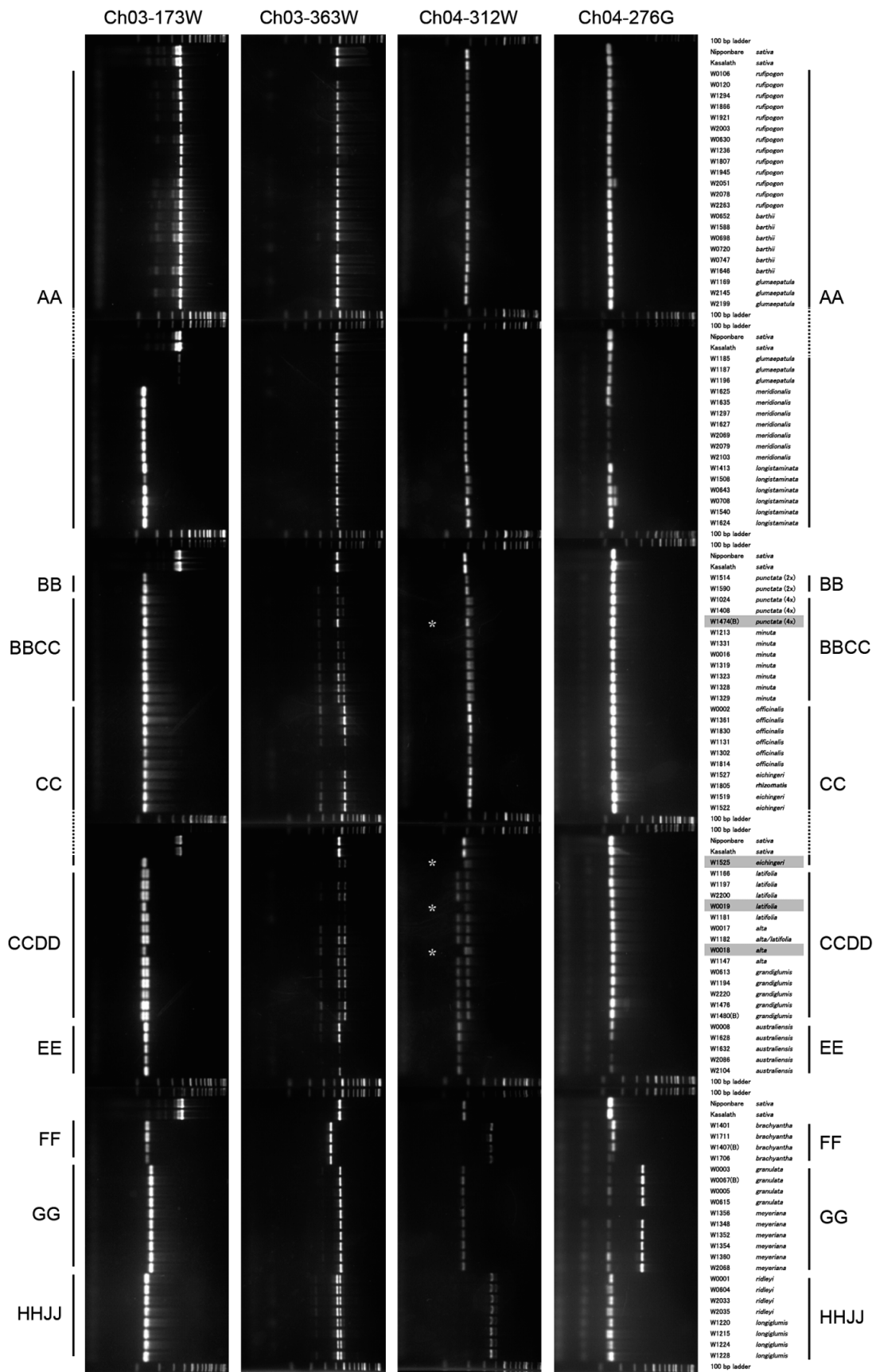
**Supplemental Fig. 1-1.** The agarose gel electrophoresis of PCR products using INDEL primers Ch06-306W, Ch07-233W, Ch05-109G and Ch05-070W. The shaded accessions indicate that the unexpected PCR products (marked with the asterisks on the image) are amplified when using several INDEL markers.



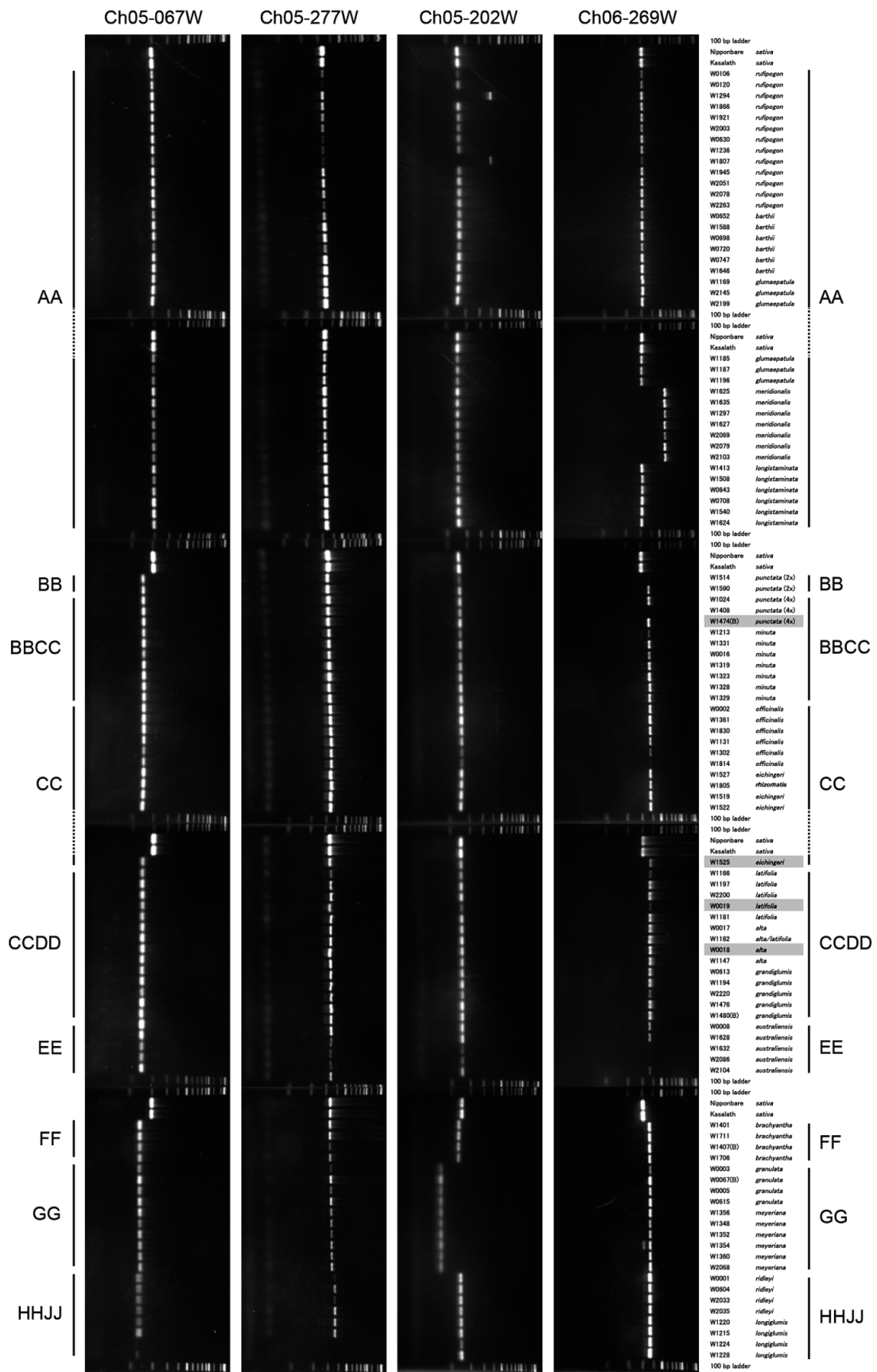
**Supplemental Fig. 1-2.** The agarose gel electrophoresis of PCR products using INDEL primers Ch02-343W, Ch06-300W, Ch10-044G and Ch01-301W.



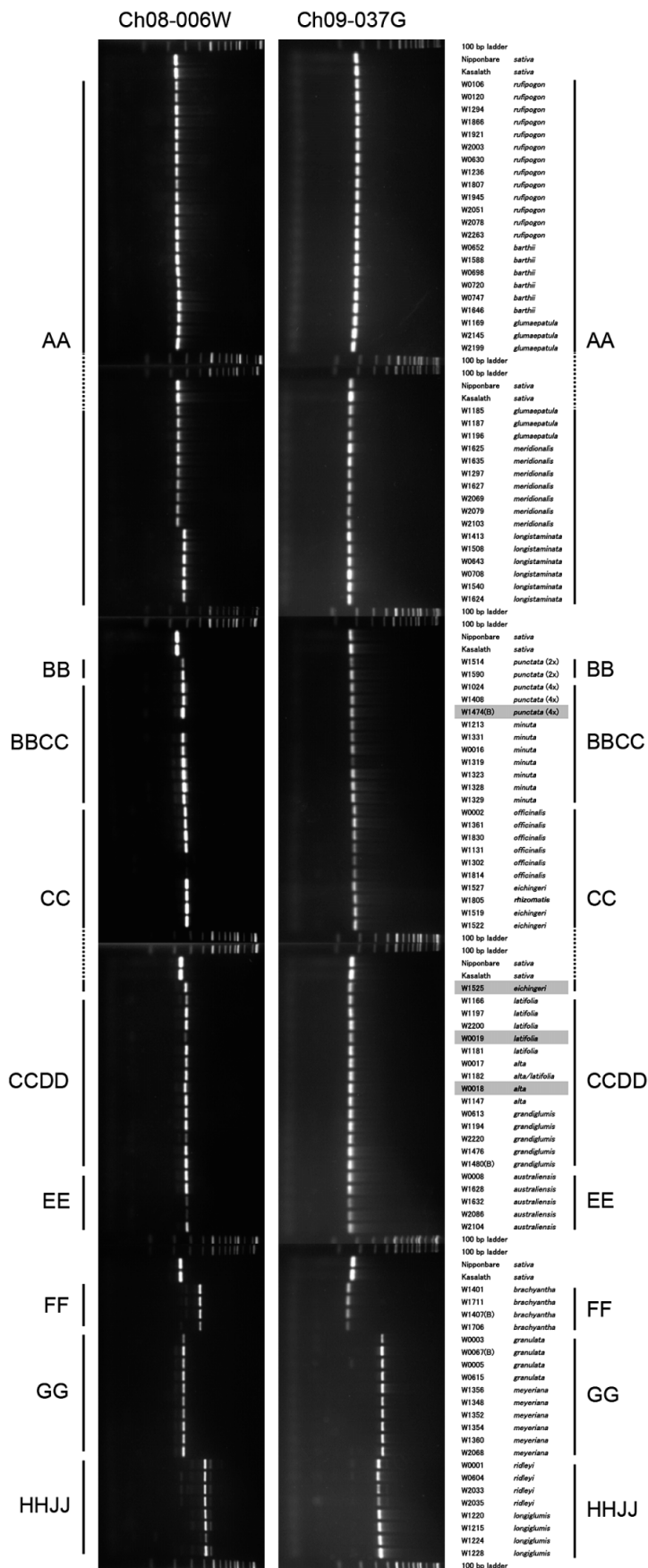
**Supplemental Fig. 1-3.** The agarose gel electrophoresis of PCR products using INDEL primers Ch02-269W, Ch02-342W, Ch02-308W and Ch03-128W.



**Supplemental Fig. 1-4.** The agarose gel electrophoresis of PCR products using INDEL primers Ch03-173W, Ch03-363W, Ch04-312W and Ch04-276G.



**Supplemental Fig. 1-5.** The agarose gel electrophoresis of PCR products using INDEL primers Ch05-067W, Ch05-277W, Ch05-202W and Ch06-269W.



Supplemental Fig. 1-6. The agarose gel electrophoresis of PCR products using INDEL primers Ch08-006W and Ch09-037G.

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W1413 AGGCAAAGTTT CAGAATGCAATACAGGATTTCTCTATTGGCATTGAGGTAATATACTT-----CTTGTAGTGCC-----CATGTTGGCCTTCTGTATACAG----- 90
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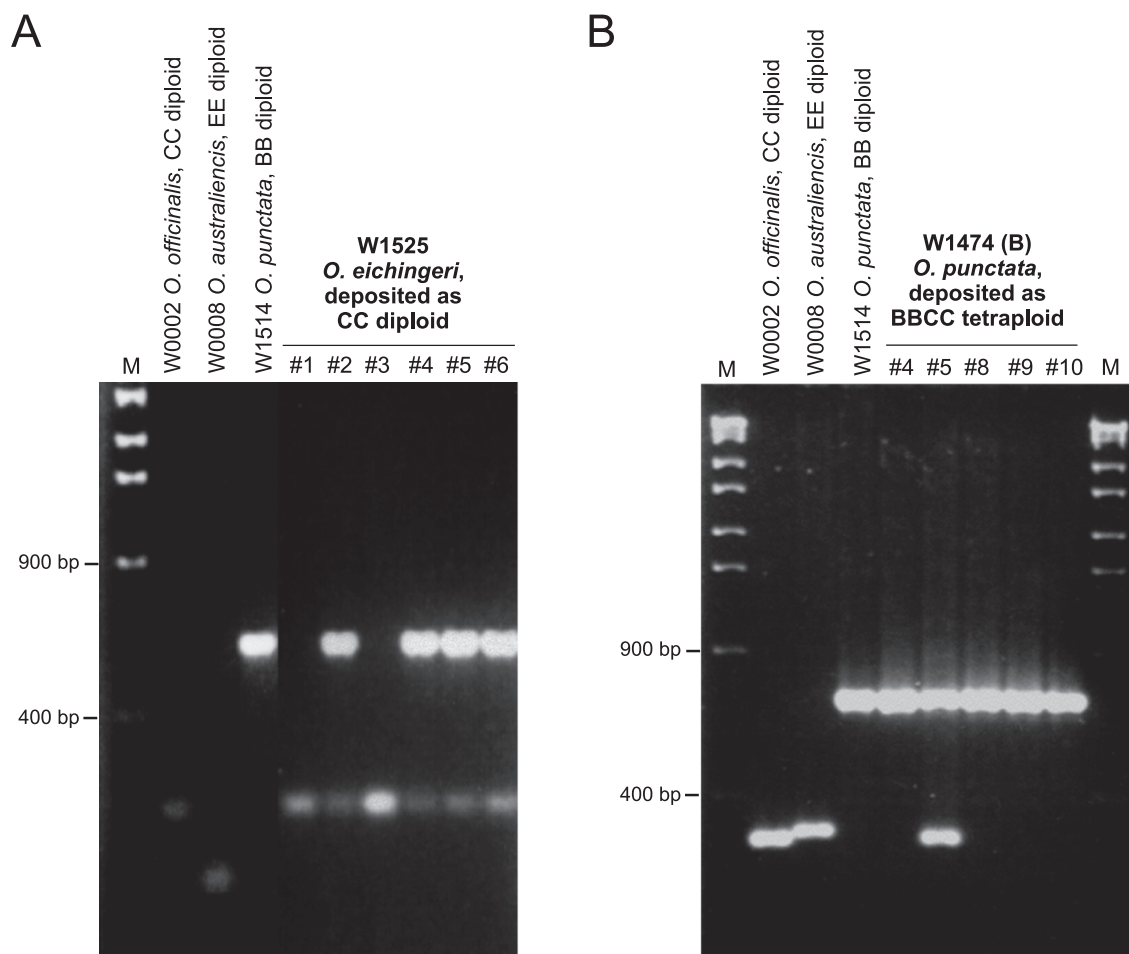
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W0002 -----
W1024_a -----
W1213_a -----
W1527 -----
W1024_b -----
W1213_b -----
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W0613_b -----
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W0001 -----
W1220 -----
W1401 -----
W0003 -----
W1356 -----

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* ** *

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**Supplemental Fig. 2.** The DNA sequence alignment of PCR products from the syntenic locus using the INDEL marker Ch03-173W. The large deletions are found in the fragments from *meridionalis* (W1625), *longistaminata* (W1413) and non-AA genome type species. The both terminal sequences enclosed with open squares are forward and reverse primers of Ch03-173W, respectively. In the accession numbers, the “a” and “b” suffixed to the same accession indicate that they are experimental replications.



Sample plant No.	Median of fluorescent intensity		Normalized (a/b)
	Sample (a)	Haploid (b)	
W1525 #1	25.96	9.89	2.6
W1525 #2	50.37	10.02	5.0
W1525 #3	27.78	10.35	2.7
W1525 #4	43.01	8.80	4.9
W1525 #5	37.28	7.91	4.7
W1525 #6	42.29	8.68	4.9

Sample plant No.	Median of fluorescent intensity		Normalized (a/b)
	Sample (a)	Haploid (b)	
W1474(B) #4	26.51	10.22	2.6
W1474(B) #5	46.00	9.96	4.6
W1474(B) #8	28.06	11.64	2.4
W1474(B) #9	25.54	10.62	2.4
W1474(B) #10	29.26	11.40	2.6

**Supplemental Fig. 3.** The wild *Oryza* accessions which segregated two different ploidies. In each panel, the top photo indicates the polymorphic INDEL pattern on the 3% agarose-gel electrophoresis. M; DNA size marker ( $\lambda$  DNA/*StyI*). The left three lanes are the standard diploid accessions; W0002 is *O. officinalis*, CC; W0008 is *O. australiensis*, EE; W1514 is *O. punctata*, BB. It is supposed that DD genome is originated from EE genome (Ge *et al.* 1999), and so *O. australiensis* is used as a standard for evaluation of DD genome bands. The bottom table indicates the results of flow-cytometric analysis for nuclear DNA contents. The median of fluorescent intensity from the nuclei of each plant (a) was normalized with that of the haploid plant (b). (A) W0002, the accession deposited as CC diploid species, *O. eichingeri*. Two of 6 plants were confirmed to be the CC diploid, while 4 plants were the tetraploid, probably the BBCC type. (B) W1474, the accession deposited as BBCC tetraploid species, *O. punctata*. One of 5 plants were confirmed to be the BBCC tetraploid, while 4 plants were the BB diploid.