

a) *dndB*

1 99
 55989¹ CGTAAAGCGATTGAAGACGCTTTAGAAGCTCGCCCGAGCTGGGGCAGGATAAACATACCIGTGCTGTTITTTGTTCGATGAAGGATTAACCGCAGCCAA
 PPN8b-EC2²
 EC1003-8³
 EC1004-8⁴
 SE11⁵ A T
 EC062/10⁶ T T T G G G
 EC075/10⁷ T C T C G T C G T G
 B7A⁸ T C T C G T C G T G
 100 198
 55989 CAGATGTTIGCGGATCTGAATAAATAIGCIATTCGCCAGICCGTCGTGGCATCGITGTAIGATCATCGGGAIGCCAGTTCAAATITGGCGGTTAT
 PPN8b-EC2
 EC1003-8
 EC1004-8
 SE11 T C A C
 EC062/10 C T A C C T AC C C T C T CC
 EC075/10 C C C A C G C A C C T G C
 B7A C C C A C G C A C C T G C
 207
 55989 CTGGCAATG
 PPN8b-EC2
 EC1003-8
 EC1004-8
 SE11
 EC062/10
 EC075/10
 B7A

b) *dndC*

1 99
 55989 CCCCCGAAATGCGCAACAAGATGTTTTGTAGTGTATCCGATACGCTGGTGGAAACACCAGTGGTAGTAGATIT AATTAAGAAAACGATGTTGCAA
 PPN8b-EC2
 EC1003-8
 EC1004-8
 SE11 G A C A G
 EC062/10 T GT T G A G A G G C C C G
 EC075/10 G A G G G C G A C G C G G
 B7A G A G G G C G A C G C G G
 100 198
 55989 TIGAGGCAGGCGCAAAGCGTAATGGCCTGCCGATCACTCAACATGCGGTAACGCCIAAAACIAATGAAACCTCTGGGTCAATTTACTGGGAAAGGTT
 PPN8b-EC2
 EC1003-8
 EC1004-8
 SE11 A
 EC062/10 C A C T A T A T G C T T G T C
 EC075/10 G A G C T C C G G G G G G G
 B7A G A G C T C C G G G G G G
 199 297
 55989 ATCCGGCCCCAACCCGCGAGTTTCGCTGGTGTACCGAACGCGATGAAAATCAAICCGGTGAGIGACTTTATTAAAGAAAGGTACGCCAGTTIGATGAAG
 PPN8b-EC2
 EC1003-8
 EC1004-8
 SE11 T G T C A
 EC062/10 T T T G T C T C T A C
 EC075/10 T T T C T C T G C T T
 B7A T T T C T C T G C T
 298 396
 55989 TAATTGTTGTCTAGGTTACCGTAGIAGIGAGAGTGCCTTCGTCGCGCAGGTATCGCAAACACAAAATTGATGGCTACCGCTTGGCCCGGCATACCA
 PPN8b-EC2
 EC1003-8
 EC1004-8
 SE11 G C C C
 EC062/10 G G GT G A G C C C A T T G A G T AC T T
 EC075/10 C C C A T G C A T G G G A C T
 B7A C C A T G C A T G G A A C T
 397 495
 55989 CACTGGCAAATGCGTTIATCTATACCCCIATTGATACCTGGGATGTAGAAGACGTCTGGAAACTGCTGCGCGGCCGCTTCCGCTATGCICCTGAAIATA
 PPN8b-EC2
 EC1003-8
 EC1004-8
 SE11 G
 EC062/10 C G C T G C G C T GT A A G
 EC075/10 G A C C C T G G G G C G
 B7A G A C C C T G G G G C G
 520
 55989 TCGACGAATGGGAAAGCCCGTGGGG
 PPN8b-EC2
 EC1003-8
 EC1004-8
 SE11
 EC062/10 T T
 EC075/10 G
 B7A G

c) *dndD*

1 99
55989 TGTGTCCGTCAGGTGCAAAAACIGCATGATGCGGCCCGCAGTCAGCATGGCTTITAGTAGCGCCTTCAAAAATGCCGAGAAACAATIAATITACTCGAT
PPN8b-EC2T.....
EC1003-8T.....
EC1004-8T.....
SE11T.....A.G..GCA...CATCA...T.C.A...T.G.C...A.T.....C...CC.G.....
EC062/10T.....
EC075/10T.....A.T.....GC...C.C.T.TTA...CA.T.A...C.T.G.T.G...T.....G.A.....
B7AT.....A.T.....GC...C.C.T.TTA...CA.T.A...C.T.G.T.G...T.....G.A.....
100 198
55989 CCGGTATAGCGAGCTAITAACTCAGGCGAGAGTAAAGACGCTATCTGCTAACTTGAAGTTGCCTATCGCAAACCTGGCTCGIAAAGAAGATATGCAACTG
PPN8b-EC2
EC1003-8
EC1004-8
SE11 TAC..C...T...C.T..G...C...G..A.AAT...G...A...C.A...G..T.A..G..T
EC062/10
EC075/10C..C...T...C...TC.G...A...G.GA.A...C.GC...T.C.T.GT...C...G..T.A...T
B7AC..C...T...C...TC.G...A...G.GA.A...C.GC...T.C.T.GT...C...G..T.A...T
199 297
55989 AGTGCTCATATIAACCCAGAGACATTTGACGTTAGGITAATIGATGAGAAGGGAICTGTCAATTAATCGTAAGTITACTATCTGCCGGTAAAAGCAGATT
PPN8b-EC2
EC1003-8
EC1004-8
SE11 .A..G...A.T..GC...T...AC.GG.G...A...T.G..G...C.G.T...G...
EC062/10T...G...C...A...
EC075/10G...C...TC.A..G...T...A...T.C.A.A...C...T...T...A...
B7AG...C...TC.A..G...T...A...T.C.A.A...C...T...T...A...
298 396
55989 TATGCCATTGCTATTCTTGAGGCGCTAGCAAAAACITCTGGTCGTGATTGGCCGGTATTAATGATACGCCATTAGGACGCTCTGGAITCACAACATCGG
PPN8b-EC2
EC1003-8
EC1004-8
SE11G...C...G...C...G...C...G...G...T...G...
EC062/10G...
EC075/10A...G...C...C...A..A...C...A...G..T...C..T...A...
B7AA...G...C...C...A..A...C...A...G..T...C..T...A...
397 495
55989 GATAAACTAATTAACCAITAITTCCCATIIGCCAGGCATCAAGTGGTCTAITGTCTIACCAGTACGGAAGTGGAIGAACGTTATTTIGTIGACCAAITA
PPN8b-EC2
EC1003-8
EC1004-8
SE11T.G...T...GGAA...G..T...GC.A..C...T...C..G...C..C..T...C.G
EC062/10T...
EC075/10T.G...T..C..C...TGAA...T...G..T...T.GC.T...T...A...T..G..G
B7AT.G...T..C..C...TGAA...T...G..T...T.GC.T...T...A...T..G..G
496 551
55989 CGIGATGATATITCTCATGCTTACGAGATAGTATTTAACACGCATACTAAATCATC
PPN8b-EC2
EC1003-8
EC1004-8
SE11T...T..G...TG...
EC062/10C...
EC075/10C...T...T..G...TG.A...G...
B7AC...T...T..G...TG.A...G...

d) *dndE*

1 99
55989 TCGGTGGAGAGTGGATTTCGCTATTCAICAGAACGGGATAATCGGAACTAGATGGTTCGCTGGTGTGGATAAAGATTACGTGGCTGGGGAGACAITA
PPN8b-EC2
EC1003-8
EC1004-8
SE11GC.T..G...G.AA..G..G...C...A..C...A...T...A...C.G
EC062/10C.G...G...A...
EC075/10C.T...A...G.AA..G..G...A...C...A...C...
B7AC.T...A...G.AA..G..G...A...C...A...C...
100 194
55989 CAGACTACGGAATGGTAITGAAGATGCTTTATCCGCAGITAGCTCAGAAGGATATGGTTAAAGCATGGGCGCCATGTGGAGGATGGGATTCG
PPN8b-EC2T...A..C...
EC1003-8T...A..C...
EC1004-8T...A..C...
SE11 ..AG...A...C...G..A...TA.TC.C.AC..A..ATTG..AA...A..A...T...A..C...
EC062/10C...T...A..C...
EC075/10AG...A...GC...A..A...AG..A...CGT..A...G...T...T...A..C...
B7AAG...A...GC...A..A...AG..A...CGT..A...G...T...T...A..C...

Figure S1: Multiple-sequence alignment of *dnd* genes using Clustal W.