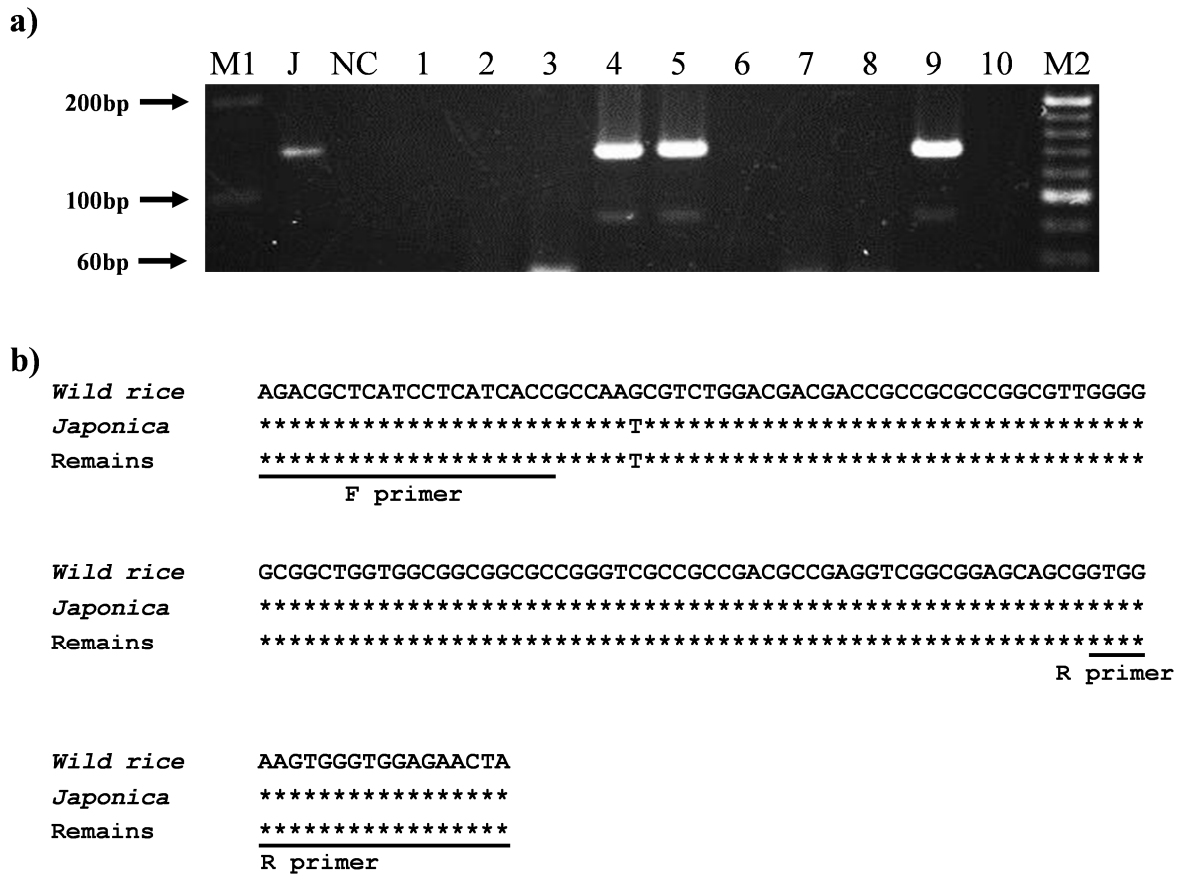
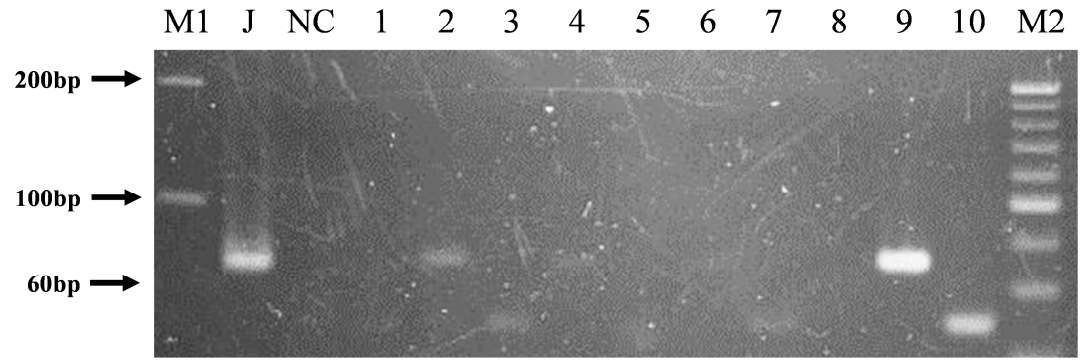


Figure S1: PCR amplification for the nuclear genome region *Sh4;* and the sequence analysis. **(a)** Electrophoresis of 10 PCR products amplified with specific primer sets, F2 and R2 primers. M1: 100bp DNA Ladder (TaKaRa, Japan), M2: 20bp DNA Ladder (TaKaRa, Japan), J: Modern *japonica* cv. 'Nipponbare', NC: negative control (dH_2O), 1-10: represent remains from Ban Non Wat V200 7:∑3 Δ2 Samples 11-20. **(b)** Sequence detected in wild rice, *japonica* and archaeological remains from Ban Non Wat V200 7:∑3 Δ2. *Wild rice*: Modern *O. rufipogon* (EU999926); *Japonica*: Modern *japonica* cv. 'Nipponbare' (NC_008397); Remains: from Ban Non Wat V200 7:∑3 Δ2 represent 14, 15 and 19. "*" shows identical nucleotide sequencing to *Wild rice.*

a)



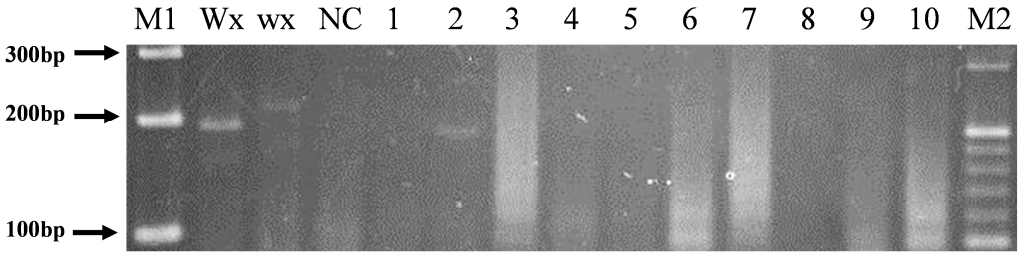
b)

```
Wild rice     ATGGTATTGATGTATACTGGACATTGCATGATACACGTACCACCAAATGCTAAGGATCTT
Japonica      ************************T*********************************
Remains       ************************G*********************************
                      F primer                                R primer

Wild rice     TGGACGAGATG
Japonica      ***********
Remains       ***********
                R primer
```

Figure S2: PCR amplification for the nuclear genome region *qSh1;* and the sequence analysis. **(a)** Electrophoresis of 10 PCR products amplified with specific primer sets, F and R primers. M1: 100bp DNA Ladder (TaKaRa, Japan), M2: 20bp DNA Ladder (TaKaRa, Japan), J: Modern *japonica* cv. 'Nipponbare', NC: negative control (dH_2O), 1-10: represent remains from Noen U-Loke #105 Samples 1-10. **(b)** Sequence detected in wild rice, *japonica* and archaeological remains from Noen U-Loke #105. *Wild rice*: Modern *O. rufipogon* (EU999846); *Japonica*: Modern *japonica* cv. 'Nipponbare' (NC_008394); Remains: from Noen U-Loke #105 represent 2 and 9. "*" shows identical nucleotide sequencing to *Wild rice.*

a)



b)

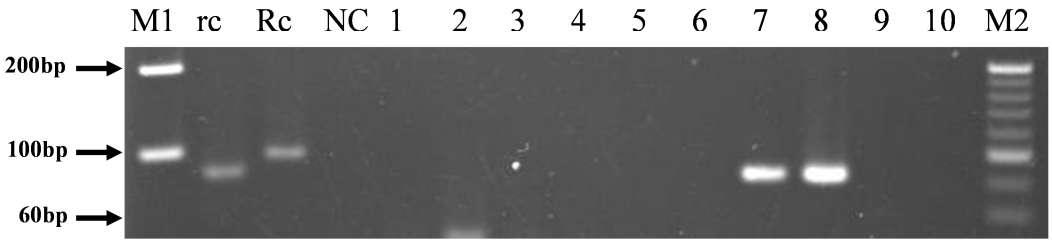
```
Non-glutinous rice    TGCAGAGATCTTCCACAGCAACAGCTAGACAACCACCATG ~(70 bp)~ CGTCGCTGCT
Glutinous rice        **************************************** ~(70 bp)~ **********
Remain                **************************************** ~(70 bp)~ **********
                           23F primer

Non-glutinous rice    CCGCCACGGGTTCCAGGGCCTCAAGCCC----------------------CGCAGCCCC
Glutinous rice        ***************************ACGGGTTCCAGGGCCTCAAGCCC*********
Remain                ***************************----------------------*********

Non-glutinous rice    GCAGCCCCGCCGGCGGCGACGCGACGTCGCTCAGCGTGACGACCAGC
Glutinous rice        *********************************************
Remain                *********************************************
                                                  23R primer
```

Figure S3: PCR amplification for the nuclear genome region *Waxy;* and the sequence analysis. **(a)** Electrophoresis of 10 PCR products amplified with specific primer sets, F and R primers. M1: 100bp DNA Ladder (TaKaRa, Japan), M2: 20bp DNA Ladder (TaKaRa, Japan), *Wx*: Modern *japonica* cv. 'Nipponbare'*, wx:* Modern *japonica* glutinous cv. accession no. DQ280635, NC: negative control (dH_2O), 1-10: represent remains from Ban Non Wat K500 4:2 GEN Δ Samples 1-10. **(b)** Sequence detected in non-glutinous rice, glutinous rice and archaeological remains from Ban Non Wat K500 4:2 GEN Δ. *Non-glutinous rice*: Modern *japonica* cv. 'Nipponbare' (NC_008399); *Glutinous rice*: accession no. DQ280635; Remains: from Ban Non Wat K500 4:2 GEN Δ represent 12. "-" in the sequence symbolises a gap introduced to optimise alignment, whereas "*" shows identical nucleotide sequencing to *non-glutinous rice.*

a)



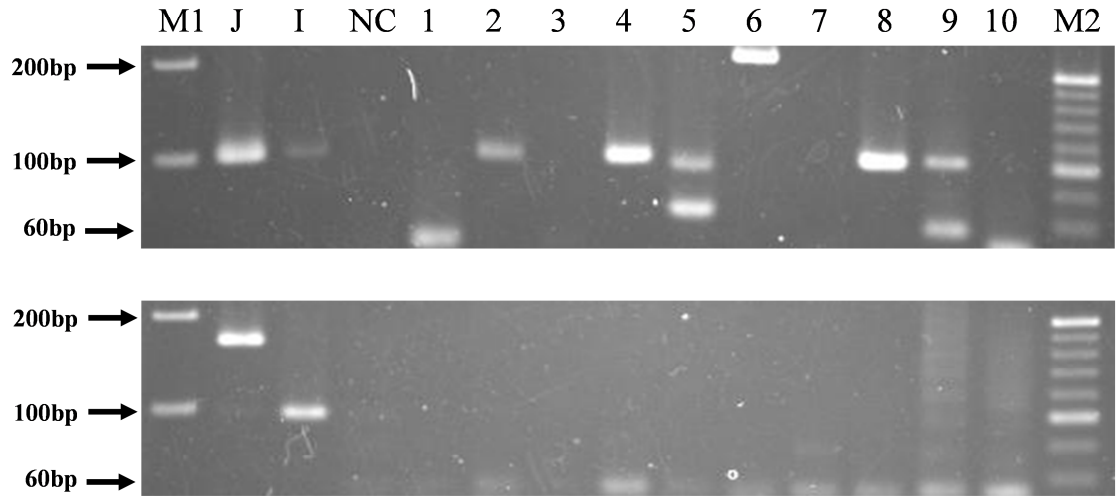
b)

```
White pericarp      CACCTGAATCAAGGGGCGGGAAAGGCGCAAGTGGA--------------TGCCATCCAAG
Red pericarp        **********************************ACGCGAAAAGTCGG***********
Remain              ************************************************************
                          F primer

White pericarp      GTGATTTCAGTGCCAACCATGTGCTGAAAGAGA
Red pericarp        *********************************
Remain              *********************************
                                      R primer
```

Figure S4: PCR amplification for exon 7 in the *Rc* gene*;* and the sequence analysis. **(a)** Electrophoresis of 10 PCR products amplified with specific primer sets, F and R primers. M1: 100bp DNA Ladder (TaKaRa, Japan), M2: 20bp DNA Ladder (TaKaRa, Japan), *rc*: Modern *japonica* cv. 'Nipponbare'*, Rc:* Modern *indica* cv. 'AC417', NC: negative control (dH_2O), 1-10: represent remains from Ban Non Wat K500 4:2 GEN Δ Samples 1-10. **(b)** Sequence detected in rice with a white and red pericarp, and archaeological remains from Ban Non Wat K500 4:2 GEN Δ. *White pericarp*: Modern *japonica* cv. 'Nipponbare' (NC_008400); *Red pericarp*: Modern *indica* cv. 'Kasalath' (AB247503); Remains: from Ban Non Wat K500 4:2 GEN Δ represent 7 and 8. "-" in the sequence symbolises a gap introduced to optimise alignment, whereas "*" shows identical nucleotide sequencing to *White pericarp.*

a)



b)

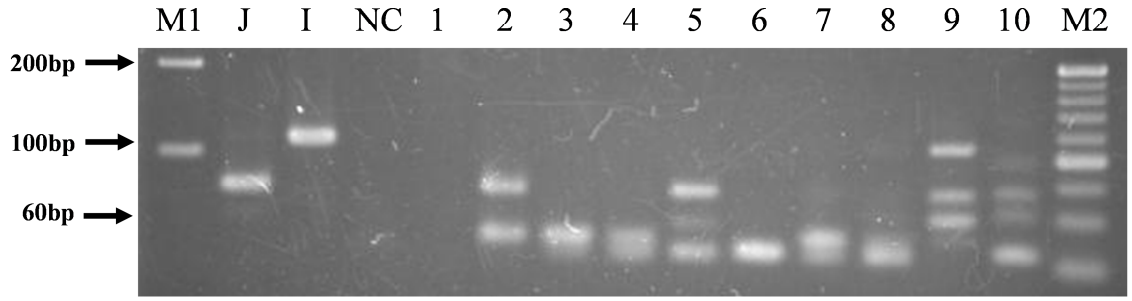
```
Indica          TGGATTTCGAAAGTCAATTTTTCTTTTCAATATCTTTACTTTTTTTCA------------
Japonica        **********************************************GAATCCTATTTT
Remains         **********************************************GAATCCTATTTT
                      F1 primer

Indica          ------------------------------------------------------------TTT
Japonica        TGTTCTTATACCCATGCAATAGAGAGCGAGTGGGAAAAGGGAGGTTACTTTTTTTCA***
Remains         TGTTCTTATACCCATGCAATAGAGAGCGAGTGGGAAAAGG
                                        R1 primer

Indica          TTCCCTTAAAAAATAGGCTTTCTTGGAAATAGGAATCATGGA
Japonica        ******************************************
                                          R2 primer
```

Figure S5: Examples of PCR amplification for the chloroplast genome region *Orf100* and the sequence analysis. **(a)** Electrophoresis of 10 PCR products amplified with F and R1 primer set (upper image) and F and R2 primer set (lower). M1: 100bp DNA Ladder (TaKaRa, Japan), M2: 20bp DNA Ladder (TaKaRa, Japan), J: Modern *japonica* cv. 'Nipponbare', I: Modern *indica* cv. 'IR36', NC: negative control (dH_2O), 1-10: represent remains from Noen U-Loke #105 Samples 1-10. **(b)** Sequence detected in *indica, japonica* and archaeological remains from Noen U-Loke. *Indica*: Modern *indica* (NC_008155); *Japonica*: Modern *japonica* cv. 'Nipponbare' (NC_001320); Remains: from Noen U-Loke represent samples 2,4,5,8 and 9. "-" in the sequence symbolises a gap introduced to optimise alignment, whereas "*" shows identical sequencing to *indica.*

a)



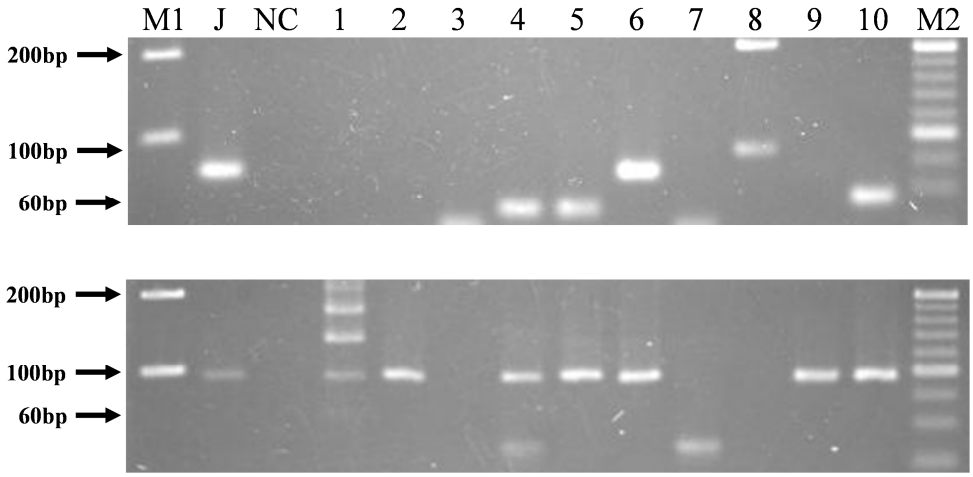
b)

```
Indica      ATCAGTTCAAAGAATTTACTCTTAACAAATTCTTAGAGTATTTCTGGTAGAATTTAACAA
Japonica    **************************************************------
Remains     **************************************************------
                  F2 primer

Indica      ATTCTTAGAGTATTTCTGGTAGAATTGGGGAGCATTAAGTATAAATA
Japonica    -------------------------**********************
Remains     -------------------------**********************
                                          R2 primer
```

Figure S6: Examples of PCR amplification for the chloroplast genome region *PetN-TrnC* and the sequence analysis, indicating presence of deletion characteristic of *japonica* rice in archaeological specimens. **(a)** Electrophoresis of 10 PCR products amplified with specific primer set, F and R primers. M1: 100bp DNA Ladder (TaKaRa, Japan), M2: 20bp DNA Ladder (TaKaRa, Japan), J: Modern *japonica* cv. 'Nipponbare', I: Modern *indica* cv. 'IR36', NC: negative control (dH_2O), 1-10: represent remains from Noen U-Loke #105 Samples 1-10. **(b)** Sequence detected in *indica, japonica* and archaeological remains from Noen U-Loke. *Indica*: Modern *indica* (NC_008155); *Japonica*: Modern *japonica* cv. 'Nipponbare' (NC_001320); Remains: from Noen U-Loke represent 2,5,9 and 10. "-" in the sequence symbolises a gap introduced to optimise alignment, whereas "*" shows identical sequencing to *indica.*

a)



b)

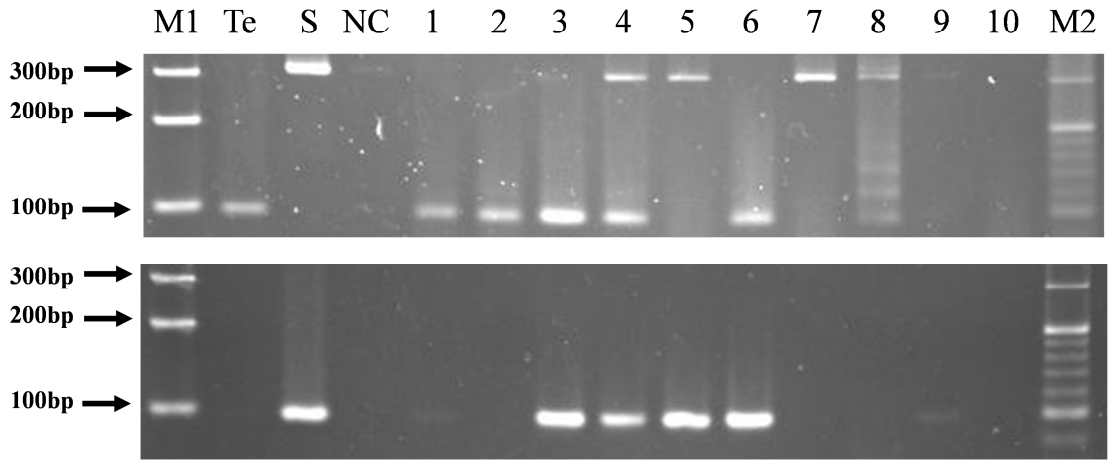
```
Indica      GGCGGAGTATCCGAAACTGTAGCTAGAGTAGCTATTTCCATAGCTGCCAGCAAAATGCCC
Japonica    **************************CG*******************************
Remains     **************************CG*******************************
                    F primer                                R primer

Indica      ATACGAAGTCAATTTCTTCGGTTAGAAATATAACCCCCCCCAAAAAAAAGTAGTATTGAA
Japonica    ****************************************--********-***********
Remains     ****************************************--********-***********
                          2F primer
            R primer

Indica      AATAAAAACCAGGTTCTTCTTTCTGGAAAGACAATATTTCTTTC
Japonica    *******************************************
Remains     *******************************************
                                      2R primer
```

Figure S7: Examples of PCR amplification for the chloroplast genome region *Rp114-Rp116* and *Rp116* (the PS-ID region)*;* and the sequence analysis. **(a)** Electrophoresis of 10 PCR products amplified with *Rp116* specific primer set (upper) and *Rp114-Rp116* specific primer sets (lower). M1: 100bp DNA Ladder (TaKaRa, Japan), M2: 20bp DNA Ladder (TaKaRa, Japan), J: Modern *japonica* cv. 'Nipponbare', NC: negative control (dH_2O), 1-10: represent remains from Ban Non Wat K500 4:2 GEN Samples 1-10. **(b)** Sequence detected in *indica, japonica* and archaeological remains from Ban Non Wat K500 4:2 GEN. *Indica*: Modern *indica* (NC_008155); *Japonica*: Modern *japonica* cv. 'Nipponbare' (NC_001320); Remains: from Ban Non Wat K500 4:2 GEN represent 1,2,4,5,6,9 and 10. "-" in the sequence symbolises a gap introduced to optimise alignment, whereas "*" shows identical nucleotide sequence to *indica.*

a)



b)

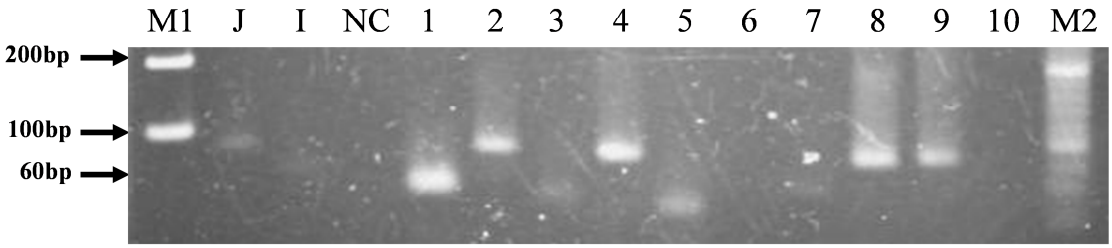
```
Temperate       TGACCGGTTCTGTAGCAGTGGACAAGTCAG ~(30 bp)~ CTC-----------------
Tropical        ************************G****** ~(26 bp)~ ***CGTAGGAACCTTCCCTC
Indica          ************************G****** ~(26 bp)~ ***CGTAGGAACCTTCCCTC
Remain Te       ***************************** ~(30 bp)~ ***-----------------
Remain S        ************************G****** ~(26 bp)~ ***CGTAGGAACCTTCCCTC
                      F primer

Temperate       ------------------------------- ~(160 bp)~ ------------TATAT
Tropical        CCGGCACGGAAAACGGAAAATCACATTAGCAT ~(160 bp)~ AAGAACGCAGCC*****
Indica          CCGGCACGGAAAACGGAAAATCACATTAGCAT ~(160 bp)~ AAGAACGCAGCC*****
Remain Te       ------------------------------- ~(160 bp)~ ------------*****
Remain S        CCGGCACGGAAAACGGAAAATCACATTAGCAT ~(160 bp)~ AAGAACGCAGCC*****
                      R2 primer

Temperate       AGCTTTGGCAATGAGAAAACATTAAACTGG
Tropical        *A***********A***************
Indica          *A***********A***************
Remain Te       **************R***************
Remain S        *A***********R***************
                          R1 primer
```

Figure S8: Polymorphism in a non-cording region in chromosome 6 (Ch6)*;* and the sequence analysis. **(a)** Electrophoresis of PCR products amplified with specific primer sets, Ch6 F and R1 primers (upper) and Ch6 and R2 primers (lower). M1: 100bp DNA Ladder (TaKaRa, Japan), M2: 20bp DNA Ladder (TaKaRa, Japan), Te: Modern temperate *japonica* cv. 'Nipponbare', S: Modern tropical *japonica* cv. 'AC220', NC: negative control (dH_2O), 1-10: represent remains from Ban Non Wat K500 4:2 GEN Δ Sample 11-20. **(b)** Sequence detected in temperate *japonica*, tropical *japonica* and archaeological remains from Ban Non Wat K500 4:2 GEN Δ. *Temperate*: Modern *japonica* cv. 'Nipponbare' (NC_008399); *Tropical*: Modern *japonica* cv. ''AC220'; *Indica:* Modern *indica* cv. 'IR36'; *Remain Te*: from Ban Non Wat K500 4:2 GEN Δ represent samples 11, 12, 13, 14 and 16; *Remain S*: from Ban Non Wat K500 4:2 GEN Δ represent samples 14, 17, 18 and 19. "-" in the sequence symbolises a gap introduced to optimise alignment, whereas "*" shows identical nucleotide sequencing to *Temperate.*

a)



b)

```
Indica          AATCTTTTAAGCCTAATCGCGTCATGATTTGACA------------------------CG
Japonica        **********************************ATGTGGTGCTACAGTAAACATTTA**
Remains         **********************************ATGTGGTGCTACAGTAAACATTTA**
                       F primer

Indica          AATGACATGTTAATTAGGCTTGATAAA
Japonica        ***************************
Remains         ***************************
                          R primer
```

Figure S9: PCR amplification for the nuclear genome region *Acp1;* and the sequence analysis. **(a)** Electrophoresis of 10 PCR products amplified with specific primer sets, F and R primers. M1: 100bp DNA Ladder (TaKaRa, Japan), M2: 20bp DNA Ladder (TaKaRa, Japan), J: Modern *japonica* cv. 'Nipponbare', I: Modern *indica* cv. 'IR36', NC: negative control (dH_2O), *1-10:* represent remains from Ban Non Wat V200 7:∑4 Δ27 Samples 11-20. **(b)** Sequence detected in *indica*, *japonica* and archaeological remains from Ban Non Wat V200 7:∑4 Δ27. *Indica*: Modern *indica* cv. 'IR36'; *Japonica*: Modern *japonica* cv. 'Nipponbare' (AL731762); Remains: from Ban Non Wat V200 7:∑4 Δ27 represent 12, 14, 18 and 19. "-" in the sequence symbolises a gap introduced to optimise alignment, whereas "*" shows identical nucleotide sequencing to *indica.*