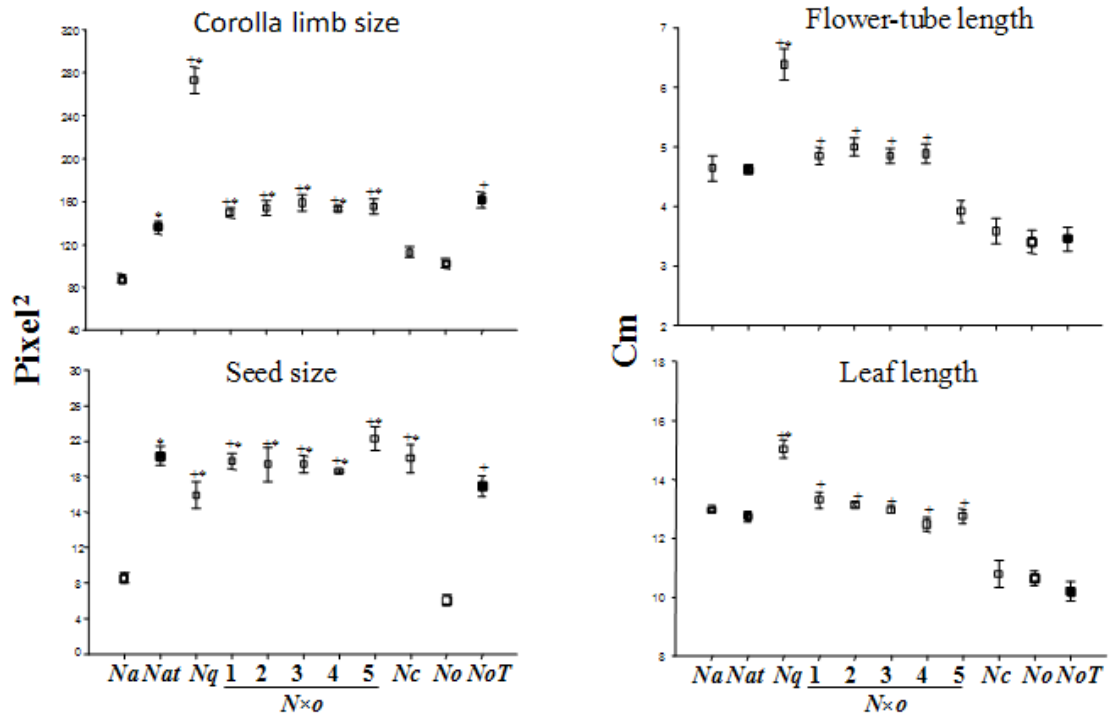


SUPPLEMENTARY DATA

FIG. S1. Corolla limb size, seed size, flower tube and leaf length were measured in *N. attenuata* (*Na*), *N. attenuata* autotetraploid (*NaT*) (F_5), *N. obtusifolia* (*No*), *N. obtusifolia* autotetraploid (*NoT*) (F_4), $N \times$ *obtusifolia* ($N \times o$) (lines 1–5, F_5), *N. clevelandii* (*Nc*) and *N. quadrivalvis* (*Nq*). Digital pictures of corolla limbs and seeds were taken from each studied species, and sizes were measured using the Axio Vision LE software and expressed in Pixel² (1 pixel = 0.26 mm).



*, Significantly different from *Na* ($P < 0.05$); + significantly different from *No* ($P < 0.05$).

FIG. S2. Genome sizes ($n = 10$) measured in seeds of *N. × obtusiata* ($N \times o$) lines 2 (F_2 to F_5) using flow cytometry for single seeds (FCSS).

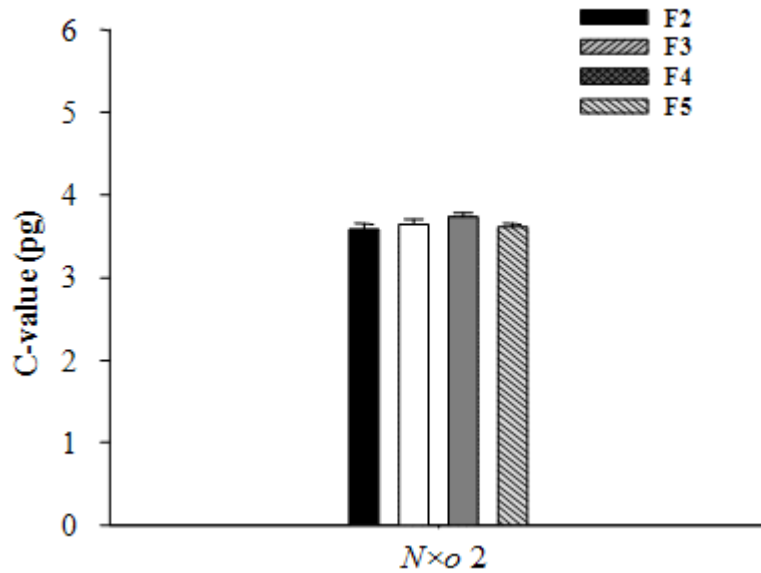
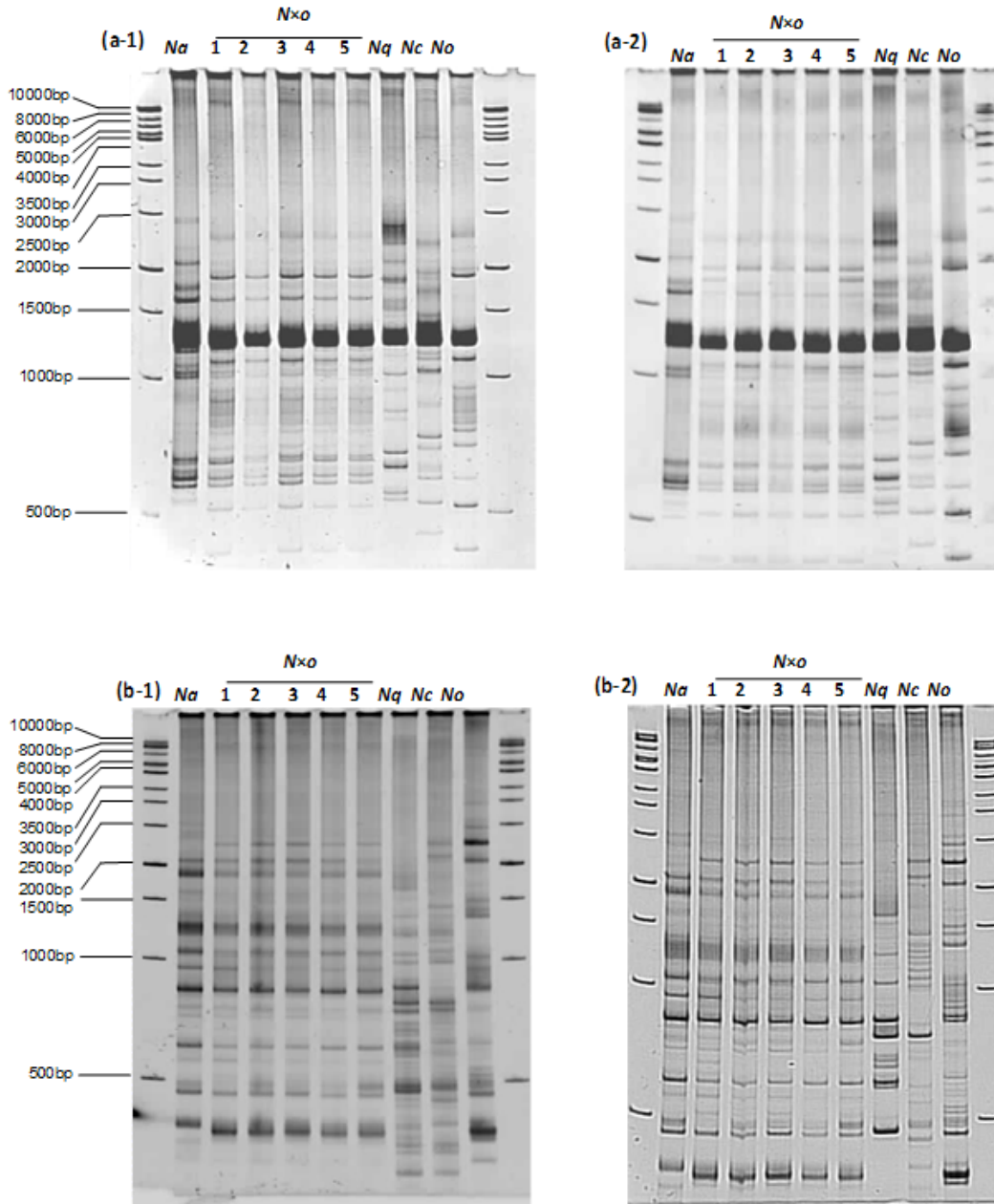
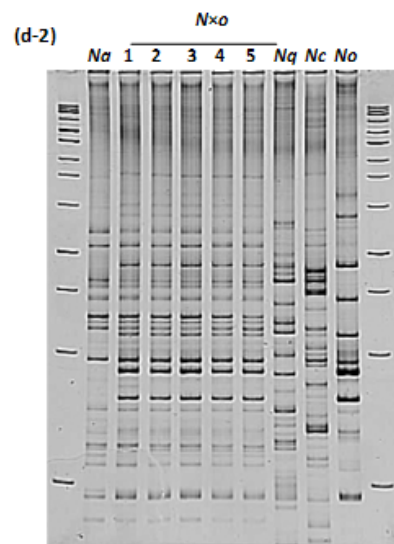
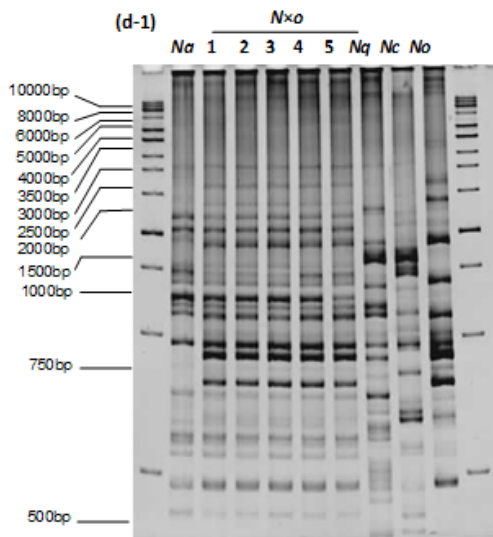
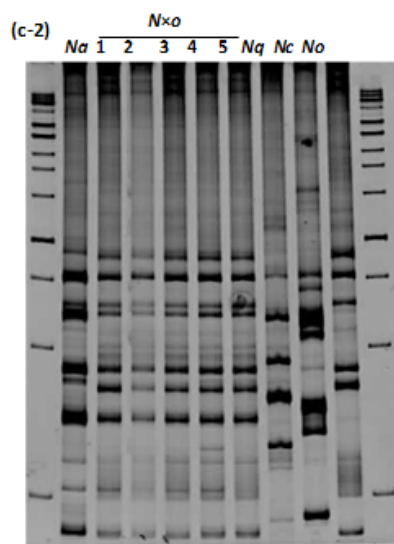
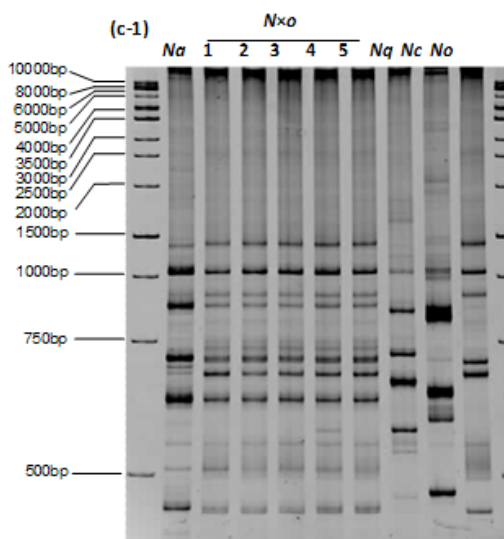
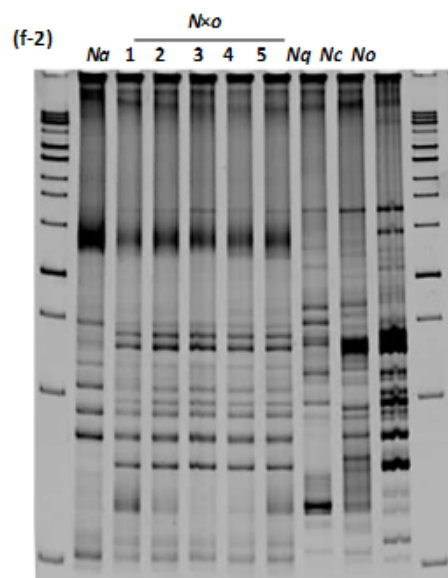
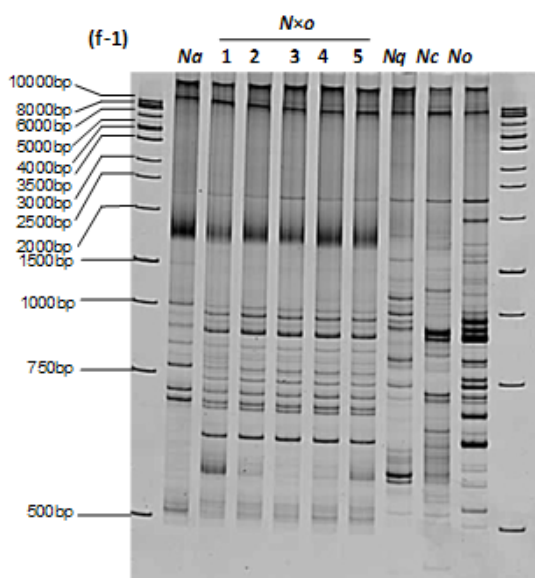
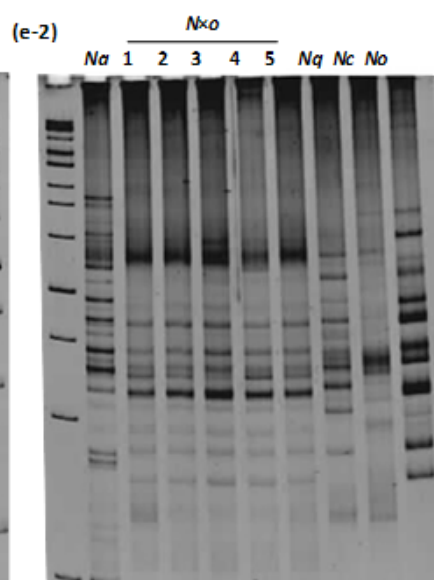
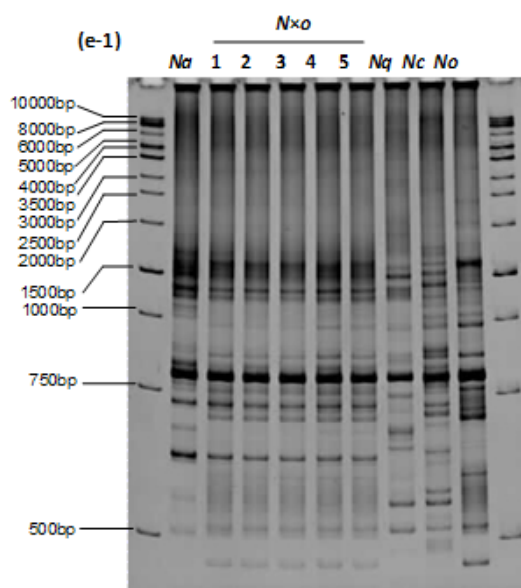


FIG. S3. UP-PCR DNA fingerprinting profiles of *N. attenuata*, *N. × obtusiata* lines 1–5, *N. quadrivalvis*, *N. clevelandii*, *N. attenuata* and *N. obtusifolia*. The figures represent UP-PCR DNA fingerprinting profiles of two biological replicates of the above-cited species using seven universal primers (see Table S1).







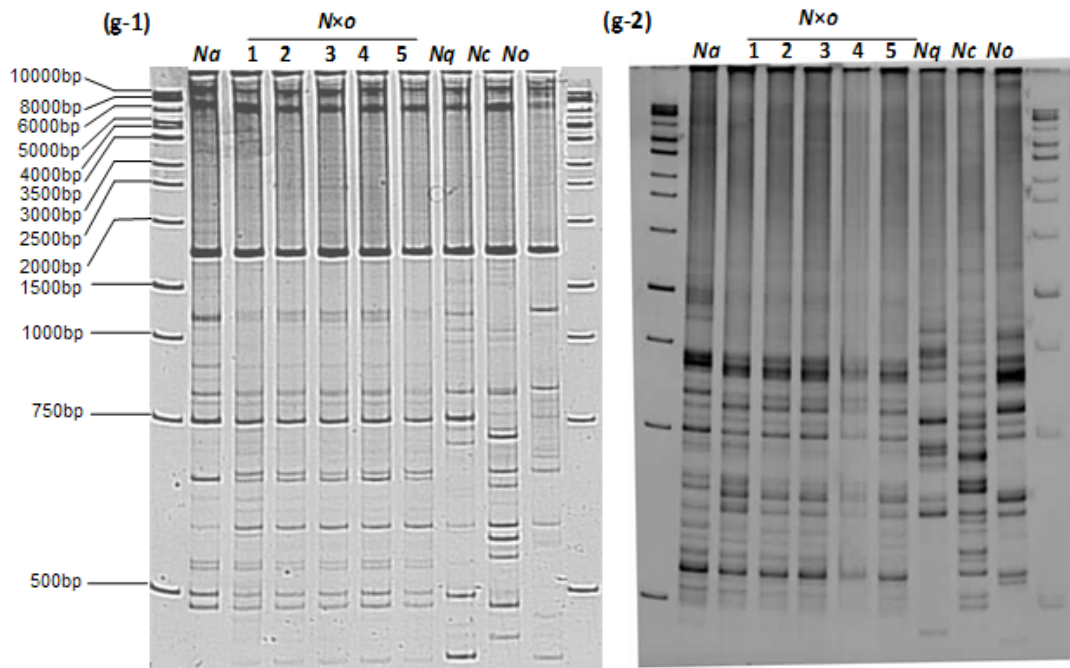


TABLE S1. Sequences of universal primers used in UP-PCR DNA fingerprinting profiles of *N. attenuata*, *N. × obtusiata* lines 1–5, *N. quadrivalvis*, *N. clevelandii*, *N. attenuata* and *N. obtusifolia*

Primer	Sequence
(a) L21	5'-GGA GAG GGT GGC GGT TCT-3'
(b) L2li	5'-GGA TCC GAG GGT GGA TCT -3'
(c) 2M2	5'-CTG CGG ACC CAG ACC CAG AGC GG-3'
(d) AS15	5'-CAT TGC TGG CGA ATC -3'
(e) AS15i	5'-GGC TAA GCG GTC CTT AC-3'
(f) AS4	5'-TGT GGG CGC TCG ACA-3'
(g) M13i	5'-GAG GGT GGT GGA TCT-3'