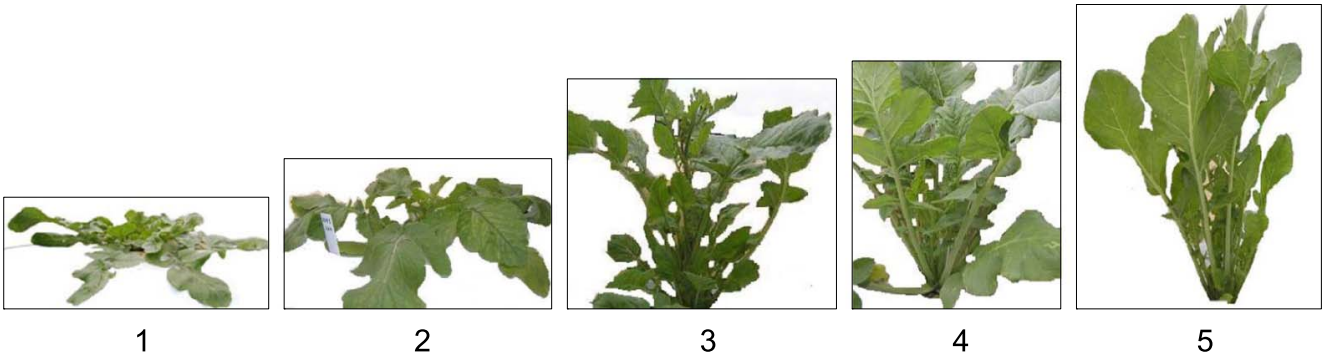
Supplemental Fig. 1. Morphologies of a rat-tailed radish (A) and the 'Harufuku' inbred line Haru-S (B) at harvest (three months after sowing). Only a single individual is shown as a representative for each line. Note that this rat-tailed radish is a commercial cultivar (Chia Tai Co. Ltd., Bangkok, Thailand) because of the severe inbred depression of the parental line Saya-S (see Materials and Methods). Scale bar = 10 cm.



Supplemental Fig. 2. Categories of plant shape (*PS*) in F_5 recombinant inbred lines (RILs). Only representative individuals in RILs are shown, which were classified into one of five categories based on visual inspection (1 = prostrate, 2 = semi-prostrate, 3 = intermediate, 4 = open and 5 = erect).

> RS1CL7063Contig1

GGACAAGTTTATACTTTAAGTGCTCTCTCTCTCTCTACGTACCAAACAAA
TAATCAGTCTAGAGATGGAAGGCAAAACTGTGATTTTAAGTGTGCTCATA
ATGAGTCTTGTCATGGCGCAGAATCAAGTCGAAGGAAAGAGTTGTTGCC
CGGACACCACTGCCAGAAACGCATATAATATATGCCGTCTTACTGGATCC
TCTAGGAAAACTTGTGCAAAAATCAGTGGATGCATCGTTTCTAGGACCGAG
ACATGTCCTCAGGGATATCCATATGACATTCTCGAAAACTCTGGTGATGCTGT
CAATGAATACTGCAAGTTGGGGTGTGCATCCTCTGTGTGTGGTGCCTTAACCA
TTCTCCAGAACTCCGATGCAAGTGAAACTGTGAATGGAGCGGTTGCACAATG
CACCAAGGCATGTTCTAATTTCTGCAGCAAGGACTCGGCTAATGCAGTTGAA
ACTGCTTAAAAAGCATATCCACTATCTATGTGTTGCGTGTGTTGTTGTTCTCCT
CGTTTTCAATAATTATCGTGTATGTGGCAAAATGACTCTTGTGTTATTTCCTGG
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> RS2CL1232Contig1

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GTTAAGAAGAACTAACTATATTTTCATAACTTTTGCTTAAGTAGAACTCACTTA
ACACCCTTATCTTTAATTGGATGCT**AGCCTGGTAAGCATCTCCAA**AAACCTA
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TGTGTCCC

> RS2CL1263Contig1

Supplemental Fig. 3. Nucleotide sequences of markers designed from radish cDNA contig data, which were retrieved from the RadishDatabase (http://radish.plantbiology.msu.edu/index.php/Sequences:All). Forward and reverse primers for each marker are underlined and the predicted amplified regions are indicated with bold-face types.

GGATCAAGCCTCTGGCAAGAAGTCAAAGGGGAACTTGAAAAGAAAGGGCG
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GTTAGGAAGCCAAGCTTCGGACAGATGCTGGCTGATGCAAGTTCTCAGAGTA
ATACTACTGGTGA**GATCCAAGGTTCCATGCCCATG**AAGCCAGTGGCCCCG
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CTAACCGTGAATCCGCTAGGCGGTCCAGATTGCGCAAGCAGGCGGAAT
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> RS2CL2285Contig1
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Supplemental Fig. 3. (continued)

> RS2CL3325Contig1

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TGGGATCACTGATAAACACGCAGTGGTTCAAGGAATGCCACTTGTACAA
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TT

> RS2CL3416Contig1

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ATGTACAAA**TACCAAAGAAGAGACCCTTATG**CCTTAAACACTGGTTCAAT
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Supplemental Fig. 3. (continued)

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GTGCTTGTTCTTCACTCCACTCTGAGCCAGTGAGTACATTGCTCTGTCA
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<u>GATCAAGGGTTCTTAGA</u>TCAGGACAGCCATAAGATAAACTCATGACTCCAT
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> RS2CL6006Contig1
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CCTCTCCATCCTTACAACCCATGCTCAAGGAAGAAAGGTATCACAGTCATATG
AAACATTCGAATA**<u>CACAGCCATCACTTGCAGATCC</u>CACAGCGCCTCCATA**
ACAGACTTCGGTGCTGTCGGAGACGGCAAAACATTGAACACAAAAGCA
TTCCAGAGCGCCGTAGATCATCTCAGCCAATACTCATCCGACGGTGGAG
CTCAGCTCTTGTCCCCGCCGGGAAATGGCTCACCGGAAGTTTCAGCCTC
ACAAGCCATTTCACTCTGTTCCTTCACAAAGACGCTACTCTTCTCGCTG
CTCAAGACTTAGAAGAATACCCAATTCTAAAAGCTTTGCCTTCTTACGGA
AGAGGCCGTGATGCCGCCGGTGGAAGATTCGCTAGTCTTGTCTTCGGG
ACTAATCTCTCCGACGTTATCATAACCGGAAACAATGGTACGATCGATGG
TCAGGGATCGTTTTGGTGGCAGAAGTTTCACGGTGGTAAACTTAAATAC
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GAACATAACGCTCATTGATTCTCCGTCGTGGAATATTC<u>ACCCGGTGTACA</u>
<u>GTAGCAGCAT</u>CATCGTGAAAGGTGTCACGATCATCGCCCCGGTGAAATCTCC
GAACACCGACGGAATCAACCCAGACTCGTGCACGAACACCAGGATCGAAGA
CTGCTACATAATCTCCGGCGACGACTGCGTCGCCGTGAAAAGCGGATGGGAC
GAGTGGTGTTGATCCTAAGCCGTGCGGTTTGCTTGATGGGGGAGGTGATTCC
GAGAAGAAGAAGAGGATGGACAACGGTGGTGGGTGTGAGTTTCCGAGTGAT
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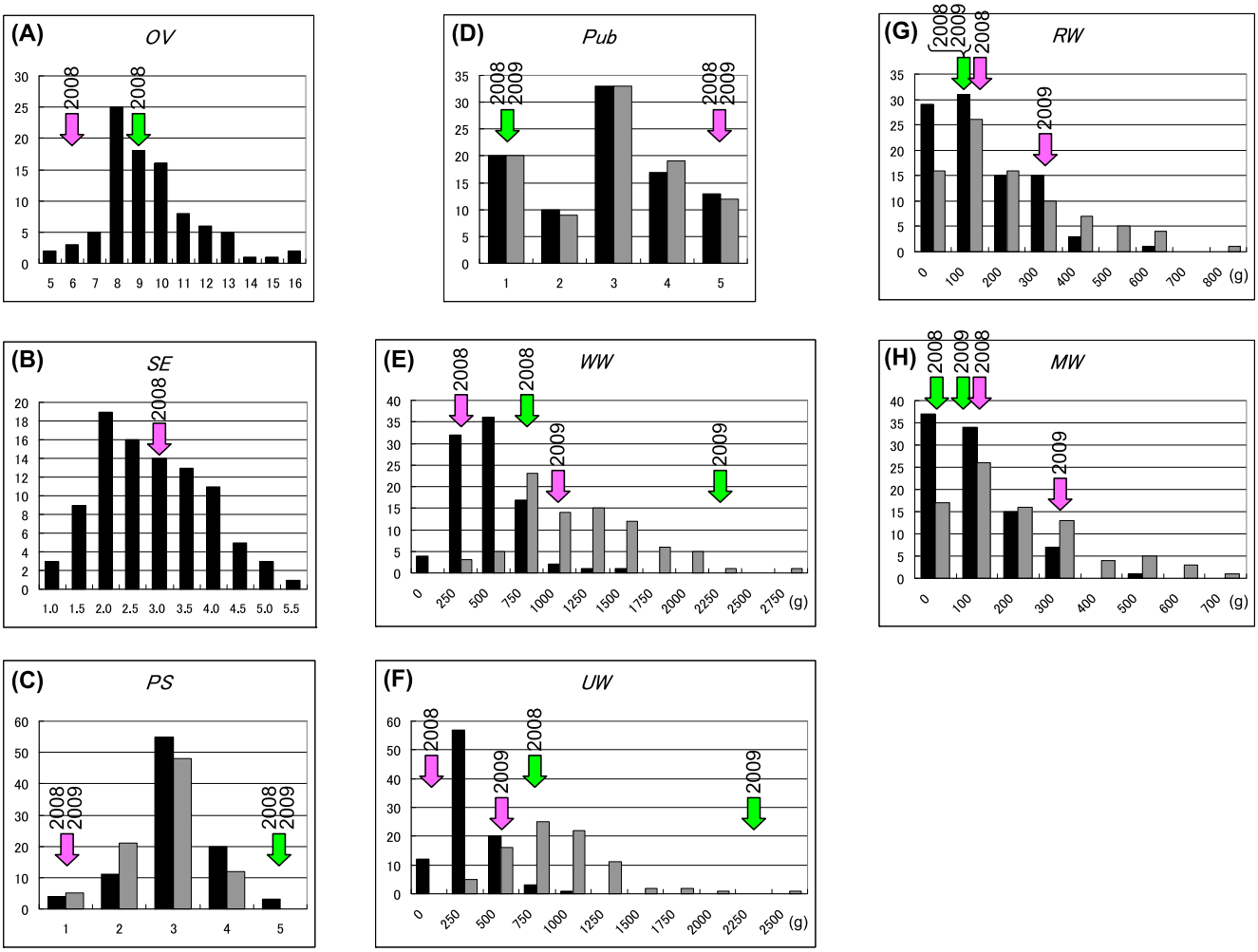
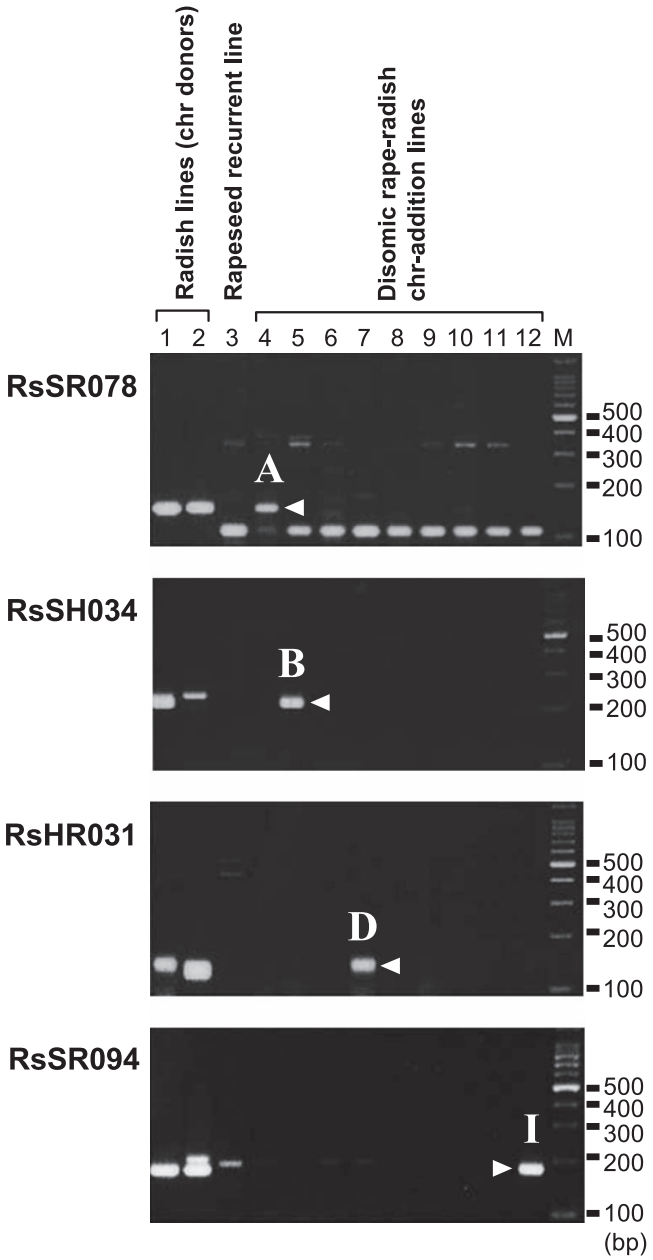
Supplemental Fig. 3. (continued)



Supplemental Fig. 4. Frequency distributions of traits in the RIL population. The trait names (*OV*-*MW*) (A–H) are shown on the top of each graph. Black and gray bars represent the data of RILs in 2008 and 2009, respectively. Green and pink arrows indicate values of the parental lines (rat-tail radish and Haru-S) in the two years, respectively.



Supplemental Fig. 5. Assignment of radish linkage groups to the corresponding chromosomes, using the complete set of disomic rape-radish chromosome-addition lines (Budahn *et al.* 2008) and the radish sequence-tagged markers. Only examples of four SSR markers are shown, whose names are indicated on the left. Lanes 1 and 2: oil radish strain 2655 and fodder radish strain 101/177, used as donors of radish chromosomes to the disomic addition lines. Lane 3: rapeseed variety 'Madora' used as recurrent line in successive backcrosses. Lanes 4–12: disomic addition lines, each of which has one of the nine radish chromosome pairs AA-II (from left to right) in the *B. napus* background. Lane M: molecular weight standards (100 bp ladder), whose sizes (≤500 bp) are indicated on the right. Radish-specific bands in the disomic addition lines are indicated with arrowheads and the assigned chromosomes are denoted with letters on the bands.