

Supplementary File 1 (Fig. S1). Flow chart of work of the present study.

**Resequencing reads alignment against
993v2.0/Gy14v1.0 to confirm CNV at *F* locus**



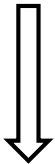
FISH verification of the CNV (based on 9930 v2.0)



One-end anchored PCR to confirm *F* locus size



**Genomic DNA qPCR in natural population
to confirm copy numbers of individual genes at *F* locus**



**Validation, annotation of *F* locus with
9930v3.0/Gy14v2.0 assemblies**



Hypothesis: gynoecey instability is due to UCO among CNV

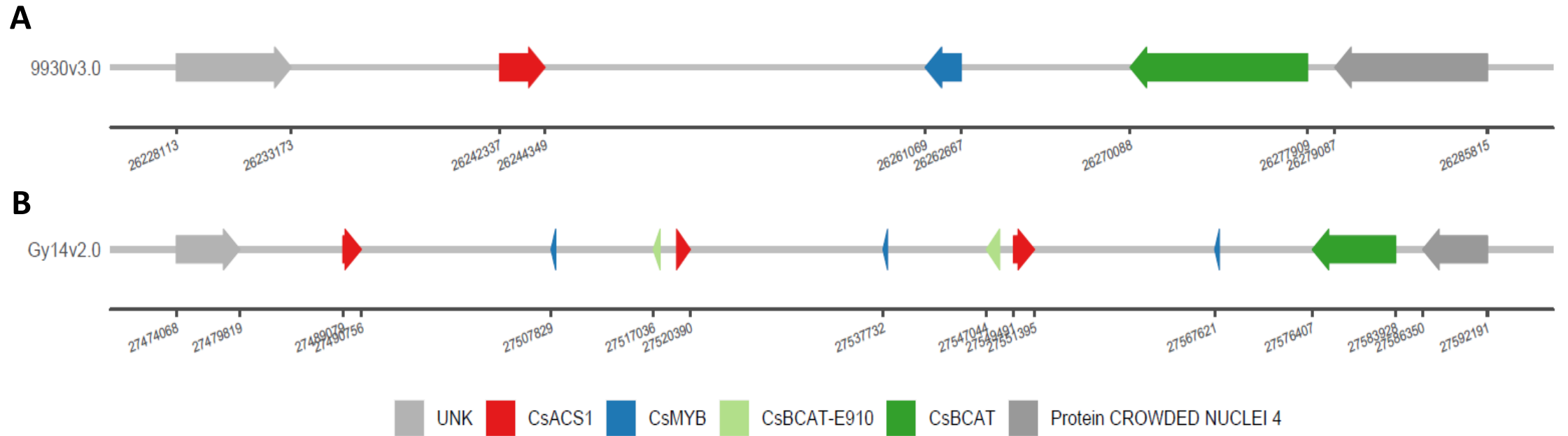


Experimental evidence to prove hypothesis:

- identification/characterization of 'gynoecey loss'
mutants in two gynoeceious lines**

Supplementary File 2 (Table S1). Information of primers used in this study.

Primer names	Forward primer (5' to 3')	Chromosome	9930 V2.0	9930 V3.0	Gy14 V2.0	Reverse primer (5' to 3')	9930 V2.0	9930 V3.0	Gy14 V2.0
Fiber FISH probes									
FISH-01	TATGTCCCTACGCCCTAT	Chr6	24,215,158	26,239,898	27,486,394	CATGATACATTTACCCACA	24,216,862	26,241,602	No hit
FISH-02	CCCTCTGTCCCTCTATT	Chr6	24,217,202	26,241,914	27,488,444	CCAAAGTTCCCTCGTCTCT	24,218,852	26,243,564	27,490,093
FISH-03	AGTAACGAAGACGAGGAA	Chr6	24,218,829	26,243,541	27,490,070	AAAGTTGGAGGAAAGAA	24,220,593	26,245,317	27,491,848
FISH-04	TTTCGGTATCTTCTATG	Chr6	24,220,946	26,245,670	27,492,201	TCTCCCTACCCCTATTTT	24,222,677	26,247,409	27,493,940
FISH-05	TTTACC GTTGATGCTCGTC	Chr6	24,222,941	26,247,648	27,494,215	AGGTCTAATGGGTGATAG	24,224,814	26,249,564	27,496,088
FISH-06	ATTAGACCTATTCAACCCAT	Chr6	24,224,806	26,249,556	27,496,080	CAAGAAACATATCCTGCA	24,226,799	26,251,411	27,497,934
FISH-07	TCATTTCTGGGCGTTCCT	Chr6	24,226,841	26,251,453	27,497,976	TCCTTTCATTTCCGGCTCT	24,228,592	26,253,204	27,499,726
FISH-08	AAAGAAAGTGAATCAAGGTT	Chr6	24,228,794	26,253,406	27,499,928	CAATGAAGGGAAAAGAAA	24,230,740	26,255,351	27,501,865
FISH-09	TTGATTGGAAGGAGAAGC	Chr6	24,230,997	26,255,608	27,502,122	CAACTCCATAACGGGTCA	24,232,547	26,257,170	27,503,684
FISH-10	TTTATTACTAGTTGTGCTTAC	Chr6	24,232,682	26,257,305	27,503,819	ATGCTGATAGTTATCGGA	24,234,668	26,259,291	27,505,805
FISH-11	CATCCCTTCTCATTGTAA	Chr6	24,234,865	26,259,488	27,506,002	TGTTTTCGTTCCTTTTAC	24,236,554	26,261,177	27,507,690
FISH-12	TCCTCCACTAACCCATTC	Chr6	24,236,874	26,261,497	27,508,010	TTTCCCTTCTCCTGACT	24,238,436	26,263,059	27,509,570
FISH-13	CTGTTTTGAATCGGTCAG	Chr6	24,238,574	26,263,197	27,509,708	CCTTTTCTTTTATTACC	24,240,466	26,265,089	27,511,599
FISH-14	GAAGAAGGAAGGAGGAAT	Chr6	24,240,721	26,265,344	27,511,847	TCTCACAATGAAAGGGA	24,242,490	26,267,113	27,513,655
FISH-15	GATAATGAAGCAATACCC	Chr6	24,242,435	26,267,058	27,513,600	AAGTTCGACCAATAAGTT	24,244,342	26,268,963	27,515,501
FISH-16	AAGGGTACTAATTATTGG	Chr6	24,244,316	26,268,937	27,515,475	AATGATGTGATGGCTGA	24,246,112	26,270,699	27,517,178
FISH-17	CAAATGAATACGGGAACA	Chr6	24,246,313	26,270,900	27,517,379	TTACTTCAGGTGCGATGC	24,248,153	26,272,740	27,578,997
FISH-18	GAAGATAGGCAGGCAACG	Chr6	24,248,349	26,272,936	27,579,193	TTGGAACTATTTCAAGTTTG	24,249,976	26,274,563	27,580,820
FISH-19	ACCTGAGATGCAAGAGCA	Chr6	24,250,090	26,274,677	27,580,934	CCTTTGACCGAACCTGTA	24,251,893	26,276,480	27,582,737
Anchor PCR, CNV, 5' end (left)									
Anchor-L1	AGCTTAAACACGTAGGTATGAATAAA	Chr6	24,213,203	26,237,942	27,484,439	TGGTGTGAATCAACCACACTTA	24,214,158	26,238,894	27,485,395
Anchor-L2		Chr6				TAACATATCAAAGGCTCATGTCGI	24,215,208	26,239,948	27,486,444
Anchor-L3		Chr6				TAAAAGGAATTGGAACCTAAATC	24,216,223	26,240,963	27,487,481
Anchor-L4		Chr6				TCTGCCATTTTCTTTTTCACCTT	24,217,064	26,241,804	27,488,334
Anchor-L5		Chr6				TAATTACTTGATTCTCGGCAAGAC	24,217,991	26,242,703	27,489,232
Anchor PCR, CNV, CsACSI-BCAT junction point									
Anchor-JP1	TTTTAAGATCCAGGTGTCCTTTGAG	Chr6	24,243,275	26,267,896	27,514,434	AATGCGGGTAAGCCGTGGT	24,218,222	26,242,934	27,489,463
Anchor-JP2	GATTAGTCAAGATGTTGGTGGTTGG	Chr6	24,244,215	26,268,836	27,515,374				
Anchor-JP3	CGATGTTTCCTTCTTGATATA	Chr6	24,245,335	26,269,922	27,516,400				
Anchor-JP4	TCAAAAACAAATGAATACGGGAACA	Chr6	24,246,306	26,270,893	27,517,372				
Anchor-JP5	TCAAACGGCCTATTTCTTTCTT	Chr6	24,247,284	26,271,871	27,518,344				
Anchor PCR, CNV, 3' end									
Anchor-R1	AGATGAAGGTTTTGCGTTGAAGTAT	Chr6	24,245,068	26,269,655	27,516,135	TTACCAGATTACAAATGGGGCTT	24,246,031	26,270,618	27,517,097
Anchor-R2		Chr6				CTGACAATTTAGCTTTGGACGGTA	24,247,026	26,271,613	27,518,087
Anchor-R3		Chr6				TACAACCTGAATCTTCCGAACAGT	24,248,022	26,272,609	27,578,866
Anchor-R4		Chr6				AAAAGCAAAAGGCTATTCTGATG	24,249,012	26,273,599	27,579,856
Anchor-R5		Chr6				ATGTTTACCTGTTGGGAACACTAT	24,249,988	26,274,575	27,580,832
Anchor-R6		Chr6				TTGACCATTGGATTGGAACAGAA	24,251,012	26,275,599	27,581,856
Sequencing, CsACSIg promoter									
CsACSIg-seq	TCAAAAACAAATGAATACGGGAACA	Chr6	24,246,306	26,270,893	27,517,372	AATGCGGGTAAGCCGTGGT	24,218,222	26,242,934	27,489,463
qPCR for copy # of genomic DNA									
CsACSIg-gDNA	AAGGCATTGGTAGAATTTATGGCGG	Chr6	24,218,227	26,242,939	27,489,468	TGGATAGTATGGAGTTGGGAGGA	24,218,388	26,243,100	27,489,629
CsMYB-gDNA	TAGATTGATGAGCAAAAGCAGGAGC	Chr6	24,236,713	26,261,336	27,507,849	TATGGGATGATGCCAAGCAGTAG	24,236,863	26,261,486	27,507,999
CsBCAT-gDNA1 (Exons 9 and 10)	AAATCTCTTGGGACTGGCAGAAAAG	Chr6	24,245,913	26,270,500	27,516,979	AAATGGTGTGGGGTTGTTTAC	24,246,072	26,270,659	27,517,138
BCAT-gDNA2 (Exons 1-8)	TACTGCTTCCACAACTGATCAAC	Chr6	24,251,141	26,275,728	27,581,985	TGAGGGTCTAAAGGCGTACAGAA	24,251,280	26,275,867	27,582,124
F-gDNA (CsACSIg junction point)	CGGACGGGCATAGTTATGAGC	Chr6	24,247,441	26,272,028	27,518,501	AGTGTCTCCGACCAGAGCAGGTA	24,217,355	26,242,067	27,488,597
qPCR for mRNA expression									
CsACSI-mRNA	GGGTCTTGGCAGAACTCAACTAT	Chr6	24,217,966	26,269,922	27,489,207	GGGTAAGCCGTGGTAATCTTGG	24,218,217	26,242,929	27,489,458
CsMYB-mRNA	TCGGAGAAGCCTCCATGTTTG	Chr6	24,237,529	26,262,152	27,508,665	GCCTTGCCTCAAAAATAGGTCTT	24,237,712	26,262,355	27,508,868
CsACS2	CCTTACTATCCTGGATTGACAGAG	Chr1	21,939,051	no hit	no hit	AATGTCTCGATTGTGGAGCGTTC	21,939,944	12,940,823	12,959,445
CsActin2 (reference)	ATTCTTGATCTCTAAGTACCTTCC	Chr6	22,425,592	24,457,766	25,695,808	CCAACTAAAGGGAAATAACTCAC	22,425,839	24,458,013	25,696,055



Supplementary File 3 (Figure S2). Annotation of the *F/f* locus in 9930 V3.0 (up) and Gy14 V2.0 (down) region. The *CsACS1* region in monoecious 9930 spans ~35.5 kb harboring three predicted genes (*CsACS1*, *CsMYB* and *CsBCAT*) which is ~94.8 kb in Gy14 V2.0 that is predicted to have three tandem repeats including one copy of *CsACS1*, and two copies of *CsACSIG*. Each *CsACSIG* consists of a recombinant promoter from BCAT exons 9 and 10, and *CsACS1*. Note the orientations of each gene are different.

Supplementary File 4 (Figure S3). Alignment of genomic DNA sequences of *CsACS1* from 9930 and Gy14, and *CsACS1G* from Gy14 and a gynocious line (Marketmore 76F, DQ839406) reported in Knopf and Trebitsh³⁸. The annotated regions in 9930 *CsACS1* are highlighted in yellow following Trebitsh et al³⁴.

```
9930_ACS1      AATAATAATAAGAACAAGAACAACAAAAAGGCTGTTTTGGATGGAAAAACTATTTTTT 60
Gy14_ACS1     -----GAACAAGAACAACAACAAAAAGGCTGTTTTGGATGGAAAAACTATTTTTT 49
Gy14_ACS1G    -----
DQ839406_ACS1G.1 AAAGGTAACGATGATTCTACAAAATCACCCATATGCTACGATAGACTGACGGTCCAATT 60

9930_ACS1     CTTCCTATTTTTGGGTGGTAAA---CGTAGAATATTGAATAATATAATGAATTGATTTG 117
Gy14_ACS1     CTTCCTATTTTTGGGTGGTAAA---CGTAGAATATTGAATAATATAATGAATTGATTTG 106
Gy14_ACS1G    -----
DQ839406_ACS1G.1 CTTTTTATCTTCGATAAGTCCCATTGTAACTCGGTAAGTACAGAATAGAGTTGTTGTA 120

9930_ACS1     AAAAATACTTACCA-----ACCCCTAAAGGGAAATTAGGTG 152
Gy14_ACS1     AAAAATACTTACCA-----ACCCCTAAAGGGAAATTAGGTG 141
Gy14_ACS1G    -----TCCATAAGCAATCCTGCAAAAAATTCAGCCATCACATCAATTG 42
DQ839406_ACS1G.1 AACACCCCAACACCATTTCATAAGCAAATCCATGCAAAAATTCAGCCATCACATCAATTG 180
                      * * * * *
Begin BCAT Exon 10 (reverse)
9930_ACS1     TGTGTGTATAGAGTATAGAGAG-----ACATGAAGTAGGGTGTCTCCGGCCGACG 204
Gy14_ACS1     TGTGTGTATAGAGTATAGAGAG-----ACATGAAGTAGGGTGTCTCCGGCCGACG 193
Gy14_ACS1G    TAAGGAAAATGCTTCAAAAACACACGTCATATTATGCCCCTACTCGAGCAACCACG 102
DQ839406_ACS1G.1 TAAGGAAAATGCTTCAAAAACACACGTCATATTATGCCCCTACTCGAGCAACCACG 240
                      * * * * *
9930_ACS1     GACATAAACTTTTGATATGAGACCTGTTTTGTCCAACCTTTTCAGCCTTTTACAAAGTGT 264
Gy14_ACS1     GACATAAACTTTTGATATGAGACCTGTTTTGTCCAACCTTTTCAGCCTTTTACAAAGTGT 253
Gy14_ACS1G    TAAAAAGAGTGGAGATATAAGCTCAATCTAGTCAAACGATTTCCCATTTCCAAGACCAC 162
DQ839406_ACS1G.1 TAAAAAGAGTGGAGATATAAGCTCAATCTAGTCAAACGATTTCCCATTTCCAAGACCAC 300
                      * * * * *
9930_ACS1     GTTTGTTGCTTTGATATGGACGGGTTTTAGACTACAGGTGGAATTAAGATCCTACTTAT 324
Gy14_ACS1     GTTTGTTGCTTTGATATGGACGGGTTTTAGACTACAGGTGGAATTAAGATCCTACTTAT 313
Gy14_ACS1G    TAGTGA-----TGATGAATGGTTTGTGTTGAAGAGACTTAAATACCATTCTACGTAT 214
DQ839406_ACS1G.1 TAGTGA-----TGATGAATGGTTTGTGTTGAAGAGACTTAAATACCATTCTACGTAT 352
                      * * * * *
                      -1622 (DQ839406)
9930_ACS1     GCTTTTCAATTTTATTA-ATTCATTGACGATAGATTTTACT---CTCTAATGTTTATTTG 380
Gy14_ACS1     GCTTTTCAATTTTATTA-ATTCATTGACGATAGATTTTACT---CTCTAATGTTTATTTG 369
Gy14_ACS1G    GTGTTGCAATCTCTCTAGTTTCAAAAACAATGAATACGGGAACATGTACTTTCTTTCAA 274
DQ839406_ACS1G.1 GTGTTGCAATCTCTCTAGTTTCAAAAACAATGAATACGGGAACATGTACTTTCTTTCAA 412
                      * * * * *
9930_ACS1     TCA----TCATTTGAGATTT-----AGGTTCCAATTCCTTTTACTCAC 419
Gy14_ACS1     TCA----TCATTTGAGATTT-----AGGTTCCAATTCCTTTTACTCAC 408
Gy14_ACS1G    TCAGAACTCAATTTCAATTTCCCAACTACTCATTCACGTGTTTCGCTGTCTCAATGTG 334
DQ839406_ACS1G.1 TCAGAACTCAATTTCAATTTCCCAACTACTCATTCACGTGTTTCGCTGTCTCAATGTG 472
                      * * * * *
                      Auxin Responsive factor binding
9930_ACS1     TAAATATTTAT-----TCTTTATCCATTTAATGTTAATGTTTTCGTTAAT 464
Gy14_ACS1     TAAATATTTAT-----TCTTTATCCATTTAATGTTAATGTTTTCCTTAAAT 453
Gy14_ACS1G    TCCAGATATTGTTTTGTAAAATTTACCTTTTCCGAGATATGTGACGCTGCCACACAGGT 394
DQ839406_ACS1G.1 TCCAGATATTGTTTTGTAAAATTTACCTTTTCCGAGATATGTGACGCTGCCACACAGGT 532
                      * * * * *
                      Start of 9th intron (reverse)
9930_ACS1     TAAATTTTCACTATTTT-----TCATCCTTTTTTACACTTAAATTTAGAATTTCCC- 514
Gy14_ACS1     TAAATTTTCACTATTTT-----TCATCCTTTTTTACACTTAAATTTAGAATTTCCC- 503
Gy14_ACS1G    GATATAACCAGCTGCTGTCCCGTACAAAAGACCTCGTCAGCTCAAGTAATTCATCCACT 454
DQ839406_ACS1G.1 GATATAACCAGCTGCTGTCCCGTACAAAAGACCTCGTCAGCTCAAGTAATTCATCCACT 592
                      * * * * *
9930_ACS1     -----TTCATAATTTTATAATTTTAAATTTGATGAAAGTGAGTATTATTT 562
Gy14_ACS1     -----TTCATAATTTTATAATTTTAAATTTGATGAAAGTGAGTATTATTT 551
Gy14_ACS1G    GCCACAAGTCGTTCCCTCGACCTGACACTCATTCAAATCAGTGCCCACTTCTCTCGTCTTT 514
DQ839406_ACS1G.1 GCCACAAGTCGTTCCCTCGACCTGACACTCATTCAAATCAGTGCCCACTTCTCTCGTCTTT 652
                      * * * * *
BACT Exon 9 (reverse)
```

```

9930_ACS1      AATGAAAAATCAATTGTAGA----AGTGCAA-----AATTTA 595
Gy14_ACS1     AATGAAAAATCAATTGTAGA----AGTGCAA-----AATTTA 584
Gy14_ACS1G    TTATCACAATCCATTATTTTACCAAGACAAACAATAATTCCTTACGCAGGTATTTAA 574
DQ839406_ACS1G.1 TTATCACAATCCATTATTTTACCAAGACAAACAATAATTCCTTACGCAGGTATTTAA 712
                * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                Potential ORF start (ATG reverse)
9930_ACS1     AAAACTTATATT---CGACTAAACTGAAACTGAAATTAACCTTAGGAACTAAGTCCTCC 651
Gy14_ACS1     AAAACTTATATT---CGACTAAACTGAAACTGAAATTAACCTTAGGAACTAAGTCCTCC 640
Gy14_ACS1G    ACAACGTACAAAAGAGAGAACCAACTCAATCACATTTTCGACTTACAAAACATTTGTAAA 634
DQ839406_ACS1G.1 ACAACGTACAAAAGAGAGAACCAACTCAATCACATTTTCGACTTACAAAACATTTGTAAA 772
                * * * * * * * * * * * * * * * * * * * * * * * * * * * *

9930_ACS1     TTTGCTTATAACCATTTAGAATCCTAGATTATGTTTTGTCTTTAAAAATAGGTTTATTT 711
Gy14_ACS1     TTTGCTTATAACCATTTAGAATCCTAGATTATGTTTTGTCTTTAAAAATAGGTTTATTT 700
Gy14_ACS1G    TATGT-TGAGATGAGATCAAATCTAAATATAGGAAATTAATTTGAAAGTAGTTTTTTT- 692
DQ839406_ACS1G.1 TATGT-TGAGATGAGATCAAATCTAAATATAGGAAATTAATTTGAAAGTAGTTTTTTT- 830
                * * * * * * * * * * * * * * * * * * * * * * * * * * * *

9930_ACS1     TCTCTTTTATTTTCATCTTTGTTGGGTAAAAGAATTGAATTAATTTAAAAACAAAAACA 771
Gy14_ACS1     TCTCTTTTATTTTCATCTTTGTTGGGTAAAAGAATTGAATTAATTTAAAAACAAAAATA 760
Gy14_ACS1G    ----TTAG--TACAC-CCAAGTGAA----CACCACAATTAATCTCATAAGAGAAATTC 739
DQ839406_ACS1G.1 ----TTAG--TACAC-CCAAGTGAA----CACCACAATTAATCTCATAAGAGAAATTC 877
                * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                -1594 (DQ839406)
9930_ACS1     AAATTTTAAAAACTATCTTTTAAAGTTTTCAAATTTTAACTTAGTTTTTGAAA----- 824
Gy14_ACS1     AAATTTTAAAAACTATCTTTTAAAGTTTTCAAATTTTAACTTAGTTTTTGAGAATGTGGA 820
Gy14_ACS1G    TAAGATATAAAATCCTGGTAAAGGTCATCTTGATTGAACCTATTCTCTTCAACTCTTTT 799
DQ839406_ACS1G.1 TAAGATATAAAATCCTGGTAAAGGTCATCTTGATTGAACCTATTCTCTTCAACTCTTTT 937
                * * * * * * * * * * * * * * * * * * * * * * * * * * * *

9930_ACS1     -----ATGTTGATAGAGAGTAAATAACAAAATAAGA--ATTTTAAAGTG 867
Gy14_ACS1     TAGAGGTTTTTGAGAATGTTGATAGAGTAAATAACAAAATAAGA--ATTTTAAAGTG 878
Gy14_ACS1G    ATCAATCCTATAGATATTTAGAATTTGACCATTAGACCAACTCAAATGGTTTATACCTT 859
DQ839406_ACS1G.1 ATCAATCCTATAGATATTTAGAATTTGACCATTAGACCAACTCAAATGGTTTATACCTT 997
                * * * * * * * * * * * * * * * * * * * * * * * * * * * *

9930_ACS1     AAAGAGATGTTATTTATGATCTAATTGAGATTTTAAAAAATTTAAAACAAAAAAGT-TAT 926
Gy14_ACS1     AAAGAGATGTTATTTATGATCTAATTGAGATTTTAAAAAATTTAAAACAAAAAAGT-TAC 937
Gy14_ACS1G    TAAAAGTTCAGAGTATAACAACCTTTAA-TATTAC-----AAATCCCACAGTAAAT 912
DQ839406_ACS1G.1 TAAAAGTTCAGAGTATAACAACCTTTAA-TATTAC-----AAATCCCACAGTAAAT 1050
                * * * * * * * * * * * * * * * * * * * * * * * * * * * *

9930_ACS1     AGAACTATTTTAAATATTAATAAAAT-----AAACAAAACATTTACAAAATATACTAAA 981
Gy14_ACS1     ATAACTATTTTAAATAT-AATAAAAT-----AAACAAAACAATTACAAAATATACTAAA 991
Gy14_ACS1G    AGTATTTCTTTTAAATACCGTCCAAGCTAAATGTGCAAGCATGCATTTTATTGACAA 972
DQ839406_ACS1G.1 AGTATTTCTTTTAAATACCGTCCAAGCTAAATGTGCAAGCATGCATTTTATTGACAA 1110
                * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                CArG transcription regulator
9930_ACS1     ATATCAAAGTCTACAA-----TAAACAACAATTTATCAAATAGATTAGACTATTACATG 1036
Gy14_ACS1     ATATCAAAGTCTACAA-----TAAATAACAATTTATCAAATAGATTAGACTATTAT--G 1044
Gy14_ACS1G    CTAGACCAACCTAAGATGTTTCCCTCTAAAAATATTTTCAGAAATTTATTATACAA-TACTAG 1031
DQ839406_ACS1G.1 CTAGACCAACCTAAGATGTTTCCCTCTAAAAATATTTTCAGAAATTTATTATACAA-TACTAG 1169
                * * * * * * * * * * * * * * * * * * * * * * * * * * * *

9930_ACS1     TGGTAAATGTATCATGAACAAAA-----TAGTAGT---CTATGATAGTTTACTATAG 1087
Gy14_ACS1     TGATAAATGTATCATGAACAAAA-----TAGCAGT---CTATGATAGTTTACTATAG 1095
Gy14_ACS1G    TTGCTAAATAGATCCATTTTACAAATAATACGAGTAAGCTTCACAAATGGT-T-TTATTA 1089
DQ839406_ACS1G.1 TTGCTAAATAGATCCATTTTACAAATAATACGAGTAAGCTTCACAAATGGT-TTATTA 1228
                * * * * * * * * * * * * * * * * * * * * * * * * * * * *

9930_ACS1     ATTGTGATATTTTAGTATAGTGATAAATGTT---TGTATAAATTTTATCATTTAAAATA 1143
Gy14_ACS1     ATTGTGATATTTTAGTATAGTGATAAATGTT---TGTATAAATTTTATCATTTAAAATA 1151
Gy14_ACS1G    CATGCATTATATGGACATTTTAAAGTGATCTAATAAGACAATTTTGGACCTATTACGAA 1149
DQ839406_ACS1G.1 CATGCATTATATGGACATTTTAAAGTGATCTAATAAGACAATTATTTGACCCTATTACGAA 1288
                * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                CArG transcription regulator
9930_ACS1     AAAATTGAGAGTAAAAATACATTTAAAAGAAAAAAGAAAGAAATGAATTAATTAGGAGG- 1202
Gy14_ACS1     AAATTCGAGAGTAAAAATACATTTAAAAGAA-AAAAGAAAAGAAATGAATTAATTAGGAGG- 1209
Gy14_ACS1G    AAAGACAATGTCAAAGAT---ATCTAGGCTGCCACTGGAGCATGCCCTCACTGAACAAA 1205
DQ839406_ACS1G.1 AAAGACAATGTCAAAGAT---ATCTAGGCTGCCACTGGAGCATGCCCTCACTGAACAAA 1344
                * * * * * * * * * * * * * * * * * * * * * * * * * * * *

```

```

9930_ACS1      ---AGAAAGAGTAAATGGTAAATGGATGTTAATTAAGGTGAAAGAAGAAAATGGCAGACAGA 1259
Gy14_ACS1     ---AG-----AAAGAGTAAATGGATGTTAATTAAGGTGAAAGAAGAAAATGGCAGACAGA 1260
Gy14_ACS1G    ATCAAACGGCCATTTTCCCTTTCTTTT-TGTTTTTCATTAAAATAATC--ACTCCTT 1262
DQ839406_ACS1G.1 ATCAAACGGCCATTTTCCCTTTCTTTT-TGTTTTTCATTAAAATAATC--ACTCCTT 1401
                *       *       *       *       *       *       *       *       *       *
                -600                                     -550

9930_ACS1     GAGTGGCTGGTGATTGTGT-AATGAGGGAACACATTGAGCCCACCCACAGTTCATATT 1318
Gy14_ACS1     GAGTGGCTGGTGATTGTGT-AATGAGGGAACACATTGAGCCCACCCACAGTTCATATT 1319
Gy14_ACS1G    CATTGATATGCAACTTAGCAAAATATATAAAATACTAGATAAGAAAACCC-AAATCAAGAG 1321
DQ839406_ACS1G.1 CATTGATATGCAACTTAGCAAAATATATAAAATACTAGATAAGAAAACCC-AAATCAAGAG 1460
                * * *       * * *       * * *       * * *       * * *       * * *

9930_ACS1     TTGATTTTGGAGATCAGGTGGGTCTTTTTTCCCATCTTCTCTAACCCCTCCTGTCCCTC 1378
Gy14_ACS1     TTGATTTTGGAGATCAGGTGGGTCTTTTTTCCCATCTTCTCTAACCCCTCCTGTCCCTC 1379
Gy14_ACS1G    AAGCAACGACAAAAACAGGGTGGTTT--AAGTATTTAACTACTTCGGACGGGCATAGTT 1378
DQ839406_ACS1G.1 AAGCAACGACAAAAACAGGGTGGTTT--AAGTATTTAACTACTTCGGACGGGCATAGTT 1517
                *       *       * * * * *       * * *       * * *       *

                Distal promoter (start of BCAT 8th intron)

9930_ACS1     TATTTTCTTCTTTCTATGTTTTCCCTAACAAATTAACCCCCAAATCATTAACTTTT 1438
Gy14_ACS1     TATTTTCTTCTTTCTATGTTTTCCCTAACAAATTAACCCCCAAATCATTAACTTTT 1439
Gy14_ACS1G    ATGAGCAACATTAATTATGTTTTCCCTAACAAATTAACCCCCAAATCATTAACTTTT 1438
DQ839406_ACS1G.1 ATGAGCAACATTAATTATGTTTTCCCTAACAAATTAACCCCCAAATCATTAACTTTT 1577
                *
                *****

                -410 Proximal promoter start/braking point

9930_ACS1     CATTATCCCATTCATTTTTGTTTCATAATCCCATTTCATCTCCATATCAAACCATAC 1498
Gy14_ACS1     CATTATCCCATTCATTTTTGTTTCATAATCCCATTTCATCTCCATATCAAACCATAC 1499
Gy14_ACS1G    CATTATCCCATTCATTTTTGTTTCATAATCCCATTTCATCTCCATATCAAACCATAC 1498
DQ839406_ACS1G.1 CATTATCCCATTCATTTTTGTTTCATAATCCCATTTCATCTCCATATCAAACCATAC 1637
                *****

9930_ACS1     CTGCTCTGGTCGGAGACACTTTCATAAATAATTCCTCAAATCATCACTGTTTATCAACC 1558
Gy14_ACS1     CTGCTCTGGTCGGAGACACTTTCATAAATAATTCCTCAAATCATCACTGTTTATCAACC 1559
Gy14_ACS1G    CTGCTCTGGTCGGAGACACTTTCATAAATAATTCCTCAAATCATCACTGTTTATCAACC 1558
DQ839406_ACS1G.1 CTGCTCTGGTCGGAGACACTTTCATAAATAATTCCTCAAATCATCACTGTTTATCAACC 1697
                *****

9930_ACS1     CCCTTAATTAATTAATTAATATCAAACACACTCTCTATATTATCTCTACAATCTAAATAA 1618
Gy14_ACS1     CCCTTAATTAATTAATTAATATCAAACACACTCTCTATATTATCTCTACAATCTAAATAA 1619
Gy14_ACS1G    CCCTTAATTAATTAATTAATATCAAACACACTCTCTATATTATCTCTACAATCTAAATAA 1618
DQ839406_ACS1G.1 CCCTTAATTAATTAATTAATATCAAACACACTCTCTATATTATCTCTACAATCTAAATAA 1757
                *****

9930_ACS1     TATACCTATATATATATATATTTGTCTCTTATTTAATTAGACCAATTAATTAATCTAT 1678
Gy14_ACS1     TATACCTATATATATATATATTTGTCTCTTATTTAATTAGACCAATTAATTAATCTAT 1679
Gy14_ACS1G    TATACCTATATATATATATATTTGTCTCTTATTTAATTAGACCAATTAATTAATCTAT 1678
DQ839406_ACS1G.1 TATACCTATATATATATATTTGTCTCTTATTTAATTAGACCAATTAATTAATCTAT 1817
                *****

                Auxin Responsive factor binding

9930_ACS1     AACCAAATCCCAGACCCACATGTGGTCAAAGTTTTTGTGTCACCATCTACGTGGCCT 1738
Gy14_ACS1     AACCAAATCCCAGACCCACATGTGGTCAAAGTTTTTGTGTCACCATCTACGTGGCCT 1739
Gy14_ACS1G    AACCAAATCCCAGACCCACATGTGGTCAAAGTTTTTGTGTCACCATCTACGTGGCCT 1738
DQ839406_ACS1G.1 AACCAAATCCCAGACCCACATGTGGTCAAAGTTTTTGTGTCACCATCTACGTGGCCT 1877
                *****

                ABA responsive

9930_ACS1     ATGGATTTGTCTTATAAATACCACCCTATGTTGCTGAACACCTCTCCAACCTCAAACAT 1798
Gy14_ACS1     ATGGATTTGTCTTATAAATACCACCCTATGTTGCTGAACACCTCTCCAACCTCAAACAT 1799
Gy14_ACS1G    ATGGATTTGTCTTATAAATACCACCCTATGTTGCTGAACACCTCTCCAACCTCAAACAT 1798
DQ839406_ACS1G.1 ATGGATTTGTCTTATAAATACCACCCTATGTTGCTGAACACCTCTCCAACCTCAAACAT 1937
                *****

                TATA box

9930_ACS1     TCGAAGAACTATCTACCATATTTCCAACCAATACAAACCACCTCTTTTCTCTCTCTATT 1858
Gy14_ACS1     TCGAAGAACTATCTACCATATTTCCAACCAATACAAACCACCTCTTTTCTCTCTCTATT 1859
Gy14_ACS1G    TCGAAGAACTATCTACCATATTTCCAACCAATACAAACCACCTCTTTTCTCTCTCTATT 1858
DQ839406_ACS1G.1 TCGAAGAACTATCTACCATATTTCCAACCAATACAAACCACCTCTTTTCTCTCTCTATT 1997
                *****

                ACS1 transcription start/5' UTR (+1, 197 bp from ATG)

9930_ACS1     TCTATTTCTCAACATTTCTCTCAATCTCATAATCTTTTGTACCTATATACCTCACCTCAA 1918
Gy14_ACS1     TCTATTTCTCAACATTTCTCTCAATCTCATAATCTTTTGTACCTATATACCTCACCTCAA 1919
Gy14_ACS1G    TCTATTTCTCAACATTTCTCTCAATCTCATAATCTTTTGTACCTATATACCTCACCTCAA 1918
DQ839406_ACS1G.1 TCTATTTCTCAACATTTCTCTCAATCTCATAATCTTTTGTACCTATATACCTCACCTCAA 2057
                *****

```

9930_ACS1 CATTAATCTTAATCTTAAATCATCAGATTCTTCTTCCATCCATCCCTAGGCTAGCTTAT 1978
Gy14_ACS1 CATTAATCTTAATCTTAAATCATCAGATTCTTCTTCCATCCATCCCTAGGCTAGCTTAT 1979
Gy14_ACS1G CATTAATCTTAATCTTAAATCATCAGATTCTTCTTCCATCCATCCCTAGGCTAGCTTAT 1978
DQ839406_ACS1G.1 CATTAATCTTAATCTTAAATCATCAGATTCTTCTTCCATCCATCCCTAGGCTAGCTTAT 2117

9930_ACS1 TAGCAGCACAACCGAAGAAAAATGAAGATGCTTCCACAAAAGCCACGTGCAATTCCCA 2038
Gy14_ACS1 TAGCAGCACAACCGAAGAAAAATGAAGATGCTTCCACAAAAGCCACGTGCAATTCCCA 2038
Gy14_ACS1G TAGCAGCACAACCGAAGAAAAATGAAGATGCTTCCACAAAAGCCACGTGCAATTCCCA 2038
DQ839406_ACS1G.1 TAGCAGCACAACCGAAGAAAAATGAAGATGCTTCCACAAAAGCCACGTGCAATTCCCA 2177

ACS1 CDS start (Exon 1, 147 bp)

9930_ACS1 CCGTCAAGATTCCCTCCTACTTCTTAGGATGGGAAGCTTATGAGAAAAACCCCTTTGATGA 2098
Gy14_ACS1 CCGTCAAGATTCCCTCCTACTTCTTAGGATGGGAAGCTTATGAGAAAAACCCCTTTGATGA 2098
Gy14_ACS1G CCGTCAAGATTCCCTCCTACTTCTTAGGATGGGAAGCTTATGAGAAAAACCCCTTTGATGA 2098
DQ839406_ACS1G.1 CCGTCAAGATTCCCTCCTACTTCTTAGGATGGGAAGCTTATGAGAAAAACCCCTTTGATGA 2237

9930_ACS1 GACTTCTAATCCCAACGGCATCATTCAGATGGGTCTTGCCGAGAATCAA GTAATTATATA 2158
Gy14_ACS1 GACTTCTAATCCCAACGGCATCATTCAGATGGGTCTTGCCGAGAATCAA GTAATTATATA 2158
Gy14_ACS1G GACTTCTAATCCCAACGGCATCATTCAGATGGGTCTTGCCGAGAATCAA GTAATTATATA 2158
DQ839406_ACS1G.1 GACTTCTAATCCCAACGGCATCATTCAGATGGGTCTTGCCGAGAATCAA GTAATTATATA 2297

9930_ACS1 TATTCTTCTCGTATATATATATGTATACAAAAAAATCACCATTTTTATGTTCTATTAA 2218
Gy14_ACS1 TATTCTTCTCGTATATATATATGTATACAAAAAAATCACCATTTTTATGTTCTATTAA 2218
Gy14_ACS1G TATTCTTCTCGTATATATATATGTATACAAAAAAATCACCATTTTTATGTTCTATTAA 2218
DQ839406_ACS1G.1 TATTCTTCTCGTATATATATATGTATACAAAAAAATCACCATTTTTATGTTCTATTAA 2357

9930_ACS1 GAGCTCTATTACTCACCTTTTTTTTTTCACTTTTTTTTTCAGCTATCATTGATCTTCTT 2278
Gy14_ACS1 GAGCTCTATTACTCACCTTTTTTTTTTCACTTTTTTTTTCAGCTATCATTGATCTTCTT 2278
Gy14_ACS1G GAGCTCTATTACTCACCTTTTTTTTTTCACTTTTTTTTTCAGCTATCATTGATCTTCTT 2278
DQ839406_ACS1G.1 GAGCTCTATTACTCACCTTTTTTTTTTCACTTTTTTTTTCAGCTATCATTGATCTTCTT 2417

ACS1 Exon 2 (291 bp)

9930_ACS1 GAATCATGGCTTACAAAAAATCCAGACGCAGCCAGCTTTAAACGTGATGGCAAATCAATT 2338
Gy14_ACS1 GAATCATGGCTTACAAAAAATCCAGACGCAGCCAGCTTTAAACGTGATGGCAAATCAATT 2338
Gy14_ACS1G GAATCATGGCTTACAAAAAATCCAGACGCAGCCAGCTTTAAACGTGATGGCAAATCAATT 2337
DQ839406_ACS1G.1 GAATCATGGCTTACAAAAAATCCAGACGCAGCCAGCTTTAAACGTGATGGCAAATCAATT 2477

9930_ACS1 TTTAGAGAGCTCGCTCTCTTCCAAGATTACCACGGCTTACCCGCATTCAAAAAGGCATTG 2398
Gy14_ACS1 TTTAGAGAGCTCGCTCTCTTCCAAGATTACCACGGCTTACCCGCATTCAAAAAGGCATTG 2398
Gy14_ACS1G TTTAGAGAGCTCGCTCTCTTCCAAGATTACCACGGCTTACCCGCATTCAAAAAGGCATTG 2397
DQ839406_ACS1G.1 TTTAGAGAGCTCGCTCTCTTCCAAGATTACCACGGCTTACCCGCATTCAAAAAGGCATTG 2537

9930_ACS1 GTAGAATTTATGGCGGAAATTAGAGGAAACAAAGTAACATTTGAAGCAAATAACATAGTC 2458
Gy14_ACS1 GTAGAATTTATGGCGGAAATTAGAGGAAACAAAGTAACATTTGAAGCAAATAACATAGTC 2458
Gy14_ACS1G GTAGAATTTATGGCGGAAATTAGAGGAAACAAAGTAACATTTGAAGCAAATAACATAGTC 2457
DQ839406_ACS1G.1 GTAGAATTTATGGCGGAAATTAGAGGAAACAAAGTAACATTTGAAGCAAATAACATAGTC 2597

9930_ACS1 CTTACAGCTGGCGCTACATCAGCCAATGAAACACTTATGTTCTGCCTTGCAGAGGCTGGC 2518
Gy14_ACS1 CTTACAGCTGGCGCTACATCAGCCAATGAAACACTTATGTTCTGCCTTGCAGAGGCTGGC 2518
Gy14_ACS1G CTTACAGCTGGCGCTACATCAGCCAATGAAACACTTATGTTCTGCCTTGCAGAGGCTGGC 2517
DQ839406_ACS1G.1 CTTACAGCTGGCGCTACATCAGCCAATGAAACACTTATGTTCTGCCTTGCAGAGGCTGGC 2657

9930_ACS1 GATGCCTTCTCCTCCCAACTCCA TACTATCCAGGGTTAGTAGTAATGATATTAATATTA 2578
Gy14_ACS1 GATGCCTTCTCCTCCCAACTCCATACTATCCAGGGTTAGTAGTAATGATATTAATATTA 2578
Gy14_ACS1G GATGCCTTCTCCTCCCAACTCCATACTATCCAGGGTTAGTAGTAATGATATTAATATTA 2577
DQ839406_ACS1G.1 GATGCCTTCTCCTCCCAACTCCATACTATCCAGGGTTAGTAGTAATGATATTAATATTA 2717

9930_ACS1 ATTACTTTACATTCACCTTAAACTTAAACATTTCCCTTTACTATAAECTCAAGCTAAATAA 2638
Gy14_ACS1 ATTACTTTACATTCACCTTAAACTTAAACATTTCCCTTTACTATAAECTCAAGCTAAATAA 2638
Gy14_ACS1G ATTACTTTACATTCACCTTAAACTTAAACATTTCCCTTTACTATAAECTCAAGCTAAATAA 2637
DQ839406_ACS1G.1 ATTACTTTACATTCACCTTAAACTTAAACATTTCCCTTTACTATAAECTCAAGCTAAATAA 2777

9930_ACS1 TTCTAATTAATCATGTATACTTTACTATAAACAGATTGATAGAGATTGAAATGGAGAA 2698
Gy14_ACS1 TTCTAATTAATCATGTATACTTTACTATAAACAGATTGATAGAGATTGAAATGGAGAA 2698
Gy14_ACS1G TTCTAATTAATCATGTATACTTTACTATAAACAGATTGATAGAGATTGAAATGGAGAA 2697
DQ839406_ACS1G.1 TTCTAATTAATCATGTATACTTTACTATAAACAGATTGATAGAGATTGAAATGGAGAA 2837

ACS1 Exon 3 (1005 bp)
9930_ACS1 CCGGAGTTGAGATTGTGCCAATTCATTGCAGCTAGCTCCAACGGCTTCCAAGTACCCAAC 2758
Gy14_ACS1 CCGGAGTTGAGATTGTGCCAATTCATTGCAGCTAGCTCCAACGGCTTCCAAGTACCCAAC 2758
Gy14_ACS1G CCGGAGTTGAGATTGTGCCAATTCATTGCAGCTAGCTCCAACGGCTTCCAAGTACCCAAC 2757
DQ839406_ACS1G.1 CCGGAGTTGAGATTGTGCCAATTCATTGCAGCTAGCTCCAACGGCTTCCAAGTACCCAAC 2897

9930_ACS1 CAGCTTTAGAACAAGCCTATCAAGAAGCCCAAGCTCGCAACCTACGTGTCAAAGGCGTAT 2818
Gy14_ACS1 CAGCTTTAGAACAAGCCTATCAAGAAGCCCAAGCTCGCAACCTACGTGTCAAAGGCGTAT 2818
Gy14_ACS1G CAGCTTTAGAACAAGCCTATCAAGAAGCCCAAGCTCGCAACCTACGTGTCAAAGGCGTAT 2817
DQ839406_ACS1G.1 CAGCTTTAGAACAAGCCTATCAAGAAGCCCAAGCTCGCAACCTACGTGTCAAAGGCGTAT 2957

9930_ACS1 TGGTTACCAACCCATCTAACCATTGGGAACCAATGACAAGAAATGAACTCGACTTGG 2878
Gy14_ACS1 TGGTTACCAACCCATCTAACCATTGGGAACCAATGACAAGAAATGAACTCGACTTGG 2878
Gy14_ACS1G TGGTTACCAACCCATCTAACCATTGGGAACCAATGACAAGAAATGAACTCGACTTGG 2876
DQ839406_ACS1G.1 TGGTTACCAACCCATCTAACCATTGGGAACCAATGACAAGAAATGAACTCGACTTGG 3017

9930_ACS1 TTTTGTATTTTCATAACCTCCAAGGCATTTCATTGATCAGCGACGAGATTTACTCTGGGA 2938
Gy14_ACS1 TTTTGTATTTTCATAACCTCCAAGGCATTTCATTGATCAGCGACGAGATTTACTCTGGGA 2938
Gy14_ACS1G TTTTGTATTTTCATAACCTCCAAGGCATTTCATTGATCAGCGACGAGATTTACTCTGGGA 2936
DQ839406_ACS1G.1 TTTTGTATTTTCATAACCTCCAAGGCATTTCATTGATCAGCGACGAGATTTACTCTGGGA 3077

9930_ACS1 CCGTTTTTGGGTCTCCAGGATTTCGTGAGCGCCATGGAGGTGCTTAAGGAGAGGAGTAACG 2998
Gy14_ACS1 CCGTTTTTGGGTCTCCAGGATTTCGTGAGCGCCATGGAGGTGCTTAAGGAGAGGAGTAACG 2998
Gy14_ACS1G CCGTTTTTGGGTCTCCAGGATTTCGTGAGCGCCATGGAGGTGCTTAAGGAGAGGAGTAACG 2996
DQ839406_ACS1G.1 CCGTTTTTGGGTCTCCAGGATTTCGTGAGCGCCATGGAGGTGCTTAAGGAGAGGAGTAACG 3137

9930_ACS1 AAGACGAGGAAGTTTGGGAAGAGAGTTTCATATTGTTTACAGTTTATCAAAGGATTTAGGGC 3058
Gy14_ACS1 AAGACGAGGAAGTTTGGGAAGAGAGTTTCATATTGTTTACAGTTTATCAAAGGATTTAGGGC 3058
Gy14_ACS1G AAGACGAGGAAGTTTGGGAAGAGAGTTTCATATTGTTTACAGTTTATCAAAGGATTTAGGGC 3056
DQ839406_ACS1G.1 AAGACGAGGAAGTTTGGGAAGAGAGTTTCATATTGTTTACAGTTTATCAAAGGATTTAGGGC 3197

9930_ACS1 TCCCAGGTTTTTCGAGTTGGTGCAATTTACTCTAATGATGAAATGGTCGTGGCGGTGCTA 3118
Gy14_ACS1 TCCCAGGTTTTTCGAGTTGGTGCAATTTACTCTAATGATGAAATGGTCGTGGCGGTGCTA 3118
Gy14_ACS1G TCCCAGGTTTTTCGAGTTGGTGCAATTTACTCTAATGATGAAATGGTCGTGGCGGTGCTA 3116
DQ839406_ACS1G.1 TCCCAGGTTTTTCGAGTTGGTGCAATTTACTCTAATGATGAAATGGTCGTGGCGGTGCTA 3257

9930_ACS1 CTAAAATGTCTAGCTTTGGGTTGGTGTCATCTCAAACACAATATCTTCTTTCAGCTATGC 3178
Gy14_ACS1 CTAAAATGTCTAGCTTTGGGTTGGTGTCATCTCAAACACAATATCTTCTTTCAGCTATGC 3178
Gy14_ACS1G CTAAAATGTCTAGCTTTGGGTTGGTGTCATCTCAAACACAATATCTTCTTTCAGCTATGC 3176
DQ839406_ACS1G.1 CTAAAATGTCTAGCTTTGGGTTGGTGTCATCTCAAACACAATATCTTCTTTCAGCTATGC 3317

9930_ACS1 TATCCGACAAGAAATTTACGAGAACCTATATTTCTGAGAATCAAAGAGGTTGAAACAAA 3238
Gy14_ACS1 TATCCGACAAGAAATTTACGAGAACCTATATTTCTGAGAATCAAAGAGGTTGAAACAAA 3238
Gy14_ACS1G TATCCGACAAGAAATTTACGAGAACCTATATTTCTGAGAATCAAAGAGGTTGAAAC-AA 3235
DQ839406_ACS1G.1 TATCCGACAAGAAATTTACGAGAACCTATATTTCTGAGAATCAAAGAGGTTGAAACAAA 3377

9930_ACS1 GACAGAAAATGTTGGTGAGTGGATTAGAGAAGGCTGGGATTAAGTGTGGGAGAGTAATG 3298
Gy14_ACS1 GACAGAAAATGTTGGTGAGTGGATTAGAGAAGGCTGGGATTAAGTGTGGGAGAGTAATG 3298
Gy14_ACS1G GACAGAAAATGTTGGTGAGTGGATTAGAGAAGGCTGGGATTAAGTGTGGGAGAGTAATG 3295
DQ839406_ACS1G.1 GACAGAAAATGTTGGTGAGTGGATTAGAGAAGGCTGGGATTAAGTGTGGGAGAGTAATG 3437

9930_ACS1 CTGGGTTGTTTTGTTGGGTTGATATGAGGCATTTGTTGGAATCAGATACGTTTGAATGTG 3358
Gy14_ACS1 CTGGGTTGTTTTGTTGGGTTGATATGAGGCATTTGTTGGAATCAGATACGTTTGAATGTG 3358
Gy14_ACS1G CTGGGTTGTTTTGTTGGGTTGATATGAGGCATTTGTTGGAATCAGATACGTTTGAATGTG 3354
DQ839406_ACS1G.1 CTGGGTTGTTTTGTTGGGTTGATATGAGGCATTTGTTGGAATCAGATACGTTTGAATGTG 3497

9930_ACS1 AATTAAAGCTATGGAAGAAGATTGTTTACGAAGTGGGTTTGAATATTTACCAGGATCAT 3418
Gy14_ACS1 AATTAAAGCTATGGAAGAAGATTGTTTACGAAGTGGGTTTGAATATTTACCAGGATCAT 3418
Gy14_ACS1G AATTAAAGCTATGGAAGAAGATTGTTTACGAAGTGGGTTTGAATATTTACCAGGATCAT 3413
DQ839406_ACS1G.1 AATTAAAGCTATGGAAGAAGATTGTTTACGAAGTGGGTTTGAATATTTACCAGGATCAT 3557

9930_ACS1 CTTGTCATTGCACTGAACCAGGCTGGTTTCGTGTTTGTGTTTGTGCTAATATGTCACAATCAA 3478
Gy14_ACS1 CTTGTCATTGCACTGAACCAGGCTGGTTTCGTGTTTGTGTTTGTGCTAATATGTCACAATCAA 3478
Gy14_ACS1G CTTGTCATTGCACTGAACCAGGCTGGTTTCGTGTTTGTGTTTGTGCTAATATGTCACAATCAA 3473
DQ839406_ACS1G.1 CTTGTCATTGCACTGAACCAGGCTGGTTTCGTGTTTGTGTTTGTGCTAATATGTCACAATCAA 3617

9930_ACS1 CCTTGAAACTCGTATCCGAAGATTGAAGTCGTTTGTTCGAAGAATTGAGATCCGTTTCTA 3538
Gy14_ACS1 CCTTGAAACTCGTATCCGAAGATTGAAGTCGTTTGTTCGAAGAATTGAGATCCGTTTCTA 3538
Gy14_ACS1G CCTTGAAACTCGTATCCGAAGATTGAAGTCGTTTGTTCGAAGAATTGAGATCCGTTTCTA 3533
DQ839406_ACS1G.1 CCTTGAAACTCGTATCCGAAGATTGAAGTCGTTTGTTCGAAGAATTGAGATCCGTTTCTA 3677

9930_ACS1 CACCGAACGTTTCCACTACCCTACAAATATTCATGACAGCAAATTTTCCAAGAATATCA 3598
Gy14_ACS1 CACCGAACGTTTCCACTACCCTACAAATATTCATGACAGCAAATTTTCCAAGAATATCA 3598
Gy14_ACS1G CACCGAACGTTTCCACTACCCTACAAATATTCATGACAGCAAATTTTCCAAGAATATCA 3593
DQ839406_ACS1G.1 CACCGAACGTTTCCACTACCCTACAAATATTCATGACAGCAAATTTTCCAAGAATATCA 3737

9930_ACS1 AGAAAAATATTTTACCACCAATGGGTTTTCCGGCAATCGGTTCAAGATCAAGCCAACCGCA 3658
Gy14_ACS1 AGAAAAATATTTTACCACCAATGGGTTTTCCGGCAATCGGTTCAAGATCAAGCCAACCGCA 3658
Gy14_ACS1G AGAAAAATATTTTACCACCAATGGGTTTTCCGGCAATCGGTTCAAGATCAAGCCAACCGCA 3653
DQ839406_ACS1G.1 AGAAAAATATTTTACCACCAATGGGTTTTCCGGCAATCGGTTCAAGATCAAGCCAACCGCA 3797

9930_ACS1 AGCTCCATTATGAACGATAGCCTGGTTTTTTTTTTTTTTTTTACTCATCATCCATATTTGGG 3717
Gy14_ACS1 AGCTCCATTATGAACGATAGCCTGGTTTTTTTTTTTTTTTTTACTCATCATCCATATTTGGG 3718
Gy14_ACS1G AGCTCCATTATGAACGATAGCCTGGTTTTTTTTTTTTTTTTTACTCATCATCCATATTTGGG 3712
DQ839406_ACS1G.1 AGCTCCATTATGAACGATAGCCTGGTTTTTTTTTTTTTTTTTACTCATCATCCATATTTGGG 3857

Translation stop codon

9930_ACS1 GGAATTTTTTTTTCTTAATCTTGTTGAAATATTCCAAATTTAGAATTTTCATATTTGTAAT 3777
Gy14_ACS1 GGAATTTTTTTTTCTTAATCTTGTTGAAATATTCCAAATTTAGAATTTTCATATTTGTAAT 3778
Gy14_ACS1G GGAATTTTTTTTTCTTAATCTTGTTGAAATATTCCAAATTTAGAATTTTCATATTTGTAAT 3772
DQ839406_ACS1G.1 GGAATTTTTTTTTCTTAATCTTGTTGAAATATTCCAAATTTAGAATTTTCATATTTGTAAT 3917

9930_ACS1 TAGAGAAAAAAGAAAAAGAAAAGTGCCTCGGTCATTGTGGGATTAGTAGTGGCTTTA 3837
Gy14_ACS1 TAGAGAAAAAAGAAAAAGAAAAGTGCCTCGGTCATTGTGGGATTAGTAGTGGCTTTA 3838
Gy14_ACS1G TAGAGAAAAAAGAAAAAGAAAAGTGCCTCGGTCATTGTGGGATTAGTAGTGGCTTTA 3832
DQ839406_ACS1G.1 TAGAGAAAAAAGAAAAAGAAAAGTGCCTCGGTCATTGTGGGATTAGTAGTGGCTTTA 3977

9930_ACS1 ATTAATTAATTAATTAATTATTAATCTTTTTTTCATTAATCTGATTCTCTCTCTCTC 3897
Gy14_ACS1 ATTAATTAATTAATTAATTATTAATCTTTTTTTCATTAATCTGATTCTCTCTCTCTC 3898
Gy14_ACS1G ATTAATTAATTAATTAATTATTAATCTTTTTTTCATTAATCTGATTCTCTCTCTCTC 3891
DQ839406_ACS1G.1 ATTAATTAATTAATTAATTATTAATCTTTTTTTCATTAATCTGATTCTCTCTCTCTC 4037

mRNA transcript end

9930_ACS1 TCTCTCTCTCTCTCTCTCTAATCAGAAATATTTAATGAAGTATATTAGAATCGAATGA 3957
Gy14_ACS1 TCTCTCTCTCTCTCTCTCTAATCAGAAATATTTAATGAAGTATATTAGAATCGAATGA 3958
Gy14_ACS1G TCTCTCTCTCTCTCTCTCTAATCAGAAATATTTAATGAAGTATATTAGAATCGAATGA 3951
DQ839406_ACS1G.1 TCTCTCTCTCTCTCTCTCTAATCAGAAATATTTAATGAAGTATATTAGAATCGAATGA 4097

9930_ACS1 ATTTTCCAACGTGGAGGATTTTATGCGAGATGTTATCATGTGTTGAAACGATAATGGTTG 4017
Gy14_ACS1 ATTTTCCAACGTGGAGGATTTTATGCGAGATGTTATCATGTGTTGAAACGATAATGGTTG 4018
Gy14_ACS1G ATTTTCCAACGTGGAGGATTTTATGCGAGATGTTATCATGTGTTGAAACGATAATGGTTG 4011
DQ839406_ACS1G.1 ATTTTCCAACGTGGAGGATTTTATGCGAGATGTTATCATGTGTTGAAACGATAATGGTTG 4157

9930_ACS1 GCCATGTGAGAAGATTTTATTTATTAATCAATTATTATTATTATTATTATTATTATTATTGTTAATGT 4077
Gy14_ACS1 GCCATGTGAGAAGATTTTATTTATTAATCAATTATTATTATTATTATTATTATTATTATTATTGTTAATGT 4078
Gy14_ACS1G GCCATGTGAGAAGATTTTATTTATTAATCAATTATTATTATTATTATTATTATTATTATTATTATTGTTAATGT 4071
DQ839406_ACS1G.1 GCCATGTGAGAAGATTTTATTTATTAATCAATTATTATTATTATTATTATTATTATTATTATTGTTAATGT 4217

9930_ACS1	ATAGAGAAAATAATAATAATAATAATATAGAAAAGAGATGGCTTGCAAAGTGAAACGGCGC	4137
Gy14_ACS1	ATAGAGAAAATAATAATAATAATAATATAGAAAAGAGATGGCTTGCAAAGTGAAACGGCGC	4138
Gy14_ACS1G	ATAGAGAAAATAATAATAATAATAATATAGAAAAGAGATGGCTTGCAAAGTGAAACGGCGC	4131
DQ839406_ACS1G.1	ATAGAGAAAATAATAATAATAATAATATAGAAAAGAGATGGCTTGCAAAGTGAAACGGCGC	4277

9930_ACS1	CGTTGGCGAGAATAGCGGCTGAAAGACGGTGGGTTTTT-TTTTTAATAGTAAGAAGATGT	4196
Gy14_ACS1	CGTTGGCGAGAATAGCGGCTGAAAGACGGTGGGTTTTTTTTTTTTAATAGTAAGAAGATGT	4198
Gy14_ACS1G	CGTTGGCGAGAATAGCGC-TGAAAGACGGTGGTTTTT-TTTTTAATAGTAAGAAGATGT	4189
DQ839406_ACS1G.1	CGTTGGCGAGAATAGCGGCTGAAAGACGGTGGGTTTT-TTTTTAATAGTAAGAAGATGT	4336

9930_ACS1	GCCGACATGAACCGGTTAATTTGGTTGAGTCATTGGTTACCCAACCGAAACCGACCTCT	4256
Gy14_ACS1	GCCGACATGAACCGGTTAATTTGGTTGAGTCATTGGTTACCCAACCGAAACCGACCTCT	4258
Gy14_ACS1G	GCCGACATGAACCGGTTAATTTGGTTGAGTCATTGGTTACCCAACCGAAACCGACCTCT	4249
DQ839406_ACS1G.1	GCCGACATGAACCGGTTAATTTGGTTGAGTCATTGGTTACCCAACCGAAACCGACCTCT	4396

9930_ACS1	TTCTTTCACACAAAACCCAAATACACAAATAATAATAATAAAGTGTGTGATTTTAAGC	4316
Gy14_ACS1	TTCTTTCACACAAAACCCAAATACACAAATAATAATAATAAAGTGTGTGATTTTAAGC	4318
Gy14_ACS1G	TTCTTTCACACAAAACCCAAATACACAAATAATAATAAT-ATAAGTGTGTGATTTTAAGC	4308
DQ839406_ACS1G.1	TTCTTTCACACAAAACCCAAATACACAAATAATAATAATAAAGTGTGTGATTTTAAGC	4456

9930_ACS1	AATTTGTGTGTTGTGTTGTACAGCAAAAAGAAGGCCAATCCCAAGTGGGTTGTTGGTCAGA	4376
Gy14_ACS1	AATTTGTGTGTTGTGTTGTACAGCAAAAAGAAGGCCAATCCCAAGTGGGTTGTTGGTCAGA	4378
Gy14_ACS1G	AATTTGTGTGTTGTGTTGTACAGCAAAAAGAAGGCCAATCCCAAGT-GGTTGTTGGTCAGA	4367
DQ839406_ACS1G.1	AATTTGTGTGTTGTGTTGTACAGCAAAAAGAAGGCCAATCCCAAGTGGGTTGTTGGTCAGA	4516

9930_ACS1	ATAGCCGAAGACAGTCAAACCTATTACGTTTGCCTAGGCCCTCCAAGAATCAAACCTTTGTC	4436
Gy14_ACS1	ATAGCCGAAGACAGTCAAACCTATTACGTTTGCCTAGGCCCTCCAAGAATCAAACCTTTGTC	4438
Gy14_ACS1G	ATAGCCGAAGACAGTCAAACCTATTACGTTTGCCTAGGCCCTCCAAGAATCAAACCTTTGTC	4427
DQ839406_ACS1G.1	ATAGCCGAAGACAGTCAAACCTATTACGTTTGCCTAGGCCCTCCAAGAATCAAACCTTTGTC	4576

9930_ACS1	CCCATTTCAACATTTCAACATTTCTTTTCTATTTTTTTTTTTCCTTTTCGTTAACCTATA	4496
Gy14_ACS1	CCCATTTCAACATTTCAACATTTCTTTTCTATTTTTTTTTTTCCTTTTCGTTAACCTATA	4498
Gy14_ACS1G	CCCATTTCAACATTTCAACATTTCTTTTCTATTTTT-TTTTTCCTTTTCGTTAACCTATA	4486
DQ839406_ACS1G.1	CCCATTTCAACATTTCAACATTTCTTTTCTATTTTTTTTTTTCCTTTTCGTTAACCTATA	4636

9930_ACS1	TATAAAATCTCACTCTTTTTTATTTTCTTTTAAACCATTTTAAATTAACCTAATCAAAAT	4556
Gy14_ACS1	TATAAAATCTCACTCTTTTTTATTTTCTTTTAAACCATTTTAAATTAACCTAATCAAAAT	4558
Gy14_ACS1G	TATAAAATCTCACTCTTTTTTATTTTCTTTTAAACCATTTTAAATTAACCTAATCAAAAT	4546
DQ839406_ACS1G.1	TATAAAATCTCACTCTTTTTTATTTTCTTTTAAACCATTTTAAATTAACCTAATCAAAAT	4696

9930_ACS1	TATTGGATATTATTGATCTCACATGACGATGCTTCTTCAAATTGCTTTATAAAAATTATG	4616
Gy14_ACS1	TATTGGATATTATTGATCTCACATGACGATGCTTCTTCAAATTGCTTTATAAAAATTATG	4618
Gy14_ACS1G	TAT-TGATATTATTGATCTCACATGACGATGCTTCTTCAAATTGCTTTATAAAAATTATG	4605
DQ839406_ACS1G.1	TATTGGATATTATTGATCTCACATGACGATGCTTCTTCAAATTGCTTTATAAAAATTATG	4756
*** *****		
9930_ACS1	ACATTAATTATATATAGGATAAATCCAAAAATAATTGAGTCAAAGTATTAAATTAACCT	4676
Gy14_ACS1	ACATTAATTATATATAGGATAAATCCAAAAATAATTGAGTCAAAGTATTAAATTAACCT	4678
Gy14_ACS1G	ACATTAATTATATATAGGATAAATCCAAAAATAATTGAGTCAAAGTATTAAATTAACCT	4665
DQ839406_ACS1G.1	ACATTAATTATATATAGGATAAATCCAAAAATAATTGAGTCAAAGTATTAAATTAACCT	4816

9930_ACS1	TT-----	4678
Gy14_ACS1	-----	4678
Gy14_ACS1G	TTGTCTTT-----	4673
DQ839406_ACS1G.1	TTGTCTTTATTTTACTT	4833

Supplementary File 5 (Table S2). Sex expression of the cucumber materials used in this study.

#	Accessions	Sex expression*	Objectives
1	WI2757	G	G01 (Fig. 3)
2	2A	G	G02 (Fig. 3)
3	NZ1	G	G03 (Fig. 3)
4	GP5818	G	G04 (Fig. 3)
5	Gy14	G	G05 (Fig. 3)
6	PI 308915	G	G06 (Fig. 3)
7	1351A1	G	G07 (Fig. 3)
8	7155B	G	G08 (Fig. 3)
9	BA-m10-139	G	G09 (Fig. 3)
10	ZS0806	G	G10 (Fig. 3)
11	ZS0833	G	G11 (Fig. 3)
12	DP1	G	G12 (Fig. 3)
13	MSU 713-5	G	G13 (Fig. 3)
14	AM297	G	G14 (Fig. 3)
15	PI 292012	H	H01 (Fig. 3)
16	PI 356809	H	H02 (Fig. 3)
17	PI 370643	H	H03 (Fig. 3)
18	PI 500365	H	H04 (Fig. 3)
19	WI1983H	H	H05 (Fig. 3)
20	WI7012A	M	M01 (Fig. 3)
21	Midget	M	M02 (Fig. 3)
22	PI 267942	M	M03 (Fig. 3)
23	PI 271327	M	M04 (Fig. 3)
24	PI 271328	M	M05 (Fig. 3)
25	SV4719S-M	M	M07 (Fig. 3)
26	Northern Pickling	M	M08 (Fig. 3)
27	Gy14*WI7284 F1	SubG	SubG01 (Fig. 3)
28	Gy14*AM056 F1	SubG	SubG02 (Fig. 3)
29	AM007 x AM001 F1	SubG	SubG03 (Fig. 3)
30	Gy14M-17	M	CNV UCO, qPCR
31	Gy14M-42	M	CNV UCO, qPCR
32	Gy14M-63	M	CNV UCO, qPCR
33	9930	M	Reference
34	PI 183967	M	CNV, reads alignment
35	PI 197088	M	CNV, reads alignment
36	WI7167	M	CNV, reads alignment
37	G421	G	CNV, reads alignment

* From 2014 and 2015 field data. A = andromonoecious; G = gynoecious, M = monoecious, H = hermaphrodite.

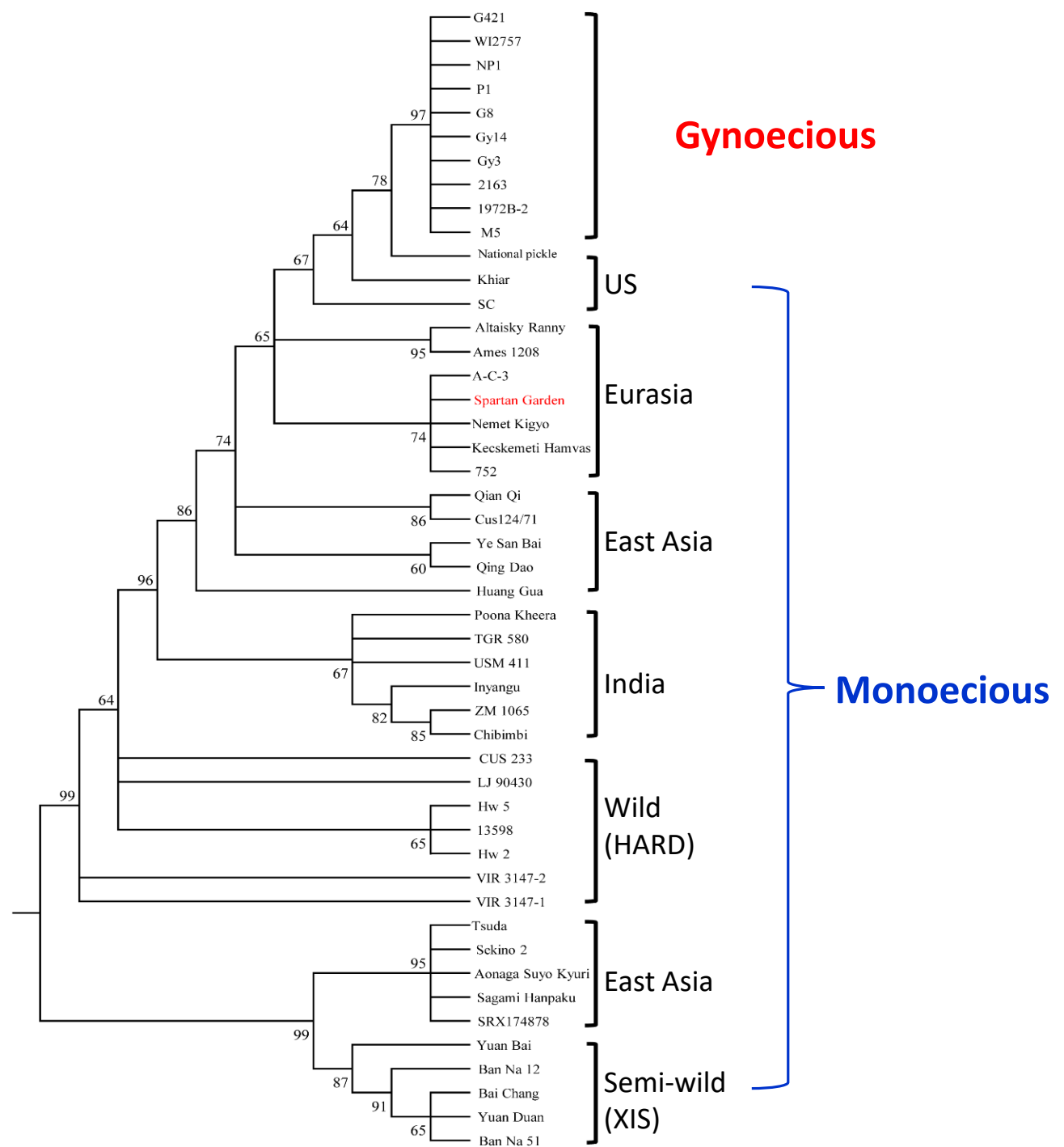
Supplementary File 6 (Table S3). Nucleotide diversity at the 50 kb *F* locus (*CsACS1G*) among 48 cucumber varieties.

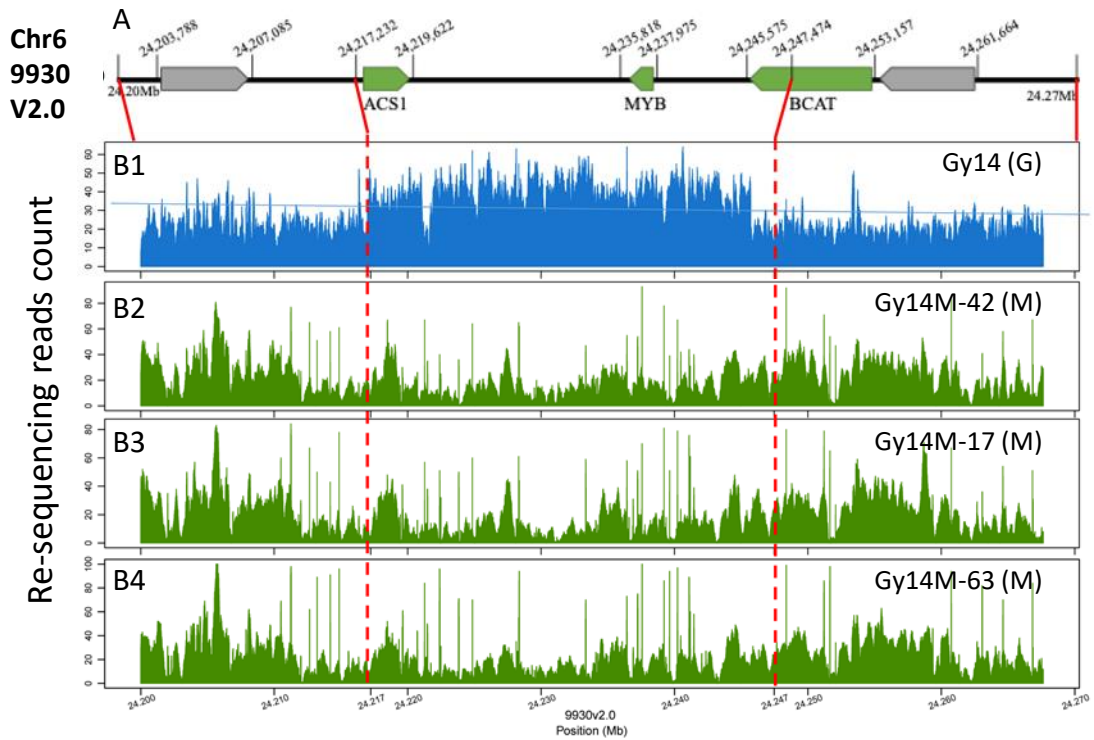
Serial #	PI or CGN #	Accession names	Sex expression	Botanical groups	Origin of accessions	Haplotypes*																			
						24,207,363	24,207,424	24,207,547	24,207,976	24,208,099	24,208,574	24,209,013	24,209,048	24,209,091	24,209,317	24,209,361	24,209,584	24,211,499	24,211,585	24,216,268	24,218,009	24,218,987	24,220,561	24,221,073	24,221,548
1	CGN19579	1972B-2	G	<i>Cs. var. sativus</i>	United States	T	G	A	A	G	C	C	C	G	C	T	C	C	A	C	A	T	T	C	T
2	CGN19677	M5	G	<i>Cs. var. sativus</i>	Netherlands	T	G	A	A	G	C	C	C	G	C	T	C	C	A	C	A	T	T	C	T
3	CGN19844	2163	G	<i>Cs. var. sativus</i>	United States	T	G	A	A	G	C	C	C	G	C	T	C	C	A	C	A	T	T	C	T
4	CGN20515	Gy3(S4)	G	<i>Cs. var. sativus</i>	Poland	T	G	A	A	G	T	C	C	G	C	T	C	C	A	C	A	T	T	C	T
5	G421	G421	G	<i>Cs. var. sativus</i>	United States	T	G	A	A	G	T	C	C	G	C	T	C	C	A	C	A	T	T	C	A
6	G8	G8	G	<i>Cs. var. sativus</i>	United States	T	G	A	A	G	T	C	C	G	C	T	C	C	A	C	A	T	T	C	T
7	Gy14	Gy14	G	<i>Cs. var. sativus</i>	United States	T	G	A	A	G	T	C	C	G	C	T	C	C	A	C	A	T	T	C	T
8	NP1	NP1	G	<i>Cs. var. sativus</i>	United States	T	G	A	A	G	T	C	C	G	C	T	C	C	A	C	A	T	T	C	A
9	P1	P1	G	<i>Cs. var. sativus</i>	United States	T	G	A	A	G	T	C	C	G	C	T	C	C	A	C	A	T	T	C	A
10	W12757	W12757	G	<i>Cs. var. sativus</i>	United States	T	G	A	A	G	T	C	C	G	C	T	C	C	A	C	A	T	T	C	A
11	PI 221440	Khair; Badreng-i-Savareh	M	<i>Cs. var. sativus</i>	Afghanistan	T	G	A	A	G	C	C	C	G	C	T	C	C	A	C	A	T	T	C	A
12	CGN20243	Cus12471	M	<i>Cs. var. sativus</i>	China	T	G	A	A	G	T	C	C	G	C	T	C	C	A	C	A	T	T	C	T
13	V05A0522	Huang Gua	M	<i>Cs. var. sativus</i>	China	T	G	A	A	G	T	C	C	G	C	T	C	C	A	C	A	T	T	C	T
14	V05A0552	Qing Dao Qiu Ye Er San	M	<i>Cs. var. sativus</i>	China	T	G	A	A	G	T	C	C	G	C	T	C	C	A	C	A	T	T	C	T
15	V05A0985	Ye San Bai	M	<i>Cs. var. sativus</i>	China	T	G	A	A	G	T	C	C	A	C	T	C	C	A	C	A	T	T	C	A
16	V05A1115	Qian Qi Li Huang Gua	M	<i>Cs. var. sativus</i>	China	T	G	A	A	G	T	C	C	G	C	T	C	C	A	C	A	T	T	C	T
17	CG9142	Ban Na Huang Gua 12	M	<i>Cs. var. xishuangbanensis</i>	China, Yunnan	T	G	A	A	G	C	C	C	G	C	T	C	C	A	C	A	T	T	C	A
18	CG9153	Bai Chang Yuan Huang Gua	M	<i>Cs. var. xishuangbanensis</i>	China, Yunnan	T	G	A	A	G	C	C	C	G	C	T	C	C	A	C	A	T	T	C	T
19	CG9164	Yuan Bai Huang Gua	M	<i>Cs. var. xishuangbanensis</i>	China, Yunnan	T	G	A	A	G	C	C	C	G	C	T	C	C	A	C	A	T	T	C	T
20	CG9169	Yuan Duan Huang Pi	M	<i>Cs. var. xishuangbanensis</i>	China, Yunnan	T	G	A	A	G	C	C	C	G	C	T	C	C	A	C	A	T	T	C	T
21	CG9185	Ban Na Huang Gua 51	M	<i>Cs. var. xishuangbanensis</i>	China, Yunnan	T	G	A	A	G	C	C	C	G	C	T	C	C	A	C	A	T	T	C	T
22	PI 288995	Nemet Kigyo	M	<i>Cs. var. sativus</i>	Hungary	T	G	A	A	G	C	C	C	G	C	T	C	C	A	C	A	T	T	C	T
23	PI 326594	Keeskeneti Hamvas	M	<i>Cs. var. sativus</i>	Hungary	T	G	A	A	G	C	C	C	G	C	T	C	C	A	C	A	T	T	C	T
24	13598	13598	M	<i>Cs. var. hardwickii</i>	India	C	A	G	G	T	T	T	T	A	T	T	C	C	A	C	A	T	T	C	T
25	CUS 233	CUS 233	M	<i>Cs. var. hardwickii</i>	India	C	A	G	G	T	T	T	T	A	T	T	C	T	T	C	A	T	T	C	T
26	Hw 2	Hw 2	M	<i>Cs. var. hardwickii</i>	India	C	A	G	G	T	T	T	T	A	T	T	C	C	A	C	A	T	T	C	A
27	Hw 5	Hw 5	M	<i>Cs. var. hardwickii</i>	India	C	A	G	G	T	T	T	T	A	T	T	C	C	A	C	A	T	T	C	T
28	LJ90430	LJ 90430	M	<i>Cs. var. hardwickii</i>	India	C	A	G	G	T	T	T	T	C	T	T	C	C	A	C	A	T	T	C	T
29	PI 504564	VIR 3147	M	<i>Cs. var. hardwickii</i>	India	C	A	G	G	T	T	T	T	C	T	T	C	C	A	C	A	T	T	C	T
30	PI 605988	USM 411	M	<i>Cs. var. sativus</i>	India	C	A	G	G	T	C	T	T	G	T	A	C	T	A	C	A	T	T	C	A
31	PI 606033	Poona Kheera	M	<i>Cs. var. sativus</i>	India	C	A	G	G	T	T	T	T	G	T	T	C	C	A	C	A	T	T	C	A
32	VIR 3147	VIR 3147	M	<i>Cs. var. hardwickii</i>	India	C	A	G	G	T	T	T	T	C	T	T	C	C	A	C	A	T	T	C	T
33	CG3010	Sagami Hanpaku Fushinari Kyuri	M	<i>Cs. var. sativus</i>	Japan	C	A	G	G	T	T	T	T	A	T	A	T	T	T	G	G	A	T	G	A
34	CGN19828	CGN19828	M	<i>Cs. var. sativus</i>	Japan	C	A	G	G	T	T	T	T	A	T	A	T	T	T	G	G	A	T	G	T
35	CGN20854	Aonaga Suyo Kyuri	M	<i>Cs. var. sativus</i>	Japan	C	A	G	G	T	T	T	T	A	T	A	T	T	T	G	G	A	A	G	T
36	PI 267942	Sekino No. 2 (Ochiai No.2)	M	<i>Cs. var. sativus</i>	Japan	C	A	G	G	T	T	T	T	A	T	A	T	T	T	G	G	A	A	G	A
37	PI 504563	Tsuda	M	<i>Cs. var. sativus</i>	Japan	C	A	G	G	T	T	T	T	A	T	A	T	T	T	G	G	A	A	G	A
38	CGN20512	752	M	<i>Cs. var. sativus</i>	Netherlands	T	G	A	A	G	C	C	C	G	C	T	C	C	A	C	A	T	T	C	T
39	PI 263047	Altaiisky Ranny	M	<i>Cs. var. sativus</i>	Russia	T	G	A	A	G	C	C	C	G	C	T	C	C	A	C	A	T	T	C	A
40	PI 512596	Ac-3	M	<i>Cs. var. sativus</i>	Spain	T	G	A	A	G	C	C	C	G	C	T	C	C	A	C	A	T	T	C	T
41	PI 338236	Ames 1208	M	<i>Cs. var. sativus</i>	Turkey	T	G	A	A	G	C	C	C	G	C	T	C	C	A	C	A	T	T	C	A
42	CGN19655	SC 53-B (6)	M	<i>Cs. var. sativus</i>	United States	T	G	A	A	G	C	C	C	G	C	T	C	C	A	C	A	T	T	C	T
43	CGN21626	National Pickle	M	<i>Cs. var. sativus</i>	United States	T	G	A	A	G	C	C	C	G	C	T	C	C	A	C	A	T	T	C	T
44	CGN21627	Spartan Garden	M	<i>Cs. var. sativus</i>	United States	T	G	A	A	G	C	C	C	G	C	T	C	C	A	C	A	T	T	C	T
45	PI 500359	ZM 1065	M	<i>Cs. var. sativus</i>	Zambia	C	A	G	G	T	T	T	T	A	T	T	C	C	A	C	A	T	T	G	A
46	PI 500361	Inyangu	M	<i>Cs. var. sativus</i>	Zambia	C	A	G	G	T	C	T	T	A	T	T	C	C	A	C	A	T	T	C	A
47	PI 500365	Chibimbi	M	<i>Cs. var. sativus</i>	Zambia	C	A	G	G	T	T	T	T	A	T	T	C	C	A	C	A	T	T	C	A
48	PI 482412	TGR 580	M	<i>Cs. var. sativus</i>	Zimbabwe	C	A	G	G	T	T	T	T	G	T	T	C	C	A	C	A	T	T	C	A

* The SNP positions are based on 9930 V2.0. Genome data are from Yang et al. (2012), and Qi et al. (2013). The repeat unit of the *F* locus (~30 kb) is from 24,217,232 to 24,247,474 in 9930 V2.0.

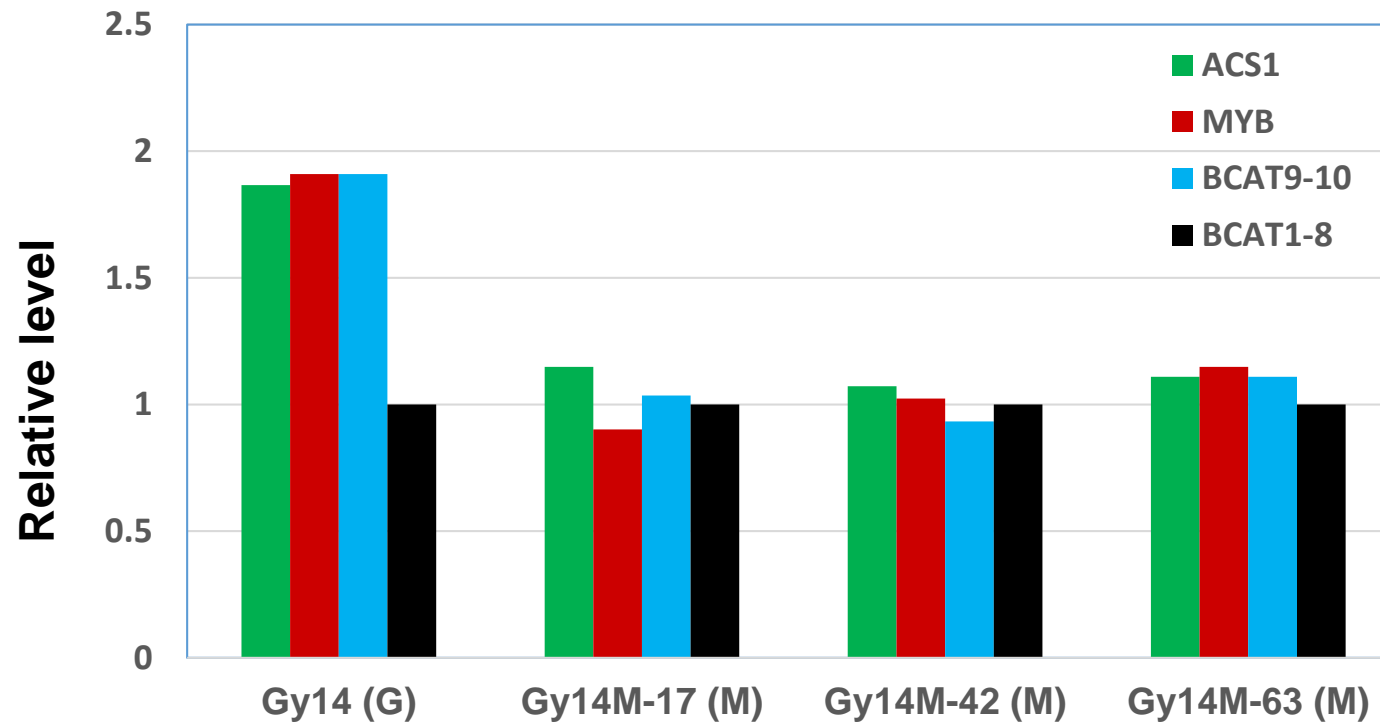
	24.222.140	24.223.241	24.223.245	24.226.857	24.227.034	24.227.349	24.229.168	24.229.194	24.229.482	24.229.619	24.233.704	24.234.010	24.236.089	24.236.195	24.236.212	24.236.380	24.236.801	24.237.028	24.237.206	24.237.254	24.238.678	24.238.966	24.240.300	24.242.378	24.244.219	24.245.834	24.245.869	24.245.888	24.246.390	24.247.113
		MYB	MYB	MYB	MYB	MYB	MYB	MYB	MYB	MYB	MYB	MYB	MYB	MYB	MYB	MYB	MYB	MYB	MYB	MYB					BCAT	BCAT	BCAT	BCAT	BCAT	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	G	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	
C	G	G	T	T	A	A	-	G	G	A	C	A	C	A	T	G	G	T	T	G	T	C	G	A	A	T	T	G	A	

Supplementary File 7 (Figure S4). Phylogenetic tree of 48 cucumber lines based on 68 SNPs and 3 indels within the 50-kb genomic region at the *F* locus. Details of the accessions, and markers are provided in Table S2.





Supplemental File 8 (Figure S5). Copy number variation at this *F* locus in ‘gynoecy loss’ cucumber mutants. This region has ~30 kb in the monoecious line 9930 with three predicted genes (top, coordinates based on V2.0). Alignment of re-sequencing reads against the 30 kb region of 9930 reveals loss of the extra copy in the three monoecious mutants (B2-B4) as compared to their parental line Gy14 (B1). Vertical red dotted lines delimit the CNV region.



Supplementary File 9 (Figure S6). Copy numbers of different regions revealed by qPCR among Gy14 and the three ‘gynocy-loss’ (Gy14M-17/42/63) lines. The detailed assay is according to Fig. 3B and C.

Supplementary File 10 (Figure S7).

Sex expression of the F₁ plants from Gy14 × 9930 (A and B), Gy14M-17 × 9930 (C), and Gy14M42 × 9930 crosses (D). Plants in A and B are subgynoecious, and those in C and D are monoecious. Red and blue arrows indicate the male flowers in subgynoecious plants (A and B), and ovaries (female flowers) in monoecious plants (C and D), respectively.

