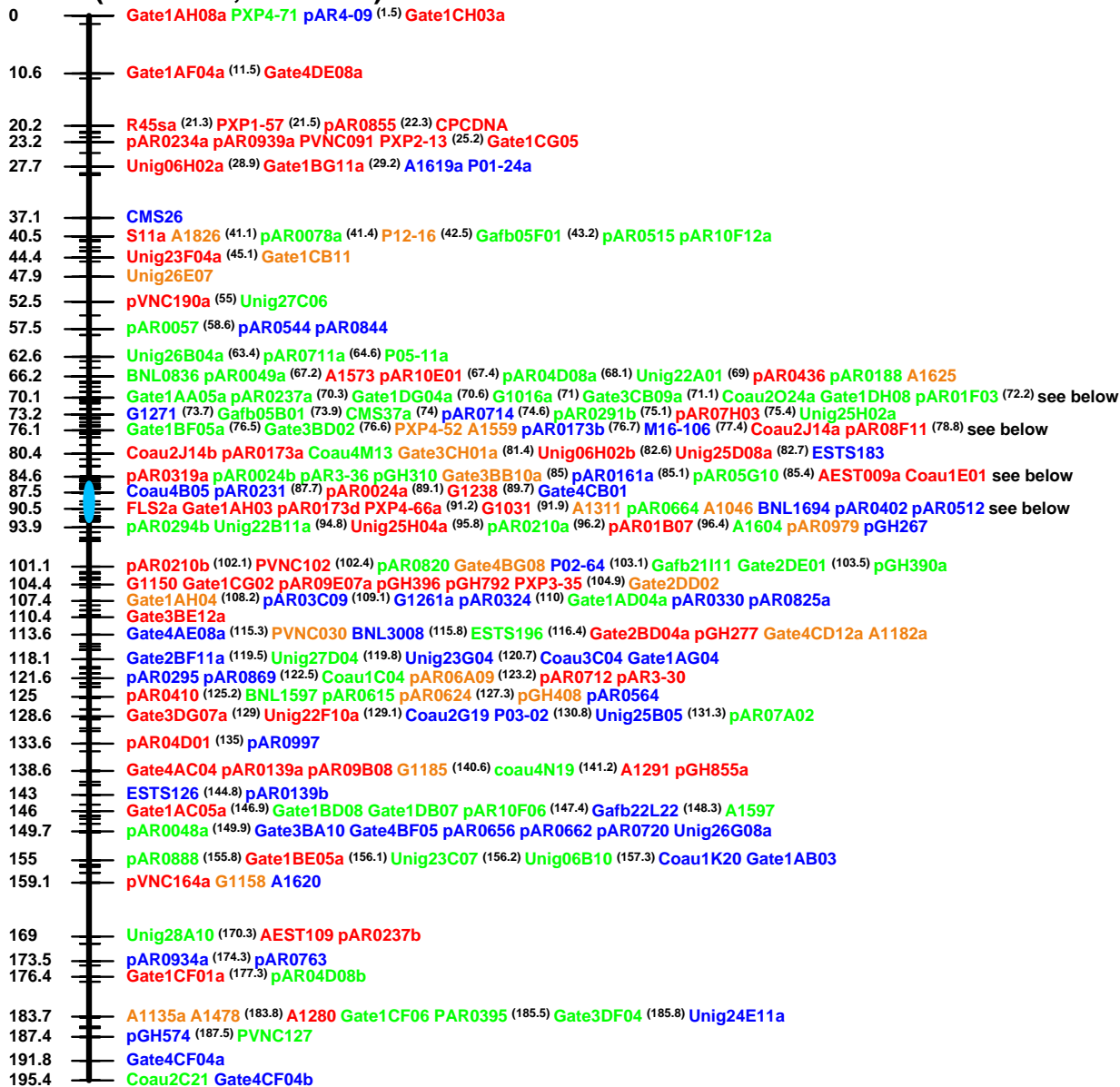


Legend for the supplemental figure:

13 cotton Consensus maps from 13 corresponding homoeologous groups. Markers colored with green, blue and red were originally from At, Dt and diploid D, respectively. Markers colored with brown were common loci originally from two or more homoeologous chromosomes. Vertical bars colored with yellow and green represented inverted regions on diploid D and At chromosomes compared to the consensus map, respectively. The vertical ellipses highlighted with blue on the map represented the possible location of centromeres, inferred as described elsewhere (Rong et al 2004).

C01 (195.4 cM, 245 Loci)



(72.2) Gate3BE11a Unig26C04a

(78.8) Unig06D05a

(85.4) pAR04B03 (85.9) Gate1AE01 PXP4-05 (86.2) G1006 G1045a (86.5) pAR0161b (86.6) pAR0319b pAR0040 pAR0173c

(86.6) pAR0887 CMS14 BNL1551 BNL3090a pAR0285a pAR0291a Unig23A09 Unig25G01a (86.9) pAR0285b

(91.9) pAR0579 Unig28E03 Unig28G08 (92.4) pAR0941a pGH646 (92.8) pAR0294a A1437 Coau3J21

C02 (176.4 cM, 194 Loci)



(61.2) A1691a P09-54 pAR0705 A1097

(128.8) Gate1DB11b

(130.6) Gafb26N16a (130.8) G1188 (130.9) BNL3888a A1204a (131) Unig25D08b Coau1O13

C03 (120.7 cM, 149 Loci)



(56.2) Gate3CB03 pAR0149b pAR2-26
 (60.4) Unig24C11a (60.8) A1536a A1683 Coau2O04 pXP4-01a
 (62.9) pGH549a (63.5) Unig24G11a (63.7) Gate1CD07b (63.8) PXP4-01b (64.3) BNL1667 BNL3971 (64.4) A1146 G1258a Gafb13B07
 (64.4) Gate3BE03 Gate3CF08 Gate4CB06 Gate4DE11 BNL3408 pAR0250a pAR0318 PAR0499 pAR0701 pGH395
 (64.4) pGH399 pGH430 Unig24G02
 (76.6) BNL1145 pAR04H03

C04 (183.8 cM, 208 Loci)



(77) Unig06D12a
 (111) pVNC149a (111.4) pAR0854 pAR07D04c (112.1) A1345b A1828 pAR3-15
 (117.6) Gate2CD01 pAR0118a pGH318 A1667a Gate4AC08
 (119.7) pAR0118b (119.8) A1168 (120.2) A1590a G1013 Gate2CF02 P05-24 (120.3) pGH422 (120.4) BNL3257 P01-02 (120.5) pAR0973 (121.1)
 (121.1) Gate1CC03 (121.6) P05-18 pAR0950 pAR3-07

C05 (191.9 cM, 246 Loci)



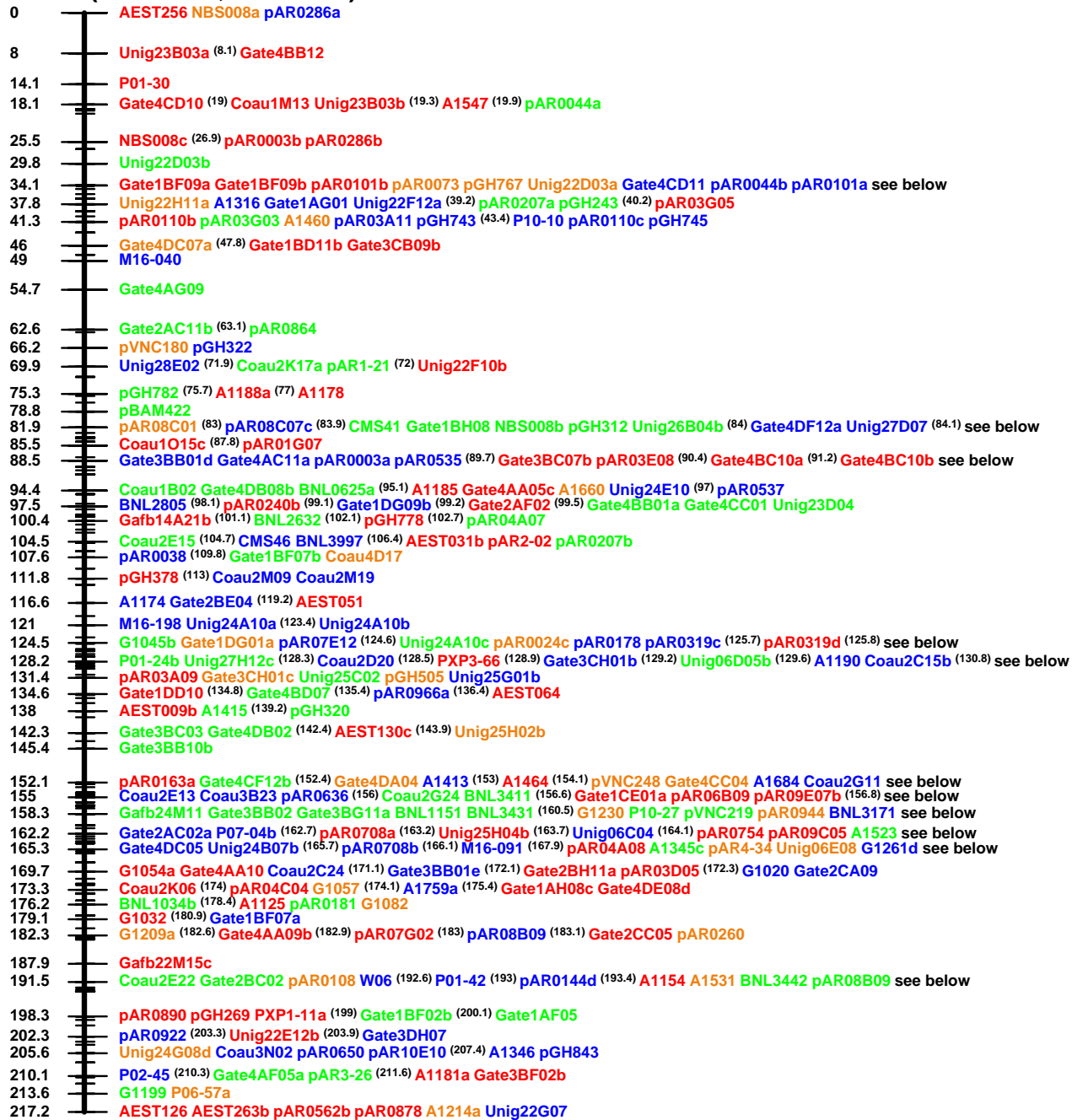
(60.6) Coau1M15 Gate1DA03 PXP4-65
 (69.6) Coau1L22 BNL3502 pAR0358 pGH812 (69.7) A1325 BNL1667b (69.9) Gate3DC02a (70) BNL1667a pGH549c (70.1)
 (70.1) BNL3971 (70.2) pGH625 Unig26C03a (70.6) A1171b Coau3B05a G34A3-3b (70.7) Gate4CD03c gate2DG02a pAR0050a
 (70.7) pAR0879
 (71.9) Gate2BD04b Unig28F06 Coau1J10 (72) pVNC313 (72.3) G1269a Gate3CF07 A1148 pGH442 BNL1059 (72.9) pAR4-14a
 (72.9) pGH364 pAR0071 (73.3) pAR04G06a (73.5) ESTS154 (73.6) pAR01A03 pAR0429 pAR04D09 pAR04G06b pAR08E07 (73.7)
 (73.7) pAR03E02 (74) Gate1BG11b
 (105.6) P01-18 (105.9) Gate4AE05 G1147 (106.2) A1727 G1044 M16-161 UN1121 (106.7) Coau1L18
 (109.6) A1418

C06 (172.6 cM, 235 Loci)



(68.2) BNL3903a pAR0257b pAR04B01 Unig27G07a
(71.8) P08-36 pAR0068 pAR0144b Unig23E02 P12-12 Coau1H02b Coau2C12 Gafb23A18 Gate4CA02 pAR0127b pAR1-33
(71.8) pGH730 pVNC164c Unig22C04 Unig22F09b Unig27G07b
(95) Coau1L24 BNL3582a
(100.2) pAR0771a^(101.1) Gate3DC04 P03-07
(111.6) A1471a M16-125a^(111.9) PXP4-23 pGH783^(112.4) pAR0096a
(162.8) pAR0144c Unig24E02

C07 (217.2 cM, 290 Loci)



(34.1) pAR0566 pAR0576 (34.8) A1623 (35.8) A1202 (36.7) pVNC012 BNL1231 Gafb14F08
 (84.1) pAR0716 (84.7) M16-105 pAR10E04
 (91.2) A1296 pBAM291b pGH854 PXP3-26
 (125.8) Gate1DD03 (126.1) A1400 Gate1BC11 A1717 (126.7) G1095 (127.2) Gate1DG01b pGH445 Unig24A10d
 (130.8) Unig24D01
 (154.1) pAR0843 (154.4) P13-07 (154.7) pAR0163b
 (156.8) Unig23D11 (157.2) Unig22B11b
 (160.5) pGH436 (161.1) pGH334
 (164.1) BNL2589 pGH819 pGH560 Gate1BA07
 (167.9) P10-56b
 (193.4) PXP3-14 pAR0570

C08 (159.5 cM, 247 Loci)



- (35.8) pVNC098
- (45.2) Gate1DC11 pAR4-14b Gate4BG06b
- (68.8) pGH785
- (72.8) pAR0244 Unig22H11b
- (112) pAR0534 pAR06B11 pAR06E10
- (119.9) Gate4DF03b
- (151.3) pGH337

C09 (264.6 cM, 382 Loci)



C10 (172.6 cM, 164 Loci)



(96.5) pAR0897b (97.4) Gate4AH05
 (108.2) G1161 Gate4CD01
 (112.9) pAR0717 pGH663 (113.4) pAR0145b (113.7) pAR0264a pGH290 (114.2) A1196 (114.5) pAR0211 pAR0768

C11 (170.2 cM, 227 Loci)



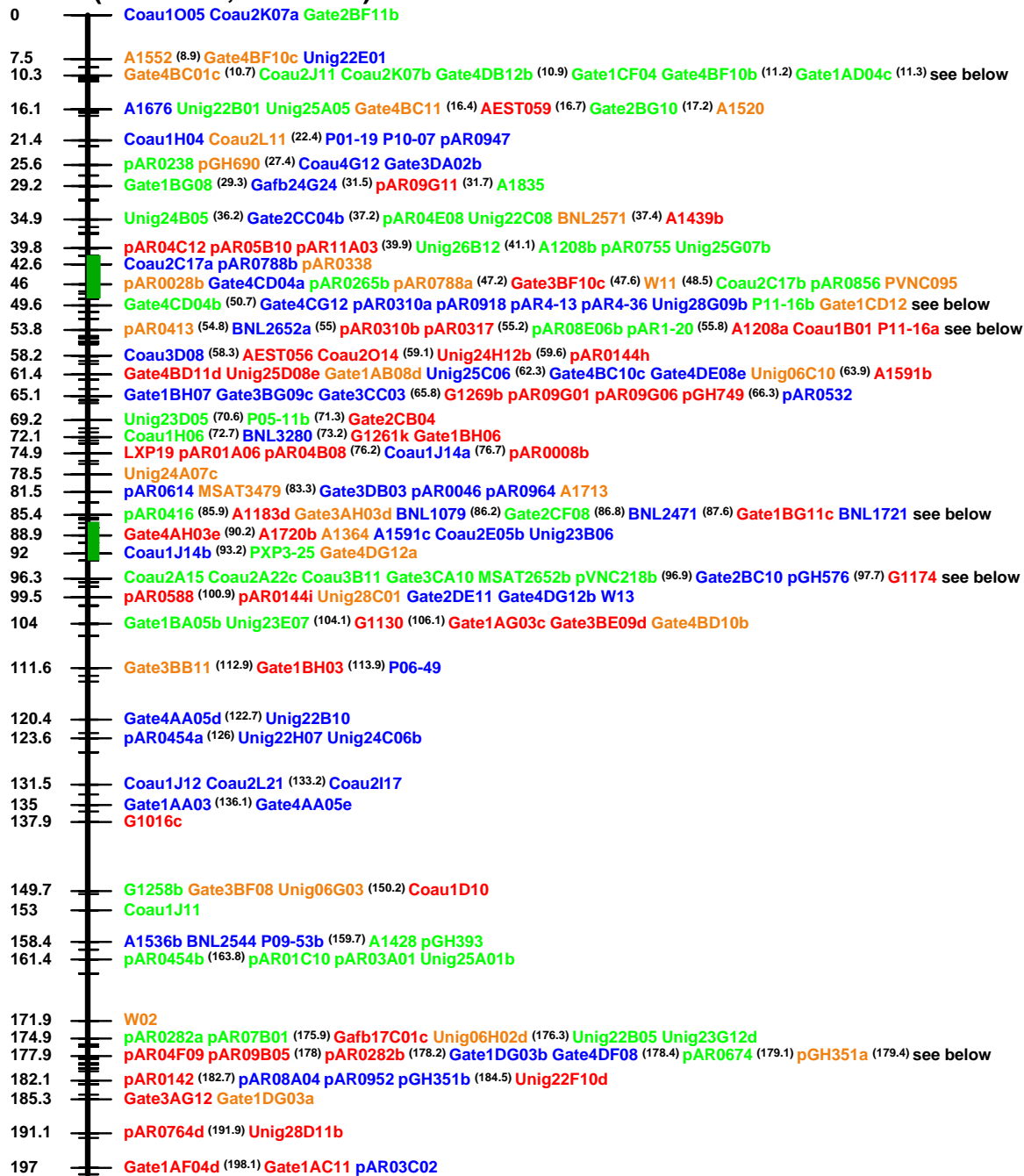
(45.7) Gafb28K14 (45.9) pGH588c (46.1) A1344 (46.8) pBAM250 pGH653b
 (56.9) G1257b
 (60.4) Gate3BF11 pGH384
 (63.1) Gate2DF07 Gate4DH08d pAR0946 pGH270 Unig22B09⁽⁶⁴⁾ Coau3F17a P06-47^(64.4) Coau1C21 Gate3CA08 pAR0055b
 (67.5) Gate3CB09c Gate3CG03
 (77.6) Unig24E01
 (88.1) Gate4DD11 pAR04E05^(88.6) BNL1161^(89.2) G1261g PXP4-66b Unig06E10^(89.5) Unig25A02d
 (104.9) Coau2O08

C12 (101.7 cM, 187 Loci)



- (23.7) G1261i
- (26.8) Gate2BF04
- (29.7) Gate3BA08 BNL3433 Gate1BA05a BNL3955b
- (39.6) pAR0450b (40) Unig27A11a Unig27B06a (40.1) Coau2I05b (40.4) Gate4AE08b pVNC058
- (42.1) pGH857b A1172 (43.1) G1033 (43.5) P05-32c (43.9) Unig27B06b Unig28C06 Unig28H09
- (45.3) pAR0939c (46) P11-38 (46.8) pAR04E02b
- (48.7) Gate1AF04c Gate4AD05c A1638 Gate4AE10 pAR08H07 (48.9) PXP1-77b (49.1) A1254 A1159c (49.4) pAR06E04
- (49.4) Coau1E03 pAR0131 A1159a (49.5) ESTS178 Gate1CH01b (49.6) pAR0078b Unig26B02b A1619d BNL1673 (50) Unig25D10
- (51.7) Unig23G07b (52.3) Gate4DF07b pAR0042 pAR0206c pAR0144g
- (56.3) Gate4AA07 P05-02 Unig25E12 (56.7) Gate1CH01a Gate2BG01 Gate4BA04

C13 (198.1 cM, 242 Loci)



(11.3) G1115b Gafb23B18 pAR0601 Gate3AH03b
 (50.7) pAR06C06 (51.9) P02-16b pAR08H05
 (55.8) pAR08F06 pAR0930 Unig26D07b (56) Gate1AG05 Unig22D09 (56.1) Gate2AB07 (56.2) Unig22F12b Gate3DA09
 (56.2) pAR0274 Unig22A02
 (87.6) PXP1-11c Coau2A19 Coau2K17b Gate3CC08 Gate4BE04 pAR0958 pAR4-39 PXP1-69 PXP2-25 pVNC256 G1125
 (97.7) pAR0049c
 (179.4) pAR0898 (180) pAR04B07 pGH544 pAR0923 (180.5) pAR0924