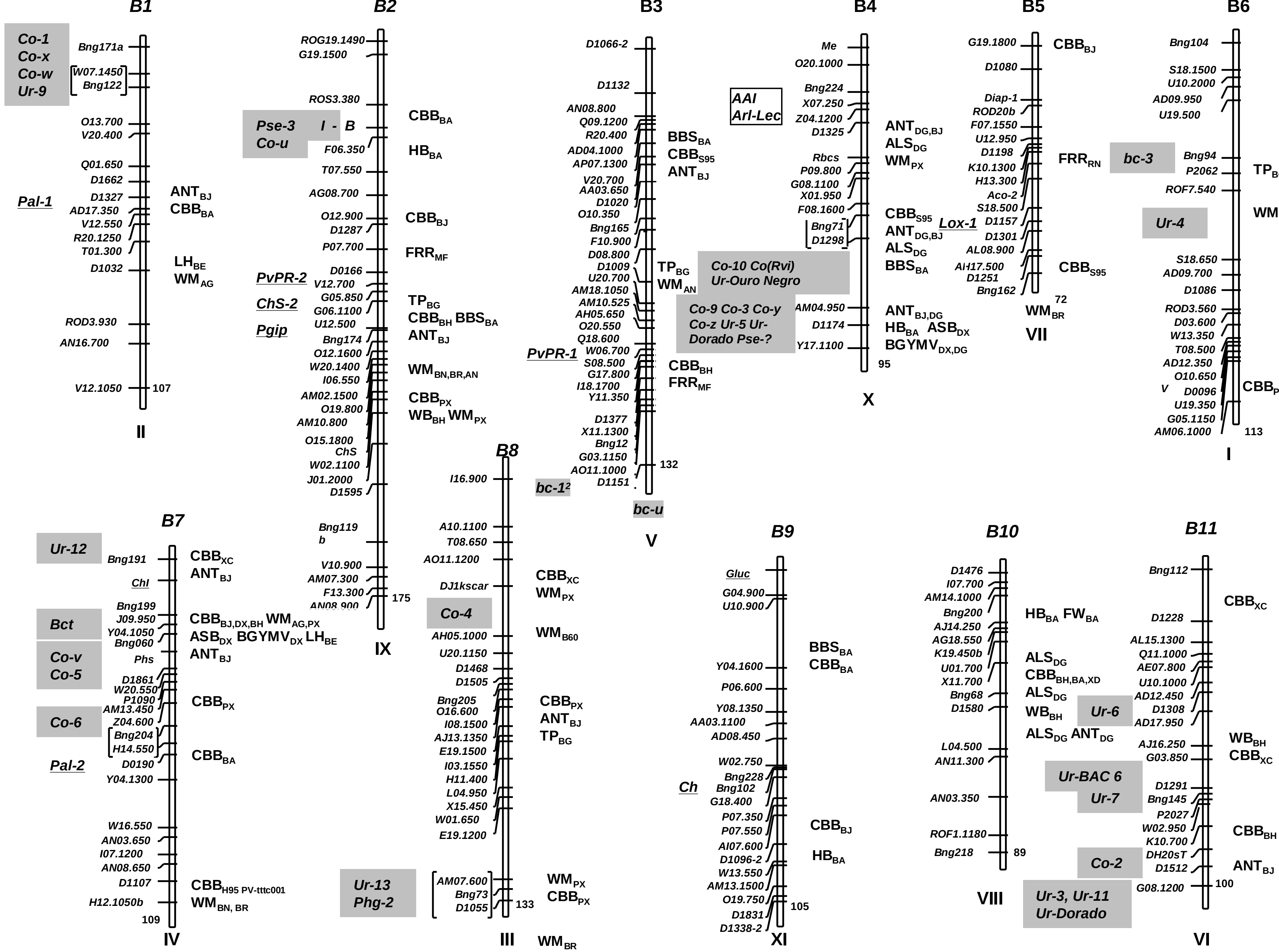
B1
Co-1
Co-x
Co-w
Ur-9
Bng171a
W07.1450
Bng122
O13.700
V20.400
Q01.650
D1662
D1327
Pal-1
AD17.350
V12.550
R20.1250
T01.300
D1032
ROD3.930
AN16.700
V12.1050
107
ANT$_{BJ}$
CBB$_{BA}$
LH$_{BE}$
WM$_{AG}$
II
B2
ROG19.1490
G19.1500
ROS3.380
Pse-3
Co-u
I - B
F06.350
T07.550
AG08.700
O12.900
D1287
P07.700
D0166
PvPR-2
V12.700
ChS-2
G05.850
G06.1100
Pgip
U12.500
Bng174
O12.1600
W20.1400
I06.550
AM02.1500
O19.800
AM10.800
O15.1800
ChS
W02.1100
J01.2000
D1595
Bng119 b
V10.900
AM07.300
F13.300
AN08.900
175
CBB$_{BA}$
HB$_{BA}$
CBB$_{BJ}$
FRR$_{MF}$
TP$_{BG}$
CBB$_{BH}$ BBS$_{BA}$
ANT$_{BJ}$
WM$_{BN,BR,AN}$
CBB$_{PX}$
WB$_{BH}$ WM$_{PX}$
IX
B3
D1066-2
D1132
AN08.800
Q09.1200
R20.400
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AP07.1300
V20.700
AA03.650
D1020
O10.350
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F10.900
D08.800
D1009
U20.700
AM18.1050
AM10.525
AH05.650
O20.550
Q18.600
PvPR-1
W06.700
S08.500
G17.800
I18.1700
Y11.350
D1377
X11.1300
Bng12
G03.1150
AO11.1000
D1151
bc-1^{2}
bc-u
132
BBS$_{BA}$
CBB$_{S95}$
ANT$_{BJ}$
TP$_{BG}$
WM$_{AN}$
CBB$_{BH}$
FRR$_{MF}$
V
B4
AAI
Arl-Lec
Me
O20.1000
Bng224
X07.250
Z04.1200
D1325
Rbcs
P09.800
G08.1100
X01.950
F08.1600
Bng71
D1298
Co-10 Co(Rvi)
Ur-Ouro Negro
Co-9 Co-3 Co-y
Co-z Ur-5 Ur-
Dorado Pse-?
AM04.950
D1174
Y17.1100
95
ANT$_{DG,BJ}$
ALS$_{DG}$
WM$_{PX}$
CBB$_{S95}$
ANT$_{DG,BJ}$
ALS$_{DG}$
BBS$_{BA}$
ANT$_{BJ,DG}$
HB$_{BA}$ ASB$_{DX}$
BGYMV$_{DX,DG}$
X
B5
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ROD20b
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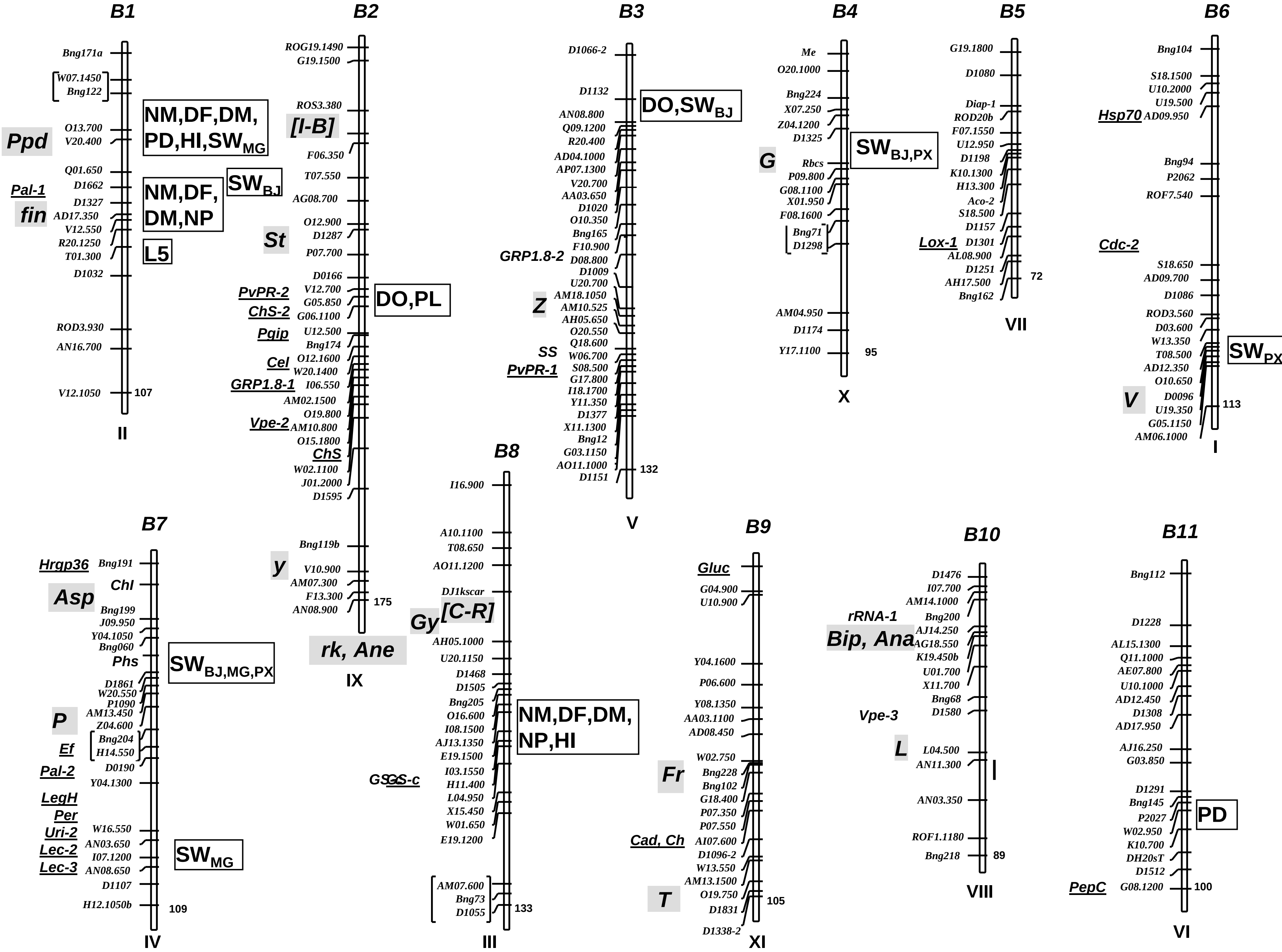
K10.1300
H13.300
Aco-2
S18.500
Lox-1
D1157
D1301
AL08.900
AH17.500
D1251
Bng162
72
CBB$_{BJ}$
FRR$_{RN}$
CBB$_{S95}$
WM$_{BR}$
VII
B6
bc-3
Ur-4
Bng104
S18.1500
U10.2000
AD09.950
U19.500
Bng94
P2062
ROF7.540
S18.650
AD09.700
D1086
ROD3.560
D03.600
W13.350
T08.500
AD12.350
O10.650
V
D0096
U19.350
G05.1150
AM06.1000
113
TP$_{B}$
WM
CBB$_{P}$
I
B7
Ur-12
Bng191
Chl
Bng199
Bct
J09.950
Y04.1050
Bng060
Co-v
Co-5
Phs
D1861
W20.550
P1090
AM13.450
Co-6
Z04.600
Bng204
H14.550
Pal-2
D0190
Y04.1300
W16.550
AN03.650
I07.1200
AN08.650
D1107
H12.1050b
109
CBB$_{XC}$
ANT$_{BJ}$
CBB$_{BJ,DX,BH}$ WM$_{AG,PX}$
ASB$_{DX}$ BGYMV$_{DX}$ LH$_{BE}$
ANT$_{BJ}$
CBB$_{PX}$
CBB$_{BA}$
CBB$_{H95\ PV\text{-}tttc001}$
WM$_{BN,\ BR}$
IV
B8
I16.900
A10.1100
T08.650
AO11.1200
DJ1kscar
Co-4
AH05.1000
U20.1150
D1468
D1505
Bng205
O16.600
I08.1500
AJ13.1350
E19.1500
I03.1550
H11.400
L04.950
X15.450
W01.650
E19.1200
Ur-13
Phg-2
AM07.600
Bng73
D1055
133
CBB$_{XC}$
WM$_{PX}$
WM$_{B60}$
CBB$_{PX}$
ANT$_{BJ}$
TP$_{BG}$
WM$_{PX}$
CBB$_{PX}$
WM$_{BR}$
III
B9
Gluc
G04.900
U10.900
Y04.1600
P06.600
Y08.1350
AA03.1100
AD08.450
W02.750
Ch
Bng228
Bng102
G18.400
P07.350
P07.550
AI07.600
D1096-2
W13.550
AM13.1500
O19.750
D1831
D1338-2
105
BBS$_{BA}$
CBB$_{BA}$
CBB$_{BJ}$
HB$_{BA}$
XI
B10
D1476
I07.700
AM14.1000
Bng200
AJ14.250
AG18.550
K19.450b
U01.700
X11.700
Bng68
D1580
L04.500
AN11.300
AN03.350
ROF1.1180
Bng218
89
HB$_{BA}$ FW$_{BA}$
ALS$_{DG}$
CBB$_{BH,BA,XD}$
ALS$_{DG}$
WB$_{BH}$
ALS$_{DG}$ ANT$_{DG}$
VIII
B11
Ur-6
Ur-BAC 6
Ur-7
Co-2
Ur-3, Ur-11
Ur-Dorado
Bng112
D1228
AL15.1300
Q11.1000
AE07.800
U10.1000
AD12.450
D1308
AD17.950
AJ16.250
G03.850
D1291
Bng145
P2027
W02.950
K10.700
DH20sT
D1512
G08.1200
100
CBB$_{XC}$
WB$_{BH}$
CBB$_{XC}$
CBB$_{BH}$
ANT$_{BJ}$
VI

Legend

Comprehensive genomic map of disease resistance genes and QTL in common bean [Abstracted from Miklas et al., 2006]. The linkage groups correspond to the core map version of Freyre et al. (1998), based on original map (Nodari et al., 1993) and resembles maps previously presented by Kelly et al. (2003), Kelly and Vallejo (2004) and Blair et al. (2003). The chromosome number (I –X1; Pedrosa et al., 2003) of each linkage group (B1 –B11) is shown at bottom of each linkage group. Directly to the left of each linkage group are the framework molecular markers (smaller font), the monogenic disease resistance genes (shaded boxes), defense related genes (underlined), and arcelin, lectin and alpha-amylase inhibitor genes (clear box). The *Co* are anthracnose resistance loci, *Ur* rust resistance loci (*Ur-Dorado, Ur-Ouro Negro,* and *Ur-BAC 6* refer to the line source of unnamed genes), *Pse* halo blight resistance loci, *I* and *bc* are dominant and recessive genes respectively for resistance to BCMV, *Phg* angular leaf spot resistance locus, and *Bct* is a locus for resistance to BCTV. For further explanations on DNA markers and gene symbols see Gepts (1999) and Bassett (2004). To the right of each linkage group are QTL mapped in different populations: ALS resistance to angular leaf spot, ANT anthracnose, ASB ashy stem blight, BGYMV bean golden yellow mosaic virus, BBS bacterial brown spot, CBB common bacterial blight, FRR *Fusarium* root rot, HB halo blight, LH leaf hopper, TP thrips, WB web blight, and WM white mold resistance. Symbols in subscript represent the source population of the QTL: AG A55/G 122 (Miklas et al., 2001), AN Aztec/ND88-106-04 (Miklas et al., 2007), BA Belneb-RR-1/A55 (Ariyarathne et al., 1999; Fourie et al., 2004; Jung et al., 2003), BE Berna/EMP 419 (Murray et al., 2004), BG BAT 881/G 21212 (Frei et al., 2005), BJ BAT 93/Jalo EEP558 (Freyre et al., 1998; Gepts, 1999; Geffroy et al., 2000), BH BAC 6/HT 7719 (Jung et al., 1996), BN Bunsi/Newport (Kolkman & Kelly, 2003), BR Bunsi/Raven (Ender & Kelly, 2005), B60 Benton/NY6020-4 (Miklas et al., 2003), DG DOR 364/G 19833 (López et al., 2003), DX DOR 364/XAN 176 (Miklas et al., 2000), H95 HR67/OAC 95 (Yu et al., 2004), MF (Montcalm/FR266 (Schneider et al., 2001), PX PC50/XAN 159 (Jung et al., 1997, 1998; Park et al., 2001), RN Red Hawk/Negro San Luis (Román-Avilés &. Kelly, 2005), S95 Seaforth/OAC 95 (Tar’an et al., 2001), and XC XR-235-1-1/Calima (Yu et al., 1998). Gene and QTL locations are approximate because most were not directly mapped in the BAT 93/Jalo EEP558 population. The total distance of each linkage group is expressed in Kosambi cM (bottom-right).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Bng171a
W07.1450
Bng122
O13.700
V20.400
Q01.650
D1662
D1327
AD17.350
V12.550
R20.1250
T01.300
D1032
ROD3.930
AN16.700
V12.1050
107
II
Ppd
Pal-1
fin
NM,DF,DM, PD,HI,SW$_{MG}$
NM,DF, DM,NP
L5
SW$_{BJ}$
B2
ROG19.1490
G19.1500
ROS3.380
F06.350
T07.550
AG08.700
O12.900
D1287
P07.700
D0166
V12.700
G05.850
G06.1100
U12.500
Bng174
O12.1600
W20.1400
I06.550
AM02.1500
O19.800
AM10.800
O15.1800
W02.1100
J01.2000
D1595
Bng119b
V10.900
AM07.300
F13.300
AN08.900
175
IX
[I-B]
St
PvPR-2
ChS-2
Pgip
Cel
GRP1.8-1
Vpe-2
ChS
y
rk, Ane
DO,PL
B3
D1066-2
D1132
AN08.800
Q09.1200
R20.400
AD04.1000
AP07.1300
V20.700
AA03.650
D1020
O10.350
Bng165
F10.900
D08.800
D1009
U20.700
AM18.1050
AM10.525
AH05.650
O20.550
Q18.600
W06.700
S08.500
G17.800
I18.1700
Y11.350
D1377
X11.1300
Bng12
G03.1150
AO11.1000
D1151
132
V
DO,SW$_{BJ}$
GRP1.8-2
Z
SS
PvPR-1
B4
Me
O20.1000
Bng224
X07.250
Z04.1200
D1325
Rbcs
P09.800
G08.1100
X01.950
F08.1600
Bng71
D1298
AM04.950
D1174
Y17.1100
95
X
G
SW$_{BJ,PX}$
B5
G19.1800
D1080
Diap-1
ROD20b
F07.1550
U12.950
D1198
K10.1300
H13.300
Aco-2
S18.500
D1157
D1301
AL08.900
D1251
AH17.500
Bng162
72
VII
Lox-1
B6
Bng104
S18.1500
U10.2000
U19.500
AD09.950
Bng94
P2062
ROF7.540
S18.650
AD09.700
D1086
ROD3.560
D03.600
W13.350
T08.500
AD12.350
O10.650
D0096
U19.350
G05.1150
AM06.1000
113
I
Hsp70
Cdc-2
V
SW$_{PX}$
B7
Bng191
Chl
Bng199
J09.950
Y04.1050
Bng060
Phs
D1861
W20.550
P1090
AM13.450
Z04.600
Bng204
H14.550
D0190
Y04.1300
W16.550
AN03.650
I07.1200
AN08.650
D1107
H12.1050b
109
IV
Hrgp36
Asp
P
Ef
Pal-2
LegH
Per
Uri-2
Lec-2
Lec-3
SW$_{BJ,MG,PX}$
SW$_{MG}$
B8
I16.900
A10.1100
T08.650
AO11.1200
DJ1kscar
AH05.1000
U20.1150
D1468
D1505
Bng205
O16.600
I08.1500
AJ13.1350
E19.1500
I03.1550
H11.400
L04.950
X15.450
W01.650
E19.1200
AM07.600
Bng73
D1055
133
III
Gy
[C-R]
GS
GS-c
NM,DF,DM, NP,HI
B9
Gluc
G04.900
U10.900
Y04.1600
P06.600
Y08.1350
AA03.1100
AD08.450
W02.750
Bng228
Bng102
G18.400
P07.350
P07.550
AI07.600
D1096-2
W13.550
AM13.1500
O19.750
D1831
D1338-2
105
XI
Fr
Cad, Ch
T
B10
D1476
I07.700
AM14.1000
Bng200
AJ14.250
AG18.550
K19.450b
U01.700
X11.700
Bng68
D1580
L04.500
AN11.300
AN03.350
ROF1.1180
Bng218
89
VIII
rRNA-1
Bip, Ana
Vpe-3
L
I
B11
Bng112
D1228
AL15.1300
Q11.1000
AE07.800
U10.1000
AD12.450
D1308
AD17.950
AJ16.250
G03.850
D1291
Bng145
P2027
W02.950
K10.700
DH20sT
D1512
G08.1200
100
VI
PepC
PD

Legend

Explanation: A second map is presented as it was not possible to fit all the genes and QTL on the first map due to space restrictions.

Comprehensive genomic map of the genes of known function for external phenotypic traits, and QTL in common bean, including genes with a biochemical function (mostly disease response genes), the domestication genes and color genes in common bean [Abstracted from Kelly et al., 2003]. Each linkage group is represented by its core map version (Freyre et al., 1998). To the left of each linkage group, are the framework molecular markers (smaller font) and the biochemical genes (larger font) and major phenotypic trait genes (shaded boxes). For explanations on marker and biochemical gene symbols, (Gepts, 1999); and the original map references (Vallejos et al., 1992; Nodari et al., 1993; Adam-Blondon et al., 1994). [*AI*- *Arl*-*Lec*] is the main locus coding for the -amylase inhibitor-arcelin-lectin multigene family. *Fin*, *Ppd*, *St* are genes for determinacy, sensitivity to photoperiod, and pod string formation (Koinange et al., 1996). *B, [C-R]*, *G*, *P*, and *rk* are seed color genes and *Ana*, *Ane*, *Bip*, *L*, *T* and *Z* are seed color pattern genes (McClean et al. 2002). *Asp* is a gene for seedcoat shininess (Arndt and Gepts 1989; Gepts 1999). *Fr* is a male fertility restorer gene (He et al. 1995). *SGou* and *Ms*-8 are genes controlling pod cross-section and male sterility (Adam-Blondon et al., 1994). To the right (boxed symbols), are QTLs mapped in different populations: DF and DM: number of days to flowering and to maturity, DO: seed dormancy, HI: harvest index, HT: height, L5: length of the 5th internode, LDG: lodging, NM: number of nodes on the main stem, NN: *Rhizobium* nodulation, NP: number of pods, PD: photoperiod-induced delay in flowering, PL: pod length, SW: seed weight. Location of most genes is approximate, as most were not directly mapped in the BJ population.

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