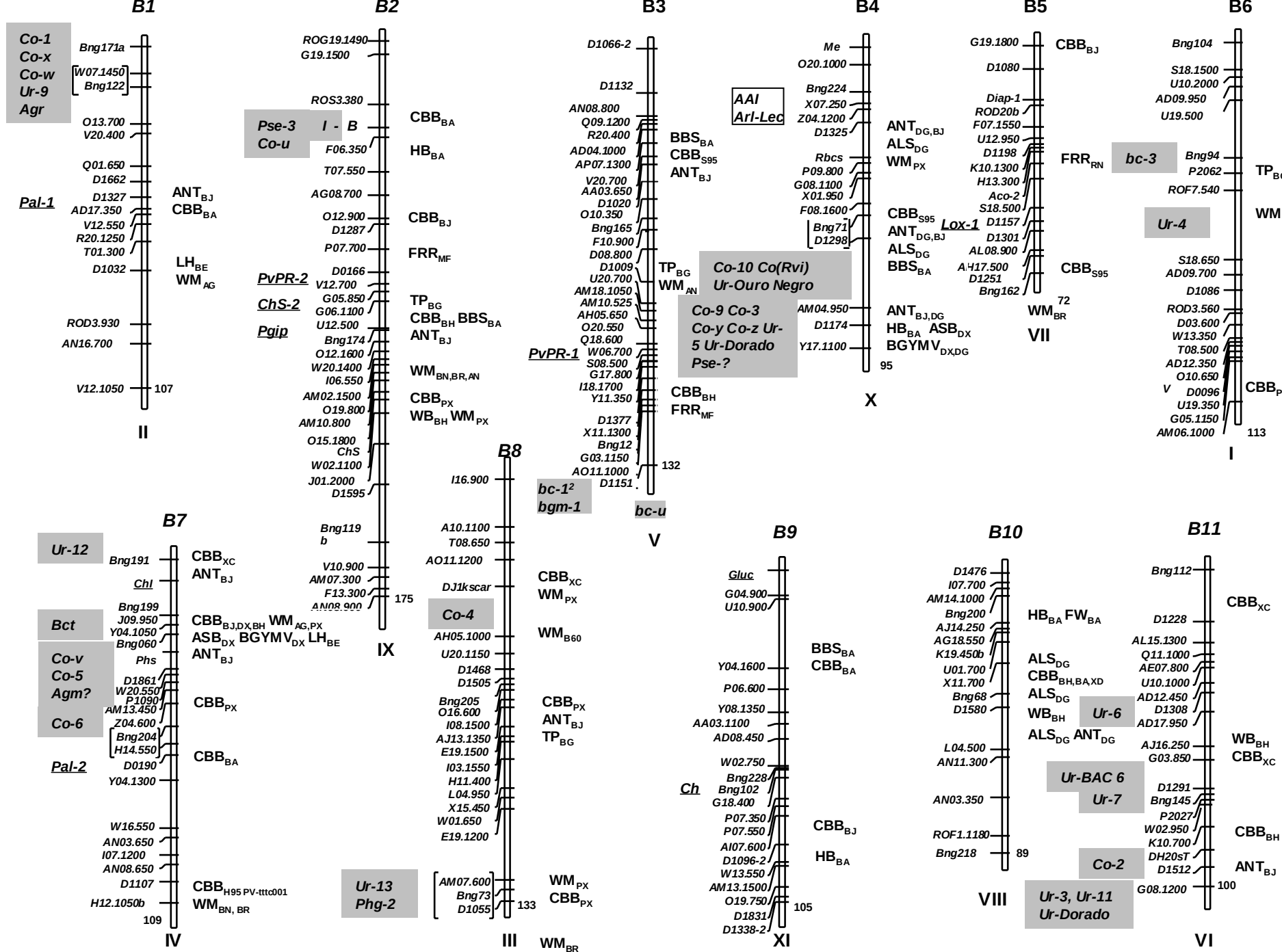


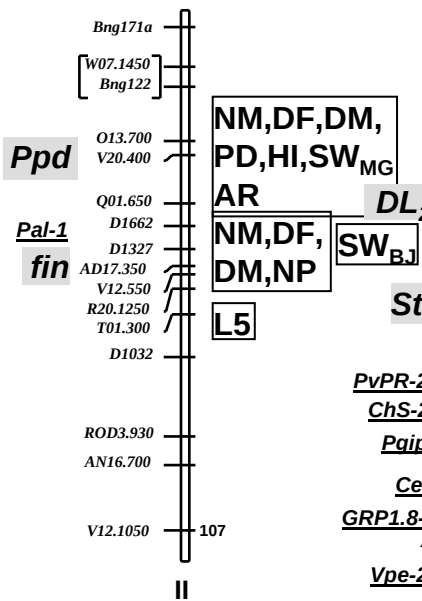


Legend

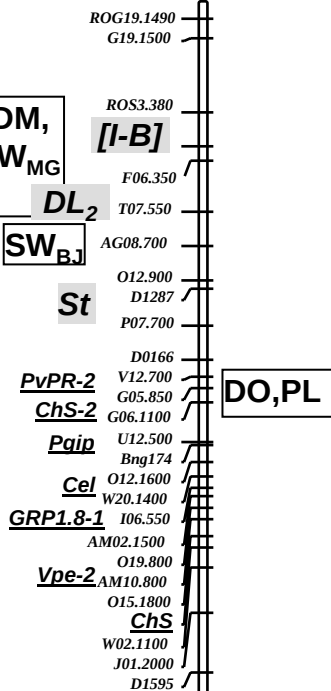
Comprehensive genomic map of disease resistance genes and QTL in common bean [Abstracted from Miklas et al., 2006]. The linkage groups correspond to the core map version of Freyre et al. (1998), based on original map (Nodari et al., 1993) and resembles maps previously presented by Kelly et al. (2003), Kelly and Vallejo (2004) and Blair et al. (2003; 2007). 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, *bgm-1* recessive resistance to BGYMV, *Phg* angular leaf spot resistance locus, *Bct* is a locus for resistance to BCTV, *Agr* and *Agm* independent genes for *Apion godmani* resistance (Garza et al., 1996; Blair et al., 2006). 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 (Ariyaratne 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 Bunsu/Newport (Kolkman & Kelly, 2003), BR Bunsu/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).

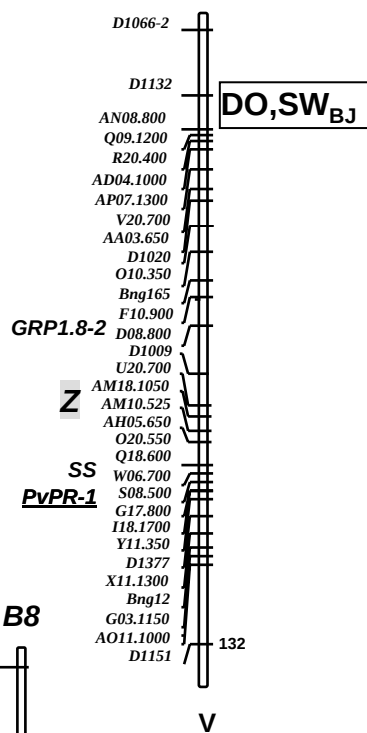
B1



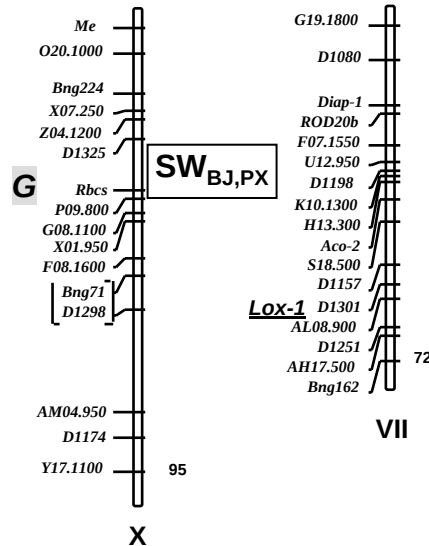
B2



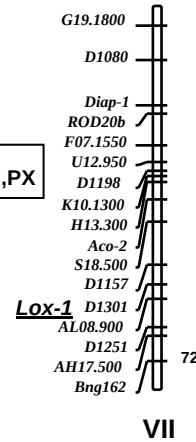
B3



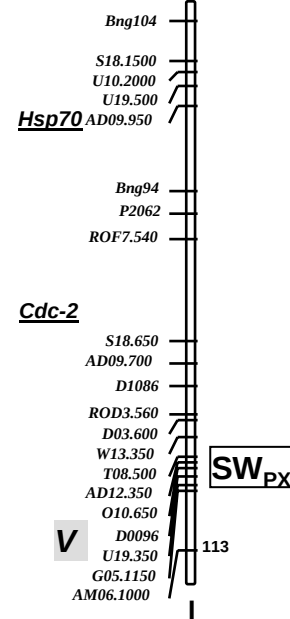
B4



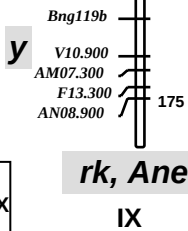
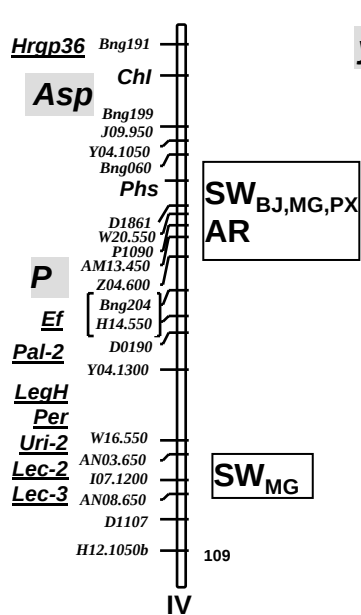
B5



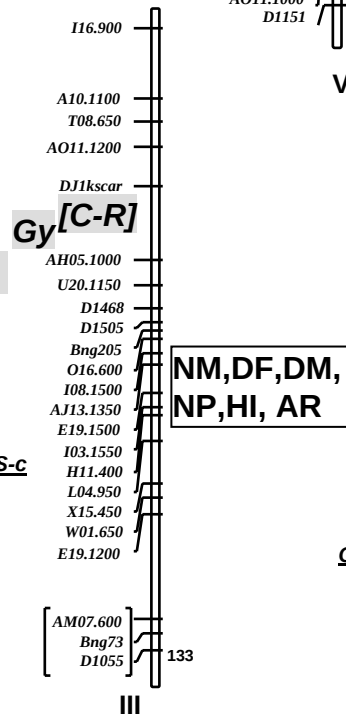
B6



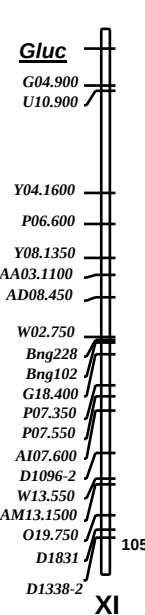
B7



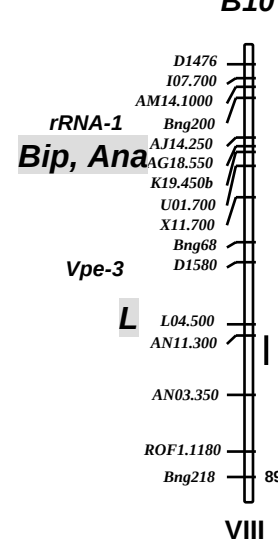
B8



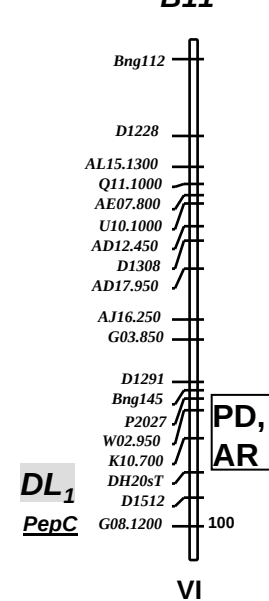
B9



B10



B11



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 α -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 (McClellan 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). *DL₁* and *DL₂* are the root and shoot expressed semidominant dosage-dependent lethal genes (Shii et al., 1980; Hannah et al., 2007).

To the right (boxed symbols), are QTLs mapped in different populations: AR: *Apion godmani* resistance (Blair et al., 2006), 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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