Supplemental Table S1. Pairwise comparison of common single nucleotide polymorphism (SNP) markers across cowpea populations.

Population [†]	M	L	K	J	I	H	G	F	E	D	C	B	A
A	84	177	164	157	89	174	183	118	195	192	290	254	–
B	89	191	133	157	47	163	195	117	193	188	279	–	
C	90	172	202	177	95	210	228	127	205	215	–		
D	59	175	132	149	68	149	180	113	184	–			
E	80	173	136	152	66	142	168	148	–				
F	48	107	100	113	49	109	121	–					
G	74	133	167	160	77	193	–						
H	81	116	142	131	63	–							
I	27	49	90	93	–								
J	67	135	136	–									
K	66	118	–										
L	60	–											
M	–												

[†]A: CB27 × IT97K-556-6; B: CB27 × IT82E-18; C: CB27 × UCR779; D: CB46 × IT93K-503-1; E: 524B × IT84S-2049; F: Dan Ila × TVu-7778; G: Yacine × 58-77; H: Sanzi × Vita 7; I: IT84S-2246 × IT93K-503; J: IT84S-2246 × Mouride; K: TVu14676 × IT84S-2246-4; L: CB27 × 24-125B-1; M: LB30#1 × LB1162#7.

Supplemental Table S2. Data processing statistics for cowpea mapping populations.

Population	Individuals genotyped [†]	Individuals used for mapping [‡]	HNPG [‡]	Genotypically identical sets of individuals	SNPs MAF > 0.25 [§]	Mapped SNPs [¶]	SNPs phase unknown [#]	SNPs phase reversed [††]
CB27 × IT97K-566-6	95	92	1	2	441	438	16	7
CB27 × IT82E-18	166	160	2	4	436	430	27	10
CB27 × UCR 779	58	56	0	2	596	560	51	26
CB46 × IT93K-503-1	130	114	16	0	423	374	17	10
524B × IT84S-2049	91	85	5	1	440	438	0	0
Dan Ila × TVu-7778 [‡‡]	113	79	11	23	296	288	107	46
Yacine × 58-77 [§§]	141	97	43	1	455	435	0	0
Sanzi × Vita 7	142	122	11	9	417	413	5	3
IT84S-2246 × IT93K-503	93	88	5	0	160	155	22	11
IT84S-2246 × Mouride	92	87	5	0	351	347	60	32
TVu14676 × IT84S-2246-4	147	136	10	1	377	345	4	3
CB27 × 24-125B-1	108	87	18	3	340	329	0	0
LB30#1 × LB1162 #7	95	90	4	1	190	180	1	0

[†]Refers to the number of individuals in the listed population that were genotyped using the Illumina 1536 GoldenGate Assay developed by Muchero et al (2009). A number of data processing steps eliminated some individuals from each population to yield a cleansed subset of individuals used for mapping.

[‡]HNPG, highly heterozygous or homozygous non-parental in genotype. Columns describe the number of individuals that were removed due to the observation that they were HNPGs or they were genotypically identical for the 1536 single nucleotide polymorphisms (SNPs) assayed.

[§]SNP, single nucleotide polymorphism; MAF, minor allele frequency. Column lists the number of SNPs for which the minor allele frequency and no call rates were above our thresholds and were subsequently considered for mapping.

[¶]The number of SNPs that were able to be mapped in the population specific maps.

[#]Lists the number of SNPs for which we were uncertain of the parental phase. This would occur if the parents for that SNP appeared monomorphic, heterozygous, or were no calls.

[††]Lists the number of SNPs from the previous column for which the phase was reversed.

[‡‡]Dan Ila × TVu-7778 required phase reversal for 46 of the mapped SNPs and also contained the highest number of genotypically identical individuals. The relatively large phase reversal requirement of this population is attributed to the amount of no-call or monomorphic genotypes for the parents of this population while the progeny were polymorphic and of high quality. This is likely the effect of different single-seed descent paths considering the actual parents of the populations are not represented in DNA stocks.

[§§]The Yacine × 58-77 population contained the greatest number of individuals, 44, that were removed prior to mapping. Forty-three of these individuals were highly heterozygous or nonparental in genotype, which likely arose from recent outcrossing during generation advancement.

Supplemental Table S3. Cowpea synteny with soybean and ***Medicago truncatula*** Gaertn.

Consensus VuLG[†]	Soybean chromosome (cowpea homeologs)	***Medicago truncatula*** chromosome (cowpea homeologs)
1	18 (24), 9 (12), 8 (10), 13 (10), 7 (7), 2 (5), 15 (5)	7 (37), 2 (10), 3 (7), 4 (6)
2	10 (54), 20 (47), 2 (14), 13 (5)	1 (51), 7 (16), 5 (13), 2 (9), 4 (8), 3 (6), 6 (6)
3	5 (58), 8 (43), 17 (37), 7 (17), 13 (17), 1 (6), 16 (6)	4 (54), 8 (52), 5 (24), 2 (18), 3 (16), 7 (9), 6 (6)
4	19 (19), 3 (14), 11 (12), 18 (10), 4 (6)	3 (33), 7 (25), 4 (5)
5	14 (47), 2 (23), 17 (8), 8 (5)	5 (56), 1 (18), 3 (7)
6	15 (34), 8 (18), 9 (14), 13 (12), 18 (11), 19 (6)	2 (54), 3 (16), 5 (10), 4 (10), 7 (10)
7	1 (26), 11 (19), 2 (12), 9 (10)	5 (50), 4 (7), 8 (7)
8	6 (30), 4 (28), 15 (6)	3 (33), 4 (14), 4 (5), 2 (5)
9	12 (33), 11 (15), 6 (10), 15 (8)	4 (28), 2 (13), 8 (13), 3 (5)
10	7 (30), 3 (19), 1 (14), 16 (12), 8 (6)	8 (23), 4 (21), 7 (12), 5 (8), 2 (6)
11	16 (16), 13 (12), 19 (10), 9 (9), 2 (7), 7 (5)	6 (23), 7 (8), 5 (7), 8 (7), 1 (5), 3 (5)

VuLG, *Vigna unguiculata* linkage group.