

Table S1 Gene model and predicted functional annotation based on Phytozome.

Gene model	Gene	Predicted functional annotation on Phytozome
<i>KTR2/3</i>	<i>Co-x</i>	Serine/Threonine-protein kinase-like protein CCR3- related
<i>Phvul.001G243800</i>	<i>Co-1</i>	Serine/Threonine-Protein Kinase-Like Protein CCR3-Related
<i>Phvul.001G244300</i>	<i>Co-AC</i>	Clathrin Heavy Chain (CLTC)
<i>Phvul.001G244400</i>	<i>Co-AC</i>	Uncharacterized protein
<i>Phvul.001G244500</i>	<i>Co-AC</i>	Basic Helix-Loop-Helix (bHLH) domain-containing protein with possible regulation of transcription function
<i>Phvul.001G245300</i>	<i>CoPv01^{CDRK}</i>	Protein Tyrosine Kinase (Pkinase_Tyr) // Leucine Rich Repeat N-terminal domain (LRRNT_2)
<i>Phvul.001G246300</i>	<i>CoPv01^{CDRK}</i>	Absciscic Acid Receptor PYL5
<i>Phvul.003G109100</i>	<i>PR1a</i>	Pathogenesis-related protein 1 (PR1)
<i>Phvul.006G196900</i>	<i>PR1b</i>	Pathogenesis-related protein Bet v I family (Bet_v_1))
<i>Phvul.009G256400</i>	<i>PR2</i>	Glucan endo-1,3-beta-D-glucosidase / Laminarinase

Table S2 Target genes, primers used, qPCR product size (amplicon), primer melting temperature (T_m), amplification efficiency (E) and coefficient of determination of linear regression (R²).

Gene Model ^a	Genes	Primers Forward (F) and Reverse (R) (5'-3')	T _m (°C)	Amplicon (bp)	E ^b	R ^{2c}
<i>Phvul.001G133200*</i>	<i>IDE</i>	F: AAGCAGGTATCTTGGCCATCTC R: AAAGCAAACCTCCAAGCTCCAATC	F: 60.16 R: 59.99	126	0.92	0.99
<i>Phvul.008G011000*</i>	<i>ACT</i>	F: ACAGCCAGGACCAGTTCATC R: TGTATGTGGTCTCGTGAATGC	F: 59.67 R: 58.38	154	0.93	0.98
<i>Phvul.001G243800</i>	<i>Co-1</i>	F: CCTCAAGGTGGGGCTTTTGAG R: TCACCGAGAACTCCCATTGC	F: 61.16 R: 60.61	118	1.01	0.99
<i>KTR2/3</i>	<i>Co-x</i>	F: ATGCACAGGGGAATGGGATG R: GCCATAGCGAGTGAGAGTGCG	F: 60.11 R: 63.42	279	1.06	0.98
<i>Phvul.001G244300</i>	<i>Co-AC</i>	F: GAAACGTCTCCGCAGAATAGTG R: GTCTTGTTGTTTCCTTGGAGTTG	F: 59.40 R: 60.44	150	0.99	0.99
<i>Phvul.001G244400</i>	<i>Co-AC</i>	F: TACAGCAAGAGAGCGGTAAAGG R: CCCTTTGTCACTTTGTTTTGAAGC	F: 60.62 R: 59.67	121	1.07	0.99
<i>Phvul.001G244500</i>	<i>Co-AC</i>	F: CAATGCACAGCTCGCAACTC R: GGAAGTGTGAAAGCTCTGCTAAC	F: 60.45 R: 59.81	141	1.09	0.98
<i>Phvul.001G245300</i>	<i>CoPv01^{CDRK}</i>	F: TCTGCTGGAAGGGTGGTAGTC R: GGACGTTATGTGAACAAGGTTTGC	F: 61.17 R: 61.08	93	1.04	0.99

<i>Phvul.001G246300</i>	<i>CoPv01^{CDRK}</i>	F: CTTCTTCCCTTCACTTCGATACC R: GTTGAGAGTGTGTTGTGGCAGT	F: 58.57 R: 58.98	87	0.95	0.99
<i>Phvul.003G109100</i>	<i>PR1a</i>	F: GTCCTAACGGAGGATCACTCA R: CAGGGATTGGCCAGAAGGTAT	F: 58.62 R: 59.50	148	1.01	0.98
<i>Phvul.006G196900</i>	<i>PR1b</i>	F: GGTTTGCCTATGATCCCAATGC R: TGTTGTGAGCGTTGAGGAAGTC	F: 59.96 R: 61.06	115	0.99	0.99
<i>Phvul.009G256400</i>	<i>PR2</i>	F: CAGAGGTTCTCATTTGCTGCTTTC R: ATGCCATAACACACCCCGATTG	F: 60.62 R: 61.75	98	1.09	0.99

^aBased on the *Phaseolus vulgaris* genome available on the Phytozome v1.2 platform:
<https://phytozome.jgi.doe.gov/pz/portal.html#>; * Reference genes;
^b Amplification efficiency obtained from the Equation $E=[10^{(-1/\text{slope})}]-1$ (Rasmussen, 2001);
^c Coefficient of determination of linear regression.

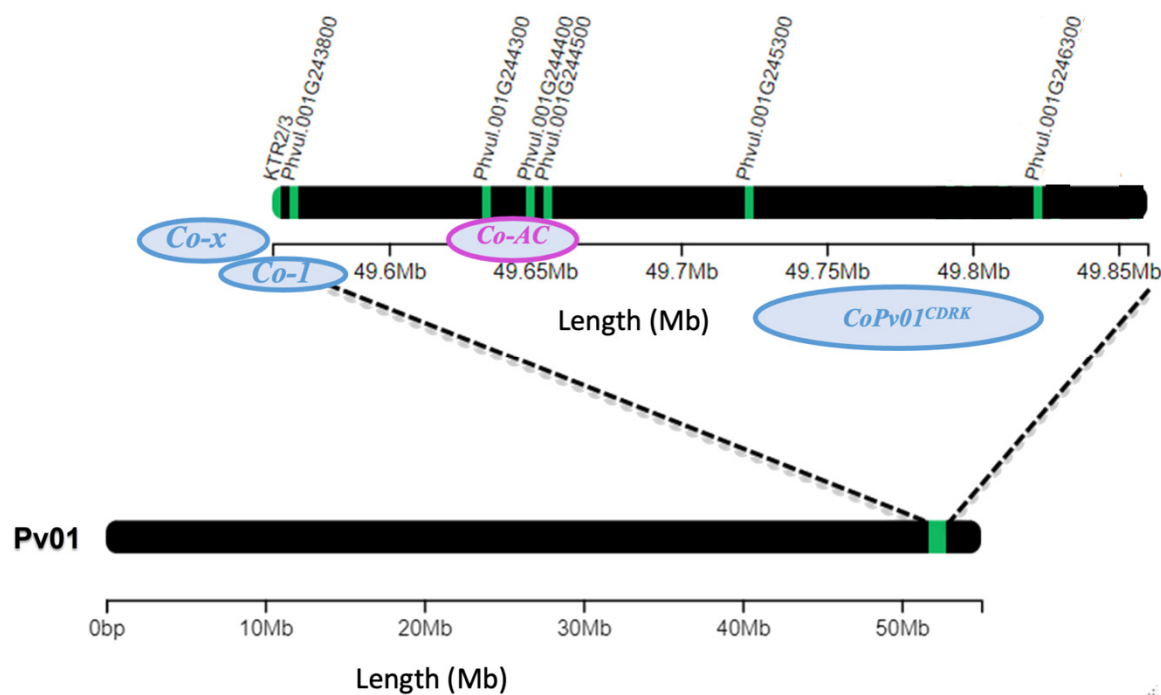


Figure S1 Common bean chromosome Pv01 containing candidate genes for anthracnose resistance genes *Co-x* (*KTR2/3*), *Co-1* (*Phvul.001G243800*), *Co-AC* (*Phvul.001G244300*, *Phvul.001G244400*, and *Phvul.001G244500*), and *CoPv01^{CDRK}/PhgPv01^{CDRK}* (*Phvul.001G245300* and *Phvul.001G246300*).