**Supporting Information**

Supplementary data for this manuscript is available at: <https://doi.org/10.18738/T8/KZFZ6K>.

**Notes.** Further details on the methods used to generate 22 phenotypes from the Cooperative Dry Bean Nursery dataset of common bean (*Phaseolus vulgaris*). Additional materials and methods concerning phenotypic data processing, greenhouse phenotypes, single nucleotide polymorphism imputation and significance and candidate gene identification criteria.

**Table S1** Summary of the Cooperative Dry Bean Nursery Dataset of common bean (*Phaseolus vulgaris*) phenotypes and the subset used in the present analysis.

**Tables S2** Excel File. Location information, genotyped Cooperative Dry Bean Nursery germplasm information, and corrected phenotype medians for 22 phenotypes used for each entry for genome-wide association on common bean (*Phaseolus vulgaris*).

**Table S3** Number of principle components that maximized the Bayesian Information Criterion for model selection in GAPIT, for each set of BLUPs derived from phenotypes in the Cooperative Dry Bean Nursery dataset.

**Table S4** Excel File. Associations from single phenotype genome-wide association significant using a Benjamini-Hochberg false discovery rate threshold of 10%. Separate tabs of the document are associations for separate phenotypes.

**Tables S5** Excel File. Associations from the multivariate shrinkage analysis significant using a local false sign rate threshold of 5%.

**Fig. S1** Correlations between best linear unbiased predictors (BLUPs) for each phenotyped entry in the Cooperative Dry Bean Nursery.

**Fig. S2** Genomic associations for six additional phenotypes with associations above a Benjamini-Hochberg false discovery rate correction.

**Fig. S3** Specific effects of top associations for four phenotypes in the Cooperative Dry Bean Nursery dataset of common bean (*Phaseolus vulgaris*).

**Fig. S4** Overlap between genetic correlation and effect size correlation groups.