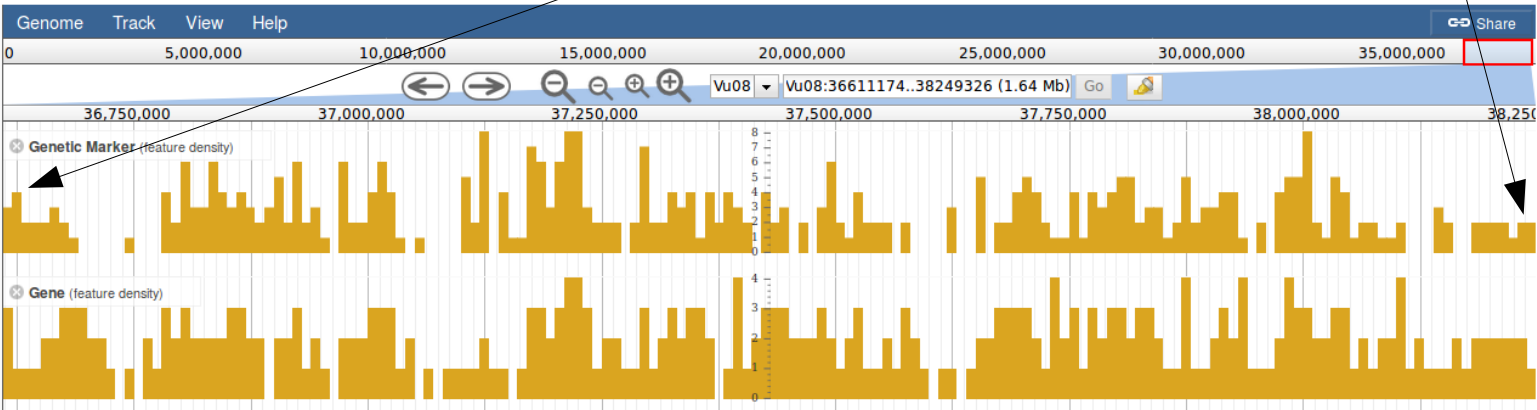


CSw8 is associated with 152 SNP markers (not all shown above). A number of other QTLs share similar regions on the linkage map.

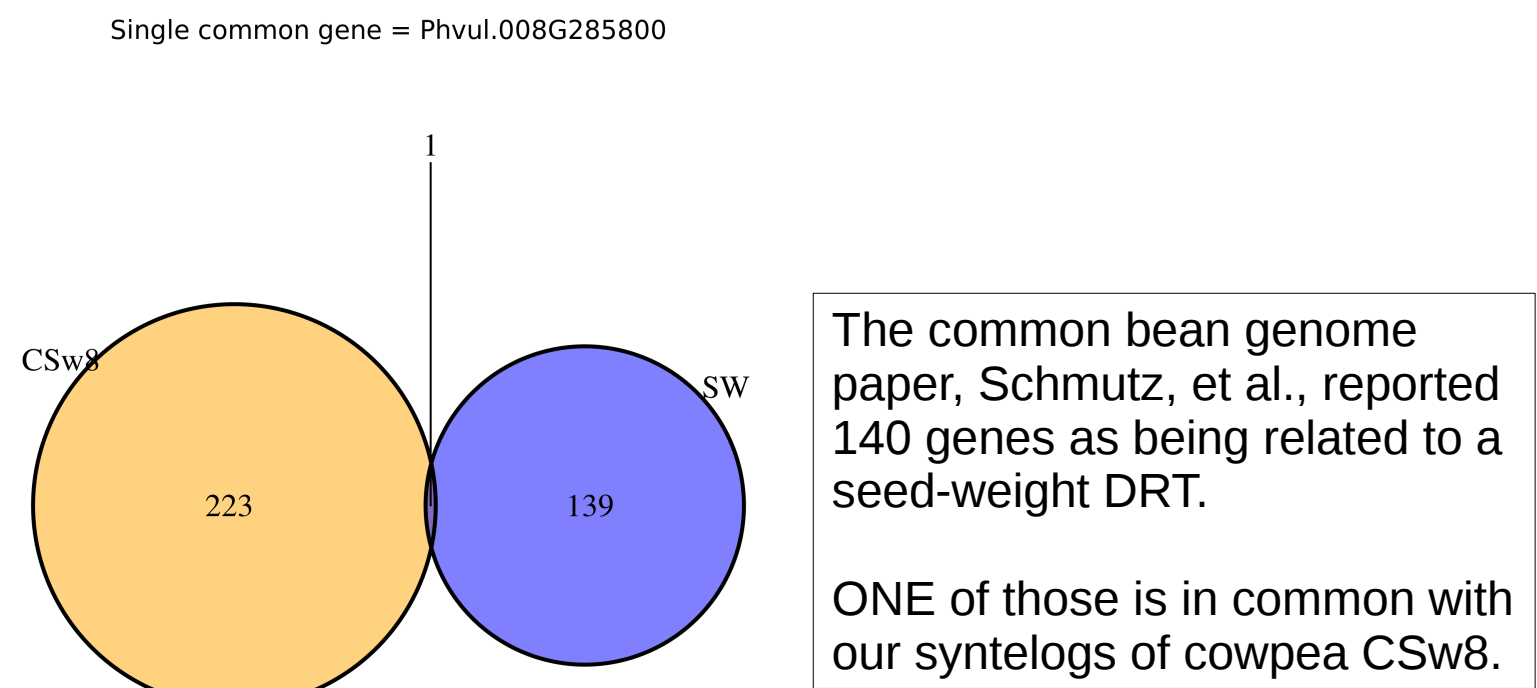


Those SNPs cover the region Vu08:36,610,400..38,248,903. That region spans 229 genes. Is one a cowpea seed-weight DRT? Compare to reported seed-weight DRT genes in common bean:



Common bean has 224 genes (“syntelogs”) across a corresponding, syntenic region on Chr08:58,048,820..59,622,008.

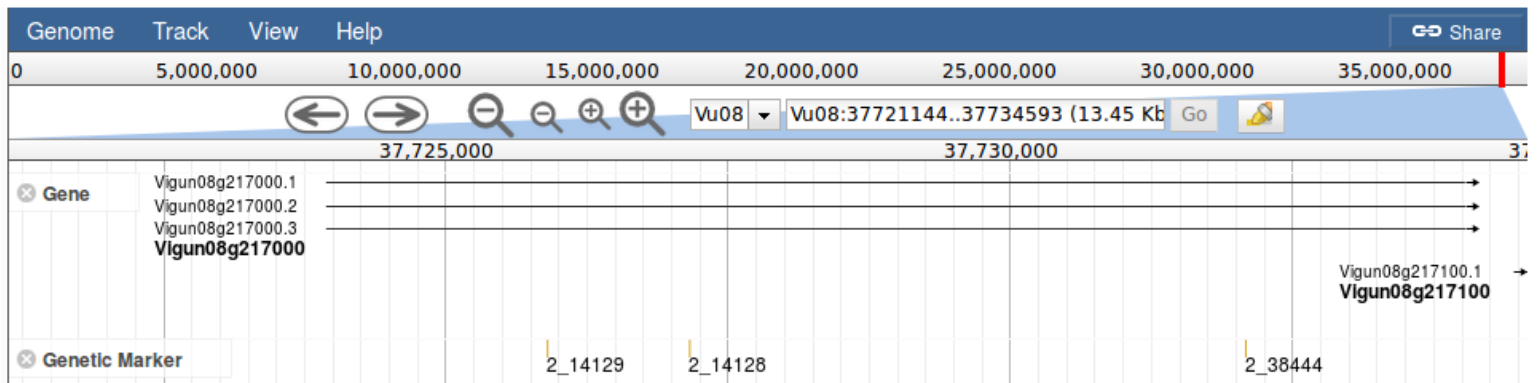
Cowpea CSw8 P.vulgaris syntelogs vs. seed-weight genes from Schmutz, et al.



That common bean gene, Phvul.008G285800, is homologous to four cowpea genes, i.e. in the same gene family:

phytozome_10_2.59232480
Signal transduction histidine kinase IPR005467 (Signal transduction histidine kinase, core), IPR006189 (CHASE), IPR009082 (Signal transduction histidine kinase, homodimeric domain), IPR011006 (CheY-like superfamily) GO:0000155 (phosphorelay sensor kinase activity), GO:0000156 (phosphorelay response regulator activity), GO:0000160 (phosphorelay signal transduction system), GO:0004871 (signal transducer activity), GO:0005524 (ATP binding), GO:0007165 (signal transduction), GO:0016020 (membrane), GO:0016310 (phosphorylation) *-** AT2G647430.1

ONE of those cowpea homologs is on Vu08! **Vigun08g21700**. Its locus spans three SNP markers:



This entire process is repeated for CSw1 and CSw6, resulting in the following candidate seed-weight DRT genes:

- Vigun01g189100** (spans SNPs 2_23240,2_23241)
Protein kinase superfamily protein; IPR011009 (Protein kinase-like domain); GO:0004672 (protein kinase activity), GO:0004674 (protein serine/threonine kinase activity), GO:0005524 (ATP binding), GO:0006468 (protein phosphorylation)
- Vigun06g209200/Vigun06g209300** (no underlying SNPs / spans 2_22118,2_36188)
equilibrative nucleoside transporter 6; IPR002259 (Equilibrative nucleoside transporter); GO:0005337 (nucleoside transmembrane transporter activity), GO:0006810 (transport), GO:0016021 (integral component of membrane)
- Vigun08g217000** (spans 2_14129,2_14128,2_38444)
Two component signal transduction system hybrid histidine kinase/response regulator with PAS sensory domain n=1 Tax=Shewanella oneidensis (strain MR-1) RepID=Q8EII0_SHEON; IPR005467 (Signal transduction histidine kinase, core), IPR006189 (CHASE), IPR009082 (Signal transduction histidine kinase, homodimeric domain), IPR011006 (CheY-like superfamily); GO:0000155 (phosphorelay sensor kinase activity), GO:0000156 (phosphorelay response regulator activity), GO:0000160 (phosphorelay signal transduction system), GO:0004871 (signal transducer activity), GO:0005524 (ATP binding), GO:0007165 (signal transduction), GO:0016020 (membrane), GO:0016310 (phosphorylation)