**Supplementary Table 1.** Summary table of parent, F1 and F2 phenotype values.



**Supplementary Table 2.** F2 phenotype correlations and their significance values.



**Supplementary Table 3.** Parent allele effects on phenotype values at each identified QTL for agronomic traits.



**Supplementary Table 4.** Summary information regarding the percent variance explained by each identified QTL cluster.



**Supplementary Table 5.** Parent allele effects on phenotype values at each identified QTL for biochemical traits.



**Supplementary Table 6.** ANOVA table showing results for tests of mean differences among F2 agronomic traits at the non-synonymous SNP within the predicted TINY coding sequence.



**Supplementary Table 7**: Table displaying the corresponding chromosomes from the Finola, CS\_10 and Purple Kush *C. sativa* assemblies.



**Supplementary Table 8:** Additive and dominance effects for individual agronomic trait QTL.



**Supplementary Table 9:** Additive and dominance effects for individual biochemical trait QTL.



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**Supplementary Figure 1.** Epistatic interaction of the stem diameter QTL SD.1 and SD.5. Line colors indicate F2 plant genotype at SD.1 while x-axis positions indicate F2 plant genotype at SD.5. Y-axis indicates the mean (± standard error) quantile normalized stem diameter quantities. Lesser y-axis values indicate smaller stem diameters while higher y-axis values indicate larger stem diameters.



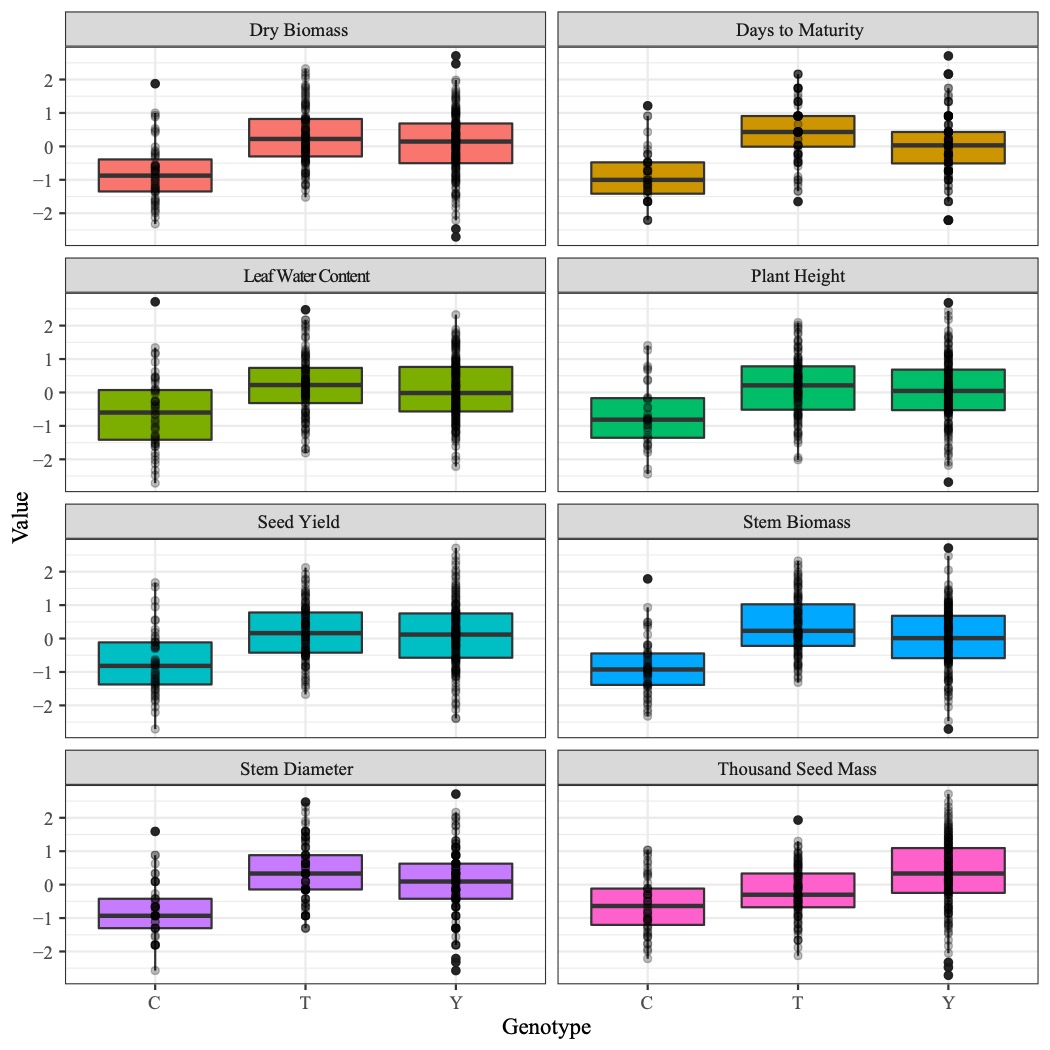
**Supplementary Figure 2**: Shown are the F2 quantile normalized phenotype values (± standard error) across each F2 plant genotype. Lesser y-axis values indicate lower seed mass while higher y-axis values indicate greater seed yield.



**Supplementary Figure 3**: Shown are the F2 quantile normalized phenotype values (± standard error) across each F2 plant genotype. Lesser y-axis values indicate lower seed mass while higher y-axis values indicate greater days to maturity.



**Supplementary Figure 4.** Shown are the F2 quantile normalized phenotype values (± standard error) across each F2 plant genotype. Lesser y-axis values indicate lower seed mass while higher y-axis values indicate greater thousand seed mass.

**Supplementary Figure 5.** Boxplots with individual points showing differences for agronomic trait performance among F2 line genotypes at the single non-synonymous SNP identified in TINY. X-axis positions indicate the F2 individual allelic state at the TINY non-synonymous SNP. “C” indicates homozygous for cytosine, “T” indicates homozygous for thymine and “Y” indicates a heterozygote. “C” alleles are derived from the USO31 parent while “T” alleles are derived from the Carmagnola parent. Y-axis positions indicate the quantile normalized values for the respective trait.



**Supplementary Figure 6.** Amino acid alignments between olivetol synthase from Taura et al. 2009 and the two transcripts we designed for Carmagnola and USO31. Amino acid substitutions are indicated by the orange points.

**Supplementary Figure 7.** Epistatic interaction of the caryophyllene oxide QTL CO.1 and CO.2. Line colors indicate F2 plant genotype at CO.1 while x-axis positions indicate F2 plant genotype at CO.2. Y-axis indicates the mean (± standard error) quantile normalized caryophyllene oxide quantities. Lesser y-axis values indicate lower quantities while higher y-axis values indicate greater quantities of caryophyllene oxide produced.

**Supplementary Figure 8**: Shown are the physical versus genetic positions for the SNPs used in linkage map construction that correspond to each chromosome in version 2 of the Finola assembly. X-axis indicates the physical positions (mega base pairs) of the SNPs in the Finola assembly while y-axis positions indicate the genetic positions (centiMorgans) of the SNPs in the linkage map.

**Supplementary Figure 9.** Epistatic interaction of the alpha-pinene QTL AP.1 and AP.5. Line colors indicate F2 plant genotype at AP.1 while x-axis positions indicate F2 plant genotype at AP.5. Y-axis indicates the mean (± standard error) quantile normalized alpha-pinene quantities. Lesser y-axis values indicate lower quantities while higher y-axis values indicate greater quantities of alpha-pinene produced.

**Supplementary Figure 10**: Design of field experiment. Shown is an illustration of the field design used for our field experiment. The experiment had three replicate blocks of 375 plants (Carmagnola, USO31, F1 and 372 F2 plants). A single plant was contained in each experimental plot (green squares).

>Carmagnola\_TINY\_predicted\_cds

ATGAGAACATGGGGAAAATGGGTATCCGAAATTAGGGAGCCCCGGAAGAAGAATCGGATCTGGCTAGGAACTTTCTCAACACCAGAAATGGCGGCGCGTGCACACGACGTGGCGGCCTTAAGCATCAAGGGTAACTCTGCAATACTCAACTTCCCCGAGCTAGCCGGATCATTACCCCGGCCGGAATCTAACTCACCCCGAGACGTTCAAGCCGCGGCTACAAAAGCGGCTTTAATGGAGTTTCCGAACCCATCTCCTTCACCTTCCACGTCATCATCGACAACAACGAGTACTTCATCGACAATGTCGCAGACTTCGTCTTCGTCTTCTTCGTCGTTGGTGGCAACTTCGTCATCGAGCTACGACGTGTCGTCTTCGCCGGAAGAGCTGAGCGAGATAGTTGAGCTGCCGAGTTTGGATACGAGTTTCGAGTCGGGGAACGAGTTCGTTTTCGAAGACTCGGTAGAGGGGTGGCTGTATCCTCCTCCGCCGTGGTACCATCATCAGAGCTTGTTTGAAGAAAATTATGGGTACTTTAGGGAAGATCAGATAGCAATGTCAGAGCCAGAGTCTGCTATTCTATCATCTTTTGAGCCTTTATTATGGCAACATTAA

>USO31\_TINY\_predicted\_cds

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>Carmagnola\_derived\_olivetol\_synthase\_cds

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>USO31\_derived\_olivetol\_synthase\_cds

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