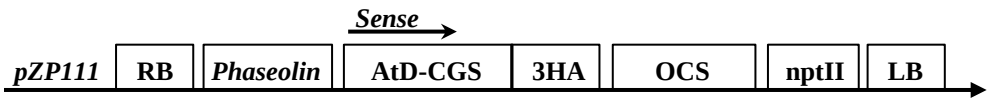

Figure S1. The plant transformation binary vector construct for seed-specific expression of AtD-CGS. The cDNA for AtD-CGS was inserted in the sense orientation under the control of the seed-specific phaseolin promoter into the binary vector *pZP111* carrying three in-frame copies of hemagglutinin (3xHA) epitope tag and an octopine synthase (OCS) terminator as illustrated. The nptII gene was used as the selectable marker for kanamycin selection.

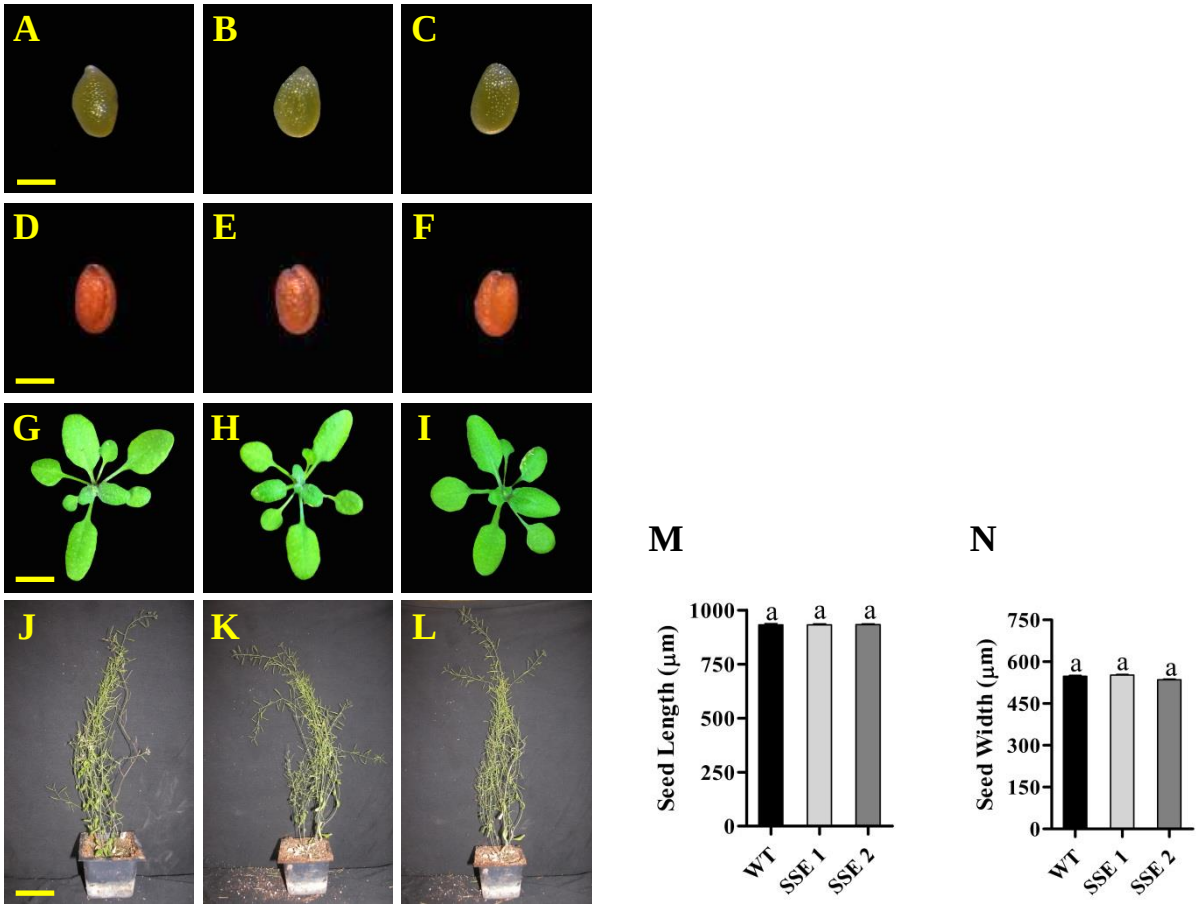

Figure S2. Morphological and phenotypic characteristics of WT and SSE seeds. Immature green seeds from (A) WT, (B) SSE 1, and (C) SSE 2 lines. Scale bar = 1 mm. Mature dry seeds from (D) WT, (E) SSE 1, and (F) SSE 2 lines. Scale bar = 1 mm. Seven weeks old seedlings from (G) WT, (H) SSE 1, and (I) SSE 2 lines. Scale bar = 1 Cm. Mature plants at the start of the desiccation processes from (J) WT, (K) SSE 1, and (L) SSE 2 lines. Scale bar = 10 Cm. M, Seed length of WT and SSE seeds. N, Seed width of WT and SSE seeds. Data shown for seed length and width parameters are means ± SE of 150 replicates. Significance was calculated using the two-way ANOVA test of $p<0.05$ and identified by different letters.

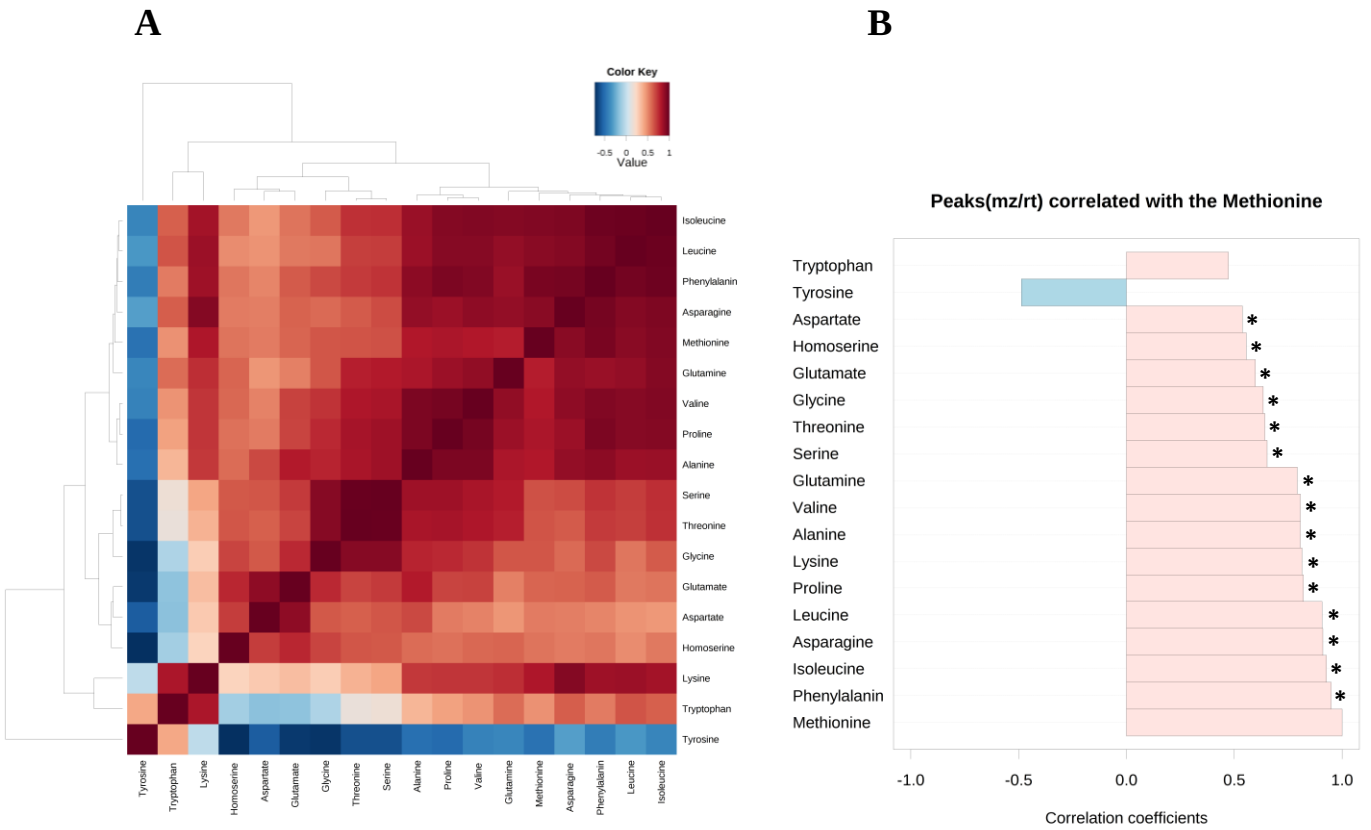

Figure S3. Correlation and pattern analyses of GC-MS metabolic profiling data. Peak intensities were $\log_{10}$-transformed and re-scaled according to the pareto scaling method where results are being mean-centered and divided by the square root of standard deviation of each metabolite. Following these manipulations, correlations (A) and patters (B) analyses were performed using the tools embedded in the MetaboAnalyst 2.0 software (http://metaboanalyst.ca/). Significance was calculated according to the Spearman rank correlation of $p<0.05$ and identified by asterisks.

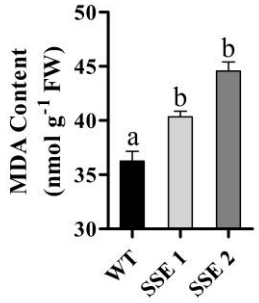

Figure S4. Determination of lipid peroxidation by malondialdehyde (MDA) assay. The thiobarbituric acid (TBA) test was used to determine MDA as an end product of lipid peroxidation. Data shown are means ± SE of four replicates. Significance was calculated using the two-way ANOVA test of $p<0.05$ and identified by different letters.

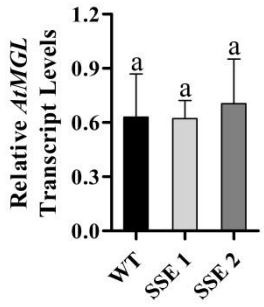

Figure S5. Transcript analysis of Met-γ-lyase (MGL). Quantitative real-time PCR analysis of AtMGL transcript levels in mature dry seeds of WT and SSE genotypes. Data shown are means ± SE of three replicates. Significance was calculated using the two-way ANOVA test of $p<0.05$ and identified by different letters.

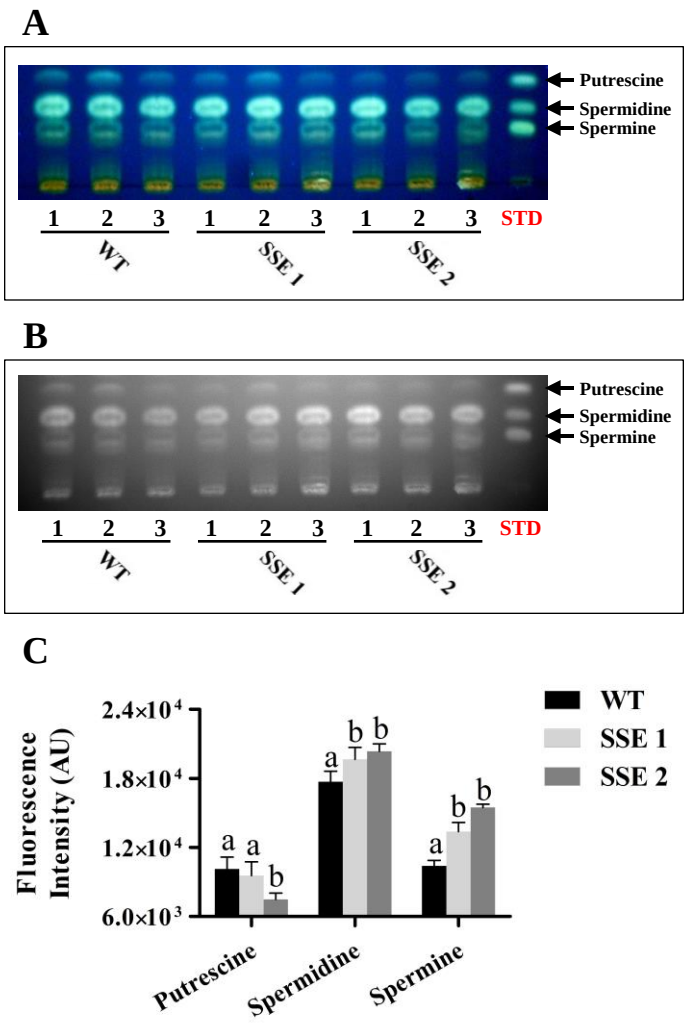

Figure S6. Polyamine contents in WT and SSE seeds. A, Photomicrographs of polyamine extracts from WT and SSE seeds according to thin layer chromatography (TLC) analysis under ultra-violet (UV) light. B, Higher resolution photomicrographs used for polyamine quantification. C, Polyamine quantification in WT and SSE seeds according to their relative fluorescence. Data shown in C are means ± SE of three replicates. Significance was calculated using the two-way ANOVA test of $p<0.05$ and identified by different letters.