Supplemental Table/figure captions:

SUPPLEMENTAL MATERIAL

Bolon_SuppFigs.pdf

**Supplemental Figure S1:** Soybean seeds and pod at early seed maturation stage. Immature green soybean seed tissue was collected from each genotype during early seed maturation for the transcript accumulation dataset. A) Image of the immature seed within the pod shell. B) The immature seed harvested with the seed coat. C) Image of seeds attached to the inner pod shell. D) View of the immature green seed with partial seed coat removed.

**Supplemental Figure S2:** Enrichment of photosynthesis and fatty acid biosynthesis and metabolism Gene Ontology categories among genes with eQTL at the chromosome 20 eQTL hotspot is shown using GOEAST (Zheng and Wang, 2008).

**Supplemental Figure S3:** Chromosome 20 (~2498 total cM) eQTL hotspot. Genes with eQTL at the ~2498 cM hotspot are represented by colored squares in different metabolic categories using Mapman (Thimm et al., 2004). The color of each square indicates the allele (red = Minsoy, blue = Noir 1) with additive effect, and the scale is based on LOD score for the eQTL. Twelve eQTL are for genes annotated to lipid biosynthesis with the same additive allele ('Minsoy').

**Supplemental Figure S4:** Network of eQTL on chromosome 7 (797 cM) and chromosome 20 (2493 cM) mapped for a common set of genes. Edges connecting the nodes are colored red for upregulation of gene transcript accumulation by the 'Minsoy' allele and blue for upregulation of transcription factor gene transcript accumulation by the 'Noir 1' allele. Edge thickness represents LOD (thicker edge = higher LOD). A zigzag edge represents a cis-acting regulatory connection.
vs. a *trans*-acting regulatory connection. Supplemental Table S12 contains the key for the genes with eQTL depicted in this figure.

**Supplemental Figure S5:** Enrichment of photosynthesis and metabolism gene ontology categories among genes with eQTL at the chromosome 7 eQTL hotspot is shown using GOEAST (Zheng and Wang, 2008).

**Supplemental Figure S6:** Phenotypic QTL mapped in MxN RILs. (A-B) Seed oil and protein QTL traces. C) MxN RILs graph of genome-wide eQTL frequency.

**Supplemental Table S1:** MxN RILs genotype data for 557 Goldengate SNP markers.

*Bolon_TableS1.xls*

**Supplemental Table S2:** Genetic map (~2500 cM) of MxN with 557 SNP markers across 20 chromosomes.

*Bolon_TableS2.xls*

**Supplemental Table S3:** Seed Oil and Protein QTL mapped in Minsoy x Noir 1. Three QTL with LOD>3.5 were mapped for seed protein in multiple years for the Minsoy x Noir 1 RIL population that included one QTL on chromosome 8 and two QTL for seed protein on chromosomes 4 and 6. Two of these seed protein QTL, on chromosomes 6 and 8, correlated inversely with seed oil QTL.

*Bolon_TableS3.xls*
**Supplemental Table S4:** List of 200 gene expression probeset values and annotations for genes with differentially accumulated transcript levels between 'Minsoy' and 'Noir 1' in stage zero of the developing soybean seed.

*Bolon_TableS4.xls*

**Supplemental Table S5:** Final normalized gene expression data from Soybean Affymetrix GeneChips on 93 MxN RILs.

*Bolon_TableS5.xls*

**Supplemental Table S6:** Genes with eQTL within the chromosome 8 eQTL hotspot enriched for flavonoid biosynthesis pathway genes.

*Bolon_TableS6.xls*

**Supplemental Table S7:** eQTL data in the MxN RILs for seed-specific genes shown in Figure 3A.

*Bolon_TableS7.xls*

**Supplemental Table S8:** eQTL data for photosynthesis genes, fatty acid biosynthesis genes and oleosin genes shown in Figures 3B-3D.

*Bolon_TableS8.xls*

**Supplemental Table S9:** Genes with eQTL peaks at the 2498 total cM eQTL hotspot on chromosome 20 enriched for seed-specific genes, photosynthesis genes, fatty acid biosynthesis-related genes and oleosin genes.

*Bolon_TableS9.xls*
**Supplemental Table S10:** Genes with eQTL peaks at the 797 total cM eQTL hotspot on chromosome 7 enriched for photosynthesis genes and metabolic pathway genes.

**Supplemental Table S11:** Photosynthesis, fatty acid biosynthesis, oleosin, and other seed-specific genes with eQTL depicted in the network among the three eQTL hotspots on chromosome 7, 13, and 20 in Figure 4.

**Supplemental Table S12:** Genes with eQTL depicted in the network between chromosome 7 (797 cM) and chromosome 20 (2493 cM) in Supplemental Figure S4.

**Supplemental Table S13:** RNA-seq data in LoPro and HiPro for genes within the chromosome 20 hotspot, including eight seed-specific genes and 36 transcription factor genes in Figure 6.

**Supplemental Table S14:** Genes with cis-acting eQTL peaks that coincide with major seed protein and oil QTL peaks.
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Figure S5
**Supplemental Figure S5.** Network of eQTL on chromosome 7 (797 cM) and chromosome 20 (2493 cM) mapped for a common set of genes. Edges connecting the nodes are colored red for upregulation of gene transcript accumulation by the 'Minsoy' allele and blue for upregulation of transcription factor gene transcript accumulation by the 'Noir 1' allele. Edge thickness represents LOD (thicker edge = higher LOD). A zigzag edge represents a *cis*-acting regulatory connection vs. a *trans*-acting regulatory connection. Supplemental Table S12 contains the key for the genes with eQTL depicted in this figure.
Figure S6
Supplemental Figure S6. Phenotypic QTL mapped in MxN RILs. (A-B) Seed oil and protein QTL traces. C) MxN RILs graph of genome-wide eQTL frequency.