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Co-expression and gene regulatory networks (GRNs) for soybean seed development: identification of key regulatory modules that impact economic traits

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Soybean is the 2<sup>nd</sup> largest crop in the USA and a very important food and feed source for human and animal health due to its high protein and oil content. The large size of the soybean genome, encoding for over 55,000 genes, creates a formidable challenge for elucidation of gene function, especially those genes important for agronomic performance. To address this challenge, we developed an extended gene expression atlas for soybean, utilizing RNA-seq performed by the DOE Joint Genome Institute. We sequenced more than 200 libraries from various soybean tissues, treatment and conditions including nine developmental stages of soybean seed. Analysis of soybean seed atlas data identified hundreds to thousands of genes and transcription factors (TFs) whose expression varied significantly between developmental stages. These genes represent promising candidates for manipulation to modify important seed, quality traits; such as, fatty acid, lipid, oil, protein, carbohydrate and amino acid content. These data were refined by generating co-expression and gene-regulatory networks revealing modules of genes and TFs that likely play key roles in oil, protein and carbohydrate biosynthesis. We are using these data in conjunction with our large soybean fast-neutron mutant population to analyze the functional role of key genes with the ultimate goal of using this information for soybean improvement.