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Computational approaches for integrating gene expression and trait information to discover high-value candidate genes in soybean

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Soybean domestication and modern breeding have resulted in narrow genetic diversity that limits yield increases each year. More information about the genes that control complex traits like yield would be valuable to breeders seeking to overcome this limitation. Genome-wide association studies are now used to find regions of the genomes associated with these high-value traits. This method, however, rarely resolves the actual gene(s) responsible. My research will address this issue by combining genome-wide association studies data with gene expression information. This will provide a platform for identifying the gene(s) associated with specific soybean health and production traits.