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Genomics survey for genes related to domestication and improvement in soybean  
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Soybean is a crop with substantial economic value, accounting for more than half of global oilseed production. It has been suggested that cultivated soybean was domesticated from wild soybean in China 5,000 years ago. Comprehensive evaluation of large scale of representative germplasm and survey for genes contributing to domestication and improvement are essential for the super variety breeding. We performed a large scale assessment of soybean domestication and improvement by resequencing of 302 wild, landrace and cultivated soybean lines with an average coverage depth of more than 11× for each line. Bioinformatics analysis identified a total of 121 and 109 selective sweeps during soybean domestication and improvement, respectively. Genome-wide association study revealed associations between 10 selected regions and 9 domestication or improvement traits and identified 13 previously uncharacterized loci for agronomic traits including oil content, plant height and pubescence form. Further investigation by combining previous quantitative trait loci (QTL) information revealed that 96 of the 230 selected regions correlate with reported oil QTLs and 21 contained fatty acid biosynthesis genes. This study facilitate us to reveal key genes responsible soybean domestication.