Soybean is a major crop providing an important source of protein and oil. A major milestone in soybean research was the recent sequencing of its genome. The sequence predicts 69,145 putative soybean genes. In order to examine their expression, we utilized the Illumina Solexa platform to sequence cDNA derived from 14 conditions. The result is a searchable soybean gene expression atlas accessible through a browser (http://digbio.missouri.edu/soybean_atlas/). The data provide experimental support for the transcription of 55,616 annotated genes and also demonstrate that 13,529 annotated soybean genes are putative pseudogenes and 1736 currently unannotated sequences are transcribed. An analysis of this atlas reveals strong differences in gene expression patterns between different tissues, especially between root and aerial organs, but also reveals similarities between gene expression in other tissues, such as flower and leaf organs. In order to demonstrate the full utility of the atlas, we investigated the expression patterns of genes implicated in nodulation and also transcription factors. The availability of the soybean gene expression atlas allowed a comparison to gene expression documented in the two model legume species, Medicago truncatula and Lotus japonicus, as well as data available for Arabidopsis thaliana, facilitating both basic and applied aspects of soybean research.