

Description of Additional Supplementary Files

Supplementary Data 1. Summary of geographical origins and re-sequencing quality of 984 soybean accessions.

Supplementary Data 2. Whole-genome annotation of SNPs, InDels, and reseq-SVs.

Supplementary Data 3. Classification of soybean accessions based on phylogenetic tree.

Supplementary Data 4. Principal components of 984 accessions.

Supplementary Data 5. Decay of linkage disequilibrium in soybean genomes by type and geographical distribution using SNP and reseq-SV data.

Supplementary Data 6. Overview of 56 assembled soybean genomes.

Supplementary Data 7. Selected reseq-SVs during domestication and improvement processes.

Supplementary Data 8. Putative reseq-SV regions under domestication sweeps identified by XP-CLR.

Supplementary Data 9. Putative reseq-SV regions under improved sweeps by XP-CLR.

Supplementary Data 10. Integration of domestication signals with known oil- and protein-associated QTLs.

Supplementary Data 11. Integration of improvement signals with known oil- and protein-associated QTLs.

Supplementary Data 12. Concordance analysis of domestication and improvement signatures with validated functional genes.

Supplementary Data 13. Agronomic and morphological traits across soybean germplasm.

Supplementary Data 14. Reseq-SVs associated with GWAS signals.

Supplementary Data 15. Comparison of reseq-SVs identified by resequencing and genome assembly.

Supplementary Data 16. Primers for vector construction and qRT-PCR.