

Article title: Identification of QTL for tolerance to flooding stress at seedling stage of soybean (*Glycine max* L. Merr.)

Journal name: Agronomy

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Supplementary Figure S1. Genetic linkage maps of 20 chromosomes showing the total 1,689 SNPs used to identify the QTL for flooding tolerance in soybean. Distances of the loci (cM) are shown on the left and the name of SNPs are shown on the right side of each chromosome.









