



S2 Fig. Association mapping of seed coat color in soybean with SNPs in Sets B and C.

(A) Expect $-\log(P)$ matched observed $-\log(P)$ best from the QQ-Plot using SNPs from Set B. (B) Manhattan plots showed $-\log(P)$ from a genome-wide scan were plotted against positions of SNPs on 20 chromosomes using SNPs from Set B. (C) Expect $-\log(P)$ matched observed $-\log(P)$ best from the QQ-Plot using SNPs from Set C. (D) Manhattan plots showed $-\log(P)$ from a genome-wide scan were plotted against positions of SNPs on 20 chromosomes using SNPs from Set C.