

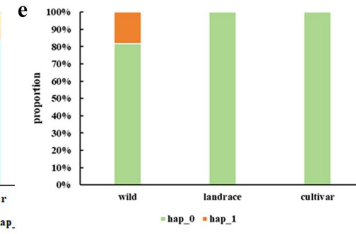
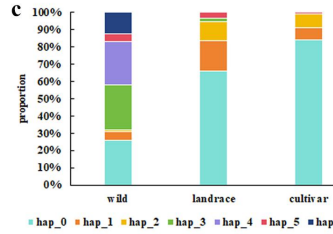
	gene number	genes with selected haplotype
dehydrin related genes	7	5 (71.43%)
oleosin related gene	11	8 (72.73%)
heat shock protein related gene	36	31 (86.11%)
LEA related genes	24	21 (87.5%)

b *GLYMA.07G043600*

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hap_0 T_A_A_G_T_T_G_C_G_G_C
hap_1 C_A_G_G_T_T_G_C_G_G_C
hap_2 C_A_G_G_A_T_T_A_C_G_A_T
hap_3 C_A_G_G_A_T_T_A_C_G_A_C
hap_4 C_G_G_G_A_C_T_G_C_G_A_C
hap_5 C_G_G_G_A_T_A_G_C_A_A_C
hap_6 C_A_G_G_A_T_T_A_T_G_A_C

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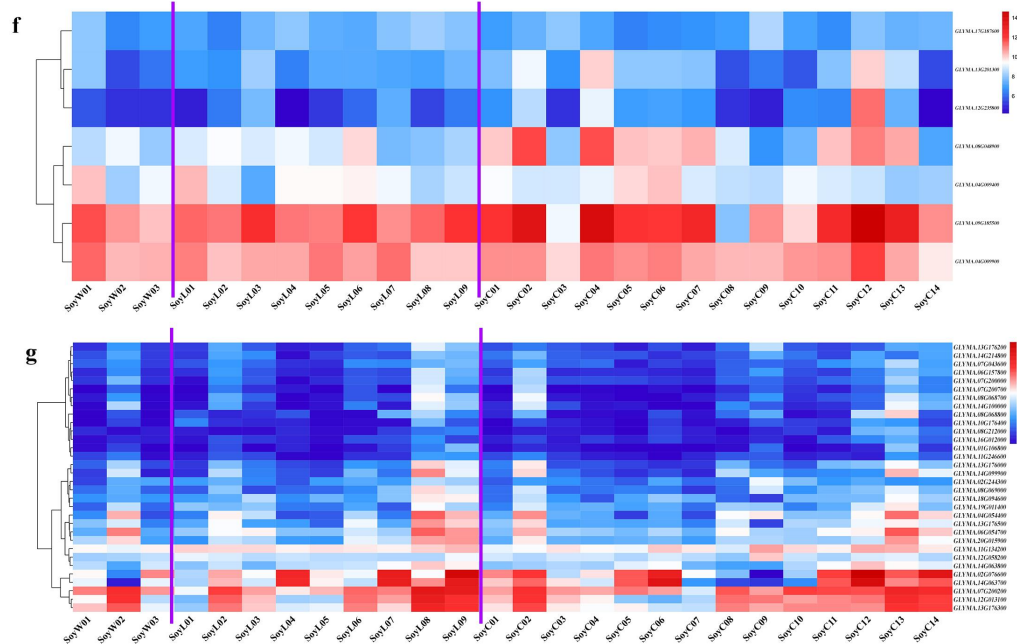


d *GLYMA.06G157800*

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hap_0 C_C_A_A_A_G_A_A_C
hap_1 C_C_A_A_G_G_A_A_C

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Supplemental Figure S7. Domestication selection of dehydration genes in soybean seed maturation. (a) The number of genes with selected haplotypes in the dehydrin, LEA, HSP, and oleosin families. (b, d) The haplotypes of *GLYMA.07G043600* (b) and *GLYMA.06G157800* (d) during soybean domestication. (c, e) The haplotype distributions of *GLYMA.07G043600* (c) and *GLYMA.06G157800* (e) in wild soybeans, landraces, and cultivars. (f, g) Heatmap showing the expression of dehydrin (f) and HSP (g) family genes in the developing seeds from wild soybeans, landraces, and cultivars. “SoyW” represents wild soybean, “SoyL” represent landrace, “SoyC” represents cultivar soybean.