

Fig. S1. At the top, the blue rectangles indicate the locations of predicted DNA-binding domains in *GmRVE8c*, while the vertical black bars represent the approximate positions of substitutions. In the middle, the red rectangles show the approximate locations of disordered regions. At the bottom, the pink rectangles indicate the approximate locations of linearly interacting peptides.

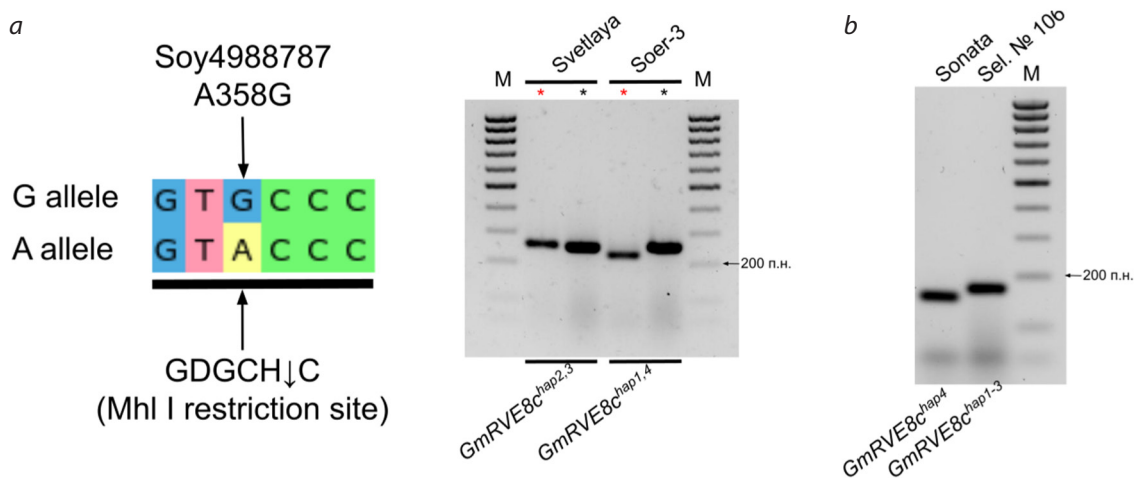


Fig. S2. *a*, Design and electrophoresis of the CAPS marker for genotyping the soy4988787 mutation. Black asterisks indicate PCR products before restriction; red asterisks indicate PCR products after restriction. M – denotes the DNA molecular weight marker “Step100+50” (Biolabmix, Russia, Novosibirsk). *b*, DNA marker for genotyping the soy32494699 mutation.

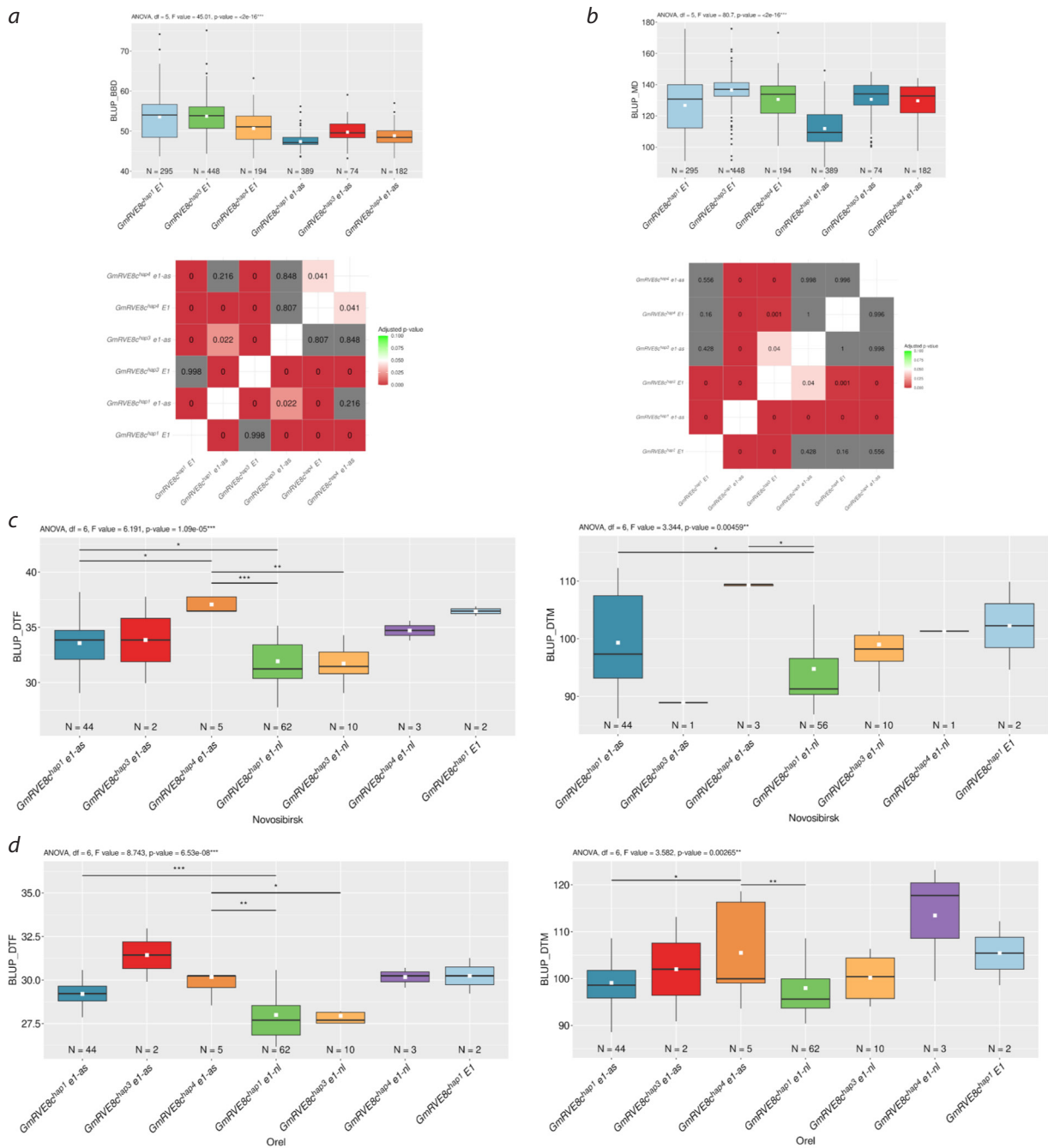


Fig. S3. a, Association of *GmRVE8c* and *E1* genotypes with BLUP_BBD. b, Association of *GmRVE8c* and *E1* genotypes with BLUP_MD. Boxplots are shown at the top, and a heatmap with the results of multiple genotype comparisons is shown at the bottom. c, Association of *GmRVE8c* and *E1* genotypes with BLUP_DTF and BLUP_DTM in Novosibirsk. d, Association of *GmRVE8c* and *E1* genotypes with BLUP_DTF and BLUP_DTM in Orel.

White squares on the boxplots indicate the mean value. Asterisks indicate significant differences between the compared genotype: *** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$. "N" denotes the number of accessions.

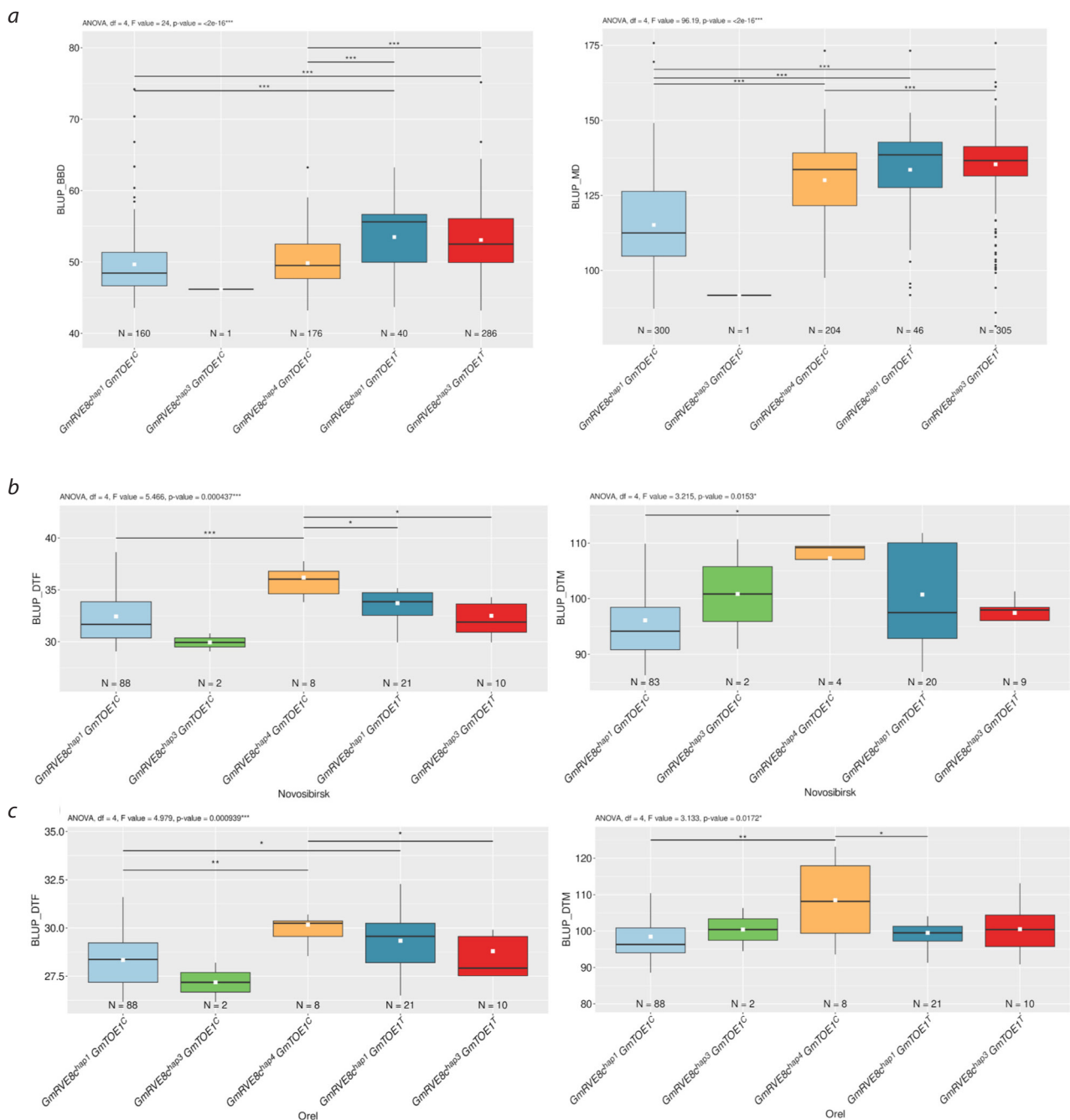


Fig. S4. *a*, Association of *GmRVE8c* and *GmTOE1* genotypes with BLUP_BBD and BLUP_MD. *b*, Association of *GmRVE8c* and *GmTOE1* genotypes with BLUP_DTF and BLUP_DTM in Novosibirsk. *c*, Association of *GmRVE8c* and *GmTOE1* genotypes with BLUP_DTF and BLUP_DTM in Orel.

White squares on the boxplots indicate the mean value. Asterisks indicate significant differences between the compared genotype: *** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$. "N" denotes the number of accessions.

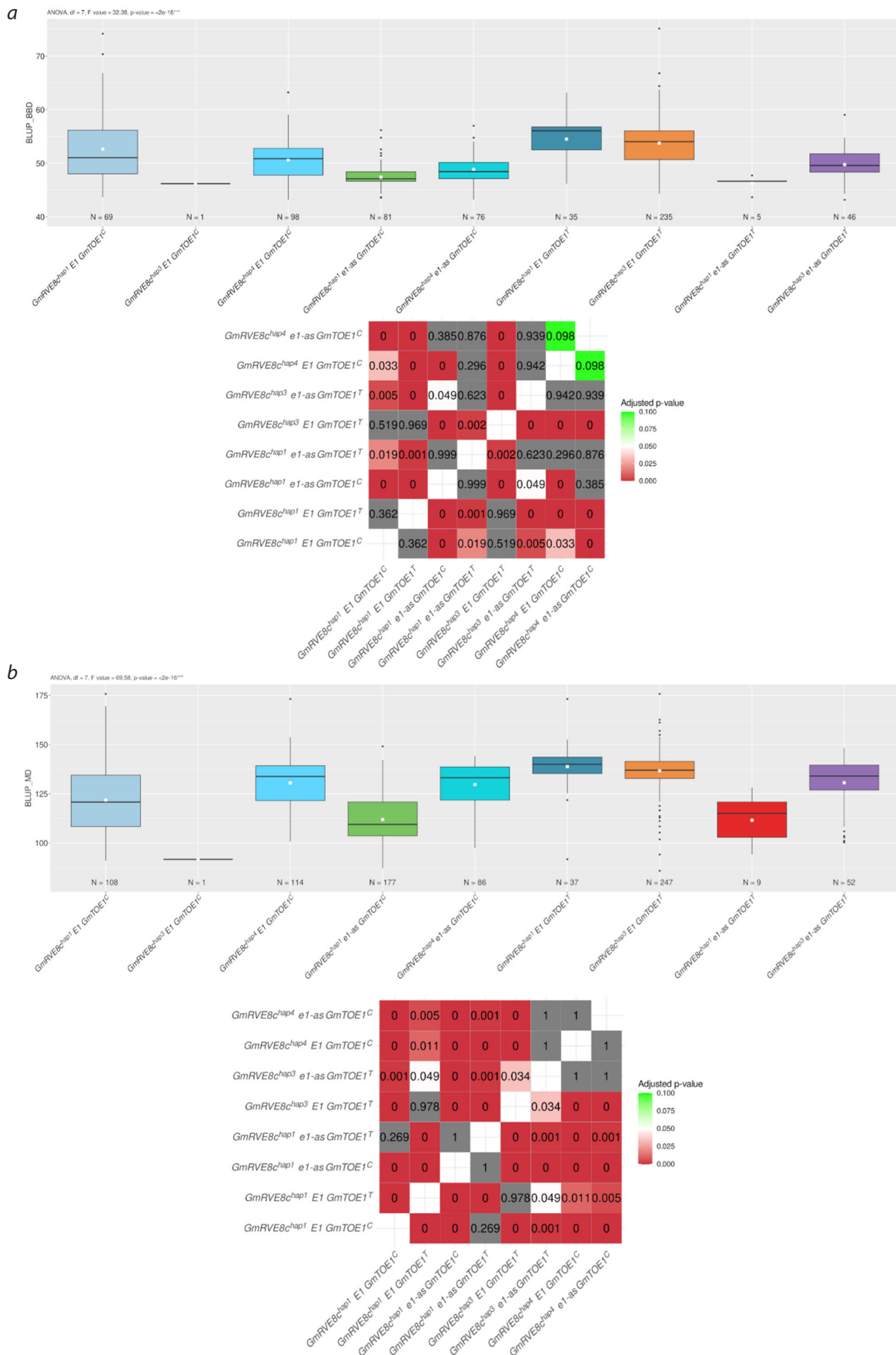


Fig. S5. *a*, Association of *GmRVE8c*, *E1* and *GmTOE1* genotypes with BLUP_BBD. *b*, Association of *GmRVE8c*, *E1* and *GmTOE1* genotypes with BLUP_MD.

Boxplots are shown at the top, and a heatmap with the results of multiple genotype comparisons is shown at the bottom. White squares on the boxplots indicate the mean value. "N" denotes the number of accessions.

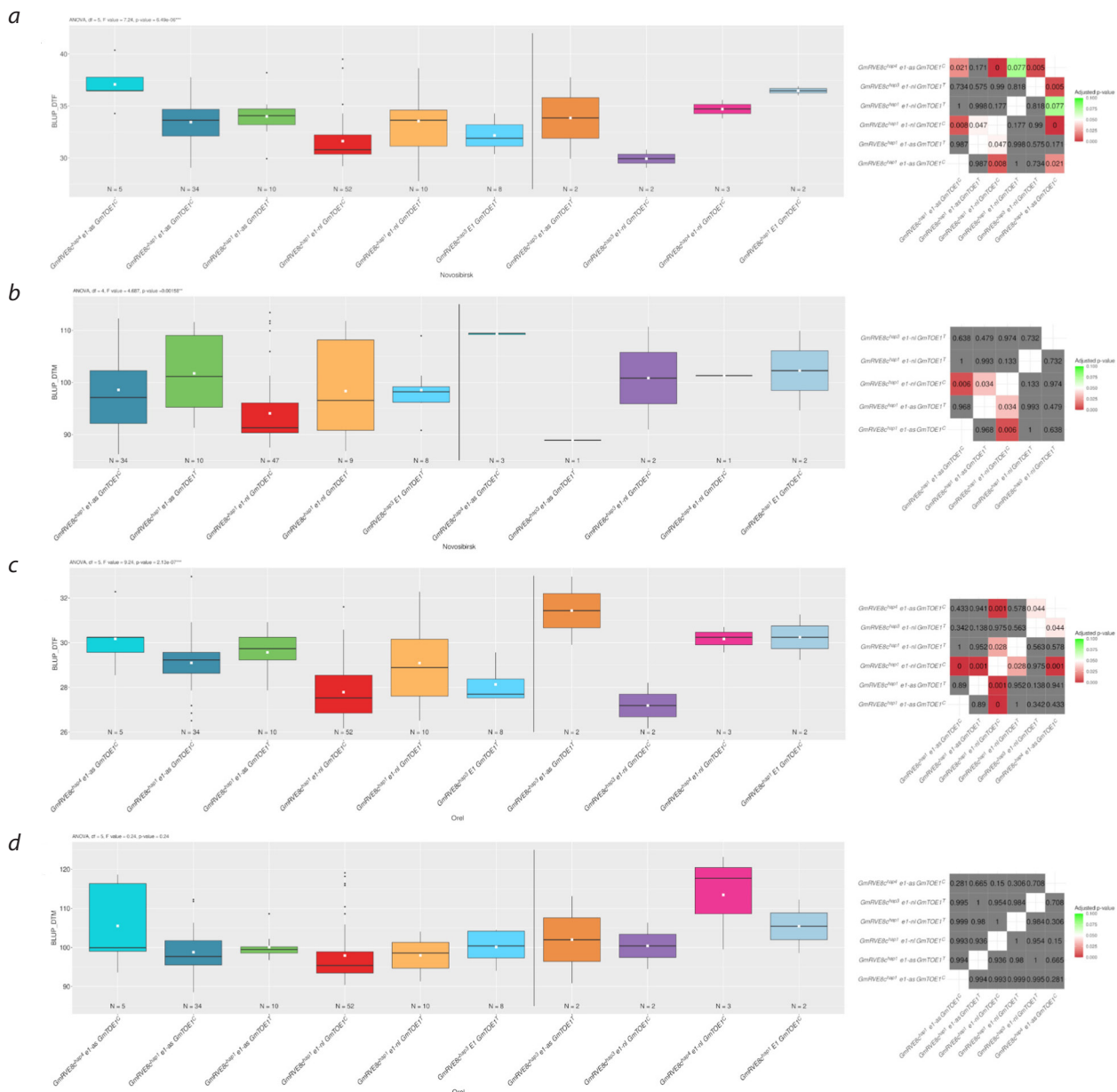


Fig. S6. *a*, Association of *GmRVE8c*, *E1* and *GmTOE1* genotypes with BLUP_DTF in Novosibirsk. *b*, Association of *GmRVE8c*, *E1* and *GmTOE1* genotypes with BLUP_DTM in Novosibirsk. *c*, Association of *GmRVE8c*, *E1* and *GmTOE1* genotypes with BLUP_DTF in Orel. *d*, Association of *GmRVE8c*, *E1* and *GmTOE1* genotypes with BLUP_DTM in Orel.

Boxplots are shown at the left, and a heatmap with the results of multiple genotype comparisons is shown at the right. White squares on the boxplots indicate the mean value. "N" denotes the number of accessions.