

Supplementary Materials

**Yanrong Gao^{1,2}, Merle Stein¹, Lilian Oshana², Wenxia Zhao^{1,5}, Shizue Matsubara^{2,3},
Benjamin Stich^{1,3,4}**

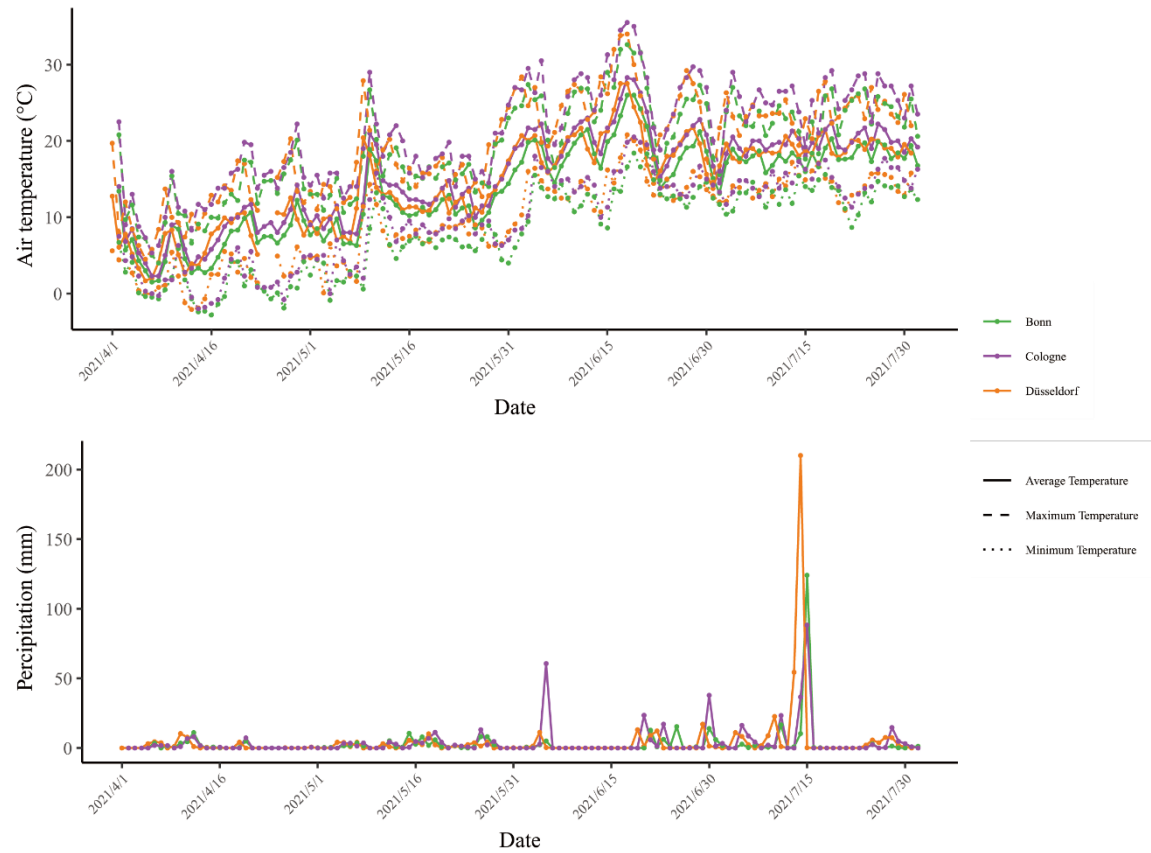
¹Institute of Quantitative Genetics and Genomics of Plants, Heinrich Heine University, Düsseldorf, Germany

²IBG-2: Plant Sciences, Forschungszentrum Jülich, Jülich, Germany

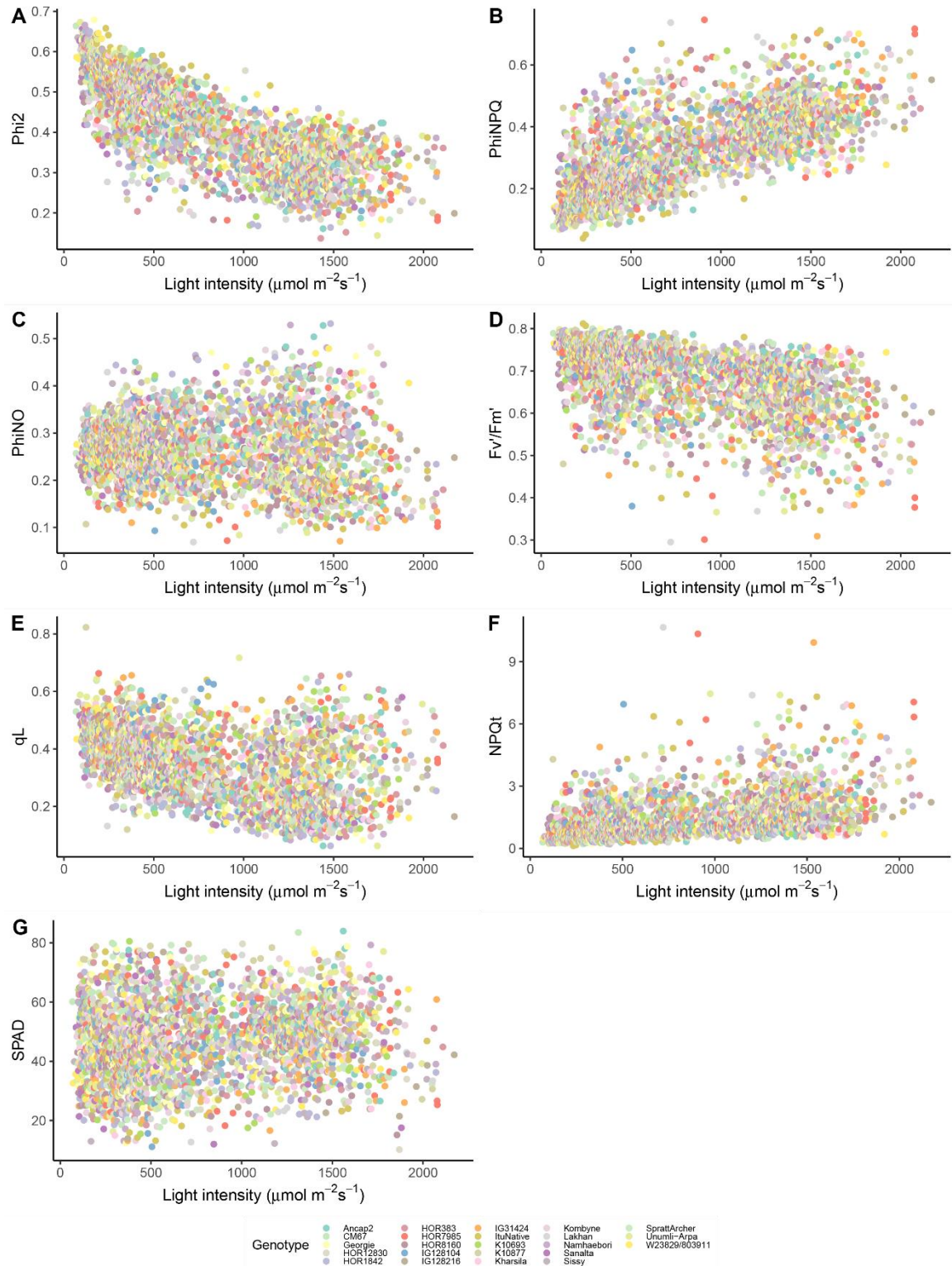
³Cluster of Excellence on Plant Sciences (CEPLAS)

⁴Julius Kühn Institute (JKI) – Federal Research Centre for Cultivated Plants, Institute for Breeding Research on Agricultural Crops, Sanitz, Germany

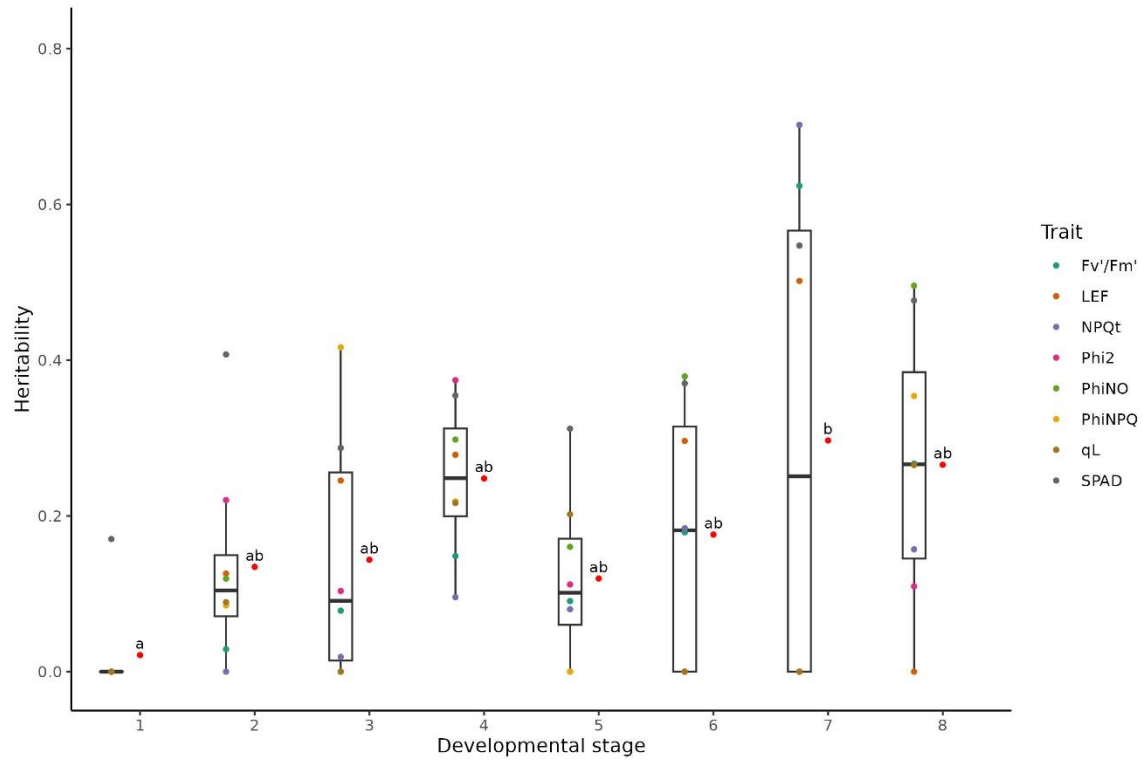
⁵Xinjiang Seed Industry Development Center of China, Urumqi, China.



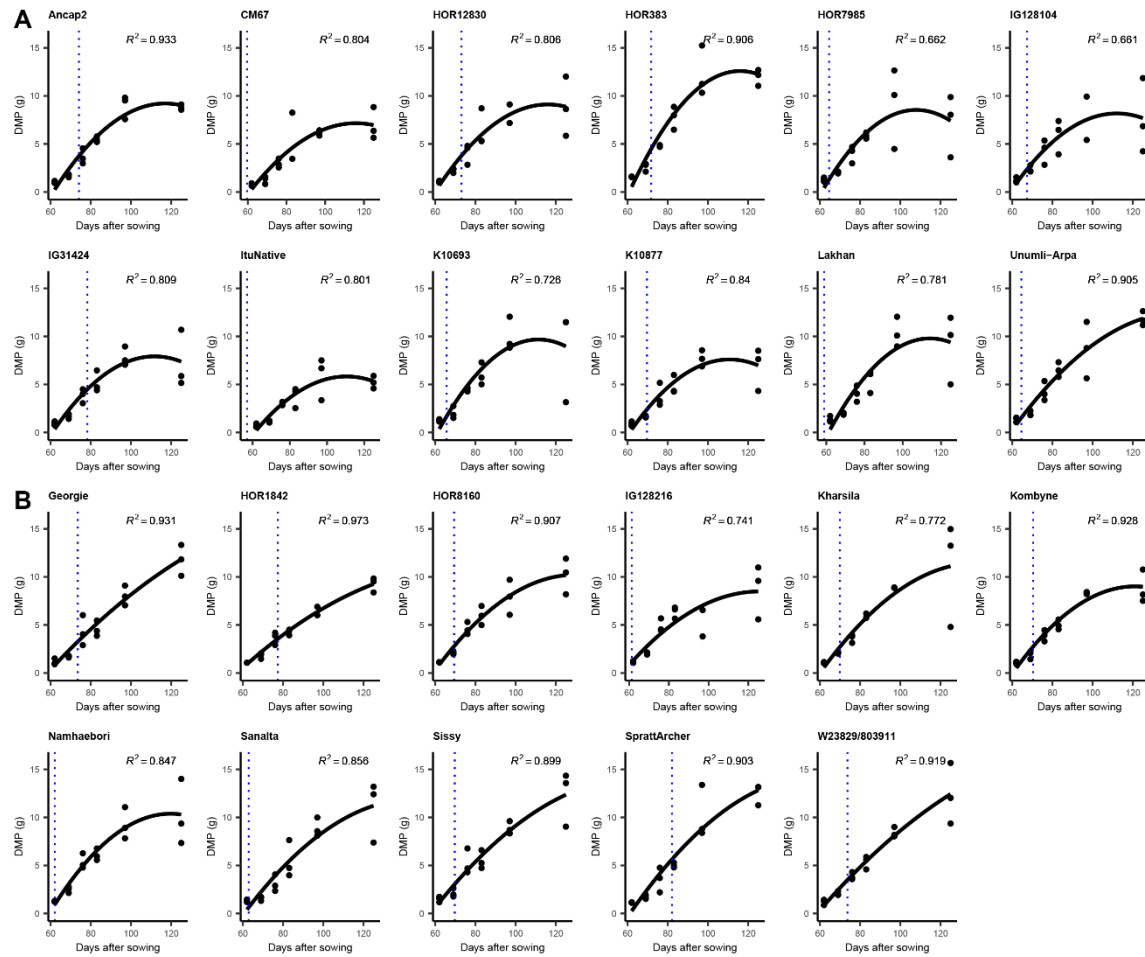
Supplementary Fig. S1: Air temperature and precipitation recorded during the field experiments in Bonn, Cologne, Düsseldorf. Dashed, solid, and dotted represent the maximum, average, and minimum temperature of one day, respectively. Green, purple and orange color represent three location Bonn, Cologne and Düsseldorf, respectively. The temperature data of Düsseldorf from 2021/04/24 to 2021/04/25 was missing.



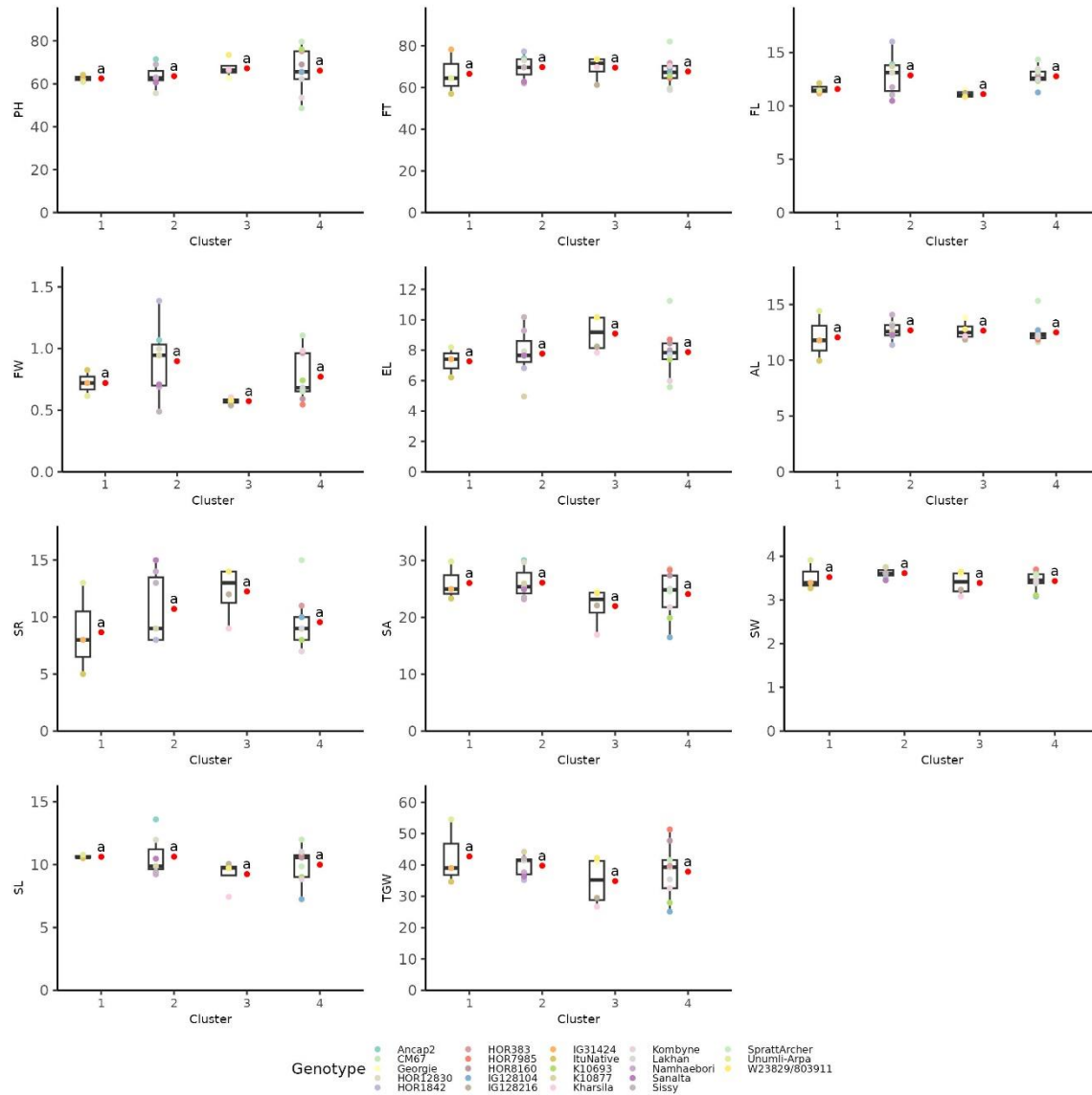
Supplementary Fig. S2: Light response curves of PSII parameters and SPAD for the 23 barley inbred lines. (A) Φ_2 , (B) Φ_{NPQ} , (C) Φ_{NO} , (D) F_v'/F_m' , (E) q_L , (F) NPQ_t and (G) SPAD.



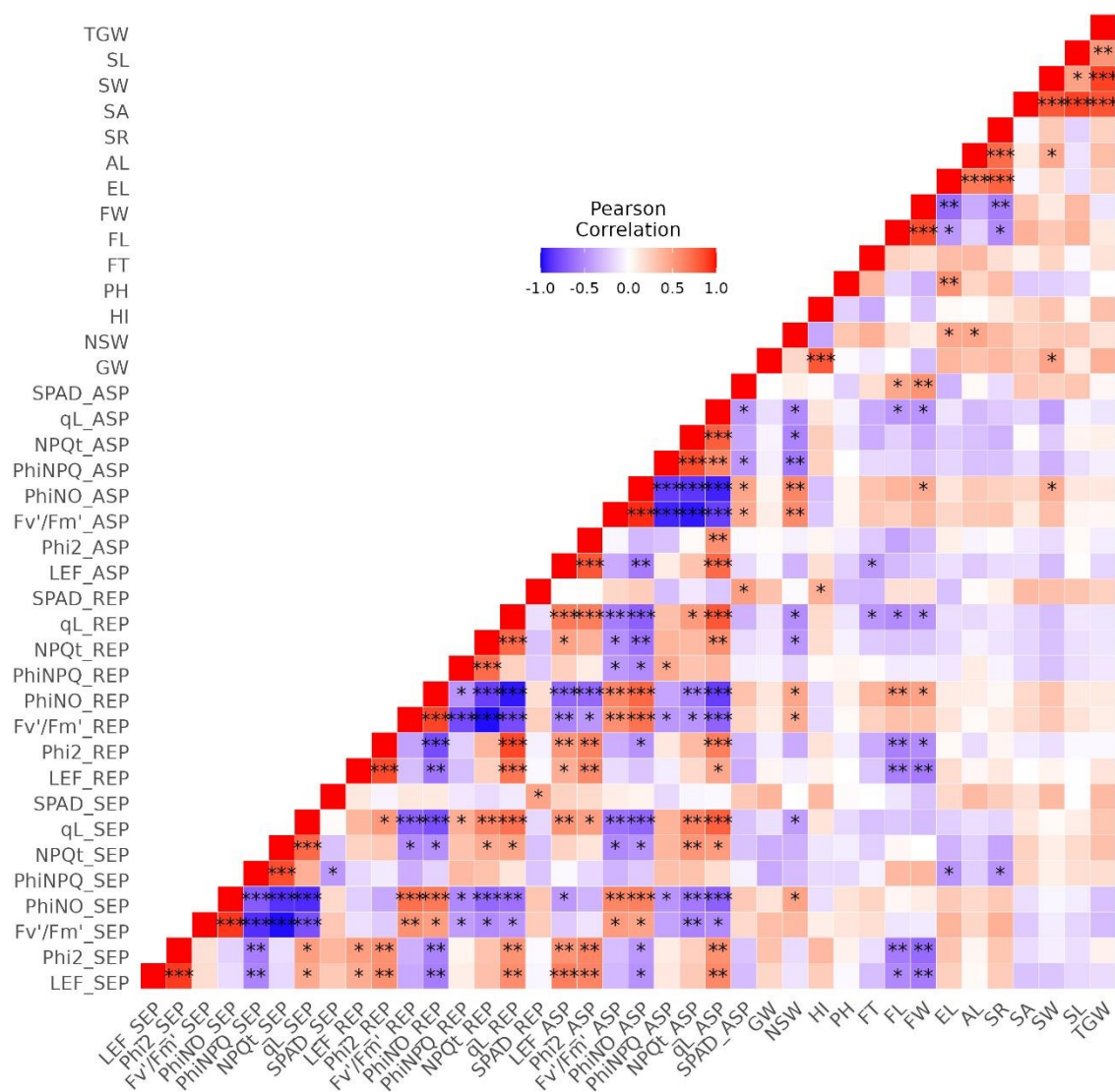
Supplementary Fig. S3: Developmental changes in heritability. Heritability of each PSII parameters and SPAD along the barley developmental stages defined by Zadok's growth scale. The red dot next to each box is the mean heritability of each stage. Different letters next to each box show significant differences by the Tukey-test ($P < 0.05$) between the mean heritability of different developmental stages.



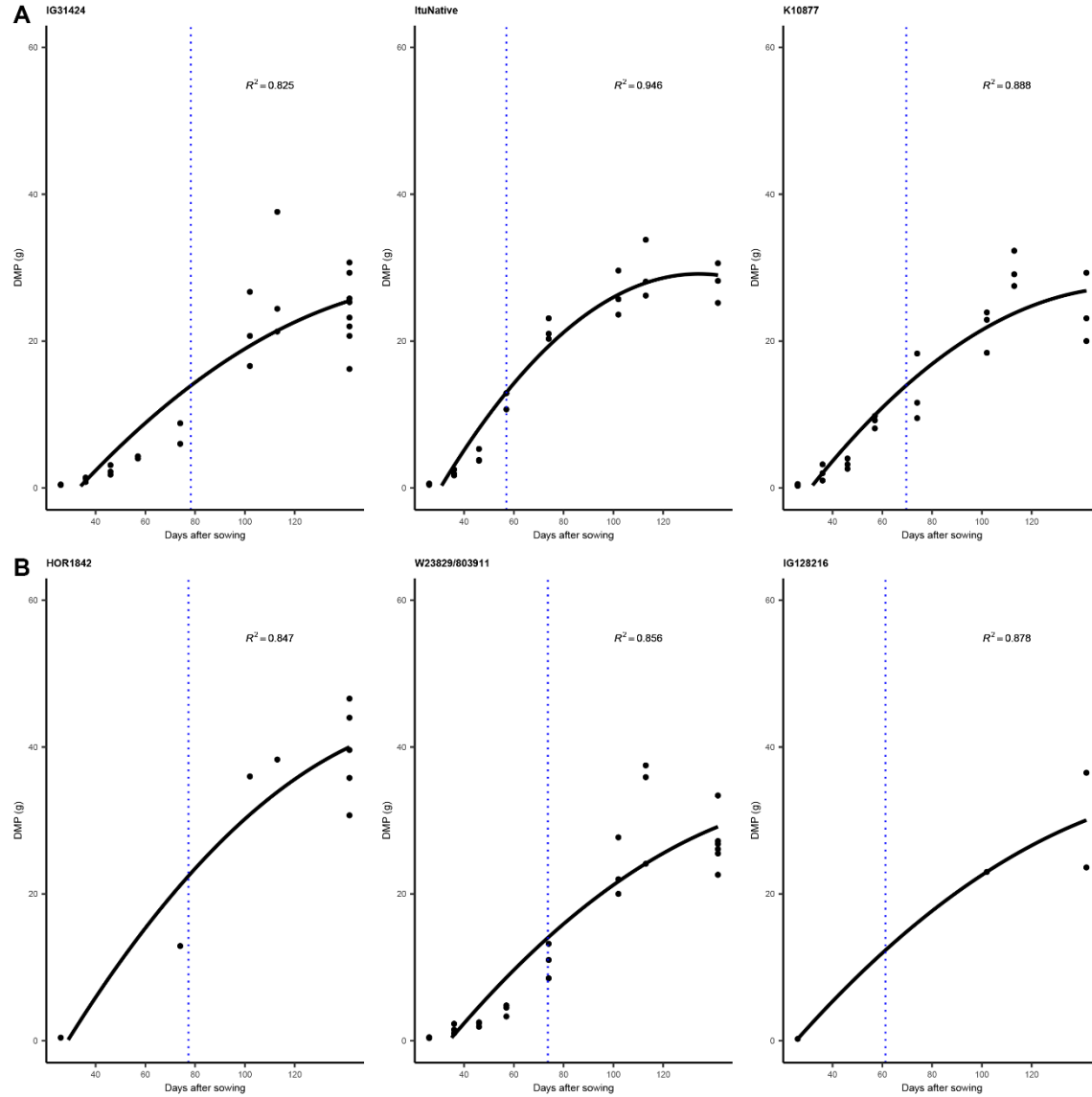
Supplementary Fig.S4: The growth trajectories for 23 barley inbred lines grown in the field. The black dots were the adjusted values of dry mass per plant (DMP) in each plot, the black lines were the DMP trajectory curves predicted by the quadratic model. The blue dashed line in each plot indicates flowering time (FT) for each inbred.



Supplementary Fig. S5: Boxplot of the adjusted entry means for 11 morphological traits of twenty-three barley inbred lines in multiple environments across multiple years experiments assigned to four clusters. The color dots represent the adjusted entry means of each morphological trait. The red dot next to each box are the mean of the trait for the genotypes in each cluster. The letters next to each box are the compact letters, which means the means for each parameter under different conditions which not sharing the same letters are significantly different based on the Tukey-test ($P < 0.05$).



Supplementary Fig. S6: Person correlation coefficients calculated between pairs of adjusted entry means based on each developmental phase of 23 barley inbreds for PSII parameters, SPAD and morphological traits collected from multiple environments and years in the field conditions. Asterisks indicate the significance level (***, **, * indicated $P < .001$, $.01$, $.05$ respectively)



Supplementary Fig. S7: The growth trajectory curves for six barley inbred lines grown in the climate chamber condition. The black dots were the adjusted value of the total aboveground dry mass (DMP), the black lines were the DMP trajectories predicted by the logistic model. The blue dashed line in each plot indicated the flowering time (FT) for each barley inbred.