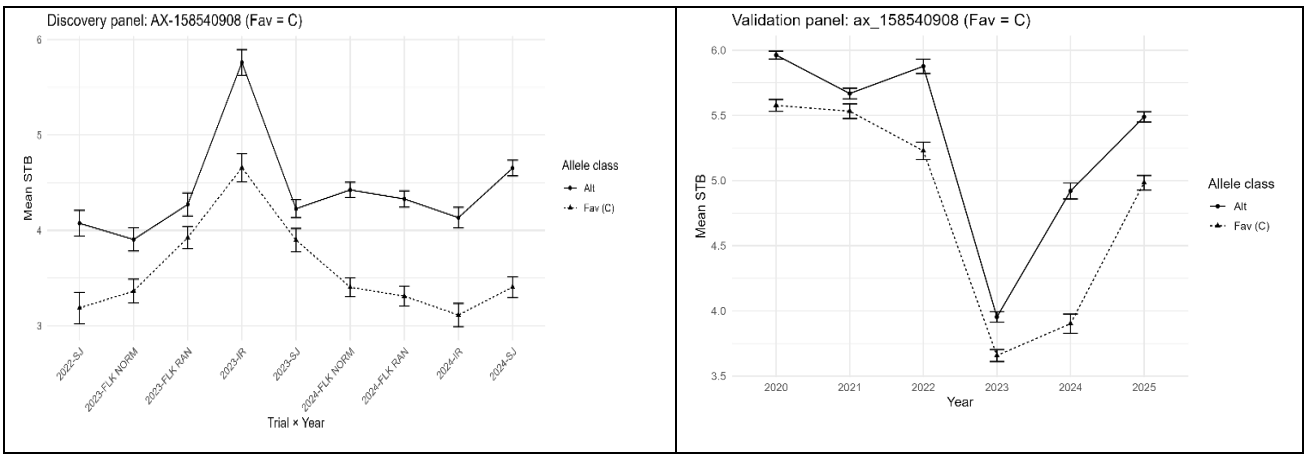
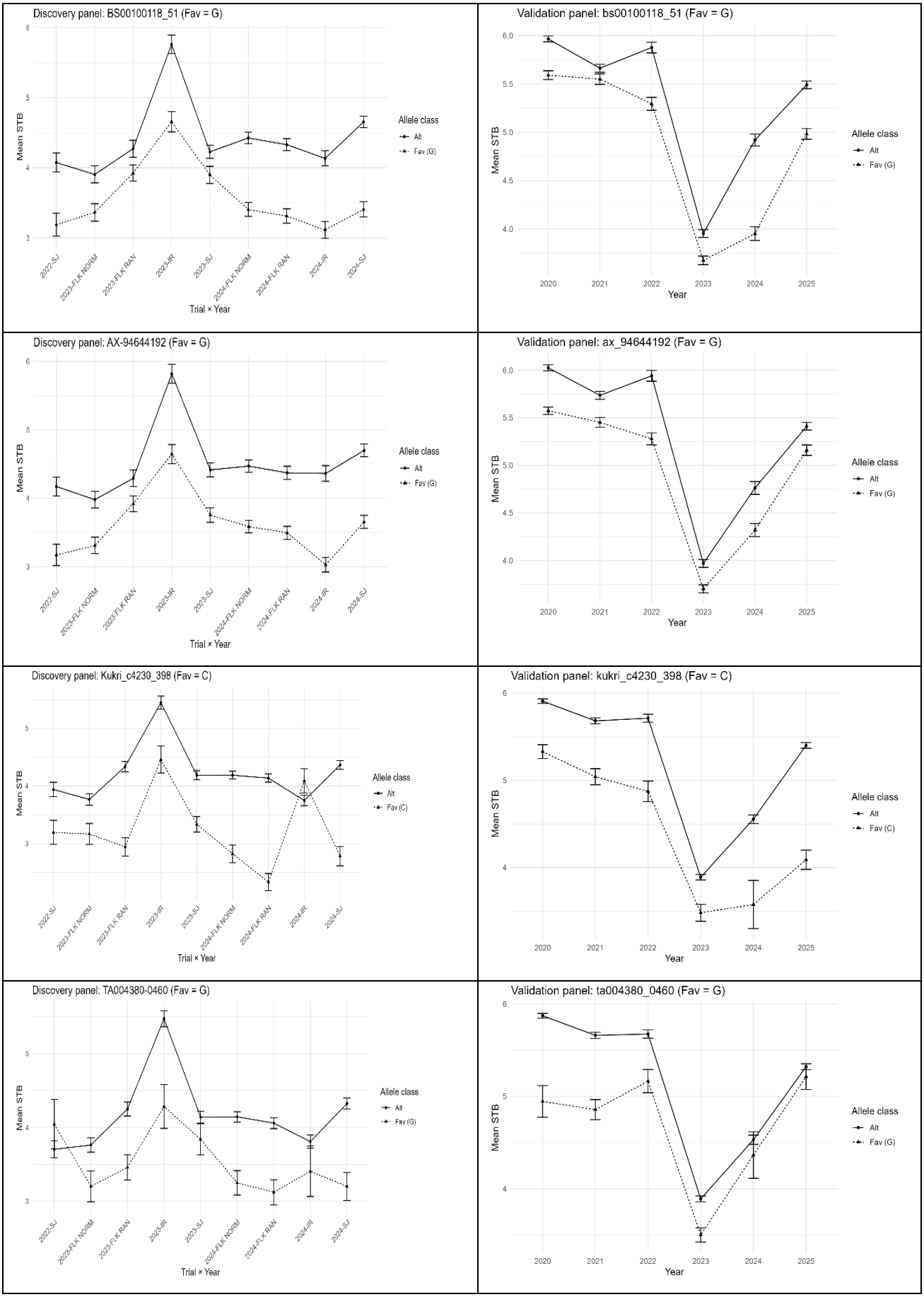
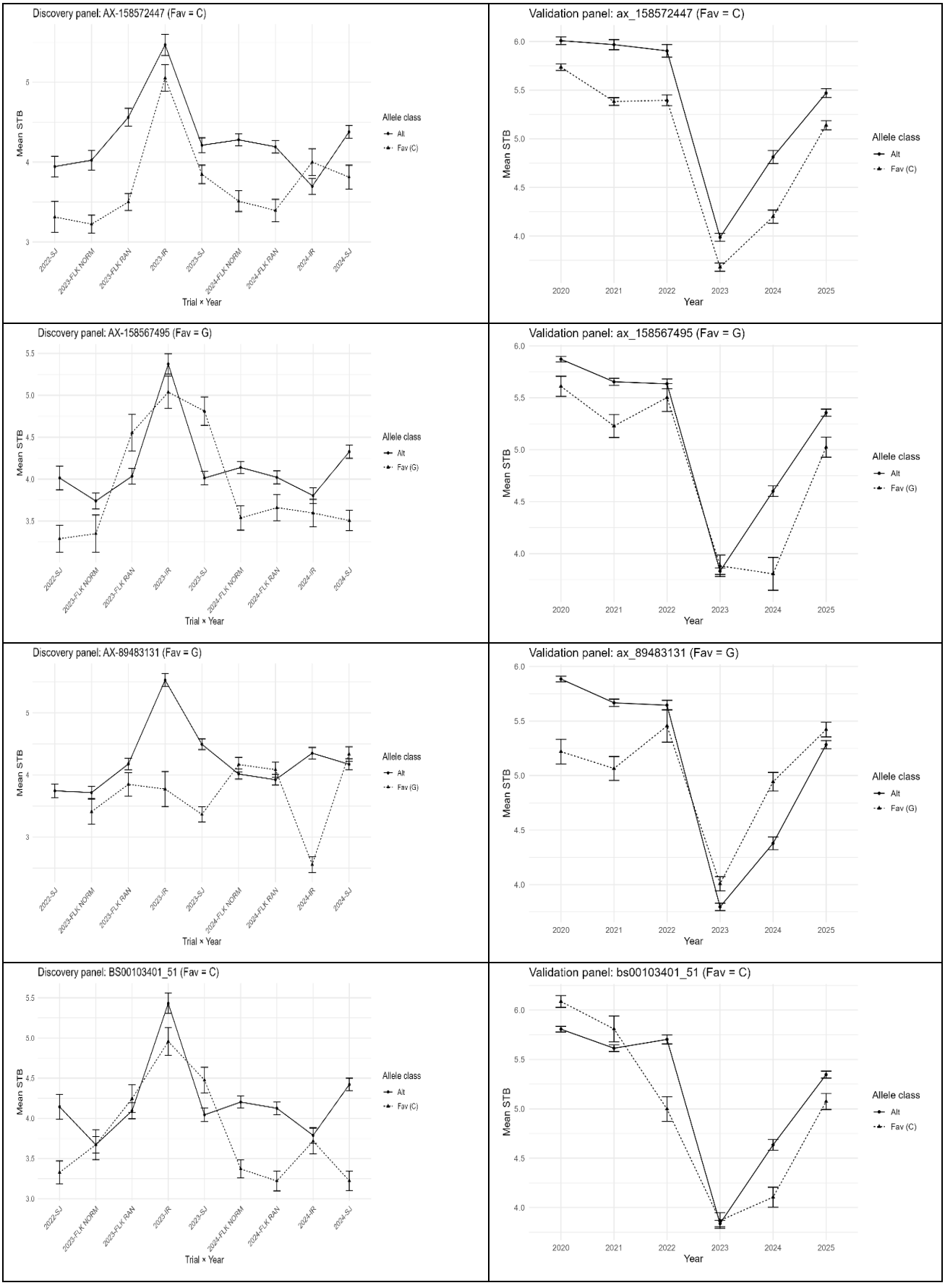
Supplementary Material

Table S1. Founder and donor varieties used in the discovery panel. Each marker is shown at the top, with each respective variety's corresponding allele. Letters in bold are the associated “favorable allele”.

Variety	Excalibur_c55959_651	TA004380-0460	AX-158572447	AX-158540908	BS00100118_51	AX-110524801	AX-94644192	Kukri_c5411_1312	Kukri_c4230_398	AX-89483131	AX-158567495	AX-94821207	BS00103401_51
Apostel	**A**	T	**C**	A	T	**G**	**G**	G	A	A	**G**	A	T
Champion	**A**	T	T	**C**	**G**	**G**	**G**	G	A	A	A	A	T
Informer	**A**	T	**C**	**C**	**G**	**G**	**G**	G	A	A	A	A	T
Knut	**A**	T	**C**	**C**	**G**	**G**	**G**	G	A	A	A	A	T
Kvium	**A**	**G**	**C**	**C**	**G**	**G**	**G**	G	A	A	A	A	T
KWS Extase	**A**	T	T	**C**	**G**	**G**	**G**	G	A	A	**G**	A	T
KWS Siskin	**A**	T	T	**C**	**G**	**G**	**G**	G	A	A	A	A	T
KWS Zyatt	**A**	T	T	A	T	A	C	G	A	A	A	**G**	**C**
LG Skyscraper	**A**	T	T	A	T	**G**	C	G	A	A	A	A	T
Pondus	G	T	T	A	T	A	C	G	A	**G**	A	A	T
Rembrandt	G	T	T	A	T	A	C	G	A	**G**	A	A	T
Revolver	**A**	T	**C**	**C**	**G**	**G**	**G**	G	**C**	A	A	A	T
RGT Stokes	**A**	T	T	A	T	A	**G**	G	A	**G**	A	A	T
SU Selke	**A**	**G**	**C**	A	T	**G**	C	**A**	**C**	A	A	**G**	**C**




Discovery panel: BS00100118_51 (Fav = G)
Validation panel: bs00100118_51 (Fav = G)
Discovery panel: AX-94644192 (Fav = G)
Validation panel: ax_94644192 (Fav = G)
Discovery panel: Kukri_c4230_398 (Fav = C)
Validation panel: kukri_c4230_398 (Fav = C)
Discovery panel: TA004380-0460 (Fav = G)
Validation panel: ta004380_0460 (Fav = G)
Mean STB
Trial × Year
Year
Allele class
Alt
Fav (G)
Fav (C)
2022-SJ
2023-FLK NORM
2023-FLK RAN
2023-IR
2023-SJ
2024-FLK NORM
2024-FLK RAN
2024-IR
2024-SJ


Discovery panel: AX-158572447 (Fav = C)
Validation panel: ax_158572447 (Fav = C)
Discovery panel: AX-158567495 (Fav = G)
Validation panel: ax_158567495 (Fav = G)
Discovery panel: AX-89483131 (Fav = G)
Validation panel: ax_89483131 (Fav = G)
Discovery panel: BS00103401_51 (Fav = C)
Validation panel: bs00103401_51 (Fav = C)
Mean STB
Trial × Year
Year
Allele class
Alt
Fav (C)
Fav (G)
2022-SJ
2023-FLK NORM
2023-FLK RAN
2023-IR
2023-SJ
2024-FLK NORM
2024-FLK RAN
2024-IR
2024-SJ

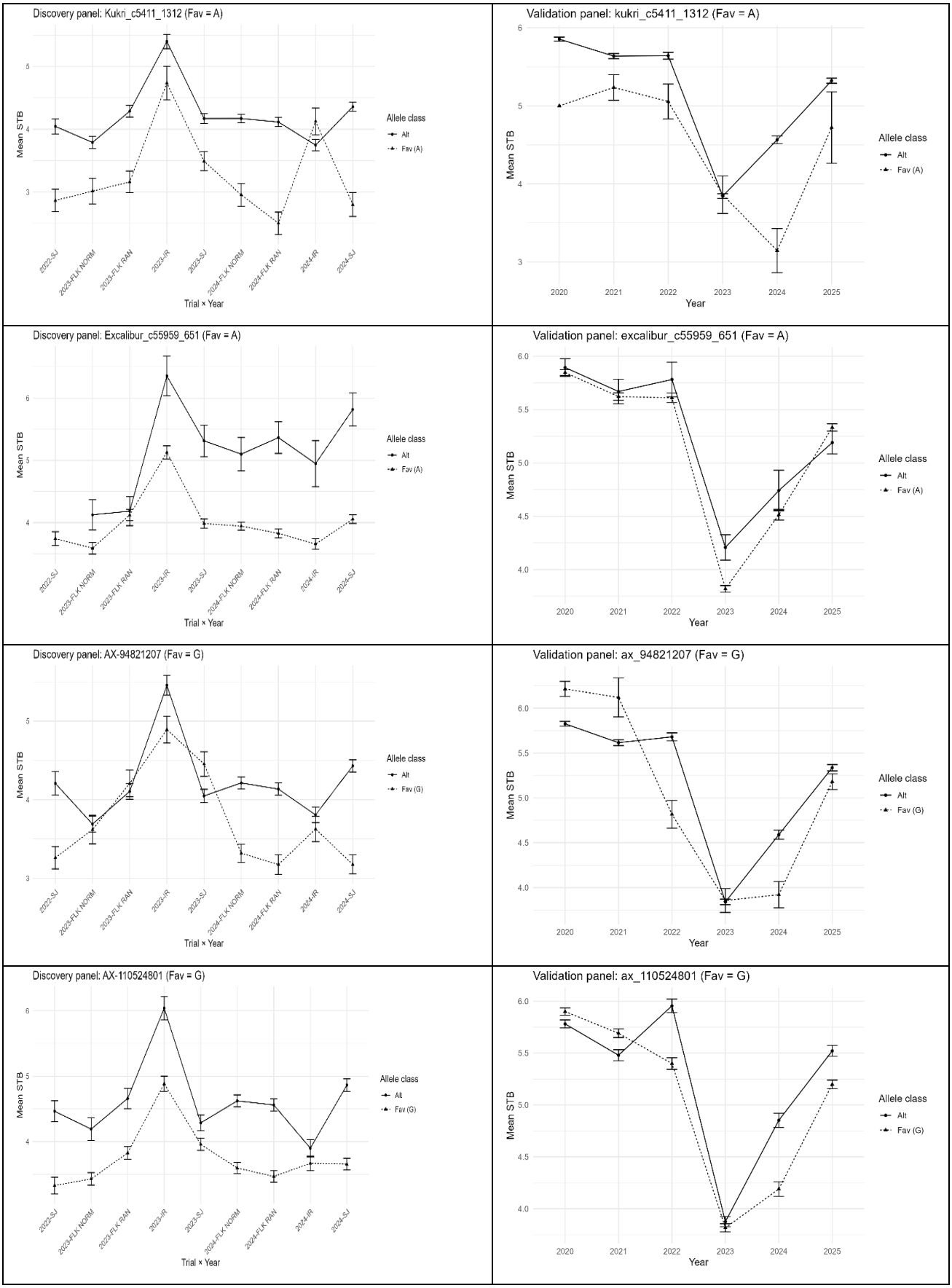


Figure S1. Marker allele effect on discovery panel (left) and validation panel (right).

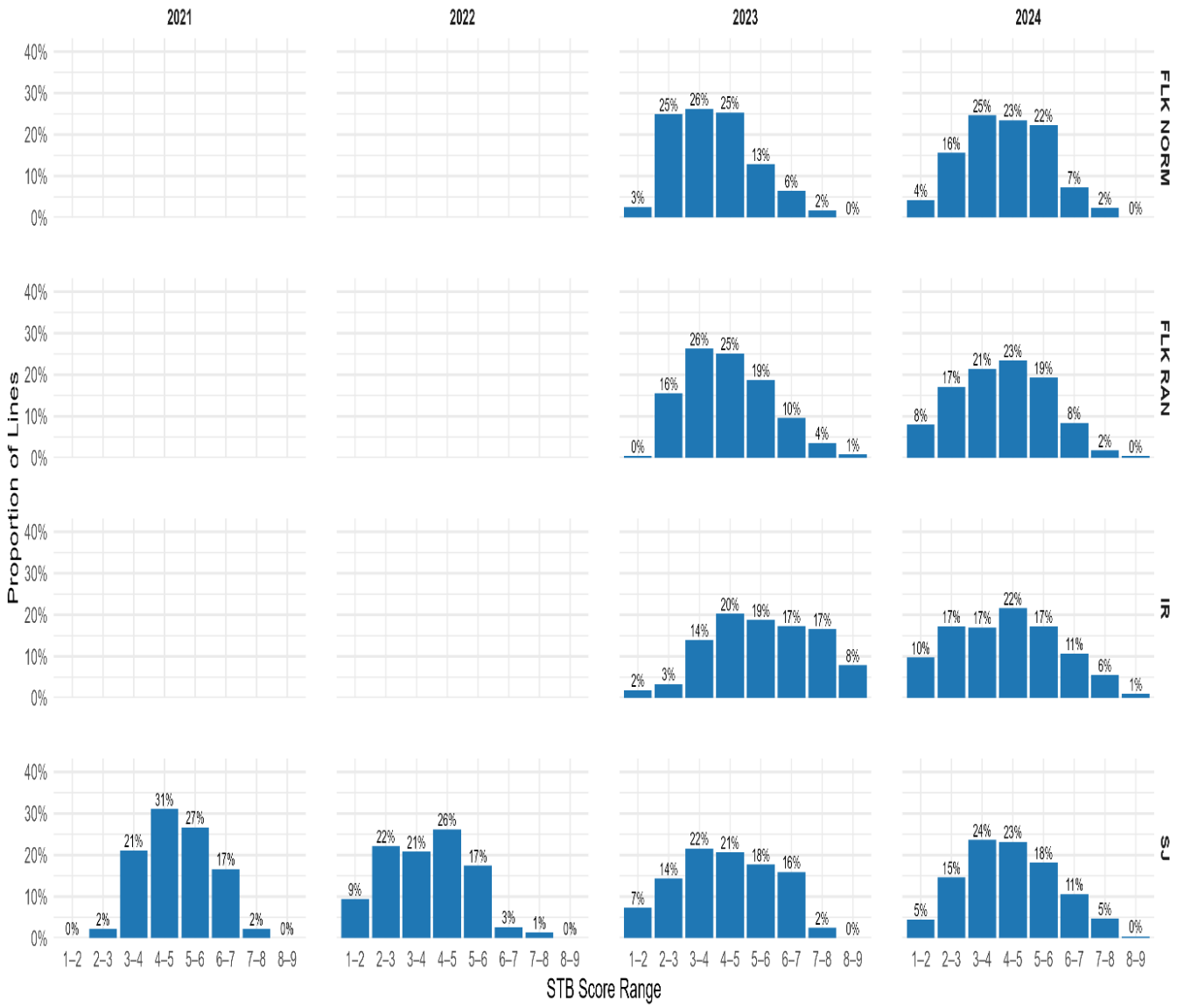


Figure S2. Proportion of breeding lines within STB severity score categories (1–9) for each year and location in the discovery panel.

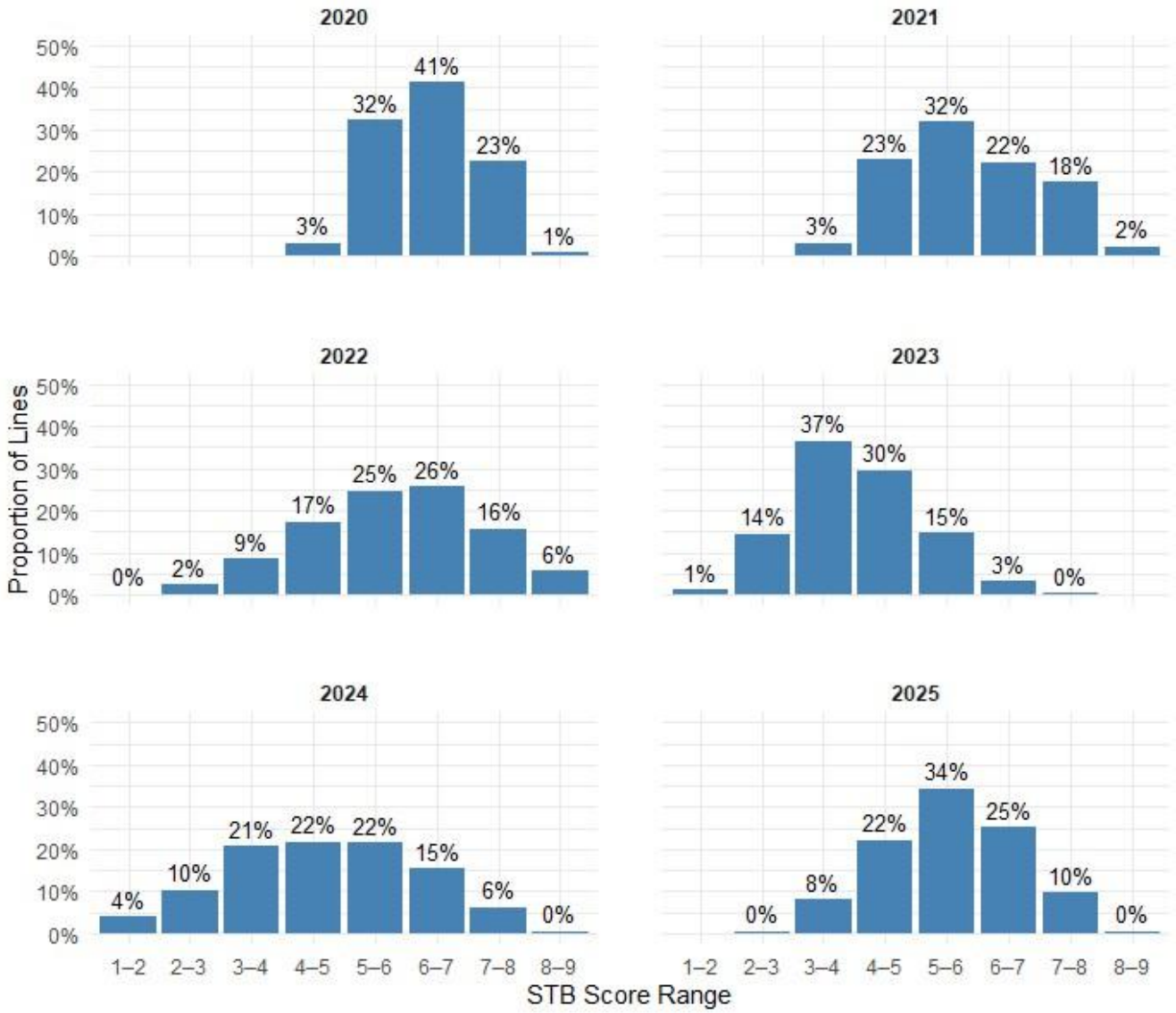


Figure S3. Proportion of breeding lines within STB severity score categories (1–9) for each year in the validation panel at Sejet.

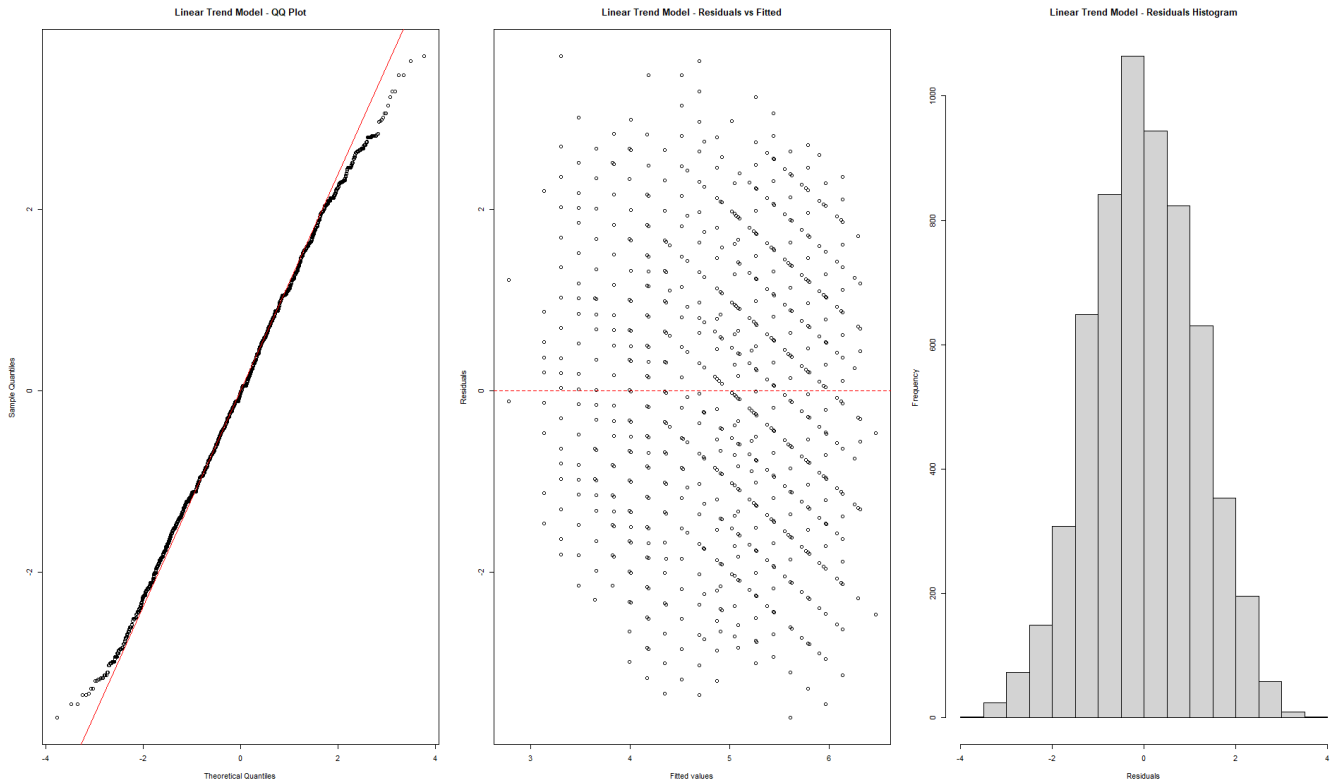


Figure S4. Diagnostic plots for the linear mixed model assessing the effects of heading date, plant height, and favorable allele count on STB severity. Panels include QQplot of residulas (left), residuals versus fitted values plot (middle) and residuals distribution (right).

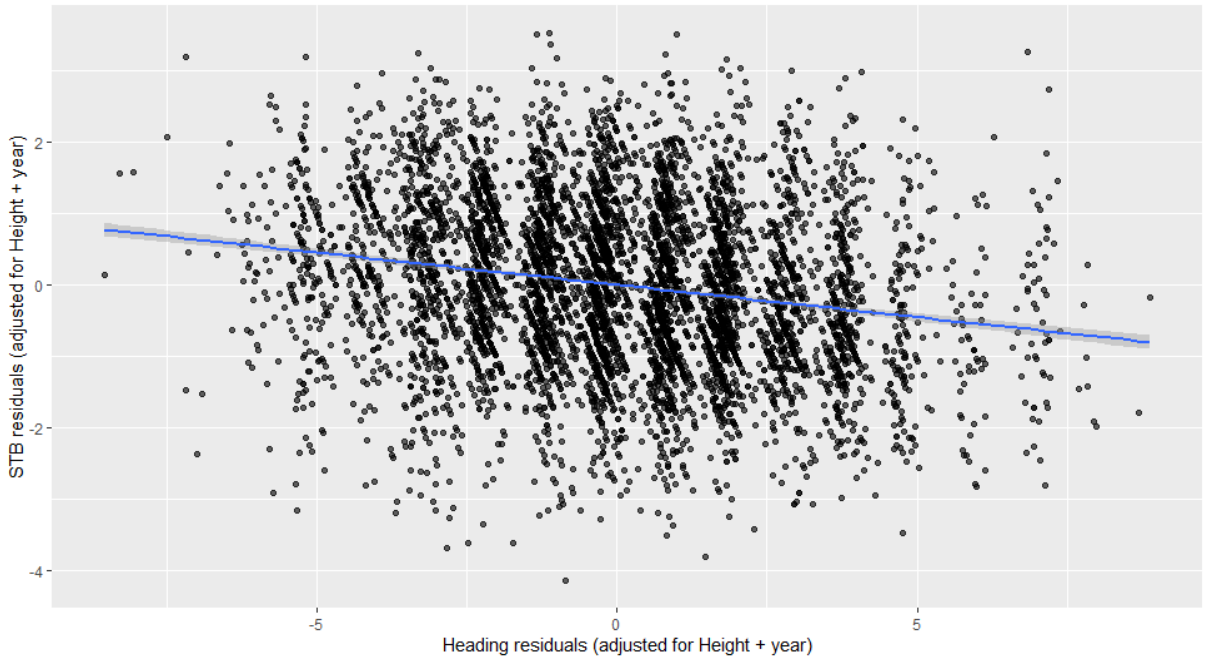


Figure S5. Partial relationship between heading date and STB after adjusting for plant height and year effects. Added-variable plot showing residual STB (after removing effects of plant height and year) versus residual heading date (adjusted for the same covariates).

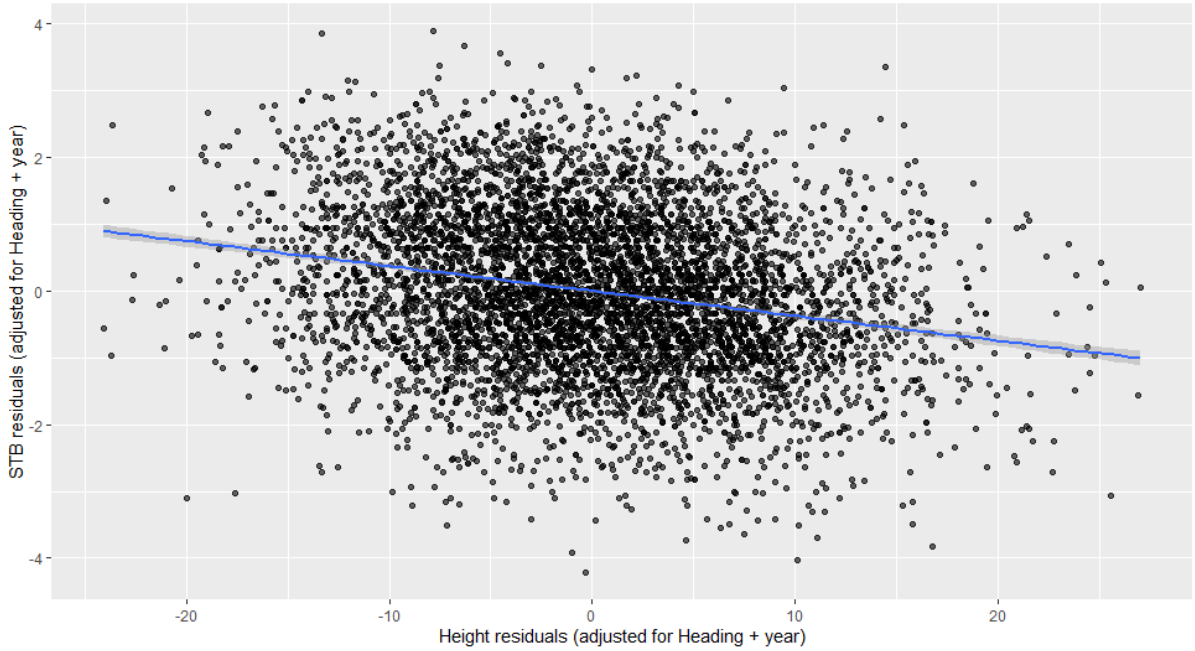


Figure S6. Partial relationship between plant height and STB after adjusting for heading date and year effects. Added-variable plot showing residual STB (after removing effects of heading date and year) versus residual plant height.

Table S2. Founder and donor varieties used in the discovery panel. Each marker is shown at the top, with each respective variety's corresponding allele. Letters in bold are the associated “favorable allele”. Scale for assessment of disease severity in cereals (adapted from [25] and corresponding UPOV scale used in plant breeding and VCU testing (adapted from [24].

Disease severity (%)	UPOV Scale	Symptoms on cereal; crop/plot level
0	1	No disease
0.1	2	Max one spot per plant
0.5	3	Max one spot per tiller
1	4	Few spots per plant (lower leaves)
5	5	Lower leaves up to 10-25% coverage
10	6	Lower leaves typically 25% coverage or more
25	7	Lower leaves 50% coverage or more
50	8	Half of leaf area is senescent. Lower leaves 75-100% coverage
>75	9	Almost no green leaf area