

## **Supplementary material**

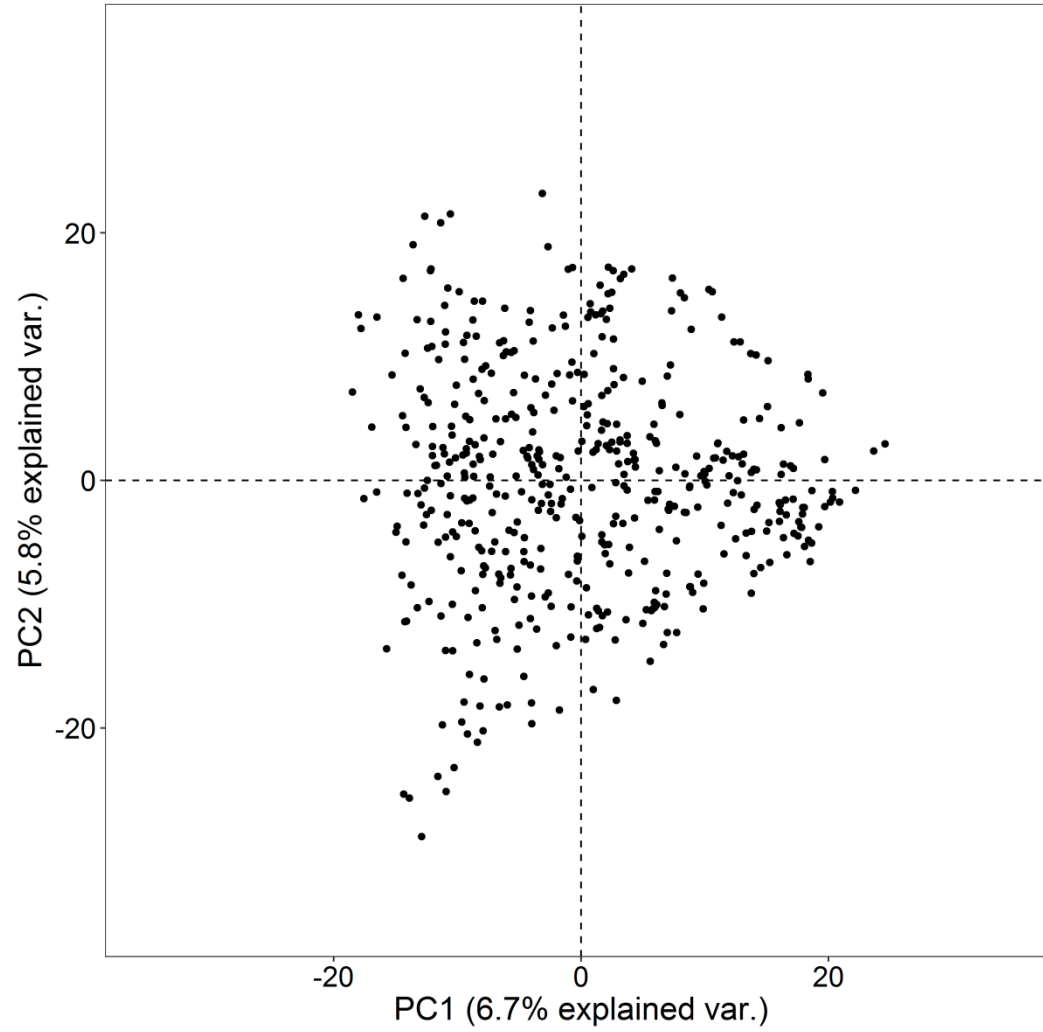
**Article Title:** Combining grain yield, protein content and protein quality by multi-trait genomic selection in bread wheat

**Journal:** Theoretical and Applied Genetics

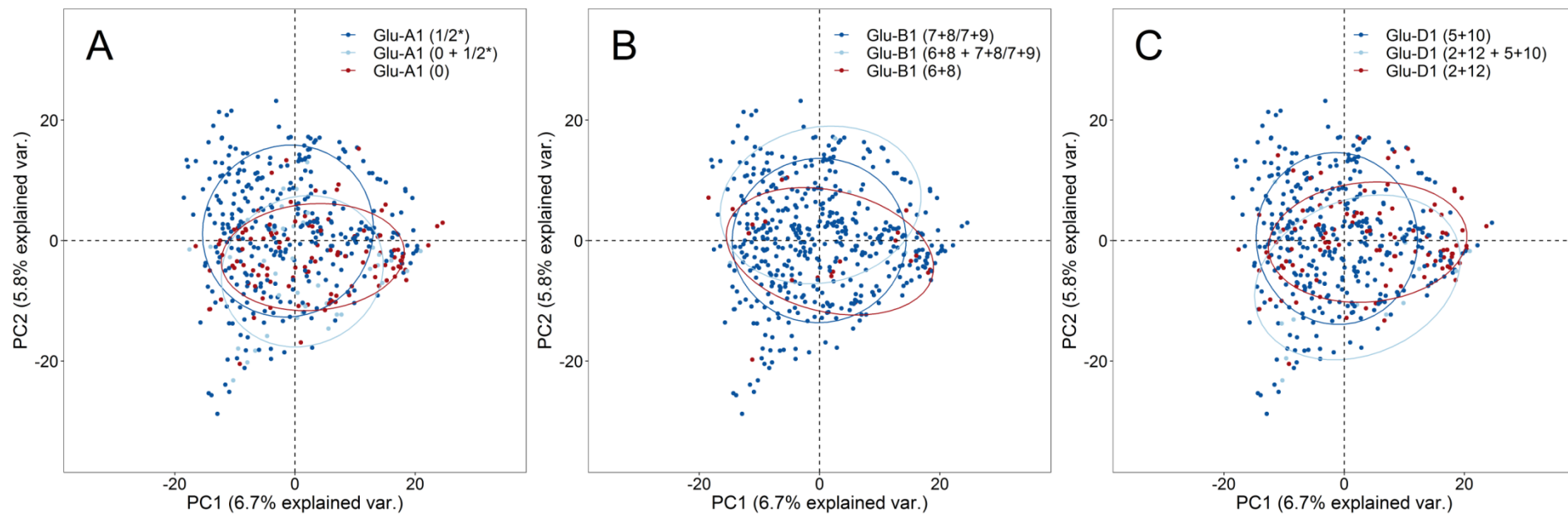
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### **Name, affiliation, and email of corresponding author:**

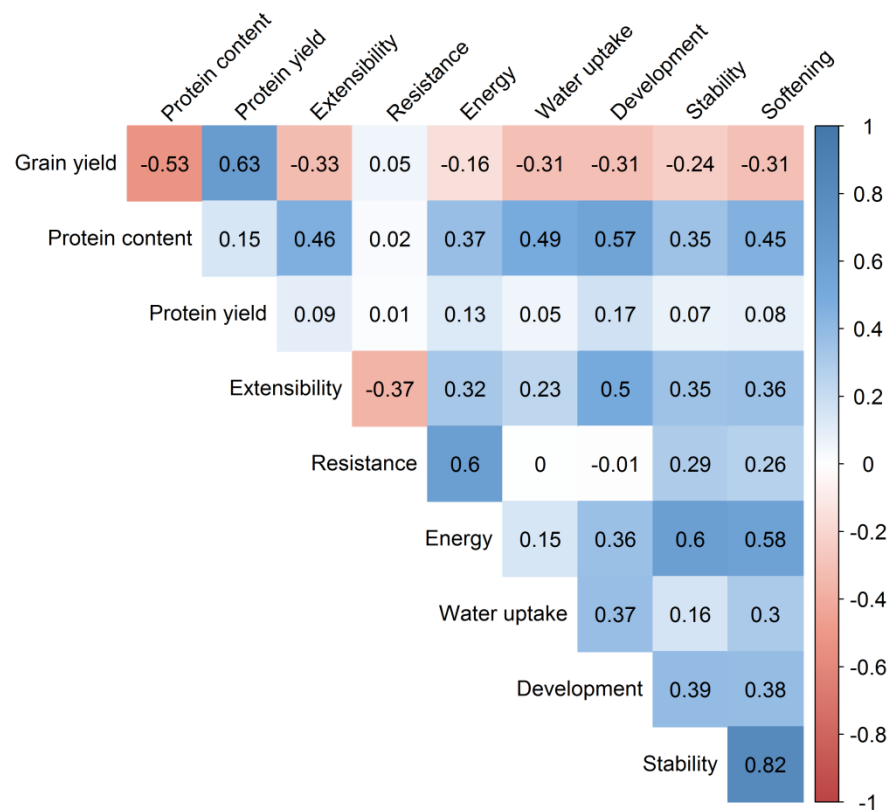
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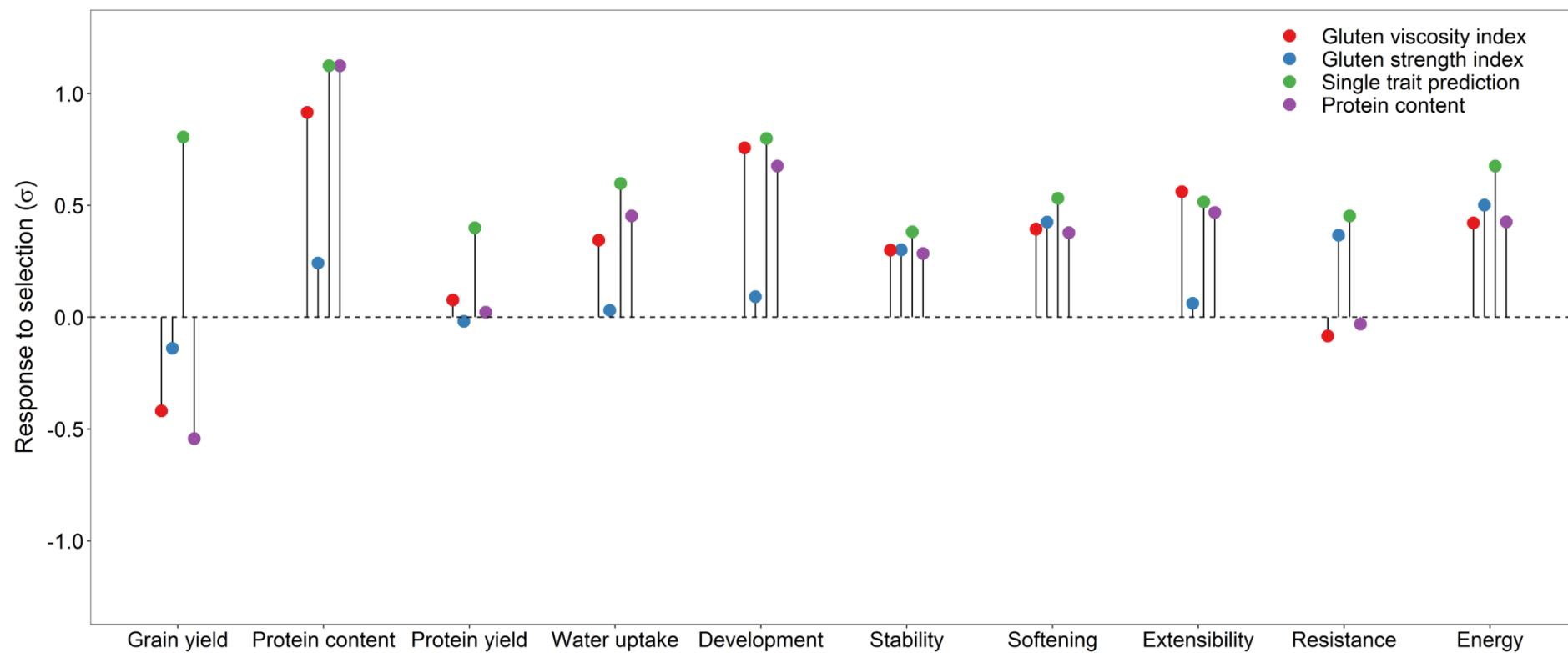
**Fig. S1** Population structure of the 480 lines involved in the study.



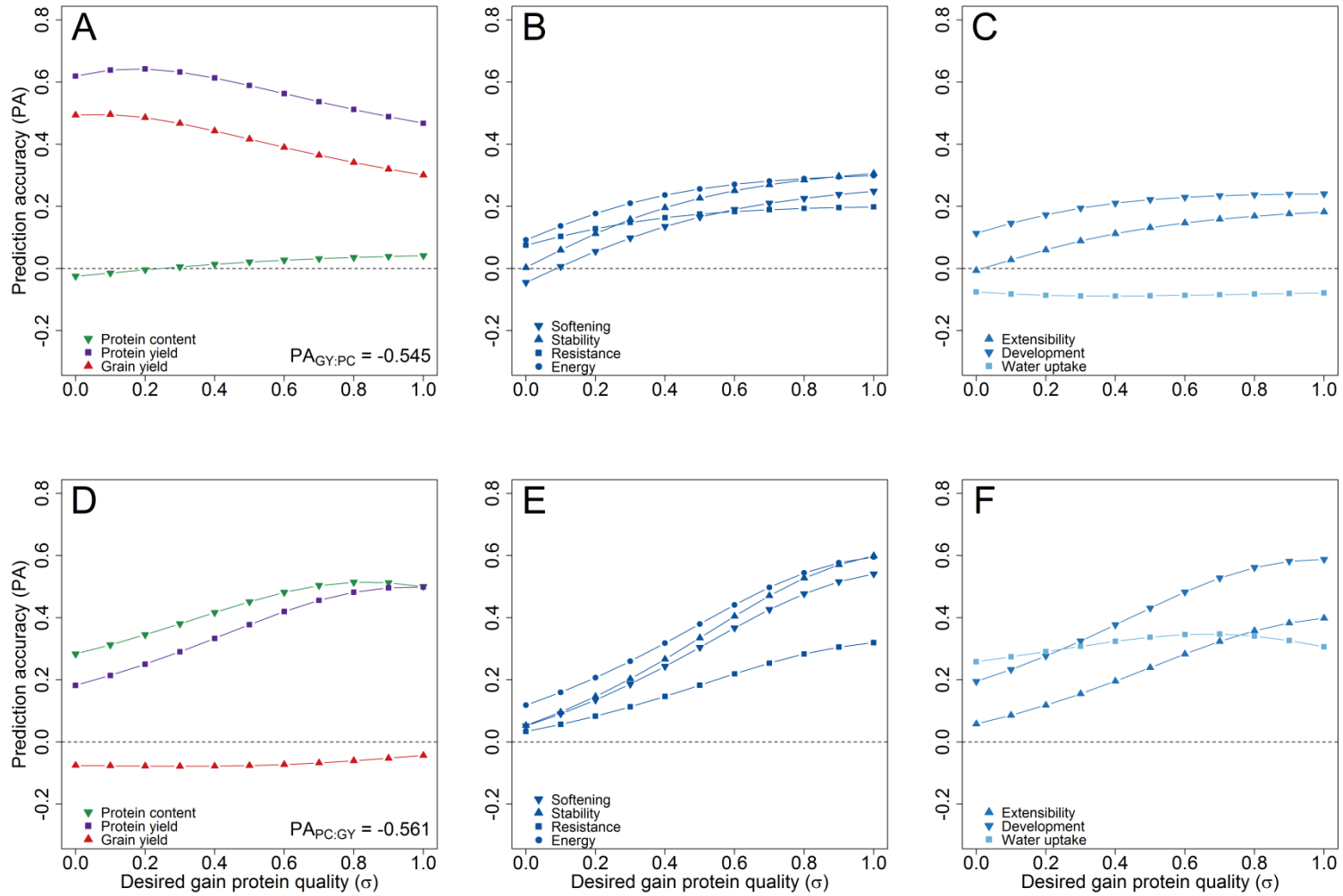
**Fig. S2** Population structure of the 480 studied lines with respect to their alleles at the Glu-A1 (A), Glu-B1 (B), and Glu-D1 (C) marker locus.



**Fig. S3** Phenotypic correlations between grain yield, protein content, protein yield and the dough rheological traits for the 480 studied lines. The phenotypic values for dough softening were inverted to achieve a positive correlation with the other dough mixing parameters.



**Fig. S4** Response to selection of the 10% best performing lines for grain yield, protein content, and protein yield as well as the dough rheological traits when using genomic estimated breeding values of the traits per se, protein content or the gluten strength and viscosity index for selection.



**Fig. S5** Prediction accuracy for major agronomic traits, gluten strength and gluten viscosity related dough rheological traits as well as the water uptake with varying desired gains for the protein quality in the grain yield deviation (top row) and grain protein deviation indices (bottom row).

**Table S1** Number of pre-selected trials, lines, variation, and entry-mean heritability for grain yield, protein content, protein yield and the assessed dough rheological traits for the phenotypic data from which the 480 lines in the study were extracted

| Trait                                | Trials | Lines | $\sigma_G^2$ | $\sigma_e^2$ | $h^2$ | Min   | Mean  | Max   |
|--------------------------------------|--------|-------|--------------|--------------|-------|-------|-------|-------|
| Grain yield (dt ha <sup>-1</sup> )   | 136    | 1838  | 11.97        | 34.45        | 0.61  | 46.4  | 66.2  | 88.8  |
| Protein content (%)                  | 86     | 1814  | 0.38         | 0.40         | 0.78  | 10.8  | 13.7  | 15.9  |
| Protein yield (dt ha <sup>-1</sup> ) | 66     | 1795  | 0.18         | 0.73         | 0.47  | 6.4   | 9.3   | 12.4  |
| Water uptake (%)                     | 28     | 753   | 2.76         | 2.27         | 0.61  | 51.7  | 59.1  | 64.7  |
| Development (min)                    | 23     | 603   | 1.24         | 2.35         | 0.41  | 0.4   | 4.0   | 11.1  |
| Stability (min)                      | 23     | 689   | 26.15        | 38.35        | 0.47  | 0.2   | 14.0  | 31.6  |
| Softening (FU)                       | 25     | 733   | 262.58       | 368.42       | 0.49  | 0.8   | 51.3  | 175.5 |
| Resistance (EU)                      | 25     | 747   | 2966.60      | 5623.41      | 0.39  | 63.2  | 389.4 | 715.1 |
| Extensibility (mm)                   | 20     | 636   | 130.92       | 173.69       | 0.49  | 120.9 | 171.1 | 226.2 |
| Energy (cm <sup>2</sup> )            | 23     | 716   | 519.31       | 341.71       | 0.66  | 24.6  | 114.3 | 192.3 |

Genotypic variance ( $\sigma_G^2$ ), residual variance ( $\sigma_e^2$ ), and heritability ( $h^2$ ).

**Table S2** Variation, genomic heritability, prediction ability and prediction accuracy for grain yield, protein content, protein yield and the assessed dough rheological traits in the investigated population of 480 lines.

| Trait                                | Min   | Mean  | Max   | h <sup>2</sup> | Prediction ability     |                           |                    |                          |                             | Prediction accuracy    |                           |                    |                          |                             |
|--------------------------------------|-------|-------|-------|----------------|------------------------|---------------------------|--------------------|--------------------------|-----------------------------|------------------------|---------------------------|--------------------|--------------------------|-----------------------------|
|                                      |       |       |       |                | MAS (fix) <sup>†</sup> | MAS (random) <sup>‡</sup> | GBLUP <sup>§</sup> | WBLUP (fix) <sup>¶</sup> | WBLUP (random) <sup>#</sup> | MAS (fix) <sup>†</sup> | MAS (random) <sup>‡</sup> | GBLUP <sup>§</sup> | WBLUP (fix) <sup>¶</sup> | WBLUP (random) <sup>#</sup> |
| Grain yield (dt ha <sup>-1</sup> )   | 48.2  | 68.3  | 83.6  | 0.60           | 0.652                  | 0.221                     | 0.223              | 0.646                    | 0.648                       | 0.259                  | 0.257                     | 0.755              | 0.748                    | 0.751                       |
| Protein content (%)                  | 11.6  | 13.5  | 15.9  | 0.80           | 0.342                  | 0.336                     | 0.725              | 0.723                    | 0.724                       | 0.363                  | 0.357                     | 0.769              | 0.766                    | 0.767                       |
| Protein yield (dt ha <sup>-1</sup> ) | 7.3   | 9.4   | 11.4  | 0.42           | 0.456                  | -0.014                    | -0.005             | 0.444                    | 0.453                       | -0.021                 | -0.008                    | 0.671              | 0.654                    | 0.667                       |
| Water uptake (%)                     | 51.7  | 58.9  | 64.7  | 0.68           | 0.225                  | 0.219                     | 0.588              | 0.583                    | 0.587                       | 0.274                  | 0.267                     | 0.728              | 0.722                    | 0.727                       |
| Development (min)                    | 0.6   | 4.0   | 11.1  | 0.49           | 0.324                  | 0.319                     | 0.565              | 0.562                    | 0.564                       | 0.418                  | 0.411                     | 0.727              | 0.723                    | 0.726                       |
| Stability (min)                      | 0.3   | 13.1  | 31.6  | 0.44           | 0.410                  | 0.410                     | 0.506              | 0.515                    | 0.518                       | 0.589                  | 0.588                     | 0.725              | 0.723                    | 0.726                       |
| Softening (FU)                       | 0.8   | 52.9  | 175.5 | 0.61           | 0.454                  | 0.455                     | 0.609              | 0.611                    | 0.613                       | 0.534                  | 0.535                     | 0.717              | 0.720                    | 0.722                       |
| Resistance (EU)                      | 135.5 | 394.5 | 715.1 | 0.53           | 0.309                  | 0.305                     | 0.437              | 0.477                    | 0.478                       | 0.454                  | 0.449                     | 0.646              | 0.704                    | 0.707                       |
| Extensibility (mm)                   | 120.9 | 170.5 | 224.1 | 0.53           | 0.239                  | 0.238                     | 0.544              | 0.545                    | 0.545                       | 0.309                  | 0.307                     | 0.702              | 0.703                    | 0.703                       |
| Energy (cm <sup>2</sup> )            | 24.6  | 115.1 | 192.3 | 0.65           | 0.471                  | 0.469                     | 0.583              | 0.611                    | 0.611                       | 0.588                  | 0.585                     | 0.727              | 0.763                    | 0.762                       |

<sup>†</sup> Linear model for marker-assisted selection with fixed *Glu-1* marker effects

<sup>‡</sup> Linear model for marker-assisted selection with random *Glu-1* marker effects

<sup>§</sup> Genomic best linear unbiased prediction model

<sup>¶</sup> Weighted genomic best linear unbiased prediction model with fixed *Glu-1* marker effects

<sup>#</sup> Weighted genomic best linear unbiased prediction model with random *Glu-1* marker effects