**TABLE S1** Phenotypic raw data and Best Linear Unbiased Estimates of each genotype (BLUEs).

**TABLE S2** Genotypic raw data of the 50K SNP array.

**TABLE S3** NIRS raw data between wavelengths of 1 250-2 400 nm, based on seed samples and based on biomass samples of seedlings.

**TABLE S4** Summary statistics for each group. Groups are abbreviated as WA = Walliser, SM = Satu Mare, SF = Strenzfelder, RT = Sankt Galler Rheintaler, GB = Gelber Badischer, CG = Campan-Galade, EF = elite Flints, and ED = elite Dents. denotes the genotypic variance, the genotype-by-environment interaction variance, and the error variance. is the broad-sense heritability. Traits are abbreviated as follows: anthesis-silking-interval (ASI), EV (early vigor), plant height at harvest (Final PH), grain dry matter content (GDM), grain yield (GYield), phosphorus grain concentration in the kernels (Pconc). All values are based on the three location-year-combinations (Hohenheim 2019 and Hohenheim 2020, Eckartsweier 2020), except for Pconc for which HOH 2020 was not available.

**TABLE S5** Phenomic prediction based on NIR spectra of seedling biomass samples (BM; green) compared to maize kernels (Seed; yellow). NIRS was assessed for all 393 available genotypes grown in EWE 2020 for seedling biomass as well as for seed samples. The analysis was performed for the three major groups elite Dents (ED, n = 100), elite Flints (EF, n = 100), and landraces (LR, n = 193). The traits anthesis-silking-interval (ASI), EV (early vigor), plant height at harvest (Final PH), grain dry matter content (GDM), grain yield (GYield), and phosphorus grain concentration in the kernels (Pconc) were predicted by phenomic prediction within and among groups. Predictions within a group were cross-validated with 100 runs.

**Figure S1** Data processing steps.The different steps of processing the phenotypic (middle), genotypic (left) and NIRS (right) data are depicted. GS stands for genomic prediction, PS for phenomic prediction, BLUEs for best linear unbiased estimates, and CV for cross-validation.

**Figure S2** Near infrared spectroscopy data. A. Raw NIR spectra of all 400 genotypes. The black line represents the mean. B. Heritabilities for each wavelength across environments. C. Variance components for each wavelength across environments. G stands for the genetic, GE for the genotype-by-environment interaction, and Residual for the error variance term. D. Correlations for each trait between best linear unbiased estimate of the trait and NIR reflectance values. Traits are abbreviated as ASI (anthesis-silking-interval), EV (early vigor), Final PH (plant height at harvest), GDM (grain dry matter content), GYield (grain yield), and Pconc (phosphorus concentration in kernels).

**Figure S3** Among-group prediction for Satu Mare and Walliser used as training set.Groups are abbreviated as ED = elite Dents, EF = elite Flints, LR = overall landraces, GB = Gelber Badischer, SM = Satu Mare, SF = Strenzfelder, and WA = Walliser. GS and PS stand for genomic and phenomic prediction, respectively. Traits are denoted as ASI (anthesis-silking-interval), EV (early vigor), Final PH (plant height at harvest), GDM (grain dry matter content), GYield (grain yield), and Pconc (phosphorus concentration in kernels).

**Figure S4** Predictive ability of among-group predictions shown by group.Groups are abbreviated as ED = elite Dents, EF = elite Flints, LR = overall landraces, GB = Gelber Badischer, SM = Satu Mare, SF = Strenzfelder, and WA = Walliser. GS (left side) and PS (right side) stand for genomic and phenomic prediction, respectively. Traits are denoted as ASI (anthesis-silking-interval), EV (early vigor), Final PH (plant height at harvest), GDM (grain dry matter content), GYield (grain yield), and Pconc (phosphorus concentration in kernels).