

Supplementary Files

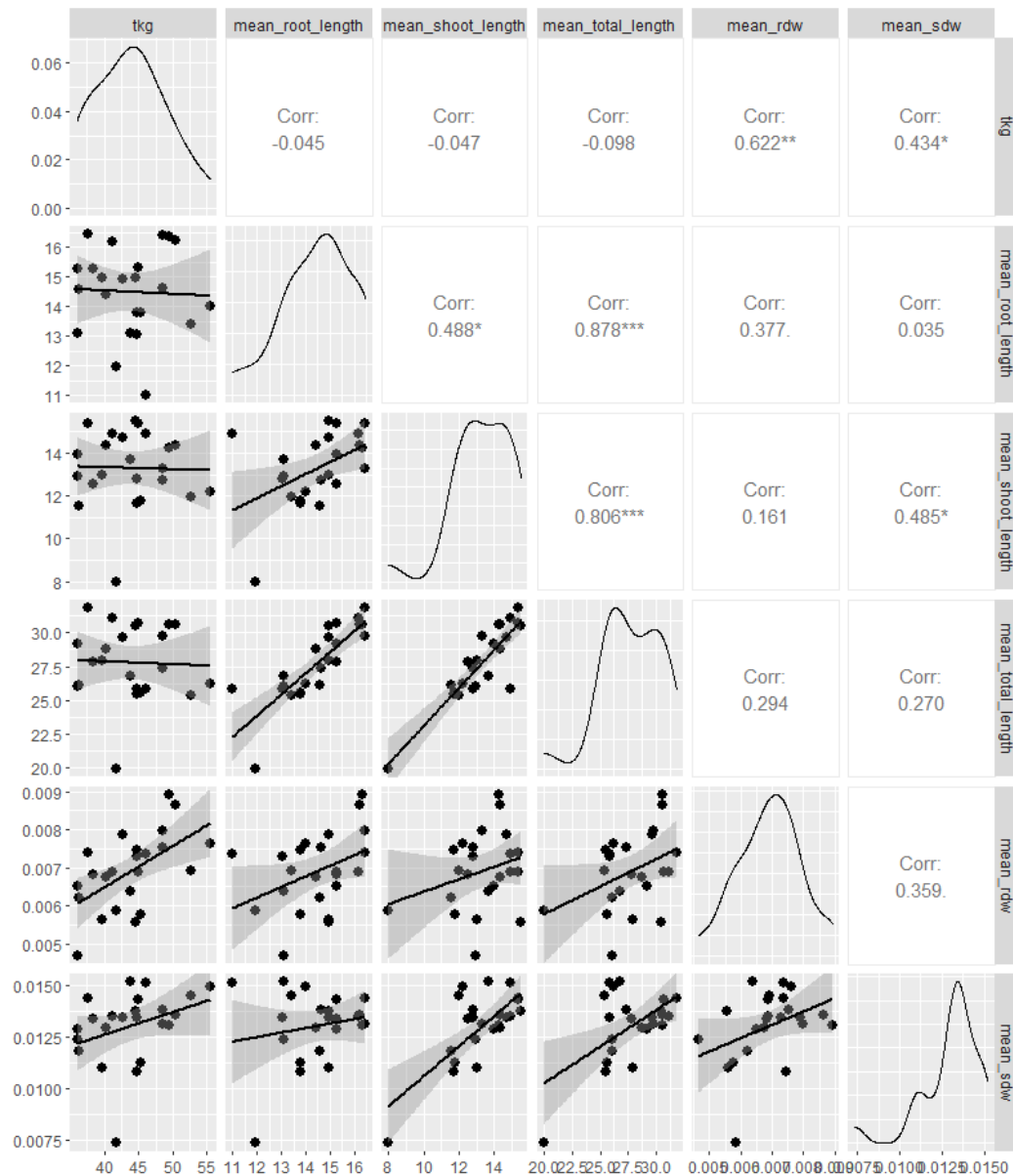


Figure S1 Correlations for various measured traits from the hydroponic experiment. Spearman correlation for SRL and TKG. SL and SRL are averaged across replicates for each genotype. Stars significant differences at $p < 0.05$ (*), $p < 0.01$ (**) and $p < 0.001$ (***).

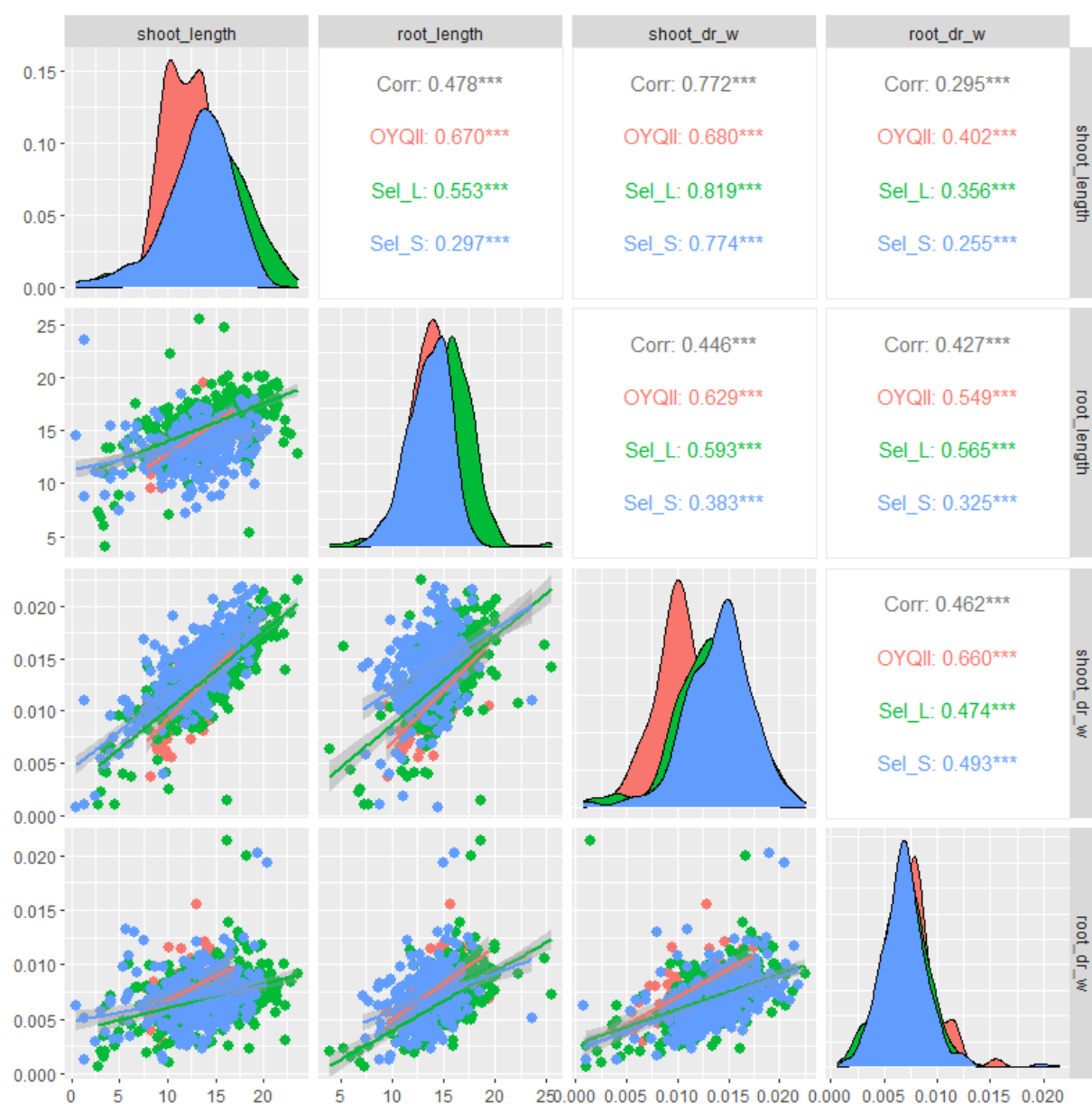


Figure S2 Spearman correlation with individual plants for shoot and root length and dry weights in the hydroponic experiment. Stars significant differences at $p < 0.0$ (*), $p < 0.01$ (**) and $p < 0.001$ (***).

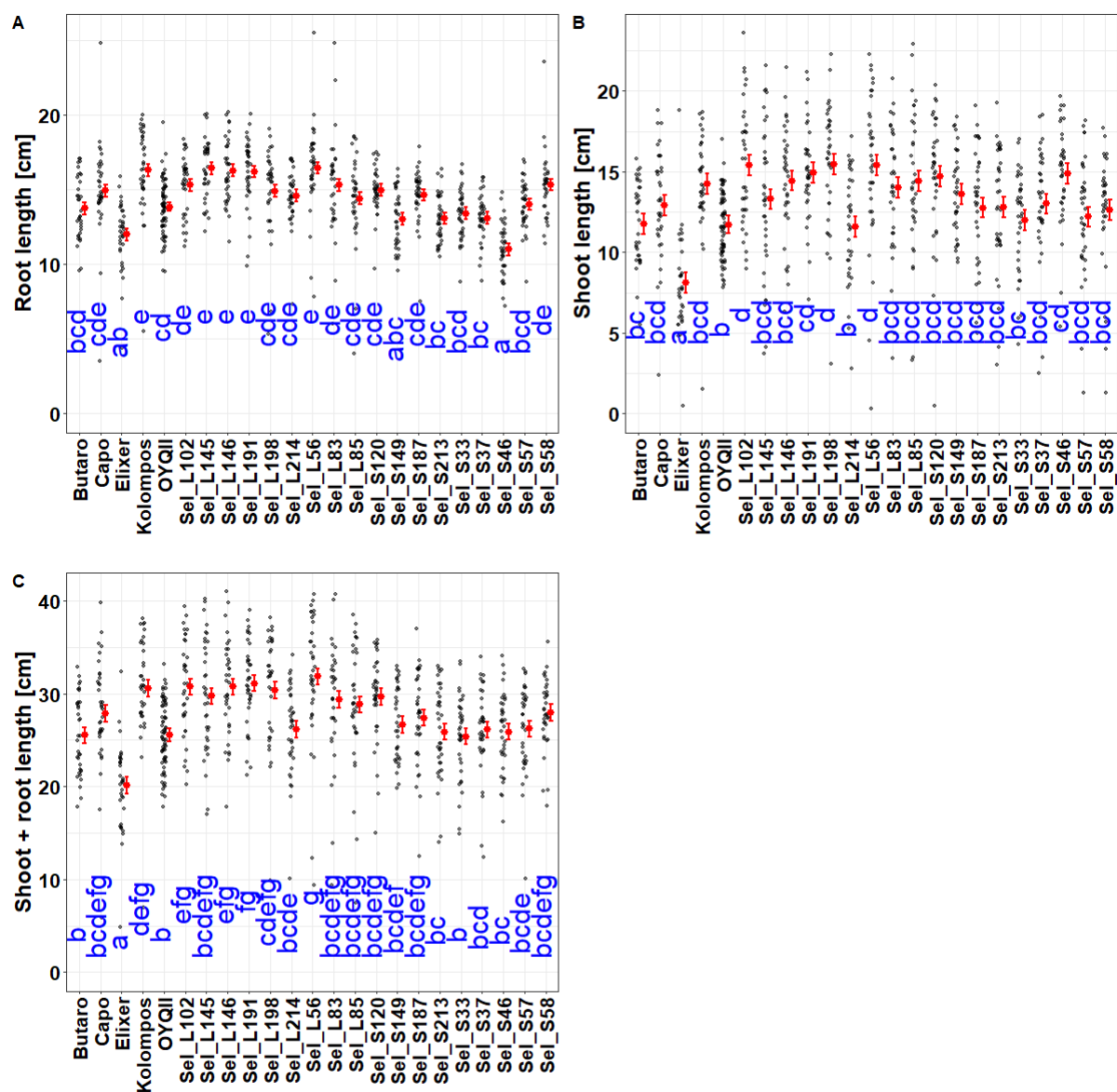


Figure S3 Root length (A), shoot length (B) and root plus shoot length (C) for individual progenies in the hydroponic experiment. Plotted are raw data for individual lines (black dots) and estimated marginal means with standard error from linear mixed effect models (lme, red). Letters indicate significant differences at $p < 0.05$ estimated from lmes with pairwise comparison and Holm correction. Sel_L includes all progenies selected for long roots and Sel_S all progenies selected for short roots.

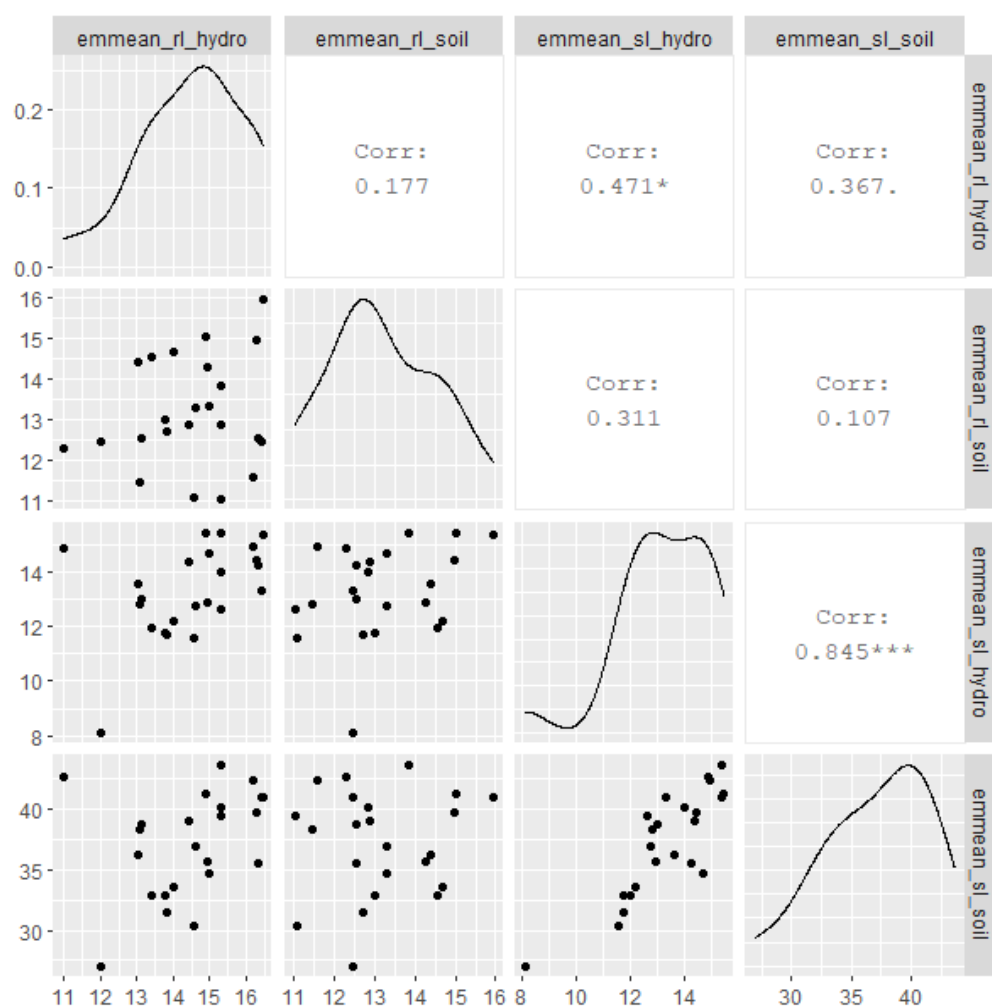


Figure S4 Spearman correlation between traits in hydroponics and soil. Stars significant differences at $p < 0.0$ (*), $p < 0.01$ (**) and $p < 0.001$ (***).

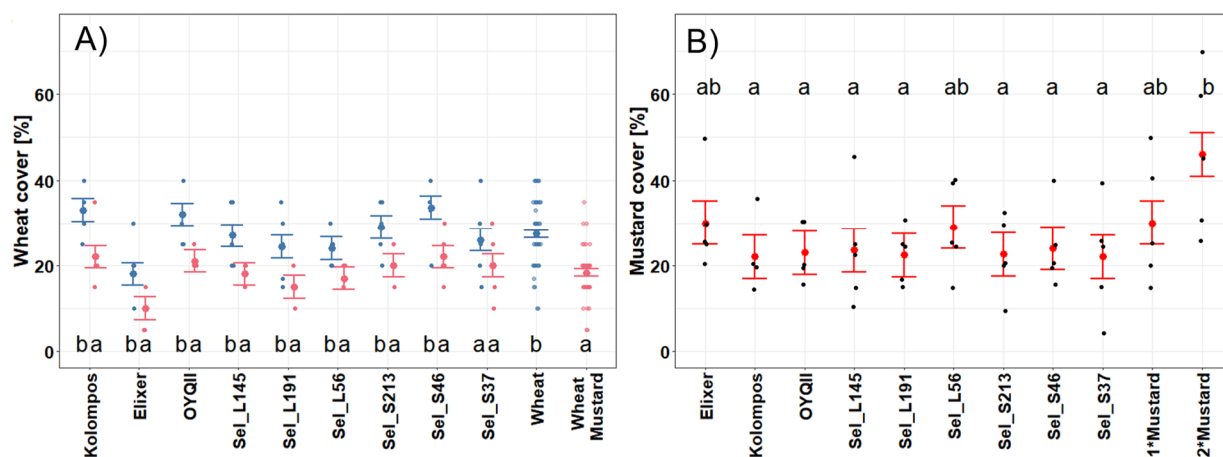


Figure S5 Soil cover for wheat (A) and Mustard (B). Plotted are raw data (dots) and estimated marginal means with standard error from linear mixed effect models. Letters indicate significant differences at $p < 0.05$ estimated from lmes with pairwise comparison and Holm correction. Sel_L includes progenies selected for long roots and Sel_S progenies selected for short roots.

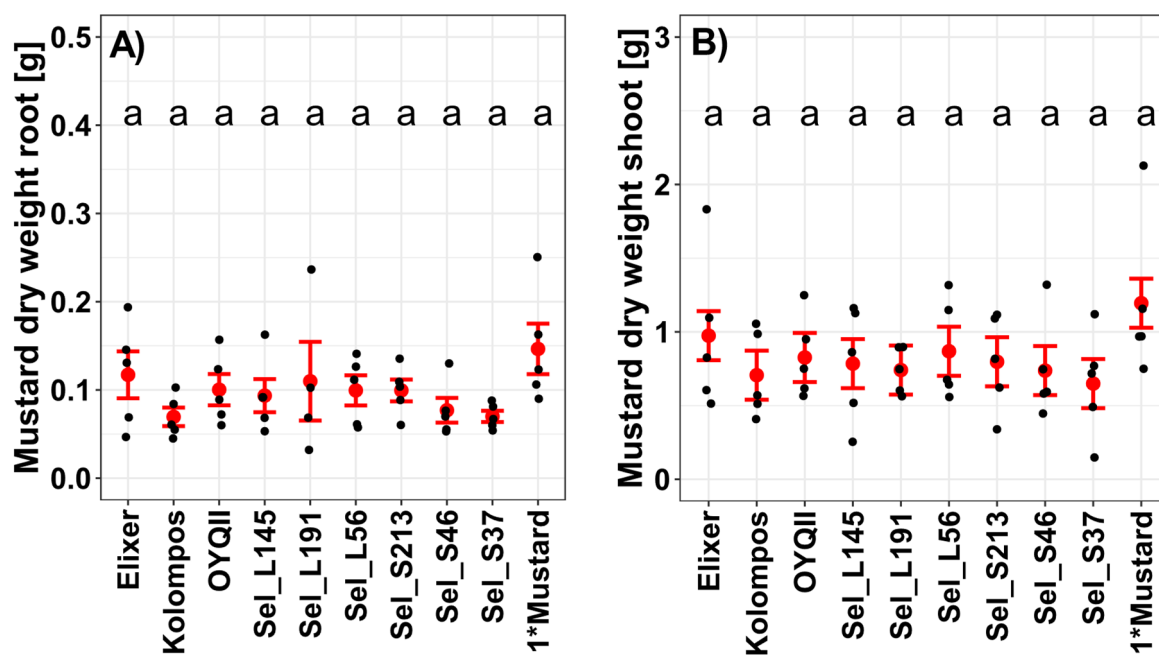


Figure S6 Mustard root and shoot dry weight. Plotted are raw data (black dots) and estimated marginal means with standard error from linear mixed effect models (lme, red). Letters indicate significant differences at $p < 0.05$ estimated from lmes with pairwise comparison and Holm correction. Sel_L includes progenies selected for long roots and Sel_S progenies selected for short roots.

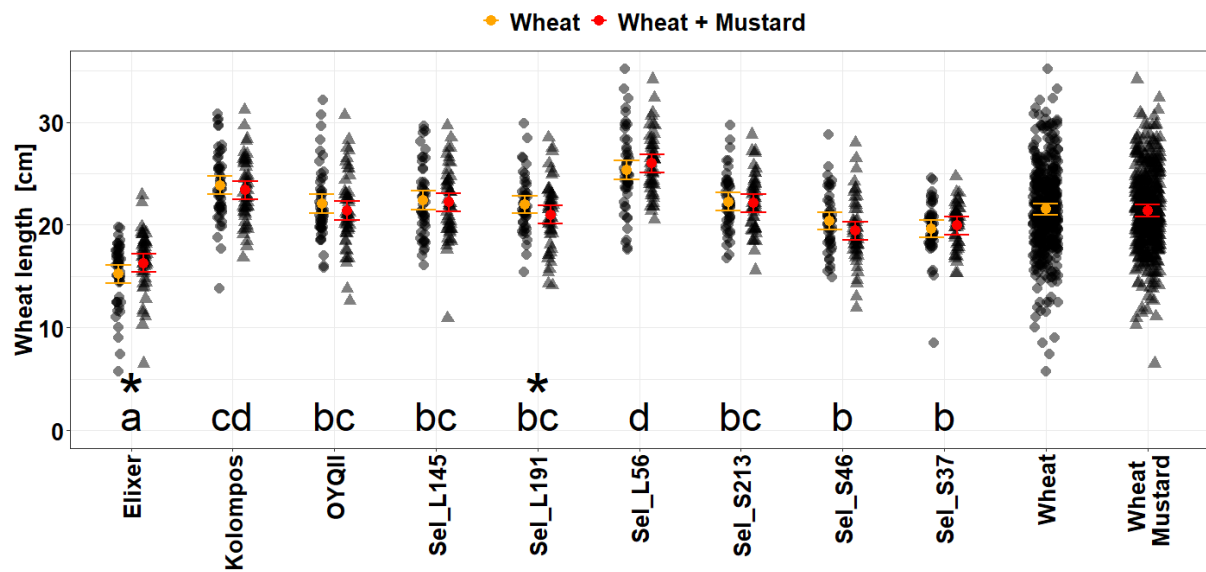
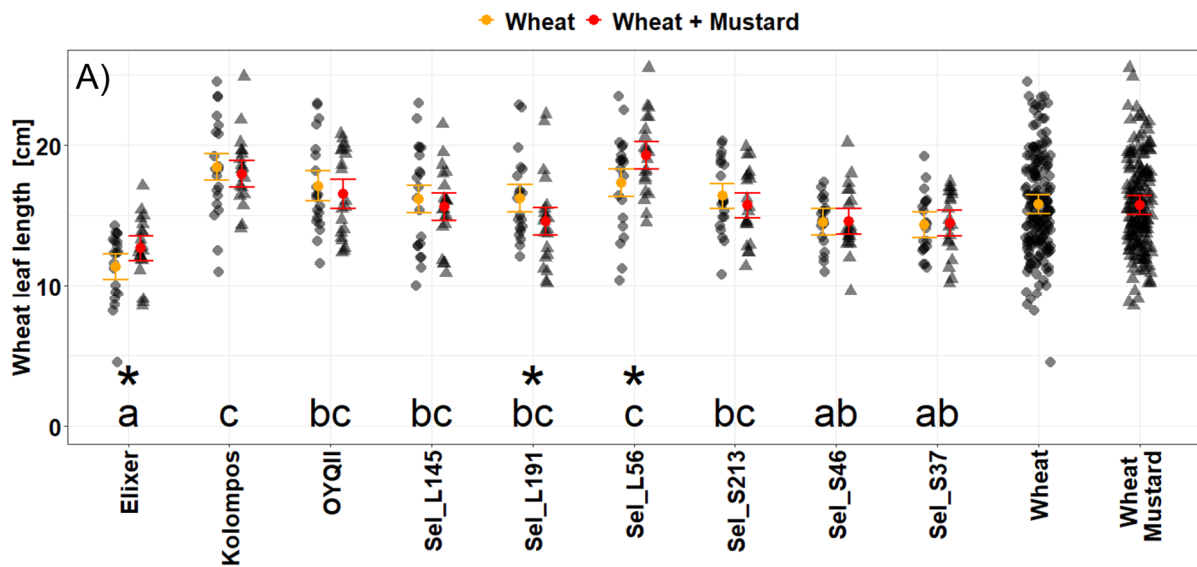


Figure S7. Length of six-week-old wheat plants grown either in pure stands or in the presence of mustard as a model weed. Raw data are plotted with dots for wheat monoculture and triangles for wheat in mixture with mustard, overlapping data points are black. Estimated marginal means with standard error from linear mixed effect models are orange for pure and red for mixed wheat. Different letters indicate significant differences among genotypes and stars between mixture and monoculture at $P < 0.05$ estimated from lmes with pairwise comparison and Holm correction. Sel_L are progenies of plants selected for long roots and Sel_S are progenies of plants selected for short roots.



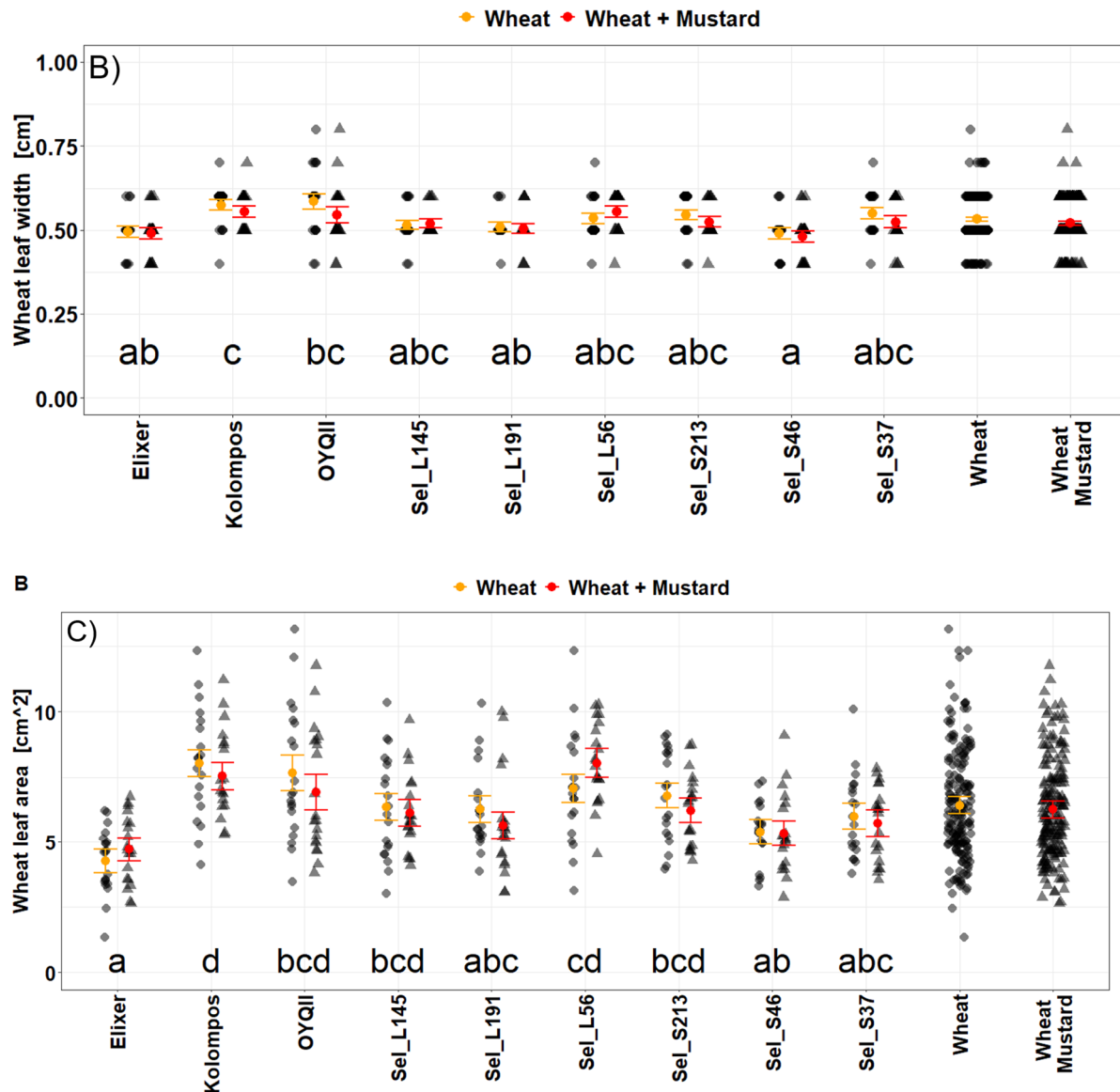


Figure S8 Leaf length (A), leaf width (B) and leaf area (C) of six weeks old wheat plants grown either in pure stands or in the presence of mustard as a model weed. Raw data are plotted with grey dots for wheat monoculture and grey triangles for wheat in mixture with mustard and black color indicates overlapping data points. Estimated marginal means with standard error from linear mixed effect models are orange for pure and red for mixed wheat. Different letters indicate significant differences between genotypes across systems and stars between mixture and monoculture at $p < 0.05$ estimated from lmes with pairwise comparison and Holm correction. Sel_L are progenies of plants selected for long roots and Sel_S are progenies of plants selected for short roots.

Table S1 List of statistical models used. Treatment refers to the two-level treatment factor (mono wheat/wheat mixed with mustard), row refers the experimental unit including multiple measured plants and rep refers to the

Experiment	Response variable	Model	Weighed variances	Used R package
Hydroponic	Wheat root length	response ~ genotype + box + (1 box:row)	no	lme4
Hydroponic	Wheat shoot length	response ~ genotype + box + (1 box:row)	no	lme4
Hydroponic	Wheat total length	response ~ genotype + box + (1 box:row)	no	lme4
Hydroponic	Wheat root length	response ~ genotype_group + box + (1 box:row)	no	lme4
Hydroponic	Wheat shoot length	response ~ genotype_group + box + (1 box:row)	no	lme4
Hydroponic	Wheat total length	response ~ genotype_group + box + (1 box:row)	no	lme4
Soil				
Experiment	Wheat RDW	response ~ entry + (1 box)	no	lme4
Soil				
Experiment	Wheat SDW	response ~ entry + (1 box)	no	lme4
Soil				
Experiment	Wheat RFW	response ~ entry + (1 box)	no	lme4
Soil				
Experiment	Wheat SFW	response ~ entry + (1 box)	no	lme4
Soil	Wheatt root length	response ~ entry + (1 box)	no	lme4
Experiment	Wheat shoot length	response ~ entry + box + (1 box:entry)	no	lme4
Competition	Wheat RDW	response ~ genotype * treat + (1 rep:pot)	no	lme4
Competition	Wheat SDW	response ~ genotype * treat + rep + (1 rep: pot)	no	lme4
Competition	Wheat SFM	response ~ genotype * treat + rep + (1 rep: pot)	no	lme4
Competition	Wheat RFM	response ~ genotype * treat + rep + (1 rep: pot)	no	lme4
Competition	Mustard RDW	response ~ genotype, random = ~1 rep	yes	nlme
Competition	Mustard SDW	response ~ genotype + (1 rep)	no	lme4
Competition	Mustard RFW	response ~ genotype, random = ~1 rep	yes	nlme
Competition	Mustard SFW	response ~ genotype + (1 rep)	no	lme4
Competition	Wheat plant length	response ~ treat*genotype, random = ~1 rep/ pot	yes	nlme
Competition	Mustard plant length	response ~ genotype + rep + (1 rep: pot)	no	lme4
Competition	Wheat leaf length	response ~ treat*genotype, random = ~1 rep/ pot	yes	nlme
Competition	Wheat leaf width	response ~ treat*genotype, random = ~1 rep/ pot	yes	nlme
Competition	Wheat leaf area	response ~ treat*genotype, random = ~1 rep/ pot	yes	nlme

experimental replicate.