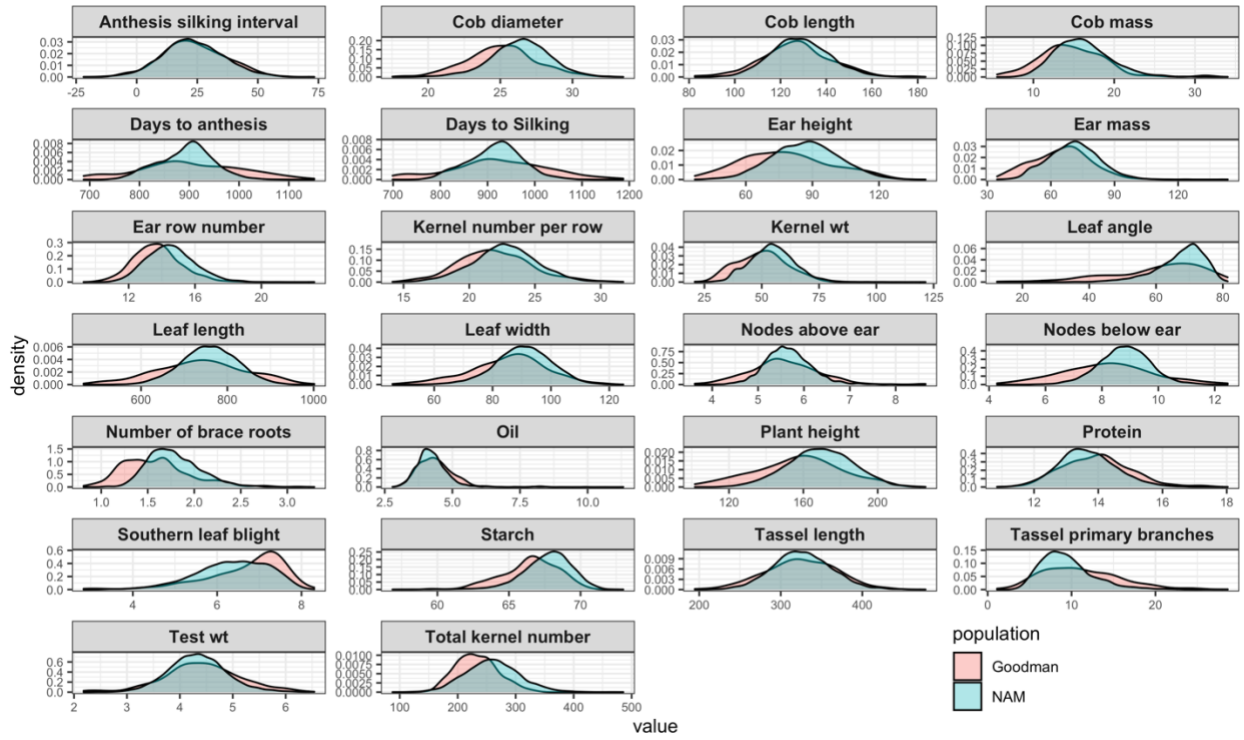
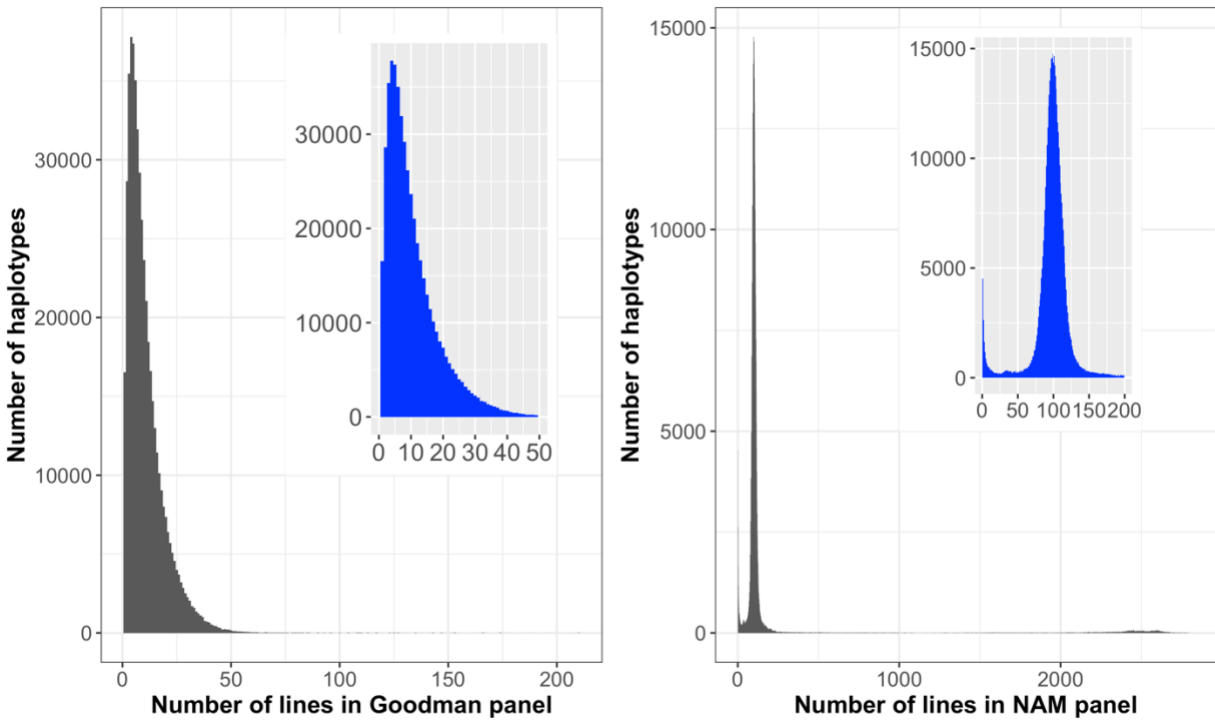


**Supporting Information:**

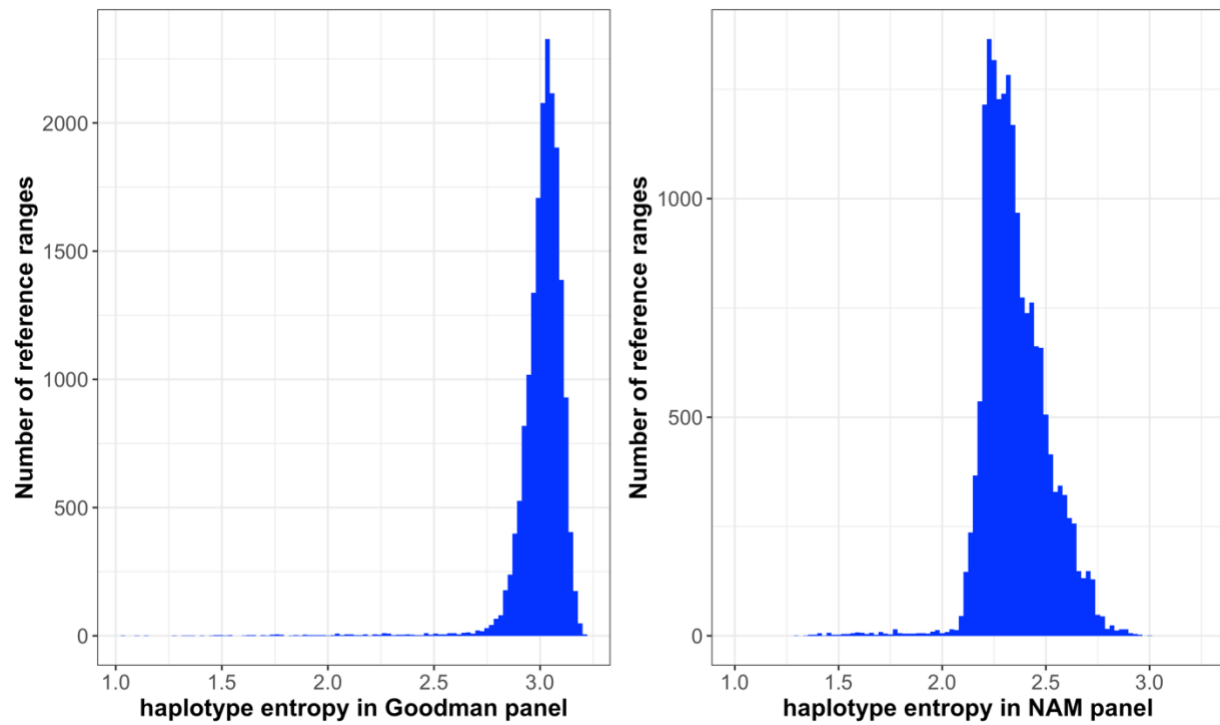


**S1 Fig. Phenotypic distribution of 26 traits in NAM and the Goodman Association panel**

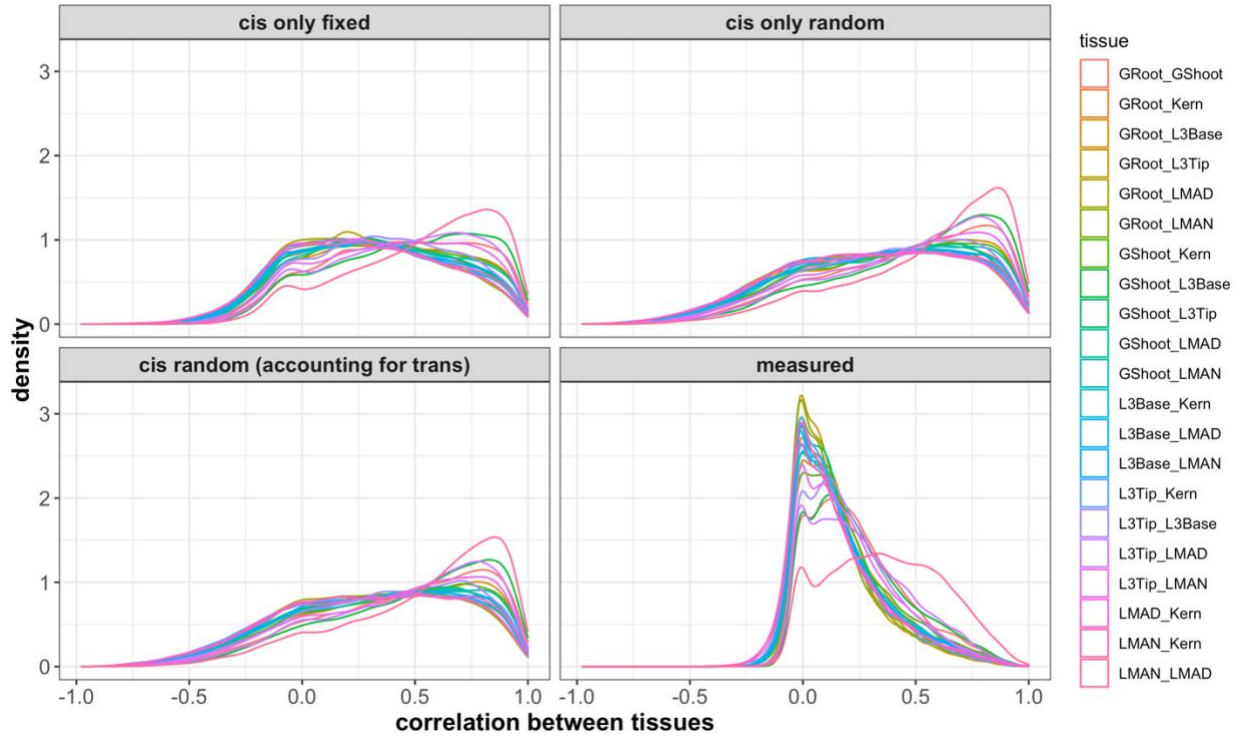
**a.**



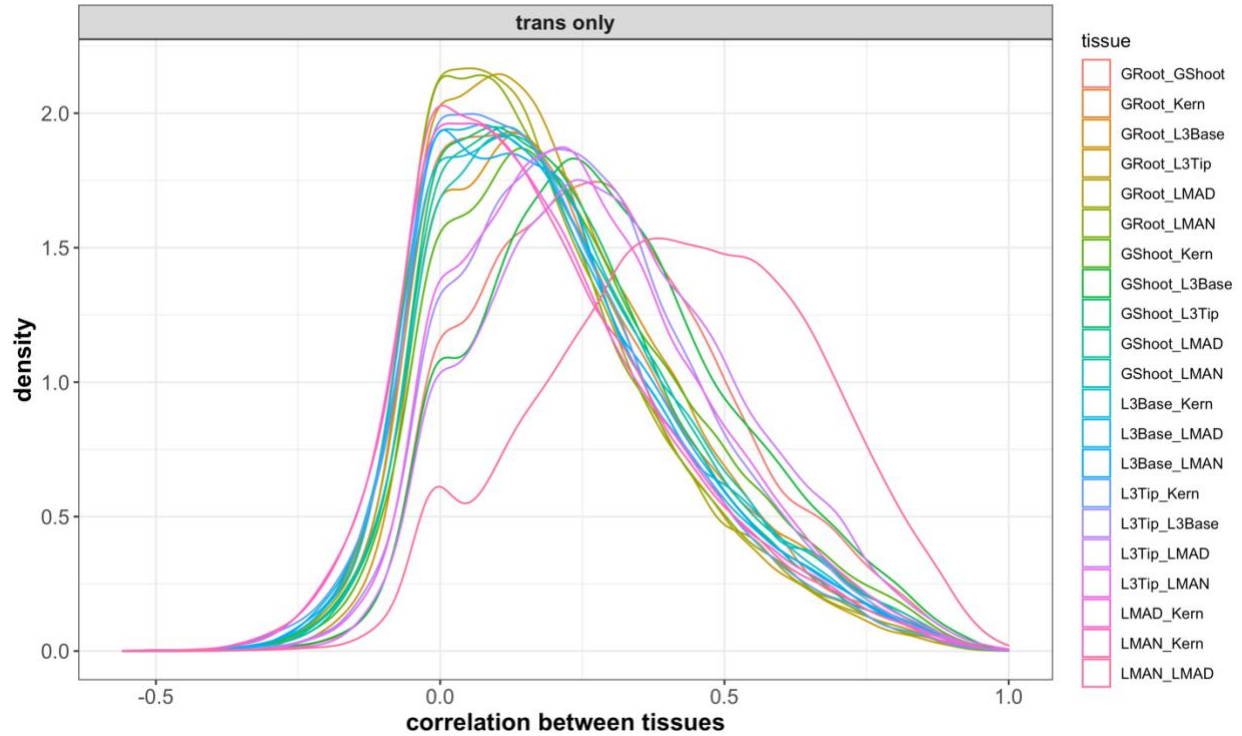
**b.**



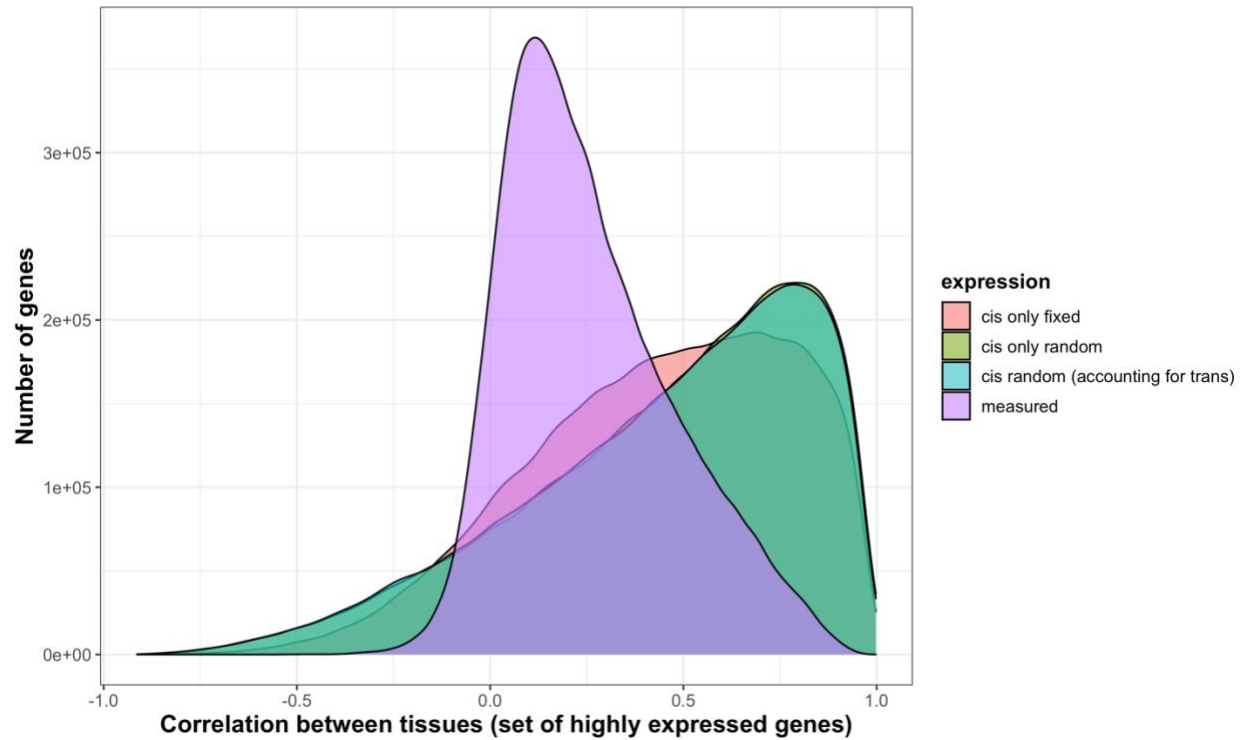
**S2 Fig. a.** Haplotype counts distribution in the Goodman association panel (left) and NAM panel (right) across all genic reference ranges. **b.** Haplotype entropy in Goodman (left) and NAM (right) panel in each reference range. Median haplotype counts were 8 and 100 in the Goodman panel and NAM, respectively, resulting in higher entropy in the Goodman panel as compared to NAM. Entropy was calculated from haplotype counts in each reference region.



**S3 Fig. Correlation distribution of expression between tissues. The four panels represent HARE estimates from models 1 (*cis* only fixed), 2 (*cis* only random), and 3 (*cis* random while accounting for *trans*), as well as measured expression. The different color lines in each panel represent 21 different combinations of the 7 different tissues as labeled on the right: germinating seedlings root (GRoot), germinating seedlings shoot (GShoot), two cm from base of leaf 3 (L3Base), two cm from tip of leaf 3 (L3Tip), mature mid-leaf tissue sampled during mid-day (LMAD), mature mid-leaf tissue sampled during mid-night (LMAN), and developing kernels harvested after 350 growing degree days after pollination (Kern). The imputed expression from models was highly correlated between tissues when compared to the measured transcript expression. In all panels, closely related tissues like matured mid-leaf tissue expression sampled during mid-day (LMAD) and matured mid-leaf tissue expression sampled during mid-night (LMAN) were highly correlated.**

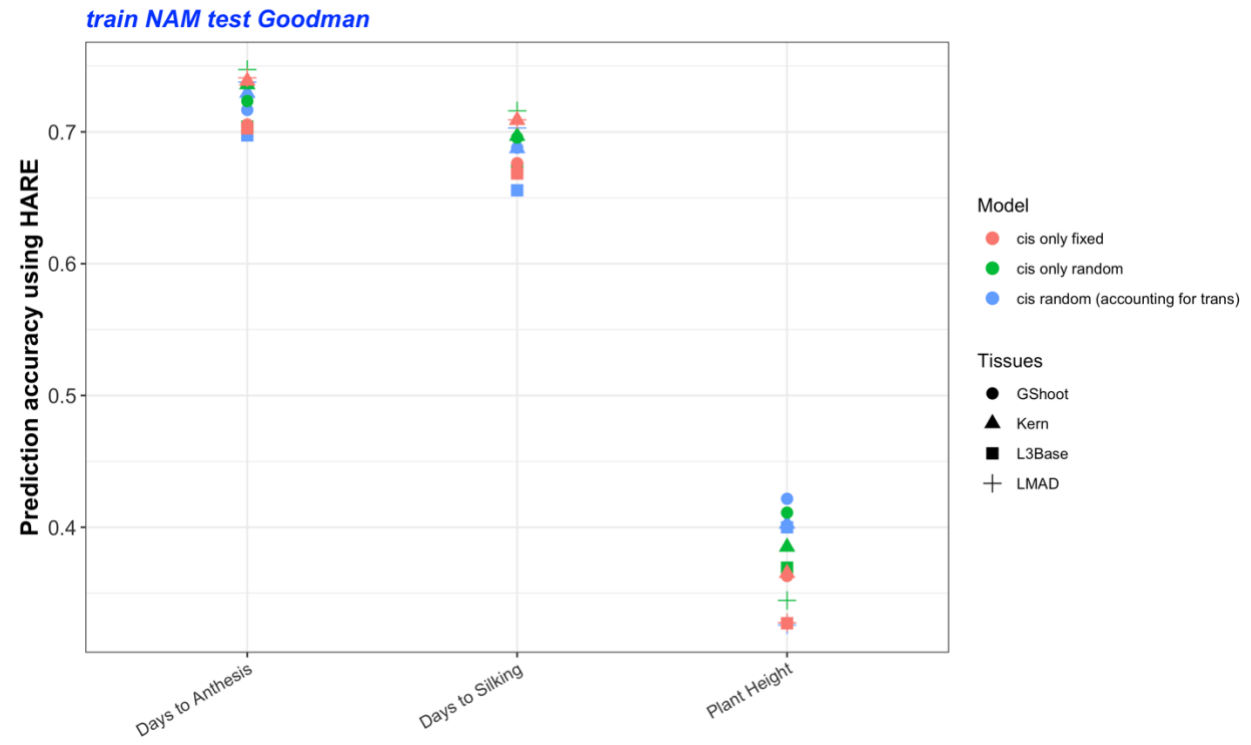


**S4 Fig.** Correlation distribution of *trans* components of expression between tissues. The different color lines in each panel represent 21 different combinations of the 7 different tissues as labeled on the right: germinating seedlings root (GRoot), germinating seedlings shoot (GShoot), two cm from base of leaf 3 (L3Base), two cm from tip of leaf 3 (L3Tip), mature mid-leaf tissue sampled during mid-day (LMAD), mature mid-leaf tissue sampled during mid-night (LMAN), and developing kernels harvested after 350 growing degree days after pollination (Kern). Similar to measured transcript expression, closely related tissues like matured leaf expression during the day (LMAD) and matured leaf expression during the night (LMAD) were highly correlated.

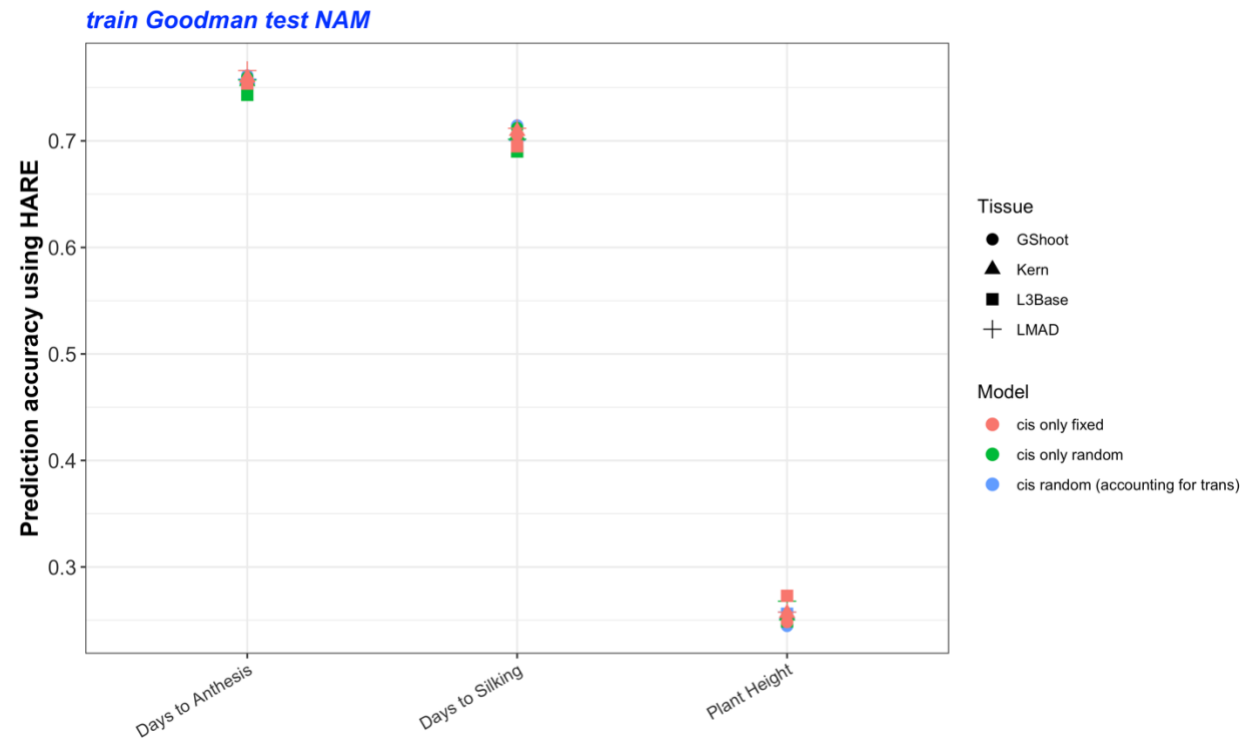


**S5 Fig. Haplotype associated RNA expression (HARE) was highly correlated across tissues as compared to measured transcript expression. Different colors represent HARE imputed from three statistical models: Model 1 (*cis* fixed effect), 2 (*cis* random effect), and 3 (*cis* + *trans* random effects), and measured transcript expression. The distribution is the pairwise correlation of ~8000 highly expressed genes across 21 different combinations from 7 different tissues.**

a.

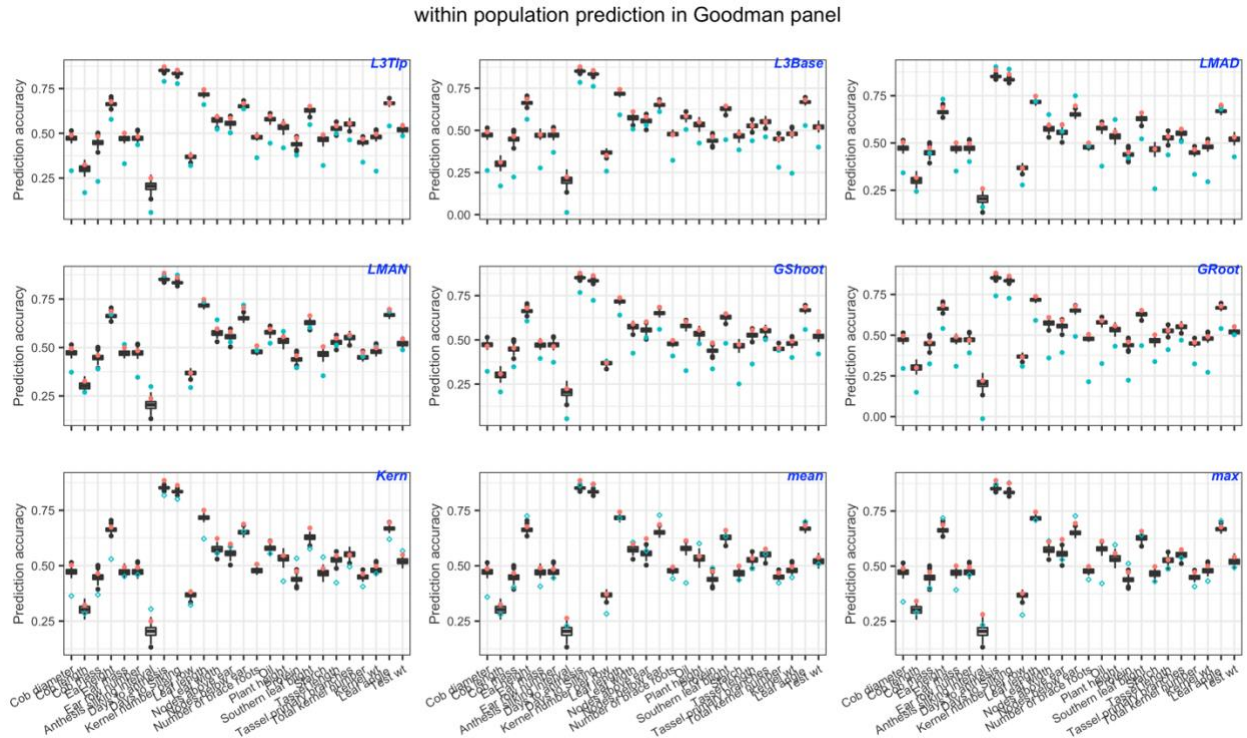


b.



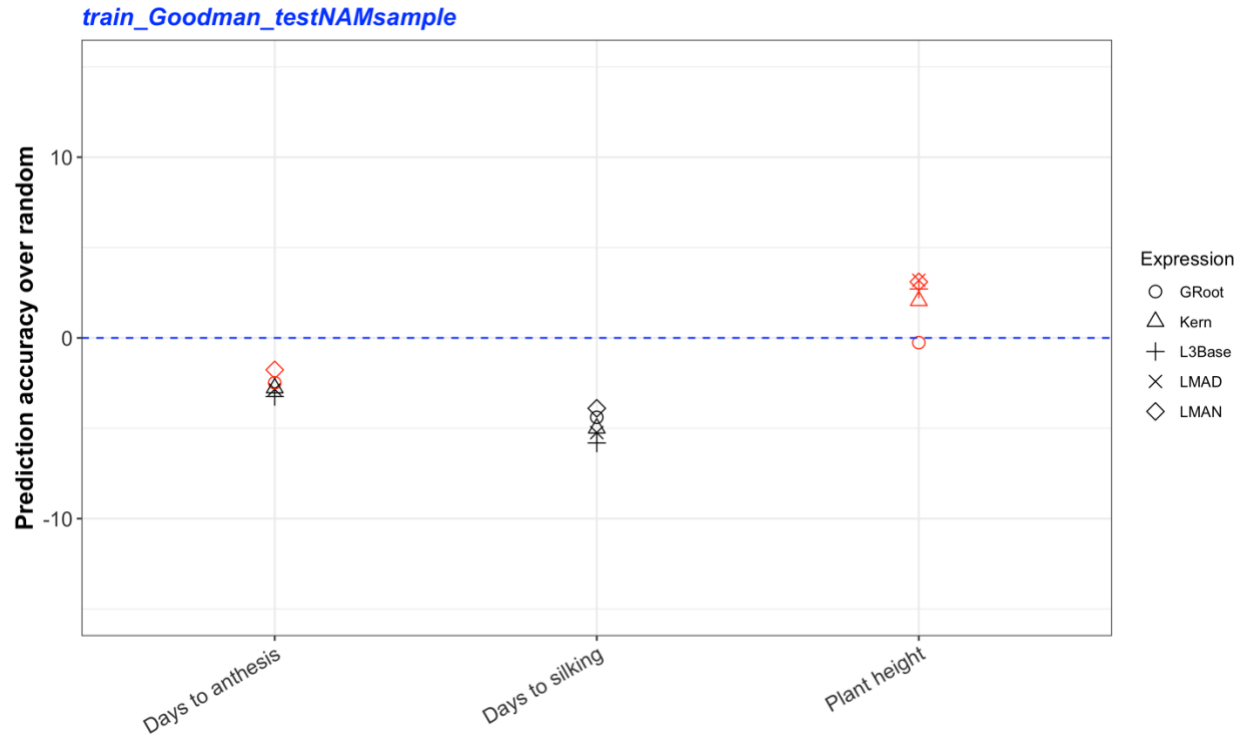
**S6 Fig. Prediction accuracy using HARE from model 1, 2, and 3 (see methods) for predicting three different traits: Days to Anthesis (DTA), Days to Silking (DTS), and Plant Height (PH) using a) model trained in NAM**

and tested in Goodman b) model trained in Goodman and tested in NAM. The different symbols represent HARE from different tissues: germinating seedlings shoot (GShoot), developing kernels harvested after 350 growing degree days after pollination (Kern), 2 cm from base of leaf 3 (L3Base), and mature mid-leaf tissue sampled during mid-day (LMAD).

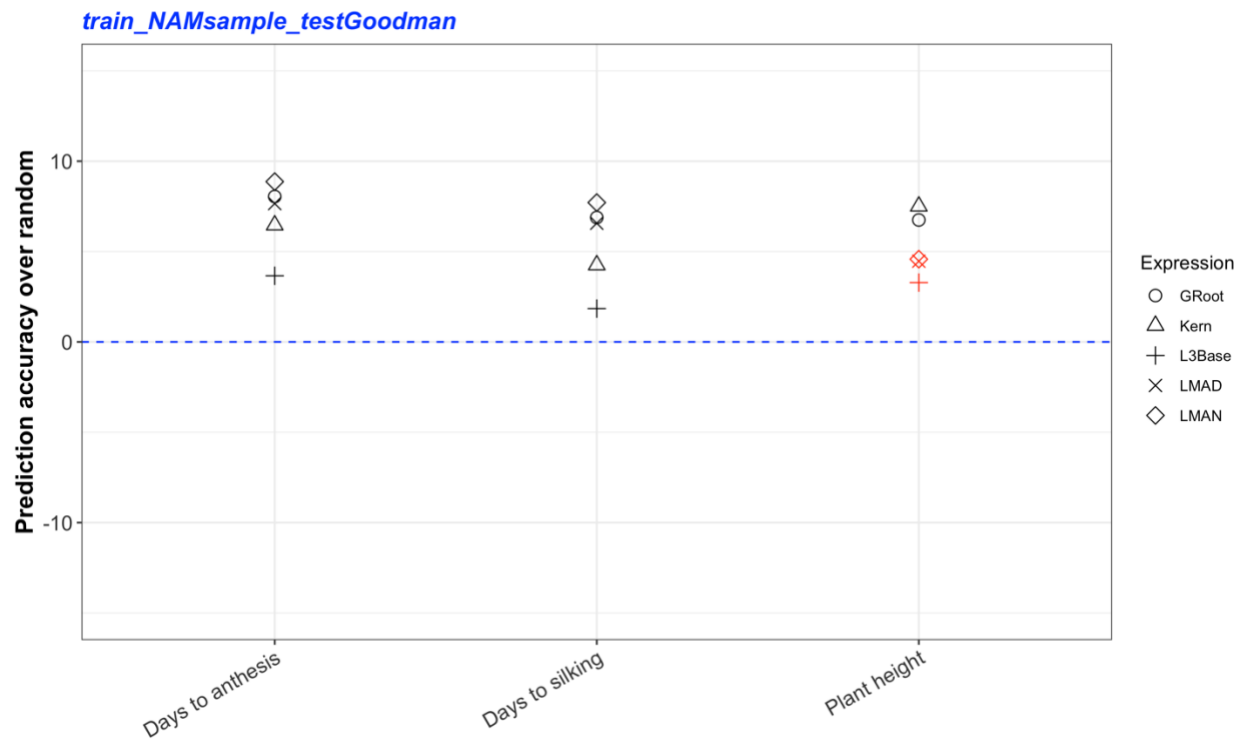


**S7 Fig.** Within-panel prediction accuracy in the Goodman panel using HARE (red dot), 100 random HARE (box plot), and measured expression (blue dot) from individual tissues or all tissues integrated as mean or maximum expression. Individual tissues included: germinating seedlings root (GRoot), germinating seedlings shoot (GShoot), two cm from base of leaf 3 (L3Base), two cm from tip of leaf 3 (L3Tip), mature mid-leaf tissue sampled during mid-day (LMAD), mature mid-leaf tissue sampled during mid-night (LMAN), and developing kernels harvested after 350 growing degree days after pollination (Kern). The model was trained in 80% of the panel and tested in the remaining 20%.

a.



b.



**S8 Fig.** Change in prediction accuracy using HARE over the mean of random expression (blue dashed line) from five different tissues: germinating seedlings root (GRoot), two cm from base of leaf 3 (L3Base), mature mid-leaf tissue sampled during mid-day (LMAD), mature mid-leaf tissue sampled during mid-night (LMAN),



and developing kernels harvested after 350 growing degree days after pollination (Kern). Genomic prediction models were (a) trained in the Goodman panel and tested in 20 subsets of NAM, (b) trained in 20 subsets of NAM and tested in the Goodman panel. The subsets of NAM were generated by randomly selecting 10 genotypes from each family resulting in a total of 250 genotypes (see methods). Accuracy was averaged over the 20 random subsets before determining significance. The black shapes represent statistically significant differences at P-values <0.05 and red shapes represent no statistical significance. P-values were calculated using a Monte Carlo procedure.

Trait	Accuracy using HARE	Mean accuracy using random HARE	P value (high)	P value (low)	Accuracy of HARE over random HARE	Tissues
Cob diameter	0.411	0.348	0.010	1.000	6.243	L3Tip
Cob length	0.146	0.157	0.673	0.337	-1.081	L3Tip
Cob mass	0.302	0.266	0.129	0.881	3.657	L3Tip
Ear height	0.559	0.473	0.010	1.000	8.620	L3Tip
Ear mass	0.387	0.365	0.099	0.911	2.242	L3Tip
Ear row number	0.387	0.381	0.426	0.584	0.668	L3Tip
Anthesis silking interval	0.001	0.059	0.901	0.109	-5.816	L3Tip
Days to anthesis	0.729	0.675	0.010	1.000	5.466	L3Tip
Days to Silking	0.693	0.642	0.010	1.000	5.057	L3Tip
Kernel number per row	0.194	0.195	0.574	0.436	-0.084	L3Tip
Leaf length	0.535	0.454	0.020	0.990	8.062	L3Tip
Leaf width	0.365	0.378	0.693	0.317	-1.314	L3Tip
Nodes above ear	0.296	0.318	0.762	0.248	-2.223	L3Tip
Nodes below ear	0.608	0.572	0.050	0.960	3.617	L3Tip
Number of brace roots	0.400	0.399	0.446	0.564	0.133	L3Tip
Oil	0.340	0.323	0.287	0.723	1.716	L3Tip
Plant height	0.341	0.264	0.030	0.980	7.644	L3Tip
Protein	0.237	0.192	0.218	0.792	4.440	L3Tip
Southern leaf blight	0.402	0.369	0.129	0.881	3.292	L3Tip
Starch	0.357	0.310	0.089	0.921	4.626	L3Tip

<b>Tassel length</b>	0.233	0.199	0.238	0.772	3.460	L3Tip
<b>Tassel primary branches</b>	0.348	0.377	0.802	0.208	-2.880	L3Tip
<b>Total kernel number</b>	0.215	0.234	0.822	0.188	-1.955	L3Tip
<b>Kernel wt</b>	0.353	0.347	0.337	0.673	0.642	L3Tip
<b>Leaf angle</b>	0.291	0.287	0.465	0.545	0.396	L3Tip
<b>Test wt</b>	0.377	0.357	0.218	0.792	1.964	L3Tip
<b>Cob diameter</b>	0.413	0.353	0.010	1.000	5.999	L3Base
<b>Cob length</b>	0.136	0.155	0.752	0.257	-1.901	L3Base
<b>Cob mass</b>	0.289	0.274	0.317	0.693	1.536	L3Base
<b>Ear height</b>	0.546	0.473	0.030	0.980	7.303	L3Base
<b>Ear mass</b>	0.394	0.370	0.109	0.901	2.407	L3Base
<b>Ear row number</b>	0.399	0.385	0.277	0.733	1.398	L3Base
<b>Anthesis silking interval</b>	0.010	0.053	0.851	0.158	-4.321	L3Base
<b>Days to anthesis</b>	0.697	0.677	0.059	0.950	2.039	L3Base
<b>Days to Silking</b>	0.656	0.644	0.218	0.792	1.185	L3Base
<b>Kernel number per row</b>	0.190	0.195	0.574	0.436	-0.500	L3Base
<b>Leaf length</b>	0.568	0.458	0.010	1.000	11.026	L3Base
<b>Leaf width</b>	0.430	0.380	0.069	0.941	4.986	L3Base
<b>Nodes above ear</b>	0.328	0.317	0.416	0.594	1.084	L3Base
<b>Nodes below ear</b>	0.599	0.576	0.119	0.891	2.361	L3Base
<b>Number of brace roots</b>	0.420	0.406	0.277	0.733	1.376	L3Base
<b>Oil</b>	0.310	0.316	0.545	0.465	-0.629	L3Base
<b>Plant height</b>	0.403	0.263	0.010	1.000	14.083	L3Base
<b>Protein</b>	0.223	0.188	0.188	0.822	3.536	L3Base
<b>Southern leaf blight</b>	0.405	0.369	0.089	0.921	3.590	L3Base
<b>Starch</b>	0.321	0.307	0.356	0.653	1.413	L3Base

<b>Tassel length</b>	0.307	0.206	0.030	0.980	10.156	L3Base
<b>Tassel primary branches</b>	0.377	0.380	0.535	0.475	-0.356	L3Base
<b>Total kernel number</b>	0.254	0.240	0.277	0.733	1.441	L3Base
<b>Kernel wt</b>	0.372	0.350	0.069	0.941	2.238	L3Base
<b>Leaf angle</b>	0.314	0.289	0.238	0.772	2.549	L3Base
<b>Test wt</b>	0.368	0.364	0.475	0.535	0.423	L3Base
<b>Cob diameter</b>	0.422	0.349	0.010	1.000	7.243	LMAD
<b>Cob length</b>	0.111	0.163	0.950	0.059	-5.248	LMAD
<b>Cob mass</b>	0.310	0.270	0.168	0.842	4.004	LMAD
<b>Ear height</b>	0.554	0.480	0.020	0.990	7.419	LMAD
<b>Ear mass</b>	0.387	0.367	0.139	0.871	1.991	LMAD
<b>Ear row number</b>	0.423	0.378	0.069	0.941	4.564	LMAD
<b>Anthesis silking interval</b>	0.015	0.061	0.782	0.228	-4.594	LMAD
<b>Days to anthesis</b>	0.737	0.677	0.010	1.000	6.014	LMAD
<b>Days to Silking</b>	0.703	0.646	0.010	1.000	5.695	LMAD
<b>Kernel number per row</b>	0.167	0.196	0.812	0.198	-2.887	LMAD
<b>Leaf length</b>	0.534	0.453	0.010	1.000	8.148	LMAD
<b>Leaf width</b>	0.420	0.383	0.119	0.891	3.713	LMAD
<b>Nodes above ear</b>	0.360	0.311	0.050	0.960	4.885	LMAD
<b>Nodes below ear</b>	0.620	0.574	0.020	0.990	4.545	LMAD
<b>Number of brace roots</b>	0.435	0.405	0.158	0.851	2.975	LMAD
<b>Oil</b>	0.263	0.318	0.970	0.040	-5.445	LMAD
<b>Plant height</b>	0.329	0.277	0.089	0.921	5.263	LMAD
<b>Protein</b>	0.131	0.197	0.921	0.089	-6.605	LMAD
<b>Southern leaf blight</b>	0.388	0.369	0.248	0.762	1.954	LMAD
<b>Starch</b>	0.262	0.310	0.950	0.059	-4.841	LMAD

<b>Tassel length</b>	0.291	0.205	0.050	0.960	8.622	LMAD
<b>Tassel primary branches</b>	0.353	0.383	0.772	0.238	-3.000	LMAD
<b>Total kernel number</b>	0.210	0.238	0.792	0.218	-2.857	LMAD
<b>Kernel wt</b>	0.361	0.349	0.257	0.752	1.240	LMAD
<b>Leaf angle</b>	0.334	0.286	0.040	0.970	4.785	LMAD
<b>Test wt</b>	0.354	0.358	0.574	0.436	-0.428	LMAD
<b>Cob diameter</b>	0.357	0.355	0.475	0.535	0.181	LMAN
<b>Cob length</b>	0.133	0.167	0.832	0.178	-3.362	LMAN
<b>Cob mass</b>	0.180	0.276	1.000	0.010	-9.632	LMAN
<b>Ear height</b>	0.569	0.476	0.020	0.990	9.353	LMAN
<b>Ear mass</b>	0.338	0.370	0.901	0.109	-3.245	LMAN
<b>Ear row number</b>	0.355	0.379	0.782	0.228	-2.383	LMAN
<b>Anthesis silking interval</b>	0.075	0.051	0.327	0.683	2.412	LMAN
<b>Days to anthesis</b>	0.759	0.678	0.010	1.000	8.061	LMAN
<b>Days to Silking</b>	0.720	0.647	0.010	1.000	7.319	LMAN
<b>Kernel number per row</b>	0.180	0.197	0.663	0.347	-1.660	LMAN
<b>Leaf length</b>	0.552	0.454	0.010	1.000	9.792	LMAN
<b>Leaf width</b>	0.397	0.385	0.366	0.644	1.180	LMAN
<b>Nodes above ear</b>	0.377	0.315	0.020	0.990	6.207	LMAN
<b>Nodes below ear</b>	0.632	0.571	0.010	1.000	6.081	LMAN
<b>Number of brace roots</b>	0.445	0.397	0.030	0.980	4.878	LMAN
<b>Oil</b>	0.291	0.319	0.832	0.178	-2.815	LMAN
<b>Plant height</b>	0.335	0.273	0.129	0.881	6.236	LMAN
<b>Protein</b>	0.125	0.194	0.901	0.109	-6.847	LMAN
<b>Southern leaf blight</b>	0.411	0.360	0.040	0.970	5.046	LMAN
<b>Starch</b>	0.314	0.311	0.485	0.525	0.315	LMAN

<b>Tassel length</b>	0.162	0.209	0.881	0.129	-4.722	LMAN
<b>Tassel primary branches</b>	0.379	0.378	0.505	0.505	0.094	LMAN
<b>Total kernel number</b>	0.214	0.241	0.782	0.228	-2.710	LMAN
<b>Kernel wt</b>	0.330	0.351	0.851	0.158	-2.135	LMAN
<b>Leaf angle</b>	0.353	0.284	0.020	0.990	6.901	LMAN
<b>Test wt</b>	0.326	0.364	0.911	0.099	-3.792	LMAN
<b>Cob diameter</b>	0.359	0.349	0.356	0.653	0.985	GShoot
<b>Cob length</b>	0.160	0.168	0.614	0.396	-0.764	GShoot
<b>Cob mass</b>	0.249	0.277	0.822	0.188	-2.848	GShoot
<b>Ear height</b>	0.566	0.476	0.020	0.990	8.937	GShoot
<b>Ear mass</b>	0.401	0.367	0.040	0.970	3.387	GShoot
<b>Ear row number</b>	0.402	0.381	0.257	0.752	2.161	GShoot
<b>Anthesis silking interval</b>	0.050	0.058	0.614	0.396	-0.829	GShoot
<b>Days to anthesis</b>	0.716	0.679	0.010	1.000	3.695	GShoot
<b>Days to Silking</b>	0.687	0.648	0.010	1.000	3.942	GShoot
<b>Kernel number per row</b>	0.244	0.197	0.089	0.921	4.729	GShoot
<b>Leaf length</b>	0.568	0.458	0.010	1.000	10.995	GShoot
<b>Leaf width</b>	0.399	0.386	0.416	0.594	1.254	GShoot
<b>Nodes above ear</b>	0.355	0.311	0.089	0.921	4.334	GShoot
<b>Nodes below ear</b>	0.623	0.573	0.010	1.000	5.033	GShoot
<b>Number of brace roots</b>	0.448	0.403	0.069	0.941	4.432	GShoot
<b>Oil</b>	0.360	0.310	0.059	0.950	4.961	GShoot
<b>Plant height</b>	0.426	0.272	0.020	0.990	15.383	GShoot
<b>Protein</b>	0.305	0.186	0.010	1.000	11.957	GShoot
<b>Southern leaf blight</b>	0.407	0.371	0.059	0.950	3.643	GShoot
<b>Starch</b>	0.339	0.309	0.168	0.842	3.024	GShoot

<b>Tassel length</b>	0.308	0.207	0.020	0.990	10.084	GShoot
<b>Tassel primary branches</b>	0.383	0.381	0.545	0.465	0.184	GShoot
<b>Total kernel number</b>	0.303	0.236	0.020	0.990	6.687	GShoot
<b>Kernel wt</b>	0.385	0.347	0.030	0.980	3.716	GShoot
<b>Leaf angle</b>	0.343	0.291	0.069	0.941	5.138	GShoot
<b>Test wt</b>	0.369	0.364	0.406	0.604	0.520	GShoot
<b>Cob diameter</b>	0.386	0.350	0.069	0.941	3.641	GRoot
<b>Cob length</b>	0.078	0.159	0.990	0.020	-8.109	GRoot
<b>Cob mass</b>	0.266	0.276	0.673	0.337	-1.000	GRoot
<b>Ear height</b>	0.604	0.474	0.010	1.000	12.951	GRoot
<b>Ear mass</b>	0.365	0.369	0.634	0.376	-0.369	GRoot
<b>Ear row number</b>	0.335	0.379	0.941	0.069	-4.348	GRoot
<b>Anthesis silking interval</b>	0.038	0.051	0.614	0.396	-1.347	GRoot
<b>Days to anthesis</b>	0.752	0.675	0.010	1.000	7.670	GRoot
<b>Days to Silking</b>	0.719	0.644	0.010	1.000	7.591	GRoot
<b>Kernel number per row</b>	0.174	0.197	0.792	0.218	-2.318	GRoot
<b>Leaf length</b>	0.565	0.453	0.010	1.000	11.190	GRoot
<b>Leaf width</b>	0.390	0.378	0.455	0.554	1.235	GRoot
<b>Nodes above ear</b>	0.356	0.313	0.089	0.921	4.331	GRoot
<b>Nodes below ear</b>	0.640	0.571	0.010	1.000	6.968	GRoot
<b>Number of brace roots</b>	0.428	0.400	0.178	0.832	2.714	GRoot
<b>Oil</b>	0.343	0.317	0.218	0.792	2.557	GRoot
<b>Plant height</b>	0.380	0.268	0.020	0.990	11.174	GRoot
<b>Protein</b>	0.267	0.181	0.040	0.970	8.611	GRoot
<b>Southern leaf blight</b>	0.412	0.363	0.030	0.980	4.904	GRoot
<b>Starch</b>	0.314	0.304	0.455	0.554	1.025	GRoot

<b>Tassel length</b>	0.277	0.202	0.079	0.931	7.556	GRoot
<b>Tassel primary branches</b>	0.371	0.378	0.545	0.465	-0.739	GRoot
<b>Total kernel number</b>	0.239	0.242	0.515	0.495	-0.282	GRoot
<b>Kernel wt</b>	0.339	0.349	0.693	0.317	-1.071	GRoot
<b>Leaf angle</b>	0.273	0.279	0.574	0.436	-0.570	GRoot
<b>Test wt</b>	0.387	0.360	0.257	0.752	2.640	GRoot
<b>Cob diameter</b>	0.379	0.353	0.178	0.832	2.590	Kern
<b>Cob length</b>	0.248	0.160	0.020	0.990	8.727	Kern
<b>Cob mass</b>	0.276	0.268	0.416	0.594	0.770	Kern
<b>Ear height</b>	0.565	0.475	0.010	1.000	9.019	Kern
<b>Ear mass</b>	0.403	0.369	0.040	0.970	3.396	Kern
<b>Ear row number</b>	0.404	0.383	0.228	0.782	2.168	Kern
<b>Anthesis silking interval</b>	0.046	0.049	0.525	0.485	-0.284	Kern
<b>Days to anthesis</b>	0.728	0.677	0.010	1.000	5.176	Kern
<b>Days to Silking</b>	0.687	0.645	0.020	0.990	4.200	Kern
<b>Kernel number per row</b>	0.245	0.197	0.079	0.931	4.849	Kern
<b>Leaf length</b>	0.549	0.458	0.010	1.000	9.084	Kern
<b>Leaf width</b>	0.420	0.381	0.119	0.891	3.909	Kern
<b>Nodes above ear</b>	0.365	0.311	0.079	0.931	5.469	Kern
<b>Nodes below ear</b>	0.627	0.579	0.010	1.000	4.877	Kern
<b>Number of brace roots</b>	0.442	0.402	0.040	0.970	3.968	Kern
<b>Oil</b>	0.352	0.316	0.119	0.891	3.553	Kern
<b>Plant height</b>	0.407	0.263	0.010	1.000	14.360	Kern
<b>Protein</b>	0.166	0.177	0.604	0.406	-1.064	Kern
<b>Southern leaf blight</b>	0.423	0.364	0.020	0.990	5.951	Kern
<b>Starch</b>	0.299	0.304	0.545	0.465	-0.519	Kern

<b>Tassel length</b>	0.278	0.204	0.030	0.980	7.417	Kern
<b>Tassel primary branches</b>	0.372	0.379	0.564	0.446	-0.644	Kern
<b>Total kernel number</b>	0.283	0.242	0.089	0.921	4.137	Kern
<b>Kernel wt</b>	0.384	0.350	0.050	0.960	3.344	Kern
<b>Leaf angle</b>	0.312	0.287	0.238	0.772	2.467	Kern
<b>Test wt</b>	0.405	0.365	0.099	0.911	3.985	Kern
<b>Cob diameter</b>	0.405	0.353	0.010	1.000	5.243	mean
<b>Cob length</b>	0.141	0.161	0.733	0.277	-2.018	mean
<b>Cob mass</b>	0.291	0.274	0.297	0.713	1.692	mean
<b>Ear height</b>	0.563	0.481	0.010	1.000	8.230	mean
<b>Ear mass</b>	0.362	0.370	0.663	0.347	-0.812	mean
<b>Ear row number</b>	0.354	0.384	0.871	0.139	-3.053	mean
<b>Anthesis silking interval</b>	0.039	0.056	0.653	0.356	-1.653	mean
<b>Days to anthesis</b>	0.748	0.679	0.010	1.000	6.858	mean
<b>Days to Silking</b>	0.716	0.648	0.010	1.000	6.797	mean
<b>Kernel number per row</b>	0.164	0.200	0.901	0.109	-3.517	mean
<b>Leaf length</b>	0.606	0.462	0.010	1.000	14.452	mean
<b>Leaf width</b>	0.412	0.388	0.287	0.723	2.321	mean
<b>Nodes above ear</b>	0.369	0.315	0.040	0.970	5.409	mean
<b>Nodes below ear</b>	0.633	0.576	0.010	1.000	5.638	mean
<b>Number of brace roots</b>	0.423	0.400	0.198	0.812	2.275	mean
<b>Oil</b>	0.349	0.320	0.188	0.822	2.942	mean
<b>Plant height</b>	0.391	0.274	0.020	0.990	11.682	mean
<b>Protein</b>	0.271	0.195	0.040	0.970	7.610	mean
<b>Southern leaf blight</b>	0.432	0.369	0.020	0.990	6.276	mean
<b>Starch</b>	0.293	0.309	0.703	0.307	-1.600	mean



<b>Tassel length</b>	0.283	0.206	0.050	0.960	7.720	mean
<b>Tassel primary branches</b>	0.394	0.380	0.356	0.653	1.407	mean
<b>Total kernel number</b>	0.201	0.243	0.960	0.050	-4.126	mean
<b>Kernel wt</b>	0.326	0.352	0.921	0.089	-2.579	mean
<b>Leaf angle</b>	0.324	0.292	0.129	0.881	3.274	mean
<b>Test wt</b>	0.378	0.362	0.337	0.673	1.536	mean
<b>Cob diameter</b>	0.406	0.351	0.030	0.980	5.506	max
<b>Cob length</b>	0.136	0.161	0.772	0.238	-2.519	max
<b>Cob mass</b>	0.306	0.276	0.218	0.792	3.065	max
<b>Ear height</b>	0.590	0.481	0.010	1.000	10.980	max
<b>Ear mass</b>	0.377	0.371	0.376	0.634	0.606	max
<b>Ear row number</b>	0.377	0.386	0.693	0.317	-0.937	max
<b>Anthesis silking interval</b>	0.090	0.053	0.188	0.822	3.738	max
<b>Days to anthesis</b>	0.755	0.679	0.010	1.000	7.588	max
<b>Days to Silking</b>	0.729	0.648	0.010	1.000	8.123	max
<b>Kernel number per row</b>	0.180	0.201	0.782	0.228	-2.056	max
<b>Leaf length</b>	0.614	0.463	0.010	1.000	15.098	max
<b>Leaf width</b>	0.402	0.386	0.297	0.713	1.518	max
<b>Nodes above ear</b>	0.392	0.312	0.010	1.000	7.931	max
<b>Nodes below ear</b>	0.634	0.576	0.010	1.000	5.759	max
<b>Number of brace roots</b>	0.393	0.403	0.683	0.327	-0.998	max
<b>Oil</b>	0.335	0.322	0.366	0.644	1.326	max
<b>Plant height</b>	0.442	0.273	0.010	1.000	16.985	max
<b>Protein</b>	0.246	0.186	0.069	0.941	5.930	max
<b>Southern leaf blight</b>	0.407	0.369	0.040	0.970	3.750	max
<b>Starch</b>	0.319	0.305	0.317	0.693	1.385	max

<b>Tassel length</b>	0.266	0.210	0.149	0.861	5.685	max
<b>Tassel primary branches</b>	0.393	0.378	0.327	0.683	1.494	max
<b>Total kernel number</b>	0.219	0.244	0.842	0.168	-2.455	max
<b>Kernel wt</b>	0.347	0.352	0.624	0.386	-0.518	max
<b>Leaf angle</b>	0.313	0.289	0.218	0.792	2.329	max
<b>Test wt</b>	0.362	0.363	0.535	0.475	-0.092	max

**S1 Table. Prediction accuracy of 26 complex traits in the Goodman Association panel using HARE from seven diverse tissues: germinating seedlings root (GRoot), germinating seedlings shoot (GShoot), 2 cm from base of leaf 3 (L3Base), two cm from tip of leaf 3 (L3Tip), mature mid-leaf tissue sampled during mid-day (LMAD), mature mid-leaf tissue sampled during mid-night (LMAN), and developing kernels harvested after 350 growing degree days after pollination (Kern), mean, and maximum expression of genes across all tissues. P value (high) and P value (low) were calculated using a Monte Carlo procedure to test if the accuracy using HARE was significantly higher or lower than random HARE. Models were trained in NAM and tested in Goodman Association panel.**

<b>Trait</b>	<b>Accuracy using HARE</b>	<b>Mean accuracy using random HARE</b>	<b>P value (high)</b>	<b>P value (low)</b>	<b>Accuracy of HARE over random HARE</b>	<b>Tissues</b>
<b>Cob diameter</b>	0.440	0.426	0.307	0.703	1.379	L3Tip
<b>Cob length</b>	0.221	0.208	0.356	0.653	1.290	L3Tip
<b>Cob mass</b>	0.450	0.404	0.030	0.980	4.553	L3Tip
<b>Ear height</b>	0.486	0.432	0.020	0.990	5.376	L3Tip
<b>Ear mass</b>	0.449	0.425	0.129	0.881	2.403	L3Tip
<b>Ear row number</b>	0.173	0.196	0.851	0.158	-2.317	L3Tip
<b>Anthesis silking interval</b>	0.061	0.054	0.406	0.604	0.724	L3Tip
<b>Days to anthesis</b>	0.751	0.742	0.257	0.752	0.943	L3Tip
<b>Days to Silking</b>	0.697	0.689	0.376	0.634	0.803	L3Tip
<b>Kernel number per row</b>	0.160	0.157	0.396	0.614	0.319	L3Tip
<b>Leaf length</b>	0.338	0.328	0.337	0.673	0.964	L3Tip
<b>Leaf width</b>	0.568	0.553	0.277	0.733	1.480	L3Tip

<b>Nodes above ear</b>	0.307	0.348	0.901	0.109	-4.182	L3Tip
<b>Nodes below ear</b>	0.619	0.591	0.089	0.921	2.826	L3Tip
<b>Number of brace roots</b>	0.331	0.303	0.069	0.941	2.794	L3Tip
<b>Oil</b>	0.234	0.217	0.317	0.693	1.695	L3Tip
<b>Plant height</b>	0.281	0.235	0.050	0.960	4.589	L3Tip
<b>Protein</b>	0.190	0.156	0.139	0.871	3.461	L3Tip
<b>Southern leaf blight</b>	0.458	0.443	0.327	0.683	1.442	L3Tip
<b>Starch</b>	0.290	0.264	0.198	0.812	2.588	L3Tip
<b>Tassel length</b>	0.174	0.163	0.356	0.653	1.147	L3Tip
<b>Tassel primary branches</b>	0.240	0.219	0.208	0.802	2.105	L3Tip
<b>Total kernel number</b>	0.179	0.169	0.297	0.713	0.996	L3Tip
<b>Kernel wt</b>	0.397	0.388	0.337	0.673	0.971	L3Tip
<b>Leaf angle</b>	0.359	0.332	0.158	0.851	2.729	L3Tip
<b>Test wt</b>	0.313	0.320	0.673	0.337	-0.723	L3Tip
<b>Cob diameter</b>	0.458	0.428	0.079	0.931	2.943	L3Base
<b>Cob length</b>	0.252	0.206	0.099	0.911	4.559	L3Base
<b>Cob mass</b>	0.455	0.406	0.030	0.980	4.864	L3Base
<b>Ear height</b>	0.462	0.433	0.149	0.861	2.886	L3Base
<b>Ear mass</b>	0.468	0.429	0.020	0.990	3.877	L3Base
<b>Ear row number</b>	0.162	0.195	0.901	0.109	-3.381	L3Base
<b>Anthesis silking interval</b>	0.043	0.050	0.614	0.396	-0.684	L3Base
<b>Days to anthesis</b>	0.751	0.742	0.317	0.693	0.921	L3Base

<b>Days to Silking</b>	0.694	0.689	0.426	0.584	0.492	L3Base
<b>Kernel number per row</b>	0.149	0.158	0.743	0.267	-0.954	L3Base
<b>Leaf length</b>	0.361	0.329	0.069	0.941	3.205	L3Base
<b>Leaf width</b>	0.564	0.554	0.356	0.653	0.949	L3Base
<b>Nodes above ear</b>	0.312	0.348	0.891	0.119	-3.533	L3Base
<b>Nodes below ear</b>	0.598	0.592	0.277	0.733	0.630	L3Base
<b>Number of brace roots</b>	0.324	0.305	0.178	0.832	1.917	L3Base
<b>Oil</b>	0.218	0.215	0.475	0.535	0.324	L3Base
<b>Plant height</b>	0.263	0.235	0.168	0.842	2.852	L3Base
<b>Protein</b>	0.209	0.155	0.040	0.970	5.378	L3Base
<b>Southern leaf blight</b>	0.449	0.441	0.376	0.634	0.853	L3Base
<b>Starch</b>	0.328	0.262	0.020	0.990	6.624	L3Base
<b>Tassel length</b>	0.220	0.160	0.020	0.990	5.999	L3Base
<b>Tassel primary branches</b>	0.258	0.224	0.139	0.871	3.420	L3Base
<b>Total kernel number</b>	0.163	0.170	0.673	0.337	-0.731	L3Base
<b>Kernel wt</b>	0.412	0.390	0.089	0.921	2.206	L3Base
<b>Leaf angle</b>	0.366	0.332	0.069	0.941	3.423	L3Base
<b>Test wt</b>	0.318	0.323	0.614	0.396	-0.455	L3Base
<b>Cob diameter</b>	0.463	0.427	0.050	0.960	3.639	LMAD
<b>Cob length</b>	0.235	0.206	0.178	0.832	2.914	LMAD
<b>Cob mass</b>	0.455	0.403	0.010	1.000	5.200	LMAD
<b>Ear height</b>	0.482	0.431	0.020	0.990	5.171	LMAD

<b>Ear mass</b>	0.442	0.427	0.267	0.743	1.542	LMAD
<b>Ear row number</b>	0.205	0.195	0.396	0.614	0.992	LMAD
<b>Anthesis silking interval</b>	0.072	0.053	0.228	0.782	1.953	LMAD
<b>Days to anthesis</b>	0.759	0.740	0.069	0.941	1.910	LMAD
<b>Days to Silking</b>	0.705	0.688	0.129	0.881	1.727	LMAD
<b>Kernel number per row</b>	0.133	0.159	0.901	0.109	-2.595	LMAD
<b>Leaf length</b>	0.346	0.328	0.257	0.752	1.756	LMAD
<b>Leaf width</b>	0.563	0.553	0.366	0.644	1.004	LMAD
<b>Nodes above ear</b>	0.343	0.347	0.564	0.446	-0.400	LMAD
<b>Nodes below ear</b>	0.616	0.589	0.089	0.921	2.717	LMAD
<b>Number of brace roots</b>	0.329	0.306	0.109	0.901	2.366	LMAD
<b>Oil</b>	0.217	0.223	0.515	0.495	-0.616	LMAD
<b>Plant height</b>	0.262	0.235	0.149	0.861	2.765	LMAD
<b>Protein</b>	0.180	0.159	0.277	0.733	2.103	LMAD
<b>Southern leaf blight</b>	0.446	0.439	0.366	0.644	0.721	LMAD
<b>Starch</b>	0.285	0.266	0.277	0.733	1.928	LMAD
<b>Tassel length</b>	0.210	0.160	0.069	0.941	5.017	LMAD
<b>Tassel primary branches</b>	0.244	0.224	0.228	0.782	2.016	LMAD
<b>Total kernel number</b>	0.168	0.170	0.574	0.436	-0.198	LMAD
<b>Kernel wt</b>	0.394	0.388	0.416	0.594	0.513	LMAD
<b>Leaf angle</b>	0.367	0.332	0.119	0.891	3.515	LMAD

<b>Test wt</b>	0.349	0.319	0.079	0.931	2.985	LMAD
<b>Cob diameter</b>	0.451	0.428	0.198	0.812	2.344	LMAN
<b>Cob length</b>	0.213	0.202	0.396	0.614	1.140	LMAN
<b>Cob mass</b>	0.443	0.405	0.059	0.950	3.763	LMAN
<b>Ear height</b>	0.479	0.430	0.030	0.980	4.894	LMAN
<b>Ear mass</b>	0.447	0.425	0.188	0.822	2.197	LMAN
<b>Ear row number</b>	0.183	0.196	0.703	0.307	-1.335	LMAN
<b>Anthesis silking interval</b>	0.053	0.051	0.426	0.584	0.210	LMAN
<b>Days to anthesis</b>	0.770	0.742	0.030	0.980	2.798	LMAN
<b>Days to Silking</b>	0.717	0.689	0.059	0.950	2.821	LMAN
<b>Kernel number per row</b>	0.144	0.155	0.713	0.297	-1.058	LMAN
<b>Leaf length</b>	0.367	0.326	0.050	0.960	4.071	LMAN
<b>Leaf width</b>	0.582	0.551	0.040	0.970	3.112	LMAN
<b>Nodes above ear</b>	0.356	0.347	0.416	0.594	0.869	LMAN
<b>Nodes below ear</b>	0.620	0.591	0.069	0.941	2.889	LMAN
<b>Number of brace roots</b>	0.337	0.301	0.040	0.970	3.638	LMAN
<b>Oil</b>	0.225	0.217	0.386	0.624	0.897	LMAN
<b>Plant height</b>	0.271	0.235	0.079	0.931	3.608	LMAN
<b>Protein</b>	0.197	0.159	0.129	0.881	3.766	LMAN
<b>Southern leaf blight</b>	0.472	0.439	0.129	0.881	3.334	LMAN
<b>Starch</b>	0.294	0.265	0.188	0.822	2.926	LMAN
<b>Tassel length</b>	0.168	0.161	0.406	0.604	0.705	LMAN

<b>Tassel primary branches</b>	0.242	0.219	0.208	0.802	2.307	LMAN
<b>Total kernel number</b>	0.180	0.167	0.267	0.743	1.257	LMAN
<b>Kernel wt</b>	0.395	0.385	0.307	0.703	0.996	LMAN
<b>Leaf angle</b>	0.363	0.330	0.139	0.871	3.252	LMAN
<b>Test wt</b>	0.326	0.320	0.475	0.535	0.576	LMAN
<b>Cob diameter</b>	0.451	0.428	0.149	0.861	2.331	GShoot
<b>Cob length</b>	0.258	0.207	0.030	0.980	5.126	GShoot
<b>Cob mass</b>	0.463	0.405	0.010	1.000	5.776	GShoot
<b>Ear height</b>	0.454	0.430	0.158	0.851	2.408	GShoot
<b>Ear mass</b>	0.464	0.429	0.030	0.980	3.502	GShoot
<b>Ear row number</b>	0.188	0.199	0.663	0.347	-1.125	GShoot
<b>Anthesis silking interval</b>	0.064	0.051	0.327	0.683	1.320	GShoot
<b>Days to anthesis</b>	0.766	0.743	0.069	0.941	2.284	GShoot
<b>Days to Silking</b>	0.715	0.691	0.079	0.931	2.395	GShoot
<b>Kernel number per row</b>	0.148	0.159	0.772	0.238	-1.085	GShoot
<b>Leaf length</b>	0.348	0.327	0.178	0.832	2.172	GShoot
<b>Leaf width</b>	0.571	0.553	0.317	0.693	1.746	GShoot
<b>Nodes above ear</b>	0.389	0.343	0.030	0.980	4.665	GShoot
<b>Nodes below ear</b>	0.604	0.590	0.228	0.782	1.411	GShoot
<b>Number of brace roots</b>	0.336	0.307	0.059	0.950	2.949	GShoot
<b>Oil</b>	0.230	0.213	0.307	0.703	1.714	GShoot
<b>Plant height</b>	0.257	0.232	0.198	0.812	2.413	GShoot

<b>Protein</b>	0.226	0.154	0.020	0.990	7.217	GShoot
<b>Southern leaf blight</b>	0.466	0.439	0.168	0.842	2.688	GShoot
<b>Starch</b>	0.311	0.263	0.079	0.931	4.809	GShoot
<b>Tassel length</b>	0.209	0.156	0.030	0.980	5.315	GShoot
<b>Tassel primary branches</b>	0.279	0.225	0.030	0.980	5.463	GShoot
<b>Total kernel number</b>	0.172	0.172	0.515	0.495	0.081	GShoot
<b>Kernel wt</b>	0.419	0.392	0.069	0.941	2.719	GShoot
<b>Leaf angle</b>	0.325	0.331	0.594	0.416	-0.595	GShoot
<b>Test wt</b>	0.314	0.321	0.624	0.386	-0.698	GShoot
<b>Cob diameter</b>	0.469	0.426	0.030	0.980	4.316	GRoot
<b>Cob length</b>	0.234	0.202	0.158	0.851	3.219	GRoot
<b>Cob mass</b>	0.452	0.403	0.020	0.990	4.970	GRoot
<b>Ear height</b>	0.454	0.433	0.198	0.812	2.158	GRoot
<b>Ear mass</b>	0.450	0.428	0.158	0.851	2.169	GRoot
<b>Ear row number</b>	0.211	0.195	0.277	0.733	1.644	GRoot
<b>Anthesis silking interval</b>	0.107	0.055	0.089	0.921	5.195	GRoot
<b>Days to anthesis</b>	0.765	0.741	0.059	0.950	2.330	GRoot
<b>Days to Silking</b>	0.716	0.689	0.079	0.931	2.652	GRoot
<b>Kernel number per row</b>	0.157	0.159	0.564	0.446	-0.156	GRoot
<b>Leaf length</b>	0.356	0.327	0.139	0.871	2.836	GRoot
<b>Leaf width</b>	0.589	0.552	0.050	0.960	3.713	GRoot
<b>Nodes above ear</b>	0.334	0.344	0.634	0.376	-1.014	GRoot



<b>Nodes below ear</b>	0.602	0.594	0.297	0.713	0.768	GRoot
<b>Number of brace roots</b>	0.331	0.306	0.119	0.891	2.451	GRoot
<b>Oil</b>	0.207	0.213	0.624	0.386	-0.620	GRoot
<b>Plant height</b>	0.231	0.235	0.564	0.446	-0.462	GRoot
<b>Protein</b>	0.174	0.153	0.218	0.792	2.123	GRoot
<b>Southern leaf blight</b>	0.485	0.439	0.030	0.980	4.594	GRoot
<b>Starch</b>	0.308	0.259	0.030	0.980	4.901	GRoot
<b>Tassel length</b>	0.195	0.161	0.139	0.871	3.354	GRoot
<b>Tassel primary branches</b>	0.243	0.224	0.218	0.792	1.845	GRoot
<b>Total kernel number</b>	0.184	0.170	0.257	0.752	1.332	GRoot
<b>Kernel wt</b>	0.415	0.388	0.089	0.921	2.703	GRoot
<b>Leaf angle</b>	0.367	0.330	0.089	0.921	3.720	GRoot
<b>Test wt</b>	0.327	0.319	0.337	0.673	0.792	GRoot
<b>Cob diameter</b>	0.464	0.426	0.040	0.970	3.833	Kern
<b>Cob length</b>	0.221	0.204	0.287	0.723	1.710	Kern
<b>Cob mass</b>	0.454	0.400	0.010	1.000	5.455	Kern
<b>Ear height</b>	0.466	0.428	0.059	0.950	3.809	Kern
<b>Ear mass</b>	0.477	0.424	0.010	1.000	5.278	Kern
<b>Ear row number</b>	0.220	0.193	0.218	0.792	2.636	Kern
<b>Anthesis silking interval</b>	0.045	0.056	0.713	0.297	-1.061	Kern
<b>Days to anthesis</b>	0.759	0.740	0.139	0.871	1.880	Kern
<b>Days to Silking</b>	0.706	0.687	0.178	0.832	1.844	Kern

<b>Kernel number per row</b>	0.158	0.156	0.436	0.574	0.197	Kern
<b>Leaf length</b>	0.363	0.327	0.069	0.941	3.580	Kern
<b>Leaf width</b>	0.583	0.547	0.069	0.941	3.639	Kern
<b>Nodes above ear</b>	0.341	0.349	0.614	0.396	-0.788	Kern
<b>Nodes below ear</b>	0.611	0.591	0.178	0.832	2.040	Kern
<b>Number of brace roots</b>	0.326	0.304	0.149	0.861	2.195	Kern
<b>Oil</b>	0.225	0.214	0.416	0.594	1.094	Kern
<b>Plant height</b>	0.257	0.234	0.218	0.792	2.299	Kern
<b>Protein</b>	0.213	0.153	0.050	0.960	6.008	Kern
<b>Southern leaf blight</b>	0.455	0.438	0.277	0.733	1.659	Kern
<b>Starch</b>	0.286	0.265	0.218	0.792	2.171	Kern
<b>Tassel length</b>	0.180	0.163	0.307	0.703	1.625	Kern
<b>Tassel primary branches</b>	0.233	0.222	0.366	0.644	1.124	Kern
<b>Total kernel number</b>	0.178	0.169	0.356	0.653	0.920	Kern
<b>Kernel wt</b>	0.394	0.387	0.366	0.644	0.636	Kern
<b>Leaf angle</b>	0.352	0.329	0.218	0.792	2.243	Kern
<b>Test wt</b>	0.313	0.322	0.713	0.297	-0.974	Kern
<b>Cob diameter</b>	0.451	0.431	0.139	0.871	2.020	mean
<b>Cob length</b>	0.233	0.204	0.198	0.812	2.923	mean
<b>Cob mass</b>	0.463	0.407	0.010	1.000	5.648	mean
<b>Ear height</b>	0.449	0.433	0.248	0.762	1.680	mean
<b>Ear mass</b>	0.457	0.429	0.069	0.941	2.787	mean

<b>Ear row number</b>	0.176	0.200	0.822	0.188	-2.364	mean
<b>Anthesis silking interval</b>	0.082	0.052	0.149	0.861	2.944	mean
<b>Days to anthesis</b>	0.787	0.745	0.010	1.000	4.231	mean
<b>Days to Silking</b>	0.740	0.692	0.010	1.000	4.860	mean
<b>Kernel number per row</b>	0.136	0.157	0.881	0.129	-2.052	mean
<b>Leaf length</b>	0.380	0.329	0.020	0.990	5.079	mean
<b>Leaf width</b>	0.579	0.555	0.099	0.911	2.350	mean
<b>Nodes above ear</b>	0.416	0.347	0.010	1.000	6.937	mean
<b>Nodes below ear</b>	0.631	0.592	0.020	0.990	3.907	mean
<b>Number of brace roots</b>	0.300	0.307	0.673	0.337	-0.756	mean
<b>Oil</b>	0.230	0.216	0.307	0.703	1.440	mean
<b>Plant height</b>	0.238	0.235	0.455	0.554	0.311	mean
<b>Protein</b>	0.230	0.155	0.010	1.000	7.506	mean
<b>Southern leaf blight</b>	0.448	0.442	0.386	0.624	0.536	mean
<b>Starch</b>	0.307	0.267	0.079	0.931	4.060	mean
<b>Tassel length</b>	0.204	0.157	0.040	0.970	4.649	mean
<b>Tassel primary branches</b>	0.266	0.225	0.050	0.960	4.046	mean
<b>Total kernel number</b>	0.147	0.170	0.901	0.109	-2.217	mean
<b>Kernel wt</b>	0.403	0.393	0.347	0.663	1.024	mean
<b>Leaf angle</b>	0.364	0.332	0.099	0.911	3.182	mean
<b>Test wt</b>	0.301	0.318	0.792	0.218	-1.686	mean

<b>Cob diameter</b>	0.479	0.432	0.020	0.990	4.700	max
<b>Cob length</b>	0.251	0.205	0.059	0.950	4.566	max
<b>Cob mass</b>	0.472	0.407	0.010	1.000	6.537	max
<b>Ear height</b>	0.471	0.433	0.059	0.950	3.791	max
<b>Ear mass</b>	0.471	0.428	0.020	0.990	4.276	max
<b>Ear row number</b>	0.181	0.199	0.782	0.228	-1.860	max
<b>Anthesis silking interval</b>	0.103	0.052	0.069	0.941	5.044	max
<b>Days to anthesis</b>	0.799	0.743	0.010	1.000	5.541	max
<b>Days to Silking</b>	0.749	0.691	0.010	1.000	5.779	max
<b>Kernel number per row</b>	0.146	0.158	0.762	0.248	-1.202	max
<b>Leaf length</b>	0.369	0.328	0.020	0.990	4.123	max
<b>Leaf width</b>	0.597	0.553	0.010	1.000	4.409	max
<b>Nodes above ear</b>	0.383	0.346	0.119	0.891	3.740	max
<b>Nodes below ear</b>	0.636	0.593	0.010	1.000	4.315	max
<b>Number of brace roots</b>	0.313	0.306	0.366	0.644	0.656	max
<b>Oil</b>	0.208	0.216	0.584	0.426	-0.860	max
<b>Plant height</b>	0.250	0.235	0.287	0.723	1.411	max
<b>Protein</b>	0.229	0.154	0.010	1.000	7.581	max
<b>Southern leaf blight</b>	0.477	0.443	0.069	0.941	3.333	max
<b>Starch</b>	0.302	0.264	0.079	0.931	3.864	max
<b>Tassel length</b>	0.194	0.161	0.149	0.861	3.307	max
<b>Tassel primary branches</b>	0.256	0.225	0.129	0.881	3.099	max

<b>Total kernel number</b>	0.155	0.170	0.832	0.178	-1.576	max
<b>Kernel wt</b>	0.406	0.390	0.238	0.772	1.643	max
<b>Leaf angle</b>	0.377	0.333	0.010	1.000	4.442	max
<b>Test wt</b>	0.302	0.319	0.802	0.208	-1.735	max

**S2 Table. Prediction accuracy of 26 complex traits in NAM using HARE from 7 diverse tissues: germinating seedlings root (GRoot), germinating seedlings shoot (GShoot), 2 cm from base of leaf 3 (L3Base), 2 cm from tip of leaf 3 (L3Tip), mature mid-leaf tissue sampled during mid-day (LMAD), mature mid-leaf tissue sampled during mid-night (LMAN), and developing kernels harvested after 350 growing degree days after pollination (Kern), mean, and maximum expression of genes across all tissues. P value (high) and P value (low) were calculated using a Monte Carlo procedure to test if the accuracy using HARE was significantly higher or lower than random HARE. Models were trained in Goodman Association panel and tested in NAM.**

