Table S11 Prediction Accuracies for 24 Grain Carotenoid Traits using the Carotenoid QTL-Targeted Prediction Marker Set Relative to Random Marker Sets

		Mean Prediction Accuracy			Fold Difference in Prediction Accuracy	
	Trait	Carotenoid QTL-Targeted Prediction **(CQTP)**	Random Candidate Regions **(Candidate)**	Random Genomic Regions **(Genomic)**	**CQTP: Candidate**	**CQTP: Genomic**
15 priority traits	Lutein	0.544	0.205	0.210	2.649	2.594
	Zeinoxanthin	0.461	0.195	0.178	2.361	2.587
	α-Carotene	0.350	0.176	0.174	1.985	2.006
	α-Carotene/Zeinoxanthin	0.527	0.221	0.196	2.388	2.687
	Zeinoxanthin/Lutein	0.479	0.192	0.156	2.497	3.076
	Zeaxanthin	0.599	0.132	0.133	4.527	4.492
	β-Cryptoxanthin	0.369	0.189	0.195	1.954	1.889
	β-Carotene	0.206	0.108	0.131	1.918	1.569
	β-Cryptoxanthin/Zeaxanthin	0.369	0.155	0.166	2.375	2.221
	β-Carotene/β-Cryptoxanthin	0.327	0.139	0.117	2.347	2.796
	Total Carotenoids	0.262	0.111	0.080	2.362	3.255
	Acyclic and Monocyclic Carotenes	0.269	0.177	0.153	1.518	1.756
	β-Xanthophylls/α-Xanthophylls	0.717	0.189	0.209	3.796	3.437
	Provitamin A	0.337	0.175	0.171	1.925	1.969
	β-Carotenoids/α-Carotenoids	0.599	0.209	0.217	2.874	2.764
9 additional traits	ζ-Carotene	0.380	0.124	0.107	3.071	3.558
	Phytofluene	0.301	0.135	0.127	2.231	2.375
	Tetrahydrolycopene	0.258	0.156	0.157	1.656	1.648
	Total β-Xanthophylls	0.435	0.092	0.109	4.720	3.981
	Total α-Xanthophylls	0.520	0.156	0.191	3.324	2.725
	Provitamin A/Total Carotenoids	0.297	0.149	0.136	1.993	2.190
	β-Carotene/(β-Cryptoxanthin+Zeaxanthin)	0.382	0.148	0.120	2.575	3.194
	Acyclic Carotenes/Cyclic Carotenes	0.171	0.046	0.066	3.716	2.586
	Total Carotenes/Total Xanthophylls	0.347	0.081	0.069	4.256	4.997

The three marker sets tested were the carotenoid quantitative trait loci (QTL)-targeted prediction set (the 944 SNP markers and 7 indels within ± 250 kb of 8 *a priori* candidate genes), random candidate gene-targeted regions (markers within ± 250 kb of 8 other candidate genes in the pathway-level prediction set), and 8 random 500 kb genomic regions (selected from the markers used in our genome-wide association studies that did not overlap with the carotenoid QTL-targeted prediction set). Average raw correlations resulting from the 5-fold cross-validation were divided by the square root of a trait's broad-sense heritability to obtain prediction accuracies, which are reported as an average across the three genomic prediction methods tested: ridge-regression best linear unbiased prediction (RR-BLUP), least absolute shrinkage and selection operator (LASSO), and elastic net (eNET). For the random candidate region and random genomic region analyses, marker selection was conducted over 100 iterations with replacement, and prediction accuracies were averaged across these iterations. R scripts for these analyses are available upon request.