Table S1 Best Linear Unbiased Predictor (BLUP) Values. BLUP values for the 24 carotenoid traits used for the genome-wide association study, pathway-level analysis, and genomic prediction for 201 inbred maize lines.

Table S1 is available for download as an Excel file at http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.114.169979/-/DC1.

Table S2 Coordinates for Additional Insertion-Deletion (Indel) and Single-Nucleotide Polymorphism (SNP) Markers

Gene-Specific Assay	PCR-Based Marker	Primer Sequence (5′-3'direction)	Specific to PCR Primer			Coordinates Spanning Longest Amplicon Length[b]		
			Chr	**Start AGP2**	**StopAGP2**	**Chr**	**Start AGP2**	**StopAGP2**
PSY1-Indel388	PSY-8F	TGAAACAAACAAAGCCAGCA	chr6	82,016,321	82,016,340			
	PSY-9R	GCCTCTCCTCTTCTTGCGTA	chr6	82,017,115	82,017,134			
	PSY-10F	GAAACAAACAAAGCCAGCAG	chr6	82,016,322	82,016,341			
	PSY-11R	CTCCGGCCTCTCCTCTTCT	chr6	82,017,121	82,017,139	chr6	82,016,321	82,017,139
LCYE-5’TE	LYCe-TE103PF-F1	CGCTAGCAAGCCCATTATTTTTA	chr8	138,882,291	138,882,313			
	LYCe-TE103PF-R1	CGGTATGGTTTTTGGTATACGG	chr8	[a]				
	LYCe-ZGt111R1-F1	AAGCATCCGACCAAAATAACAG	chr8	138,882,423	138,882,444			
	LYCe-TE105PR-R1	GAGAGGGAGACGACGAGACAC	chr8	138,882,649	138,882,670	chr8	138,882,291	138,882,670
LCYE-SNP216	LYCe-SNP216-F1	GCGGCAGTGGGCGTGGAT	chr8	138,883,009	138,883,026			
	LYCe-SNP216-R1	TGAAGTACGGCTGCAGGACAACG	chr8	138,883,381	138,883,403	chr8	138,883,009	138,883,403
LCYE-3’	LYCe-3'indl-F1	GTACGTCGTTCATCTCCCGTACCC	chr8	[a]				
	LYCe-3'indl-R1	CTTGGTGAACGCATTTCTGTTGG	chr8	[a]				
	LYCe-3'indl-F2	GGACCGGAACAGCCAACTG	chr8	[a]				
	LYCe-3'indl-R2	GGCGAAATGGGTACGGCC	chr8	[a]		chr8	138,889,812	138,892,812
CCD1-5’	CCD1-WC-L1	CCGTGCTCGGACAGAATAGT	chr8	[a]				
	CCD1-B73-rev-L1	CTCACACGTGTCAACGCC	chr9	152,093,059	152,093,042			
	CCD1-ALL-R1	GTGGTTTCGGTGGCTGTC	chr9	152,092,686	152,092,700	chr9	152,092,686	152,093,042
crtRB1-5’TE	crtRB1 H1UF	TTAGAGCCTCGACCCTCTGTG	chr10	136,061,212	136,061,232			
	crtRB1 H1UR	AATCCCTTTCCATGTTACGC	chr10	136,060,416	136,060,435	chr10	136,060,416	136,061,232
crtRB1-InDel4	crtRB1 D4F	ACCGTCACGTGCTTCGTGCC	chr10	136,059,806	136,059,787			
	crtRB1 D4R	CTTCCGCGCCTCCTTCTC	chr10	136,059,690	136,059,708	chr10	136,059,690	136,059,806
crtRB1-3’TE	crtRB1 65F	ACACCACATGGACAAGTTCG	chr10	[a]				
	crtRB1 62R	ACACTCTGGCCCATGAACAC	chr10	[a]				
	crtRB1 66R	ACAGCAATACAGGGGACCAG	chr10	[a]		chr10	136,060,219	136,063,219

RefGen_v2 Coordinates and PCR primer sequences for the additional seven indel markers and one SNP marker within and near the coding regions of one carotenoid degradation gene and three carotenoid biosynthetic pathway genes.
Amplification protocols for gene-specific PCR-based marker sets are listed in: Fu et al. 2013b for PSY1; Harjes et al. 2008 for LCYe; Kandianis et al. for CCD1; Yan et al. 2010 for crtRB1.

[a] RefGen_v2 Coordinates are not available

[b] Physical distance encompassing all possible primer combinations