Figure S1

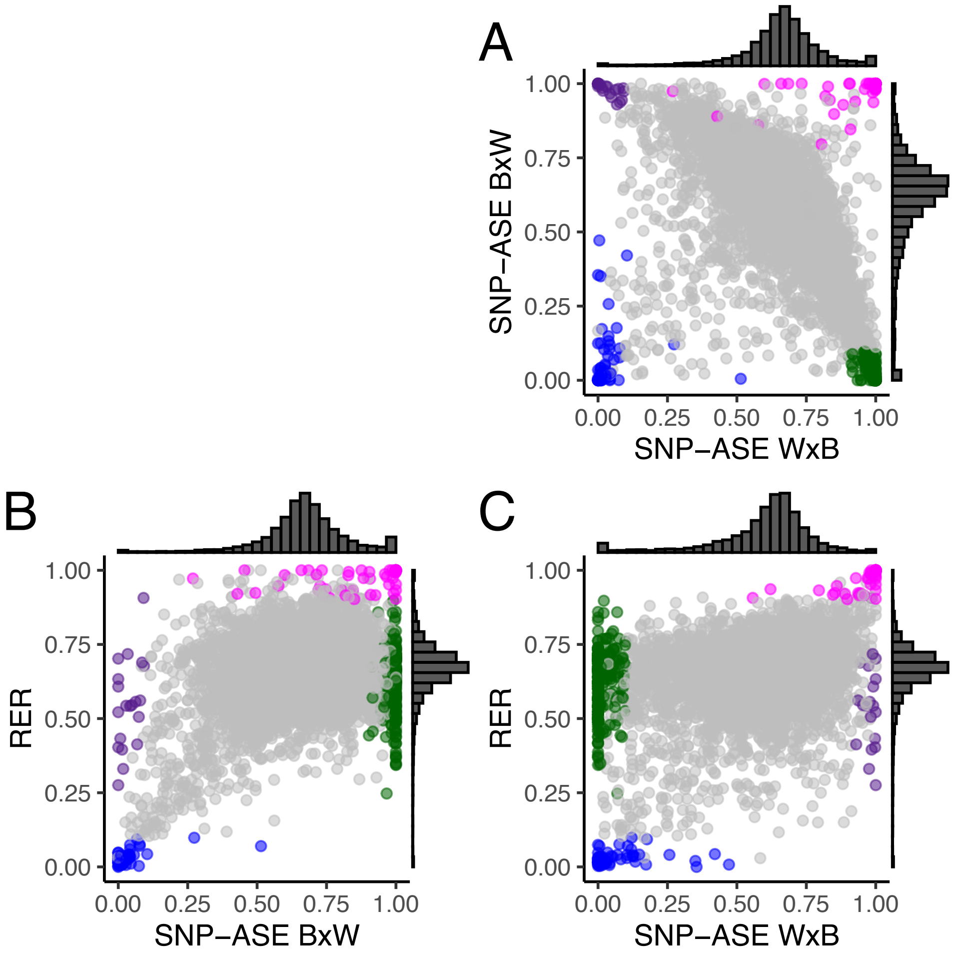


Figure S1: Comparison of SNP-ASE and RER for B73 genes accessible using both methods in the B73 x W22 cross. A) The SNP-ASE method applied across both directions of reciprocal crosses, with points colored based on imprinting calls using RER (magenta and blue) or inconsistency across reciprocals using SNP-ASE (green and purple). Colors are consistent across panels. B-C) Comparison of the two SNP-ASE values to RER. Plots are the same as shown in Figure 1B but colored to indicate imprinted genes and genes with genotype-biased expression using SNP-ASE. Genotype bias does not impact RER since the calculation is performed across reciprocals instead of across genotypes. For all panels, values plotted show the average across three biological replicates. Genes are color-coded based on expression pattern, with magenta = MEG, blue = PEG, green = B73 biased, and purple = W22 biased. Genotype bias was defined by SNP-ASE ratios > 0.85 in one direction and < 0.15 in the other direction of reciprocal crosses.

Figure S2

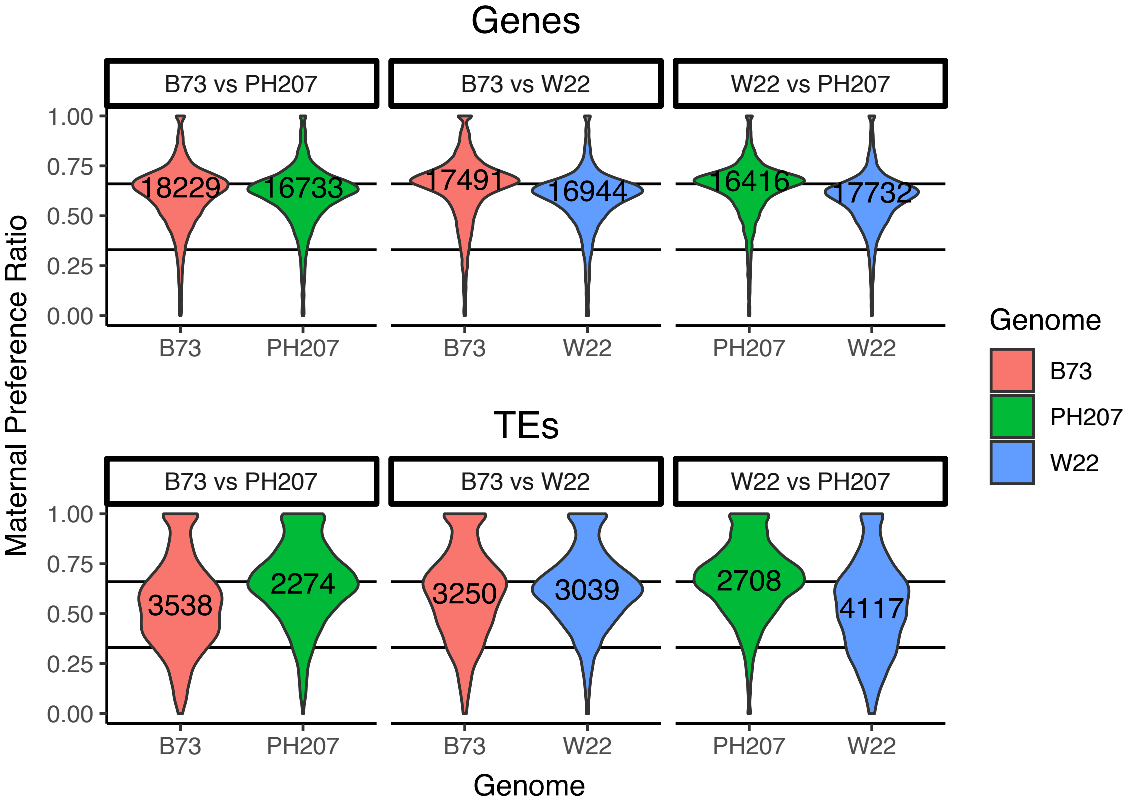


Figure S2: Distribution of RER for genes and TEs across contrasts. Most genes and TEs are expressed near the expected ratio given genome dosage (horizontal line, 0.67), with maternal and paternal expression approaching 1 or 0, respectively. TEs have a more pronounced peak of maternal expression than genes. For TEs, a bimodal peak near 0.67 and 0.33 in contrasts with PH207 suggests that some PH207 TEs may be mapping better to B73 or W22 assemblies due to poor assembly quality of PH207 in intergenic space. For this reason, paternal TEs were not counted in contrasts with PH207 in Fig 3A.

Figure S3

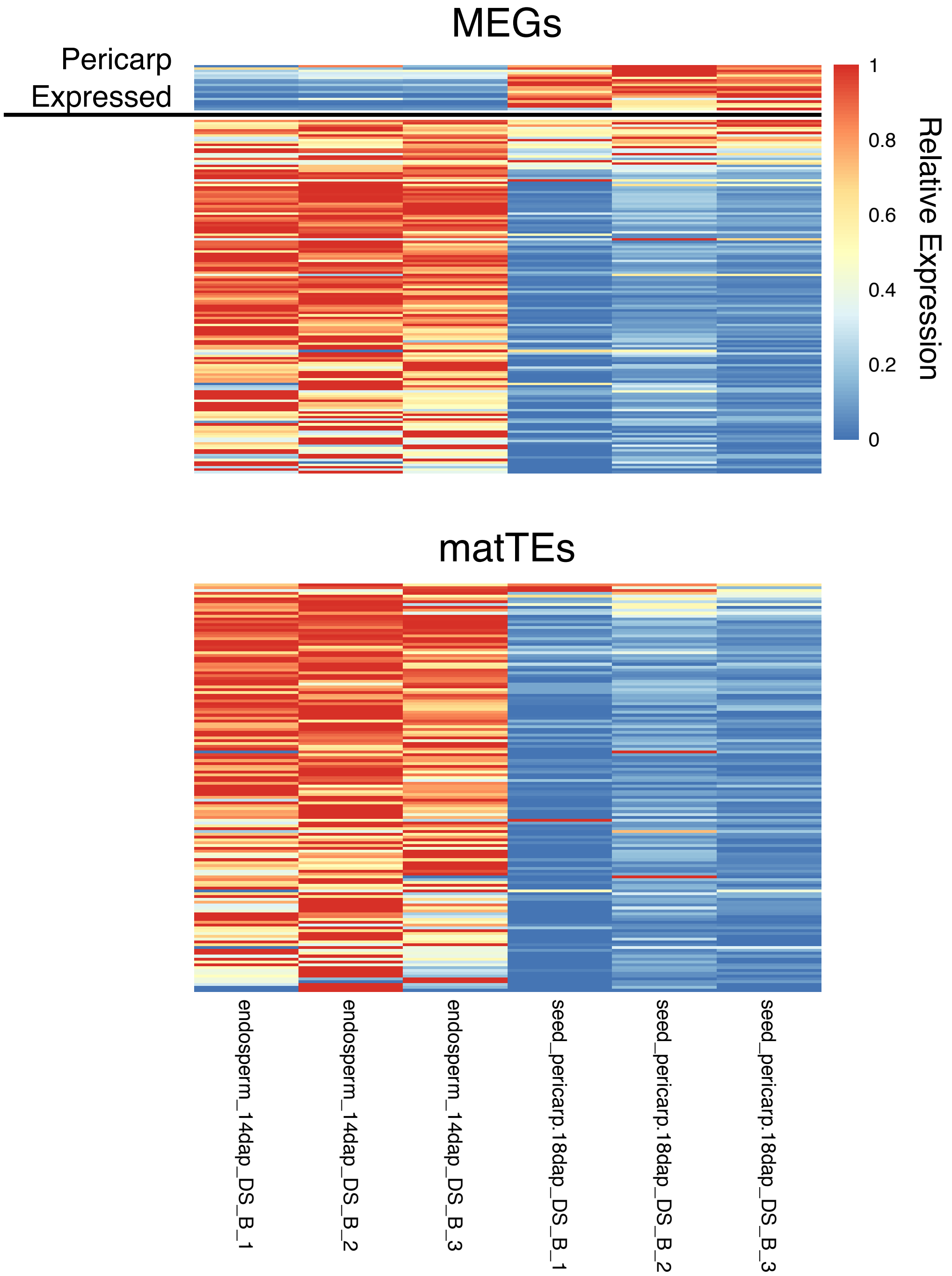


Figure S3: Expression profile of B73 MEGs and matTEs in the endosperm and pericarp using RNA-seq data from Stelpflug et al. Genes with mean expression in the pericarp > 2x the mean expression in the endosperm were filtered from the MEG list due to the potential for seed coat contamination. W22 and PH207 genes corresponding to B73 pericarp-preferred genes were also removed from MEG counts. There were no matTEs filtered out using this method. Heat of each pixel represents the expression value compared to the max in the row.

Figure S4

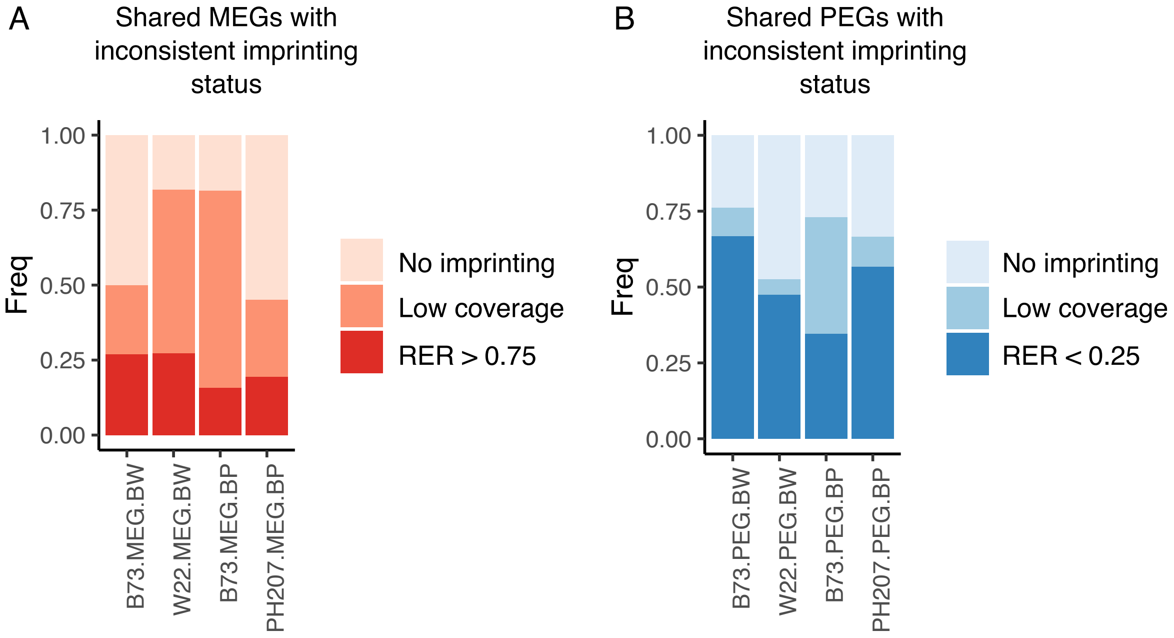


Figure S4: RER bias for genes with inconsistent imprinting in Figure 2B. For both MEGs (right) and PEGs (left), the majority of genes do not overlap due to low coverage or have RER values in the same direction as imprinted genes but failed to meet our strict statistical and/or RER threshold. X-axis labels denote the genotype where the gene is imprinted, the type of imprint, and the cross where the imprinting is variable (B = B73, W = W22, P = PH207)

Figure S5

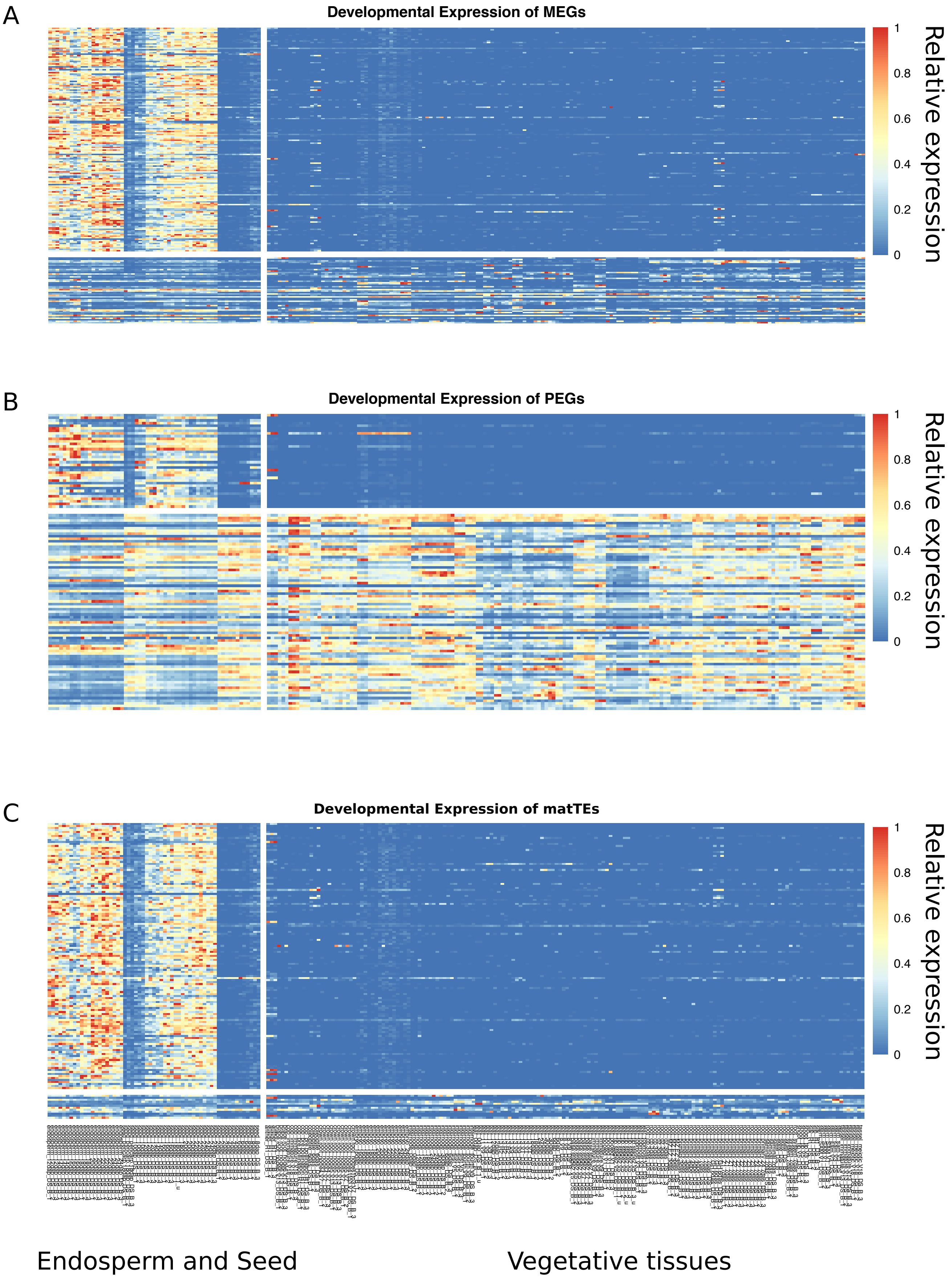


Figure S5: Expression pattern of imprinted B73 genes and TEs across development using data from Stelpflug et al. Endosperm and seed tissues are shown on the left side of the break, and all other tissues sampled are shown on the right of the break. Endosperm-preferred expression was defined where the sum of the expression across endosperm and seed libraries were more than 60% of the sum of the expression across all libraries. For each plot, endosperm-preferred features are shown above the break and constitutive features are shown below the break. Heat of each pixel represents the expression value compared to the max in the row.

Figure S6

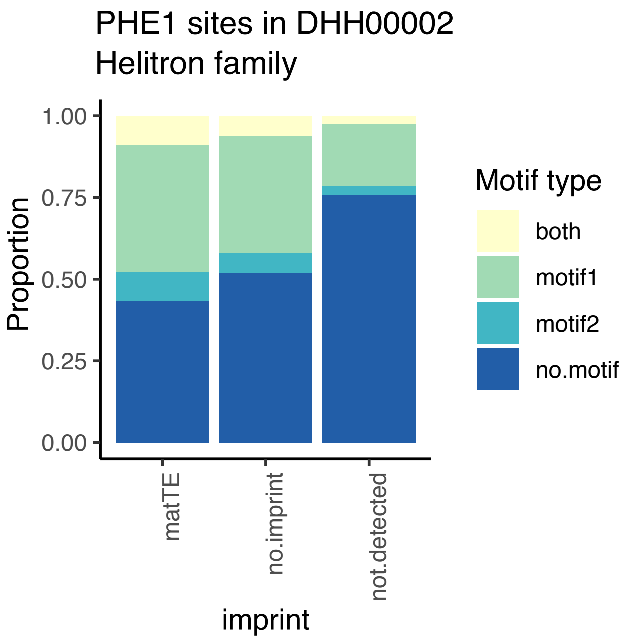


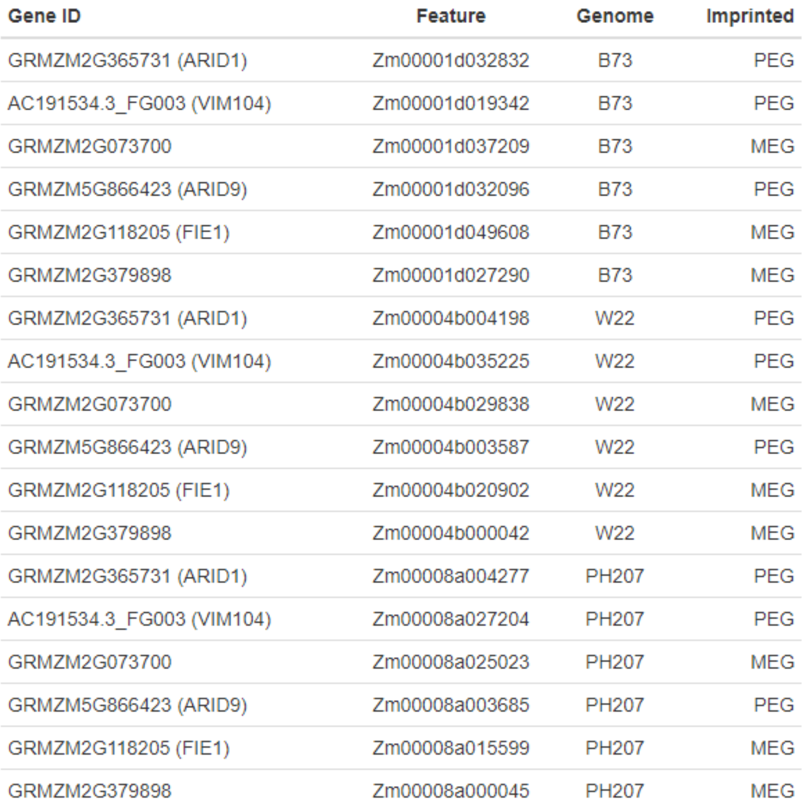
Figure S6: Presence of PHE1 binding sites within DHH2 family helitrons. Binding motifs from Batista et al. 2019 were identified in all DHH2 helitrons, and the distribution of members with zero, one, or both of the sites were determined. A similar distribution of motifs were found for matTEs and non-imprinted family members, with a lower proportion of elements with at least one motif identified in the not detected set. TEs in the not detected set include TEs that are not expressed and TEs without unique sequence that could be assessed for imprinting.

Table S1

Library	Reads	Percent_Unique
BW1	50912503	16.09983
BW2	46955481	16.63385
BW3	43297034	17.88011
WB1	42341423	18.12524
WB2	38350809	14.4479
WB3	53936174	13.86724
BP1	50287029	14.24699
BP2	51260636	16.18052
BP3	45525383	16.54365
PB1	43670832	19.41905
PB2	39706669	18.70737
PB3	41024925	15.71401
WP1	53203456	15.92903
WP2	52838664	16.56664
WP3	41023269	19.63248
PW1	53900552	15.71085
PW2	35267586	18.17527
PW3	35654524	18.32236

Table S1: Reads and mapping statistics for RNA-seq libraries in this study

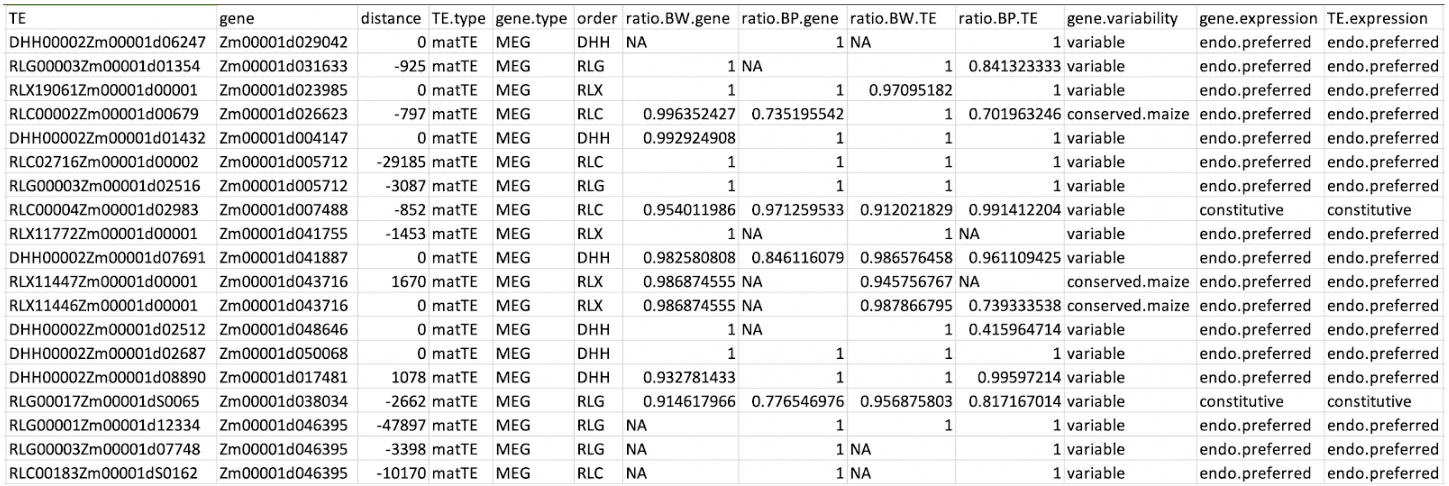
Table S2



Gene ID	Feature	Genome	Imprinted
GRMZM2G365731 (ARID1)	Zm00001d032832	B73	PEG
AC191534.3_FG003 (VIM104)	Zm00001d019342	B73	PEG
GRMZM2G073700	Zm00001d037209	B73	MEG
GRMZM5G866423 (ARID9)	Zm00001d032096	B73	PEG
GRMZM2G118205 (FIE1)	Zm00001d049608	B73	MEG
GRMZM2G379898	Zm00001d027290	B73	MEG
GRMZM2G365731 (ARID1)	Zm00004b004198	W22	PEG
AC191534.3_FG003 (VIM104)	Zm00004b035225	W22	PEG
GRMZM2G073700	Zm00004b029838	W22	MEG
GRMZM5G866423 (ARID9)	Zm00004b003587	W22	PEG
GRMZM2G118205 (FIE1)	Zm00004b020902	W22	MEG
GRMZM2G379898	Zm00004b000042	W22	MEG
GRMZM2G365731 (ARID1)	Zm00008a004277	PH207	PEG
AC191534.3_FG003 (VIM104)	Zm00008a027204	PH207	PEG
GRMZM2G073700	Zm00008a025023	PH207	MEG
GRMZM5G866423 (ARID9)	Zm00008a003685	PH207	PEG
GRMZM2G118205 (FIE1)	Zm00008a015599	PH207	MEG
GRMZM2G379898	Zm00008a000045	PH207	MEG

Table S2 - Gene IDs for conserved imprinted genes plotted in Figure 1C

Table S3



TE	gene	distance	TE.type	gene.type	order	ratio.BW.gene	ratio.BP.gene	ratio.BW.TE	ratio.BP.TE	gene.variability	gene.expression	TE.expression
DHH00002Zm00001d06247	Zm00001d029042	0	matTE	MEG	DHH	NA	1	NA	1	variable	endo.preferred	endo.preferred
RLG00003Zm00001d01354	Zm00001d031633	-925	matTE	MEG	RLG	1	NA	1	0.841323333	variable	endo.preferred	endo.preferred
RLX19061Zm00001d00001	Zm00001d023985	0	matTE	MEG	RLX	1	1	0.97095182	1	variable	endo.preferred	endo.preferred
RLC00002Zm00001d00679	Zm00001d026623	-797	matTE	MEG	RLC	0.996352427	0.735195542	1	0.701963246	conserved.maize	endo.preferred	endo.preferred
DHH00002Zm00001d01432	Zm00001d004147	0	matTE	MEG	DHH	0.992924908	1	1	1	variable	endo.preferred	endo.preferred
RLC02716Zm00001d00002	Zm00001d005712	-29185	matTE	MEG	RLC	1	1	1	1	variable	endo.preferred	endo.preferred
RLG00003Zm00001d02516	Zm00001d005712	-3087	matTE	MEG	RLG	1	1	1	1	variable	endo.preferred	endo.preferred
RLC00004Zm00001d02983	Zm00001d007488	-852	matTE	MEG	RLC	0.954011986	0.971259533	0.912021829	0.991412204	variable	constitutive	constitutive
RLX11772Zm00001d00001	Zm00001d041755	-1453	matTE	MEG	RLX	1	NA	1	NA	variable	endo.preferred	endo.preferred
DHH00002Zm00001d07691	Zm00001d041887	0	matTE	MEG	DHH	0.982580808	0.846116079	0.986576458	0.961109425	variable	endo.preferred	endo.preferred
RLX11447Zm00001d00001	Zm00001d043716	1670	matTE	MEG	RLX	0.986874555	NA	0.945756767	NA	conserved.maize	endo.preferred	endo.preferred
RLX11446Zm00001d00001	Zm00001d043716	0	matTE	MEG	RLX	0.986874555	NA	0.987866795	0.739333538	conserved.maize	endo.preferred	endo.preferred
DHH00002Zm00001d02512	Zm00001d048646	0	matTE	MEG	DHH	1	NA	1	0.415964714	variable	endo.preferred	endo.preferred
DHH00002Zm00001d02687	Zm00001d050068	0	matTE	MEG	DHH	1	1	1	1	variable	endo.preferred	endo.preferred
DHH00002Zm00001d08890	Zm00001d017481	1078	matTE	MEG	DHH	0.932781433	1	1	0.99597214	variable	endo.preferred	endo.preferred
RLG00017Zm00001dS0065	Zm00001d038034	-2662	matTE	MEG	RLG	0.914617966	0.776546976	0.956875803	0.817167014	variable	constitutive	constitutive
RLG00001Zm00001d12334	Zm00001d046395	-47897	matTE	MEG	RLG	NA	1	1	1	variable	endo.preferred	endo.preferred
RLG00003Zm00001d07748	Zm00001d046395	-3398	matTE	MEG	RLG	NA	1	NA	1	variable	endo.preferred	endo.preferred
RLC00183Zm00001dS0162	Zm00001d046395	-10170	matTE	MEG	RLC	NA	1	NA	1	variable	endo.preferred	endo.preferred

Table S3: IDs and features of matTEs near MEGs