

Figure S1. Summary of read mapping statistics. For each tissue / genotype combination we show the number of read pairs (in millions) mapped to the maize B73 AGPv4 reference. Color indicates the three biological replicates for each sample and color darkness indicates mapping quality (read pair mapped uniquely - Map\_HighQual, read pair mapped multiple times - Map\_LowQual, one read of the pair mapped but the other unmapped - Orphan, both reads of the pair

unmapped - Unmap).

Total Assigned Unassigned Map_LowQual Unmap FailedQC																		
	B73 Mo17 BxM																	
seedlingleaf_11DAS	38.9M	77%	12%	7%	4%	0%	40.2M	78%	12%	7%	3%	0%	42.6M	78%	11%	7%	3%	0%
blade_v12	31.1M	80%	10%	6%	4%	0%	29.5M	67%	9%	14%	11%	0%	33.4M	75%	11%	8%	6%	0%
flagleaf_0DAP	27.1M	79%	11%	6%	4%	0%	32.7M	83%	10%	6%	2%	0%	28.4M	81%	10%	6%	3%	0%
auricle_v12	30.1M	79%	11%	6%	4%	0%	37.5M	73%	12%	7%	8%	0%	34.0M	78%	13%	6%	3%	0%
sheath_v12	33.4M	77%	12%	6%	5%	0%	31.7M	77%	14%	7%	2%	0%	34.9M	72%	13%	6%	8%	0%
husk_0DAP	35.7M	77%	13%	6%	5%	0%	38.4M	79%	11%	6%	3%	0%	37.9M	80%	11%	6%	4%	0%
tasselstem_0DAP	36.2M	74%	14%	5%	7%	0%	27.9M	78%	14%	5%	3%	0%	27.0M	76%	14%	6%	4%	0%
internode_v12	30.5M	75%	14%	5%	6%	0%	42.3M	78%	14%	5%	3%	0%	34.4M	77%	15%	5%	3%	0%
root_0DAP	38.2M	80%	11%	5%	4%	0%	36.4M	83%	11%	5%	1%	0%	38.0M	80%	13%	5%	2%	0%
silk_0DAP	29.9M	75%	13%	5%	6%	0%	27.0M	77%	14%	5%	3%	0%	36.3M	78%	12%	5%	5%	0%
floret_0DAP	30.0M	73%	14%	8%	5%	0%	28.7M	75%	15%	8%	2%	0%	28.2M	74%	15%	7%	4%	0%
radicle_root	34.5M	76%	14%	5%	5%	0%	34.7M	79%	14%	5%	3%	0%	37.2M	79%	13%	5%	3%	0%
seedlingroot_11DAS	41.1M	77%	12%	5%	5%	0%	12.0M	76%	14%	6%	4%	0%	26.6M	77%	12%	5%	5%	0%
tassel_v12	36.9M	72%	11%	5%	12%	0%	31.9M	73%	11%	5%	11%	0%	32.1M	76%	12%	5%	7%	0%
spikelets_0DAP	38.4M	77%	13%	5%	4%	0%	37.0M	79%	13%	5%	3%	0%	35.0M	79%	12%	5%	3%	0%
coleoptile_tip	36.2M	78%	11%	5%	5%	0%	37.4M	82%	11%	5%	2%	0%	36.6M	75%	10%	5%	9%	0%
seedlingmeristem_11DAS	43.2M	79%	12%	6%	3%	0%	46.1M	81%	12%	5%	2%	0%	43.5M	78%	13%	5%	3%	0%
ear_v14	31.6M	71%	12%	5%	12%	0%	31.9M	81%	12%	5%	2%	0%	31.4M	79%	13%	5%	3%	0%
embryo_27DAP	21.0M	74%	12%	7%	7%	0%	22.9M	62%	13%	7%	18%	0%	24.1M	73%	13%	7%	7%	0%
embryo_imbibedseed	51.2M	71%	13%	5%	10%	0%	56.8M	67%	13%	4%	16%	0%	29.5M	72%	13%	5%	10%	0%
endosperm_27DAP	53.6M	57%	6%	34%	3%	0%	43.5M	54%	5%	38%	2%	0%	44.1M	58%	5%	34%	3%	0%
kernel_14DAP	32.5M	75%	9%	11%	5%	0%	38.1M	76%	9%	12%	4%	0%	34.5M	71%	8%	17%	4%	0%
endosperm_14DAP	24.4M	75%	8%	14%	4%	0%	22.2M	76%	9%	13%	3%	0%	23.0M	69%	8%	18%	4%	0%

Figure S1b. Summary of read mapping statistics. For each tissue / genotype combination we show the number of read pairs (in millions) mapped to the maize B73 AGPv4 reference, and the proportion of reads that failed QC (failedQC), failed to map to the genome (Unmap), mapped in multiple locations (Map\_LowQual), mapped in high quality to intergenic regions (Unassigned) as well as reads assigned to genes.

		Pearsor	ı (upper right) and	Spearman (lower	r left) Correlation (	Coefficient	20000		
	auricle_v12	auricle_v12			blade_v12	blade_v12	92 0.96 coleoptile_tip	coleoptile_tip	
Rep1	BR010 0.98 0.99	BxM BR016 0.99 0.94	Mo17 BR013 0.98 0.98	BR001 1.00 0.98	BxM BR006 0.99 0.99	Mo17 BR003 1.00 1.00	B73 BR166 1.00 0.99	BxM BR172 0.99 0.98	
Rep2	0.99 BR011 0.97	0.99 BR017 0.92	0.99 BR014 0.97	0.99 BR002 0.98	0.99 BR008 0.99	0.99 BR005 0.99	0.99 BR167 1.00	0.99 BR173 0.99	
Rep3	0.99 0.98 BR012	0.98 0.97 BR018	0.99 0.98 BR015	0.99 0.99 BR004	0.99 0.99 BR009	0.99 0.99 BR007	0.99 0.99 BR168	0.99 0.99 BR174	
					embryo_27DAP	embryo_27DAP			
	coleoptile_tip Mo17	ear_v14 B73	ear_v14 BxM	ear_v14 Mo17	B73	BxM	embryo_27DAP Mo17	embryo_imbibedseed B73	
Rep1	BR169 1.00 1.00	BR046 0.99 0.99	BR052 0.99 1.00	BR049 0.99 0.99	BR142 0.99 0.99	BR148 0.99 0.99	BR145 1.00 0.99	BR184 0.92 0.93	
Rep2	0.99 BR170 1.00	0.99 BR047 1.00	0.99 BR053 0.99	0.99 BR050 0.99	0.99 BR143 0.99	0.99 BR149 0.99	0.99 BR146 0.99	0.96 BR242 0.99	
Rep3	0.99 0.99 BR171	0.99 0.99 BR048	1.00 0.99 BR054	0.99 0.99 BR051	0.99 0.99 BR144	0.98 0.98 BR150	0.98 0.98 BR147	0.96 1.00 BR243	
	embryo_imbibedseed BxM	embryo_imbibedseed Mo17	endosperm_14DAP B73	endosperm_14DAP BxM	endosperm_14DAP Mo17	endosperm_27DAP B73	endosperm_27DAP BxM	endosperm_27DAP Mo17	
Rep1	BR191 0.98	BR245 0.95 0.86	BR130 1.00 1.00	BR136 1.00 1.00	BR133 1.00 1.00	BR154 0.99 0.99	BR160 1.00 1.00	BR157 1.00 1.00	
Rep2	0.99 BR192	0.97 BR188 0.91	0.99 BR131 1.00	0.98 BR137 0.99	0.99 BR134 1.00	0.98 BR155 0.97	0.99 BR161 1.00	0.99 BR158 0.99	
Rep3		0.93 0.95 BR227	0.99 0.99 BR132	0.99 0.98 BR138	0.99 0.99 BR135	0.99 0.98 BR156	0.99 0.99 BR162	0.99 0.98 BR159	
	flagleaf_0DAP	flagleaf_0DAP	flagleaf_0DAP	floret_0DAP	floret_0DAP	floret_0DAP	husk_0DAP	husk_0DAP	
Pon1	B73	BxM	Mo17	B73	BxM	Mo17	B73	BxM	
Rep1	BR100 1.00 1.00	BR106 1.00 0.99	BR103 1.00 1.00	BR091 0.97 0.99	BR097 1.00 0.99	BR094 0.98 0.98	BR073 0.99 0.98	BR079 0.98 0.98	
Rep2	0.99 BR101 1.00	0.99 BR107 1.00	0.99 BR104 1.00 0.99 0.99 BR105	0.99 BR092 0.97 0.99 0.98 BR093	0.99 BR098 0.99 0.99 0.99 BR099	0.97 BR095 0.95 0.99 0.97 BR096	0.99 BR074 0.99 0.99 0.99 BR075	0.99 BR080 0.97 0.98 0.98 BR081	
Rep3	0.99 0.99 BR102	0.99 0.99 BR108							
	husk_0DAP Mo17	internode_v12 B73	internode_v12 BxM	internode_v12 Mo17	kernel_14DAP B73	kernel_14DAP BxM	kernel_14DAP Mo17	radicle_root B73	
Rep1	BR076 0.93 0.92	BR028 0.95 0.99	BR034 0.98 0.98	BR032	BR118 1.00 1.00	BR124 1.00 1.00	BR121 1.00 0.99	BR175 0.99 0.99	
Rep2	0.95 BR077 0.99	0.97 BR030 0.98	0.99 BR035 0.99	0.97 BR031 0.97	0.99 BR119 1.00	0.99 BR125 1.00	1.00 BR122 1.00	0.99 BR176 0.99	
Rep3	0.95 0.98 BR078	0.98 0.99 BR029	0.98 0.99 BR036	0.94 0.98 BR033	0.99 0.99 BR120	0.99 0.99 BR126	0.99 0.99 BR123	0.99 0.99 BR177	
	radicle_root BxM	radicle_root Mo17	root_0DAP B73	root_0DAP BxM	root_0DAP Mo17	seedlingleaf_11DAS B73	seedlingleaf_11DAS BxM	seedlingleaf_11DAS Mo17	
Rep1	BR181 0.98 0.98	BR178 0.99 0.98	BR109 0.98 0.99	BR115 0.99 0.97	BR112 0.99 0.99	BR193 1.00 1.00	BR199 1.00 1.00	BR196 0.99 1.00	
Rep2	0.98 BR182 0.98	0.99 BR179 0.97	0.99 BR110 0.98	0.99 BR116 0.99	0.99 BR113 0.99	0.99 BR194 1.00	0.99 BR200 0.99	0.99 BR197 1.00	
Rep3	0.99 0.98 BR183	0.99 0.98 BR180	0.99 0.99 BR111	0.98 0.99 BR117	0.99 0.99 BR114	0.99 0.99 BR195	0.98 0.98 BR201	0.99 0.99 BR198	
	edlingmeristem_11DA	edlingmeristem_11DA	edlingmeristem_11DA	seedlingroot_11DAS	seedlingroot_11DAS	sheath_v12	sheath_v12	sheath_v12	
Rep1	B73 BR211 0.99 0.96	BxM BR217 1.00 0.99	Mo17 BR214 0.99 0.99	B73 BR202 0.99 0.99	BxM BR208 0.99	BR019 0.99 0.96	BxM BR025 <b>0.91 0.96</b>	Mo17 BR022 0.99 0.98	
Rep2	0.99 BR212 0.96	0.99 BR218 0.99	0.99 BR215 0.99	0.99 BR203 0.98	0.99 BR209	0.99 BR020 0.97	0.92 BR026 0.96	0.99 BR023 0.98	
Rep3	0.95 0.96 BR213	0.99 0.99 BR219	0.99 0.99 BR216	0.99 0.99 BR204	0.33 BR203	0.98 0.98 BR021	0.95 0.98 BR027	0.99 0.98 BR024	
	silk_0DAP	silk_0DAP	silk 0DAP	spikelets_0DAP	spikelets_0DAP	spikelets_0DAP	tassel_v12	tassel_v12	
	B73	BxM	Mo17	B73	BxM	Mo17	B73	BxM	
Rep1	BR055 0.99 0.99	BR061 0.99 0.99	BR058 0.98 0.97	BR064 0.98 0.98	BR070 0.99 0.99	BR067 0.97 0.97	BR037 0.99 0.97	BR043 0.90 0.91	
	0.99 BR056 1.00	0.99 BR062 0.99	0.99 BR059 0.99	0.99 BR065 0.99	0.99 BR071 0.99	0.98 BR068 0.99	0.99 BR038 0.98	0.97 BR044 0.88	
Rep3	0.99 0.99 BR057	0.99 0.99 BR063	0.98 0.99 BR060	0.99 0.99 BR066	0.99 0.99 BR072	0.98 0.99 BR069	0.98 0.98 BR039	0.96 0.97 BR045	
	tassel_v12 Mo17	tasselstem_0DAP B73	tasselstem_0DAP BxM	tasselstem_0DAP Mo17					
Rep1	BR040 0.95 0.97	BR082 <b>0.87 0.97</b>	BR088 0.96 0.96	BR085 0.99 0.98					
Rep2	0.98 BR041 0.95	0.97 BR083 0.84	0.99 BR089 0.98	0.99 BR086 0.99					
Rep3	0.98 0.98 BR042	0.95 0.92 BR084	0.99 0.99 BR090	0.97 0.97 BR087					

Figure S2. Consistency between biology replicates of each sample. Each panel shows a heatmap of the correlations between biological replicates for each tissue-genotype combination. These show both the Pearson (upper right half) and Spearman (lower left half) correlation values of gene expression levels (FPKMs) between each pair of replicates. The subset of 14,216 genes with CPM >1 in at least 90% samples were used in this analysis.

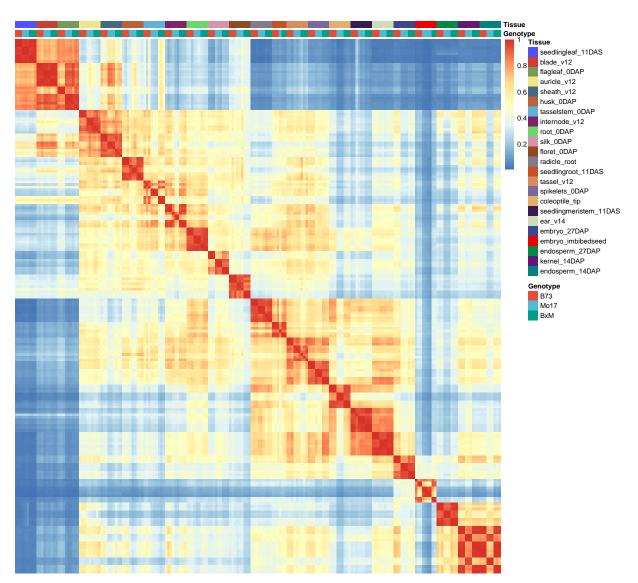


Figure S2b. Distance matrix heatmap between all samples. Pearson correlation coefficients based on gene expression levels (FPKMs) between each pair of samples were shown as a heatmap. The subset of 14,216 genes with CPM >1 in at least 90% samples were used in this analysis.

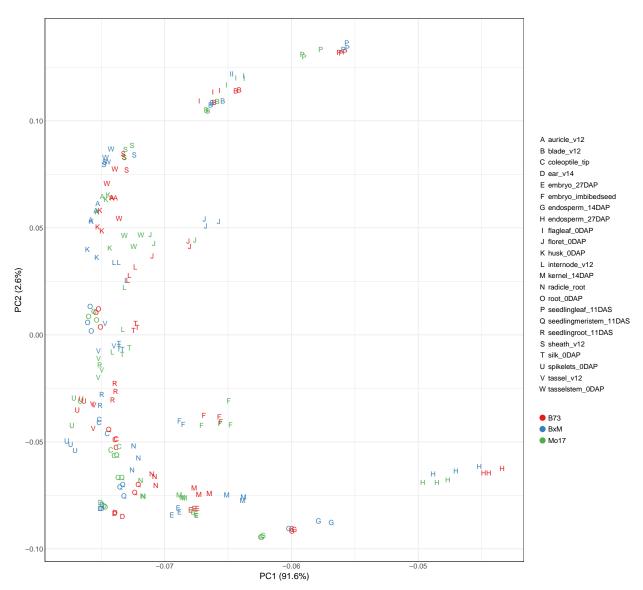


Figure S3. Principal component analysis of gene expression in 23 tissues for B73, Mo17 and the F1 hybrid. A set of 17,135 genes with CPM >1 in at least 170 out of 204 samples were used for this analysis. Clustering was done using the log2 transformed CPM values and the "prcomp" function in R with no centering or scaling. The color indicates the genotypes while the symbols indicate the tissue type (key shown on the left).

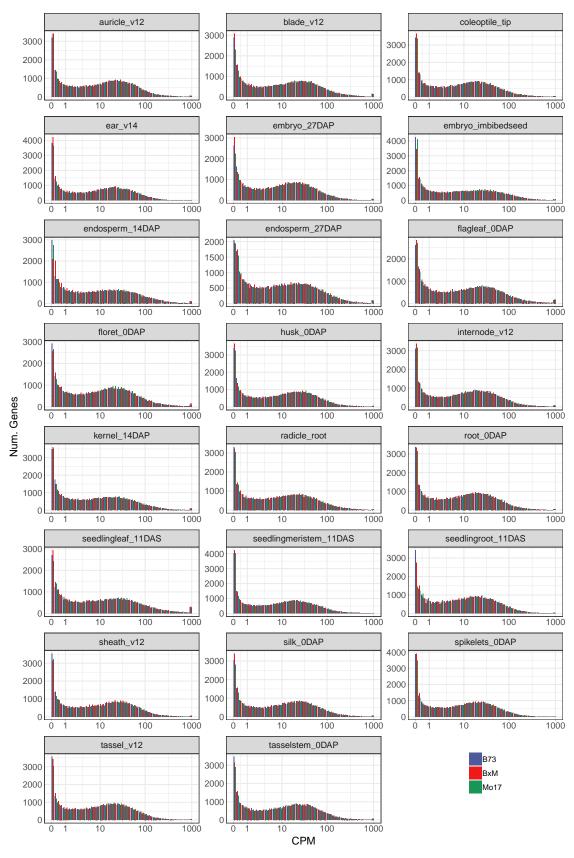


Figure S4. The distribution of gene CPM (Counts per Million) values is show for B73, Mo17

and hybrid in each tissue. The expression values are normalized using the TMM normalization approach implemented in the edgeR (see methods).

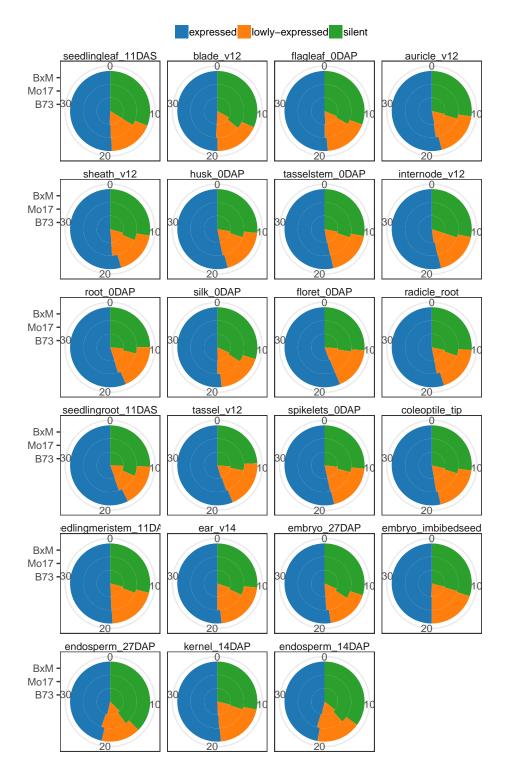


Figure S4b. Number of silent (CPM = 0), lowly-expressed (0<CPM<1) and (moderately) expressed (CPM >= 1) genes for B73, Mo17 and F1 in each tissue.

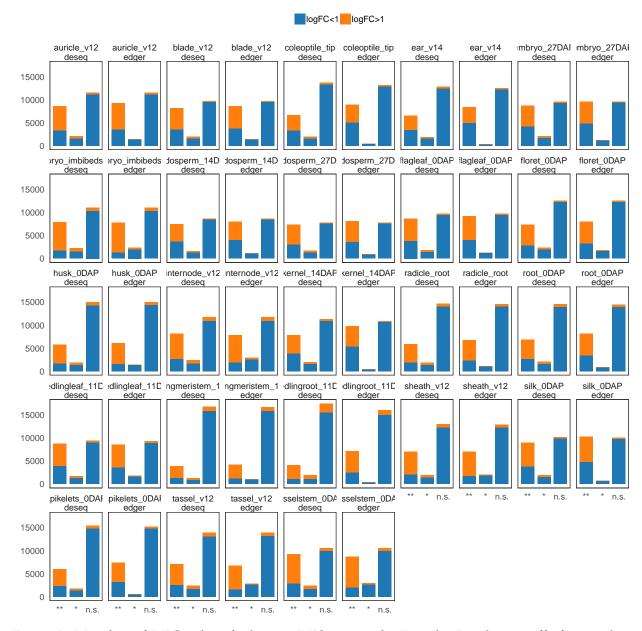


Figure X. Number of DEGs identified using DESeq2 or edgeR under P-value cutoff of .01 and .5 in each of the 23 tissues.

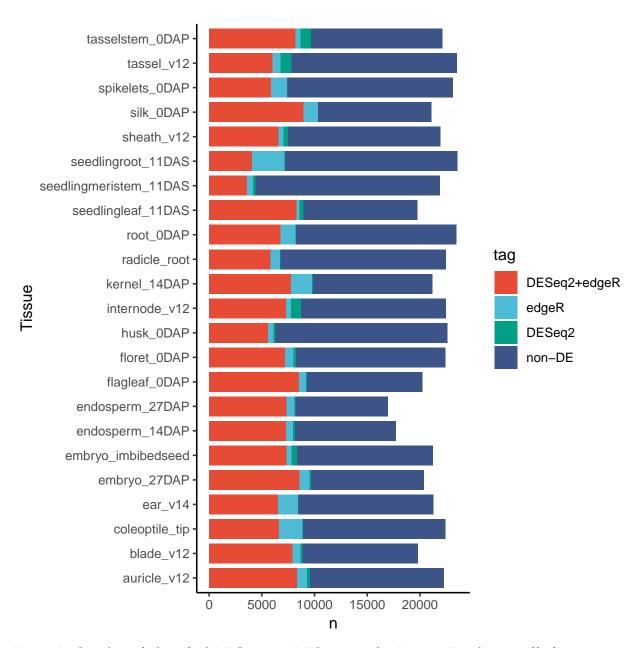


Figure X. Overlap of identified DEGs using DESeq2 or edgeR using P-value cutoff of .01.

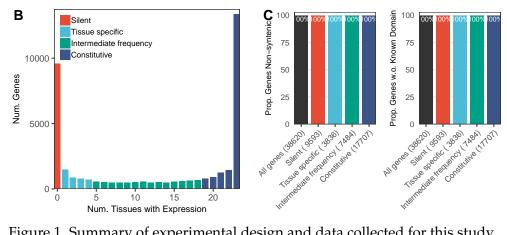


Figure 1. Summary of experimental design and data collected for this study.

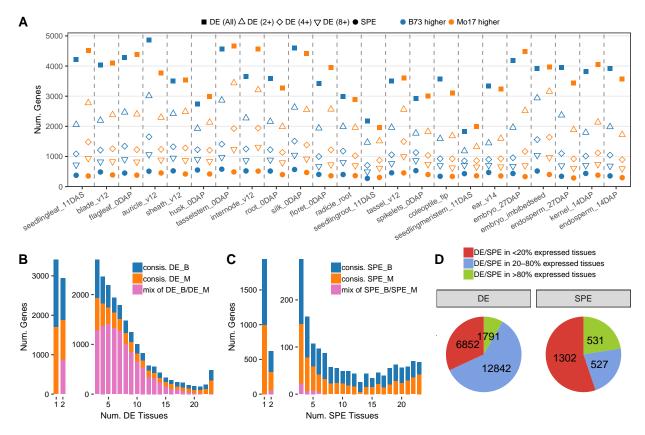


Figure 2. Analysis of developmental dynamics of differential expression.

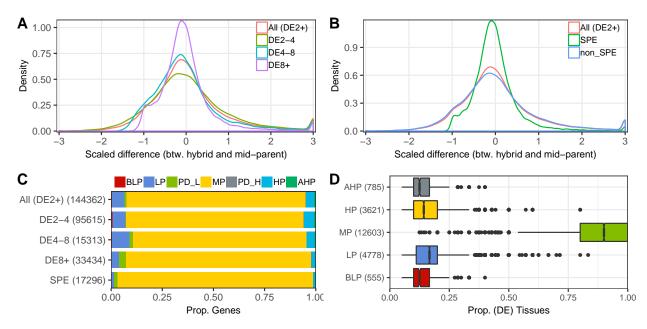


Figure 3. Classification of non-additive expression patterns.

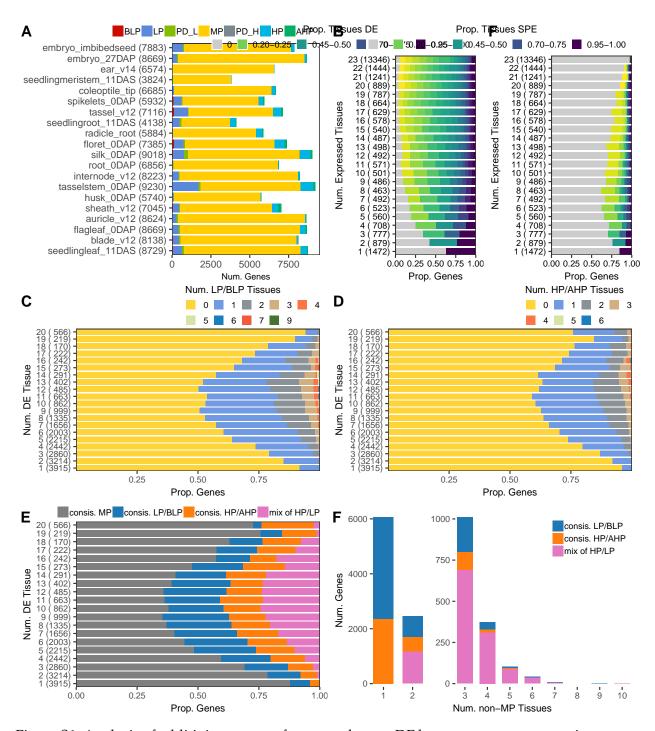


Figure S6. Analysis of additivity patterns for genes that are DE between parents across tissues.