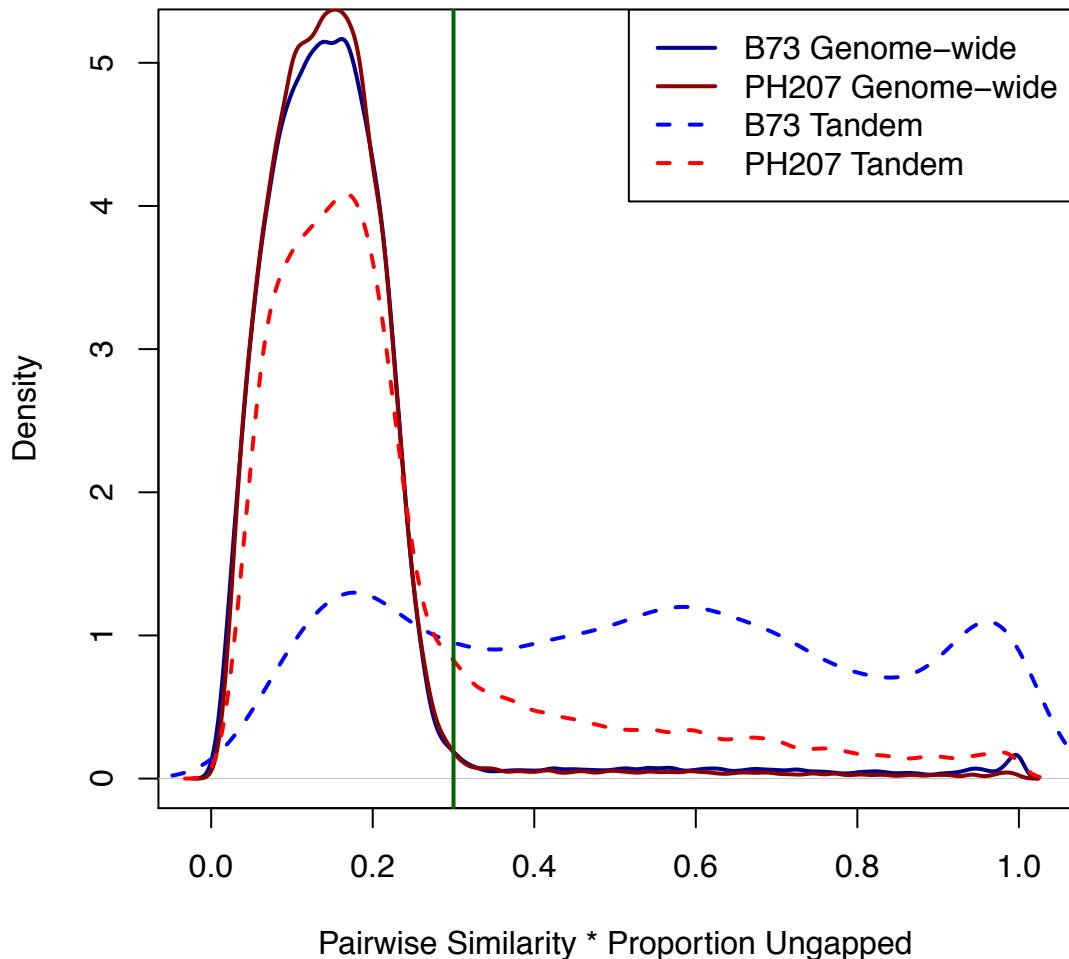
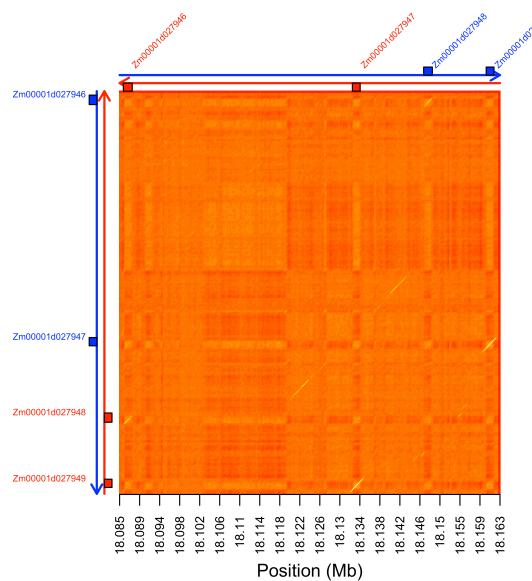


## Adjusted Pairwise Similarity



**Supplementary Fig. 1.** Weighted pairwise similarity distribution for adjacent genes in B73 and PH207. Solid lines are from all pairs of adjacent genes in the genome and the dashed lines are from pairs of adjacent genes defined as tandem duplicates from raw CoGe output. Green line at 0.3 marks the threshold used to define tandem duplicate genes for downstream analysis.

- 1: {**5** **2**} {**7** **8**} {**3** **6**} {**9** **4** **1**} {**13** **14**}
- 2: {**2** **5**} {**7** **8**} {**3** **6**} {**1** **4** **9**} {**13** **14**}
- 3: {**1** **4** **9**} {**2** **5**} {**3** **6**} {**7** **8**} {**13** **14**}
- 4: {**1** **4** **9**} {**2** **5**} {**3** **6**} {**7** **8**}
- 5: {**1** **4** **9**} {**2** **5**} {**3** **6**}
- 6: {**1** **2** **3** **4** **5** **6**} — **9**
- Putative cassette**

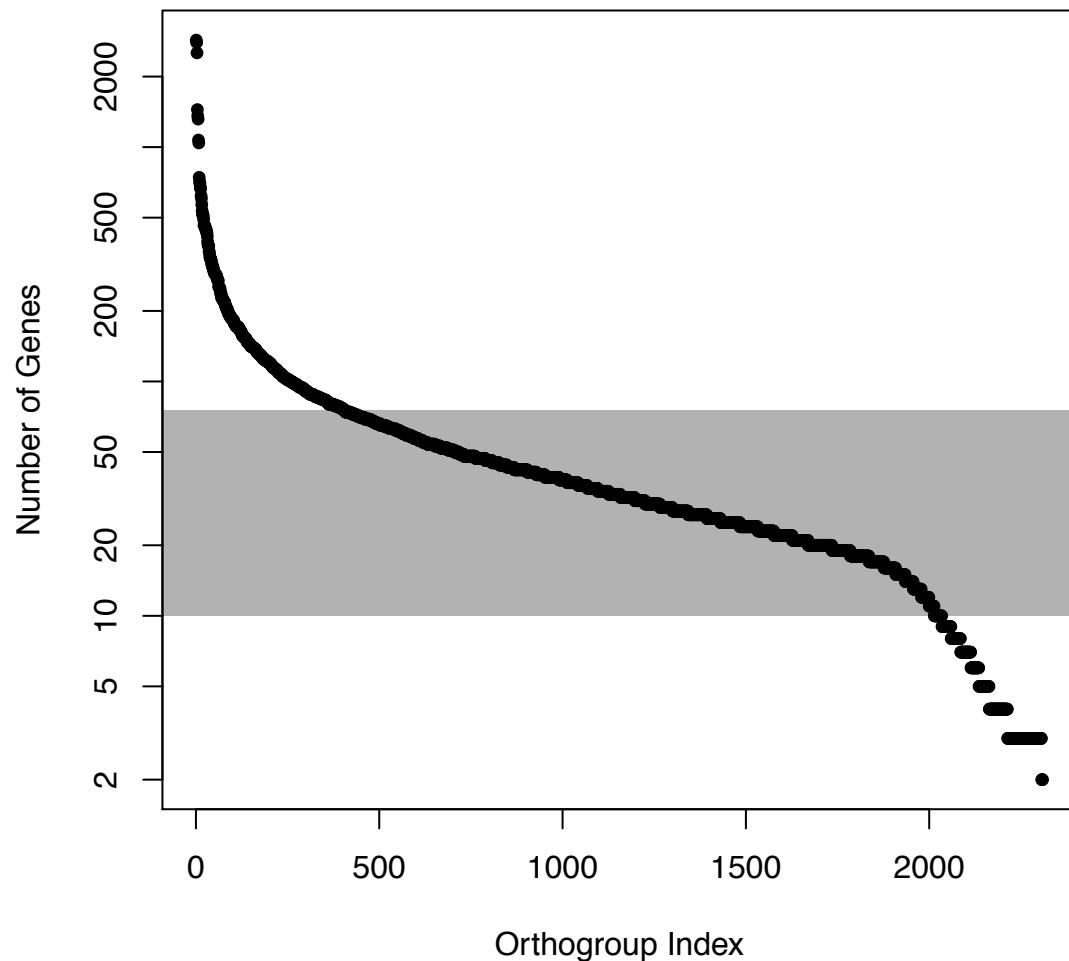


### Algorithm:

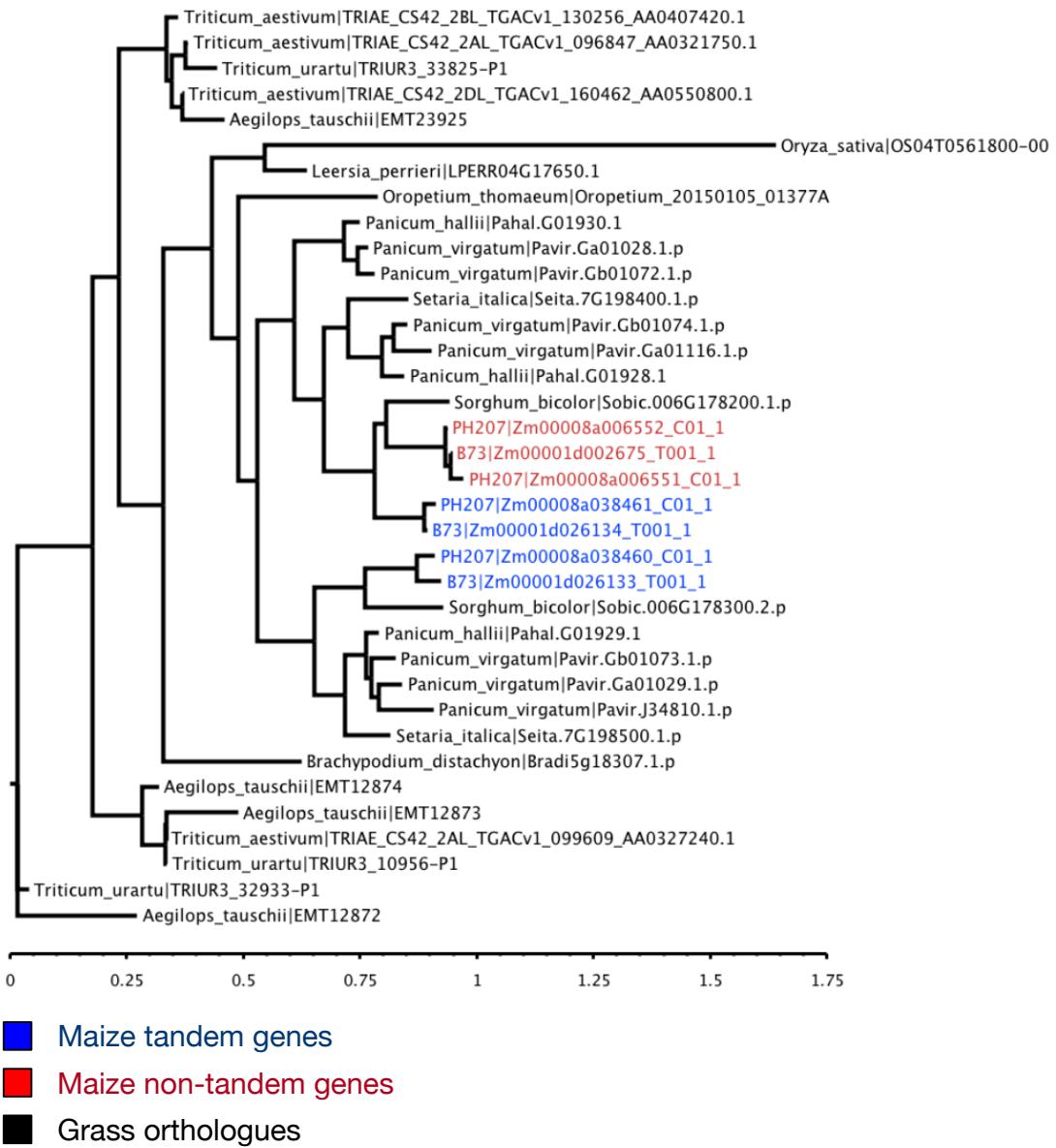
- 1) Identify tandem duplicate clusters
- 2) Sort within clusters by coordinate
- 3) Sort clusters by leftmost coordinate
- 4) Identify groups of overlapping clusters
- 5) Identify groups of non-nested clusters

**Supplementary Fig. 2.** Tandem duplicate gene cassette identification. Similarity heatmap on right shows an example tandem duplicate gene cassette in which the off-diagonal heat (yellow) shows high similarity among genes within the cassette.

### Distribution of Orthogroup Sizes with Maize Tandems



**Supplementary Fig. 3.** Distribution of orthologous group sizes as defined by OrthoFinder. Grey box (size 10 to 75) indicates orthogroups that were used in downstream PAML analysis.



120 tandem duplicate clusters tested

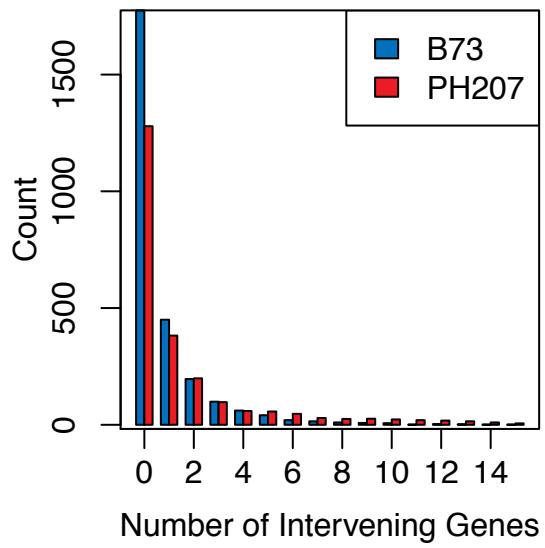
48.3% Grass = **Maize** = Tandem

25.8% Grass != **Maize** = Tandem

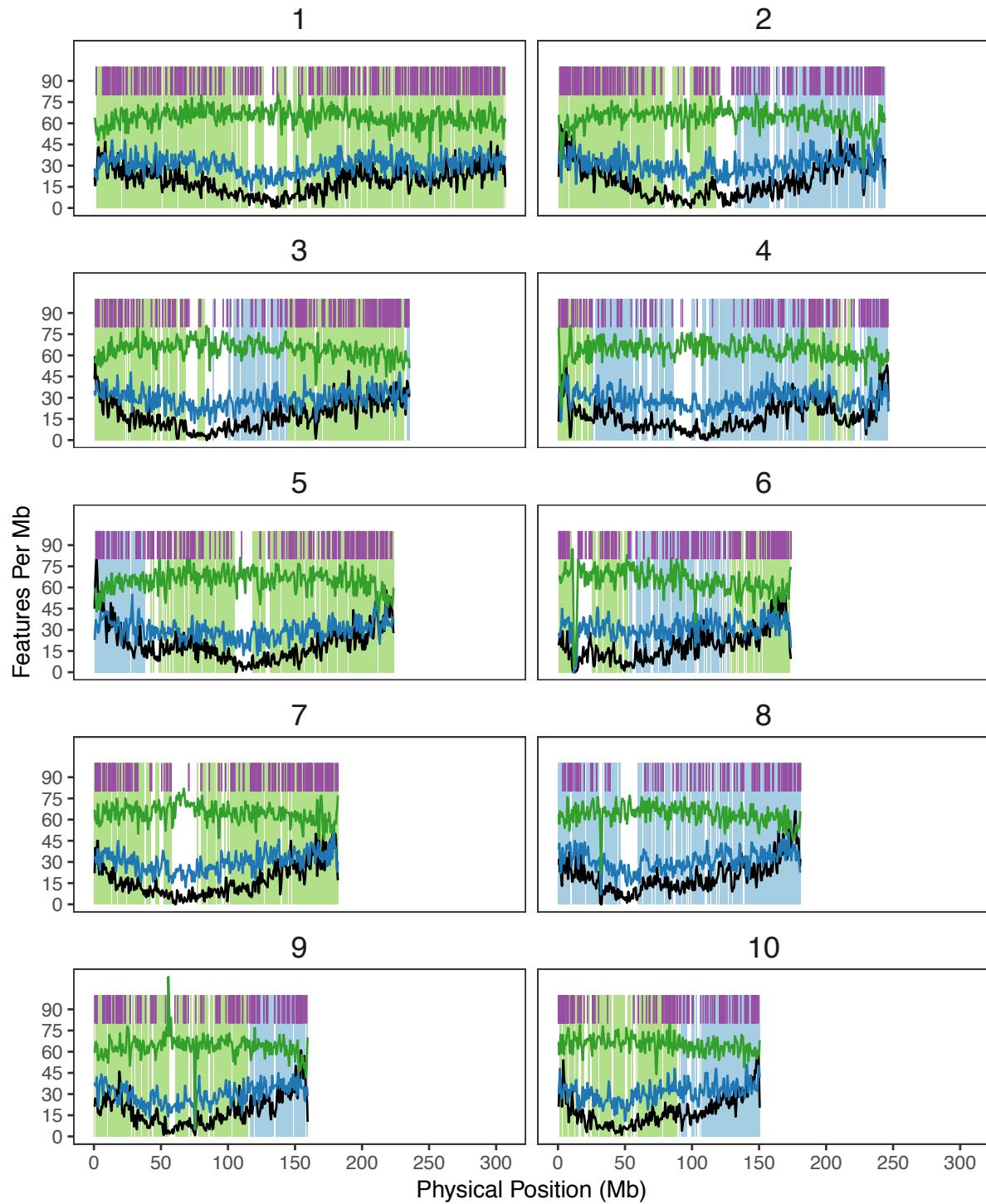
5.0% Grass = **Maize** != Tandem  
20.8% Grass != **Maize** != Tandem

} 31 tandem duplicates where **Maize** != Tandem  
10 evolving under stronger constraint  
7 evolving under weaker constraint  
14 with dS too small to test

**Supplementary Fig 4.** Example marked input tree for PAML relative rates analysis. Orthologous groups were defined using OrthoFinder.

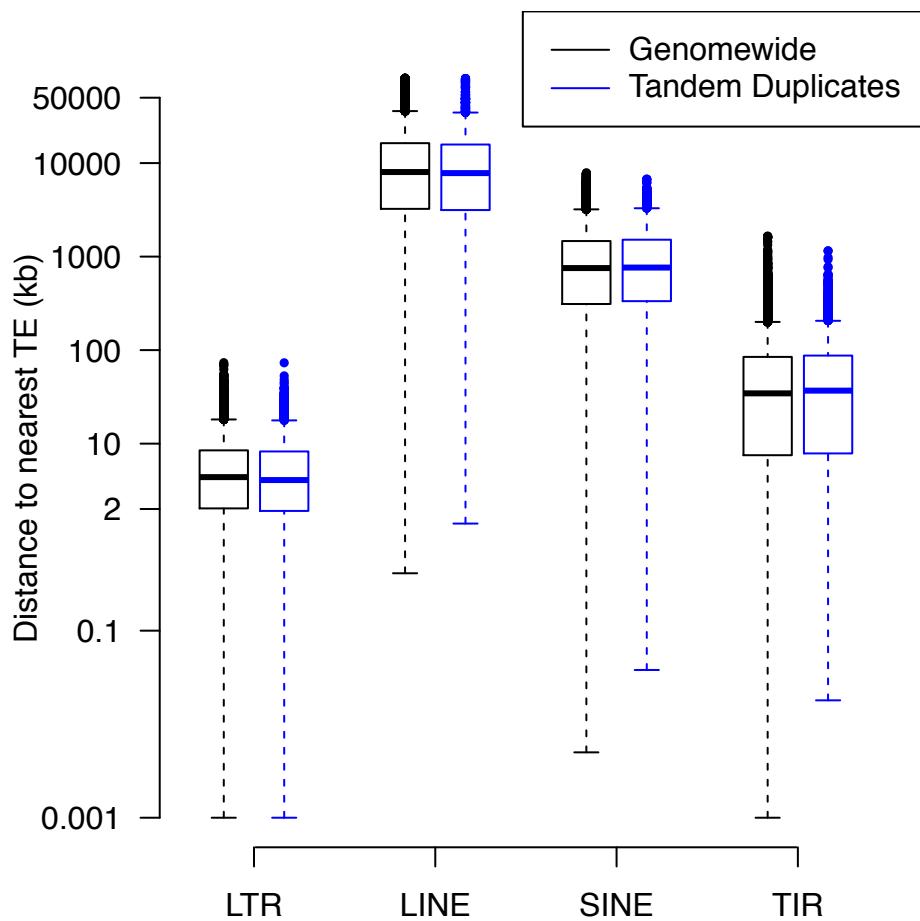


**Supplementary Fig. 5.** Number of intervening genes in tandem duplicate gene cluster. Genes that are directly adjacent have an intervening gene number of zero.



**Supplementary Fig. 6.** Genomic locations of maize tandem duplicates for all chromosomes in B73. Purple ticks show tandem duplicates. Black line shows gene density, dark grey line shows RNA transposable element density, light grey line shows DNA transposable elements per Mb. Subgenome 1 is shown in green shading and subgenome 2 is shown in blue shading.

## Distances From B73 Tandem Duplicates to Nearest TE



**Supplementary Fig. 7.** Distance to nearest transposable element (upstream or downstream) for B73 tandem duplicate genes.