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Supplemental information

**Genomic imbalance modulates transposable element expression in
maize**

**Hua Yang, Xiaowen Shi, Chen Chen, Jie Hou, Tieming Ji, Jianlin Cheng, and James A.
Birchler**

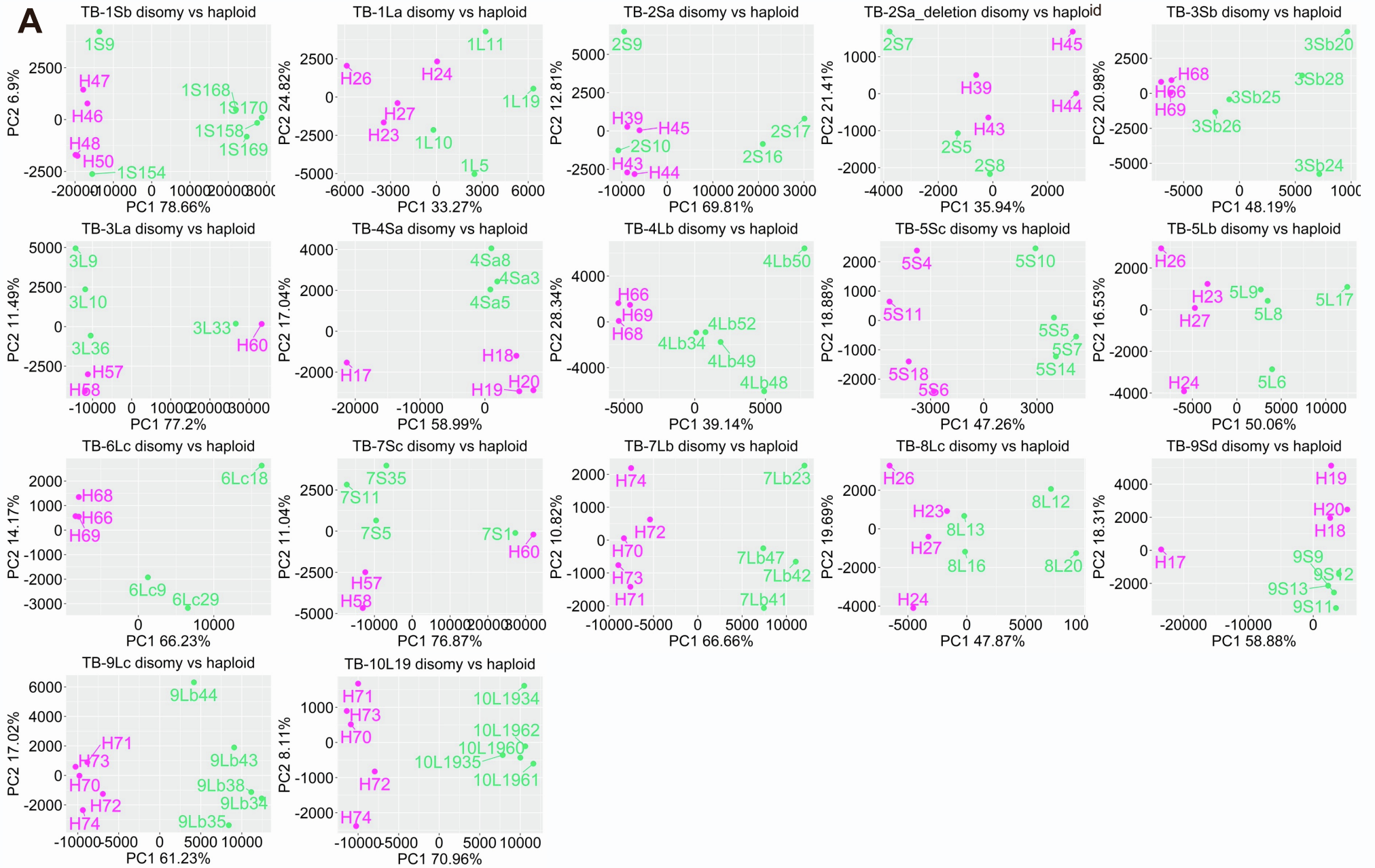
Supplemental information

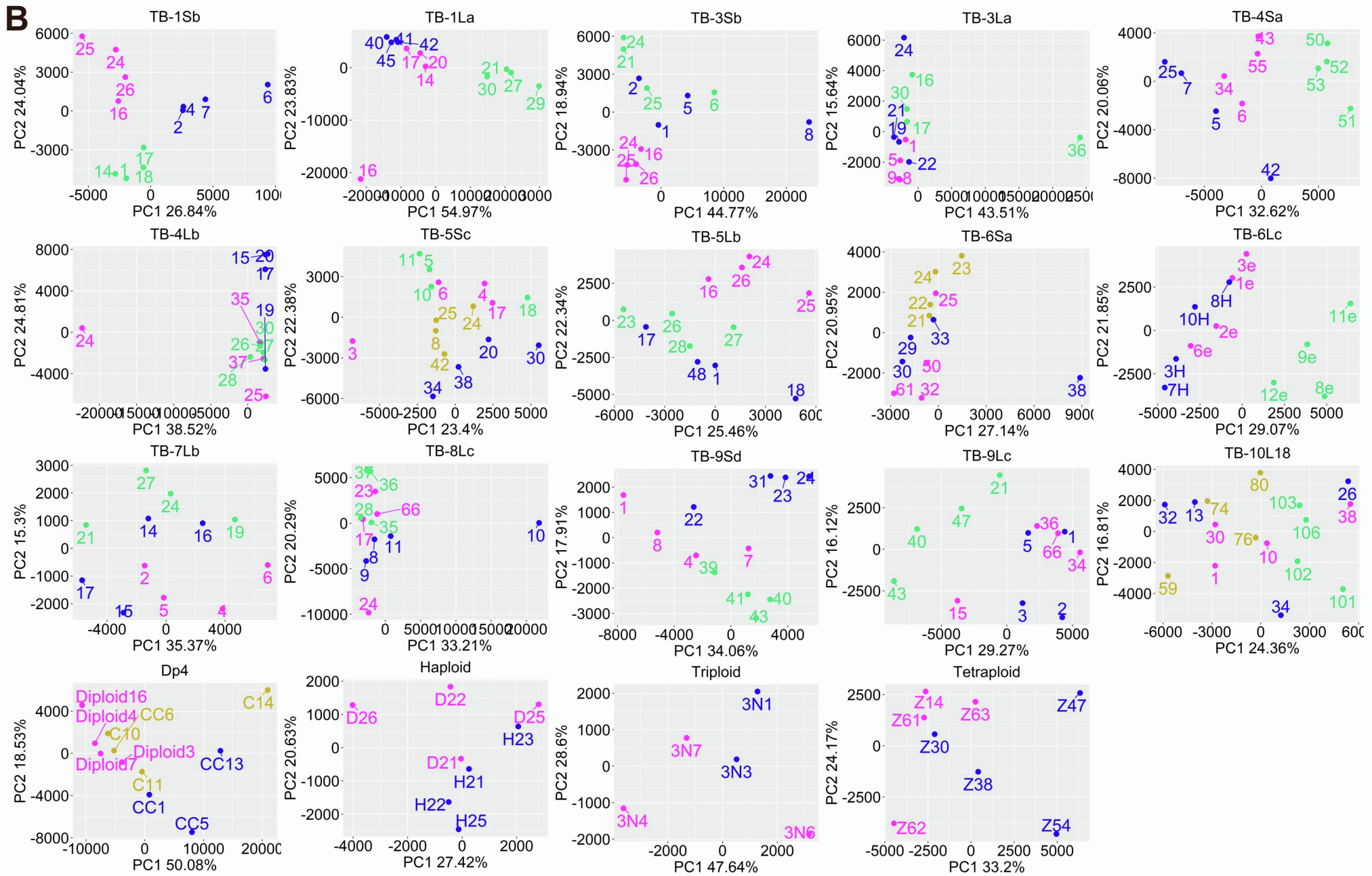
Genomic imbalance modulates transposable element expression in maize

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This PDF file includes: Supplemental Figures 1-10

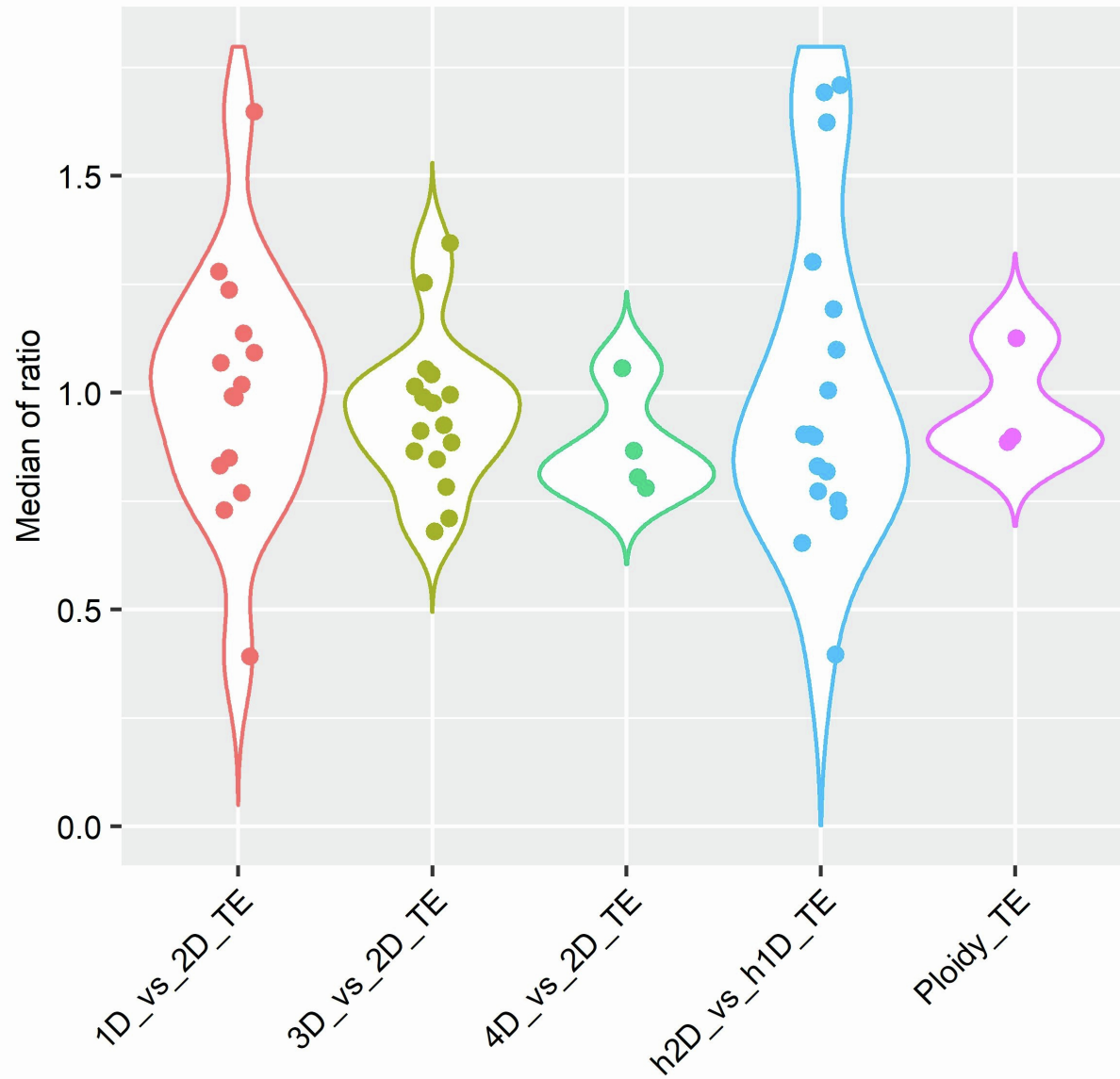
Other supplemental information for this manuscript includes the following: Supplemental Data sets 1-7

A



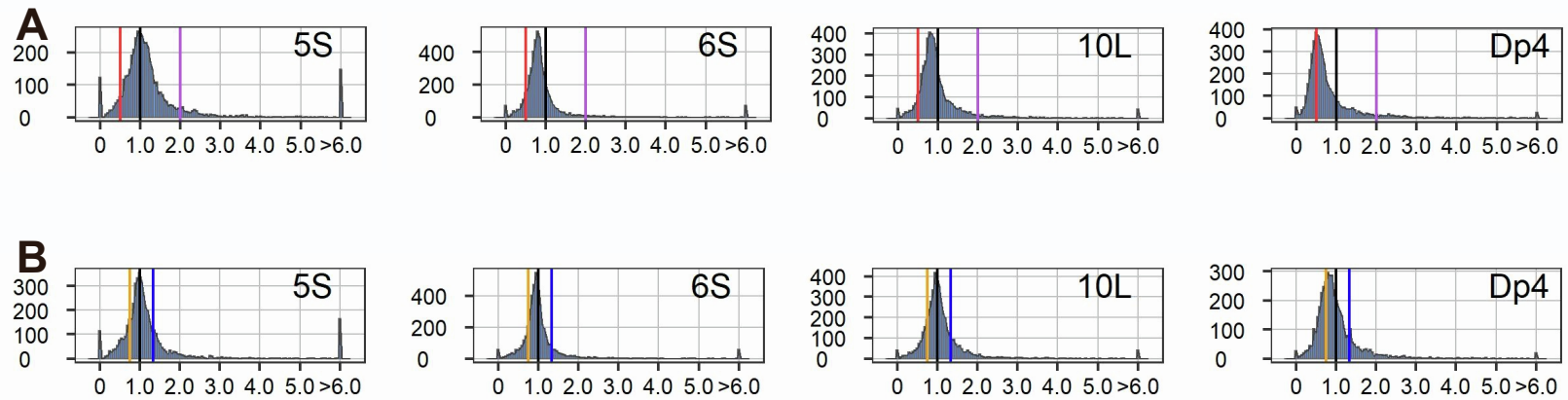
Supplementary Figure 1. PCA plots

A PCA of all biological replicates in each respective group comparison using the normalized counts is shown. **A**, In the disomic data comparison, the biological replicates of disomies were depicted as green, while the haploid controls were shown magenta. **B**, PCA of the diploid aneuploidy and ploidy series. In the diploid aneuploidy, diploid controls are depicted as magenta, monosomy is shown as green, trisomy is blue, and yellow is tetrasomy. In the ploidy series, diploid control is shown as magenta and haploid, triploid, or tetraploid were depicted as blue.



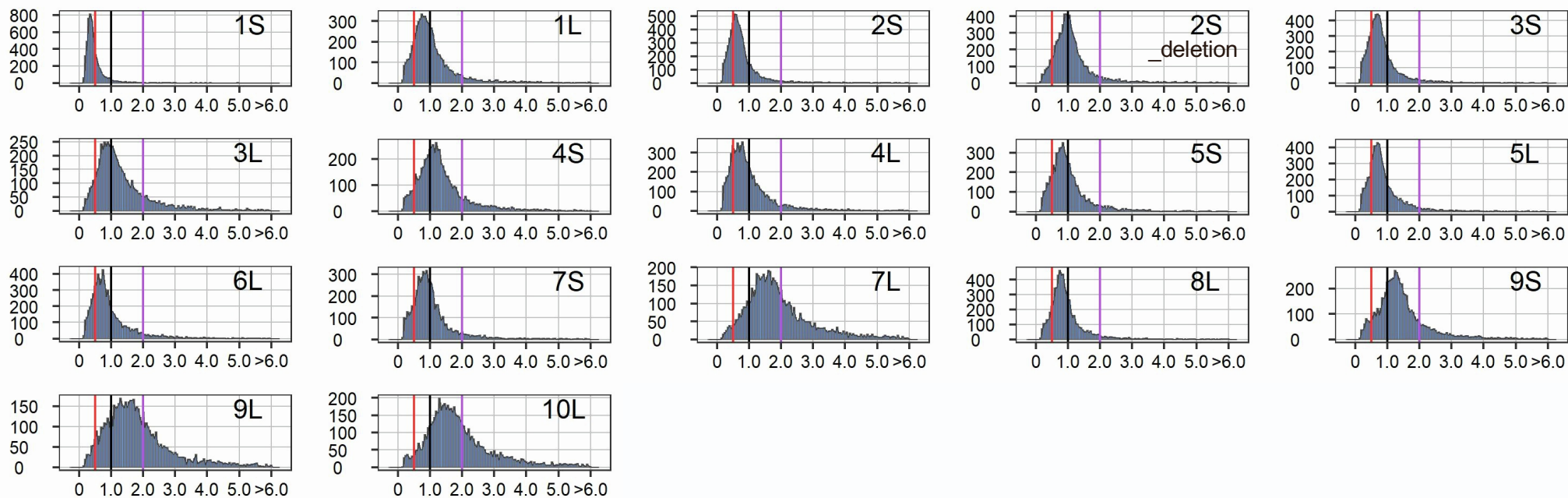
Supplemental Figure 2. Median of aneuploidy and ploidy series.

The dots are the median value of the ratios from each experimental comparison. The x-axis refers to different aneuploidy and ploidy series. The y axis notes the median value. The median was calculated as described in *Material and Methods*.



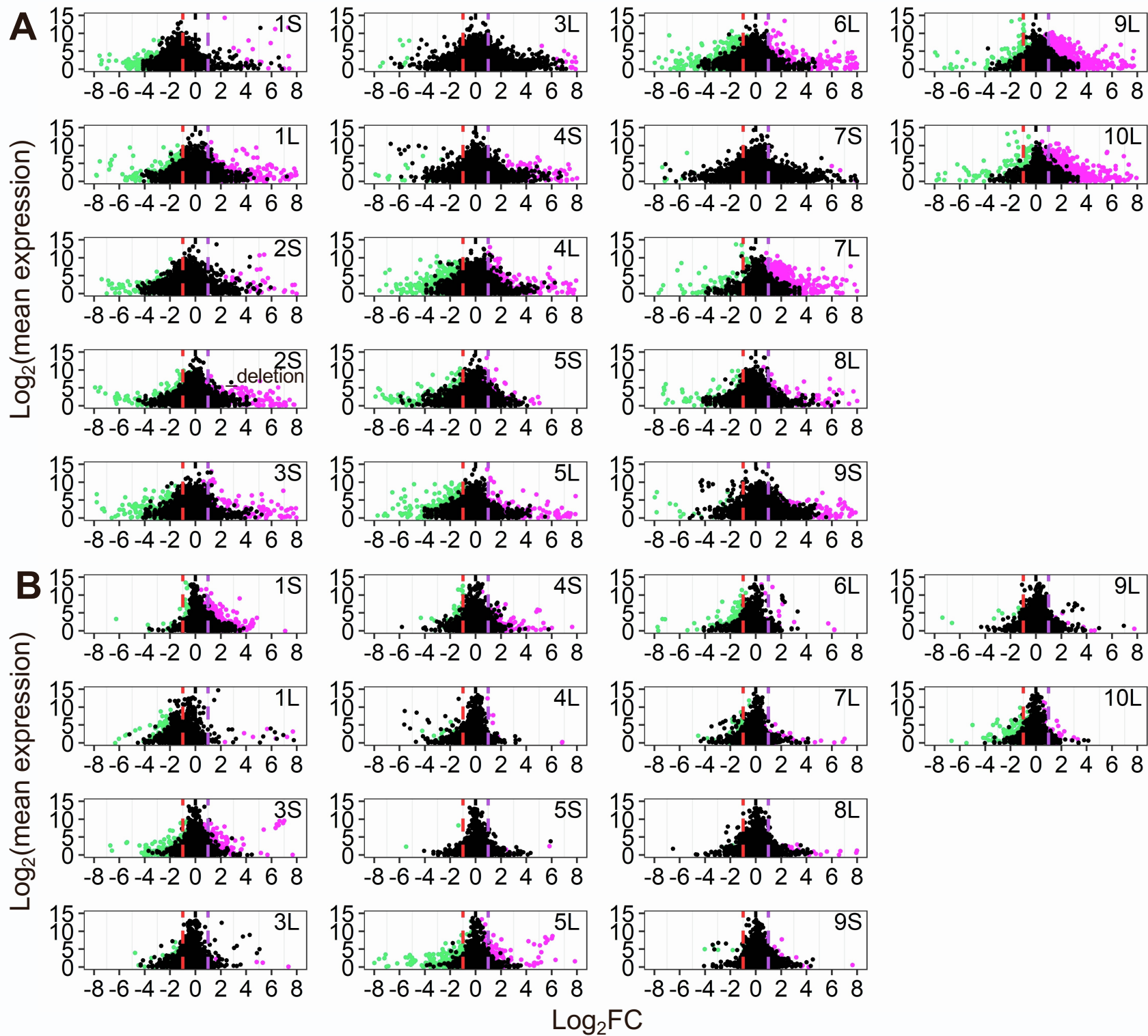
Supplemental Figure 3. Ratio distribution of tetrasomy.

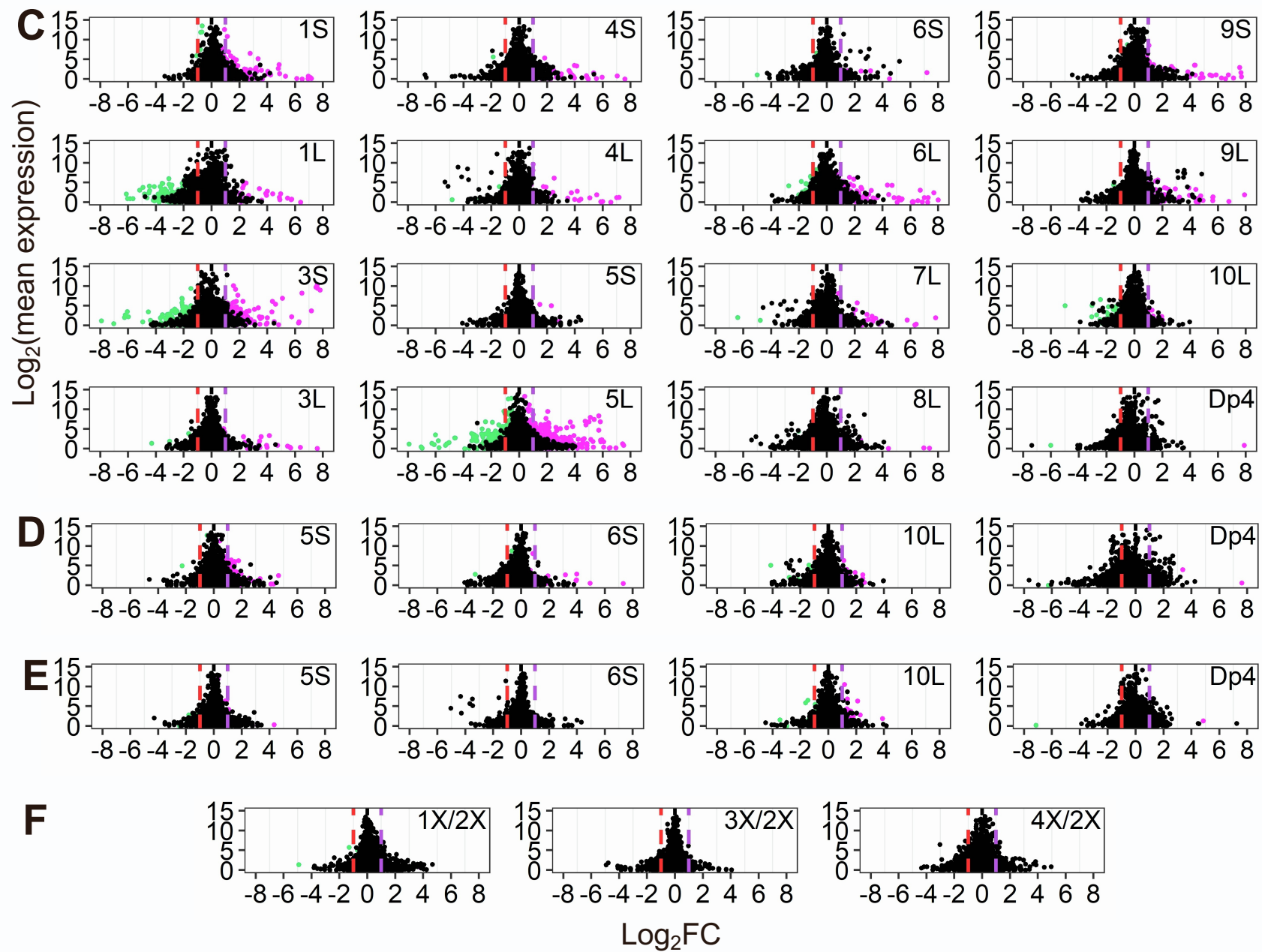
Ratio distributions of TE expression in 4D/2D (**A**) and 4D/3D (**B**). Ratio distributions were plotted as described in Figure 2. The vertical lines were depicted as purple (2) and red (0.5) in 4D/2D. While in 4D/3D, ratio values are demarcated with labeled vertical lines in blue (1.33) and yellow (0.75).



Supplemental Figure 4. Ratio distribution of h2D/h1D without outlier ratios.

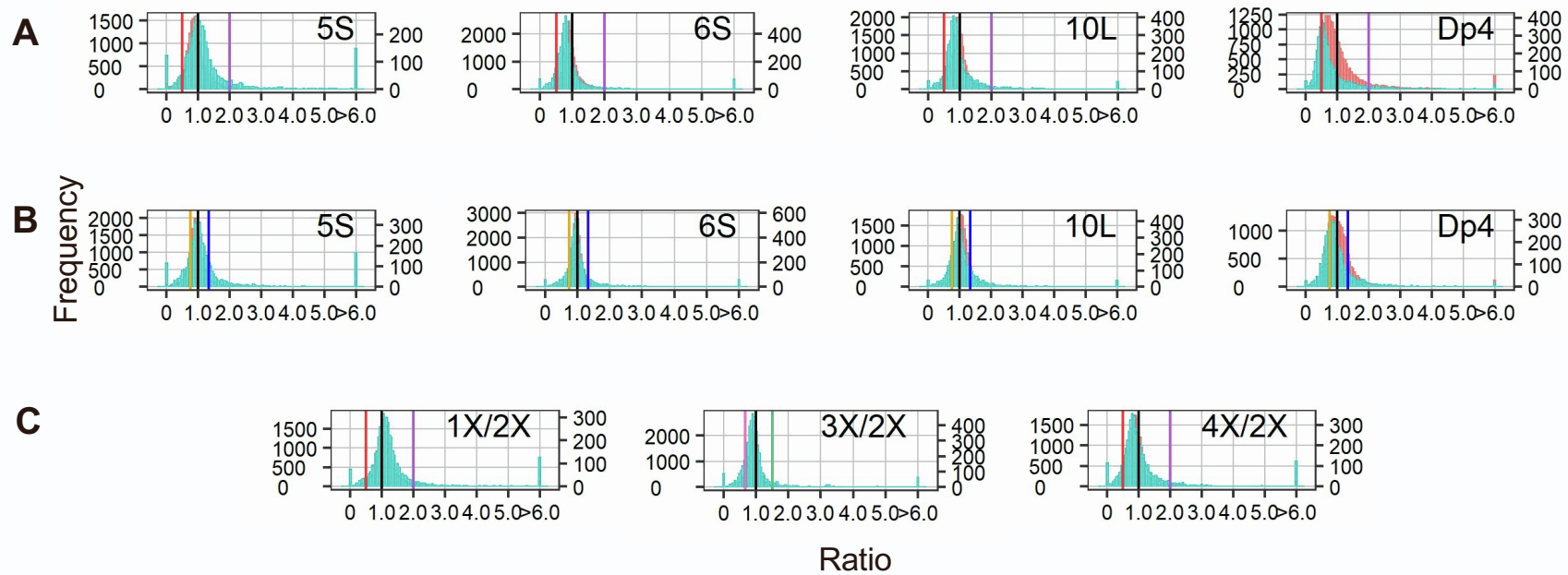
Ratio distributions were plotted as described in Figure 2. The only difference is that the ratios $\leq 1/6$ and ≥ 6 were excluded from the distributions.





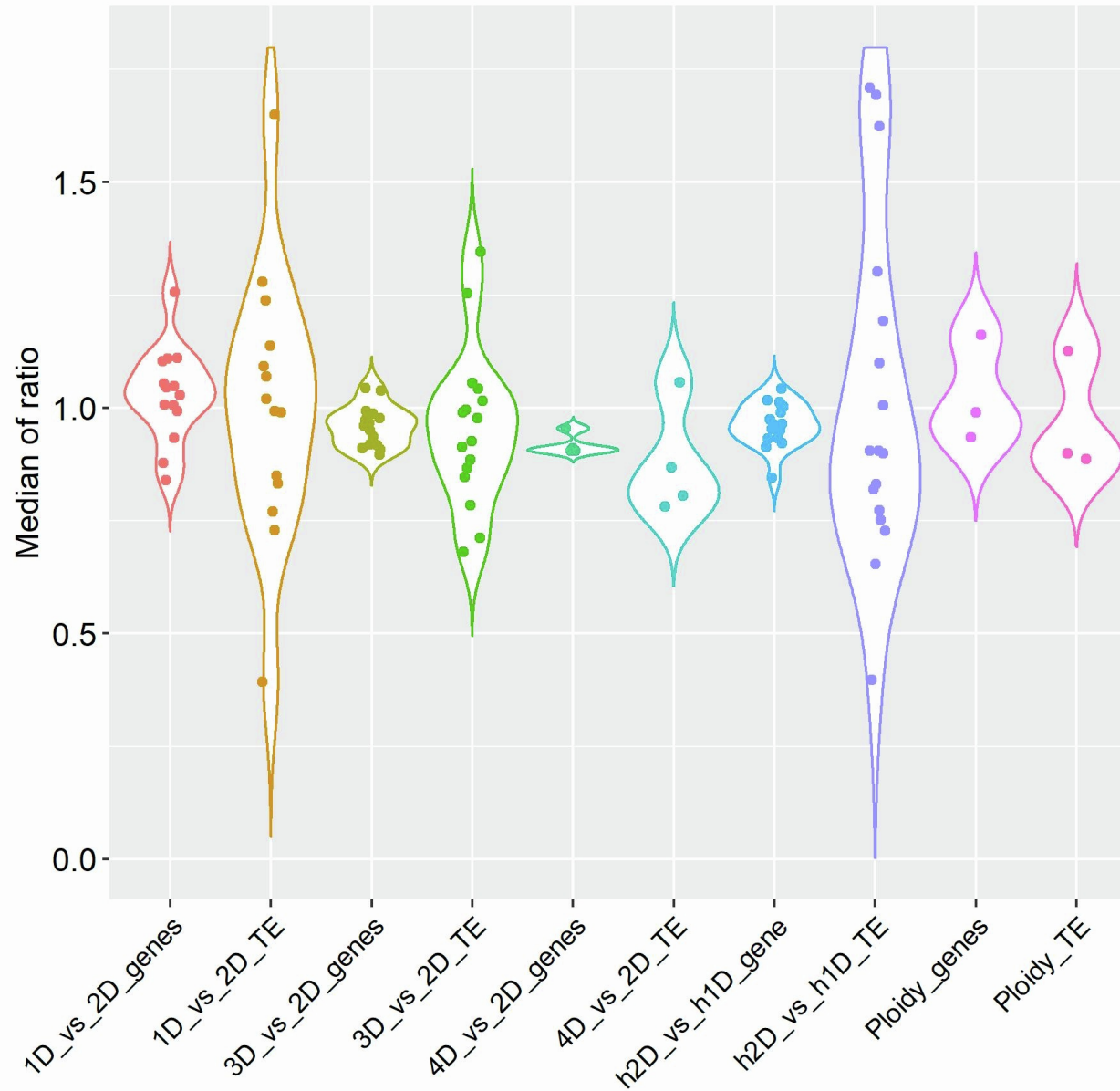
Supplemental Figure 5. Scatter plots of differential TE expression.

Scatter plots of significant differential expression (using edgeR) for each TE comparing experimental to control are shown. The scatter plot analysis was used as a complement to ratio distributions to illustrate both the magnitude of deviation from the control and the magnitude of expression difference in h2D/h1D (**A**), 1D/2D (**B**), 3D/2D (**C**), 4D/2D (**D**), 4D/3D (**E**), and ploidy series (**F**). Lowly expressed TEs were filtered using the same criteria as in the ratio distributions. The x axis represents log₂ fold change of the experimental to the control and the y axis shows the mean of normalized counts of the experimental and control. Data points with an FDR (*q* value) < 0.05 and a corresponding log fold change of experimental to control more than 0 were depicted in magenta, while points with a *q* value < 0.05 and a corresponding log fold change less than 0 were depicted in green. Otherwise, they were designated in black. Three designated ratio values, 0.5, 1.0 and 2.0, were depicted in red, black and purple vertical dashed lines, respectively.



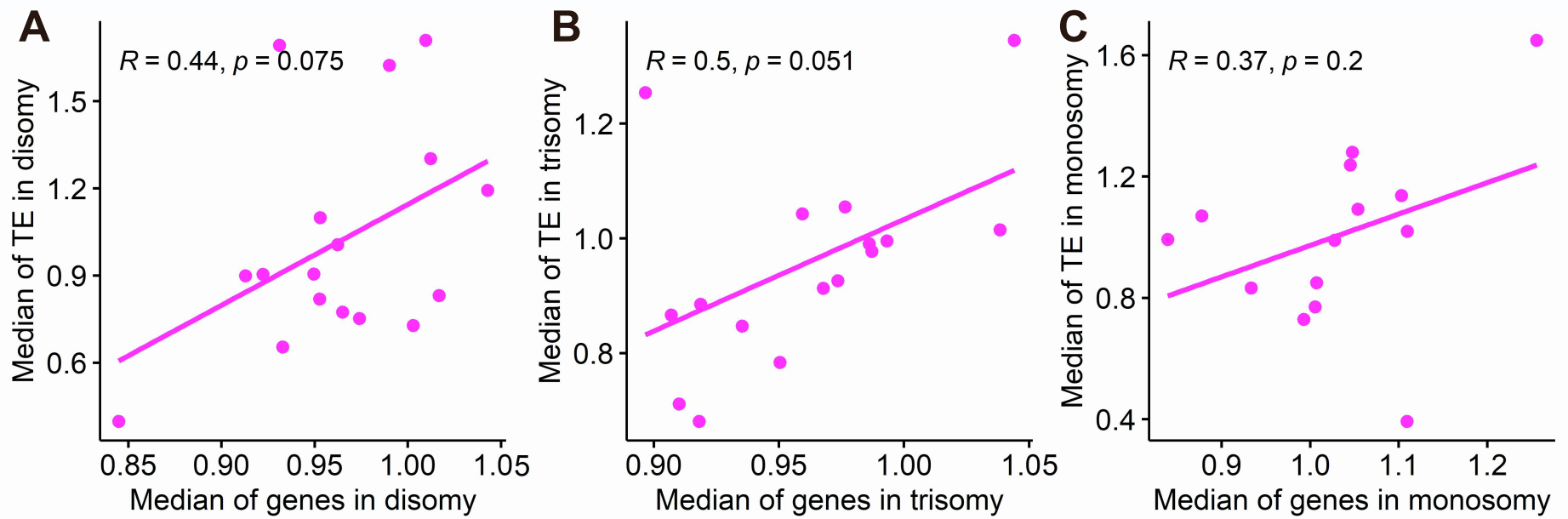
Supplemental Figure 6. Overlapping plots for genes and TEs in tetrasomy and ploidy series.

Ratio distributions were plotted as described in Figure 2. **A**, 4D/2D. **B**, 4D/3D. **C**, ploidy series. The ratio distributions for genes and TEs were depicted as red and cyan. The left y-axis is the number of genes in each bin and the right y-axis is the TE number.



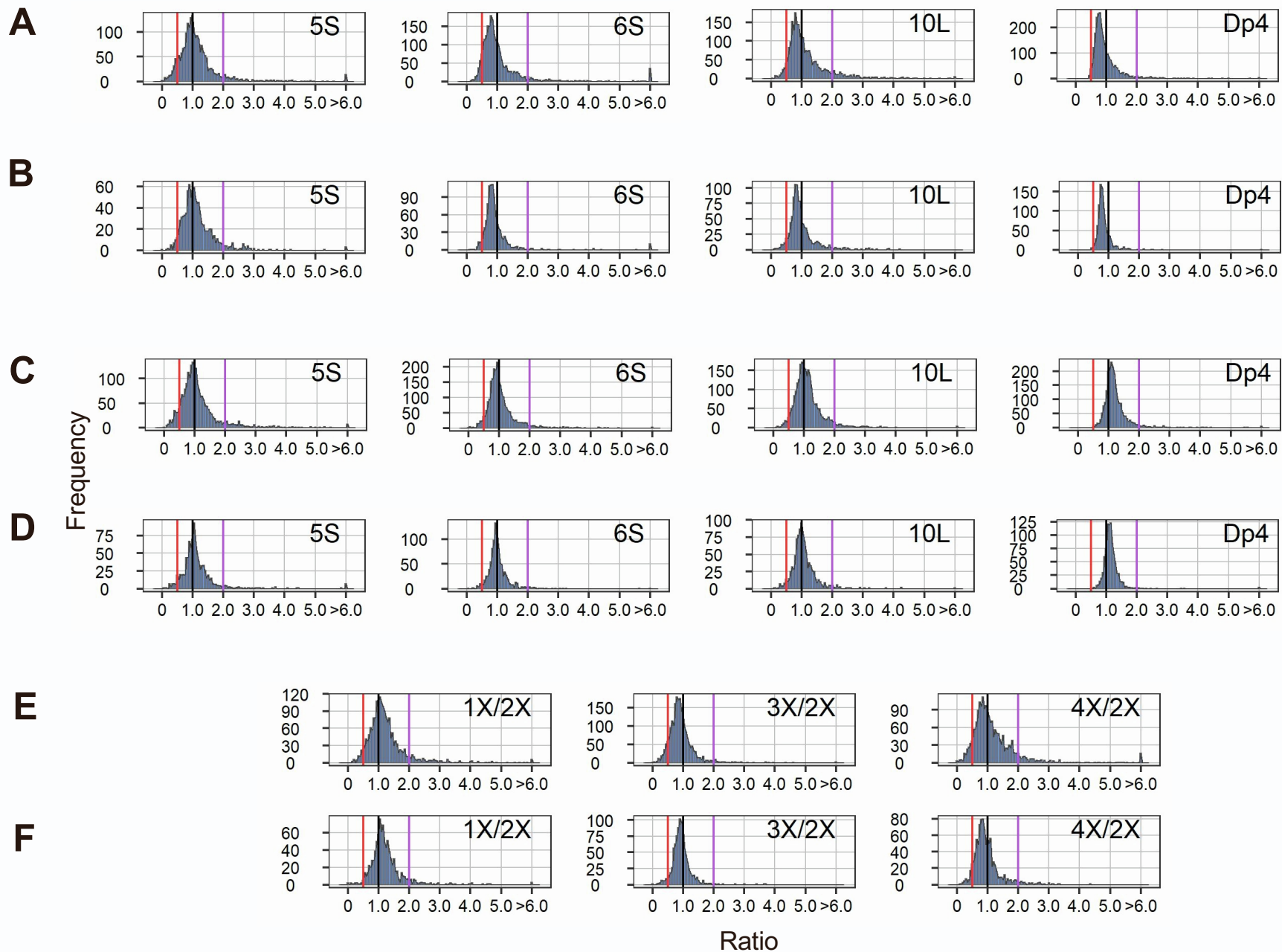
Supplemental Figure 7. Median of genes and TEs in aneuploid and ploidy series.

The dots are the median value of the ratios from each experimental comparison. The x-axis refers to different aneuploidy and ploidy series. The y axis notes the median value. The Median was calculated as described in *Material and Methods*.



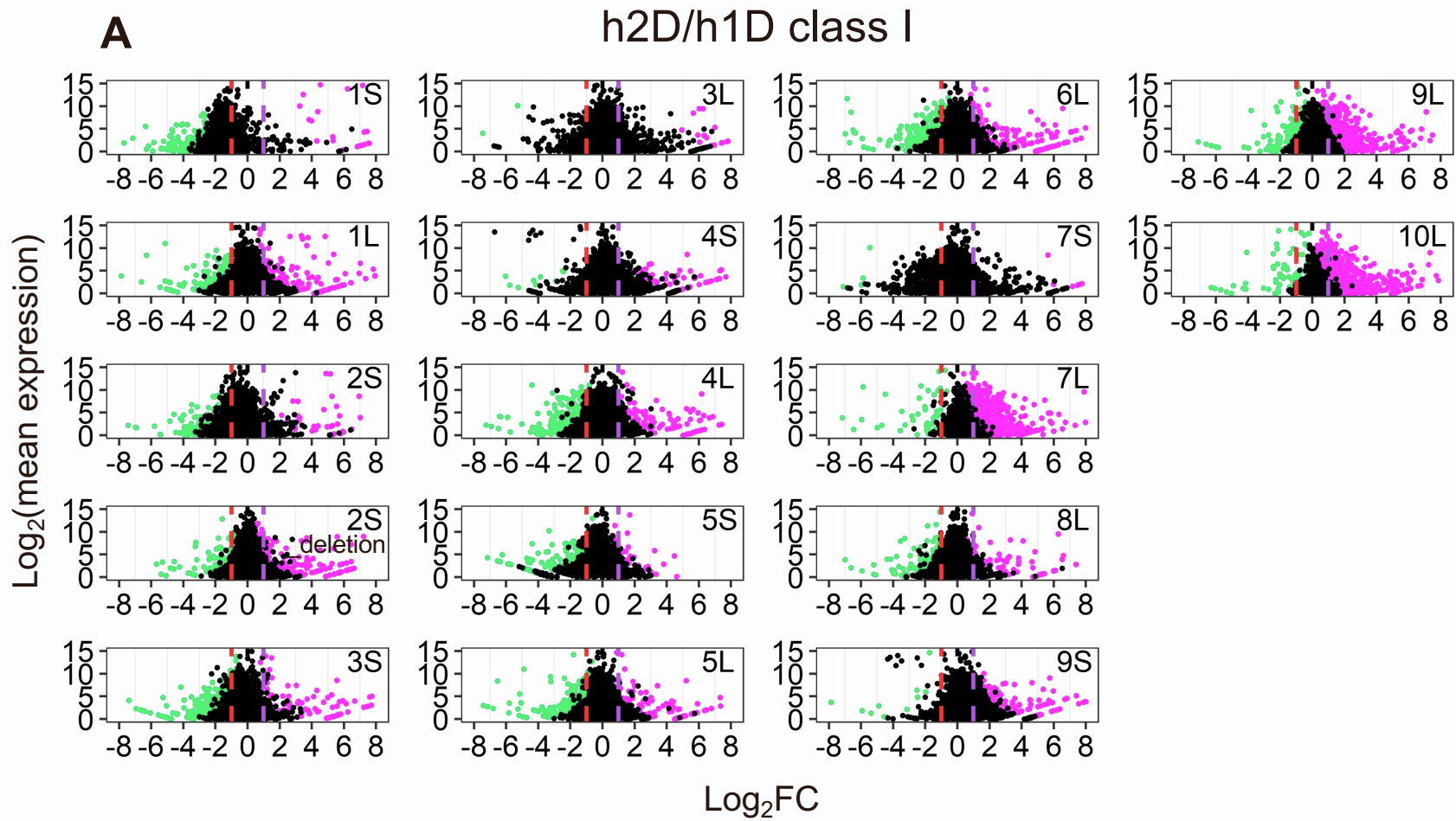
Supplementary Figure 8. Relationship between expression of genes and TEs.

Each data point represents one comparison between genes and TEs. Correlation between the median ratios of genes and TEs in disomy (**A**), trisomy (**B**) and monosomy (**C**). Medians of genes and TEs in each comparison were computed as in *Materials and Methods* and plotted on the x- and y-axes, respectively. R , Pearson correlation coefficient; p , P values for Pearson correlation.



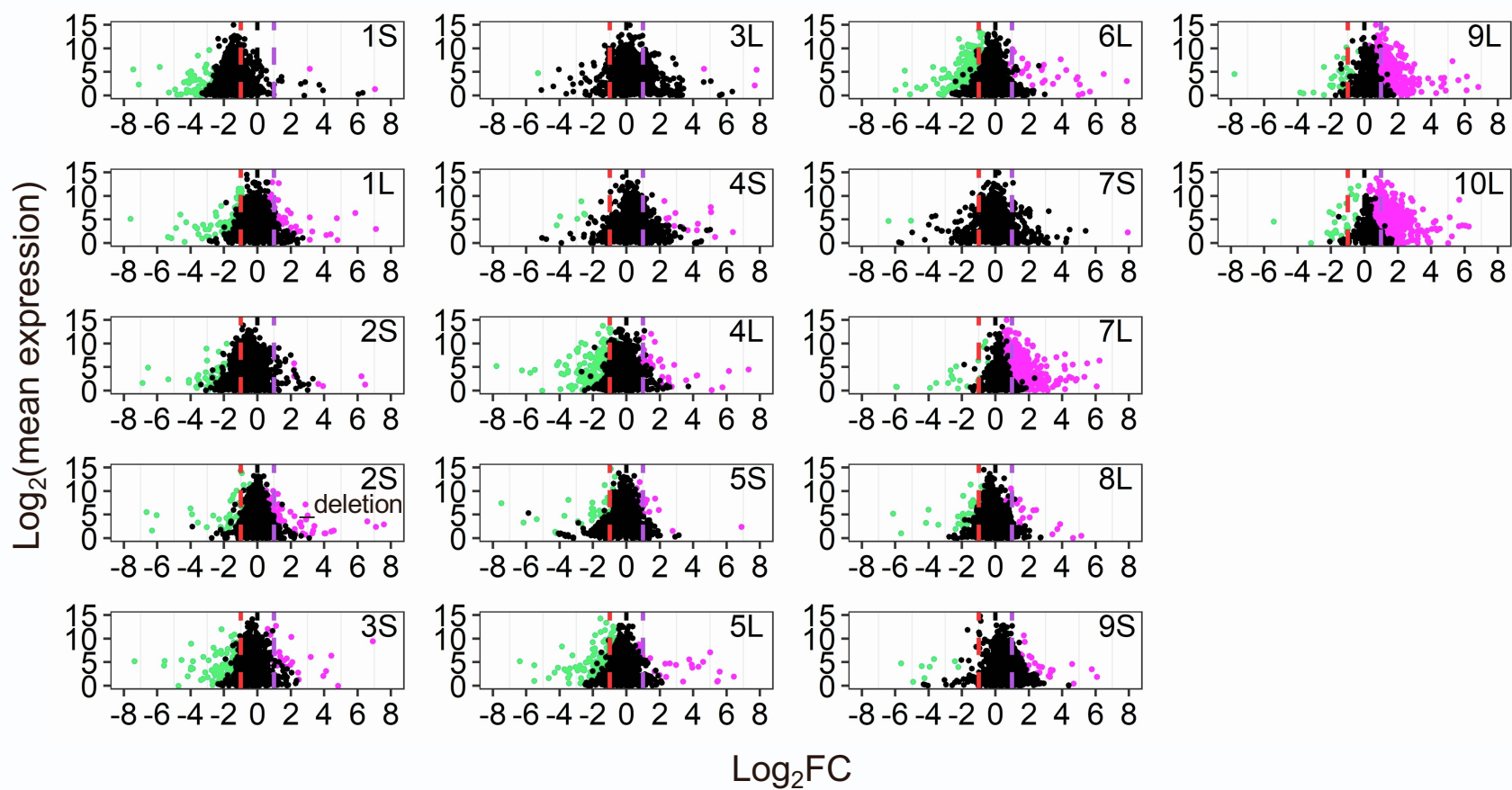
Supplemental Figure 9. Ratio distribution of two classes TEs in tetrasomy and ploidy series.

Ratio distributions were plotted as described in Figure 2. **A** and **B** for 4D/2D. **C** and **D** for 4D/3D. **E** and **F** for ploidy series. The distribution of Class I TEs is in **A**, **C** and **E**. **B**, **D** and **F** show the ratio distribution of Class II TEs.



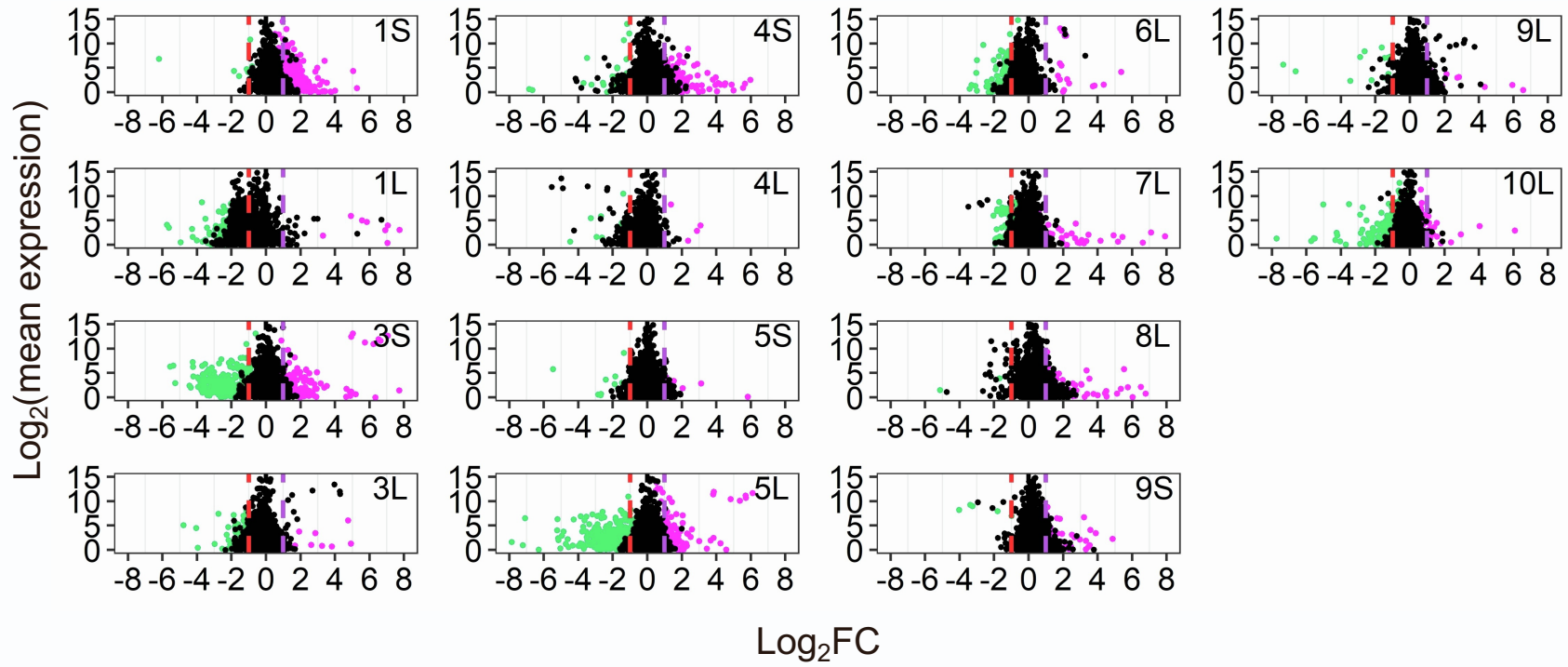
B

h2D/h1D class II

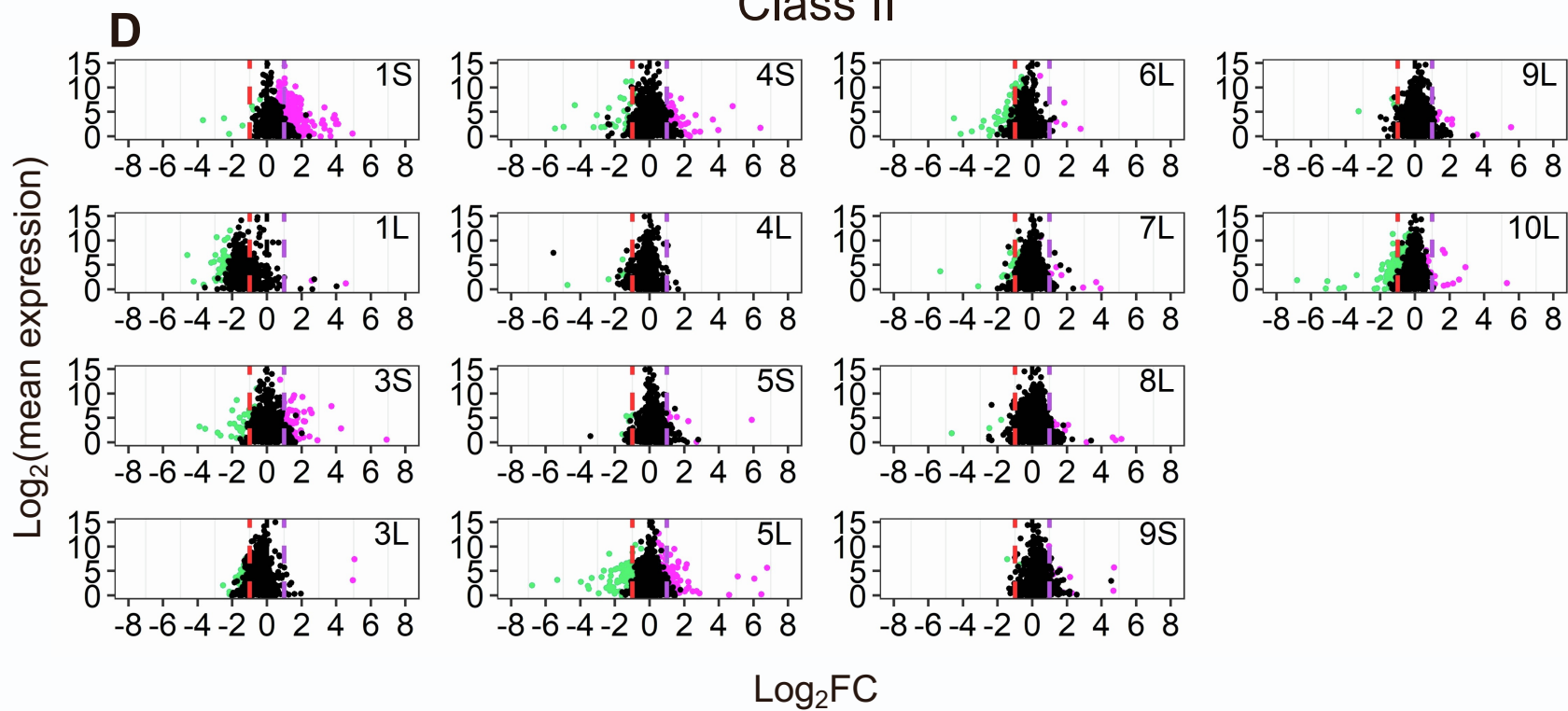


1D/2D
Class I

C



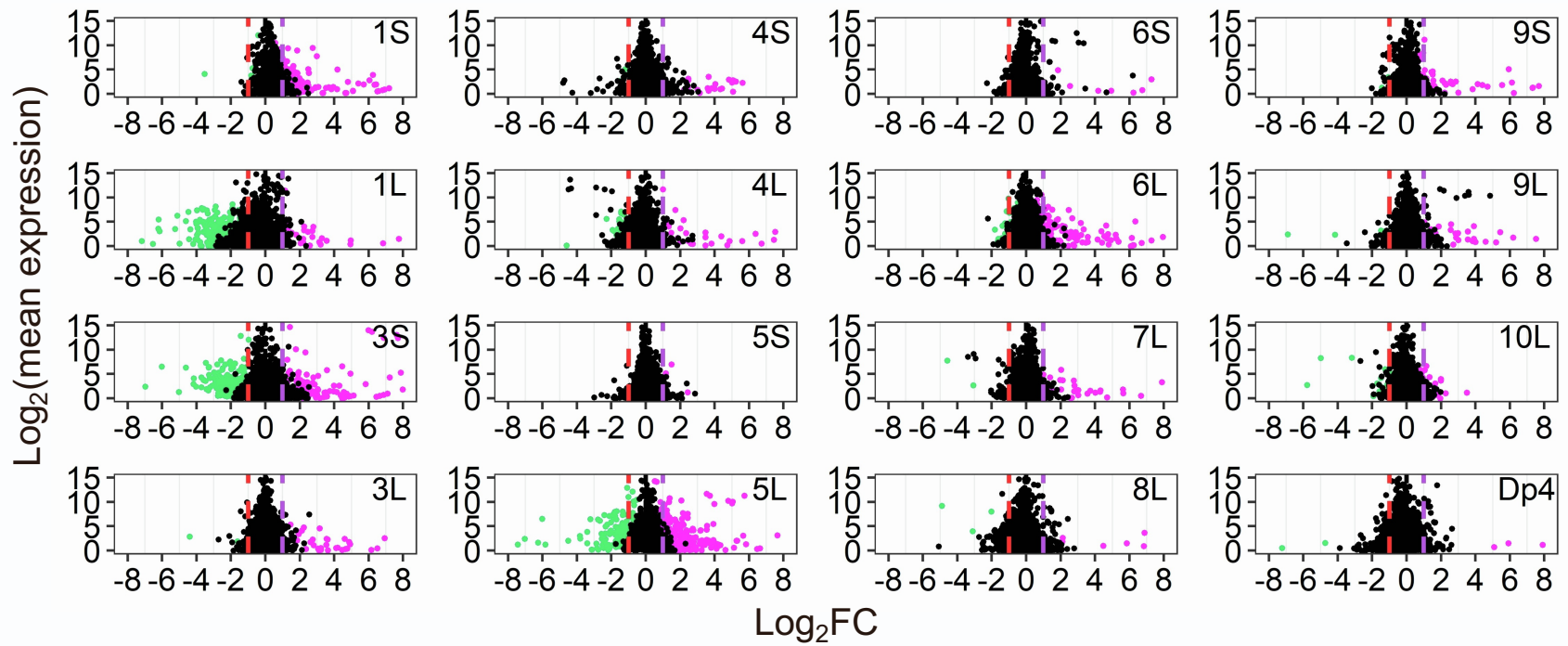
1D/2D
Class II



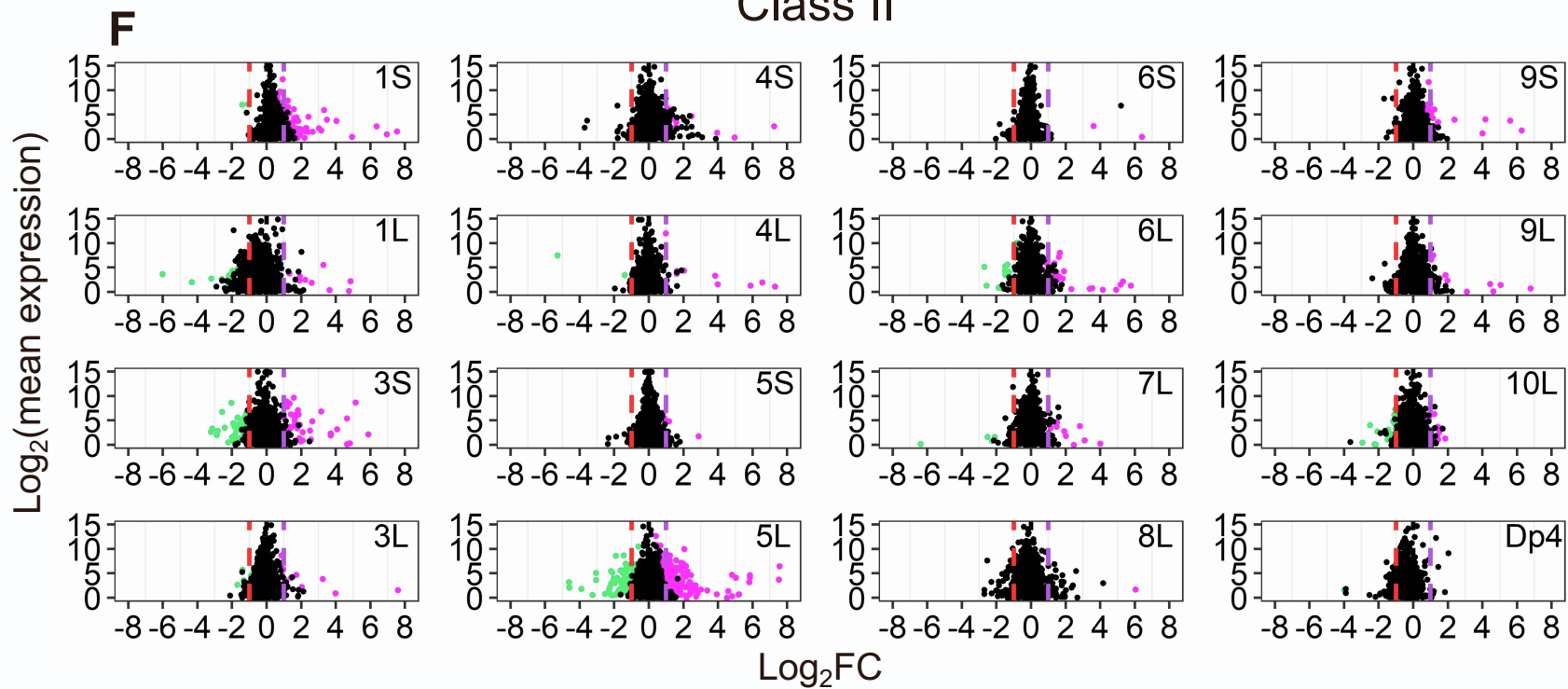
3D/2D

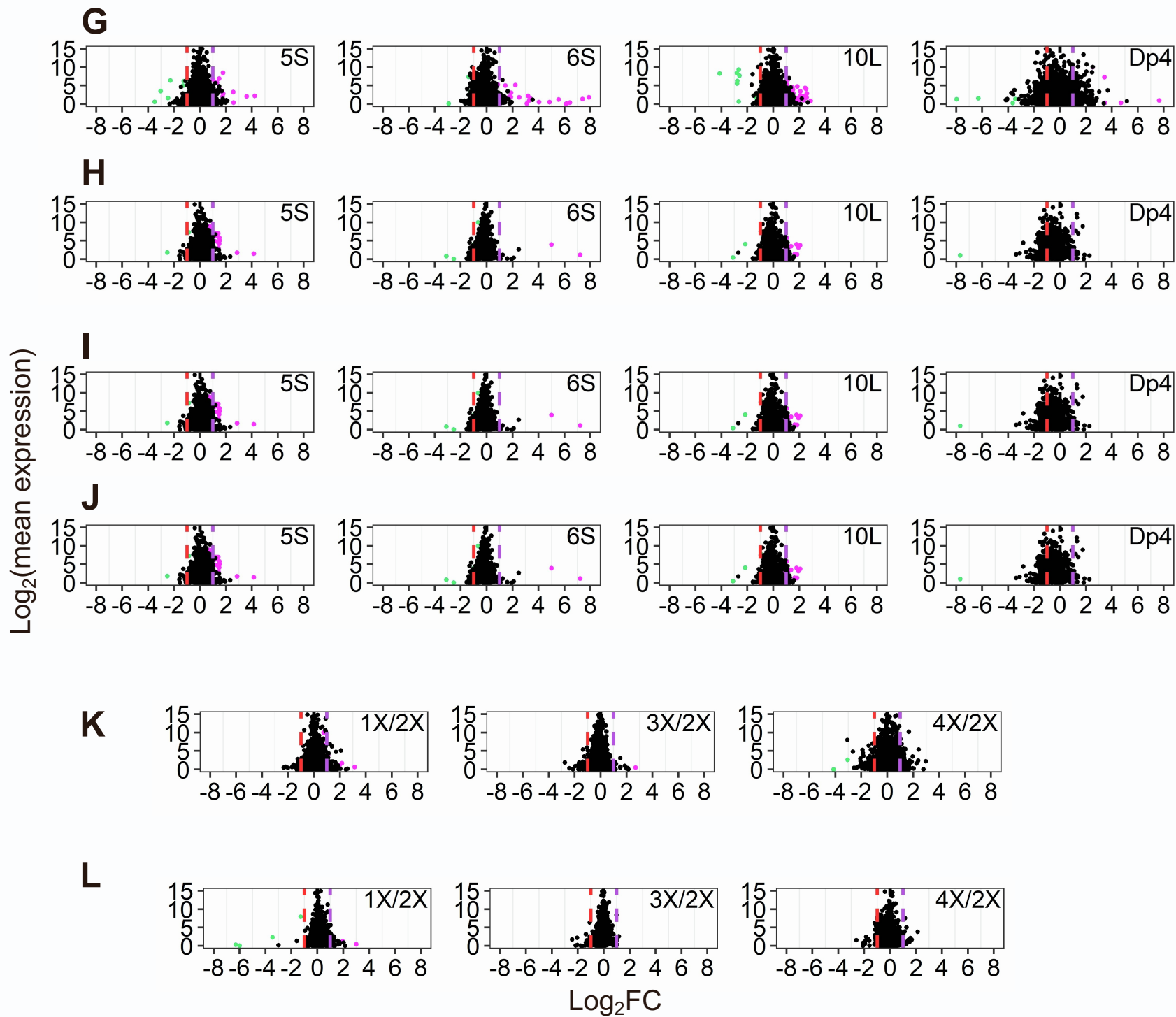
Class I

E



3D/2D
Class II





Supplemental Figure 10. Scatter plots of differential TE expression of two classes of TEs.

Scatter plots of significant differential expression of two classes of TEs comparing experimental to control in h2D/h1D (**A** and **B**), 1D/2D (**C** and **D**), 3D/2D (**E** and **F**), 4D/2D (**G** and **H**), 4D/3D (**I** and **J**) and ploidy series (**K** and **L**). The scatter plot of Class I TEs is in **A**, **C**, **E**, **G**, **I** and **K**. **B**, **D**, **F**, **H**, **J** and **L** show the ratio distribution of Class II TEs. Plots were generated as described in Supplemental Figure 5.