In 667 non-silent jDE genes in endosperm, 661 genes can be mapped on the genome. Ratio distribution of the 661 jDE genes to the 13,681 mapped highly expressed ones is shown.

In 536 non-silent jDE genes in anther, 527 genes can be mapped on the genome. Ratio distribution of the 527 jDE genes to the 13,885 mapped highly expressed ones is shown.

In 665 non-silent jDE genes in panicle, 658 genes can be mapped on the genome. Ratio distribution of the 658 jDE genes to the 14,435 mapped highly expressed ones is shown.

In 866 non-silent jDE genes in root, 855 genes can be mapped on the genome. Ratio distribution of the 855 jDE genes to the 14,281 mapped highly expressed ones is shown.

In 1,174 non-silent jDE genes in leaf, 1,161 genes can be mapped on the genome. Ratio distribution of the 1,161 jDE genes to the 14,019 mapped highly expressed ones is shown.

Figure S8. Ratio distribution of changed-tissues jDE genes of the NZ combination. Ratios of changed-tissues jDE genes to highly expressed genes in Nipponbare or Zhenshan97 tissues were plotted for every 100 mapped genes. Red asterisks (*) mean an exceptional ratio that was more than 3 times higher than the 3rd quartile value of the changed-tissues jDE gene ratio distribution, where highly expressed genes were more than the first quartile value of the highly expressed gene rate distribution in 100 mapped genes.