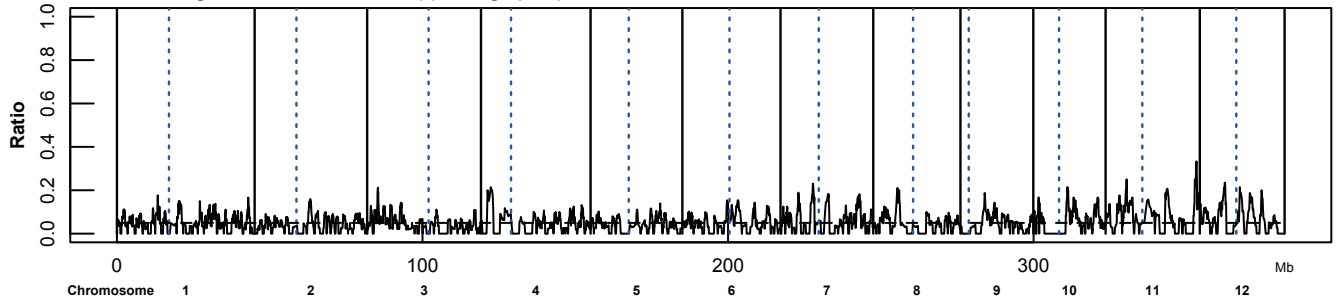
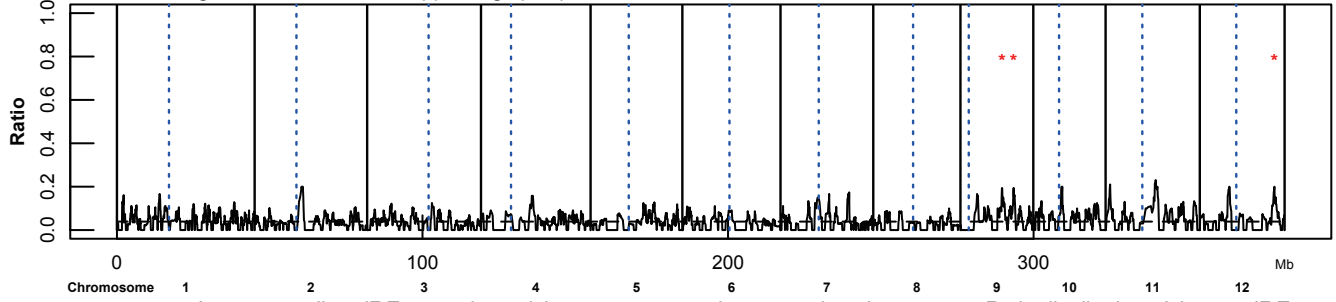


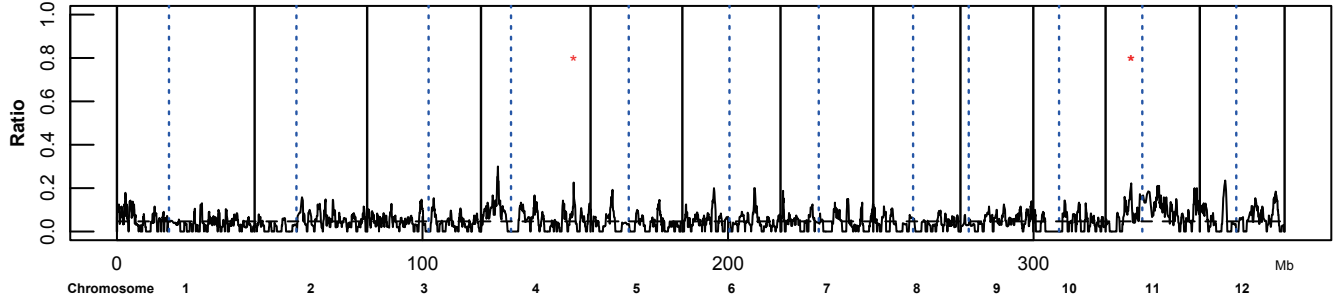
Endosperm In 667 non-silent *ji*DE genes in endosperm, 661 genes can be mapped on the genome. Ratio distribution of the 661 *ji*DE genes to the 13,681 mapped highly expressed ones is shown.



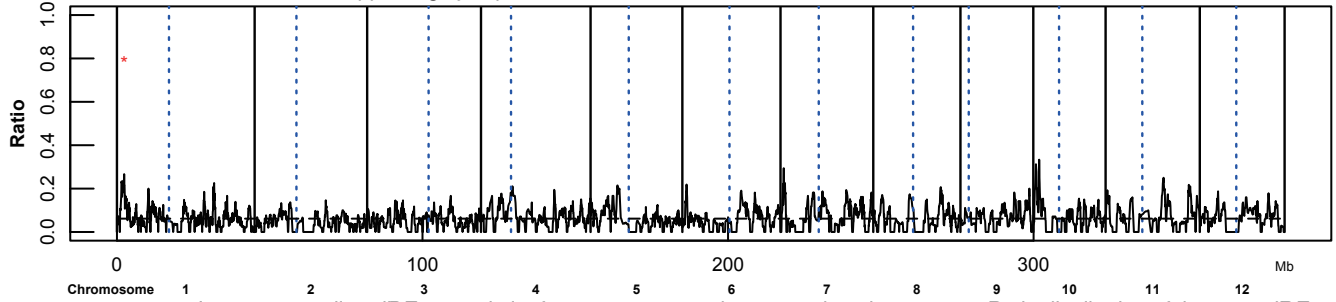
Anther In 536 non-silent *ji*DE genes in anther, 527 genes can be mapped on the genome. Ratio distribution of the 527 *ji*DE genes to the 13,885 mapped highly expressed ones is shown.



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



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



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

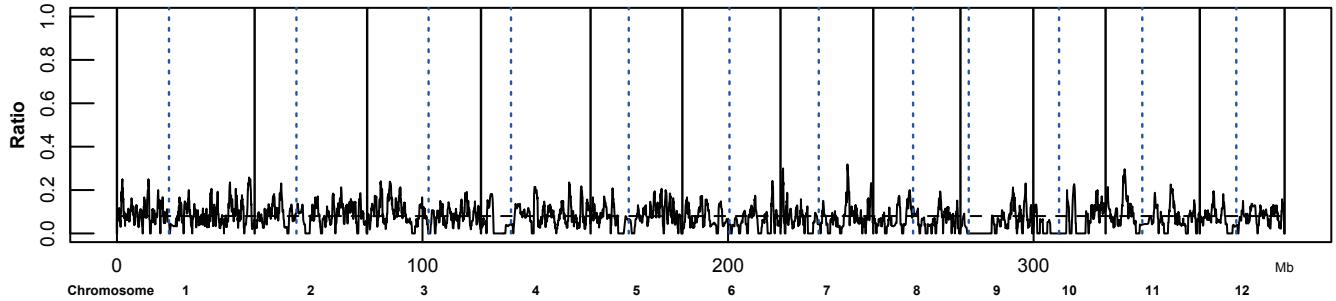


Figure S8. Ratio distribution of changed-tissues *ji*DE genes of the NZ combination. Ratios of changed-tissues *ji*DE genes to highly expressed genes in Nipponbare or Zhenshan97 tissues were plotted for every 100 mapped genes. Red asterisks (*) mean an exceptional ratio that was more than 3 times higher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