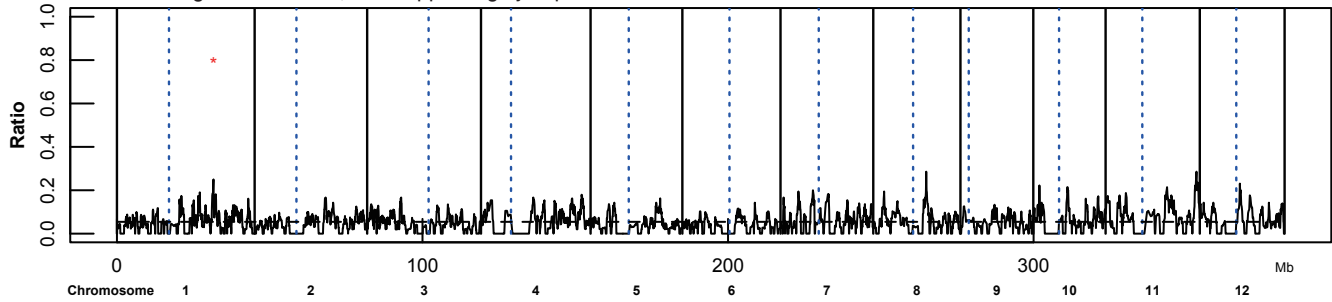
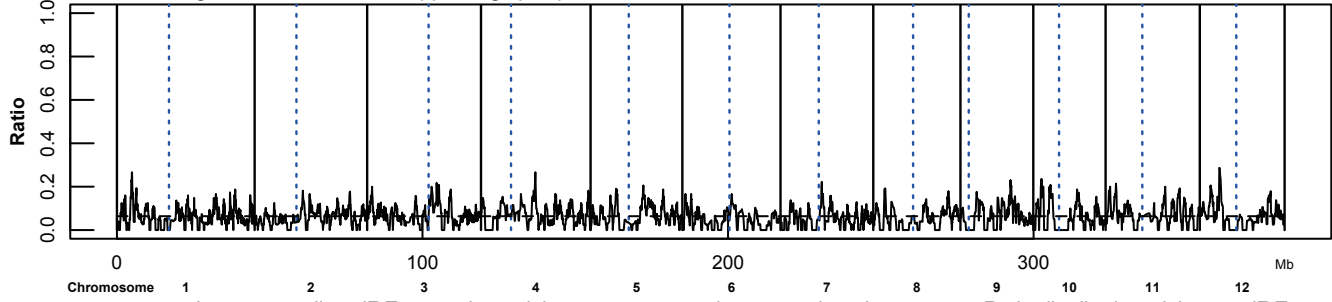


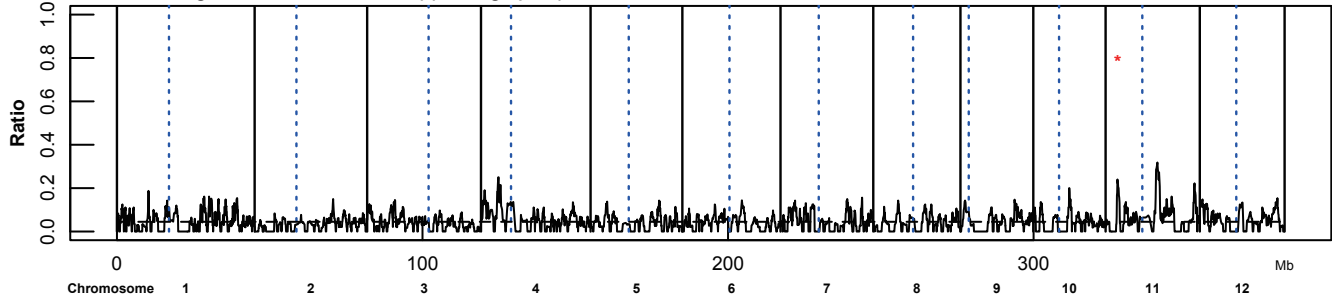
Endosperm In 748 non-silent *ji*DE genes in endosperm, 743 genes can be mapped on the genome. Ratio distribution of the 743 *ji*DE genes to the 13,771 mapped highly expressed ones is shown.



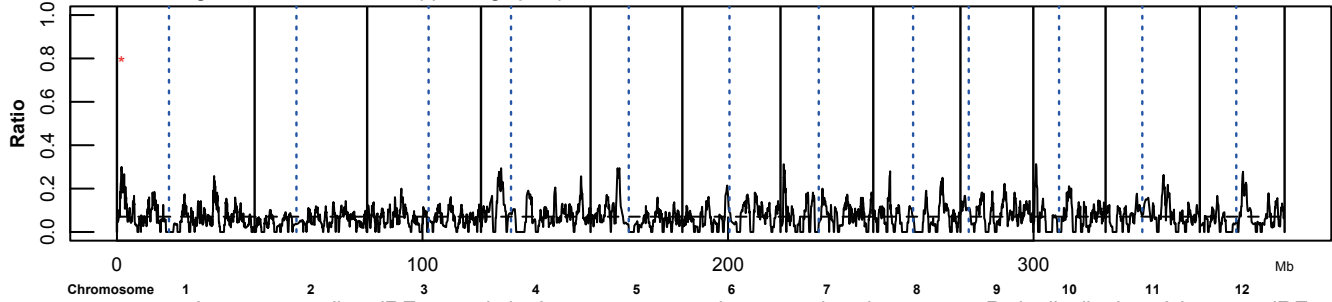
Anther In 887 non-silent *ji*DE genes in anther, 880 genes can be mapped on the genome. Ratio distribution of the 880 *ji*DE genes to the 13,781 mapped highly expressed ones is shown.



Panicle In 645 non-silent *ji*DE genes in panicle, 638 genes can be mapped on the genome. Ratio distribution of the 638 *ji*DE genes to the 14,490 mapped highly expressed ones is shown.



Root In 1,011 non-silent *ji*DE genes in root, 998 genes can be mapped on the genome. Ratio distribution of the 998 *ji*DE genes to the 14,353 mapped highly expressed ones is shown.



Leaf In 1,161 non-silent *ji*DE genes in leaf, 1,147 genes can be mapped on the genome. Ratio distribution of the 1,147 *ji*DE genes to the 14,363 mapped highly expressed ones is shown.

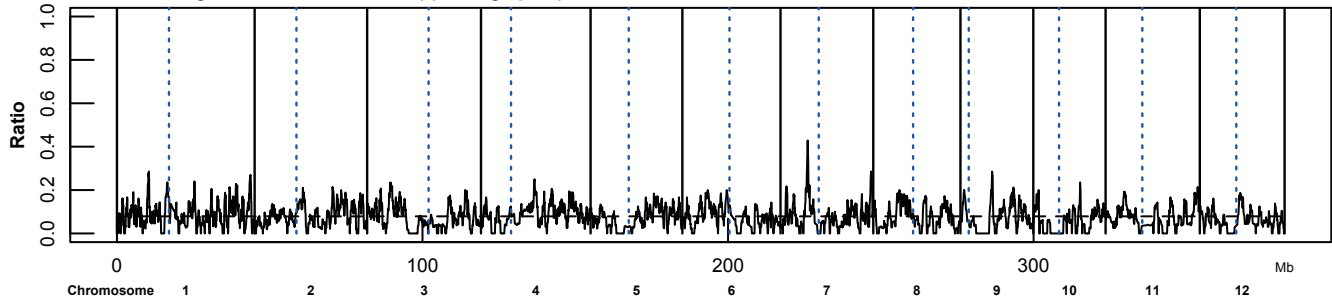


Figure S7. Ratio distribution of changed-tissues *ji*DE genes of the NM combination. Ratios of changed-tissues *ji*DE genes to highly expressed genes in Nipponbare or Minghui63 tissues were plotted for every 100 mapped genes. Red asterisks (*) mean an exceptional ratio that was more than 3 times higher 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.