



**Figure S3. Scatter plots of  $\tau$  values for highly expressed genes in respective *japonica* or *indica* tissues.** Nipponbare  $\tau$ , Minghui63  $\tau$ , and Zhenshan97  $\tau$  values were calculated using 44, 36, and 39 tissues, respectively. Red points represent changed-tissues *j*DE genes. Diagonal lines means same *japonica* and *indica*  $\tau$  values. The top and right panels of each scatter plot show the percentages of changed-tissues (solid line) and global (broken line) *j*DE genes on a window of 0.1  $\tau$  window for highly expressed genes in Nipponbare and *indica* strain tissues, respectively.