



Figure S1. Probe Selection by using SNEP two-sided test. Each transcript expression data was subjected to SNEP two-side analysis. Raw perfect match probe intensities were used. Probes were ordered by differences between *japonica* and *indica*. Values of top, middle, and bottom panels indicated original, difference between *japonica* and *indica*, selected probes to evaluate expression difference by SNEP, respectively. In top and bottom panels, blue and red shows *japonica* and *indica* probe intensities, respectively. In the middle panel, values of non-SFP probes were shown in red, and probes with nucleotide polymorphisms were shown with blue blast scores. In bottom panel, non-SFP probes were only plotted.