



Figure S3. Volcano plots showing the gene expression differences among different samples. The RPKM-normalized transcript count data sets were analysed by using the NOIseq: the x-axis shows the log-ratio (gene expression fold change after challenge) the y-axis the probability for each gene of being differentially expressed. The up-regulated and down-regulated genes were identified under the criterion of $\text{probability} \geq 0.8$ and $|\log_2(\text{fold change})| \geq 1$