



**S9 Figure. Confirmation of differentially retained introns.** Splicing of 10 genes with increased intron retention in *brr2a-2* according to the RNA-seq data was analyzed by splicing assays based on quantitative RT-PCR. RNA was extracted from 15 days old Col and *brr2a-2* seedling grown in LD conditions. Intron retention was analyzed with primers designed to amplify unspliced and spliced transcript, respectively. RNA-seq and qPCR data are compared in a log-log plot. Shown are logarithms of intron retention fold changes (IR FC) between Col and *brr2a-2*. Data points are means of triplicates.