



Figure S3 | Pairwise comparison of highly methylated 100 bp windows between ZEB-treated and control seedlings

A pairwise comparison of methylation level in untreated seedlings and the 100 μM ZEB-treated seedlings for highly methylated 100 bp windows in both the pericentromere and the chromosome arms (as defined in Figure 2A). CG and CHH contexts of DNA methylation are shown. A highly methylated window was defined as having $\geq 50\%$ methylation in the control sample for CG and $\geq 30\%$ methylation in the control sample for CHH. ZEB-treated seedling methylation level is on the y-axis and control methylation level is on the x-axis. The color spectrum—ranging from red (low) to purple (high)—illustrates the density of points at a coordinate. The slopes (m) of the dashed lines represent the following relative methylation levels: 100% (treated and control methylation level are the same), 75%, 50% (treated methylation level is half of the control), and 25%.