**Figure S2.** $RR_{met}$ of subsampled motifs. The number of occurrences for each observed nucleotide motif was counted in both human and *A. thaliana* motif pairs. For each motif, the occurrences in both sets were compared, and the set with the larger number of said motif was randomly subsampled without replacement to contain the same number as the smaller sample. After doing this for all motifs, we have a reduced set of human and *A. thaliana* methylated and unmethylated motifs with identical motif distribution. $RR_{met}$ was then calculated as described. This process was repeated 100 times, to account for biases in random sampling.