Figure S1. Quantification of novel methylation-dependent interactions between H3TMs and methyl reader domains. As shown in Figure 2, each of the seven peptide probes harboring the K4me3 mark displayed a unique interaction profile with sixteen H3K4me3 effector domains. The average signal intensities of two duplicate spots were used for quantifying each of the interactions. Interactions between sixteen H3K4me3 effector domains were quantified for each of the eight peptides, as well as for H3K4m3, which serves as a positive control.