Supporting Information

A system for enzymatic lysine methylation in a desired sequence context

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Figure S1. MS/MS spectrum of a chymotrypsin-generated peptide encompassing the lysine methylation site in the D1-H3K4 chimera. Shown is the spectrum for the 27-mer peptide representing monomethylated D1-H3K4.



Figure S2. MS/MS spectrum of a chymotrypsin-generated peptide encompassing the lysine methylation site in the D1-H3K36 chimera. Shown is the spectrum for the 26-mer peptide representing trimethylated D1-H3K36.



Figure S3. MS/MS spectrum of a chymotrypsin-generated peptide encompassing the lysine methylation site in the D1-H3K9 chimera. Shown is the spectrum for the 27-mer peptide representing monomethylated D1-H3K9.



Figure S4. MS/MS spectrum of a chymotrypsin-generated peptide encompassing the lysine methylation site in the wild-type D1 protein. Shown is the spectrum for the 27-mer peptide representing trimethylated wild-type D1.



Figure S5. Examples of extracted ion chromatograms. Shown are extracted ion chromatograms for the four possible methylation states (Me0, Me1, Me2, Me3) of 26-mer (D1-H3K36) or 27-mer (other three proteins) chymotryptic peptides derived from cellularly expressed TAP-tagged proteins.