Legends for Supplementary Figures and Tables:

Supplementary Figure S1. High propionylation efficiency of K562 whole lysate. Propionylated whole lysate of K562 was digested with trypsin and subsequently analyzed with mass spectrometry. The propionylation efficiency was estimated by the ratio of propionyllysine-bearing peptides over all lysine-containing peptides.

Supplementary Figure S2. Annotated MS/MS spectra of the Kme1 peptides identified in all cell lines.

Supplementary Figure S3. Mass spectrometric verification of lysine propionyl-methylated peptides. The annotated MS/MS spectra generated from cell-derived lysine propionyl-methylated peptides were compared with those of synthetic peptides.

Supplementary Figure S4. Pie charts of (**a**) Biological Process and (**b**) Cellular Component analysis of the methylated proteins analyzed with DAVID.

Supplementary Figure S5. Enrichment analysis of the methylated proteins according to the GO terms, KEGG pathways and Pfam database. The number on the right of the bar is the number of proteins involved in the indicated term.

Supplementary Figure S6. a) Interaction network obtained from the STRING 9.05 database with confidence score ≥0.7 (containing 205 nodes and 604 edges). The subclusters (highly interconnected regions) were identified with MCODE[62]. **b-d).**Details of three most highly connected network clusters as obtained by MCODE analysis were presented. The size of the protein node represented the topological coefficient, which is a relative measure for the extent to which a node shares neighbors with other nodes. The protein nodes was colored according to its MCODE score, which represented the density of the protein node and its neighbors. The cluster score is defined as the product of the complex subgraph, density and the number of vertices (proteins) in the complex subgraph.

Supplementary Figure S7. Mutation analysis of the sequence surrounding the methylation sites. X-axis is the amino acid position relative to the methylated lysine, Y-axis is the number of mutations found in the indicated position.

Supplementary Figure S8. Overlap of the identified mono-methylation peptides between this study, Guo's and Bremang's study.

Supplementary Table S1. List of the mono-methylated peptides from all samples.

Supplementary Table S2. Subcellular localization of the methylated proteins predicted by the PENCE Proteome Analyst databases.

Supplementary Table S3. Functional annotation analysis result.

Supplementary Table S4. Protein-protein interaction network analysis by MOCDE.

Supplementary Table S5. Protein complex analysis result from querying the CORUM database.

Supplementary Table S6. Overlap of the methylation sites with known acetylated and succinylated sites.

Supplementary Table S7. Mutation analysis of the sequence surrounding the methylation sites.