

Phosphoproteomic analysis of human mesenchymal stromal cells during osteogenic differentiation

Supplementary Figure. 1 Venn diagram representing the overlap of identified phosphoproteins in hMSCs after 0, 1, 3 and 7 days of osteogenic differentiation (abbreviated as D0, D1, D3 and D7).

Supplementary Figure. 2 Quantitative proteomics and phosphoproteomics MS data of selected proteins listed in Table 1. Phosphorylation sites of each phosphoprotein were indicated. The fold change of each protein or phosphoprotein level was calculated by dividing the mean XIC peak area from three technical replicates of sample 1 by the mean of sample 2.

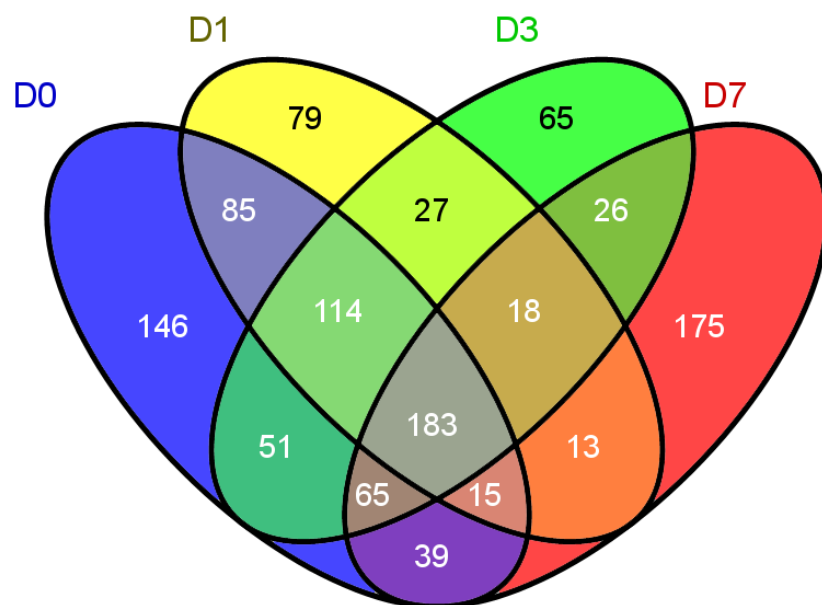
Supplementary Figure. 3 The MS/MS spectra of all the unique, quantified phosphopeptides in the quantitative comparison of hMSCs that underwent osteogenesis for 0, 1, 3 and 7 days. This information is available free via Internet at http://proj3.sinica.edu.tw/~yujuchen/2011JPR_hMSC/SupplementaryMSMS.html.

Supplementary Table. 1 Detailed identification information of all phosphopeptides identified by LC-MS/MS from D0, D1, D3 and D7. The calculated MD score listed in column O was for the confidence assessment of phosphorylation site determination (MD score > 9 suggests the top ranked phosphorylated site is confidently determined). The peptide query and index number in column Z and column AA were listed to refer to the corresponding MS/MS spectra in supplementary Figure. 3. LC-MS/MS analyses were obtained from three technical replicates.

Supplementary Table. 2 Detailed quantification information of all phosphopeptides quantified after SEMI strategy analysis. The quantitative comparison between D1/D0, D3/D0 and D7/D0 were calculated and listed in column X, Y and Z, respectively. Changes in phosphorylation level of each phosphopeptides during osteogenic differentiation were categorized into six different phosphorylation expression clusters, including: (1) Up (up during all time points), (2) Down (down during all time points), (3) Up-Down (went up then down), (4) Down-Up (went down then up), (5) Unchanged, and (6) Fluctuated (no particular pattern) through differentiation, and were listed in column AC.

Supplementary Table. 3 Enriched biological processes in hMSCs during osteogenic differentiation. Differentially phosphorylated proteins identified in hMSCs during osteogenic differentiation were used to perform functional annotation clustering analysis using DAVID analysis. Biological processes related to osteogenic commitment with significant enrichment were selected.

Supplementary Figure. 1



Supplementary Figure. 2

