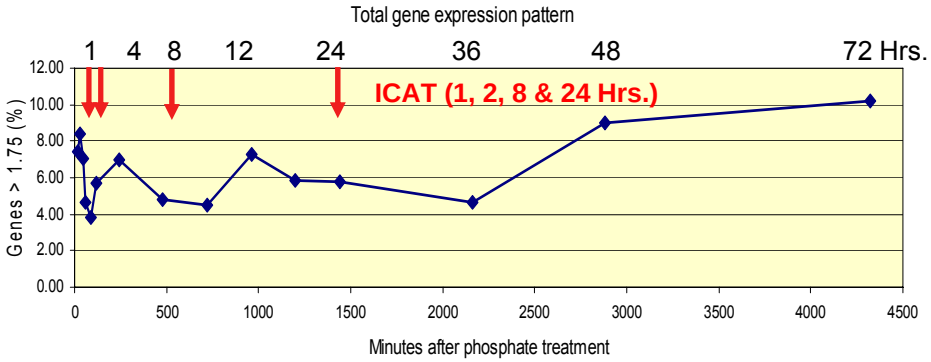
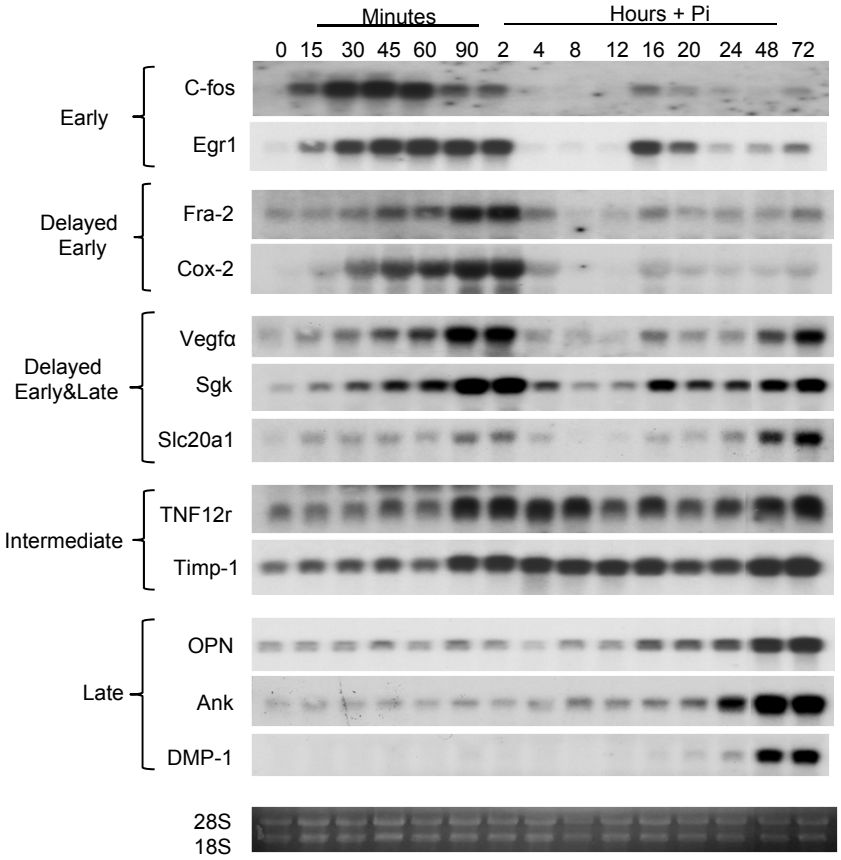
Supplemental Figure 1:

A

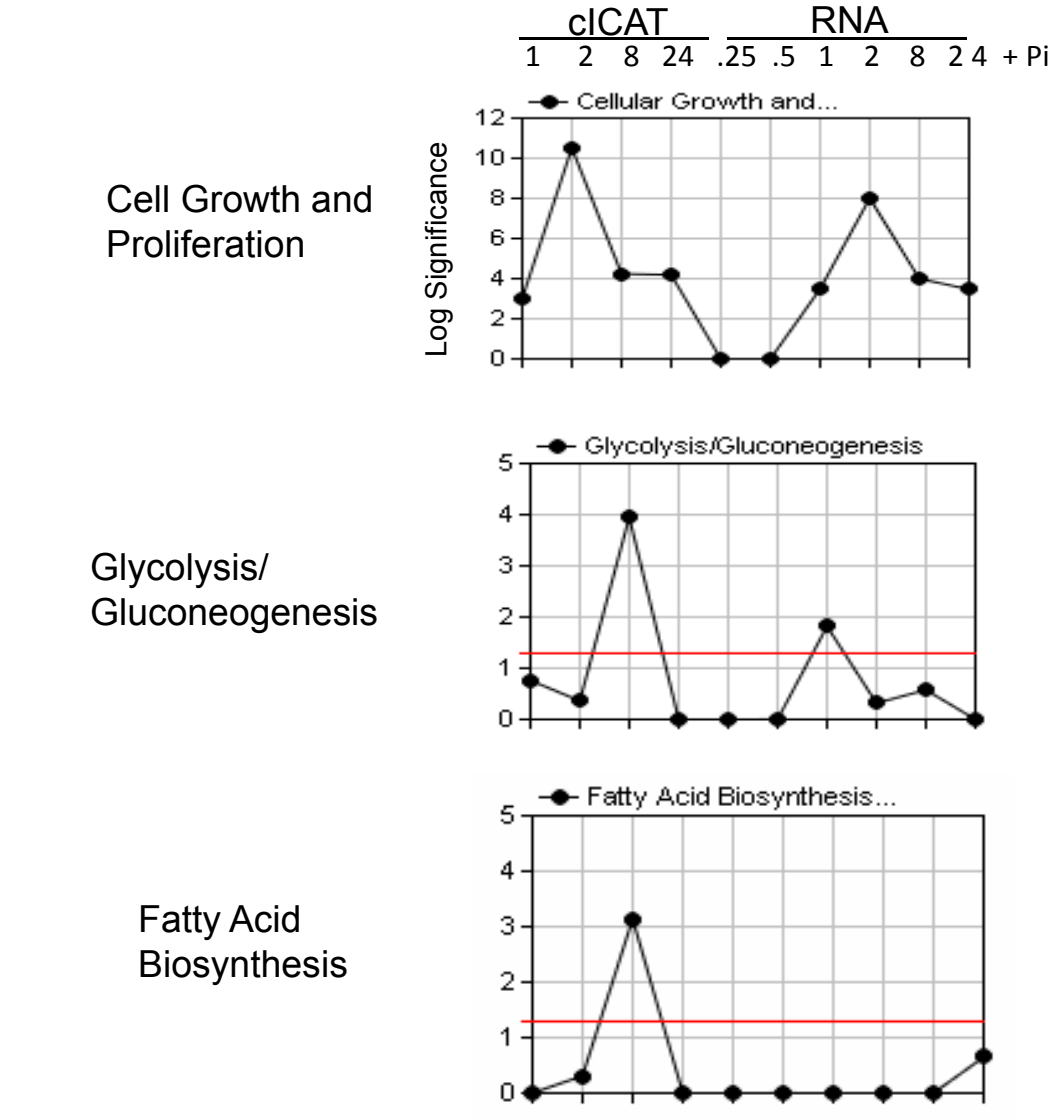


B



Supplemental Figure S1: (A) MC3T3-E1 cells were treated with 10 mM inorganic phosphate for the indicated times and duplicate samples harvested for transcriptomic and proteomic analyses. Transcriptomic results were analyzed and the percent of genes altered by greater than 1.75 fold at each time point calculated relative to untreated. (B) MC3T3-E1 cells grown in normal growth medium (1mM Pi and 10% FBS) and Pi (10mM) was added for the indicated times and samples analyzed by Northern blotting. The resulting membrane was probed as indicated. COX-2:*Ptgs2*, Fra-2:*Fosl2*, OPN:*spp1*. Results are representative of multiple experiments.

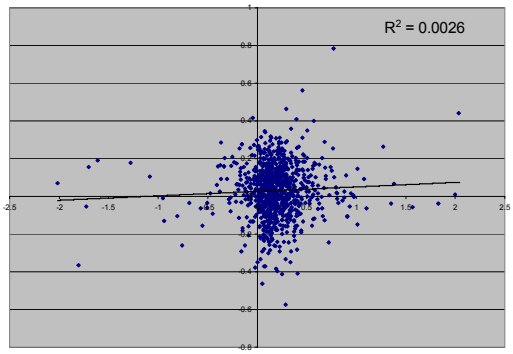
Supplemental Figure 2:



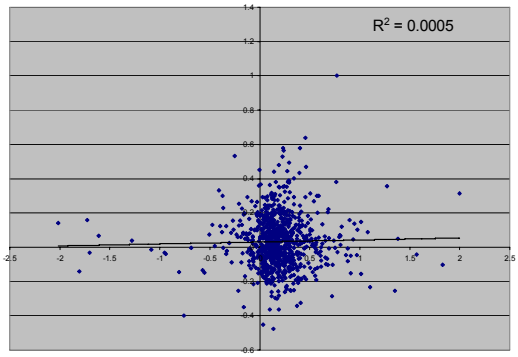
Supplemental Figure S2: Comparison of transcriptomic and proteomic datasets by Ingenuity pathway analysis. Time points as indicated were compared for functional analysis.

Supplemental Figure 3:

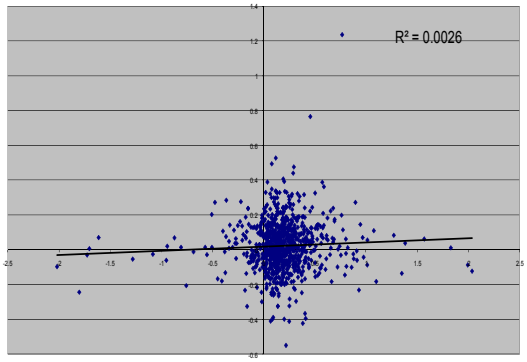
15 m RNA v. 60 m Protein



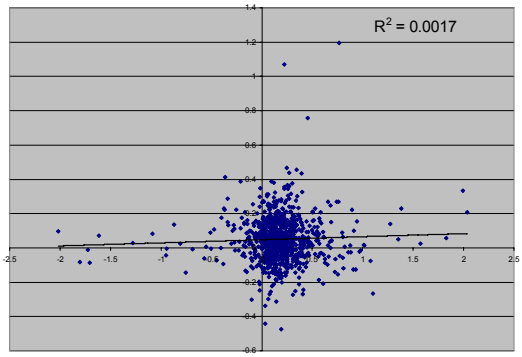
30 m RNA v. 60 m Protein



45 m RNA v. 60 m Protein

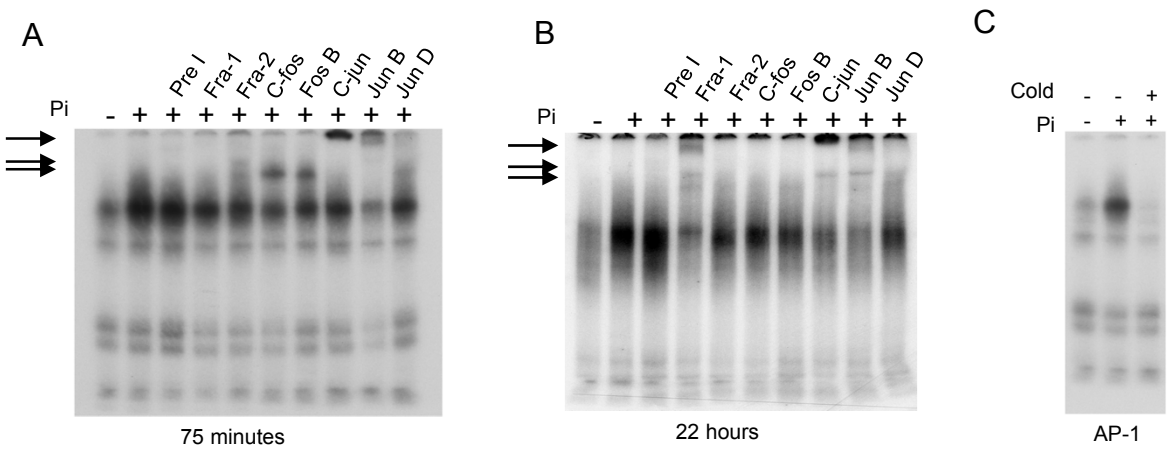


60 m RNA v. 60 m Protein



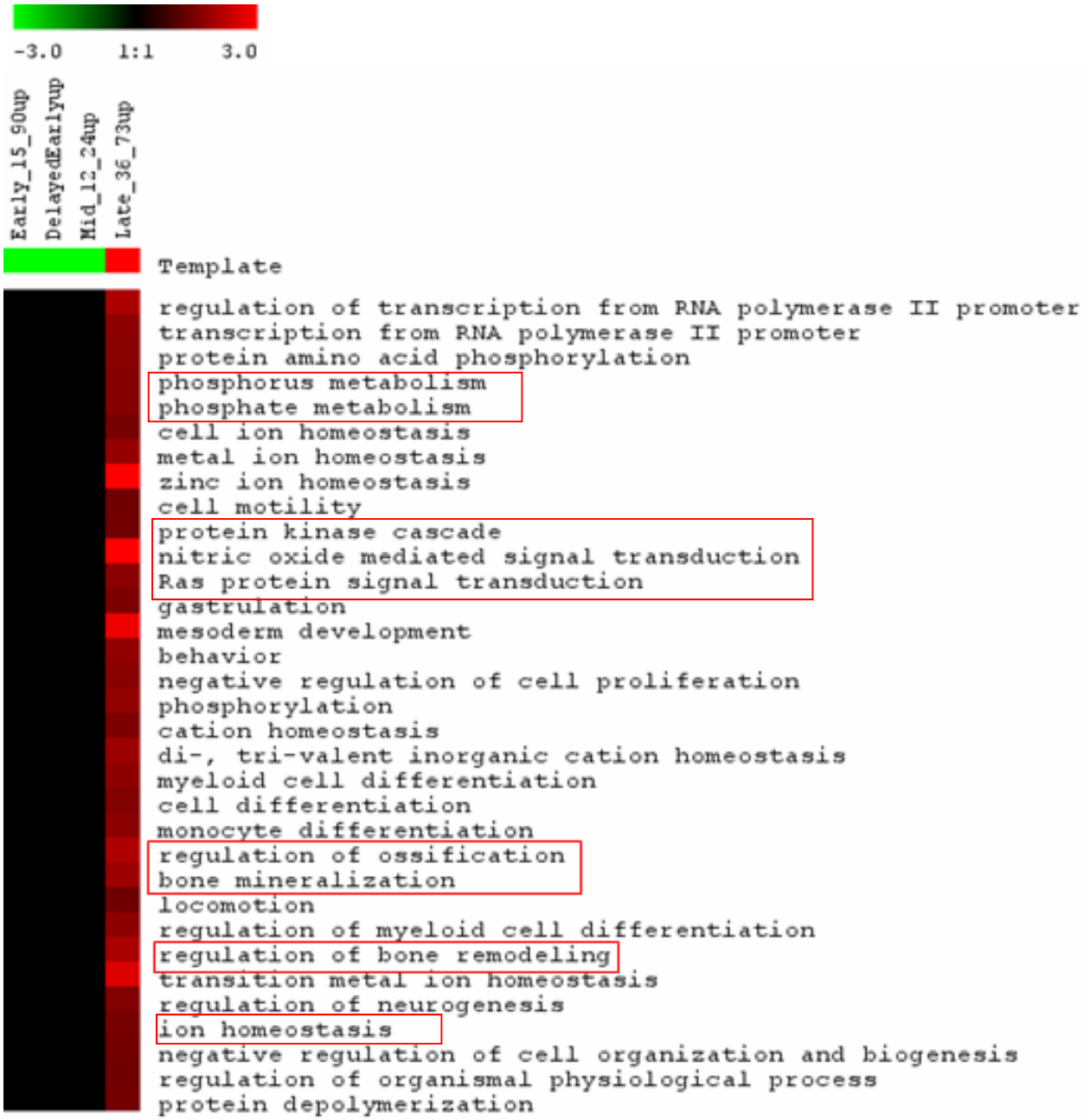
Supplemental Figure S3: Pearson correlation of relative RNA and protein abundance at various time points after Pi treatment. Transcriptomic (microarray) samples generated at 15, 30, 45, and 60 min and a parallel proteomic (cICAT) sample at 60 min after exposure to Pi were correlated.

Supplemental Figure 4:



Supplemental Figure S4: (A) MC3T3-E1 cells were serum starved overnight and cells harvested 75 min after addition of Pi. The resulting nuclear lysate was used for EMSA-supershift using antibodies specific to AP-1 family proteins. (B) Cells were harvested 22 h after addition of Pi in standard growth medium. The resulting nuclear lysate was used for an EMSA-Supershift assay as in (A). (C) Addition of cold AP-1 oligo to the 75 min Pi treated sample eliminated the increased binding.

Supplemental Figure 5:



Supplemental Figure S5: Predicted changes in cell phenotype using the GO database. Heatmap of enrichment scores of the differentiated expressed gene lists (36-72 h) in terms of Gene Ontology biological processes category. Biological processes that are activated at late stage based on up-regulated genes from pooled time points. The bone mineralization-related terms are highlighted in red rectangles.