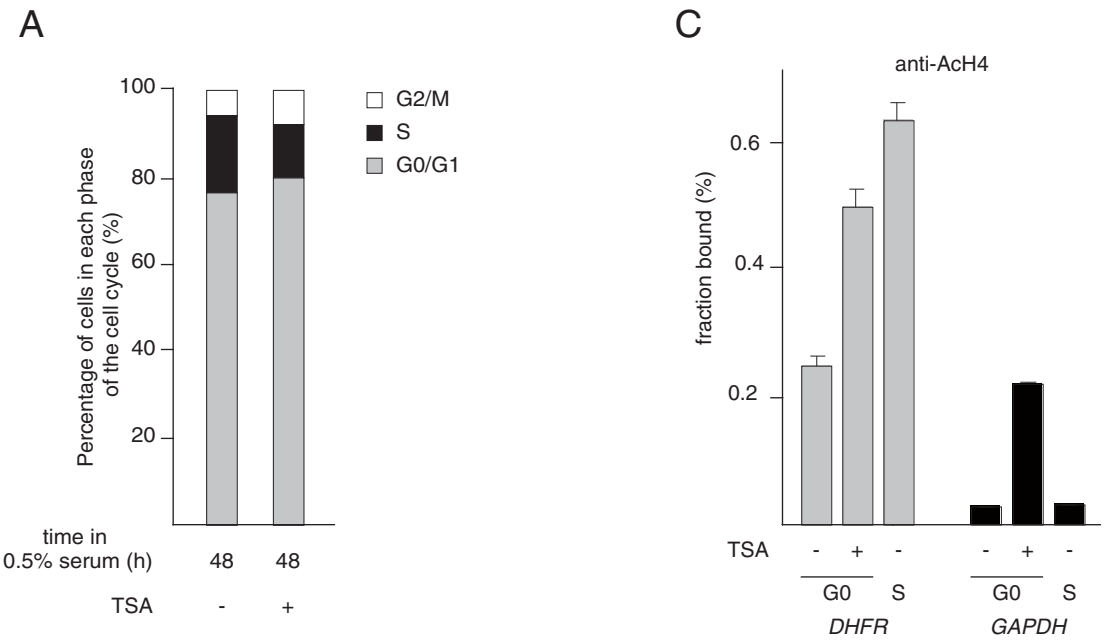

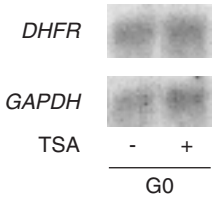

Data not shown. (A) Cell cycle analysis. NIH 3T3 cells were serum starved for 48h and incubated, for the final 10 hours, with (+) or without (-) TSA at a final concentration of 200 ng/ml. Cell cycle phase was determined by flow cytometry using propidium iodide and the percentage of cells in each phase of the cell cycle is presented.
(B) Total RNA was extracted from NIH 3T3 cells in G0 phase, with or without TSA treatment, and analysed by Northern blot using a *DHFR* or a *GAPDH* probe, as indicated.
(C) Chromatin from synchronized NIH 3T3 cells, either in G0 phase, with or without TSA treatment, or in S phase, were analysed by XChIP procedure followed by quantitative PCR of eluted DNA. Equal amounts of chromatin were subjected to immunoprecipitation using anti-acetylated histone H4 antibodies. *DHFR* (gray bars) or *GAPDH* (black bars) sequences were detected by quantitative PCR. The results are expressed as fraction of the total number of copies detected as antibody-bound material.