Early S-phase cell hypersensitivity to heat stress.

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Supplemental Data

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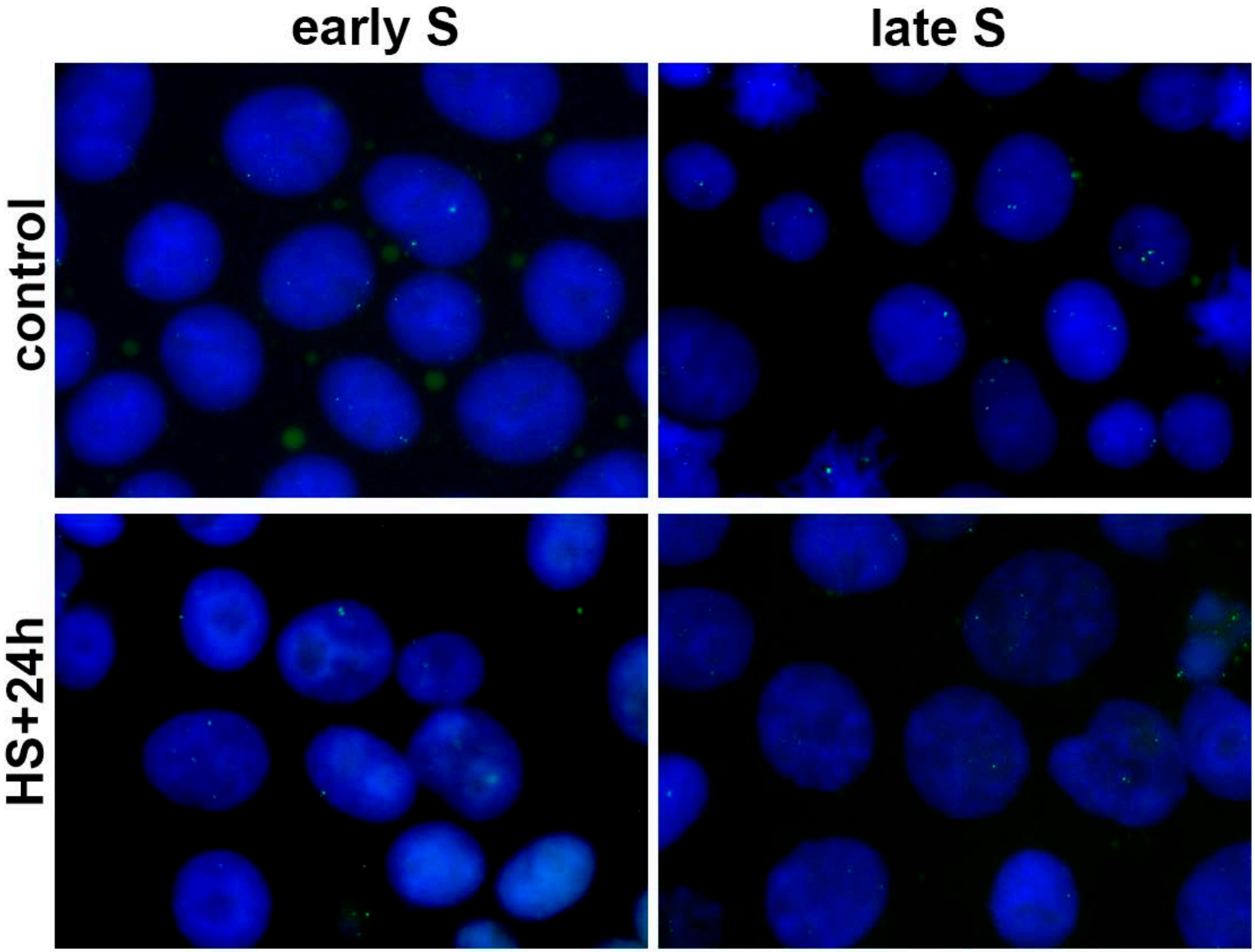
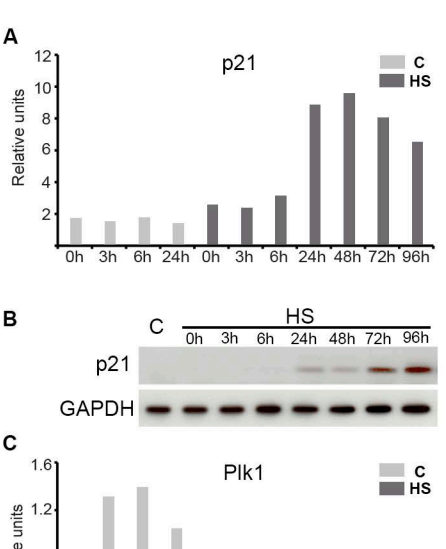
Supplemental Figure S1



Supplemental Figure S1. Early and late S-phase HeLa cells that were either untreated ("C") or HS-treated and allowed to recover for 24 h ("HS+24h") were hybridized with a probe specific for chromosome 18 α-satellite (green) and stained with DAPI (blue).



Supplemental Figure S2. Early S-phase HeLa cells that were treated with HS (45.5C, 30 min) and allowed to recover for the indicated time intervals (0, 3, 6, 24, 48, 72 and 96 h) were subjected to gene expression analysis using qRT-PCR (A and C) and WB (B). The control represents HeLa cells synchronized by a double-thymidine block and released in a drug-free medium for 0, 3, 6 or 24 h. The expression of p21CIP1 and polo-like kinase 1 (plk1) was analyzed using EvaGreen-based qRT-PCR. The amplification levels of the cDNA were normalized to the level of GAPDH cDNA. WB was carried out with an antibody against p21; GAPDH was used as the loading control.

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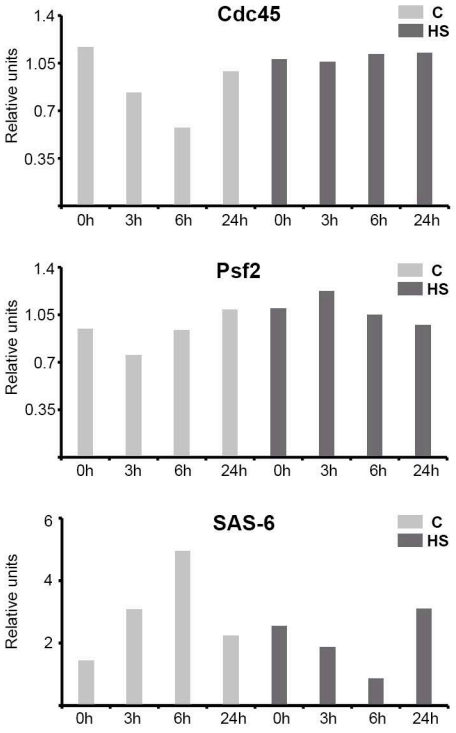
Supplemental Figure S3



Supplemental Figure S3. Early S-phase HeLa cells were either mock-treated or HS-treated (45.5C, 30 min) and recovered for indicated time periods (0, 3, 6 and 24 hr). Quantitative reverse-transcription PCR (qRT-PCR) analysis of cdc45, Psf2 and SAS-6 mRNA levels was performed. RNA extracted from treated and non-treated cells was reverse transcribed, and the cDNA obtained was analyzed using a EvaGreen-based qRT-PCR. The amplification levels of the analysed cDNAs were normalized to the amplification level of GAPDH cDNA. The results of one representative experiment are shown.