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Regulation of target proteins by small ubiquitin-like modifiers

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Citation

Xiao, Z. (2019, June 5). *Regulation of target proteins by small ubiquitin-like modifiers*. Retrieved from <https://hdl.handle.net/1887/74009>

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Author: Xiao, Z.

Title: Regulation of target proteins by small ubiquitin-like modifiers

Issue Date: 2019-06-05

Chapter 2

System-wide analysis of SUMOylation dynamics in response to replication stress reveals novel SUMO target proteins and acceptor lysines relevant for genome stability

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Chapter 2 has been published in **Molecular cell proteomics**

Mol Cell Proteomics. 2015 May;14(5):1419-34. doi: 10.1074/mcp.O114.044792. Epub 2015 Mar 9.

Supplementary Tables are available online.

Running title

SUMOylation and replication stress

Abbreviations

53BP1	Tumor suppressor p53-binding protein 1
Atg12	Ubiquitin-like protein ATG12
Atg8	Ubiquitin-like protein ATG8
BHLHE40/41	Class E basic helix-loop-helix protein 40/41
BLM	Bloom syndrome protein, RecQ helicase-like
BRCA1	Breast cancer type 1 susceptibility protein
CENPC1	CENPC, Centromere protein C
CENPH	Centromere protein H
CHAF1A	Chromatin assembly factor 1, subunit A
DDR	DNA damage response
dNTPs	deoxynucleotide triphosphates
DSBs	Double strand breaks
EME1	Crossover junction endonuclease EME1
FAT10	UBD or ubiquitin D
FOXM1	Forkhead box protein M1
FUBI	Ubiquitin-like protein FUBI
GO	Gene Ontology
HERC2	HECT domain and RCC1-like domain-containing protein 2, E3 ligase
His10-S2	His10-SUMO-2-IRES-GFP
His10-S2-K0-Q87R	His10-SUMO-2-K0-Q87R-IRES-GFP
HU	Hydroxyurea
HUB1	Ubiquitin-like modifier HUB1
IAA	Iodoacetamide
IR	Ionizing radiation
IRES	Internal ribosome entry site
ISG15	Ubiquitin-like modifier ISG15
K0	Lysine-deficient
LFQ	Label free quantification
MAFF	Transcription factor MafF
MCM4	Minichromosome maintenance complex component 4
MDC1	Mediator of DNA-damage checkpoint 1
MIS18A	Protein Mis18-alpha
MMS	Methyl methanesulfonate
MYBL2	Myb-related protein B

NACC1	Nucleus accumbens-associated protein 1
Nedd8	Ubiquitin-like protein NEDD8
PCNA	Proliferating Cell Nuclear Antigen
PIAS	E3 SUMO-protein ligase
PTM	Post-translational modification
RANBP2	RAN binding protein 2
RMI1	RecQ-mediated genome instability protein 1
RNF168	E3 ubiquitin-protein ligase RNF168
SAE1	SUMO activating enzyme subunit 1
SAE2	SUMO-activating enzyme subunit 2, UBA2
Srs2	ATP-dependent DNA helicase SRS2
STRING	Search Tool for the Retrieval of Interacting Genes and Proteins
SUMO	Small Ubiquitin-like Modifier
TCEP	Tris(2-carboxyethyl)phosphine hydrochloride
TOP2A	DNA topoisomerase II α
UBC9	SUMO-conjugating enzyme UBC9
Ubl	Ubiquitin like
UFM1	Ubiquitin-fold modifier 1
URM1	Ubiquitin related modifier 1
UV	Ultraviolet

Summary

Genotoxic agents can cause replication fork stalling in dividing cells due to DNA lesions, eventually leading to replication fork collapse when the damage is not repaired. Small Ubiquitin-like Modifiers (SUMOs) are known to counteract replication stress, nevertheless, only a small number of relevant SUMO target proteins are known. To address this, we have purified and identified SUMO-2 target proteins regulated by replication stress in human cells. The developed methodology enabled single step purification of His10-SUMO-2 conjugates under denaturing conditions with high yield and high purity. Following statistical analysis on five biological replicates, a total of 566 SUMO-2 targets were identified. After 2 hours of Hydroxyurea treatment, 10 proteins were up-regulated for SUMOylation and 2 proteins were down-regulated for SUMOylation, whereas after 24 hours, 35 proteins were up-regulated for SUMOylation and 13 proteins were down-regulated for SUMOylation. A site-specific approach was used to map over 1,000 SUMO-2 acceptor lysines in target proteins. The methodology is generic and is widely applicable in the ubiquitin field. A large subset of these identified proteins function in one network that consists of interacting replication factors, transcriptional regulators, DNA damage response factors including MDC1, ATR-interacting protein ATRIP, the Bloom syndrome protein and the BLM-binding partner RMI1, the crossover junction endonuclease EME1, BRCA1 and CHAF1A. Furthermore, centromeric proteins and signal transducers were dynamically regulated by SUMOylation upon replication stress. Our results uncover a comprehensive network of SUMO target proteins dealing with replication damage and provide a framework for detailed understanding of the role of SUMOylation to counteract replication stress. Ultimately, our study reveals how a post-translational modification is able to orchestrate a large variety of different proteins to integrate different nuclear processes with the aim of dealing with the induced DNA damage.

1 Introduction

All cellular processes are tightly regulated via post-translational modifications (PTMs) including small chemical modifications like phosphorylation and acetylation and including modifications by small proteins belonging to the ubiquitin family (1). These PTMs frequently regulate protein-protein interactions via specific domains, exemplified by the archetypical phosphor-tyrosine-interacting SH2-protein-interaction module (2). The reversible nature of these modifications enables rapid and transient cellular signal transduction. As a result of these PTMs, functional proteomes are extremely complex (3).

Ubiquitination, the process of ubiquitin conjugation to target proteins is best known for its role in targeting proteins for degradation by the proteasome, but importantly also regulates target proteins in a degradation-independent manner (4). The ubiquitin-like (Ubl) family includes Small Ubiquitin-like Modifiers (SUMOs), FUBI, HUB1, Nedd8, ISG15, FAT10, URM1, UFM1, Atg12 and Atg8 (5, 6). SUMOs are predominantly located in the nucleus, regulating all nuclear processes, including transcription, splicing, genome stability and nuclear transport (7).

Similar to the ubiquitin system, SUMO conjugation is mediated by E1, E2 and E3 enzymes (8). The SUMO E1 is a dimer consisting of SAE1 and SAE2. A single E2 enzyme, Ubc9, mediates conjugation of SUMO to all target proteins. SUMO E3 enzymes include PIAS protein family members and the nucleoporin RanBP2. SUMO proteases remove SUMOs from target proteins and mediate the maturation of SUMO precursors to enable SUMO conjugation to the epsilon amino group of lysines situated in target proteins (9). A significant set of SUMO-2 acceptor lysines are situated in the SUMO consensus motif Ψ KxE (8, 10). This motif is directly recognized by Ubc9, with coordinated binding of the lysine and the acidic residue of the motif to the catalytic core of the E2 enzyme (11).

The essential role of SUMO to maintain genome stability is particularly well studied (12-14). Organisms deficient for SUMOylation display increased sensitivity for different types of DNA damaging agents including double strand breaks (IR), intra-strand crosslinks (UV), alkylation (MMS) and replication fork blockage (HU) (12-14). Mice deficient for Ubc9 die at the early post-implantation stage showing DNA hypo-condensation and chromosomal aberrancies (15). The trimeric replication clamp PCNA is one of the best studied SUMO target proteins in yeast (16, 17), where SUMOylation enables the interaction with the helicase Srs2 to prevent recombination (18-20). Multiple SUMO target proteins relevant for the DNA Damage Response have been identified in mammalian systems, including DNA topoisomerase I (21), DNA topoisomerase II α and β (22, 23), the BLM helicase (24), 53BP1 (25), BRCA1 (26), HERC2, RNF168 (27) and MDC1 (28-31). In yeast, significant numbers of SUMO target proteins have been identified upon MMS and UV treatment using proteomics approaches (32, 33).

Currently, we are limited in our understanding of the role of SUMOylation in mammalian cells during the DDR since only a limited number of SUMO target proteins are known to be specifically SUMOylated in response to DNA damage. In this study, we are focusing on the role of SUMOylation

with respect to replication, since SUMOylation-impaired organisms are particularly sensitive to replication stress (34-36). We have used a proteomics approach to purify and identify SUMO-2 target proteins and acceptor lysines from cells exposed to replication stress. We have uncovered sets of SUMO target proteins specifically up-regulated or down-regulated in response to replication stress, revealing a highly interactive network of proteins that is coordinated by SUMOylation to cope with replication damage. Our results shed light on the target protein network that is coordinated by SUMOylation to maintain genome stability during replication stress.

2 Results

A quantitative proteomics approach to identify SUMO-2 target proteins and acceptor lysines that are dynamically SUMOylated in response to replication stress.

2.1 Strategy to enrich SUMO-2 conjugates

In order to purify SUMO-2 target proteins from cells under replication stress conditions, we first generated a U2OS cell line stably expressing His10-tagged SUMO-2 (abbreviated as His10-S2). To facilitate flow cytometry sorting of cells expressing a low level of His10-S2, GFP was linked to the His10-S2 cDNA via an internal ribosome entry site (IRES) (Fig. 1A). A homogeneous population of low level GFP expressing cells was selected by flow cytometry to avoid overexpression artifacts. Immunoblotting analysis confirmed the relatively low expression level of His10-SUMO-2 compared to endogenous SUMO-2 levels in U2OS cells, and the efficient enrichment of SUMO-2 conjugates by Ni-NTA purification. Ponceau S staining is shown as a loading control. Coomassie staining showed the low level of non-specific binding of non-SUMOylated proteins (Fig. 1B). Analysis of the cells by confocal microscopy revealed that His10-SUMO-2 was predominantly located in the nucleus (Fig. 1C).

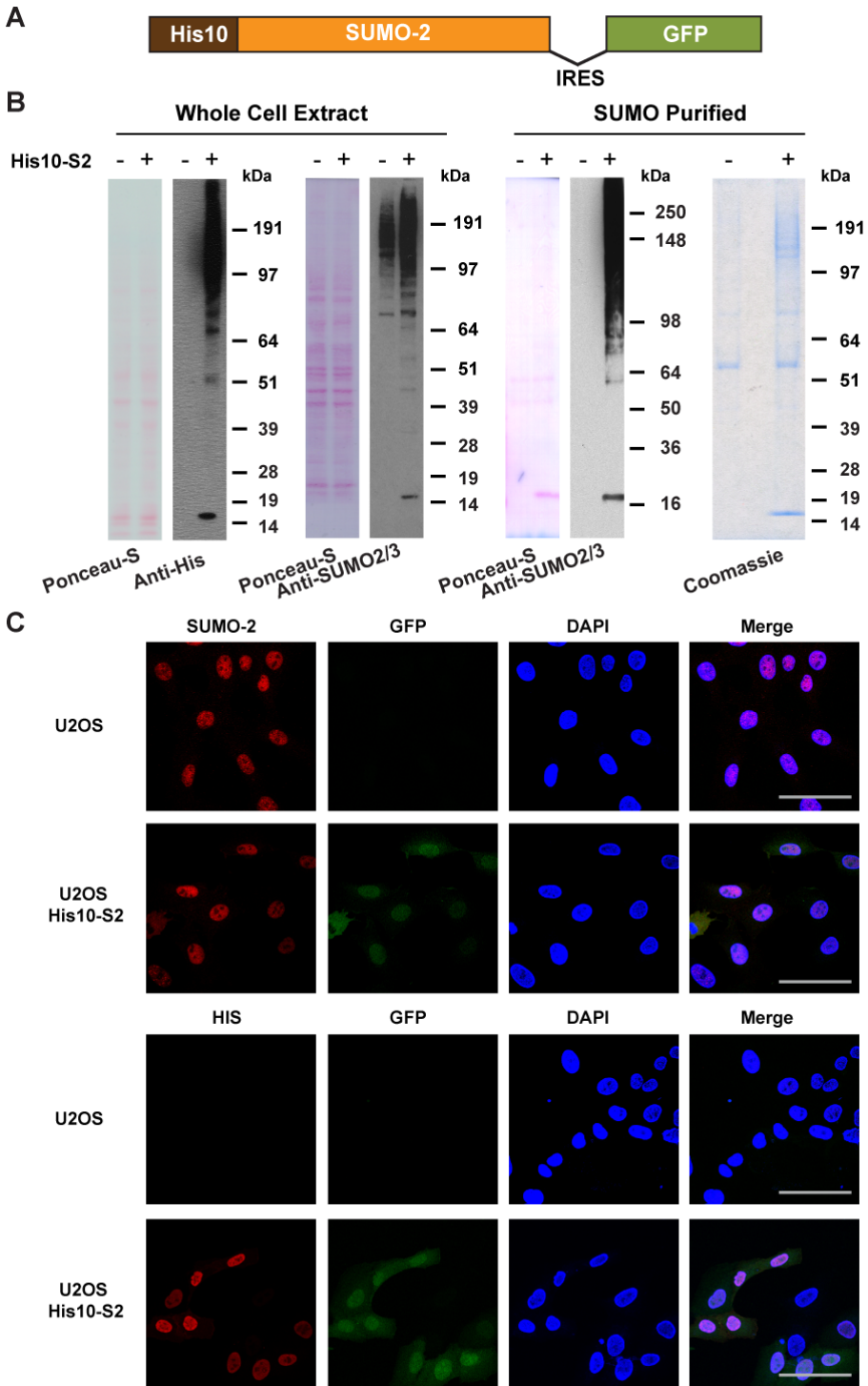


Figure 1. Generation and validation of U2OS cells stably expressing His10-SUMO-2. *A*, Schematic representation of the His10-SUMO-2-IRES-GFP construct used in this project. U2OS cells were infected with a lentivirus encoding His10-SUMO-2 (His10-S2) and GFP separated by an Internal Ribosome Entry Site (IRES) and cells stably expressing low levels of GFP were sorted by flow cytometry. *B*, Expression levels of SUMO-2 in U2OS cells and His10-SUMO-2 (His10-S2) expressing stable cells were compared by immunoblotting. Whole cell extracts were analyzed by immunoblotting using anti-polyHistidine and anti-SUMO-2/3 antibody to confirm the expression of SUMO-2 in U2OS cells and His10-SUMO-2 (His10-S2) expressing stable cells. Ponceau-S staining is shown as a loading control. Additionally, a His-pulldown was performed using Ni-NTA agarose beads to enrich SUMOylated proteins, and purification of His10-SUMO-2 conjugates was confirmed by immunoblotting using anti-SUMO-2/3 antibody. Ponceau-S staining and Coomassie staining were performed to confirm the purity of the final fraction. The experiment was performed in three biological replicates. *C*, The predominant nuclear localization of His10-SUMO-2 was visualized via confocal fluorescence microscopy after immunostaining with the indicated antibodies. DAPI staining was used to visualize the nuclei. Scale bars represent 75 μ m.

2.2 Replication stress induction upon HU treatment

To investigate global changes of proteins that are dynamically SUMOylated during early and late replication damage events, we employed a label free quantitative proteomics approach (Fig. 2A). It was reported before that after short replication blocks, replication forks can stay viable and are able to restart after release from the replication block. In contrast, prolonged stalling of replication forks is known to result in the generation of DNA double strand breaks (DSBs) in S phase and requires HR-mediated restart (43). We cultured U2OS and U2OS cells which stably expressed His10-tagged SUMO-2 (His10-S2) in regular medium and then treated these cells with 2 mM of the replication inhibiting agent hydroxyurea (HU) for 2 hours or for 24 hours in order to induce replication fork stalling.

We first used Ni-NTA purification to enrich His10-SUMO-2 conjugates from U2OS cells stably expressing His10-SUMO-2, after treatment with HU for either 2 hours, 24 hours, or after mock treatment. Parental U2OS cells were included as a negative control. Immunoblotting analysis was employed to assess global purified SUMO-2 conjugates. The total level of SUMO-2 conjugation appeared to be equal and the immunoblotting analysis also confirmed our highly efficient enrichment for SUMO-2 conjugates (Fig. 2B).

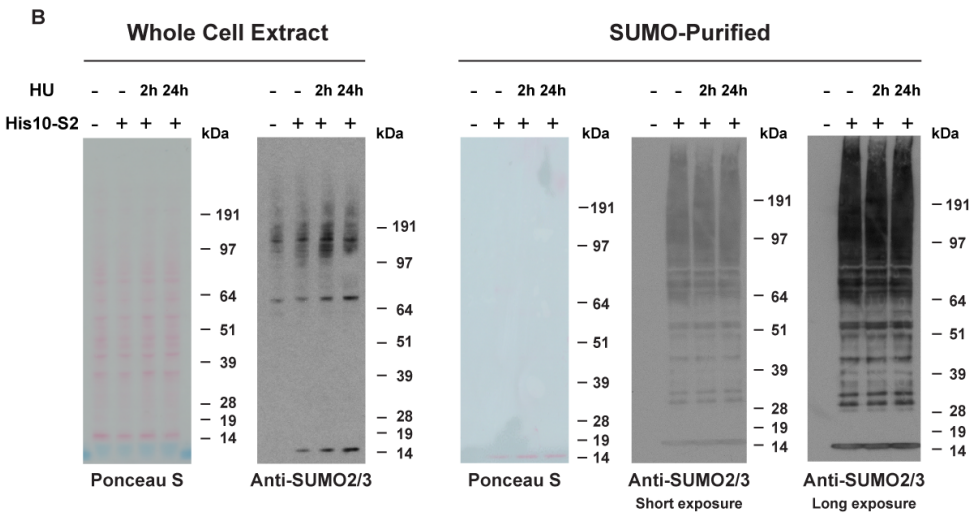
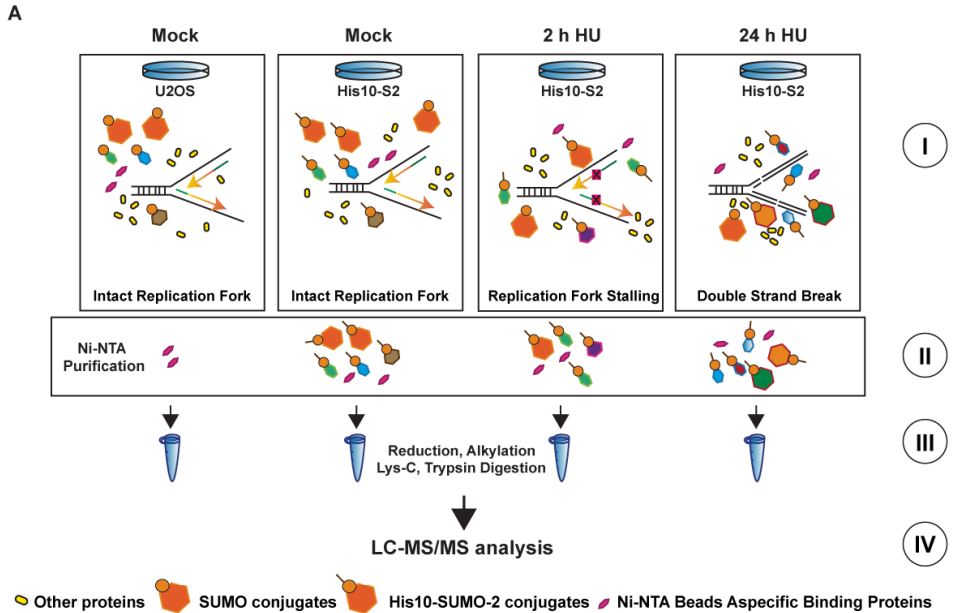


Figure 2. A strategy for discerning SUMOylation dynamics during replication stress. **A**, Cartoon depicting the strategy to study SUMOylation dynamics during replication stress. U2OS cells expressing His10-SUMO-2 were treated with 2 mM Hydroxyurea (HU) for 2 hours or 24 hours to induce DNA replication fork stalling and double strand breaks, respectively. Parental U2OS cells and U2OS cells expressing His10-SUMO-2 were mock treated as negative controls. SUMO-2 target proteins were purified by Ni-NTA purification. To study SUMO-2 targets that dynamically respond to replication stress, 5 biological replicates were performed. **B**, Purification of His10-SUMO-2 conjugates via NTA purification was confirmed by immunoblotting. Whole cell extracts and SUMO-2 purified proteins of the differently treated cells were run on 4-12% Bis-Tris polyacrylamide gels and levels of His10-SUMO-2 conjugates were compared by immunoblotting using anti-SUMO-2/3 antibody.

As indicated in Figure 3A and 3B, flow cytometry analysis from three independent experiments confirmed the enrichment of cells in the G1 phase and a decreased number of G2/M cells after 2 hours HU treatment, and a further decrease of G2/M phase cells upon 24 hours HU treatment, which confirmed stalling of the replication forks.

To further ratify that HU treatments induced the anticipated DNA damage response, we measured the formation of the phosphorylated histone variant H2AX (γ H2AX) foci after 2 hours and 24 hours HU treatment and mock treatment was used as negative control (Fig. 3C). As reported before (44), γ H2AX accumulated during 2 hours HU treatment and further increased numbers of foci were observed after 24 hours HU treatment. Furthermore, we checked the formation of Double Strand Break (DSB)-associated 53BP1 foci, and confirmed a large increase in foci upon 24 hours HU treatment (Fig. 3C).

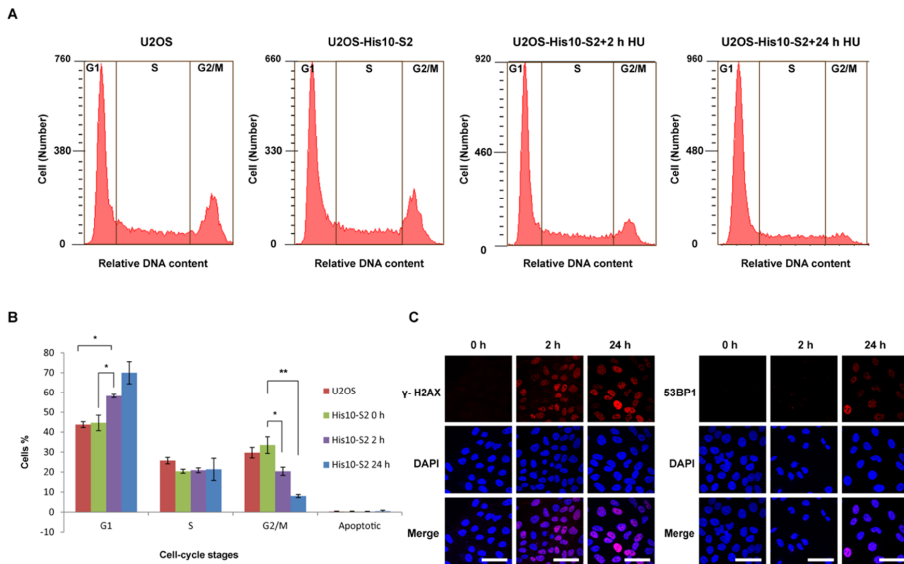


Figure 3. HU-induced DNA damage in U2OS stably expressing His10-SUMO-2. *A*, DNA content analysis of Hydroxyurea treated and non-treated cells. Flow cytometry was employed to confirm an increase in G1 phase cells upon HU treatment and a corresponding decrease in G2/M phase cells. *B*, The percentage of cells in each cell cycle phase is depicted. Error bars indicate the standard deviation from three independent replicates. Asterisks indicate significant differences by two-tailed Student's *t* testing. * $P < 0.05$, ** $P < 0.001$. *C*, Localization of γ H2AX and 53BP1 upon HU treatment. Cells were treated with 2 mM HU for 2 hours or 24 hours or left untreated. Cells were then fixed, permeabilized and immunostained for γ H2AX (red) or 53BP1 (red), and DNA was stained with DAPI (blue). Scale bars represent 75 μ m.

2.3 Identification of SUMOylated proteins using Label Free Quantification

His10-SUMO-2 purification coupled to mass spectrometry and label free quantification as described in the experimental procedures were used to study the abundance of SUMOylated proteins in response to replication stress (Fig. 4). In total, 5 biological replicates with three technical repeats for each condition were analyzed in this study. Label free quantification was performed using the MaxQuant software suite which quantifies proteins by MS1 peak intensities (41). Peak intensities measured during individual runs were matched to all other runs.

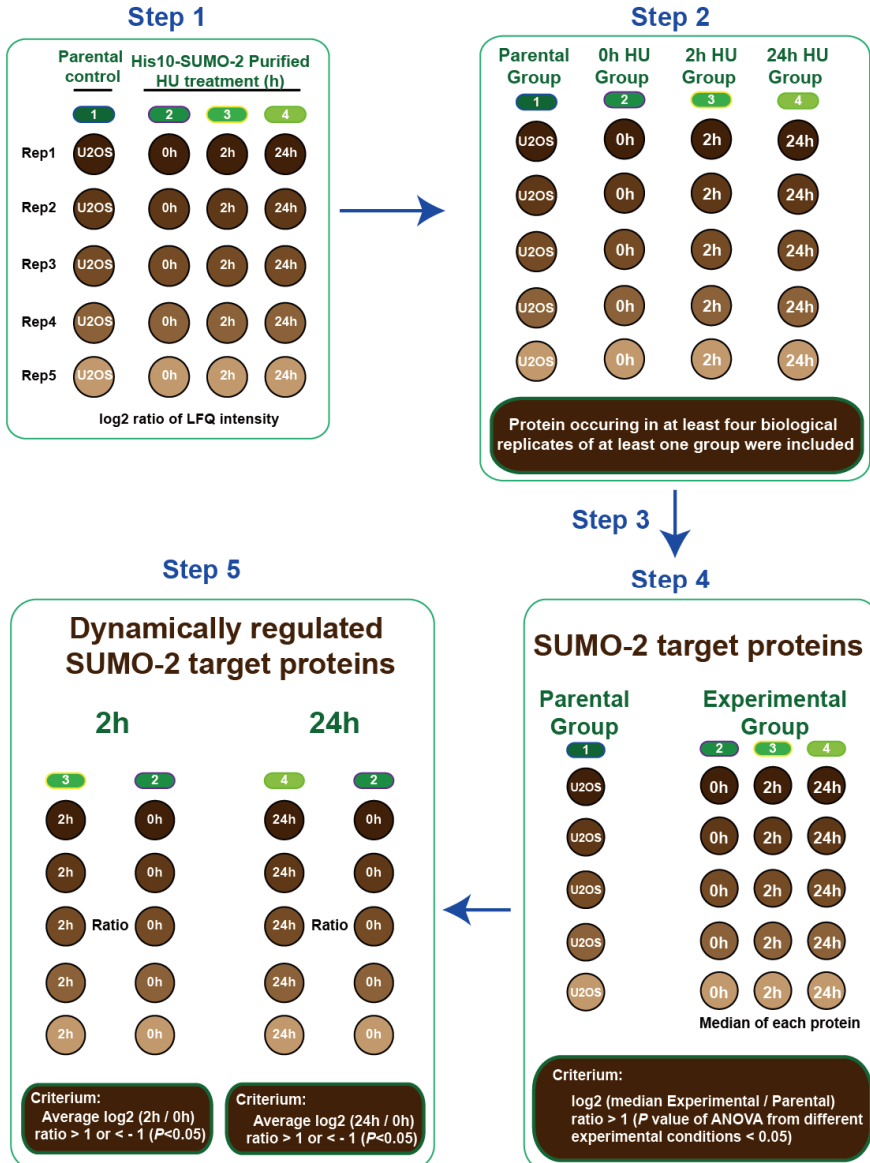


Figure 4. Label Free Quantification Strategy. Cartoon depicting our strategy for Label Free Quantification (LFQ) to select SUMO-2 target proteins and to identify significantly up- or down- regulated SUMO-2 target proteins in response to 2 hours or 24 hours HU treatment.

Step 1: Protein lists generated by MaxQuant were further analyzed by Perseus and LFQ intensities were \log_2 transformed.

Step 2: Different experiments were divided into four groups based on experimental conditions: a parental control group for U2OS control samples and three experimental groups for SUMO-2 samples purified from U2OS cells expressing His10-SUMO-2 treated with HU for 2 hours or 24 hours or mock treated. Inclusion criteria are depicted.

Step 3: Imputation of the missing values by normally distributed values with 1.8 downshift (\log_2) and 0.3 randomized width (\log_2).

Step 4: Proteins were considered as SUMO-2 target proteins using the indicated criteria.

Step 5: Significantly up- or down- regulated SUMO-2 target proteins in response to 2 hours or 24 hours HU treatment were identified as indicated.

2881 proteins were identified from 48821 peptides and 566 of them were considered as SUMO-2 target proteins in response to DNA replication stress (Fig. 5A and Table S1). After filtering out contaminants and putative false positives, all the LFQ intensities were transformed by \log_2 . The multiple scatter plot in Figure 5B shows high correlation within each condition throughout different biological replicates. SUMO-2 purified fractions showed more correlation than parental control due to specific enrichment of SUMOylated proteins by the affinity purification. Next, \log_2 ratios of all the LFQ intensities were used to generate a heat map by hierarchical clustering of all proteins. The heat map also visualized a high correlation between the biological replicates (Fig. 5C).

Subsequently, LFQ ratios corresponding to proteins derived from SUMO-2 enriched fractions purified from either the parental U2OS cell line or U2OS cells stably expressing His10-SUMO-2 were compared, in order to filter out non-specifically binding proteins (Fig. 4). After selecting proteins that were found in at least four biological replicates in at least one experimental condition in SUMO-2 purified samples, missing LFQ ratios were imputed as described in the experimental procedures. Proteins were considered as SUMO-2 target proteins when they were enriched at least two-fold from His10-SUMO-2 expressing cells compared to U2OS parental control cells. The SUMOylated protein list is provided in Table S1.

To assess the biological function of SUMOylated proteins identified in this study, we performed Gene Ontology (GO) term enrichment analysis using Perseus (Fig. 5D, Table S2 and Table S3). For GO Biological Processes, proteins involved in the DNA damage response were found to be significantly enriched. 53 proteins were related to DNA repair, 61 proteins were related to the DNA damage response. For GO Cellular Compartments, 300 proteins were found to be located in the nucleus. For GO Molecular Functions, 260 proteins were involved in DNA binding and 11 proteins were involved in damaged DNA binding.

2.4 Analysis of SUMOylated protein dynamics during replication stress

SUMOylation dynamics in response to replication stress was explored using bioinformatics analysis as described in experimental procedures and in Figure 4. Ten proteins were significantly increased in SUMOylation and 2 proteins were significantly decreased in SUMOylation after 2 hours HU treatment. After 24 hours HU treatment, 35 proteins were significantly increased in SUMOylation and 13 proteins were significantly decreased in SUMOylation (Table S4).

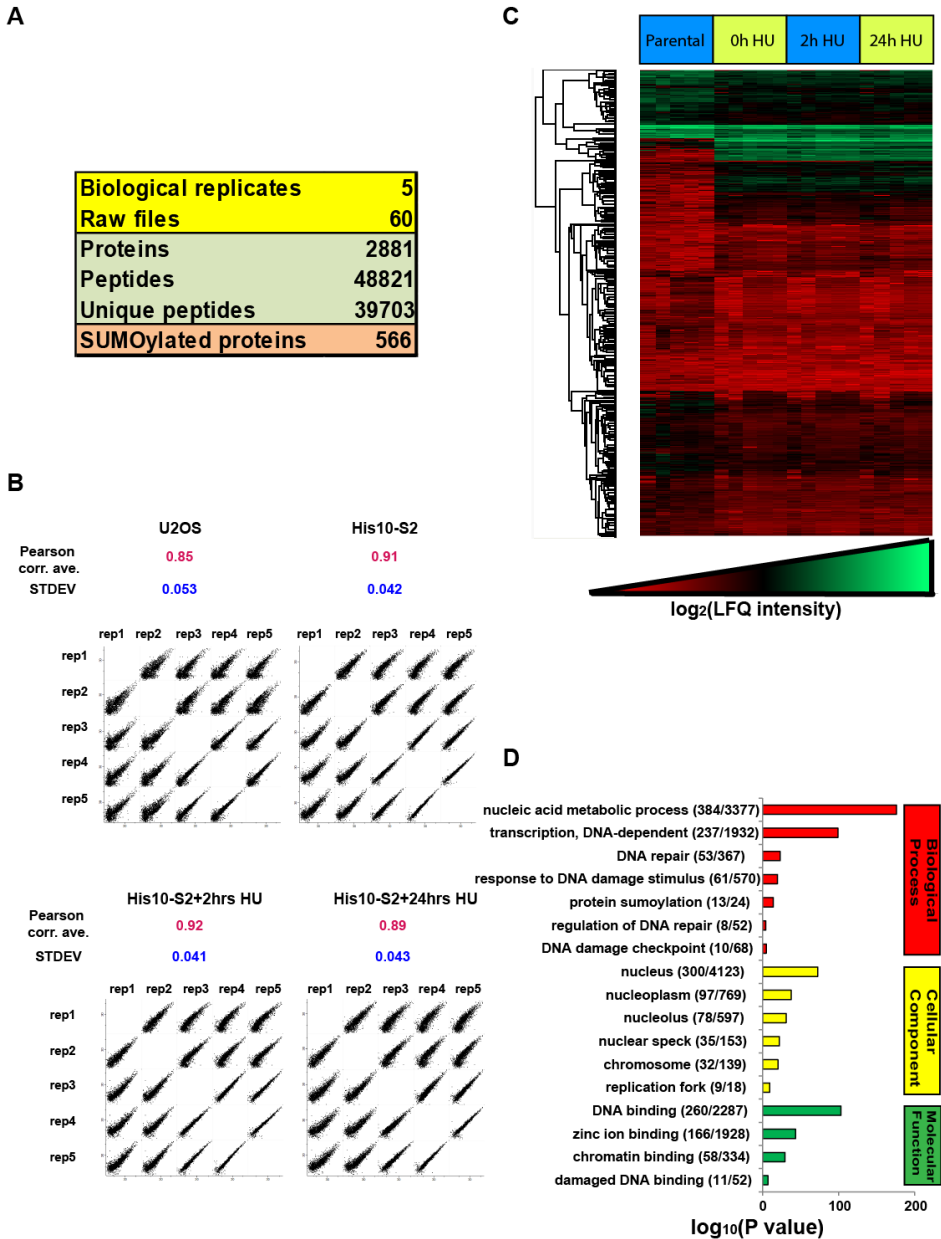


Figure 5. Overview of the SUMO proteomics results. *A*, Overview of the proteomic experiments. Out of 2,881 proteins identified with 48,821 peptides, 566 proteins were considered as SUMO-2 target proteins after filtering by LFQ intensities as described in Figure 4. *B*, LFQ intensity scatter plot. Each condition of each biological replicate was plotted together to visualize the correlation between the experiments. Pearson correlation averages were calculated for each condition and standard deviations (SD) are indicated. *C*, Heat map of log₂ LFQ intensities. Hierarchical clustering was performed for all identified

proteins. Within each biological replicate, the sample order from left to right was U2OS, U2OS His10-SUMO-2 (mock treated), U2OS His10-SUMO-2 (2 hours HU), and U2OS His10-SUMO-2 (24 hours HU). **D**, GO term enrichment analysis of the SUMOylated proteins identified. The bar chart shows GO terms for biological processes, cellular components and molecular functions.

Volcano plots shown in Figure 6A and 6B indicate the significance and magnitude of SUMO-2 target protein changes after 2h and 24h HU treatment. *P* values less than 0.05 were considered significant. STRING analysis of significantly regulated SUMOylated proteins was performed. Figure 6C shows the interaction of proteins significantly increased or decreased in SUMOylation after 2 hours of HU treatment. SUMOylation of CHAF1A and PCNA was significantly decreased. On the other hand, SUMOylation of MCM4, MYBL2 and FOXM1 was found to be increased. Similar to the finding of Li *et al.* (45), PCNA is a hub connecting several other SUMOylated proteins, including CHAF1A, FOXM1, MYBL2, ATRIP, and MCM4. After 24 hours of HU treatment (Fig. 6D), BHLHE41, CHAF1A, and DNMT1 were significantly decreased in SUMOylation. Additionally, BHLHE40, BARD1, MDC1, RMI1, and BRCA1 were greatly increased in SUMOylation. EME1 was found to be modestly down-regulated and additionally high-lighted in Figure 6B. Most of the SUMOylated proteins were significantly interacting to each other throughout the STRING network. In conclusion, DNA replication stress caused by HU treatment changed the SUMOylation of a distinct subset of proteins with key functions in the DNA damage response.

2.5 Site-specific SUMOylation dynamics during replication stress

Previously we have developed methodology to study SUMOylation at the site-specific level (Fig. S1) (38, 39). Here we used similar methodology to map SUMO-2 acceptor lysines in U2OS target proteins. First, we generated U2OS cells stably expressing lysine-deficient His10-SUMO-2 with a conserved mutation at its C-terminal part, Q87R, which mimics the localization of an arginine in yeast SUMO, Smt3. Characterization of the cell line is shown in Figure S2. We used this cell line to enrich SUMOylation sites from mock treated cells, or cells treated with HU for 2 hours or 24 hours to induce replication stress. In total, 1,043 SUMOylation sites were identified in 426 proteins (Tables S5 and S6), at a false discovery rate (FDR) below 1%. Mass accuracy was within 3 p.p.m. for 98.8% of all identified sites and within 6 p.p.m. for all sites, with an average absolute mass error of 0.78 p.p.m. We identified 83 peptides co-modified by SUMOylation and phosphorylation, of which 24 SUMOylated peptides were not found in the non-phosphorylated form (Table S9).

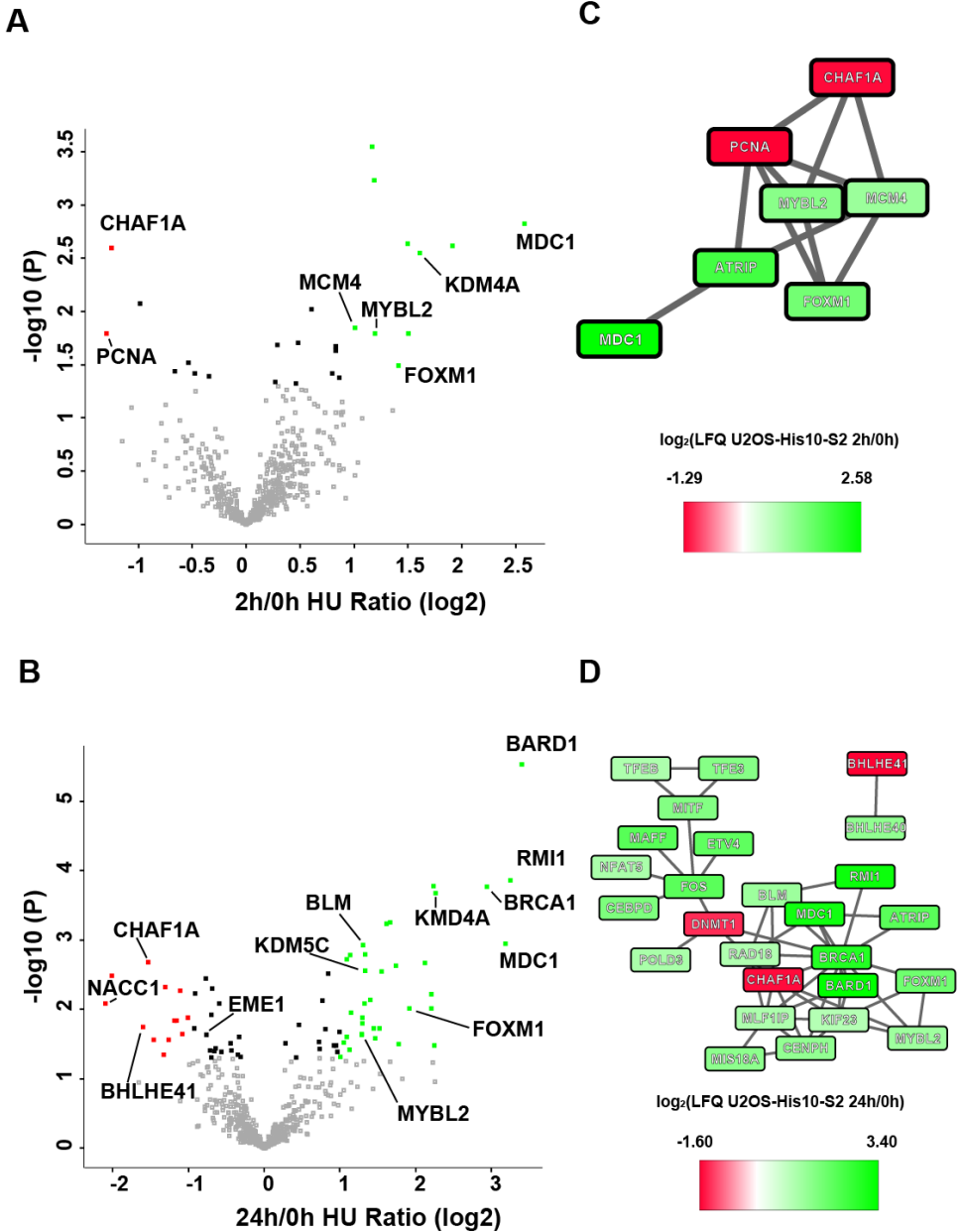


Figure 6. Volcano plots and STRING protein interaction network of dynamically regulated SUMO-2 target proteins. A, B, Volcano plots to show significantly altered SUMO-2 targets in response to 2 hours HU treatment (A) or 24 hours HU treatment (B). The $-\log_{10}(P)$ value of 2h/0h and 24h/0h from pairwise comparisons of SUMO-2 target proteins purified from mock treated cells and HU-treated cells were plotted against the average LFQ ratio 2h/0h (\log_2) and LFQ ratio 24h/0h (\log_2). The red dots represent proteins decreased for SUMOylation in response to HU with an average \log_2 ratio smaller than -1. The green dots represent proteins increased for SUMOylation in response to HU with an average \log_2 ratio greater than 1. C, STRING analysis of dynamically regulated SUMO-2 target proteins after 2 hours Hydroxyurea treatment. P value: 1.42×10^{-7} .

Upregulated SUMOylated proteins are colored in green and downregulated SUMOylated proteins are colored in red. **D**, STRING analysis of dynamically regulated SUMO-2 target proteins after 24 hours Hydroxyurea treatment. *P* value: 6.94×10^{-14} . Upregulated SUMOylated proteins are colored in green and downregulated SUMOylated proteins are colored in red.

In order to study the dynamics of SUMO-2 acceptor sites in response to HU treatment, SUMO-2 site MS1 peak intensities were normalized and compared between samples. Volcano plots were used to visualize SUMOylation site dynamics in response to 2 hours or 24 hours HU treatment. (Fig. 7A and 7B). Sites displaying a significant change of at least two-fold in response to HU treatment are highlighted. After 2 hours of HU treatment, 27 sites were significantly upregulated and 23 sites were significantly downregulated. After 24 hours of HU treatment, 49 sites were upregulated and 38 sites were downregulated (Table S7). Overall, the dynamic SUMO-2 sites correspond well with the results from our site-independent approach (Table S8).

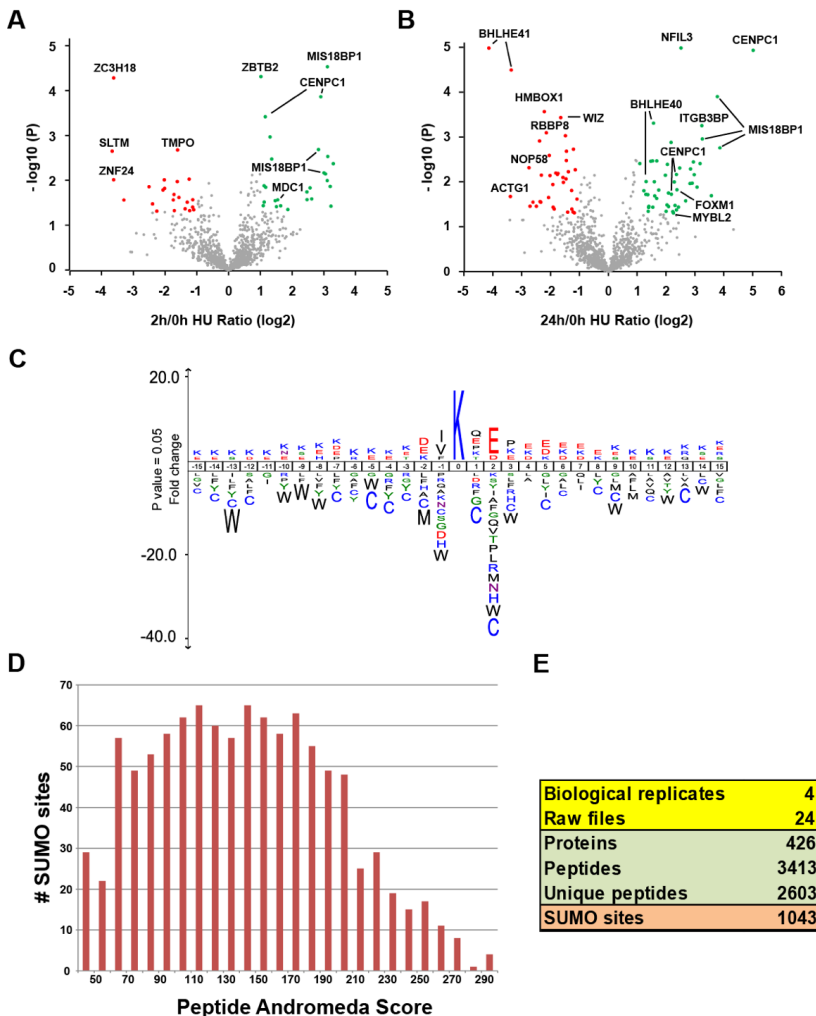


Figure 7. Volcano plots of dynamically regulated SUMOylation sites and SUMOylation motif analysis. **A, B,** Volcano plots showing dynamically regulated SUMO-2 acceptor sites in response to 2 hours HU treatment (A) or 24 hours HU treatment (B). The $-\log_{10}(P)$ value from pairwise comparisons of SUMO-2 acceptor lysines purified from mock treated cells and HU-treated cells were plotted against the average LFQ Ratio 2h /0h (\log_2) and LFQ Ratio 24h /0h (\log_2). The red dots represent sites decreased for SUMOylation in response to HU with an average \log_2 ratio smaller than -1.0 and with $P < 0.05$. The green dots represent sites increased for SUMOylation in response to HU with an average \log_2 ratio greater than 1.0 and with $P < 0.05$. **C,** All SUMO-2 acceptor lysines identified in this study (1,043 sites) were used to generate a SUMOylation motif employing IceLogo software. The height of the amino acid letters represents the fold change as compared to amino acid background frequency. All amino acid changes were significant with $P < 0.05$ by two-tailed Student's t test. **D and E,** Summary of the SUMO-2 acceptor lysines identified (E) with their peptide Andromeda scores (Median = 141.36) (D).

2.6 Verification of dynamic SUMO targets upon DNA replication stress.

We verified SUMOylation dynamics upon DNA replication stress by immunoblotting analysis for a subset of the identified dynamic SUMO-2 targets, including FOXM1, MYBL2, MDC1, and EME1 (Fig. 8). To study whether the HU treatment was efficient, flow cytometry was used to confirm the expected effects on cell cycle progression (Fig. 3A and 3B). All four of these SUMO-2 target proteins were found to be dynamically SUMOylated in accordance with the LFQ data derived from the mass spectrometry analysis, whereas the total amount of SUMO remained stable. As such, we demonstrated the feasibility of our approach, providing a powerful tool for analysis of SUMOylation dynamics in general, as well as a reliable resource of SUMO-2 target proteins dynamically regulated in response to replication stress.

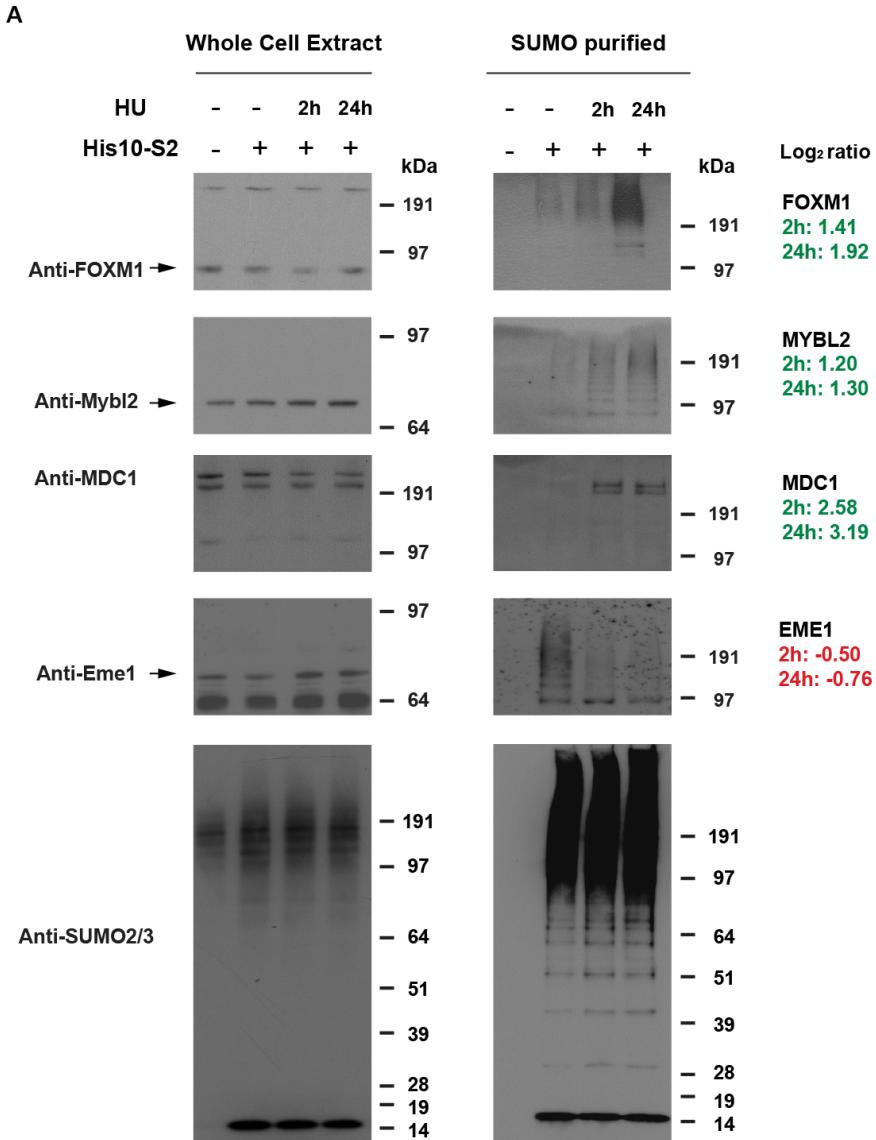


Figure 8. Verification of SUMO targets showing SUMOylation dynamics in response to replication stress. U2OS cells and U2OS cells expressing His10-tagged SUMO-2 were either mock treated or treated with Hydroxyurea (2 mM) for 2 hours or 24 hours as described, and His10-SUMO-2 conjugates were purified by Ni-NTA purification. SUMOylation dynamics induced by DNA replication stress was analyzed for four different SUMO-2 targets identified in the mass spectrometry screen using the indicated antibodies, and equal levels of SUMO conjugates in all samples were verified via immunoblotting using anti-SUMO-2/3 antibody. The fold changes in SUMOylation (log₂) of these proteins as found in our proteomics screen are indicated on the right.

3 Discussion

Our knowledge on the role of SUMOylation to maintain genome stability during replication is limited, due to limited insight into all involved SUMO target proteins. To address this, we have optimized a purification procedure to enrich SUMO target proteins, reaching a depth of 566 proteins. The optimized methodology employs the His10 tag, enabling the use of denaturing buffers to inactivate proteases and combining a high yield with a high purity; a major improvement over the His6 tag as a result of the usage of a much higher concentration of competing imidazole during the purification procedure to reduce the binding of contaminating proteins.

We have used the optimized methodology to study SUMOylation dynamics in response to HU-induced replication stress, resulting from the depletion of dNTPs required for DNA replication. A group of 12 dynamic SUMO-2 targets were identified when cells were treated for 2 hours with HU, including 10 upregulated and 2 downregulated proteins. When treating U2OS cells for 24 hours with HU, 48 dynamic SUMO-2 targets were identified including 35 upregulated and 13 downregulated proteins. As a cautionary note, we cannot exclude the possibility that changes in total levels of some proteins could underlie some of the observed changes in SUMOylation. More than half (2h: 70%, 24h: 52%) of these targets are functionally connected, indicating tight interactions between the SUMO-orchestrated proteins. The identified SUMO-regulated functional groups include key replication factors, DDR-components, a transcription-factor network, centromeric proteins and signal transducers. Identification of sites of modification is the most reliable manner to study post-translational modification of proteins (5). Powerful site-specific methodology is available to study phosphorylation and ubiquitination. In contrast, this has remained a major challenge in the SUMOylation field (5). Several years ago, we have developed a novel approach, enabling the identification of a limited set of SUMO-2 acceptor lysines in endogenous target proteins (38). Recently, we have further optimized this methodology by employing the His10-tag, enabling large-scale identification of SUMOylation sites (39). The use of a lysine-deficient version of SUMO-2 enabled the enrichment of SUMOylated peptides after Lys-C digestion. This is a key step to reduce the complexity of samples prior to mass spectrometry analysis. Using this methodology, we have identified 1,043 SUMOylation sites in this project, including 382 sites not previously identified (39). Similar methodology could be employed to study other ubiquitin-like modifications.

Proliferating Cell-Nuclear Antigen (PCNA) is one of the most strongly downregulated SUMO target proteins after two hours of HU treatment and is also one of the most highly connected components of the SUMO-target protein interaction network as depicted in Figure 6C. PCNA is a trimeric replication clamp that serves as platform for replicating polymerases. SUMOylated PCNA is known to interact with the helicase Srs2 to counteract recombination (18-20). Down-regulation of PCNA SUMOylation at early time points could represent a mechanism to explain increased recombination as a result of HU treatment, to counteract replication fork stalling (46).

MCM4 is a second key replication factor that we identified in our screen. MCM4 is a component of the DNA replication licensing factor Mini Chromosome Maintenance (MCM), which consists of MCM2-7 hexamers. The MCM complex plays an essential role in replication licensing and ensures that the entire genome is replicated exactly once during S-phase, avoiding reduplication or leaving genomic regions unreplicated (47). It acts as a helicase to unwind DNA, enabling access for the replication machinery to duplicate DNA. Interestingly, we previously found that MCM4 SUMOylation preferentially occurs during G1, a time point when MCM complexes are loaded on DNA for replication-licensing (48). Our data indicate a small increase in MCM4 SUMOylation in response to HU-treatment, which potentially could be involved in a cellular attempt to complete replication by firing of dormant origins in response to replication fork stalling (49). It is currently unclear how SUMOylation precisely regulates MCM4.

Furthermore, we identified a set of known SUMOylated DNA damage response factors, including MDC1, BRCA1 and BLM. MDC1 was previously found to be SUMOylated in response to Ionizing Radiation (28-31), and BRCA1 was found to be SUMOylated in response to cisplatin and HU (26). SUMOylation regulates the interaction of BLM and RAD51 at damaged replication forks (50) and the accumulation of ssDNA at stalled replication forks. The identification of SUMOylated BRCA1 and BLM is thus in agreement with the existing literature, and underlines the validity of our approach.

After prolonged exposure of cells to HU, SUMOylation of a cluster of centromeric proteins was induced, including CENPC1, CENPH and MIS18A (51) which is required for regulating CENPA deposition. Our data thus indicate co-regulation of centromeric proteins by SUMOylation in response to replication stress. The functional significance of these findings could further be explored, since other studies have demonstrated that SUMOylation at centromeres plays a key role to regulate cell cycle progression (23, 52-54).

Finally, it is interesting to note that SUMOylation regulates a number of factors involved in other modifications, demonstrating extensive signaling crosstalk. These proteins include the ATR-interacting protein ATRIP, ubiquitin E3 ligases RAD18 and BRCA1, the lysine-specific demethylases KDM5D, KDM5C and KDM4A. SUMOylation of HDAC1 and BRCA1 was previously demonstrated to promote enzymatic activity (26, 55), and it would be interesting to determine the functional relevance of SUMOylation for these other SUMO target proteins. Concerning crosstalk, we also obtained evidence for mixed SUMO-ubiquitin chains in our study, including linkages of SUMO-2 to lysines 11, 48 and 63 of ubiquitin. Furthermore, we found 83 peptides simultaneously modified by both SUMO-2 and phosphorylation (Table S9).

In summary, our study provides a critical framework to understand the role of SUMOylation to maintain genome stability during replication stress. The identified target proteins can be studied in detail at the functional level. Replication problems frequently lead to genome instability, one of the enabling characteristics of cancer cells (56). A detailed understanding of the role of SUMOylation in genome instability could potentially be employed to counteract oncogenesis, similarly to recent successful

efforts to disrupt signal transduction by the ubiquitin-like protein Nedd8 (57, 58). Moreover, the developed methodology could be widely employed to study SUMOylation, but also ubiquitination and signal transduction by other ubiquitin-like proteins.

Ultimately, our study reveals how SUMO regulates a network of target proteins in response to replication stress to coordinate the cellular DNA damage response. This network not only consists of known DNA damage response factors, but also includes replication factors, transcriptional regulators, chromatin modifiers and centromeric proteins, revealing how a post-translational modification is able to orchestrate a large variety of different proteins to integrate different nuclear processes with the aim of dealing with the induced DNA damage.

4 Experimental procedures

4.1 Antibodies

The primary antibodies used were: Mouse monoclonal anti-polyHistidine, clone HIS-1 (Sigma, H1029), mouse monoclonal anti-SUMO-2/3 (Abcam, ab81371), rabbit polyclonal anti-SUMO-2/3 (developed with Eurogentec) (37), rabbit polyclonal anti gamma-H2AX (Bethyl, A300-081A), rabbit polyclonal anti-53BP1 (Bethyl, A300-272A), mouse monoclonal anti EME1 (ImmuQuest, IQ284), rabbit polyclonal anti B-Myb (Mybl2) (Bethyl, A301-654A), rabbit polyclonal anti-FOXM1 (Santa Cruz Biotechnology, sc-502) and rabbit polyclonal anti-MDC1 (Bethyl, A300-052A).

4.2 Electrophoresis and immunoblotting

Whole cell extracts or purified protein samples were separated on Novex Bolt 4-12% Bis-Tris Plus gradient gels (Life Technologies) using MOPS buffer or via regular SDS-PAGE using a Tris-glycine buffer and transferred onto Hybond-C nitrocellulose membranes (GE Healthcare Life Sciences) using a submarine system (Life Technologies). Membranes were stained with Ponceau S (Sigma) to stain total protein and blocked with PBS containing 8% milk powder and 0.05% Tween-20 before incubating with the primary antibodies as indicated. Gels were stained with Coomassie using the Colloidal Blue Staining kit according to the manufacturer's instructions (Life Technologies).

4.3 Flow cytometry

Cells were harvested by a mild trypsin treatment, subsequently washed two times with phosphate-buffered saline (PBS) and resuspended in 1.3 mL of PBS. Afterwards, 3.75 mL of 100% ethanol was added and the cells were fixed at 4 °C overnight. On the day of flow cytometry analysis, the cells were centrifuged at 250 r.c.f. for 2 minutes, the supernatant was removed and the cells were washed with PBS and 2% fetal calf serum. Then, the cells were pelleted again and resuspended in 500 µL of PBS complemented with 2% fetal calf serum, 25 µg/mL propidium iodide (Sigma) and 100 µg/mL RNase A (Sigma) and then incubated for 30 minutes at 37 °C. FACS analysis was performed on a BD LSRII system and all gathered data was analyzed using BD FACS DIVA Software (BD Biosciences Clontech).

4.4 Cell culture, cell line generation and Hydroxyurea treatment

Cells were cultured in Dulbecco's modified Eagle's medium (Life Technologies) supplemented with 10% fetal bovine serum (Life Technologies) and 100 U/mL penicillin and 100 µg/mL streptomycin (Life Technologies). U2OS cells were infected using a bicistronic lentivirus encoding His10-SUMO-2 (His10-S2) and GFP separated by an IRES. Following infection, cells were sorted for low GFP levels using a FACSAria II (BD Biosciences). To induce DNA replication damage, an asynchronously growing cell population was incubated in medium containing 2 mM Hydroxyurea (Sigma) for either 2 hours or 24 hours. In all cases, the cells were then harvested and subjected to flow cytometry analysis, or Ni-NTA purification to enrich SUMO conjugates. For the proteome-wide identification of SUMO-2 acceptor lysines, U2OS cells were infected with bicistronic lentiviruses encoding His10-SUMO-2-K0-Q87R-IRES-GFP, abbreviated as His10-S2-K0-Q87R.

4.5 Immunofluorescence

Primary antibodies used for immunofluorescence were rabbit polyclonal anti-53BP1, rabbit polyclonal anti-phospho-Histone H2AX (Ser139) (gamma H2AX). Secondary antibody was anti-rabbit IgG AlexaFluor 594 (Life Technologies). Cells were cultured on circular glass slides in 24-well plates. After Hydroxyurea treatment for either 2 hours or 24 hours, medium was removed, cells were fixed with 4% paraformaldehyde for 20 minutes at room temperature in PBS and cells were permeabilized with 0.1% Triton X-100 in PBS for 15 minutes. Next, cells were washed twice with PBS and once with PBS with 0.05% Tween-20 (PBS-T). Cells were then blocked for 10 minutes with 0.5% blocking reagent (Roche) in 0.1 M Tris, pH 7.5 and 0.15 M NaCl (TNB) and incubated with primary antibody in TNB for one hour. Coverslips were washed five times with PBS-T and incubated with the secondary antibody in TNB for one hour. Next, coverslips were washed five times with PBS-T and dehydrated by washing once with 70% ethanol, once with 90% ethanol, and once with 100% ethanol. After drying the cells, coverslips were mounted onto a microscopy slide using citifluor/DAPI solution (500 ng/mL) and sealed with nail varnish. Images were recorded on a Leica TCS SP8 confocal microscope system equipped with 405, 488, 552 and 638-nm lasers for excitation, and a 63× lens for magnification, and were analyzed with Leica confocal software.

4.6 Purification of His10-SUMO-2 conjugates

U2OS cells expressing His10-SUMO-2 were washed, scraped and collected in ice-cold PBS. For total lysates, a small aliquot of cells was kept separately and lysed in 2% SDS, 1% N-P40, 50 mM TRIS pH 7.5, 150 mM NaCl. The remaining part of the cell pellets were lysed in 6 M guanidine-HCl pH 8.0 (6 M guanidine-HCl, 0.1 M Na₂HPO₄/NaH₂PO₄, 10 mM TRIS, pH 8.0). The samples were snap frozen using liquid nitrogen, and stored at -80°C.

For His10-SUMO-2 purification, the cell lysates were first thawed at room temperature and sonicated for 5 sec using a sonicator (Misonix Sonicator 3000) at 30 Watts to homogenize the lysate.

Protein concentrations were determined using the bicinchoninic acid (BCA) protein assay reagent (Thermo Scientific) and lysates were equalized. Subsequently, imidazole was added to a final concentration of 50 mM and β -mercaptoethanol was added to a final concentration of 5 mM. His10-SUMO-2 conjugates were enriched on nickel-nitrilotriacetic acid-agarose beads (Ni-NTA) (Qiagen), and subsequently the beads were washed using wash buffers A-D. Wash buffer A: 6 M guanidine-HCl, 0.1 M Na₂HPO₄/NaH₂PO₄ pH 8.0, 0.01 M Tris-HCl pH 8.0, 10 mM imidazole pH 8.0, 5 mM β -mercaptoethanol, 0.1% Triton X-100. Wash buffer B: 8 M urea, 0.1 M Na₂HPO₄/NaH₂PO₄ pH 8.0, 0.01 M Tris-HCl pH 8.0, 10 mM imidazole pH 8.0, 5 mM β -mercaptoethanol, 0.1% Triton X-100. Wash buffer C: 8 M urea, 0.1 M Na₂HPO₄/NaH₂PO₄ pH 6.3, 0.01 M Tris-HCl pH 6.3, 10 mM imidazole pH 7.0, 5 mM β -mercaptoethanol, no Triton X-100. Wash buffer D: 8 M urea, 0.1 M Na₂HPO₄/NaH₂PO₄ pH 6.3, 0.01 M Tris-HCl, pH 6.3, no imidazole, 5 mM β -mercaptoethanol, no Triton X-100. Wash buffers employed for immunoblotting experiments contained 0.2% Triton X-100. Samples were eluted in 7 M urea, 0.1 M NaH₂PO₄/Na₂HPO₄, 0.01 M Tris/HCl, pH 7.0, 500 mM imidazole pH 7.0. For site-specific purification, we used the strategy developed previously by our group (38, 39).

4.7 Sample preparation and mass spectrometry

SUMO-2 enriched samples were supplemented with 1 M Tris-(2-carboxyethyl)-phosphine hydrochloride (TCEP) to a final concentration of 5 mM, and incubated for 20 minutes at room temperature. Iodoacetamide (IAA) was then added to the samples to a 10 mM final concentration, and samples were incubated in the dark for 15 minutes at room temperature. Lys-C and Trypsin digestions were performed according to the manufacturer's specifications. Lys-C was added in a 1:50 enzyme-to-protein ratio, samples were incubated at 37 °C for 4 hours, and subsequently 3 volumes of 100 mM Tris-HCl pH 8.5 were added to dilute urea to 2 M. Trypsin (V5111, Promega) was added in a 1:50 enzyme-to-protein ratio and samples were incubated overnight at 37 °C. For site-specific samples preparation, we used the strategy developed previously by our group (39).

Subsequently, digested samples were desalted and concentrated on STAGE-tips as described previously (40) and eluted with 80% acetonitrile in 0.1% formic acid. Eluted fractions were vacuum dried employing a SpeedVac RC10.10 (Jouan, France) and dissolved in 10 μ L 0.1% formic acid before online nanoflow liquid chromatography-tandem mass spectrometry (nanoLC-MS/MS).

All the experiments were performed on an EASY-nLC 1000 system (Proxeon, Odense, Denmark) connected to a Q-Exactive Orbitrap or a Q-Exactive Plus Orbitrap (Thermo Fisher Scientific, Germany) through a nano-electrospray ion source. For the Q-Exactive, peptides were separated in a 13 cm analytical column with an inner-diameter of 75 μ m, in-house packed with 1.8 μ m C18 beads (Reprospher-DE, Pur, Dr. Manish, Ammerbuch-Entringen, Germany). The Q-Exactive Plus was coupled to 15 cm analytical columns with an inner-diameter of 75 μ m, in-house packed with 1.9 μ m

C18 beads (Reprospher-DE, Pur, Dr. Manish, Ammerbuch-Entringen, Germany), employing a column oven (PRSO-V1, Sonation, Biberach) to heat the column to 50 °C.

The gradient length was 120 minutes from 2% to 95% acetonitrile in 0.1% formic acid at a flow rate of 200 nL/minute. The mass spectrometers were operated in data-dependent acquisition mode with a top 10 method. Full-scan MS spectra were acquired at a target value of 3×10^6 and a resolution of 70,000, and the Higher-Collisional Dissociation (HCD) tandem mass spectra (MS/MS) were recorded at a target value of 1×10^5 and with a resolution of 17,500 with a normalized collision energy (NCE) of 25%. The maximum MS1 and MS2 injection times were 20 ms and 60 ms, respectively. The precursor ion masses of scanned ions were dynamically excluded (DE) from MS/MS analysis for 60 sec. Ions with charge 1, and greater than 6 were excluded from triggering MS2 events.

For samples enriched for identification of SUMO-2 acceptor lysines, a 120 minute gradient was used for chromatography. Data dependent acquisition with a top 5 method was used. Maximum MS1 and MS2 injection times were 20 ms and 250 ms, respectively. Resolutions, normalized collision energy and automatic gain control target were set as mentioned previously. Dynamic exclusion was set to 20 sec.

4.8 Protein level SUMOylation data analysis

For protein-level data analysis, four experimental conditions were performed in biological quintuplicate, and all samples were measured in technical triplicate, resulting in a total of 60 runs. All RAW data was analyzed using MaxQuant (version 1.4.1.2) and its integrated search engine Andromeda. The first search was carried out with 20 ppm, while the main search used 6 ppm for precursor ions. Mass tolerance of MS/MS spectra were set to 20 ppm to search against an *in silico* digested UniProt reference proteome for *Homo sapiens* (13 Nov 2013, 88704 proteins). Additionally, MS/MS data were searched against a list of 262 common mass spectrometry contaminants by Andromeda.

Database searches were performed with Trypsin/P and Lys-C specificity, allowing two missed cleavages. Carbamidomethylation of cysteine residues was considered as a fixed modification. Oxidation of methionine, phosphorylation and acetylation of protein N-termini were considered as variable modifications. Match between runs was performed with 0.7 min match time window and 20 min alignment time window. The minimum peptide length was set to 6. Protein groups considered for quantification required at least 2 peptides, including unique and razor peptides. Peptides and proteins were identified with a false discovery rate of 1% according to Cox *et al.* (41).

Label-free quantification was carried out, as described in Figure 4, using MaxLFQ without fast LFQ. Proteins identified by the same set of peptides were combined to a single protein group by MaxQuant.

Protein lists generated by MaxQuant were further analyzed by Perseus (version 1.5.0.31) (42). Proteins identified as a common contaminant were filtered out, and then all the LFQ intensities were \log_2 transformed as described in Figure 4, step 1. Scatter plots were generated for each experimental

condition to compare the differences between biological replicates and to derive Pearson correlations. Different experiments were annotated into four groups as described in Figure 4, step 2: a control group for the parental U2OS cell line, a 0 hours HU group (untreated), a 2 hours HU group and a 24 hours HU group for the different time points of HU treatment of the U2OS cell line expressing His10-SUMO-2. Proteins identified in at least one treatment condition and found in at least four biological replicates were included for further analysis. For each experimental condition individually, missing values were imputed using Perseus software by normally distributed values with a 1.8 downshift (\log_2) and a randomized 0.3 width (\log_2) as described in Figure 4, step 3. For heat maps, the \log_2 ratios of LFQ intensities were plotted by hierarchical clustering to compare biological replicates. For identification of SUMO-2 target proteins, selection criteria are detailed in Figure 4 step 4. Proteins are considered to be SUMO-2 target proteins when the median \log_2 ratio of the LFQ intensity in the experimental group minus the median \log_2 ratio of the LFQ intensity in the parental control group was greater than 1 and the P value of ANOVA was smaller than 0.05. Term enrichment analysis (Gene Ontology) of SUMOylated proteins by protein annotation was carried out using Perseus. Term enrichment was determined by Fisher Exact testing, and P values were corrected for multiple hypotheses testing using the Benjamini and Hochberg false discovery rate. Final corrected P values were filtered to be less than 0.02.

Subsequently, average \log_2 ratios for 2 hours of HU treatment (LFQ ratio 2h/ 0h HU treatment) and average \log_2 ratios for 24 hours of HU treatment (LFQ ratio 24h/ 0h HU treatment) were calculated, and P values of each protein across all treatment conditions were calculated by ANOVA, using permutation-based FDR. SUMOylated proteins were considered significantly up- or down-regulated when their average \log_2 ratio (2h/0h HU treatment) or average \log_2 ratio (24h/0h HU treatment) was greater than 1 or less than -1, and corresponding ANOVA P values were less than 0.05; selection criteria are detailed in Figure 4 step 5. Volcano plots to demonstrate significant changes in protein SUMOylation upon HU treatment were created by plotting the Student's t -test $-\log_{10}(P)$ value of LFQ 2h/0h against the average \log_2 (LFQ ratio 2h/0h) value, and the Student's t -test $-\log_{10}(P)$ value of 24h/0h against the average \log_2 (LFQ ratio 24h/0h). Significantly regulated SUMOylated proteins after 2 hours or 24 hours of HU treatment were selected to perform functional protein interaction analysis by STRING (string-db.org, version 9.1) using a confidence score of medium or higher ($p > 0.4$). STRING analysis results were visualized using Cytoscape (version 3.1.0).

4.9 Site level SUMOylation data analysis

Site-specific purifications were performed in biological quadruplicate, and all samples were measured in technical duplicate. All 24 RAW files were analyzed by MaxQuant (version 1.5.1.2). The first search was carried out with a mass accuracy of 20 ppm, while the main search used 6 ppm for precursor ions. Database searches were performed with Trypsin/P specificity, allowing two missed cleavages. Carbamidomethylation of cysteine residues was considered as a fixed modification. Mass tolerance of

MS/MS spectra was set to 20 ppm to search against an *in silico* digested UniProt reference proteome for *Homo sapiens* (29 October 2014, 88812 proteins). Additionally, MS/MS data was searched against a list of 245 common mass spectrometry contaminants by Andromeda. Pyro-QQTGG (K), QQTGG (K) and phosphorylation (STY) were set as variable modifications. In order to increase identification certainty, diagnostic peaks were searched within MS/MS spectra corresponding to SUMOylated peptides. The default minimum Andromeda score for accepting MS/MS spectra corresponding to modified peptides was left at 40 and the minimum delta score was left at 6. Additionally identified Pyro-QQTGG and QQTGG sites without diagnostic peaks, matching reversed sequences, or having a localization probability of less than 0.9 were excluded. Match between runs was used with 0.7 min match time window and 20 min alignment time window. Sequence windows of -15 to +15 with respect to the identified SUMO-2 acceptor lysines were used to generate a SUMOylation motif, employing iceLogo software.

Intensities of Pyro-QQTGG and QQTGG were further analyzed by Perseus (1.5.0.31). Pyro-QQTGG and QQTGG site intensities were normalized by the total site-peptide intensities in each sample, and then all the intensities were \log_2 transformed. Experiments were annotated into three groups: untreated control, 2 hours HU treatment and 24 hours HU treatment. Sites occurring in at least one treatment condition and identified in all four biological repeats, were included for further analysis. Missing values were imputed using Perseus software by normally distributed values with a 1.8 downshift (\log_2) and a randomized 0.3 width (\log_2), for each experimental condition individually. Volcano plots to demonstrate significant changes in protein SUMOylation upon HU treatment were created by plotting $-\log_{10}(P)$ values of 2h/0h HU and 24h/0h HU from pairwise comparisons of SUMO-2 target proteins against the average LFQ Ratio 2h/0h (\log_2) and LFQ Ratio 24h/0h (\log_2).

Acknowledgements

This work was supported by the Marie Curie Initial Training Network UPStream of the European Union (A.C.O.V. and J.V.O.). This work was furthermore supported by the European Research Council (A.C.O.V.) and the Netherlands Organization for Scientific Research (NWO) (A.C.O.V.). The NNF Center for Protein Research is supported by a generous donation from the Novo Nordisk Foundation. None of the authors have a financial interest related to this work.

The MS data have been deposited to the ProteomeXchange Consortium (<http://proteomecentral.proteomexchange.org>) via the PRIDE partner repository with the dataset identifier PXD001736.

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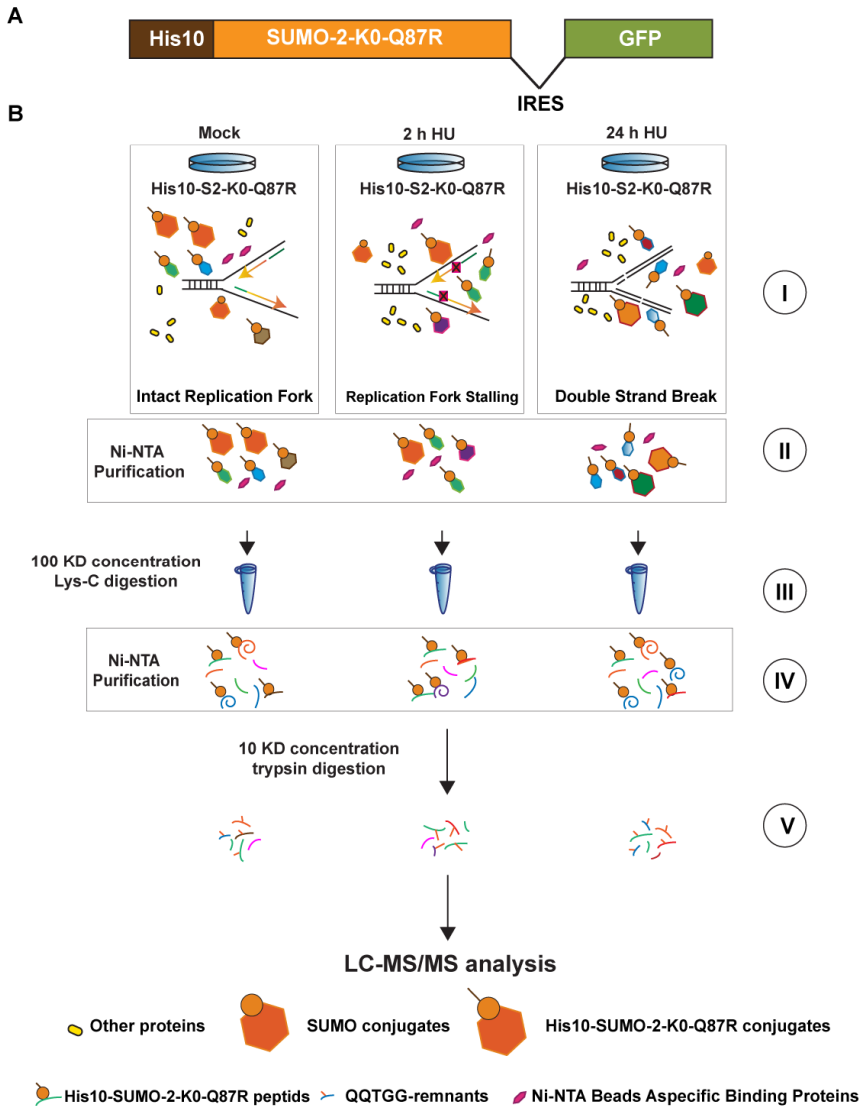


Figure S1. A strategy for identifying SUMO-2 acceptor lysines in endogenous proteins during replication stress.

A. Schematic representation of the His10-SUMO-2-K0-Q87R-IRES-GFP construct used in this project. **B.** Cartoon depicting our strategy to identify SUMO-2 acceptor lysines and their dynamics during replication stress. U2OS cells expressing His10-SUMO-2-K0-Q87R were treated with 2 mM Hydroxyurea (HU) for 2 hours or 24 hours to induce DNA replication fork stalling and double strand breaks, respectively. U2OS cells expressing His10-SUMO-2-K0-Q87R cells were mock treated as negative controls. SUMO-2 target proteins were enriched on Ni-NTA beads. SUMOylated peptides were obtained by Lys-C digestion and Ni-NTA re-purification and subsequently analyzed by mass spectrometry.

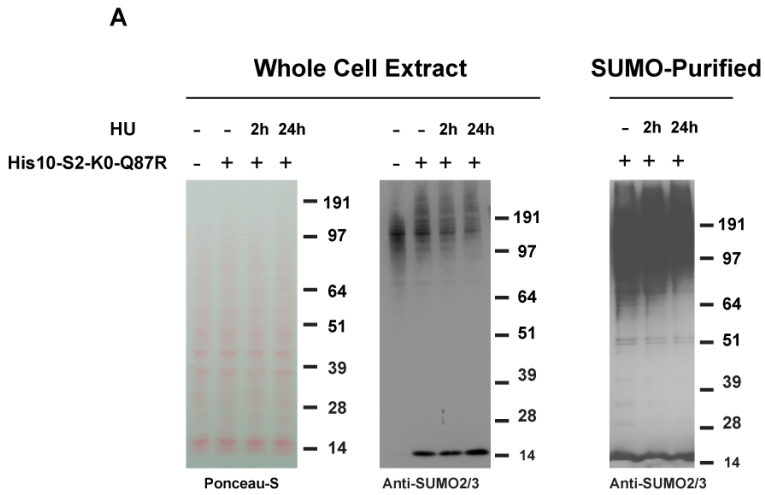


Figure S2. A U2OS cell line stably expressing His10-SUMO-2-K0-Q87R. Immunoblotting analysis was used to verify the expression levels of SUMO-2 in U2OS cells stably expressing His10-SUMO-2-K0-Q87R (His10-K0-S2-Q87R).

