

Mitochondria-derived nuclear ATP surge protects against confinement-induced proliferation defects

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Description of Source Data Files

All code to produce figures from Source Data used in this manuscript can be found at <https://github.com/SdelciLab/CINAPS>.

Source Data 1: Proteomics, NAM quantification, and nuclear shape data.

Contains data for mitochondrial enrichment upon confinement ("time_nam", "percentageNAM"), quantification of nuclear shape changes ("nucShape_data", "nucShape_NAM"), correlation of nuclear indentations with NAM ("indentation_vs_nam"), mitochondrial localization ("mitoloc"), mitochondrial and nuclear overlap line profiles ("mito_dapi_line"), and quantification of NAMs in tumor tissue microarrays ("tma").

Source Data 2: Cytoskeletal, ER dynamics, mitochondrial morphology, and ROS measurements.

Includes nuclear chromatin coefficient of variation ("CoV"), actin distribution changes upon Latrunculin A treatment ("actin_dapi_latA"), mitochondrial morphology validations ("mito_morph_validation"), actin localization ("actin"), ER dynamics kymograph data ("er_kymograph_std_dev"), and reactive oxygen species measurements ("ros").

Source Data 3: Nuclear ATP dynamics and nucleotide metabolism.

Contains nuclear ATP time course data ("time_nucATP"), FRET-based ATP measurements ("atp_fret"), ATP recovery kinetics after confinement release ("nucATP_releaseTime"), and metabolomics data of nucleotide levels during DNA repair ("de_novo_nucleotides_metabolomic").

Source Data 4: Chromatin accessibility analysis.

Contains differential accessibility annotations used for ATAC-seq analysis ("CT_vs_UT_diff_exp_annotated_pea", "CU_vs_UU_diff_exp_annotated_pea", "ct_vs_ut_diff_exp_collapsed_ann", "cu_vs_uu_diff_exp_collapsed_ann").

Source Data 5: DNA damage, proliferation, and cell cycle analysis.

Includes quantification of DNA damage foci under various treatments ("53bp1_conf_bam15_pyr", "53bp1_conf_oligo", "eto_ir_dna_damage", "53bp1_conf_latA"), NAM and DNA damage association in unconfined cells ("dna_damage_nam_unconfined"), pyruvate proliferation rescue experiments ("pyruvate_proliferation"), FUCCI-based cell cycle analysis ("fucci_gates"), western blot tubulin quantification ("wb_tubulin_normalised"), and CENPA-nucleoli association data ("cenpa_nucleoli").

Source Data 6: ATAC-seq peak data for chromatin accessibility in control conditions.

Contains peak information for ATAC-seq analysis comparing confined vs suspension cells under control (untreated) conditions.

Source Data 7: ATAC-seq peak data for chromatin accessibility in Oligomycin A-treated conditions.

Contains peak information for ATAC-seq analysis comparing confined vs suspension cells under Oligomycin A treatment.

Source Data L1: Time-lapse tracking of 53BP1 foci post-confinement

Available for download from <https://zenodo.org/records/15641870>.

Source Data L2: Cell cycle post confinement FUCCI

Available for download from <https://zenodo.org/records/15641870>.