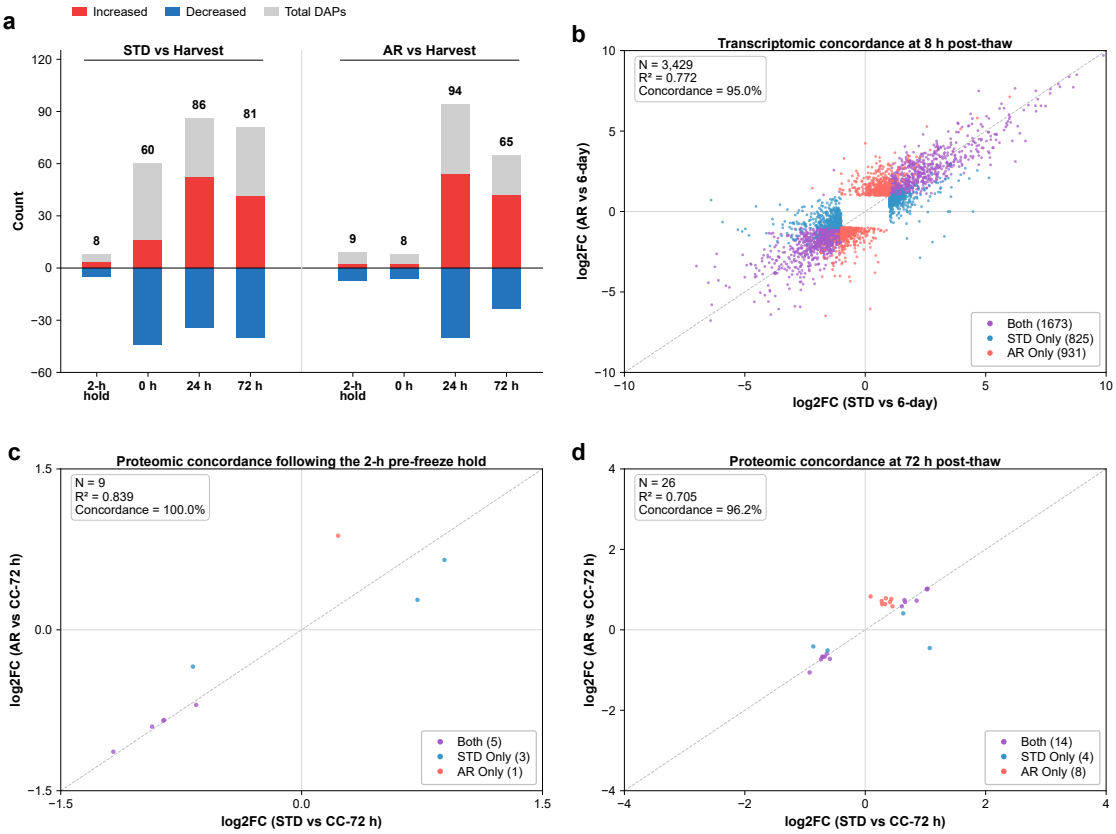
Supplementary Information

Time-Resolved Multi-Omic Characterization of Post-Thaw Remodeling in Monocytic THP-1 Cells

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Supplementary Figure S1



Supplementary Fig. S1 | Additional differential-abundance and cross-format concordance analyses. a, Differentially abundant proteins (DAPs) in STD and AR cells following the 2-h hold and at 0, 24, and 72 h relative to the shared Harvest state (adjusted $p < 0.05$, $|\log_2$ fold change$| > 0.58$). **b,** Transcriptomic STD-versus-AR response concordance at 8 h relative to the 6-day recovered reference. **c,d,** Proteomic response concordance following the 2-h hold and at 72 h relative to CC-72 h. Features meeting significance criteria in either format are shown; colors denote significance in both formats, STD only, or AR only. R^2 is the squared Pearson correlation coefficient and concordance is the percentage of features changing in the same direction. Dashed diagonals denote identity. RNA-seq: $n = 3$ biological replicates for STD 8 h and AR 8 h, and $n = 5$ for the 6-day reference; proteomics: $n = 3$ per group.

Supplementary Table S1

Supplementary Table S1 | Cryostress marker panel used for targeted transcriptomic and proteomic analysis. The panel contains 37 literature-informed markers spanning cold shock, proteostasis, endoplasmic-reticulum stress and the integrated stress response, oxidative/metabolic stress, apoptosis/survival, cell-cycle/DNA stress, osmotic/membrane regulation, and autophagy/protein clearance.

Gene	Functional category	Basis for inclusion	Supporting reference(s)	RNA evaluated	Protein detected
CIRBP	Cold shock	Cold-inducible RNA-binding protein	[1]	Yes	Yes
RBM3	Cold shock	Cold-shock RNA-binding protein	[1]	Yes	Yes
HSPA1A	Rewarming/proteostasis	Inducible HSP70 chaperone	[2,3]	Yes	No
HSPA1B	Rewarming/proteostasis	Inducible HSP70 chaperone	[2,3]	Yes	Yes
HSPA8	Rewarming/proteostasis	Constitutive HSP70 chaperone	[3]	Yes	Yes
HSP90AA1	Rewarming/proteostasis	HSP90 proteostasis chaperone	[2,3]	Yes	Yes
HSPH1	Rewarming/proteostasis	HSP110/HSP70-network chaperone	[3]	Yes	Yes
HSPB1	Rewarming/proteostasis	Small heat-shock chaperone	[3]	Yes	Yes
DNAJB1	Rewarming/proteostasis	HSP40/J-domain co-chaperone	[3]	Yes	Yes
HSPA5	ER stress / integrated stress response	ER BiP/GRP78 chaperone	[4,5]	Yes	Yes
DDIT3	ER stress / integrated stress response	CHOP stress transcription factor	[5,6]	Yes	No
HERPUD1	ER stress / integrated stress response	ER-stress/ERAD response protein	[5]	Yes	No
PPP1R15A	ER stress / integrated stress response	GADD34 ISR feedback regulator	[5,6]	Yes	No
ATF4	ER stress / integrated stress response	Central ISR transcription factor	[5,6]	Yes	No
HMOX1	Oxidative/metabolic stress	Canonical oxidative-stress/NRF2 target	[7,8]	Yes	No
NQO1	Oxidative/metabolic stress	Canonical NRF2 detoxification target	[8]	Yes	Yes
SOD2	Oxidative/metabolic stress	Mitochondrial ROS-defense enzyme	[7]	Yes	Yes
GCLC	Oxidative/metabolic stress	Glutathione-synthesis NRF2 target	[8]	Yes	Yes
GCLM	Oxidative/metabolic stress	Glutathione-synthesis NRF2 target	[8]	Yes	Yes
DDIT4	Oxidative/metabolic stress	REDD1 stress/mTOR regulator	[9]	Yes	No
SESN2	Oxidative/metabolic stress	Stress-inducible redox/mTOR regulator	[10]	Yes	No
BAX	Apoptosis/survival	Pro-apoptotic BCL-2-family effector	[11,12]	Yes	Yes
BCL2	Apoptosis/survival	Anti-apoptotic BCL-2-family protein	[11]	Yes	Yes
MCL1	Apoptosis/survival	Anti-apoptotic BCL-2-family protein	[11]	Yes	No
BBC3	Apoptosis/survival	PUMA BH3-only apoptotic regulator	[11]	Yes	No
PMAIP1	Apoptosis/survival	NOXA BH3-only apoptotic regulator	[11]	Yes	No

Gene	Functional category	Basis for inclusion	Supporting reference(s)	RNA evaluated	Protein detected
CASP3	Apoptosis/survival	Executioner caspase	[12,13]	Yes	Yes
CDKN1A	Cell-cycle/DNA stress	p21 stress-induced cell-cycle arrest	[14]	Yes	No
GADD45A	Cell-cycle/DNA stress	DNA-damage/growth-arrest response	[14]	Yes	No
AQP3	Osmotic/membrane regulation	Aquaglyceroporin; water/glycerol transport	[15]	Yes	No
AQP9	Osmotic/membrane regulation	Aquaglyceroporin; water/glycerol transport	[15]	Yes	No
LRRC8A	Osmotic/membrane regulation	VRAC volume-regulatory channel subunit	[16,17]	Yes	Yes
SLC12A2	Osmotic/membrane regulation	NKCC1 volume-regulatory cotransporter	[17]	Yes	Yes
ANXA1	Osmotic/membrane regulation	Ca2+-dependent membrane repair/remodeling	[18,19]	Yes	Yes
ANXA2	Osmotic/membrane regulation	Ca2+-dependent membrane repair/remodeling	[18,19,20]	Yes	Yes
SQSTM1	Autophagy/protein clearance	Autophagy cargo receptor	[21]	Yes	Yes
MAP1LC3B	Autophagy/protein clearance	Autophagosome-associated LC3 marker	[21]	Yes	No

Notes. RNA evaluated indicates inclusion in the targeted transcriptomic marker panel. Protein detected indicates retention of the corresponding protein in the processed TMT abundance matrix. Supporting references are numbered independently within this Supplementary Information.

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