

# Supplementary Materials: Active and Repressive Chromatin Associated Proteome after MPA Treatment and the Role of Midkine in Epithelial Monolayer Permeability

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**Table S1.** List of significantly altered proteins associated with active (H3K4me3) and or repressive (H3K27me3) histone modification marks in MPA treated Caco-2 cells.

ChIP	Accession No.	Protein Name	Fold Change	p-Value	Functions (Uniprot)
Histone Modification Active Mark (H3K4me3)	Q9UN86	Ras GTPase-activating protein-binding protein 2 OS	2.5 ↓	0.0067	mRNA transportation
	P63104	14-3-3 protein zeta/delta	1.1 ↑	0.0031	Adaptor protein
	P61978	Heterogeneous nuclear ribonucleoprotein K	1.4 ↑	0.0032	Transcription activation/repression, hnRNAs metabolism
	P07355	Annexin A2	1.2 ↑	0.0011	Heat response
	P68104	Elongation factor 1-alpha 1	1.1 ↑	0.0011	Transcription activity, protein synthesis
	Q8IU66	Histone H2A type 2-B	1.2 ↑	0.0087	Chromatin structure
	P62258	14-3-3 protein epsilon	1 ↑	0.005	Adaptor protein
	P61254	60S ribosomal protein L26	1 ↑	0.0078	
	Q01844	RNA-binding protein EWS	1.1 ↑	0.003	Repressor
	P68431	Histone H3.1	1.4 ↑	0.0011	Chromatin structure
	P16402	Histone H1.3	1.1 ↑	0.00019	Chromatin structure, regulator of individual gene transcription
	P62249	40S ribosomal protein S16	1.25 ↓	0.0042	
	Q15691	Microtubule-associated protein RP/EB family member 1	1.1 ↓	0.0046	Microtubule base cytoskeleton
	Q13242	Serine/arginine-rich splicing factor 9	1.1 ↑	0.00038	Splicing activity
	P37108	Signal recognition particle 14 kDa protein	1.0 ↑	0.0039	
	Q96AE4	Far upstream element-binding protein 1	1.4 ↑	0.0063	Transcriptional activity
	P24534	Elongation factor 1-beta	1.3 ↑	0.0015	Exchanging EF-1alpha bound GDP to GTP
	Q12906	Interleukin enhancer-binding factor 3	1.5 ↑	0.00042	Gene regulation, protein synthesis
	P10599	Thioredoxin	1.1 ↑	0.00048	Transcription activity, redox reaction
	P62081	40S ribosomal protein S7	1.3 ↑	0.0071	rRNA maturation
	P62851	40S ribosomal protein S25	0.9 ↓	0.0006	
	Q12874	Splicing factor 3A subunit 3	1.3 ↑	0.0058	Subunit of A & E complex
	P62857	40S ribosomal protein S28	1.1 ↓	0.0043	
	P09234	U1 small nuclear ribonucleoprotein C	1.1 ↑	0.0054	Splicing activity
	Q14157	Ubiquitin-associated protein 2-like	1.3 ↑	0.00014	Ubiquitin-proteasome pathway, growth and migration of prostate cancer cells
	P25398	40S ribosomal protein S12	1.25 ↓	0.0082	
	Q99459	Cell division cycle 5-like protein	1.6 ↑	0.0032	Cell cycle regulator, transcription activity
	O95793	Double-stranded RNA-binding protein Stauf homolog 1	1.5 ↑	0.0028	Cross linking cytoskeleton, RNA component, translation
	P62424	60S ribosomal protein L7a	1.3 ↑	0.0074	
	Q92522	Histone H1x	1.7 ↑	0.008	Chromatin condensation
	Q71UI9	Histone H2A.V	1.2 ↑	0.0017	Chromosome segregation, cell division
	Q9NYL4	Peptidyl-prolyl <i>cis-trans</i> isomerase FKBP11	1.11 ↓	0.0065	Protein folding
	P12277	Creatine kinase B-type	1.4 ↑	0.0096	Energy transduction
	P14866	Heterogeneous nuclear ribonucleoprotein L	1.8 ↑	0.0022	Splicing activity, regulator of exon inclusion
	P02545	Prelamin-A/C	1.7 ↑	0.0022	Nuclear lamina, chromatin organization, telomere dynamics
	P20700	Lamin-B1	1.8 ↑	0.002	Nuclear lamina, chromatin organization, telomere dynamics
	P23528	Cofilin-1	1.4 ↑	0.0016	Cell morphology, cytoskeletal organization
	Q13813	Spectrin alpha chain, non-erythrocytic 1	5.5 ↑	0.0038	Cytoskeleton
	P21796	Voltage-dependent anion-selective channel protein 1	1.9 ↑	0.0046	Cell volume, apoptosis

Table S1. Cont.

ChIP	Accession No.	Protein Name	Fold Change	p-Value	Functions (Uniprot)
	Q15365	Poly(rC)-binding protein 1	1.8 ↑	0.0029	Nucleic acid binding protein
	P53999	Activated RNA polymerase II transcriptional coactivator p15	2.1 ↑	0.006	Stabilizing the multiproteins transcription complex
	P09327	Villin-1	2.5 ↑	0.005	Cell morphology, division, migration and apoptosis
	<b>P21741</b>	<b>Midkine</b>	<b>3.8 ↑</b>	<b>0.00010</b>	<b>Growth factor, activator of PI3K, MAPK pathways</b>
	Q15366	Poly(rC)-binding protein 2	2.2 ↑	0.0093	Nucleic acid binding protein, adaptor & regulator protein
	P61586	Transforming protein RhoA	3 ↑	0.0071	Signal transduction pathway, activator, cell migration
<b>Histone Modification Repressive Mark (H3K27me3)</b>	Q06830	Peroxiredoxin-1	1.67 ↓	0.00094	Redox regulation
	P13639	Elongation factor 2	1.67 ↓	0.00010	ribosomal translocation
	P12956	X-ray repair cross-complementing protein 6	5 ↓	0.00098	Helicase activity, chromosome translocation, negative transcription regulators
	Q9ULV4	Coronin-1C	3.33 ↓	0.00044	Cytokinesis, motility, and signal transduction
	P14174	Macrophage migration inhibitory factor	1.25 ↓	0.00058	Pro inflammatory cytokines
	P10599	Thioredoxin	1.1 ↑	0.00010	Redox reactions, DNA binding activity
	Q9NX24	H/ACA ribonucleoprotein complex subunit 2	4.3 ↑	0.00010	Ribosome biogenesis, telomere maintenance

Arrows indicate “↑” upregulation and “↓” downregulation of the respective proteins after MPA treatment as compared with DMSO (control in fold change). Protein highlighted in the **bold** (Midkine) was further characterized by exploring its role in the increased permeability of Tight Junctions in Caco-2 cells monolayer after MPA treatment.