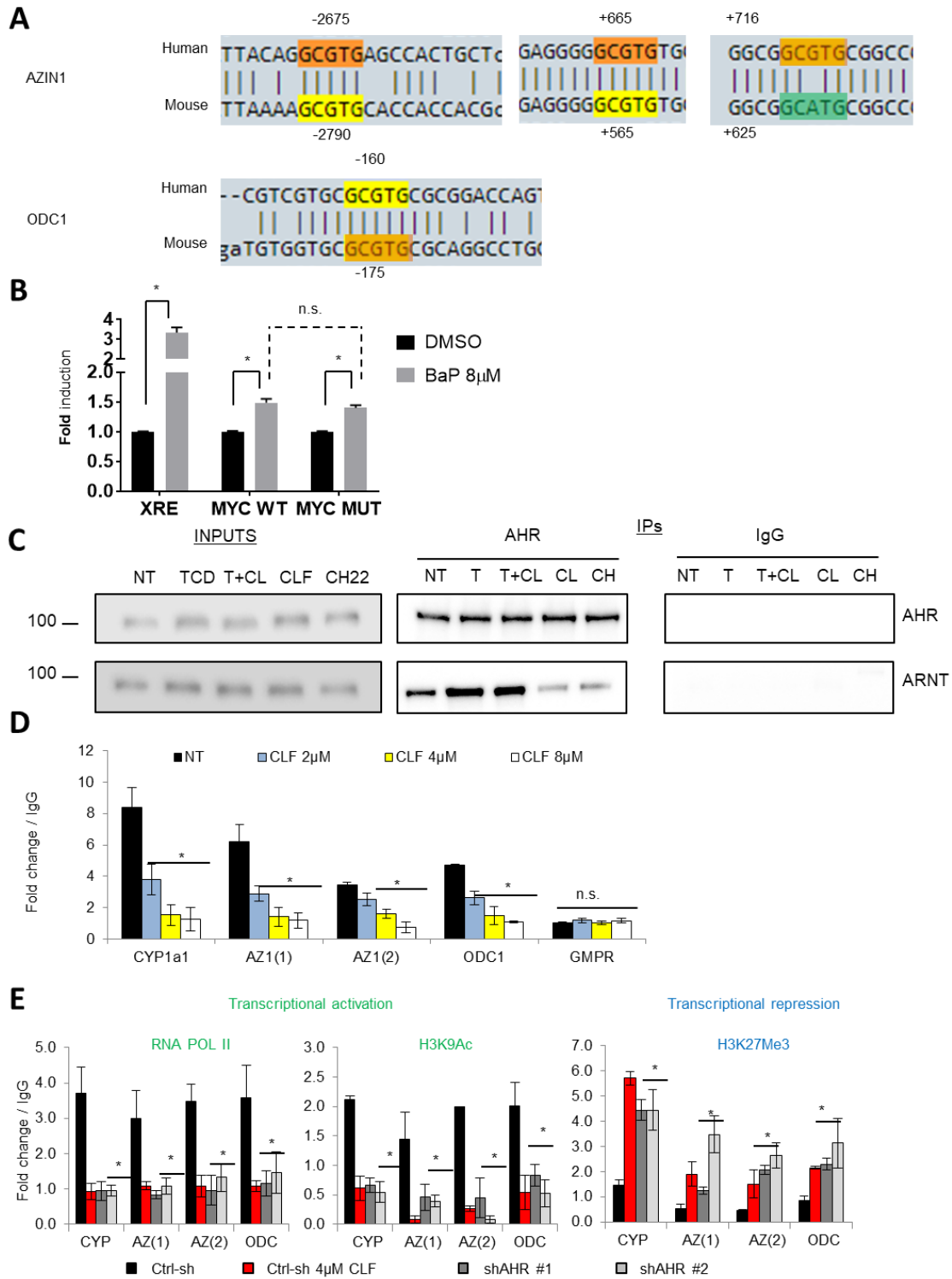
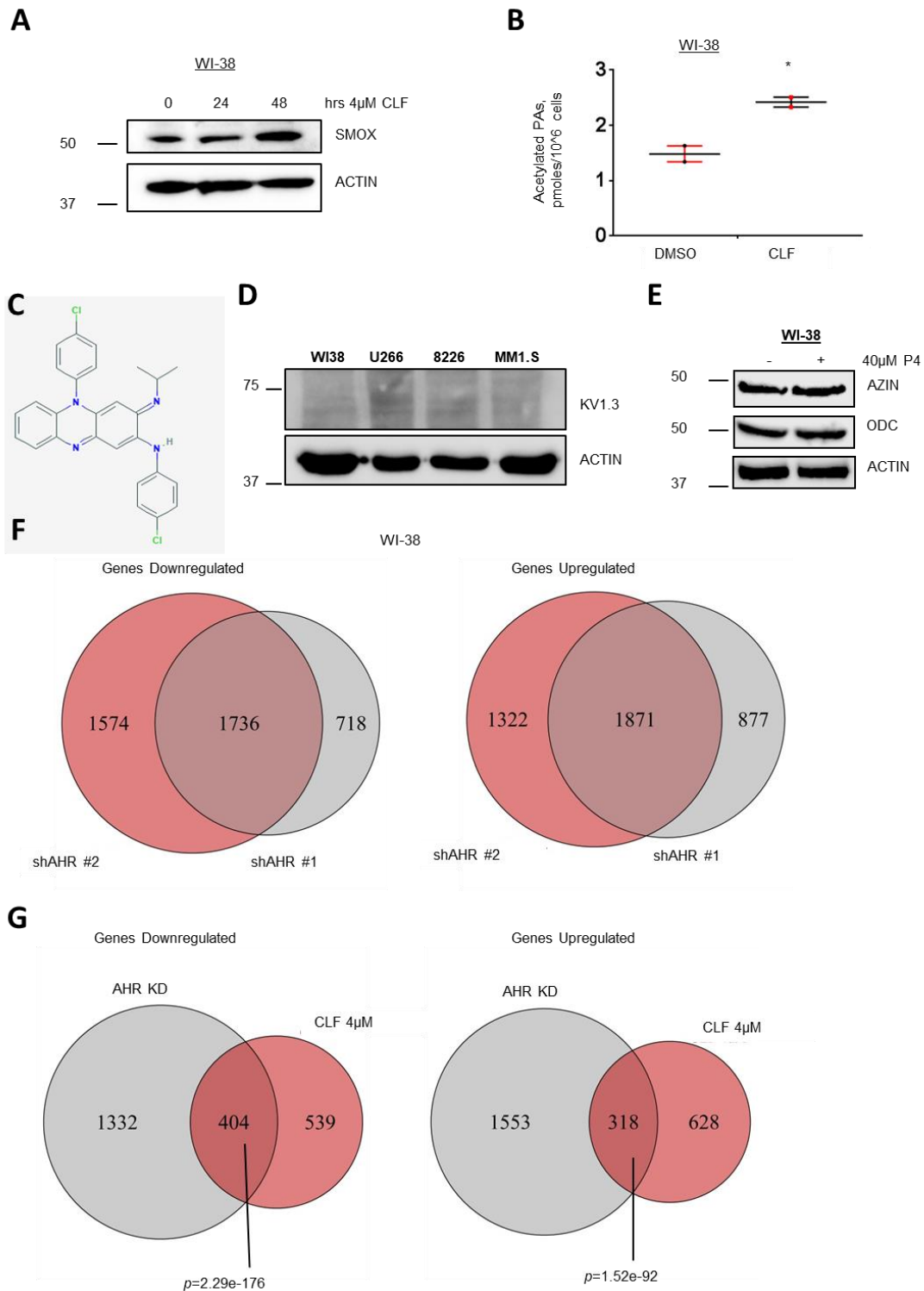


Supplementary Materials:



Supplementary Fig. S1. AhR binds to *AZIN1* and *ODC1* promoters

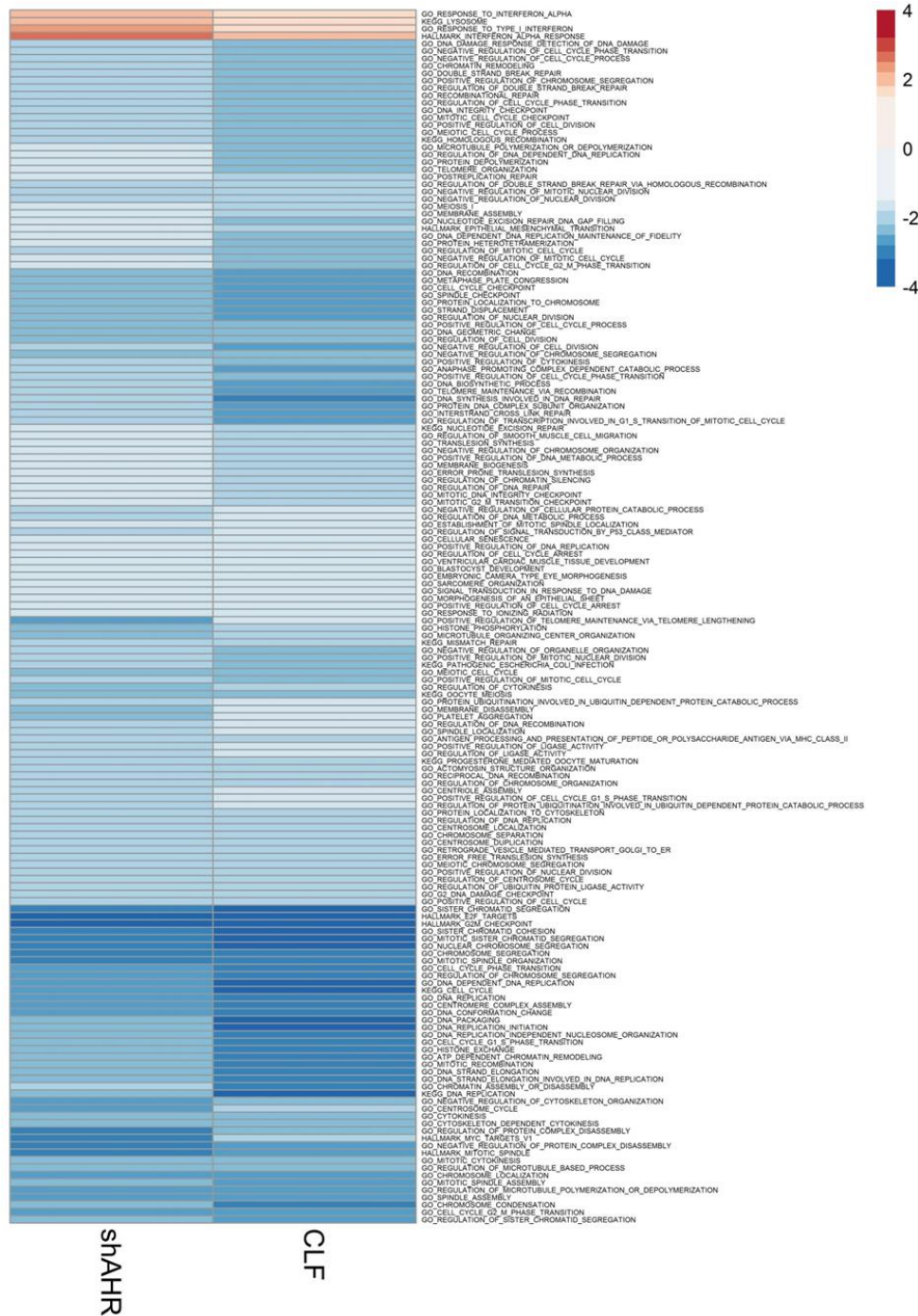
(A) Alignment of the conserved AhR binding sites in *AZIN1* and *ODC1* promoters between human and mouse. Mouse +625 site in *Azin1* is highlighted in green as it is partially conserved. **(B)** pGL3-basic-*ODC1p* constructs designed to include MYC responsive elements (either WT or mutated) were transduced into HEK293FT cells along with the pRLSV40 plasmid expressing the Renilla luciferase gene. Cells were treated for 24hrs with increasing amounts of BaP to stimulate AHR activity and luciferase activity was measured 48hrs post-transfection. The XRE-Luc plasmid was used as a control. Data are presented as the average \pm SEM of 2 independent experiments performed in duplicate. **(C)** WI-38 cells were either left untreated or treated for 30min with TCDD 20nM, TCDD20nM +CLF 4 μ M, CLF 4 μ M, or CH223191 20 μ M. Total proteins were extracted in lysis buffer and 500 μ g of each extract were used in immunoprecipitation assays with either AHR or normal mouse IgG antibodies. Inputs and IP materials were probed in immunoblot for AHR and ARNT. **(D)** DNA from WI-38 cells treated with increasing concentrations of CLF was immunoprecipitated with control (IgG) or AhR-specific (AhR) antibodies. The precipitated material was probed in qPCR with primers for *CYP1a1* promoter (positive control), for regions in *AZIN1* and *ODC1* promoters described in (B), or for a nonspecific promoter (GMPR). Data are presented as the average \pm SEM of 3 independent experiments performed in triplicate. **(E)** DNA from WI38 cells treated with vehicle or increasing concentrations of CLF was immunoprecipitated with control (IgG) or antibodies against RNAPol-II, H3K9AC, H3K4Me3, H3K9Me2, or H3K27Me3. The precipitated material was probed in qPCR with primers described in (Fig. 1D). Data are presented as the average \pm SEM of 3 independent experiments performed in triplicate. Statistics performed with two-tailed Student *t*-Test. * p < 0.05; ** p <0.001, n.s. not significant.



Supplementary Fig. S2. AhR and CLF regulate overlapping sets of genes in WI-38 cells

(A) Cell extracts of WI-38 treated for 24-48hrs with 4μM CLF were probed in immunoblot for SMOX. Actin was used as loading control. **(B)** Acetylated polyamine content analysis by HPLC in

media of WI-38 cells treated with 4 μ M CLF for 48hrs. Data are presented as the average \pm SEM of 2 independent experiments. **(C)** Structure of CLF, as obtained from the PubChem website (<https://pubchem.ncbi.nlm.nih.gov/compound/clofazimine#section=2D-Structure>) **(D)** Cell extracts of WI-38, U266, RPMI-8226, and MM.1S were probed in immunoblot for Kv1.3. Actin was used as loading control. **(E)** Cell extracts of WI-38 treated for 2hrs with 40 μ M PSORA-4 (P4) were probed in immunoblot for AZIN1 and ODC1. **(F)** Venn diagrams comparing the overlaps of genes downregulated or upregulated in the two shAHR treatment groups. **(G)** Venn diagrams comparing the overlaps of genes downregulated or upregulated in AHR KD (common genes from (D)) and CLF treatment. Overlap statistics were calculated with a hypergeometric test, based on 18411 detectable genes (mean normalized counts across samples > 5).

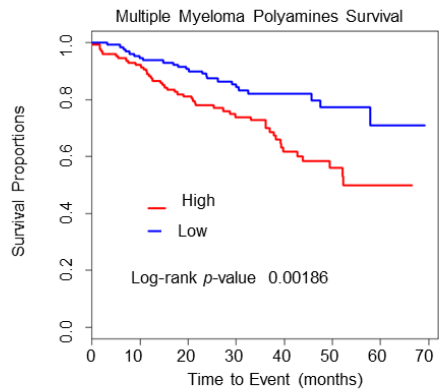
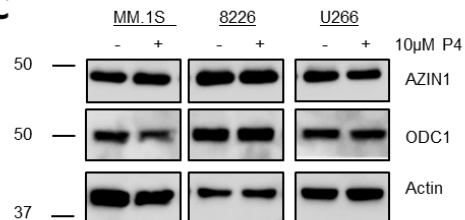
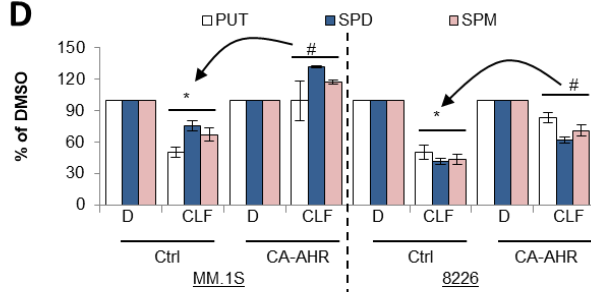
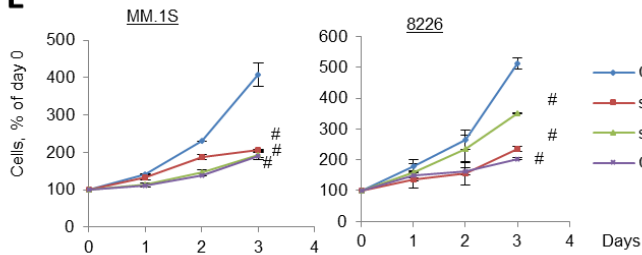
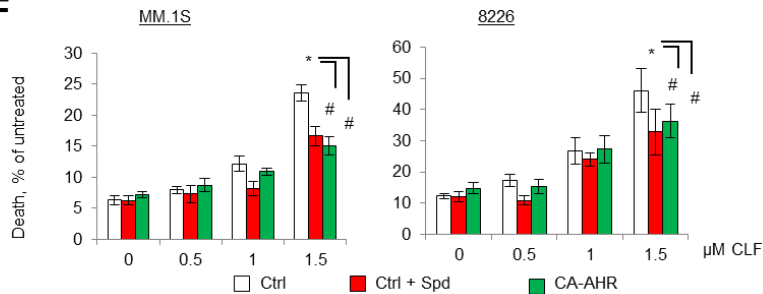


Supplementary Fig. S3. AhR and CLF regulate overlapping pathways in WI-38 cells

Heat-map of pathways commonly regulated by AHR KD and CLF in WI-38 cells generated by crossing the overlapping genes identified in Supplementary Figure S2c,d against GO biological processes, KEGG pathways and Hallmark pathways available through the MSigDB (FDR<0.1).

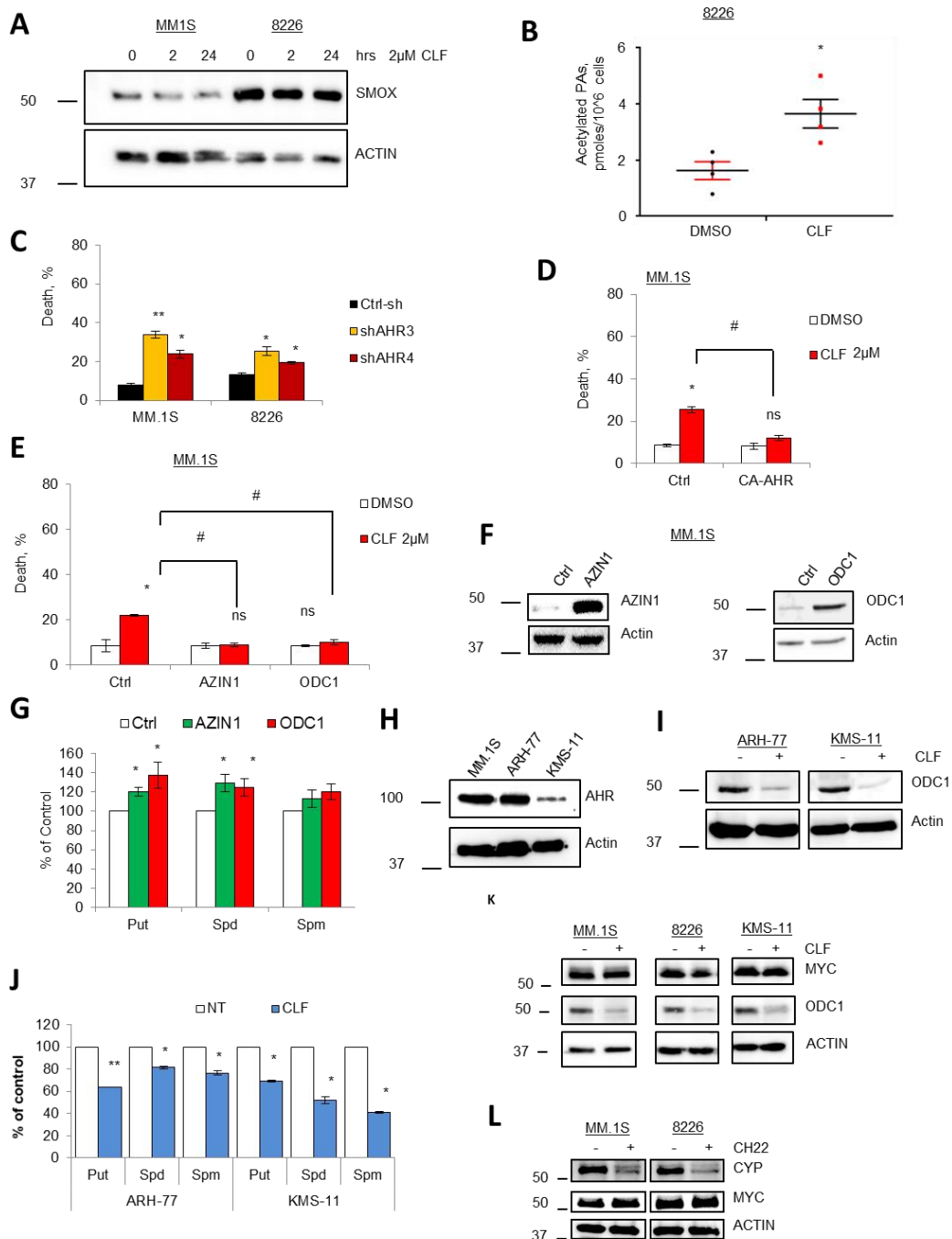
A

Cohort	AHR levels vs Survival	Log-rank p-value
MM	High - Poor	0.000906
CESC	High - Poor	0.0371
GBM	High - Poor	0.0469
ESCA	High - Good	0.0322
KIRC	High - Good	0.0249
PAAD	No correlation	0.0501
AML	No correlation	0.644
BLAD	No correlation	0.0765
BRCA	No correlation	0.18
CHOL	No correlation	0.417
COAD	No correlation	0.924
DLBC	No correlation	0.847
HNSC	No correlation	0.791
KICH	No correlation	0.99
KIRP	No correlation	0.109
LIHC	No correlation	0.722
LUAD	No correlation	0.853
LUSC	No correlation	0.45
PCPG	No correlation	0.521
PRAD	No correlation	0.579
SARC	No correlation	0.743
SKCM	No correlation	0.14
STAD	No correlation	0.331
THCA	No correlation	0.579
THYM	No correlation	0.676
UCEC	No correlation	0.638

B**C****D****E****F**

Supplementary Fig. S4. AHR expression levels correlate patient survival in some cancers

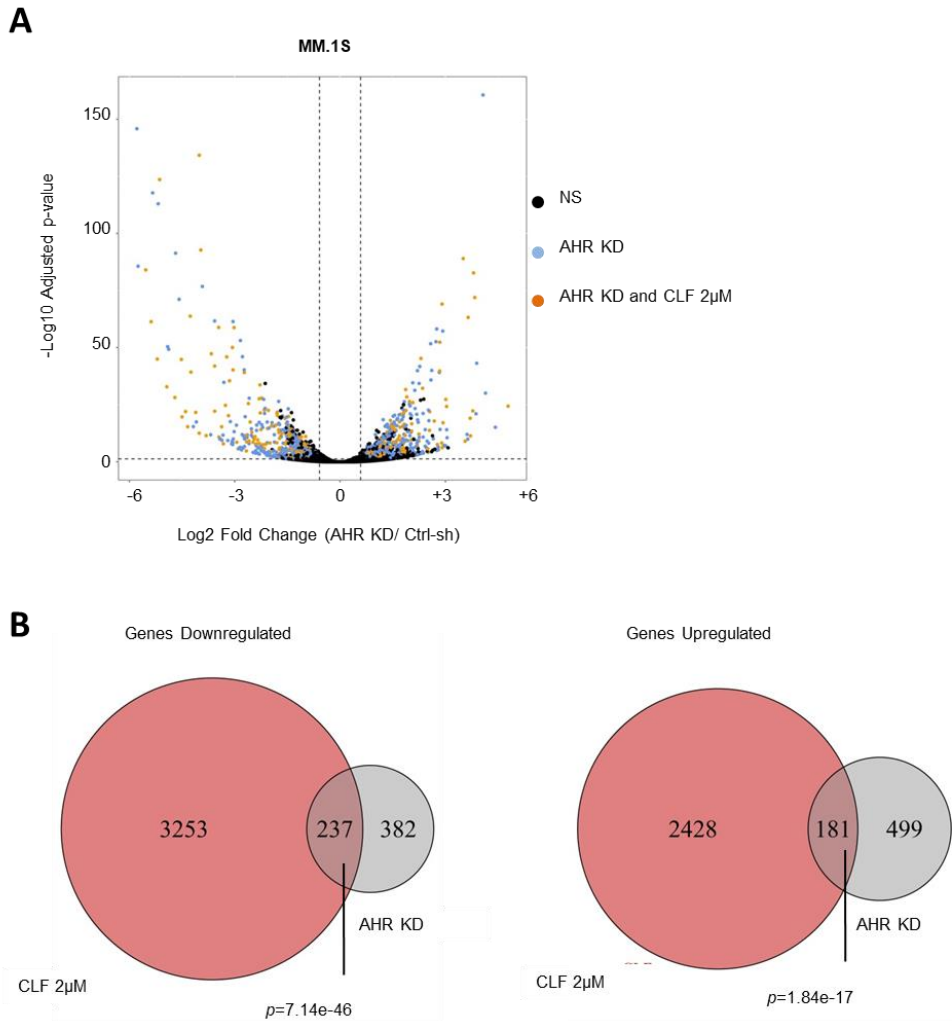
(A) Correlation of AhR expression levels and patients survival in 26 cancer cohorts. Log-rank p -values are reported. **(B)** Correlation of Polyamine Biosynthetic Score (PBS, defined as the sum of the gene expression levels of AZIN1, OAZ1, OAZ2, ODC1, SMS, SRM, and AMD1) and patients' survival in the multiple myeloma cohort. The cohort consisted of 256 patients, 127 of which were classified as "high PBS" (average expression value = 53328.85) and 129 classified as "low PBS" (average expression value = 42241.16). Statistics performed with Log-rank test. **(C)** Cell extracts of human multiple myeloma cells MM.1S, RPMI-8226, and U266 treated with 10 μ M PSORA-4 for 2hrs were probed in immunoblot for AZIN1, and ODC1. Actin was used as a loading control. **(D)** Polyamine content analysis by HPLC in MM.1S and 8226 cells transduced with Ctrl or CA-AHR and treated with DMSO (D) or 2 μ M CLF for 24hrs. Values are normalized to the DMSO in each group. Data are presented as the average \pm SEM of 3 independent experiments. **(E)** Proliferation of MM.1S and RPMI-8226 cells transduced with two independent shAHR was measured *via* trypan blue exclusion cell counts. Control cells were treated with 0.5 μ M CLF. Data are presented as the average \pm SEM of 3 independent experiments performed in duplicate **(F)** Percentage cell death in MM.1S or 8226 cells from Fig. 4g,h was assessed via trypan blue exclusion cell counts. Statistics performed with two-tailed Student t -Test * p <0.05 compared to untreated control; # p <0.05 compared to treated control.



Supplementary Fig. S5. AhR depletion and CLF treatment induced cell death

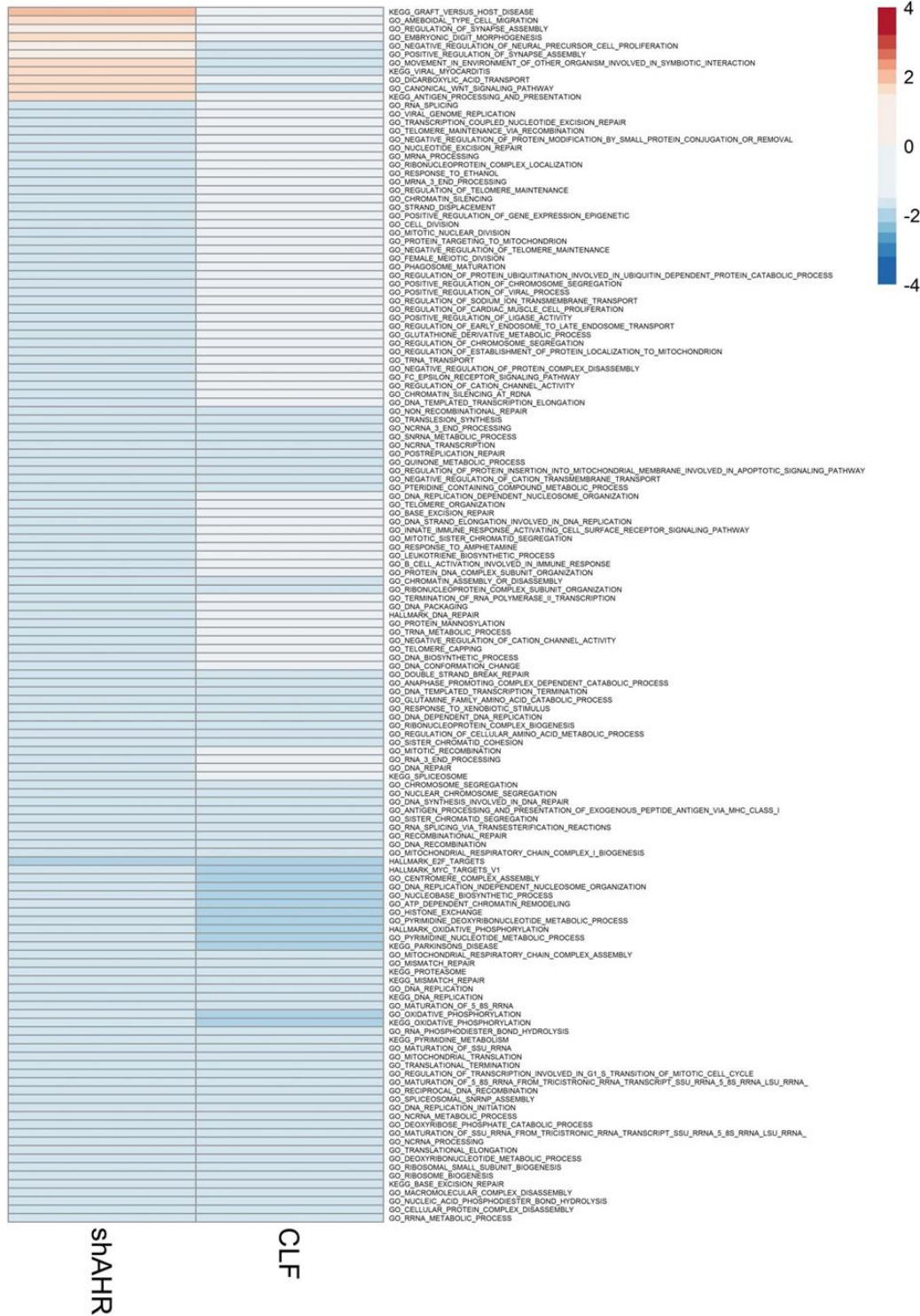
(A) Immunoblot of MM.1S and 8226 cells treated for 24hrs with 2μM CLF. **(B)** Acetylated polyamine content in media of 8226 cells treated with 2μM CLF for 24hrs. Data are presented as the average \pm SEM of 4 independent experiments. **(C)** Cell death in MM.1S and RPMI-8226 cells transduced with two independent shAHR. Data are presented as the average \pm SEM of 3

independent experiments in duplicate. **(D)** Cell death of MM.1S cells transduced with Ctrl or CA-AHR vectors, after 24hrs treatment with vehicle (DMSO) or 2 μ M CLF. Data are presented as the average \pm SEM of 4 independent experiments in duplicate. **(E)** Cell death of MM.1S cells transduced with Ctrl, AZIN1, or ODC1 vectors, after 24hrs treatment with vehicle (DMSO) or 2 μ M CLF. Data are presented as the average \pm SEM of 3 independent experiments in duplicate. **(F)** Immunoblot of cells as in (E). **(G)** Polyamine content in MM.1S cells transduced as in (E). **(H)** Cell extracts of MM.1S, ARH-77, and KMS-1 cells were probed in immunoblot for AHR. **(I)** Cell extracts of ARH-77 and KMS-11 cells treated for 24hrs with 4 μ M CLF probed in immunoblot for ODC1 and AZIN1. **(J)** Polyamine content in ARH-77 and KMS-11 cells treated for 24hrs with 4 μ M CLF. Data are presented as the average \pm SEM of 2 independent experiments. **(K)** Cell extracts of MM.1S, 8226, and KMS-11 cells treated for 4hrs with 2 μ M CLF were probed in immunoblot for MYC and ODC1. **(L)** Cell extracts of MM.1S and 8226 cells treated with CH223191 (CH22, 20 μ M, 24hrs) probed in immunoblot for MYC and CYP1a1 (CYP). Statistics performed with two-tailed Student *t*-Test * p <0.05; ** p <0.001 compared to untreated control cells; # p <0.05 compared to treated control cells.



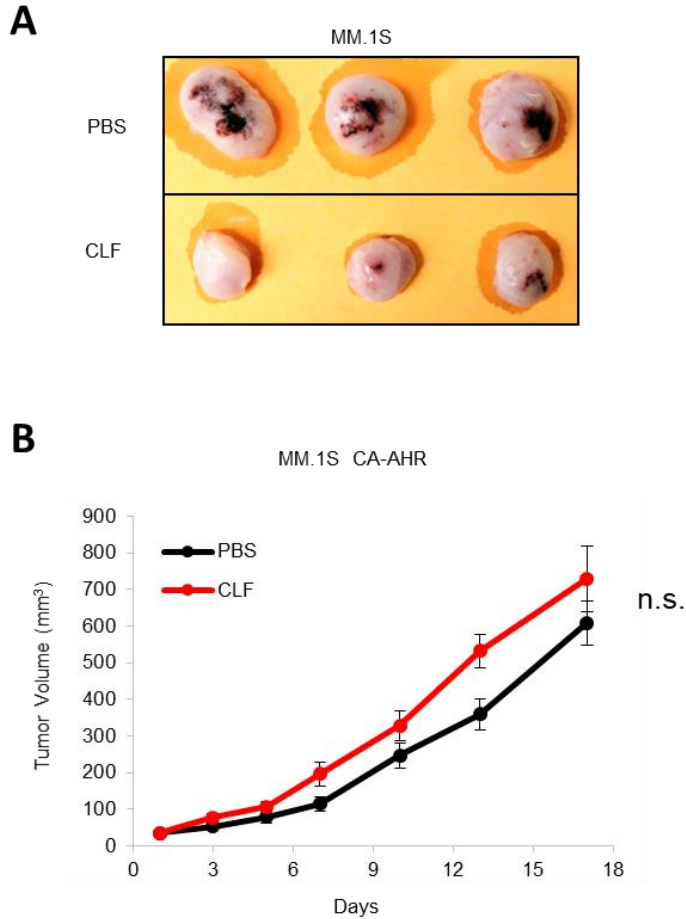
Supplementary Fig. S6. AhR and CLF regulate overlapping sets of genes in MM.1S cells

(A) Volcano plot of differentially expressed genes in AHR KD and CLF-treated MM.1S cells. A 1.5FC and $p < 0.05$ threshold was applied. Black symbols, not significant; blue symbols genes changed significantly only with AHR KD; orange symbols, genes changed significantly in both AHR KD and CLF treatment. **(B)** Venn diagrams comparing the overlaps of genes downregulated or upregulated in AHR KD and CLF treatment. Overlap statistics were calculated with a hypergeometric test, based on 23368 detectable genes (mean normalized counts across samples > 5).



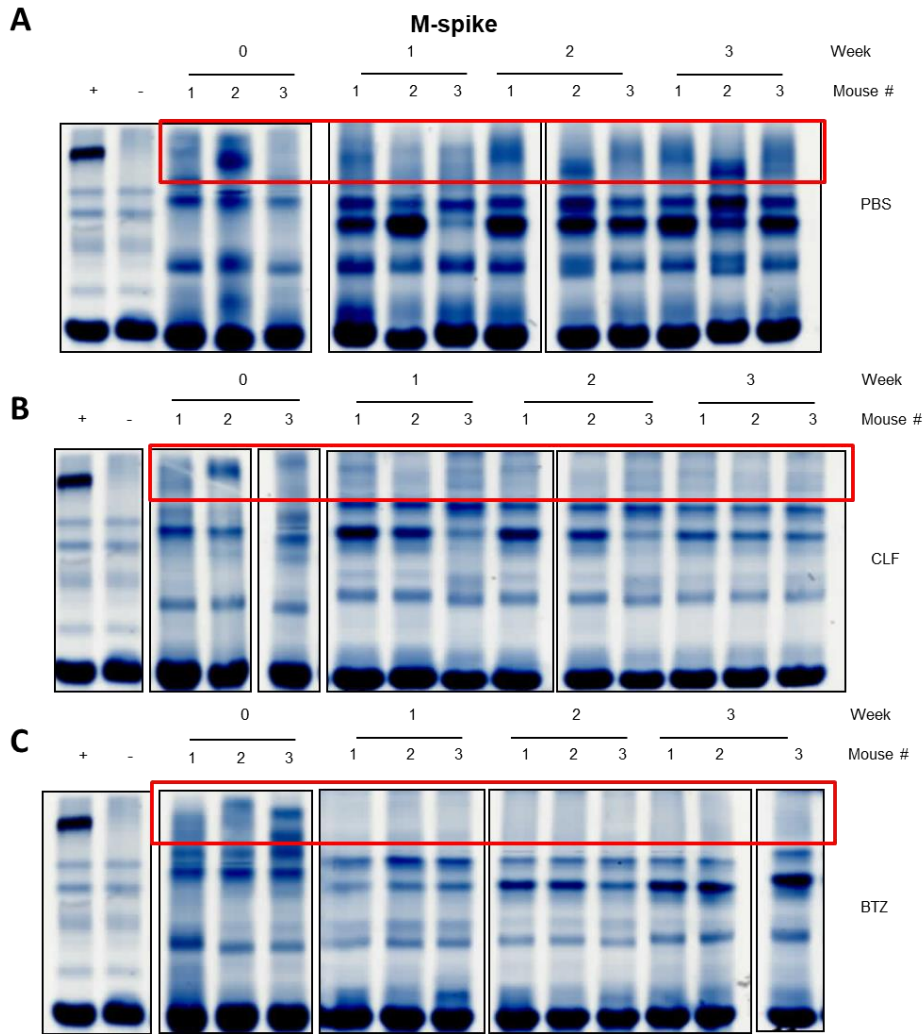
Supplementary Fig. S7. AhR and CLF regulate overlapping pathways in MM.1S cells

Heat-map of pathways commonly regulated by AHR KD and CLF in MM.1S cells generated by crossing the overlapping genes identified in Supplementary Figure S4 against GO biological processes, KEGG pathways and Hallmark pathways available through the MSigDB (FDR<0.2).



Supplementary Fig. S8. CA-AHR prevents CLF-mediated xenograft growth suppression

(A) Representative images of tumors from MM.1S cells xenografts from Fig. 5a. **(B)** MM.1S cells over-expressing CA-AHR were inoculated in subcutaneously in both flanks of 4-6 week-old female SCID mice. When tumors reached a volume of 100mm³ the animals were randomized into one of two groups (5 animals/control, 7 animals/CLF) and treated with daily i.p. injections of vehicle in PBS or clofazimine (10mg/Kg). Tumor volumes were recorded every 2-3 days and mice were sacrificed when tumor volume reached 2cm³ or when a tumor became ulcerated. Statistics performed with two-tailed Student *t*-Test ***p*<0.001.



Supplementary Fig. S9. Clofazimine suppresses M-spike in $V\kappa^*$ MYC mice.

Blood collected from the same $V\kappa^*$ MYC mice as in Fig. 6b treated with PBS (**A**); CLF (**B**), or BTZ (**C**) was analyzed by serum protein electrophoresis (SPEP).

Supplementary Table 1. List of compounds down-regulating *AZIN1* or *ODC1*.

Query	Compound Name	Score 0-100	Supporting Data Types	# of Studies	Effect on Query	Toxic or Unsuitable for Therapy
<i>AZIN1</i>	Khellin	74	RNA expression	1	Down	
<i>AZIN1</i>	Harmol	72	RNA expression	1	Down	
<i>AZIN1</i>	N-nitrosomorpholine	70	RNA expression	2	Down	X
<i>AZIN1</i>	Bromobenzene	70	RNA expression	3	Down	X
<i>AZIN1</i>	4-dichlorobenzene	67	RNA expression	4	Down	X
<i>AZIN1</i>	2-dichlorobenzene	65	RNA expression	2	Down	X
<i>AZIN1</i>	1,2-dithiol-3-thione	60	RNA expression	4	Down	X
<i>AZIN1</i>	Clofazimine	58	RNA expression	1	Down	
<i>AZIN1</i>	Enrofloxacin	54	RNA expression	1	Down	
<i>AZIN1</i>	7,8-Dihydro-7,8-dihydroxybenzo(a)pyrene 9,10-oxide	53	RNA expression	2	Down	X
<i>AZIN1</i>	Dextran Sulfate	51	RNA expression	1	Down	X
<i>AZIN1</i>	Nitrofurantoin	51	RNA expression	3	Down	
<i>AZIN1</i>	AICA ribonucleotide	51	RNA expression	1	Down	X
<i>AZIN1</i>	Apratoxin A	50	RNA expression	1	Down	X
<i>AZIN1</i>	Polychlorinated Biphenyls	50	RNA expression	2	Down	X
<i>ODC1</i>	Hydrochloric Acid	74	RNA expression	1	Down	X
<i>ODC1</i>	Fenofibrate	73	RNA expression	9	Down	
<i>ODC1</i>	Lactic Acid	59	RNA expression	2	Down	
<i>ODC1</i>	Ethylene Oxide	58	RNA expression	1	Down	X
<i>ODC1</i>	Bevacizumab	57	RNA expression	2	Down	

<i>ODC1</i>	Harmol	57	RNA expression	1	Down	
<i>ODC1</i>	Calcium	55	RNA expression	4	Down	X
<i>ODC1</i>	CpG ODN 2216	54	RNA expression	1	Down	

Supplementary Table 2. List of top pathways commonly regulated in WI-38 cells by shAHR and CLF treatment.

GeneSets	shAHR_NES	shAHR_pval	shAHR_FDR	CLF_NES	CLF_pval	CLF_FDR
GO_ACTOMYOSIN_STRUCTURE_ORGANIZATION	-1.9272	0.0000	0.0096	-1.9447	0.0000	0.0093
GO_ANAPHASE_PROMOTING_COMPLEX_DEPENDENT_CATABOLIC_PROCESS	-2.1394	0.0000	0.0012	-2.5287	0.0000	0.0000
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_OR_POLYSACCHARIDE_ANTIGEN_VIA_MHC_CLASS_II	-2.1063	0.0000	0.0018	-1.8609	0.0000	0.0168
GO_ATP_DEPENDENT_CHROMATIN_REMODELING	-2.2331	0.0000	0.0004	-2.9406	0.0000	0.0000
GO_BLASTOCYST_DEVELOPMENT	-1.5981	0.0033	0.0811	-1.5415	0.0000	0.0941
GO_CELL_CYCLE_CHECKPOINT	-2.3881	0.0000	0.0001	-2.6631	0.0000	0.0000
GO_CELL_CYCLE_G1_S_PHASE_TRANSITION	-2.3943	0.0000	0.0001	-3.0367	0.0000	0.0000
GO_CELL_CYCLE_G2_M_PHASE_TRANSITION	-2.5444	0.0000	0.0000	-2.7514	0.0000	0.0000
GO_CELL_CYCLE_PHASE_TRANSITION	-2.6797	0.0000	0.0000	-3.0285	0.0000	0.0000
GO_CELLULAR_SENESCENCE	-1.5469	0.0265	0.0997	-1.5820	0.0124	0.0773
GO_CENTRIOLE_ASSEMBLY	-1.9837	0.0000	0.0057	-1.7079	0.0133	0.0413
GO_CENTROMERE_COMPLEX_ASSEMBLY	-2.5102	0.0000	0.0000	-3.1995	0.0000	0.0000
GO_CENTROSOME_CYCLE	-2.5456	0.0000	0.0000	-2.1723	0.0000	0.0011
GO_CENTROSOME_DUPLICATION	-2.1383	0.0000	0.0012	-1.9858	0.0061	0.0066
GO_CENTROSOME_LOCALIZATION	-1.9365	0.0026	0.0088	-1.8793	0.0051	0.0150
GO_CHROMATIN_ASSEMBLY_OR_DISASSEMBLY	-2.0272	0.0000	0.0039	-3.0433	0.0000	0.0000
GO_CHROMATIN_REMODELING	-1.8469	0.0000	0.0191	-2.3215	0.0000	0.0003
GO_CHROMOSOME_CONDENSATION	-2.4444	0.0000	0.0000	-2.8193	0.0000	0.0000
GO_CHROMOSOME_LOCALIZATION	-2.5166	0.0000	0.0000	-2.6172	0.0000	0.0000
GO_CHROMOSOME_SEGREGATION	-3.1058	0.0000	0.0000	-3.1515	0.0000	0.0000
GO_CHROMOSOME_SEPARATION	-1.9510	0.0000	0.0078	-1.8424	0.0050	0.0187
GO_CYTOKINESIS	-2.4867	0.0000	0.0000	-2.2599	0.0000	0.0005
GO_CYTOSKELETON_DEPENDENT_CYTOKINESIS	-2.4509	0.0000	0.0000	-2.3504	0.0000	0.0002
GO_DNA_BIOSYNTHETIC_PROCESS	-2.1011	0.0000	0.0017	-2.7311	0.0000	0.0000
GO_DNA_CONFORMATION_CHANGE	-2.5253	0.0000	0.0000	-3.1716	0.0000	0.0000
GO_DNA_DAMAGE_RESPONSE_DETECTION_OF_DNA_DAMAGE	-1.8915	0.0000	0.0128	-2.2672	0.0000	0.0005
GO_DNA_DEPENDENT_DNA_REPLICATION	-2.6016	0.0000	0.0000	-3.3733	0.0000	0.0000
GO_DNA_DEPENDENT_DNA_REPLICATION_MAINTENANCE_OF_FIDELITY	-1.7050	0.0054	0.0469	-2.2887	0.0000	0.0004
GO_DNA_GEOMETRIC_CHANGE	-2.3335	0.0000	0.0002	-2.4767	0.0000	0.0000

GO_DNA_INTEGRITY_CHECKPOINT	-2.0507	0.0000	0.0030	-2.2623	0.0000	0.0005
GO_DNA_PACKAGING	-2.4090	0.0000	0.0000	-3.2109	0.0000	0.0000
GO_DNA_RECOMBINATION	-2.2454	0.0000	0.0004	-2.7306	0.0000	0.0000
GO_DNA_REPLICATION	-2.5854	0.0000	0.0000	-3.1786	0.0000	0.0000
GO_DNA_REPLICATION_INDEPENDENT_NUCLEOSOME_ORGANIZATION	-2.3066	0.0000	0.0002	-3.1279	0.0000	0.0000
GO_DNA_REPLICATION_INITIATION	-2.4241	0.0000	0.0000	-3.2933	0.0000	0.0000
GO_DNA_STRAND_ELONGATION	-2.3103	0.0000	0.0002	-2.9450	0.0000	0.0000
GO_DNA_STRAND_ELONGATION_INVOLVED_IN_DNA_REPLICATION	-2.3138	0.0000	0.0002	-2.9335	0.0000	0.0000
GO_DNA_SYNTHESIS_INVOLVED_IN_DNA_REPAIR	-2.1195	0.0000	0.0014	-2.8103	0.0000	0.0000
GO_DOUBLE_STRAND_BREAK_REPAIR	-1.9035	0.0000	0.0114	-2.3274	0.0000	0.0003
GO_EMBRYONIC_CAMERA_TYPE_EYE_MORPHOGENESIS	-1.6634	0.0160	0.0575	-1.5289	0.0476	0.0989
GO_ERROR_FREE_TRANSLESION_SYNTHESIS	-2.0619	0.0000	0.0026	-2.0828	0.0000	0.0026
GO_ERROR_PRONE_TRANSLESION_SYNTHESIS	-1.6483	0.0283	0.0635	-1.9977	0.0000	0.0062
GO_ESTABLISHMENT_OF_MITOTIC_SPINDLE_LOCALIZATION	-1.7848	0.0052	0.0289	-1.7245	0.0000	0.0377
GO_G2_DNA_DAMAGE_CHECKPOINT	-1.9233	0.0027	0.0099	-2.0184	0.0000	0.0049
GO_HISTONE_EXCHANGE	-2.4107	0.0000	0.0000	-3.0666	0.0000	0.0000
GO_HISTONE_PHOSPHORYLATION	-2.3909	0.0000	0.0001	-1.9916	0.0000	0.0064
GO_INTERSTRAND_CROSS_LINK_REPAIR	-1.8133	0.0029	0.0238	-2.6098	0.0000	0.0000
GO_MEIOSIS_I	-1.7395	0.0068	0.0385	-2.1829	0.0000	0.0010
GO_MEIOTIC_CELL_CYCLE	-2.2021	0.0000	0.0006	-2.2745	0.0000	0.0005
GO_MEIOTIC_CELL_CYCLE_PROCESS	-2.1215	0.0000	0.0014	-2.2956	0.0000	0.0004
GO_MEIOTIC_CHROMOSOME_SEGREGATION	-2.0337	0.0000	0.0036	-2.0677	0.0000	0.0030
GO_MEMBRANE_ASSEMBLY	-1.7157	0.0137	0.0444	-2.1608	0.0000	0.0012
GO_MEMBRANE_BIOGENESIS	-1.5793	0.0229	0.0880	-1.9137	0.0067	0.0120
GO_MEMBRANE_DISASSEMBLY	-2.2122	0.0000	0.0005	-1.6949	0.0085	0.0444
GO_METAPHASE_PLATE_CONGRESSION	-2.3052	0.0000	0.0002	-2.6920	0.0000	0.0000
GO_MICROTUBULE_ORGANIZING_CENTER_ORGANIZATION	-2.4256	0.0000	0.0000	-2.0552	0.0000	0.0034
GO_MICROTUBULE_POLYMERIZATION_OR_DEPOLYMERIZATION	-1.6002	0.0166	0.0807	-2.3402	0.0000	0.0002
GO_MITOTIC_CELL_CYCLE_CHECKPOINT	-2.0797	0.0000	0.0022	-2.2856	0.0000	0.0005
GO_MITOTIC_CYTOKINESIS	-2.4529	0.0000	0.0000	-2.4929	0.0000	0.0000
GO_MITOTIC_DNA_INTEGRITY_CHECKPOINT	-1.7186	0.0000	0.0439	-1.9772	0.0000	0.0072
GO_MITOTIC_G2_M_TRANSITION_CHECKPOINT	-1.6974	0.0150	0.0494	-1.9520	0.0000	0.0091
GO_MITOTIC_RECOMBINATION	-2.3720	0.0000	0.0001	-2.9238	0.0000	0.0000
GO_MITOTIC_SISTER_CHROMATID_SEGREGATION	-3.0107	0.0000	0.0000	-3.4125	0.0000	0.0000
GO_MITOTIC_SPINDLE_ASSEMBLY	-2.4805	0.0000	0.0000	-2.5669	0.0000	0.0000

GO_MITOTIC_SPINDLE_ORGANIZATION	-2.9156	0.0000	0.0000	-2.9918	0.0000	0.0000
GO_MORPHOGENESIS_OF_AN_EPITHELIAL_SHEET	-1.6815	0.0030	0.0534	-1.7468	0.0000	0.0333
GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	-1.8375	0.0000	0.0205	-2.2535	0.0000	0.0005
GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_PROCESS	-1.8567	0.0000	0.0178	-2.2358	0.0000	0.0005
GO_NEGATIVE_REGULATION_OF_CELL_DIVISION	-2.1362	0.0000	0.0011	-2.6001	0.0000	0.0000
GO_NEGATIVE_REGULATION_OF_CELLULAR_PROTEIN_CATABOLIC_PROCESS	-1.8258	0.0000	0.0225	-1.5411	0.0192	0.0940
GO_NEGATIVE_REGULATION_OF_CHROMOSOME_ORGANIZATION	-1.6661	0.0000	0.0570	-1.8577	0.0000	0.0171
GO_NEGATIVE_REGULATION_OF_CHROMOSOME_SEGREGATION	-2.2162	0.0000	0.0005	-2.4281	0.0000	0.0000
GO_NEGATIVE_REGULATION_OF_CYTOSKELETON_ORGANIZATION	-2.6399	0.0000	0.0000	-2.3984	0.0000	0.0001
GO_NEGATIVE_REGULATION_OF_MITOTIC_CELL_CYCLE	-1.7849	0.0000	0.0290	-2.2381	0.0000	0.0005
GO_NEGATIVE_REGULATION_OF_MITOTIC_NUCLEAR_DIVISION	-1.8740	0.0000	0.0150	-2.1225	0.0000	0.0017
GO_NEGATIVE_REGULATION_OF_NUCLEAR_DIVISION	-1.8378	0.0000	0.0205	-2.1350	0.0000	0.0014
GO_NEGATIVE_REGULATION_OF_ORGANELLE_ORGANIZATION	-2.1387	0.0000	0.0012	-2.2150	0.0000	0.0007
GO_NEGATIVE_REGULATION_OF_PROTEIN_COMPLEX_DISASSEMBLY	-2.9520	0.0000	0.0000	-2.6118	0.0000	0.0000
GO_NUCLEAR_CHROMOSOME_SEGREGATION	-3.1018	0.0000	0.0000	-3.3794	0.0000	0.0000
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_GAP_FILLING	-1.6664	0.0058	0.0571	-2.2021	0.0000	0.0007
GO_PLATELET_AGGREGATION	-2.2094	0.0000	0.0006	-1.7284	0.0069	0.0368
GO_POSITIVE_REGULATION_OF_CELL_CYCLE	-1.8978	0.0000	0.0121	-2.0520	0.0000	0.0036
GO_POSITIVE_REGULATION_OF_CELL_CYCLE_ARREST	-1.6904	0.0000	0.0515	-1.6536	0.0000	0.0553
GO_POSITIVE_REGULATION_OF_CELL_CYCLE_G1_S_PHASE_TRANSITION	-1.8533	0.0000	0.0183	-1.7758	0.0057	0.0280
GO_POSITIVE_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	-2.1041	0.0000	0.0017	-2.4733	0.0000	0.0000
GO_POSITIVE_REGULATION_OF_CELL_CYCLE_PROCESS	-2.2836	0.0000	0.0003	-2.4494	0.0000	0.0000
GO_POSITIVE_REGULATION_OF_CELL_DIVISION	-2.0718	0.0000	0.0024	-2.2803	0.0000	0.0005
GO_POSITIVE_REGULATION_OF_CHROMOSOME_SEGREGATION	-1.9229	0.0054	0.0099	-2.2996	0.0000	0.0004
GO_POSITIVE_REGULATION_OF_CYTOKINESIS	-2.1903	0.0000	0.0007	-2.4758	0.0000	0.0000
GO_POSITIVE_REGULATION_OF_DNA_METABOLIC_PROCESS	-1.7400	0.0000	0.0385	-1.8539	0.0000	0.0174
GO_POSITIVE_REGULATION_OF_DNA_REPLICATION	-1.5971	0.0037	0.0815	-1.6055	0.0000	0.0696
GO_POSITIVE_REGULATION_OF_LIGASE_ACTIVITY	-2.0713	0.0000	0.0024	-1.7997	0.0000	0.0241
GO_POSITIVE_REGULATION_OF_MITOTIC_CELL_CYCLE	-2.1954	0.0000	0.0007	-2.3232	0.0000	0.0003
GO_POSITIVE_REGULATION_OF_MITOTIC_NUCLEAR_DIVISION	-2.1685	0.0000	0.0008	-2.2442	0.0000	0.0006
GO_POSITIVE_REGULATION_OF_NUCLEAR_DIVISION	-2.0541	0.0000	0.0029	-2.0445	0.0000	0.0039
GO_POSITIVE_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	-2.5485	0.0000	0.0000	-1.5269	0.0219	0.0995
GO_POSTREPLICATION_REPAIR	-1.7640	0.0094	0.0330	-2.0817	0.0000	0.0026
GO_PROTEIN_DEPOLYMERIZATION	-1.7928	0.0051	0.0274	-2.4195	0.0000	0.0001
GO_PROTEIN_DNA_COMPLEX_SUBUNIT_ORGANIZATION	-2.0524	0.0000	0.0030	-2.7639	0.0000	0.0000

GO_PROTEIN_HETEROTETRAMERIZATION	-1.7795	0.0061	0.0301	-2.2011	0.0000	0.0008
GO_PROTEIN_LOCALIZATION_TO_CHROMOSOME	-2.3148	0.0000	0.0002	-2.6370	0.0000	0.0000
GO_PROTEIN_LOCALIZATION_TO_CYTOSKELETON	-1.8905	0.0000	0.0128	-1.8599	0.0120	0.0168
GO_PROTEIN_UBIQUITINATION_INVOLVED_IN_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS	-2.1322	0.0000	0.0012	-1.5343	0.0000	0.0965
GO_RECIPROCAL_DNA_RECOMBINATION	-1.9247	0.0000	0.0098	-1.9109	0.0000	0.0122
GO_RECOMBINATIONAL_REPAIR	-2.0053	0.0000	0.0047	-2.3494	0.0000	0.0002
GO_REGULATION_OF_CELL_CYCLE_ARREST	-1.5786	0.0039	0.0882	-1.6052	0.0000	0.0695
GO_REGULATION_OF_CELL_CYCLE_G2_M_PHASE_TRANSITION	-1.7728	0.0000	0.0309	-2.2480	0.0000	0.0005
GO_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	-1.9943	0.0000	0.0052	-2.3704	0.0000	0.0002
GO_REGULATION_OF_CELL_DIVISION	-2.3414	0.0000	0.0001	-2.4834	0.0000	0.0000
GO_REGULATION_OF_CENTROSOME_CYCLE	-2.0614	0.0000	0.0026	-2.0629	0.0000	0.0031
GO_REGULATION_OF_CHROMATIN_SILENCING	-1.6246	0.0160	0.0716	-1.9931	0.0000	0.0064
GO_REGULATION_OF_CHROMOSOME_ORGANIZATION	-1.9050	0.0000	0.0113	-1.9046	0.0000	0.0127
GO_REGULATION_OF_CHROMOSOME_SEGREGATION	-2.6655	0.0000	0.0000	-3.0689	0.0000	0.0000
GO_REGULATION_OF_CYTOKINESIS	-2.3010	0.0000	0.0002	-2.1775	0.0000	0.0010
GO_REGULATION_OF_DNA_DEPENDENT_DNA_REPLICATION	-1.5719	0.0158	0.0910	-2.4323	0.0000	0.0000
GO_REGULATION_OF_DNA_METABOLIC_PROCESS	-1.8435	0.0000	0.0197	-1.5410	0.0000	0.0937
GO_REGULATION_OF_DNA_RECOMBINATION	-2.1354	0.0000	0.0011	-1.7310	0.0086	0.0364
GO_REGULATION_OF_DNA_REPAIR	-1.7106	0.0000	0.0452	-2.0176	0.0000	0.0049
GO_REGULATION_OF_DNA_REPLICATION	-1.8764	0.0000	0.0147	-1.8242	0.0000	0.0207
GO_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR	-1.9125	0.0000	0.0108	-2.3042	0.0000	0.0004
GO_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR_VIA_HOMOLOGOUS_RECOMBINATION	-1.8320	0.0054	0.0213	-2.0902	0.0000	0.0024
GO_REGULATION_OF_LIGASE_ACTIVITY	-2.0245	0.0000	0.0039	-1.7925	0.0000	0.0255
GO_REGULATION_OF_MICROTUBULE_BASED_PROCESS	-2.4759	0.0000	0.0000	-2.4949	0.0000	0.0000
GO_REGULATION_OF_MICROTUBULE_POLYMERIZATION_OR_DEPOLYMERIZATION	-2.5780	0.0000	0.0000	-2.6869	0.0000	0.0000
GO_REGULATION_OF_MITOTIC_CELL_CYCLE	-1.8021	0.0000	0.0258	-2.2437	0.0000	0.0005
GO_REGULATION_OF_NUCLEAR_DIVISION	-2.2652	0.0000	0.0003	-2.5215	0.0000	0.0000
GO_REGULATION_OF_PROTEIN_COMPLEX_DISASSEMBLY	-2.9758	0.0000	0.0000	-2.4088	0.0000	0.0001
GO_REGULATION_OF_PROTEIN_UBIQUITINATION_INVOLVED_IN_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS	-1.8977	0.0000	0.0120	-1.7572	0.0000	0.0312
GO_REGULATION_OF_SIGNAL_TRANSDUCTION_BY_P53_CLASS_MEDIATOR	-1.8014	0.0000	0.0258	-1.6537	0.0000	0.0555
GO_REGULATION_OF_SISTER_CHROMATID_SEGREGATION	-2.4627	0.0000	0.0000	-2.7148	0.0000	0.0000
GO_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	-1.5797	0.0099	0.0881	-2.0682	0.0000	0.0030
GO_REGULATION_OF_TRANSCRIPTION_INVOLVED_IN_G1_S_TRANSITION_OF_MITOTIC_CELL_CYCLE	-1.9662	0.0000	0.0067	-2.6321	0.0000	0.0000

GO_REGULATION_OF_UBIQUITIN_PROTEIN_LIGASE_ACTIVITY	-1.9625	0.0025	0.0069	-1.9871	0.0000	0.0066
GO_RESPONSE_TO_INTERFERON_ALPHA	1.9046	0.0000	0.0371	1.7696	0.0000	0.0431
GO_RESPONSE_TO_IONIZING_RADIATION	-1.6283	0.0000	0.0697	-1.6497	0.0000	0.0561
GO_RESPONSE_TO_TYPE_I_INTERFERON	2.4541	0.0000	0.0000	1.7572	0.0000	0.0448
GO_RETROGRADE_VESICLE_MEDIATED_TRANSPORT_GOLGI_TO_ER	-2.1781	0.0000	0.0007	-1.9751	0.0000	0.0074
GO_SARCOMERE_ORGANIZATION	-1.5513	0.0387	0.0992	-1.7191	0.0000	0.0386
GO_SIGNAL_TRANSDUCTION_IN_RESPONSE_TO_DNA_DAMAGE	-1.5626	0.0037	0.0939	-1.6550	0.0000	0.0556
GO_SISTER_CHROMATID_COHESION	-3.1104	0.0000	0.0000	-3.4931	0.0000	0.0000
GO_SISTER_CHROMATID_SEGREGATION	-3.1836	0.0000	0.0000	-3.6991	0.0000	0.0000
GO_SPINDLE_ASSEMBLY	-2.6295	0.0000	0.0000	-2.6728	0.0000	0.0000
GO_SPINDLE_CHECKPOINT	-2.3548	0.0000	0.0001	-2.5766	0.0000	0.0000
GO_SPINDLE_LOCALIZATION	-2.1398	0.0000	0.0012	-1.7646	0.0000	0.0305
GO_STRAND_DISPLACEMENT	-2.3370	0.0000	0.0002	-2.6216	0.0000	0.0000
GO_TELOMERE_MAINTENANCE_VIA_RECOMBINATION	-2.1565	0.0000	0.0009	-2.7328	0.0000	0.0000
GO_TELOMERE_ORGANIZATION	-1.6808	0.0000	0.0535	-2.4380	0.0000	0.0000
GO_TRANSLESION_SYNTHESIS	-1.5664	0.0240	0.0939	-2.1038	0.0000	0.0020
GO_VENTRICULAR_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	-1.5633	0.0256	0.0940	-1.6003	0.0122	0.0717
HALLMARK_E2F_TARGETS	-3.3660	0.0000	0.0000	-3.7997	0.0000	0.0000
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	-1.6541	0.0000	0.0610	-2.1539	0.0000	0.0012
HALLMARK_G2M_CHECKPOINT	-3.4579	0.0000	0.0000	-3.7415	0.0000	0.0000
HALLMARK_INTERFERON_ALPHA_RESPONSE	2.5392	0.0000	0.0000	1.8191	0.0000	0.0362
HALLMARK_MITOTIC_SPINDLE	-2.9564	0.0000	0.0000	-2.7011	0.0000	0.0000
HALLMARK_MYC_TARGETS_V1	-2.8411	0.0000	0.0000	-2.1608	0.0000	0.0012
KEGG_CELL_CYCLE	-2.5901	0.0000	0.0000	-3.2917	0.0000	0.0000
KEGG_DNA_REPLICATION	-2.2014	0.0000	0.0006	-3.2202	0.0000	0.0000
KEGG_HOMOLOGOUS_RECOMBINATION	-2.0979	0.0000	0.0018	-2.3529	0.0000	0.0002
KEGG_LYSOSOME	1.9426	0.0000	0.0246	1.7221	0.0000	0.0697
KEGG_MISMATCH_REPAIR	-2.0842	0.0000	0.0021	-2.1657	0.0000	0.0011
KEGG_NUCLEOTIDE_EXCISION_REPAIR	-1.6602	0.0066	0.0588	-2.0847	0.0000	0.0026
KEGG_OOCYTE_MEIOSIS	-2.2724	0.0000	0.0003	-2.2207	0.0000	0.0006
KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	-2.1524	0.0000	0.0010	-2.2512	0.0000	0.0005
KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	-1.8183	0.0000	0.0232	-1.8980	0.0000	0.0133

Supplementary Table 3. List of top pathways commonly regulated in MM.1S cells by shAHR and CLF treatment.

GeneSets	shAHR_NES	shAHR_pval	shAHR_FDR	CLF_NES	CLF_pval	CLF_FDR
HALLMARK_E2F_TARGETS	-1.9055	0.0000	0.0238	-2.0431	0.0000	0.0010
KEGG_GRAFT_VERSUS_HOST_DISEASE	1.9194	0.0043	0.0522	-1.3790	0.0491	0.1652
KEGG_SPLICEOSOME	-1.7440	0.0000	0.0905	-1.4941	0.0010	0.0901
KEGG_DNA_REPLICATION	-1.7499	0.0012	0.0941	-1.7630	0.0000	0.0090
KEGG_MISMATCH_REPAIR	-1.7453	0.0013	0.0945	-1.7335	0.0011	0.0121
GO_RECOMBINATIONAL_REPAIR	-1.7580	0.0000	0.0967	-1.5524	0.0000	0.0616
GO_DNA_REPAIR	-1.7197	0.0000	0.1021	-1.4700	0.0000	0.1050
GO_MISMATCH_REPAIR	-1.7226	0.0025	0.1026	-1.7121	0.0000	0.0154
KEGG_VIRAL_MYOCARDITIS	1.7758	0.0000	0.1027	-1.5274	0.0031	0.0734
GO_MRNA_PROCESSING	-1.7165	0.0000	0.1030	-1.3366	0.0000	0.1970
GO_RNA_3_END_PROCESSING	-1.6873	0.0000	0.1037	-1.4824	0.0020	0.0971
GO_MITOTIC_RECOMBINATION	-1.6888	0.0036	0.1047	-1.4598	0.0171	0.1118
GO_RIBONUCLEOPROTEIN_COMPLEX_LOCALIZATION	-1.7590	0.0000	0.1048	-1.3700	0.0111	0.1719
GO_NUCLEAR_CHROMOSOME_SEGREGATION	-1.6832	0.0000	0.1066	-1.5251	0.0000	0.0736
GO_TELOMERE_MAINTENANCE_VIA_RECOMBINATION	-1.6891	0.0025	0.1071	-1.4225	0.0351	0.1319
GO_SISTER_CHROMATID_SEGREGATION	-1.7061	0.0000	0.1072	-1.5801	0.0000	0.0495
GO_CHROMOSOME_SEGREGATION	-1.7085	0.0000	0.1078	-1.5121	0.0000	0.0789
GO_DNA_SYNTHESIS_INVOLVED_IN_DNA_REPAIR	-1.7229	0.0000	0.1078	-1.5544	0.0021	0.0603
GO_NEGATIVE_REGULATION_OF_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATION_OR_REMOVAL	-1.6769	0.0000	0.1080	-1.4167	0.0010	0.1360
GO_VIRAL_GENOME_REPLICATION	-1.6783	0.0013	0.1083	-1.3829	0.0728	0.1620
GO_DNA_DEPENDENT_DNA_REPLICATION	-1.6598	0.0000	0.1084	-1.6924	0.0000	0.0185
GO_DNA_REPLICATION	-1.7633	0.0000	0.1084	-1.7563	0.0000	0.0095
GO_TRANSCRIPTION_COUPLED_NUCLEOTIDE_EXCISION_REPAIR	-1.6694	0.0000	0.1084	-1.4095	0.0132	0.1401
GO_RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS	-1.6746	0.0000	0.1086	-1.6765	0.0000	0.0215
KEGG_PROTEASOME	-1.7254	0.0000	0.1092	-1.7047	0.0000	0.0163
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I	-1.7022	0.0012	0.1097	-1.5653	0.0010	0.0550
GO_SISTER_CHROMATID_COHESION	-1.7283	0.0000	0.1097	-1.6257	0.0000	0.0339
GO_DNA_REPLICATION_INDEPENDENT_NUCLEOSOME_ORGANIZATION	-1.6897	0.0012	0.1098	-1.9239	0.0000	0.0028
GO_ANAPHASE_PROMOTING_COMPLEX_DEPENDENT_CATABOLIC_PROCESS	-1.6697	0.0000	0.1105	-1.5942	0.0010	0.0441

GO_CENTROMERE_COMPLEX_ASSEMBLY	-1.6644	0.0024	0.1105	-1.8954	0.0000	0.0055
GO_DOUBLE_STRAND_BREAK_REPAIR	-1.6599	0.0000	0.1105	-1.6085	0.0000	0.0401
GO_NUCLEOTIDE_EXCISION_REPAIR	-1.6786	0.0000	0.1109	-1.4238	0.0040	0.1311
GO_DNA_RECOMBINATION	-1.7935	0.0000	0.1112	-1.5720	0.0000	0.0515
GO_RNA_SPLICING	-1.6934	0.0000	0.1113	-1.3750	0.0000	0.1683
GO_LEUKOTRIENE_BIOSYNTHETIC_PROCESS	-1.6545	0.0064	0.1124	-1.4482	0.0355	0.1195
GO_DNA_TEMPLATED_TRANSCRIPTION_TERMINATION	-1.6646	0.0022	0.1130	-1.5847	0.0000	0.0473
HALLMARK_MYC_TARGETS_V1	-1.7825	0.0000	0.1142	-2.0919	0.0000	0.0000
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_I_BIOGENESIS	-1.7655	0.0000	0.1176	-1.5934	0.0000	0.0441
GO_REGULATION_OF_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	-1.6944	0.0011	0.1183	-1.6312	0.0000	0.0326
GO_RESPONSE_TO AMPHETAMINE	-1.6459	0.0064	0.1190	-1.4676	0.0323	0.1070
GO_B_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	-1.6428	0.0089	0.1221	-1.4480	0.0261	0.1195
GO_STRAND_DISPLACEMENT	-1.6337	0.0038	0.1250	-1.3433	0.0728	0.1906
GO_PROTEIN_DNA_COMPLEX_SUBUNIT_ORGANIZATION	-1.6343	0.0000	0.1261	-1.4480	0.0000	0.1193
GO_RIBOSOME_BIOGENESIS	-1.6388	0.0000	0.1267	-1.7041	0.0000	0.0163
GO_RESPONSE_TO ETHANOL	-1.6343	0.0011	0.1281	-1.3746	0.0142	0.1682
GO_RESPONSE_TO_XENOBIOTIC_STIMULUS	-1.6362	0.0011	0.1290	-1.5635	0.0000	0.0561
GO GLUTAMINE_FAMILY_AMINO_ACID_CATABOLIC_PROCESS	-1.6052	0.0103	0.1291	-1.5780	0.0058	0.0494
GO_REGULATION_OF_TELOMERE_MAINTENANCE	-1.6038	0.0011	0.1300	-1.3550	0.0332	0.1841
GO_HISTONE_EXCHANGE	-1.6080	0.0059	0.1306	-1.8479	0.0000	0.0044
GO_MITOTIC_SISTER_CHROMATID_SEGREGATION	-1.6263	0.0011	0.1314	-1.4259	0.0061	0.1310
GO_ATP_DEPENDENT_CHROMATIN_REMODELING	-1.6109	0.0011	0.1322	-1.8468	0.0000	0.0041
GO_RIBOSOMAL_SMALL_SUBUNIT_BIOGENESIS	-1.6080	0.0023	0.1322	-1.7442	0.0000	0.0111
GO_OXIDATIVE_PHOSPHORYLATION	-1.6283	0.0000	0.1323	-1.8001	0.0000	0.0073
GO_MATURATION_OF_5_8S_RRNA	-1.6086	0.0100	0.1330	-1.7770	0.0000	0.0084
GO_RIBONUCLEOPROTEIN_COMPLEX_SUBUNIT_ORGANIZATION	-1.6095	0.0000	0.1331	-1.5225	0.0000	0.0740
GO_MACROMOLECULAR_COMPLEX_DISASSEMBLY	-1.6113	0.0000	0.1333	-1.6581	0.0000	0.0256
GO_DEOXYRIBONUCLEOTIDE_METABOLIC_PROCESS	-1.6264	0.0061	0.1334	-1.7362	0.0000	0.0120
GO_CELLULAR_PROTEIN_COMPLEX_DISASSEMBLY	-1.5970	0.0000	0.1337	-1.6973	0.0000	0.0178
GO_TELOMERE_ORGANIZATION	-1.5984	0.0000	0.1341	-1.4491	0.0061	0.1200
GO_INNATE_IMMUNE_RESPONSE_ACTIVATING_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY	-1.5973	0.0011	0.1348	-1.4195	0.0030	0.1343
GO_TERMINATION_OF_RNA_POLYMERASE_II_TRANSCRIPTION	-1.6115	0.0034	0.1348	-1.4723	0.0052	0.1034
GO_MRNA_3_END_PROCESSING	-1.6134	0.0022	0.1350	-1.3649	0.0163	0.1766
GO_CHROMATIN_ASSEMBLY_OR_DISASSEMBLY	-1.6230	0.0000	0.1352	-1.5161	0.0000	0.0770

GO_DNA_BIOSYNTHETIC_PROCESS	-1.5937	0.0011	0.1352	-1.4746	0.0010	0.1037
GO_DICARBOXYLIC_ACID_TRANSPORT	1.6952	0.0000	0.1355	-1.3831	0.0392	0.1620
GO_CHROMATIN_SILENCING	-1.6152	0.0011	0.1357	-1.3448	0.0328	0.1902
GO_DNA_CONFORMATION_CHANGE	-1.5940	0.0000	0.1361	-1.4787	0.0000	0.1002
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	1.6731	0.0083	0.1366	-1.4685	0.0094	0.1063
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY	-1.7941	0.0000	0.1369	-1.6386	0.0000	0.0313
KEGG_BASE_EXCISION_REPAIR	-1.6166	0.0060	0.1371	-1.7093	0.0000	0.0157
HALLMARK_DNA_REPAIR	-1.6154	0.0011	0.1374	-1.4867	0.0000	0.0955
KEGG_OXIDATIVE_PHOSPHORYLATION	-1.6166	0.0011	0.1391	-1.8080	0.0000	0.0073
GO_DNA_STRAND_ELONGATION_INVOLVED_IN_DNA_REPLICATION	-1.5905	0.0174	0.1392	-1.4261	0.0301	0.1311
GO_DNA_PACKAGING	-1.6179	0.0000	0.1402	-1.4858	0.0000	0.0951
GO_CANONICAL_WNT_SIGNALING_PATHWAY	1.6334	0.0099	0.1453	-1.5042	0.0042	0.0835
GO_DNA_REPLICATION_DEPENDENT_NUCLEOSOME_ORGANIZATION	-1.5845	0.0138	0.1473	-1.4453	0.0324	0.1194
GO_MITOCHONDRIAL_TRANSLATION	-1.5815	0.0000	0.1482	-1.7232	0.0000	0.0136
GO_PYRIMIDINE_DEOXYRIBONUCLEOTIDE_METABOLIC_PROCESS	-1.5829	0.0079	0.1484	-1.8509	0.0000	0.0044
GO_RRNA_METABOLIC_PROCESS	-1.5800	0.0000	0.1496	-1.7021	0.0000	0.0167
GO_NUCLEIC_ACID_PHOSPHODIESTER_BOND_HYDROLYSIS	-1.5815	0.0000	0.1496	-1.6819	0.0000	0.0209
GO_MOVEMENT_IN_ENVIRONMENT_OF_OTHER_ORGANISM_INVOLVED_IN_SYMBIOTIC_INTERACTION	1.6177	0.0000	0.1506	-1.6574	0.0000	0.0256
GO_BASE_EXCISION_REPAIR	-1.5727	0.0097	0.1516	-1.4242	0.0235	0.1315
GO_SPLICEOSOMAL_SNRNP_ASSEMBLY	-1.5681	0.0120	0.1517	-1.6507	0.0011	0.0275
GO_MATURATION_OF_SSU_RRNA	-1.5668	0.0120	0.1517	-1.7171	0.0000	0.0146
GO_NCRNA_TRANSCRIPTION	-1.5701	0.0011	0.1518	-1.5992	0.0000	0.0439
GO_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANSPORT	-1.5732	0.0155	0.1522	-1.3721	0.0416	0.1701
GO_TRNA_METABOLIC_PROCESS	-1.5532	0.0000	0.1523	-1.4487	0.0000	0.1197
GO_NEGATIVE_REGULATION_OF_CATION_CHANNEL_ACTIVITY	-1.5684	0.0128	0.1525	-1.4998	0.0156	0.0867
GO_PTERIDINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	-1.5536	0.0131	0.1527	-1.5595	0.0076	0.0581
GO_NEGATIVE_REGULATION_OF_PROTEIN_COMPLEX_DISASSEMBLY	-1.5703	0.0010	0.1529	-1.3361	0.0120	0.1965
GO_POSITIVE_REGULATION_OF_LIGASE_ACTIVITY	-1.5585	0.0000	0.1529	-1.3735	0.0091	0.1692
GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_PROLIFERATION	-1.5540	0.0115	0.1532	-1.3805	0.0688	0.1637
GO_NEGATIVE_REGULATION_OF_CATION_TRANSMEMBRANE_TRANSPORT	-1.5508	0.0098	0.1534	-1.5515	0.0053	0.0621
GO_TRANSLATIONAL_TERMINATION	-1.5544	0.0033	0.1534	-1.7706	0.0000	0.0083
GO_TELOMERE_CAPPING	-1.5774	0.0115	0.1534	-1.4811	0.0154	0.0981
GO_QUINONE_METABOLIC_PROCESS	-1.5741	0.0141	0.1534	-1.5845	0.0101	0.0470
GO_REGULATION_OF_PROTEIN_INSERTION_INTO_MITOCHONDRIAL_MEMBRANE_INVOLVED_IN_APOPTOTIC_SIGNALING_PATHWAY	-1.5588	0.0109	0.1536	-1.5686	0.0088	0.0534

GO_REGULATION_OF_EARLY_ENDOSOME_TO_LATE_ENDOSOME_TRANSPORT	-1.5600	0.0157	0.1539	-1.3782	0.0674	0.1653
GO_POSTREPLICATION_REPAIR	-1.5754	0.0034	0.1539	-1.5920	0.0053	0.0444
GO_CHROMATIN_SILENCING_AT_RDNA	-1.5509	0.0156	0.1544	-1.3363	0.0660	0.1969
GO_POSITIVE_REGULATION_OF_VIRAL_PROCESS	-1.5744	0.0022	0.1545	-1.3595	0.0246	0.1800
GO_DNA_REPLICATION_INITIATION	-1.5513	0.0122	0.1547	-1.6268	0.0011	0.0336
GO_POSITIVE_REGULATION_OF_CHROMOSOME_SEGREGATION	-1.5617	0.0129	0.1548	-1.3560	0.0717	0.1830
GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS	-1.5588	0.0000	0.1548	-1.7341	0.0000	0.0122
KEGG_PYRIMIDINE_METABOLISM	-1.5638	0.0011	0.1549	-1.7284	0.0000	0.0126
GO_PYRIMIDINE_NUCLEOTIDE_METABOLIC_PROCESS	-1.5644	0.0143	0.1550	-1.8027	0.0000	0.0071
HALLMARK_OXIDATIVE_PHOSPHORYLATION	-1.5622	0.0000	0.1552	-1.8592	0.0000	0.0047
GO_REGULATION_OF_CHROMOSOME_SEGREGATION	-1.5626	0.0055	0.1556	-1.3989	0.0122	0.1491
GO_PROTEIN_MANNOSYLATION	-1.5604	0.0108	0.1558	-1.4701	0.0342	0.1050
GO_NCRNA_METABOLIC_PROCESS	-1.5442	0.0000	0.1606	-1.6269	0.0000	0.0338
GO_GLUTATHIONE_DERIVATIVE_METABOLIC_PROCESS	-1.5432	0.0172	0.1614	-1.3917	0.0389	0.1545
GO_DNA_TEMPLATED_TRANSCRIPTION_ELONGATION	-1.5444	0.0022	0.1624	-1.3444	0.0295	0.1900
GO_FC_EPSILON_RECEPTOR_SIGNALING_PATHWAY	-1.5402	0.0011	0.1637	-1.3337	0.0121	0.1983
GO_POSITIVE_REGULATION_OF_GENE_EXPRESSION_EPIGENETIC	-1.5394	0.0022	0.1640	-1.4329	0.0052	0.1272
GO_REGULATION_OF_TRANSCRIPTION_INVOLVED_IN_G1_S_TRANSITION_OF_MITOTIC_CELL_CYCLE	-1.5404	0.0139	0.1644	-1.7416	0.0000	0.0111
GO_REGULATION_OF_CATION_CHANNEL_ACTIVITY	-1.5380	0.0034	0.1656	-1.3327	0.0403	0.1992
GO_NCRNA_3_END_PROCESSING	-1.5371	0.0203	0.1661	-1.5876	0.0046	0.0461
GO_PROTEIN_TARGETING_TO_MITOCHONDRION	-1.5330	0.0105	0.1706	-1.4376	0.0301	0.1233
GO_EMBRYONIC_DIGIT_MORPHOGENESIS	1.5652	0.0069	0.1717	-1.4567	0.0137	0.1139
GO_AMEBOIDAL_TYPE_CELL_MIGRATION	1.5382	0.0000	0.1746	-1.3354	0.0211	0.1971
GO_TRANSLATIONAL_ELONGATION	-1.5287	0.0021	0.1765	-1.6632	0.0000	0.0251
GO_CELL_DIVISION	-1.5221	0.0000	0.1785	-1.4299	0.0000	0.1283
GO_MITOTIC_NUCLEAR_DIVISION	-1.5255	0.0000	0.1785	-1.4387	0.0000	0.1230
GO_TRNA_TRANSPORT	-1.5184	0.0269	0.1785	-1.3399	0.0810	0.1928
GO_PHAGOSOME_MATURATION	-1.5162	0.0196	0.1787	-1.3957	0.0430	0.1515
GO_REGULATION_OF_PROTEIN_UBIQUITINATION_INVOLVED_IN_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS	-1.5236	0.0022	0.1788	-1.4047	0.0071	0.1447
GO_RECIPROCAL_DNA_RECOMBINATION	-1.5224	0.0181	0.1791	-1.7652	0.0000	0.0088
GO_SNRNA_METABOLIC_PROCESS	-1.5164	0.0045	0.1792	-1.6035	0.0000	0.0417
GO_MATURATION_OF_5_8S_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_LSU_RRNA_	-1.5263	0.0268	0.1793	-1.7613	0.0000	0.0089
KEGG_PARKINSONS_DISEASE	-1.5189	0.0054	0.1796	-1.8393	0.0000	0.0045

GO_NCRNA_PROCESSING	-1.5244	0.0000	0.1796	-1.6584	0.0000	0.0257
GO_DEOXYRIBOSE_PHOSPHATE_CATABOLIC_PROCESS	-1.5194	0.0214	0.1796	-1.7057	0.0000	0.0162
GO_NON_RECOMBINATIONAL_REPAIR	-1.5146	0.0101	0.1799	-1.5209	0.0041	0.0741
GO_NEGATIVE_REGULATION_OF_TELOMERE_MAINTENANCE	-1.5197	0.0252	0.1802	-1.3761	0.0522	0.1676
GO_RNA_SPLICING_VIA_TRANSESTERIFICATION_REACTIONS	-1.7944	0.0000	0.1811	-1.5136	0.0000	0.0780
GO_NEGATIVE_REGULATION_OF_NEURAL_PRECURSOR_CELL_PROLIFERATION	1.4901	0.0471	0.1815	-1.5350	0.0083	0.0704
GO_MATURATION_OF_SSU_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8_S_RRNA_LSU_RRNA_	-1.5097	0.0123	0.1878	-1.6766	0.0000	0.0217
GO_POSITIVE_REGULATION_OF_SYNAPSE_ASSEMBLY	1.4766	0.0316	0.1916	-1.5144	0.0077	0.0776
GO_REGULATION_OF_SYNAPSE_ASSEMBLY	1.4734	0.0276	0.1925	-1.4045	0.0273	0.1448
GO_TRANSLESION_SYNTHESIS	-1.5060	0.0228	0.1941	-1.5209	0.0097	0.0743
GO_NUCLEOBASE_BIOSYNTHETIC_PROCESS	-1.5051	0.0280	0.1951	-1.9288	0.0000	0.0029
GO_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_MITOCHONDRION	-1.5034	0.0011	0.1967	-1.3409	0.0181	0.1924
GO_FEMALE_MEIOTIC_DIVISION	-1.5002	0.0280	0.1986	-1.3947	0.0571	0.1525