SUPPLEMENTARY MATERIALS AND METHODS

Synthesis of MC2392, MC2678, and MC2677.

General procedure for the preparation of N-(2-, 3-, 4-aminophenyl)retinamides. Example: N-(2-aminophenyl)retinamide (MC2392). A mixture of all-trans retinoic acid (ATRA) (0.50 g, 1.66 mmol), triethylamine (0.93 mL, 0.67 g, 6.65 mmol), and benzotriazole-1-yloxytris(dimethylamino)phosphonium hexafluorophosphate (BOP-reagent) (0.88 g, 1.99 mmol) in dry DMF (5 mL) was stirred at room temperature for 40 minutes under inert atmosphere (N2). After the addition of 1,2-phenylenediamine (0.19 g, 1.83 mmol), the resulting mixture was stirred at room temperature under N2 for 2h. The reaction was quenched by water addition (50 mL). The resulting suspension was then filtered and the crude solid product was purified by passing it through a silica gel column eluting with ethyl acetate/chloroform (1:15). Yield: 67%; mp:150-152°C; recrystallization solvent: cyclohexane. 1H-NMR (CDCl3) δ 1.01 (m, 6H, C(CH3)2), 1.44 (m, 2H, CH2), 1.59 (m, 2H, CH2), 1.69 (s, 3H, CH3), 1.99 (m, 5H, CH2 and CH3), 2.39 (s, 3H, CH3), 3.86 (s, 2H, NH2), 5.84 (s, 1H, NH), 6.11 (m, 2H, ethylenic H), 6.25 (m, 2H, ethylenic H), 6.78 (m, 2H, ethylenic H), 6.92-7.05 (m, 2H, benzene ring), 7.15-7.20 (m, 2H, benzene ring). N-(3-aminophenyl)retinamide (MC2678), prepared from ATRA and 1,3-phenylendiamine. Yield: 59%; mp: 78-80°C; recrystallization solvent: n-hexane. 1H-NMR (CDCl3) δ 1.05 (m, 6H, C(CH3)2), 1.50 (m, 2H, CH2), 1.63 (m, 2H, CH2), 1.74 (s, 3H, CH3), 2.00 (m, 5H, CH2 and CH3), 2.43 (s, 3H, CH3), 3.79 (s, 2H, NH2), 5.79 (s, 1H, NH), 6.16 (m, 2H, ethylenic H), 6.30 (m, 2H, ethylenic H), 6.44 (m, 1H, ethylenic H), 6.67 (m, 1H, ethylenic H), 7.01 (m, 1H, benzene ring), 7.05 (m, 2H, benzene ring), 7.26 (m, 1H, benzene ring). N-(4-aminophenyl)retinamide (MC2677), prepared from ATRA and 1,4-phenylendiamine. Yield: 71%; mp: 155-158°C; recrystallization solvent: cyclohexane. 1H-NMR (CDCl3) δ 1.05 (m, 6H, C(CH3)2), 1.48 (m, 2H, CH2), 1.62 (m, 2H, CH2), 1.73 (s, 3H, CH3), 2.02 (m, 5H, CH2 and CH3), 2.43 (s, 3H, CH3), 3.61 (s, 2H, NH2), 5.78 (s, 1H, NH), 6.16 (m, 2H, ethylenic H), 6.28 (m, 2H, ethylenic H), 6.67 (m, 2H, ethylenic H), 7.02 (m, 2H, benzene ring), 7.34 (m, 2H, benzene ring). The HDAC inhibitory activities of 3- and 4-aminoanilides (MC2677 and MC2678) are reported absent or very low (only present for concentrations higher than 100 μM).

Cell cycle analysis. 2.0×10^5 cells were collected and resuspended in 500 □L of an hypotonic buffer (0,1% NP-40, 0.1% sodium citrate, 50 microg/mL propidium iodide (PI), RNAse A). Cells were incubated in the dark for 30 min. Samples were measured on a FACS (fluorescence-activated cell sorting) Calibur flow cytometer using the Cell Quest software (Becton Dickinson) and analyzed

with standard procedures using the Cell Quest software (Becton Dickinson) and the ModFit LT version 3 Software (Verity). All the experiments were performed in triplicate.

Granulocytic differentiation. Cells were harvested and resuspended in 10 μL phycoerythrine-conjugated CD11c (CD11c-PE). Control samples were incubated with 10 μL PE conjugated mouse IgG1, incubated for 30 min at 4°C in the dark, washed in PBS, and resuspended in 500 μL PBS containing PI (0.25 μg/mL). Samples were analyzed by FACS with Cell Quest technology (Becton Dickinson). PI positive cells were excluded from the analysis.

Protein extraction. Cells were harvested and washed once with cold PBS and lysed in 50 mM Tris-HCl pH 7.4, 150 mM NaCl, 1% NP40, 10 mM NaF, 1 mM PMSF (phenyl-methylsulphonylfluoride) and protease inhibitor cocktail (Roche). The lysates were centrifuged at 14000 rpm for 30 min at 4°C. Protein concentrations were determined by Bradford assay (Bio-Rad).

Histone extraction. U937 and NB4 were harvested and histone extracts were prepared as further described. Cells were washed twice with cold PBS and than resuspended in Triton Extraction Buffer (TEB: PBS containing 0.5% Triton X 100 (v/v), 2 mM phenylmethylsulfonyl fluoride (PMSF), 0.02% (w/v) NaN3) at a cell density of 10^7 cells per ml. Lyses was performed on ice for 10 minutes with gentle stirring and centrifuged at 6,500 x g for 10 minutes at 4°C to spin down the nuclei. The supernatant was discarded and the nuclei were washed in half the volume of TEB and centrifuged as before. The pellet was resuspended in 0.2 N HCl overnight at 4°C. The samples were centrifuged for 10 minutes at 4°C and the supernatant, which contains the histone protein, was stored. The protein content was determined using the Bradford assay.

Western blot. 50 □g of total proteins and 10□g of histone extract were separated on a 8% and 15% polyacrylamide gel and blotted as previously described (30). Antibodies used were: TRAIL, H2Ax phosphoS139 (Abcam), Bcl2 (Stressgene), Bid (Stressgene), Bad, FADD, caspase3, 8 (Cell Signaling), FAS (prosci), $Flip_L$ (Alexis), RIP1, $p21^{Cip1/Waf1}$ (Transduction Laboratories), PML, ERKs, histone H1 (Santa Cruz) and AcH3 (Millipore).

Transfections and luciferase assay. The HeLa cells were transfected with lipofectamine (Invitrogen). Briefly, HeLa cells were plated at 90% confluence and transfected with 100 ng of plasmid $(RARE)_3$ tk-luc; 50 ng of pmaxGFP (GFP, used as an internal control to normalize variations in the transfection efficiency). After induction with ATRA and MC2392, cells were harvested and washed twice in PBS 1X. Then the cells were lysed with 100 □L of cellular lysys buffer (Promega) for 1 h at room temperature. 20 □L of lysated was carried out in a 96 well and the luciferase assay was performed by adding the luciferase substrate to the cell lysate, using standard protocols with the TECAN Inphinite 200. The light (produced by converting the chemical energy of luciferin oxidation through an electron transition, forming the product molecule oxyluciferin) was measured in relative light units (RLU).

Immunoprecipitation. After HeLa transient transfection with the plasmid pLenti6/V5-DEST PML/RARα(Invitrogen), HeLa cells were lysed in TAP buffer (tris HCl pH 7.0 50 mM, NaCl 180 mM, NP-40 0.15%, glycerol 10%, $MgCl_2$ 1.5 mM, $NaMO_4$ 1 mM, NaF 0.5 mM) with protease inhibitor cocktail (Sigma), DTT 1 mM and PMSF 0.2 mM for 10 minutes in ice and centrifugated at 13000rpm for 30 minutes. 1000 □g of extracts were diluted in TAP buffer up to 1 ml and pre-cleared by incubating with 20 □L A/G plus Agarose (Santa Cruz) for 30 minutes to 1 hour on a rocking table at 4°C. Supernatant was transferred in a new tube and the antibody (around 3-4 □g) added and IP was allowed to proceed overnight at 4°C on a rocking table. The antibody was anti-PML (Santa Cruz). As a negative control, protein extracts were immunoprecipitated with purified IgG rabbit (Santa Cruz). After day 10-15□L A/G plus Agarose were added and incubation was continued for 2 hours. The beads were recovered by brief centrifugation and washed with cold TAP buffer several times. After the last washing 20□L of 2X concentrated electrophoresis sample buffer (tris HCl pH 8 217 mM, SDS 5.3%, glycerol 17.4%, □-mercaptoethanol 8.7%, bromophenol blue 0.026%) were added, and samples boiled for 5 minutes. Supernatants were loaded onto an SDS-PAGE gel.

Illumina High-Throughput ChIP Sequencing

DNA samples were prepared for sequencing by end repair of 20 ng DNA as measured by Qubit (Invitrogen) using Klenow and T4 PNK enzymes. A 30 protruding A base was generated using Taq polymerase and adapters were ligated. The DNA was loaded on gel and a band corresponding to about 300bp (ChIP fragment + adapters) was excised. The DNA was isolated, amplified by 14 cycles of PCR, and used for cluster generation on the Illumina Genome Analyzer II. Quality control of DNA libraries prepared for sequencing was made by qPCR and by running the products on a Bioanalyzer (BioRad). The image files generated by the Genome Analyzer were processed to extract DNA sequence data and the 36 bp tags were mapped to the human genome hg18 using the Eland program allowing one mismatch. The 36 bp sequence reads were directionally extended to 300 bp, corresponding to the length of the original fragments used for sequencing. Data can be accessed on GEO: GSE50958. The output data were converted to Browser Extensible Data (BED) files for downstream analysis and Wiggle (WIG) files for viewing as tag-density in the University of California Santa Cruz genome browser (http://genome.ucsc.edu). As Zhang et al, (35) discussed, large differences in sequencing depth may lead to an increase of FDR (false discovered rate) and result in false-positive peaks. In order to compensate for differences in sequencing depth and mapping efficiency among ChIP-seq samples at different conditions, the total number of tags of each samples was equalized by uniformly removing tags relatively to the sample with the lower number of tags. After equalization, the tracks contained the same number of sequence reads and could be compared quantitatively.

Overview of sequenced and mapped tags for all data sets.

Sample	Total reads	Mapped reads	%mapped reads
NB4_DMSO	29412721	24753856	84.16
NB4_ATRA_4h	36264992	30727370	84.73
NB4_ATRA_24h	37690280	31952702	84.78
NB4_MS275_4h	33947367	28936792	85.24
NB4_MC2392_4h	31390125	26652886	84.91
NB4_MC2392_24h	35407148	29554235	83.47
NB4_MC2392_48h	35267181	30179637	85.57

Peak Detection and Clustering analysis. All the H3K9K14ac combined peaks were detected using MACS (35) with a P =10^{-6} and the normalized number of tags of the treated and untreated samples were counted. The results, represented in log2 of tag density, were used in k-mean clustering

analysis using the Pearson correlation distance (Mev). The regulated genes of the clusters of particular interest were assigned to biological functions based on Gene Ontology (GO) analysis using the web tool David (http://david.abcc.ncifcrf.gov/home.jsp).

Motif Search. De novo motif search was performed using a combination of widely used software coupled with motif quantity control, clustering and statistical significance metrics (36). The top scoring clustered motifs were curated and converted to Position Weight Matrices (PWMs) which were compared against the JASPAE v3 database using STAMP (37). The PWSs data were used to scan all peak subset for the occurrence of the respective motifs.

RNA extraction, reverse transcription (RT) and quantitative PCR in real time (RT-PCR). See Supplementary Materials and M Cells were homogenized in 1 mL TRIzol (Invitrogen) and RNA extracted following supplier's instruction (GIBCO). RNA concentration was measured using a Nanodrop spectrophotometer (Thermo Scientific, USA). Total RNA (1 □g) was reverse transcribed with oligo (dT) primer using Superscript III Reverse Transcriptase (Invitrogen) as described by supplier. Quantitative realtime PCR was carried out in a Bio-Rad iCycler Real-Time PCR using the iQ Sybr Green SuperMix (Biorad).

Supplemental Table 1. Primers

Name	Sequence
IRF1 up	5'-GCA GGC CCT GAC TCC AGC AC-3'
IRF1 down	5'-GC CAC TCC GAC TGC TCC AA-3'
TNF up	5'-CAG AGG GAA GAG GTT CCC CAG-3'
TNF down	5'-CCT TGG TCT GGT AGG AGA CG-3'
casp3 up	5'-TGG AAT TGA TGC GTG ATG TT-3'
casp3 down	5'-GGC AGG CCT GAA TAA TGA AA-3'
casp9 up	5'- CTA GTT TGC CCA CAC CCA GT-3'
casp9 down	5'-CCT TTC ACC GAA ACA GCA TT-3'
bcl2 up	5'-TTG TTC AAA CGG GAT TCA CA-3'
bcl2 down	5'-GAG CAA GTG CAG CCA CAA TA-3'
bax up	5'-TTT GCT TCA GGG TTT CAT CC-3'
bax down	5'-ATC CTC TGC AGC TCC ATG TT-3'
casp8 up	5'-AAG CAA ACC TCG GGG ATA CT-3'
casp8 down	5'-GGG GCT TGA TCT CAA AAT GA-3'
FADD up	5'-CAC AGA CCA CCT GCT TCT GA-3'
FADD down	5'-CTG GAC ACG GTT CCA ACT TT-3'
Fas up	5'-CAA GGG ATT GGA ATT GAG GA-3'
Fas down	5'-TGG AAG AAA AAT GGG CTT TG-3'
TRAIL up	5'-CAA CTC CGT CAG CTC GTT AGA AAG-3'
TRAIL down	5'-TTA GAC CAA CAA CTA TTT CTA GCA CT-3'
DR5 up	5'-GCCTCA TGG ACA ATG AGA TAA AGG TGGCT-3'
DR5 down	5'-CCA AAT CTC AAA GTA CGC ACA AAC GG-3'
p40 phox up	5'-CAG CCA CTT TGT TTT CGT CA-3'
p40 phox down	5'- TCC TGT TTC ACA CCC ACG TA-3'
p47 phox up	5'-AGT CCT GAC GAG ACG GAA GA-3'
p47 phox down	5'-TAC ATG GAC GGG AAG TAG CC-3'
p67 phox up	5'-TGG AGT GTG TCT GGA AGC AG-3'
p67 phox down	5'-ATC TCT GGG GTT TTC GGT CT-3'
casp2 up	5'-AAG GAG CTG ATG GCC GCT GA-3'
casp2 down	5'-GCC CAC TTT GGC CTG GAT GA-3'
nox2 up	5'-TCA CTT CCT CCA CCA AAA CC-3'
nox2 down	5'-GGG ATT GGG CAT TCC TTT AT-3'
p65 up	5' ATC TTG AGC TCG TCG GCA GTG TT 3'
p65 down	5' ACA ACC CCT TCC AAG TTC CT -3'
Ikkalpha up	5'- ATT GCC CTG TTC CTC ATT TG -3'
Ikkalpha down	5'- GAA GGT GCA GTA ACC CTT CA -3'

RNA-sequencing. Total RNA was isolated using Trizol (Invitrogen) according to the manufacturer's recommendations. The amounts of 100 ng mRNA was fragmented by hydrolysis and purified using the RNAeasy Minelute Kit (Qiagen). cDNA first and Ds-cDNA synthesis then, was performed following supplier's instructions (Invitrogen). Ds-cDNA samples were prepared for sequencing by end repair of 20 ng DNA as measured by Qubit (Invitrogen). Adaptors were ligated to DNA fragments, followed by size selection (~300 bp) and limited PCR amplification (14 cycles). The resulting sample libraries were subjected to DSN treatment (Evrogen) according to the manufacturer's recommendations. Cluster generation and sequencing-by-synthesis (36 bp) were performed using the Illumina Genome Analyzer IIx (GAIIx) platform according to standard protocols (Illumina). Samples were sequenced to a depth of approximately 20 million mapped tags per sample. Sequences were aligned to hg18 reference genome using the Illumina Analysis Pipeline allowing one mismatch. Only the tags uniquely aligning to the genome were considered for further analysis. To obtain gene expression values from the RNA-Seq output, we counted the number of tags present in the coding bodies of genes. The gene expression values were converted to standardized RNA-Seq expression values "Reads Per Kilobase exon Model per million mapped read" (RPKM). To obtain gene expression values (RPKM) from the RNA-Seq output, we used Genomatix (www.genomatix.de) software. GO and Pathway analysis were performed using Panther (http://www.pantherdb.org).

Supplemental Table 2. Analysis of the transcription level of the 148 genes associated with apoptosis (http://www.reactome.org) revealed main differences between ATRA and MC2392.

	Atra_24h	Atra_48h	MC2392_24h	MC2392_48h
PSMB6	-0.05	0.32	-6.83	-6.83
GSN	-0.05	1.71	0.01	-7.96
UNC5A	1.52	1.72	-6.38	0.07
SATB1	1.75	2.14	-6.44	-0.33
DAPK1	0.63	2.31	2.84	-4.32
HIST1H1E	-0.05	-7.89	2.30	1.23
PSMA5	1.77	-7.14	1.66	0.30
TNFRSF1A	0.57	0.50	0.18	-0.23
CASP6	6.66	8.13	0.00	0.00
PKP1	6.66	8.29	0.00	0.00
ACIN1	4.81	0.00	0.00	0.00
BID	0.00	6.19	0.00	0.00
CASP3	0.00	8.22	0.00	0.00
MAPK8	0.00	6.46	0.00	0.00
PPP3R1	0.00	5.32	0.00	0.00
UBA52	0.00	5.81	0.00	0.00
PPP3CC	-2.25	-1.51	-0.53	0.03
UBB	-0.04	0.39	-0.19	0.25
CTNNB1	-5.09	-5.09	2.45	-5.09
ADD1	0.84	1.45	1.29	-0.63
HIST1H1D	-3.24	-1.80	0.22	-1.76
PSMC5	-5.21	-5.21	0.96	-5.21
APPL1	0.21	0.98	0.11	0.45
RIPK1	-5.64	-5.64	-0.22	-5.64
PSMB7	5.04	6.32	6.58	0.00
DIABLO	1.85	1.91	1.47	0.72
APC	6.92	8.18	4.25	5.09
APAF1	-0.07	1.29	0.00	0.76
DFFA	0.94	1.39	1.50	0.06
BCAP31	0.50	1.34	-0.19	1.43
PRKCD	6.87	7.06	6.34	4.58
PSMD11	-5.93	-1.76	-5.93	-0.50
PAK2	1.38	2.43	1.85	1.49
LMNB1	-0.85	-1.59	-1.76	-0.43
PSMF1	0.00	7.31	7.21	0.00
STK24	-5.21	-5.21	-5.21	-5.21
FNTA	5.86	0.00	5.91	0.00
PSMB10	-0.66	-0.23	-0.33	-0.60
PSMD2	6.79	8.38	8.64	8.70
BBC3	5.43	0.00	0.00	6.52
FASLG	7.49	5.32	7.67	8.19
RPS27A	0.00	6.19	8.03	0.00
MST4	-1.11	-5.81	-5.81	-5.81
CASP9	-1.40	0.26	-0.79	-1.15
CYCS	-6.54	-1.18	-6.54	-6.54
TRAF2	0.00	6.83	7.99	6.13
PSMB2	-6.11	0.58	-6.11	-6.11
PSMD3	0.00	4.25	4.52	5.52
E2F1	0.00	4.64	6.86	7.91
CDH1	-0.39	-0.34	-1.91	-0.72
PSMD9	-0.22	-0.62	-3.14	-0.10
CLSPN	-1.82	1.99	2.14	-0.43
PSMC3	-0.12	0.05	-1.02	-0.36
DBNL	0.00	0.00	6.44	0.00
DFFB	0.00	0.00	0.00	0.00
DYNLL1	0.00	0.00	7.58	0.00
DYNLL2	0.00	0.00	5.00	5.04
H1F0	0.00	0.00	6.34	6.00
HMGB2	0.00	0.00	0.00	5.73
KPNB1	0.00	0.00	7.81	0.00
PSMA3	0.00	0.00	5.73	0.00
PSMA6	0.00	0.00	0.00	0.00
PSMB11	0.00	0.00	0.00	0.00
PSMC4	0.00	0.00	0.00	0.00
XIAP	0.00	0.00	0.00	6.87

Supplemental Table 3. Primers used

Name	Sequence
IRF1 up	5'-GCA GGC CCT GAC TCC AGC AC-3'
IRF1 down	5'-GC CAC TCC GAC TGC TCC AA-3'
TNF up	5'-CAG AGG GAA GAG GTT CCC CAG-3'
TNF down	5'-CCT TGG TCT GGT AGG AGA CG-3'
casp3 up	5'-TGG AAT TGA TGC GTG ATG TT-3'
casp3 down	5'-GGC AGG CCT GAA TAA TGA AA-3'
casp9 up	5'- CTA GTT TGC CCA CAC CCA GT-3'
casp9 down	5'-CCT TTC ACC GAA ACA GCA TT-3'
bcl2 up	5'-TTG TTC AAA CGG GAT TCA CA-3'
bcl2 down	5'-GAG CAA GTG CAG CCA CAA TA-3'
bax up	5'-TTT GCT TCA GGG TTT CAT CC-3'
bax down	5'-ATC CTC TGC AGC TCC ATG TT-3'
casp8 up	5'-AAG CAA ACC TCG GGG ATA CT-3'
casp8 down	5'-GGG GCT TGA TCT CAA AAT GA-3'
FADD up	5'-CAC AGA CCA CCT GCT TCT GA-3'
FADD down	5'-CTG GAC ACG GTT CCA ACT TT-3'
Fas up	5'-CAA GGG ATT GGA ATT GAG GA-3'
Fas down	5'-TGG AAG AAA AAT GGG CTT TG-3'
TRAIL up	5'-CAA CTC CGT CAG CTC GTT AGA AAG-3'
TRAIL down	5'-TTA GAC CAA CAA CTA TTT CTA GCA CT-3'
DR5 up	5'-GCCTCA TGG ACA ATG AGA TAA AGG TGGCT-3'
DR5 down	5'-CCA AAT CTC AAA GTA CGC ACA AAC GG-3'
p40 phox up p40 phox down	5'-CAG CCA CTT TGT TTT CGT CA-3' 5'- TCC TGT TTC ACA CCC ACG TA-3'
p47 phox up	5'-AGT CCT GAC GAG ACG GAA GA-3'
p47 phox down	5'-TAC ATG GAC GGG AAG TAG CC-3'
p67 phox up	5'-TGG AGT GTG TCT GGA AGC AG-3'
p67 phox down	5'-ATC TCT GGG GTT TTC GGT CT-3'
casp2 up	5'-AAG GAG CTG ATG GCC GCT GA-3'
casp2 down	5'-GCC CAC TTT GGC CTG GAT GA-3'
nox2 up nox2 down	5'-TCA CTT CCT CCA CCA AAA CC-3' 5'-GGG ATT GGG CAT TCC TTT AT-3'
p65 up p65 down	5' ATC TTG AGC TCG TCG GCA GTG TT 3' 5' ACA ACC CCT TCC AAG TTC CT -3'

Ikkalpha up	5’- ATT GCC CTG TTC CTC ATT TG -3’
Ikkalpha down	5’- GAA GGT GCA GTA ACC CTT CA -3’

Supplemental Table 4. Primers used in qPCR ChIP

Name	Sequence
NQO1 up	5’- CCC TTT TAG CCT TGG CAC GAA A -3’
NQO1 down	5’- TGC ACC CAG GGA AGT GTG TTG TAT -3’
NQO1upstream (CTR-) up	5’- TAA AAA GTA GAG TGG TTG GAG TGA TGA GC -3’
NQO1 upstream(CTR-) down	5’- TCT CAG TTT TTG CCC TTA TTT AAT CCC -3’
hMox1 up	5’- CCC TGC TGA GTA ATC CTT TCC CGA -3’
hMox1 down	5’- ATG TCC CGA CTC CAG ACT CCA -3’
RXRA up	5’- GGG TTT GCA GAA GTG GAG GCT -3’
RXRA down	5’- AAC AGC TGC AGC GTG CAG TGA CA -3’
GCLC up	5’- TGA GGC CAA GCT GAG CAT -3’
GCLC down	5’- ATG GAC TGA GAC TTT GCC CT -3’
GPD2 up	5’- CTG GTC AGG CCT CCG GGA -3’
GPD2 down	5’- CCC AGA ATC AGA GCC TCG G -3’
CSF1 up	5’- CAA AGG ATT TCC CTC CCT TC -3’
CSF1 down	5’- ACC CTG GCC AGG CGC C -3’
TNFSF10 up	5’- GGG CCA GGT TAT GAC ATC TG -3’
TNFSF10 down	5’- GAC AGG TAG GAA GTA GTT GA -3’
IL1B up	5’- GAA TAA CGG GAA CAG CGG TC -3’
IL1B down	5’- CTA GCG AGT TTC AAA CCC GC -3’
FANCF up	5’- AGG TGC TGA CGT AGG TAG TG -3’
FANCF down	5’- AAG ACG CTG GGA GAT TGA CA -3’
Ogg1 up	5’- CCACCCTGATTTCTCATTGG -3’
Ogg1 down	5’- CAACCACCGCTCATTTCAC -3’
KREMEN up	5’- CGAGAGTGACATCCAGTTGC -3’
KREMEN down	5’- TTCACAACCGTTCCAGATGA -3’
NFE2 up	5’- GGTTAGCAGCATACGTGGAG -3’
NFE2 down	5’- ACGATACGGAGAAAACCACG -3’
Myog up	5’- AAGTTTGACAAGTTCAAGCACCTG -3’
Myog down	5’- TGGCACCATGCTTCTTTAAGTC -3’
H2B up	5’- TTGCATAAGCGATTCTATATAAAAGCG -3’
H2B down	5’- ATAAAGCGCCAACGAAAAGG -3’