

Table S1: Oligonucleotide primer sequences for quantitative real-time PCR

Gene symbol	Gene name	Reference sequence accession #	Primer sequence (5'→3')	Size (bp)	Primer (F/R, μ M)
DNMT1	DNA methyltransferase 1	NM_182651	F: CAGACATCAAGATCAGGGTCAA R: CTCCTCATCGCTCCAGTAAAG	110	0.3/0.3
DNMT3A	DNA methyltransferase 3A	NM_001206502	F:CAAGTTCTCAGTGGTGTGTGT R: TACATGGGCTGCTTGTGTAG	93	0.3/0.3
HAT1	Histone acetyltransferase 1	NM_001034347	F: GGCAATAGAGGCTCAACAGAA R: CACTCATGTCAGTTACCAGTAGTC	92	0.6/0.6
KAT2A	K(lysine) acetyltransferase 2A	XM_001788901	F: GTGGCTACCTACAAGGTCAATTA R: CAAAGACGTGAGTGGTCTCAT	100	0.3/0.3
KAT5	K(lysine) acetyltransferase 5	NM_001192066	F: CACAGACCCTTTCCTCTTCTAC R: TAGTCTTCCGTGGACTCCCT	99	0.3/0.3
CREBBP	CREB binding protein	NM_001164022	F: GACAAGACAGTGGAGGTCAAG R: TCTCCTCAAAGGCAAAGAGTG	109	0.6/0.6
HDAC1	Histone deacetylase 1	NM_001037444	F: TGGACACGGAGATCCCTAAT R: GGTTAGTCATATTGGAAGGACTGATA	99	0.3/0.3
HDAC2	Histone deacetylase 2	NM_001075146	F: GTGCTTGCCATCCTTGAATTAC R: AAAGCCTCCTCAACACCATC	92	0.3/0.3
HDAC3	Histone deacetylase 3	NM_001206243	F: ATATCCCTCTACTGGTGCTAGG R: CTCTTCACTAATGGCCTCTTCTAC	107	0.3/0.3
SIRT1	Sirtuin 1	NM_001192980	F: GGGTTTCTGTTTCTTGTGGAATAC R: GATCTGGAAGGTCTGGAAAGTC	90	0.3/0.3
SIRT2	Sirtuin 2	NM_001113531	F: CTCTCGCCAAGGAACTCTATC R: CTCCAGGGTGTCTATGTTCTG	122	0.3/0.3
PRMT1	Protein arginine methyltransferase 1	NM_001015624.1	F:CGTCAAAGCCAACAAGTTAGAC R: CCACTCGCTGATGATGATGT	103	0.3/0.3
EHMT2	Euchromatic histone-lysine N-methyltransferase 2	NM_001206263	F: GATGTGAGAGAGGACGATTCTTATC R: GGCTGATGTTGCCGTAGTAA	94	0.3/0.3
PPIA	Peptidylprolyl isomerase A	NM_178320	F: ATGCTGGCCCAACACAA R: CCCTCTTTCACCTTGCCAAA	101	0.3/0.3
UXT	Ubiquitously expressed transcript	NM_001037471	F: TGGCAGAAGCTCTCAAGTTCATT R: CATGTGGATATGGGCCTTGAT	104	0.6/0.6
GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	NM_001034034.2	F: TGGAAAGGCCATCACCATCT R: CCCACTTGATGTTGGCAG	62	0.3/0.3
RPS9	Ribosomal protein S9	NM_001101152.2	F: TTTCCAGAGCGTTGGCTTAG R: GGACTTCTCGAAGGGTCTCC	114	0.3/0.3

Table S2: Adjusted mean values for each time (day-1 [control period], days+7 and +28 [treatment period] and day+56 [post treatment period]), p-values of time effect and multiple comparisons were conducted with Tukey adjustments, and fold change in gene expression as compared to day-1

Gene	Mean values					P-value							Fold change		
	Day-1	D+7	D+28	D+54	sem_max	time	-1 vs 7	-1 vs 28	-1 vs 56	7vs28	7 vs 56	28 vs 56	fold_7	fold_28	fold_56
Linseed oil treatment															
CREBBP	0.231	0.109	0.125	0.097	0.054	0.1372	0.1397	0.3729	0.2569	0.9907	0.9983	0.9651	0.47	0.54	0.42
DNMT1	0.113	0.089	0.082	0.077	0.018	0.2349	0.2871	0.2817	0.2685	0.9361	0.8806	0.9800	0.79	0.72	0.68
DNMT3A	0.127	0.080	0.059	0.085	0.022	0.0596	0.1185	0.0525	0.4580	0.7381	0.9967	0.6036	0.63	0.46	0.67
EHMT2	1.660	1.038	0.963	1.290	0.271	0.0276	0.0300	0.0737	0.6482	0.9851	0.8067	0.4605	0.62	0.58	0.78
HAT1	0.090	0.084	0.082	0.087	0.016	0.9186	0.9527	0.9432	0.9977	0.9964	0.9977	0.9671	0.93	0.91	0.96
HDAC1	2.688	1.689	1.715	1.619	0.616	0.2535	0.2121	0.4481	0.4692	0.9999	0.9995	0.9975	0.63	0.64	0.60
HDAC2	2.354	1.381	1.535	1.312	0.473	0.0591	0.0473	0.3208	0.2313	0.9745	0.9988	0.9346	0.59	0.65	0.56
HDAC3	1.894	1.284	1.435	1.456	0.381	0.0658	0.0425	0.4248	0.5989	0.9011	0.9377	0.9997	0.68	0.76	0.77
KAT2A	0.104	0.073	0.054	0.071	0.015	0.0244	0.0761	0.0189	0.2756	0.4302	0.9990	0.5384	0.70	0.52	0.68
KAT5	0.177	0.100	0.085	0.122	0.032	0.1828	0.2432	0.1877	0.6176	0.9845	0.9601	0.8067	0.56	0.48	0.69
PRMT1	1.210	0.989	0.944	0.852	0.189	0.3148	0.3947	0.4740	0.3309	0.9881	0.8740	0.9074	0.82	0.78	0.70
SIRT1	3.848	1.847	1.742	1.740	0.818	0.1464	0.1750	0.2220	0.2582	0.9995	0.9997	1.0000	0.48	0.45	0.45
SIRT2	1.325	0.975	0.728	1.046	0.182	0.0136	0.1029	0.0181	0.5697	0.3501	0.9826	0.1568	0.74	0.55	0.79
Safflower oil treatment															
CREBBP	0.109	0.122	0.116	0.097	0.018	0.4616	0.8062	0.9855	0.9301	0.9694	0.5248	0.5495	1.12	1.06	0.89
DNMT1	0.096	0.109	0.102	0.101	0.021	0.7906	0.7837	0.9870	0.9955	0.9599	0.9722	0.9998	1.14	1.06	1.05

Gene	Mean values					P-value								Fold change		
DNMT3A	0.094	0.093	0.101	0.134	0.032	0.2362	0.9999	0.9872	0.4372	0.9558	0.2721	0.2054	0.99	1.08	1.43	
EHMT2	1.144	1.131	0.997	1.351	0.199	0.0153	0.9993	0.7398	0.6251	0.5907	0.4383	0.0115	0.99	0.87	1.18	
HAT1	0.094	0.098	0.104	0.095	0.019	0.9164	0.9962	0.9617	1.0000	0.9772	0.9986	0.9291	1.04	1.10	1.00	
HDAC1	1.407	1.541	1.461	1.254	0.278	0.5745	0.8760	0.9959	0.9457	0.9692	0.6317	0.6575	1.10	1.04	0.89	
HDAC2	1.563	1.599	1.486	1.320	0.297	0.8876	0.9993	0.9963	0.9230	0.9789	0.8618	0.9393	1.02	0.95	0.84	
HDAC3	1.595	1.516	1.635	1.484	0.262	0.8439	0.9829	0.9989	0.9842	0.9454	0.9994	0.8958	0.95	1.03	0.93	
KAT2A	0.088	0.088	0.089	0.100	0.021	0.7878	1.0000	0.9997	0.8947	0.9995	0.8458	0.7455	1.00	1.02	1.14	
KAT5	0.116	0.094	0.090	0.110	0.018	0.2398	0.3662	0.4689	0.9919	0.9933	0.7974	0.4917	0.81	0.78	0.95	
PRMT1	0.904	1.068	1.011	1.009	0.184	0.5562	0.5034	0.9031	0.9387	0.9598	0.9809	1.0000	1.18	1.12	1.12	
SIRT1	2.051	1.900	1.724	1.690	0.228	0.6640	0.9217	0.6744	0.6495	0.8856	0.8872	0.9990	0.93	0.84	0.82	
SIRT2	1.182	1.096	1.006	1.267	0.241	0.1041	0.8589	0.6488	0.9648	0.8421	0.6710	0.1010	0.93	0.85	1.07	

*P<0.05 implies significance.

0.05<p<0.10 implies tendency towards significance.