

Supplementary material to:

Thaler R, Spitzer S, Karlic H, Klaushofer K, Varga F. DMSO is a strong inducer of DNA hydroxymethylation in pre-osteoblastic MC3T3-E1 cells. *Epigenetics* 2012; 7(6);

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10428707	8.46	7.72	-0.74	8.21	6.70	-1.51	NM_008216	Has2	hyaluronan synthase 2
10435712	5.60	5.07	-0.53	6.65	5.15	-1.51	BC131959	Cd80	CD80 antigen
10492355	8.85	8.78	-0.07	10.35	8.85	-1.50	NM_008604	Mme	membrane metallo endopeptidase
10582658	7.26	7.40	0.13	9.94	8.44	-1.50	NM_007428	Agt	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
10481627	4.68	4.33	-0.35	12.58	11.10	-1.48	NM_008491	Lcn2	lipocalin 2
10593460	4.35	3.85	-0.50	5.73	4.25	-1.47	BC046587	4833427C06R	RIKEN cDNA 4833427C06 gene
1045954	4.22	4.97	0.75	8.39	6.91	-1.47	NM_00103376	EG240327	predicted gene, EG240327
10598569	3.23	3.99	0.77	4.69	3.23	-1.46	NM_00103865	EG434729	predicted gene, EG434729
10502791	7.99	7.92	-0.06	10.19	8.73	-1.46	NM_133871	Ifi44	interferon-induced protein 44
10502855	7.77	7.40	-0.36	10.93	9.47	-1.46	NM_008966	Pgrfr	prostaglandin F receptor
10356262	6.54	6.58	0.04	8.71	7.27	-1.44	NM_00108174	EG665378	predicted gene, EG665378
10401238	8.68	8.18	-0.50	11.50	8.88	-1.44	NM_007564	Zfp361	zinc finger protein 36, C3H type-like 1
10393573	8.00	8.23	0.23	10.31	10.07	-1.44	NM_011150	Lgals3bp	lectin, galactoside-binding, soluble, 3 binding protein
1047125	8.50	8.30	-0.20	9.46	8.02	-1.44	NM_008344	Igf2bp5	insulin-like growth factor binding protein 6
10569020	4.77	4.52	-0.25	7.49	6.05	-1.43	NM_00103363	Irfm6	interferon induced transmembrane protein 6
10429564	9.47	7.28	-2.20	10.64	9.22	-1.42	NM_010738	Ly6a	lymphocyte antigen 6 complex, locus A
10362294	6.71	6.13	-0.58	8.63	7.22	-1.42	NM_176837	Ahgap18	Rho GTPase activating protein 18
10566358	6.87	7.39	0.51	10.04	8.63	-1.41	NM_009099	Trim30	tripartite motif-containing 30
10389877	3.47	3.83	0.36	5.33	3.93	-1.41	ENSMUST0001	Wfknk2	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2
10478048	4.93	5.18	0.25	9.43	8.02	-1.41	NM_008489	Lbp	lipopolysaccharide binding protein
10464836	5.27	5.02	-0.25	6.93	5.53	-1.40	NM_013456	Actn3	actinin alpha 3
10604661	6.73	4.64	-2.09	6.29	4.90	-1.39	XM_00147822	Gm1862	gene model 1862, (NCBI)
10395039	3.95	4.11	0.16	6.29	4.90	-1.39	NM_020557	Cmpk2	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial
10569466	10.81	9.72	-1.09	10.16	8.77	-1.39	NM_007631	Cnd1	cyclin D1
10444780	8.16	8.22	0.06	9.39	8.00	-1.38	NM_010380	H2-D1	histocompatibility 2, D region locus 1
10451287	5.69	5.36	-0.33	7.86	6.49	-1.37	NM_015783	Igfb1	IGF1 ubiquitin-like modifier
10533246	4.41	4.25	-0.17	5.71	4.34	-1.37	NM_011852	Oas1g	2'-5' oligoadenylate synthetase 1G
10411235	8.10	7.66	-0.45	9.19	7.83	-1.36	NM_027711	Igga2	IQ motif containing GTPase activating protein 2
10347948	5.50	5.76	0.26	7.46	6.10	-1.36	NM_013673	Sp100	nuclear antigen Sp100
10395559	4.74	4.80	0.06	6.67	5.31	-1.36	NM_00115963	Atp6v1c2	ATPase, H+ transporting, lysosomal V1 subunit C2
10347925	5.80	6.44	0.64	8.47	7.11	-1.36	NM_00108174	EG665378	predicted gene, EG665378
10588037	8.33	7.91	-0.42	10.87	9.52	-1.36	NM_011254	Rbp1	retinol binding protein 1, cellular
10399470	8.21	7.98	-0.23	9.69	8.34	-1.35	NM_144551	Trib2	tribbles homolog 2 (Drosophila)
10434666	1.91	2.67	0.76	3.19	1.84	-1.35	ENSMUST0001	---	---
10361234	3.12	3.34	0.21	3.97	2.63	-1.34	NM_008298	Hsd11b1	hydroxysteroid 11-beta dehydrogenase 1
10495206	4.18	5.23	1.05	5.81	4.46	-1.34	NM_146136	Slc16a4	solute carrier family 16 (monocarboxylic acid transporters), member 4
10360382	7.06	6.54	-0.52	7.33	6.00	-1.33	NM_008329	Ifi204	interferon activated gene 204
10460585	8.07	6.76	-1.32	7.45	6.12	-1.33	NM_010235	Fos1	fos-like antigen 1
10592007	7.67	6.98	-0.69	8.37	7.04	-1.32	NM_019391	Lcp1	lymphocyte specific 1
10601659	7.76	7.43	-0.34	6.81	5.36	-1.32	NM_026838	Srxp2	sushi-repeat-containing protein, X-linked 2
10356274	5.36	5.98	0.63	7.92	6.60	-1.32	NM_033616	Csprs	component of Sp100-rs
1048463	4.22	4.21	-0.01	6.78	5.46	-1.31	NM_009776	Serpin1	serine (or cysteine) peptidase inhibitor, clade G, member 1
10531980	5.62	5.25	-0.37	7.73	6.41	-1.31	NM_172777	BC057170	cDNA sequence BC057170
10435457	6.77	6.74	-0.03	8.47	7.16	-1.31	NM_030253	Parp9	poly (ADP-ribose) polymerase family, member 9
10519314	4.32	3.76	-0.56	4.70	3.40	-1.30	GENSCAN0001	---	---
10453250	2.93	2.93	0.00	4.23	2.94	-1.29	---	---	---
10510580	5.48	5.31	-0.16	7.55	6.27	-1.28	NM_011612	Tnfrsf9	tumor necrosis factor receptor superfamily, member 9
10533213	4.60	3.78	-0.83	5.13	3.86	-1.28	NM_145226	Oas3	2'-5' oligoadenylate synthetase 3
10450374	9.27	8.15	-1.12	8.83	7.55	-1.27	L78788	D17H6556E.5	DNA segment, Chr 17, human D6556E.5
10599286	4.05	3.75	-0.29	4.85	3.58	-1.27	NM_00108534	Rhox2e	reproductive homeobox 2E
10383200	7.32	7.61	0.29	9.07	7.81	-1.26	ENSMUST0001	---	---
10436598	7.00	6.98	-0.01	6.99	5.74	-1.25	ENSMUST0001	Z810055G20R	RIKEN cDNA Z810055G20 gene
10415081	5.15	4.39	-0.75	4.82	3.58	-1.24	FJ556972	EG665955	predicted gene, EG665955
10520121	5.15	4.39	-0.75	4.82	3.58	-1.24	FJ556972	EG665955	predicted gene, EG665955
10578405	5.15	4.39	-0.75	4.82	3.58	-1.24	FJ556972	EG665955	predicted gene, EG665955
10586076	5.15	4.39	-0.75	4.82	3.58	-1.24	FJ556972	EG665955	predicted gene, EG665955
10347915	6.12	6.69	0.57	8.81	7.57	-1.24	NM_00108174	EG665378	predicted gene, EG665378
10420488	3.86	4.13	0.27	5.86	4.63	-1.24	BC145673	D14Ert668e	DNA segment, Chr 14, ERATO Doi 668, expressed
10381371	6.11	6.05	-0.06	7.79	6.56	-1.23	NM_009675	Aoc2	amine oxidase, copper containing 3
10491952	7.83	8.21	0.38	8.92	7.69	-1.23	NM_174995	Nrg2	microsomal glutathione S-transferase 2
10492021	12.61	12.36	-0.25	12.98	11.76	-1.22	NM_015784	Postn	periostin, osteoblast specific factor
10363735	7.10	6.34	-0.76	7.50	6.28	-1.22	NM_010118	Egr2	early growth response 2
10383206	7.85	8.12	0.27	9.60	8.38	-1.21	ENSMUST0001	---	---
10389879	4.54	4.52	-0.02	6.64	5.43	-1.21	NM_181819	Wfknk2	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2
10439289	3.06	2.97	-0.09	3.55	2.35	-1.21	NM_00100133	BC117090	// cDNA sequence BC117090
10582879	5.65	6.20	0.55	8.19	6.99	-1.20	NM_033616	Csprs	component of Sp100-rs
10379228	4.84	4.46	-0.38	6.25	5.05	-1.20	NM_010927	Nos2	nitric oxide synthase 2, inducible
10359571	5.16	5.21	0.06	7.21	6.01	-1.20	NM_010231	Fmo1	flavin containing monooxygenase 1
10426425	4.63	4.07	-0.56	7.91	6.71	-1.20	BC151034	Pdzrn4	PDZ domain containing RING finger 4
10532709	8.08	8.13	0.06	6.99	5.79	-1.20	---	---	---

Gene	Co basal expression	1d 1%DMSO	5d 1%DMSO
<i>Aicda</i>	3.54	0.99	1.00
<i>Apobec1</i>	6.33	0.73	0.81
<i>Apobec2</i>	3.69	1.21	0.66
<i>Apobec3</i>	6.45	0.80	0.73
<i>Apobec4</i>	2.48	0.84	1.12
<i>Smug1</i>	5.27	1.18	1.79
<i>Tdg</i>	8.70	0.84	0.97
<i>Ercc1</i>	7.84	0.84	1.10
<i>Ercc2</i>	7.19	1.01	1.22
<i>Ercc3</i>	8.48	1.16	1.10
<i>Ercc4</i>	7.04	1.27	1.56
<i>Ercc5</i>	8.32	1.17	1.03
<i>Ercc6</i>	7.22	1.04	1.39
<i>Ercc8</i>	5.60	1.24	1.30

Suppl. table 1

Fold increase in mRNA expression of genes compared to untreated control culture, which are suggested to be involved in demethylation and repair mechanisms. Genes up regulated beyond 1.1-fold or 1.5 fold are marked in bright red or dark red, respectively. Genes down regulated beyond 1.1-fold (<0.91) or 1.5 fold (<0.67) are marked in bright green or dark green, respectively. Co basal expression: the log2 signal of untreated cells at day 1.

