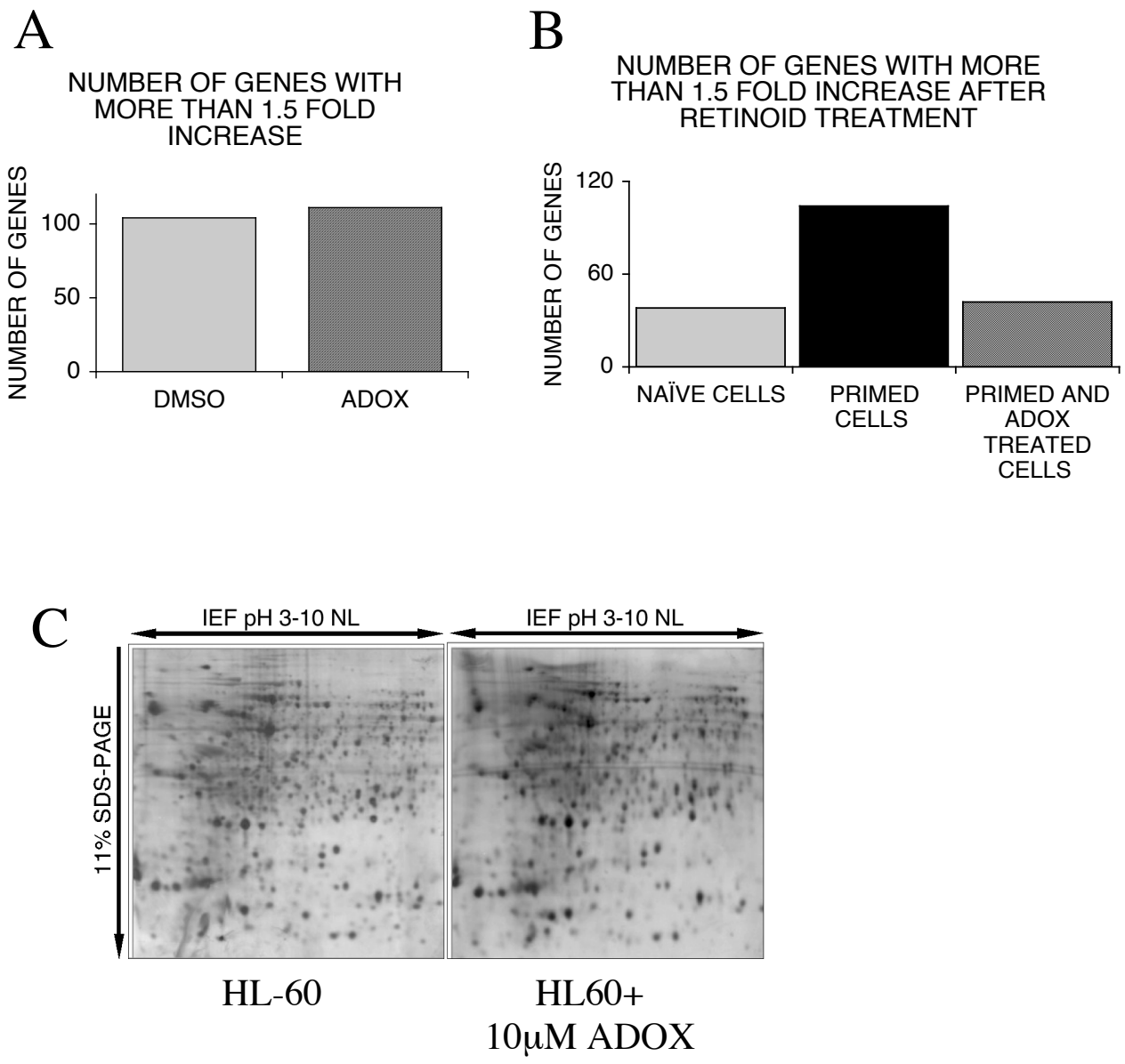
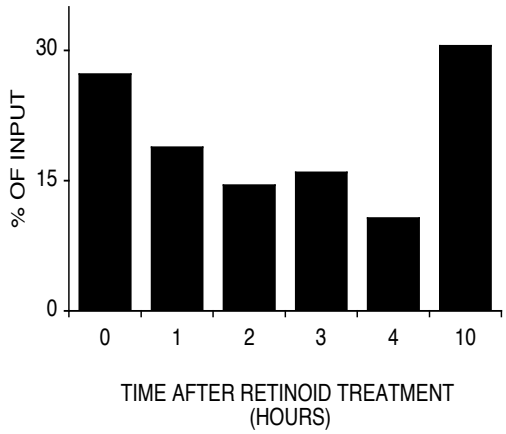



**Balint et al. Fig. S1**

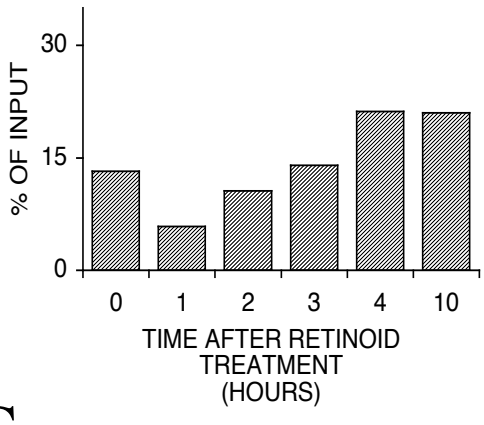
Figure S1. Analysis of methylation mute cells on genomic and proteomic levels. (A) Blocking methyltransferases with ADOX is not blocking transcription. Both ADOX and DMSO are inducing approximately the same number of genes (111 for ADOX and 104 for DMSO). Global gene expression analysis was performed on a cDNA microarray that contained 3200 features in duplicates as described in Materials and Methods. (B) Number of genes with a higher than 1.5 fold increase in expression after retinoid induction in three different conditions: naïve, primed with DMSO or primed with DMSO in the presence of ADOX. Retinoid treated samples were compared to their appropriate controls (naïve, primed with DMSO or primed with DMSO in the presence of ADOX) Global gene expression analysis was performed on a cDNA microarray that contained 3200 features in duplicates. (C) Comparison on proteomic level of HL-60 cells and HL-60 cells treated with 10 mM ADOX for 16 hours. 2D electrophoresis, silver staining and analysis were performed as described in Materials and Methods.

A



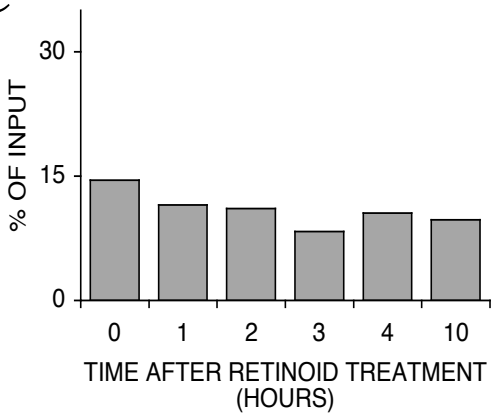

H3 K4-DI MET
IN NAÏVE CELLS

B




H3 K4-DI MET
IN PRIMED CELLS

C




H3 K4-DI MET IN PRIMED
METHYLATION MUTE
CELLS

**Balint et al. Fig. S2**

Figure S2. H3 Lysine4 methylation studied by chromatin immunoprecipitation on the core promoter. H3 Lysine4 methylatylation in naïve, primed and primed methylation mute cells after retinoid treatment. All chromatin immunoprecipitation values are the means of three independent QPCR measurements of a representative experiment. Chromatin immunoprecipitation results were confirmed in at least three independent chromatin preps.

Balint et al.3 Supplemental Data.

| **GENOMIC ASSAYS** | **FW 5'-3'** | **REV 5'-3'** | **PROBE 5'-3'** |
|---|---|---|---|
| TGM2-CORE | GAGACCCTCCAAGTGCGAC | CCAAAGCGGGCTATAAGTTAGC | FAM-CCGCCTCGGCAGTGCCA-TAMRA |
| TGM2-D | CAGACACACACCAGGACATAG | CTCTGGACACCTGCTCATCT | FAM-TGTGTGTGGCTCGCGGACAAGG-TAMRA |
| TGM2-C | ACACCAATGCCACTGTCAGAT | GTCTGTACCTGAGTCCATGCCTG | FAM-CTGTGGGTGCCCTCTCTGATTTTGGG-TAMRA |
| TGM2-B | GTCCTAGGCTGAGTCCCTGGA | TCCACTGAGCTTTCTTGAGGC | FAM-AGTCTTGCTCCTTTCTGGCACACAGTGGTAMRA |
| TGM2-A | GAGACTCCAGCCAGAGCCC | TCAGGGAAAACAACCCGTGT | FAM TTTGACCCAGGGAGAAATATCCACTGAAGC TAMRA |
| TGM2-HR1 | TGCTCCCTGCAGCTGGT | CCTCTCGGTCGGGTGATT | FAM-TCCTCACGCTGCTCTTTCCTCCAA-TAMRA |
| RARb RARE | TGTCAGACTAGTTGGGTCATTTGAAG | TTGCCTAATATATGCGAGTGAACTTT | FAM-TTAGCAGCCCGGGTAGGGTTCACC-TAMRA |
| | | | |
| **GENE EXPRESSION ASSAYS** | | | |
| hCyclophilin | ACGGCGAGCCCTTGG | TTTCTGCTGTCTTTGGGACCT | FAM-CGCGTCTCCTTTGAGCTGTTTGCA-TAMRA |
| hCyp27 | AGATGCACGTGAACCTGGC | TACTTTCCCTCTTGCCGCA | FAM-AGTGCCCCGCTCTTGGAGCAAGT-TAMRA |
| hRARa | CCAGCACCAGCTTCCAGTTA | GGGAGGGCTGGGCAC | FAM-CTCTTCAGAACTGCTGCTCTGGGTCTCAA-TAMRA |
| hRARb | GGAAACTTTCCCTTCACTCTGC | CCAGTCGGACTCGATGGTC | FAM-TGGGTAAATACACCACGAATTCCAGTGCTG-TAMRA |
| hRARg | TGCATCATCAAGATCGTGGAG | GTGATCTGGTCAGCAATGCTG | FAM-CCAAGCGGTTGCCTGGCTTTACA-TAMRA |
| hRXRa | GGCCTACTGCAAGCACAAGTA | CAGGCGGAGCAAGAGCTTA | FAM-CGAACCTTCCCGGCTGCTCTG-TAMRA |
| hRXRb | CCCATTCAGCAGGAGTAGG | CTCATGTCACGCATTTTGGA | FAM-TCTGTCAGCACCCGATCAAAGATGG-TAMRA |
| hRXRg | GGGAAGCTGTGCAAGAAGA | GGTAGCACATTCTGCCTCACT | FAM-AGACAGAGGAGCCGAGAGCGAG-TAMRA |
| hCD38 | CGTCAAGTACACTGAAATTCATCCT | AATAAATGCACCCTTGAAAGCA | FAM-CCCATACACTTTGGCAGTCTACATGTCTCATCT -TAMRA |
| hRAOH | TTCTCCAGAAAGTGCGAGAAGAG | CTTAATAACACACCCGATGTATTTAAG | FAM-CAAATTTCCATGTCTAACTTGTTGTCTTGATTGCT-TAMRA |
| hTGM2 | CTGGGCCACTTCATTTTGC | ACTCCTGCCGCTCCTCTTC | FAM-TCCAGGTACACAGCATCCGCTGGG-TAMRA |
| | | | |
| **PREDESIGNED GENE EXPRESSION ASSAYS** | Applera Assay I.D. | | |
| hPADI4 | Hs00202612_m1 | | |
| hPRMT1 | Hs00266002_m1 | | |
| | | | |

Supplemental Table 1.

Real time quantitative PCR oligo sets used in the presented experiments.