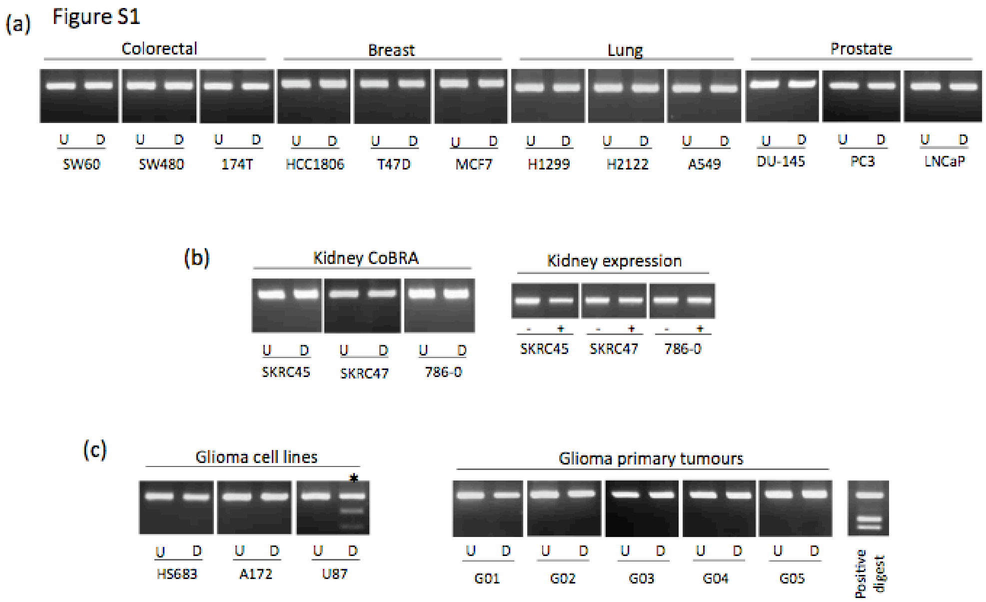
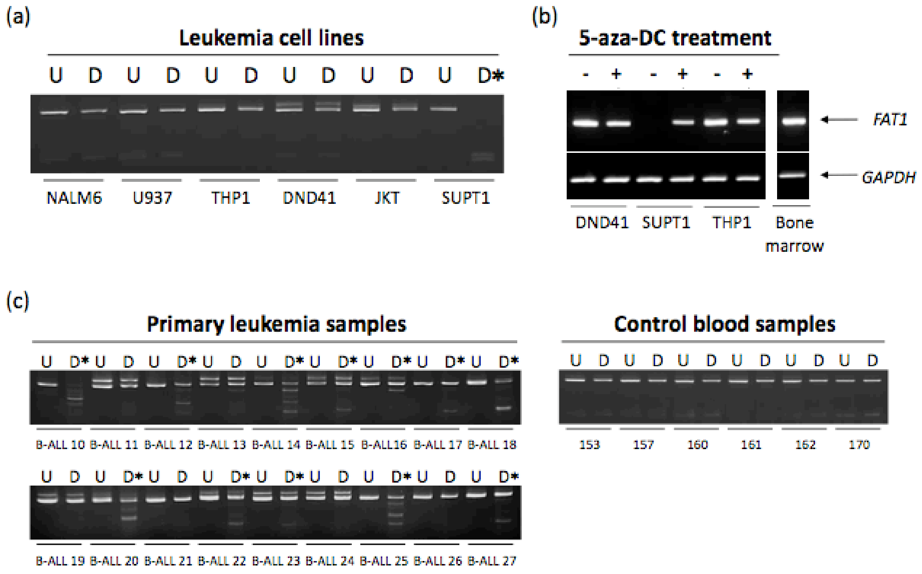
Figure S1



**Supplementary figure S1 *KIBRA* methylation analysis of epithelial cancers.**

CoBRA results are shown for colorectal, breast, lung and prostate cancer cell lines (a). Kidney cancer cell line CoBRA results and expression results pre (-) and post (+) treatment with 5-aza-2’-deoxycitidine are shown (b). CoBRA results are shown for glioma cancer cell lines and five primary tumors (c). U = undigested product, D = digested product and *=methylated samples.

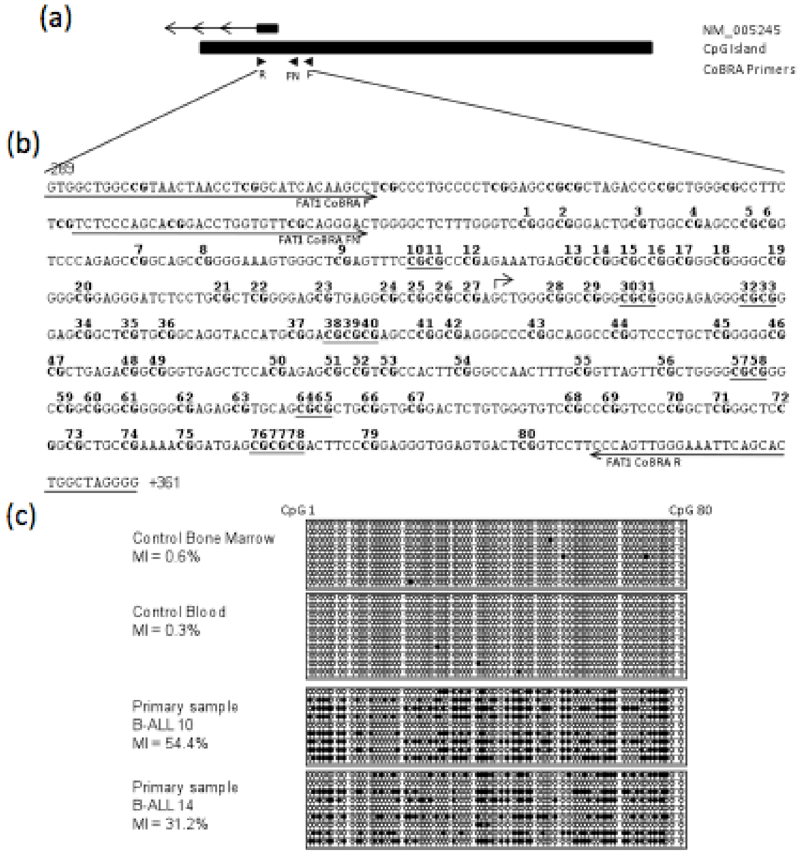
Figure S2



**Supplementary figure S2. *FAT1* methylation and expression analysis.**

CoBRA results are shown for leukemia cell lines (a) along with expression results for three corresponding lines pre (-) and post (+) treatment with 5-aza-2’-deoxycitidine (b). CoBRA results are also shown for primary leukemia samples and control blood samples (c). U = undigested product, D = digested product and * = methylated samples. Methylation and expression primer sequences provided on request.

Figure S3



**Supplementary figure S3. Sequencing of the *FAT1* CpG island in primary samples.**

A schematic showing the location of the *FAT1* CpG island in relation to the transcription start site is shown indicating the positions of the semi-nested PCR primers, forward (F), reverse (R) and forward nested (FN) (a). The region being sequenced is shown underneath with numbered CpG dinucleotides within the amplified region and the location of the first and last nucleotides relative to the *FAT1* transcription start site. *Bst*UI sites are underlined. (b). Sequencing of cloned CoBRA PCR products showing extent of methylation across the *FAT1* CpG island are shown. Each line is representative of an allele, empty circles represent unmethylated CpGs. Filled circles represent methylated CpGs (c).