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# Base-pair resolution DNA methylome of the EBV-positive Endemic Burkitt lymphoma cell line DAUDI determined by SOLiD bisulfite-sequencing

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The Burkitt translocation t(8;14), first identified in the 1970s in biopsies and cell lines from Burkitt lymphoma (BL),<sup>1,2</sup> and its variants juxtapose the MYC oncogene to one of the immunoglobulin (IG

We could confirm that in DAUDI cells 91.21% of these genes have a DNA methylation level  $\geq 60\%$  in their promoter region and lack transcription. As compared with all other RefSeq genes, the mean CpG methylation level within promoter regions of the 969 genes was significantly higher (84% vs 41%; Supplementary Tables S2).

Gene expression analyses confirmed that DAUDI cells show the typical signature of molecular BL.<sup>17</sup> Correlating methylation and expression patterns in our data revealed that significant presence of transcripts is associated with absence of DNA methylation particular at and closely around the transcription start site (TSS). In contrast, DNA methylation exactly at the TSS correlates with lack of transcription (Figure 2). Although the group of non-expressed genes showed an overall high mean DNA methylation level across the whole gene with highest methylation levels in exons, genomic regions comprising expressed genes were characterized by

methylation. As the DAUDI cell line has been used over decades in many laboratories in the world, the obtained methylome data might serve as a 'reference epigenome' for future studies.

Data availability: methylome data are available at <sftp://134.245.63.215/export/home/daudi> (login: daudi; password: daudismethylome2012).

#### **CONFLICT OF INTEREST**

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