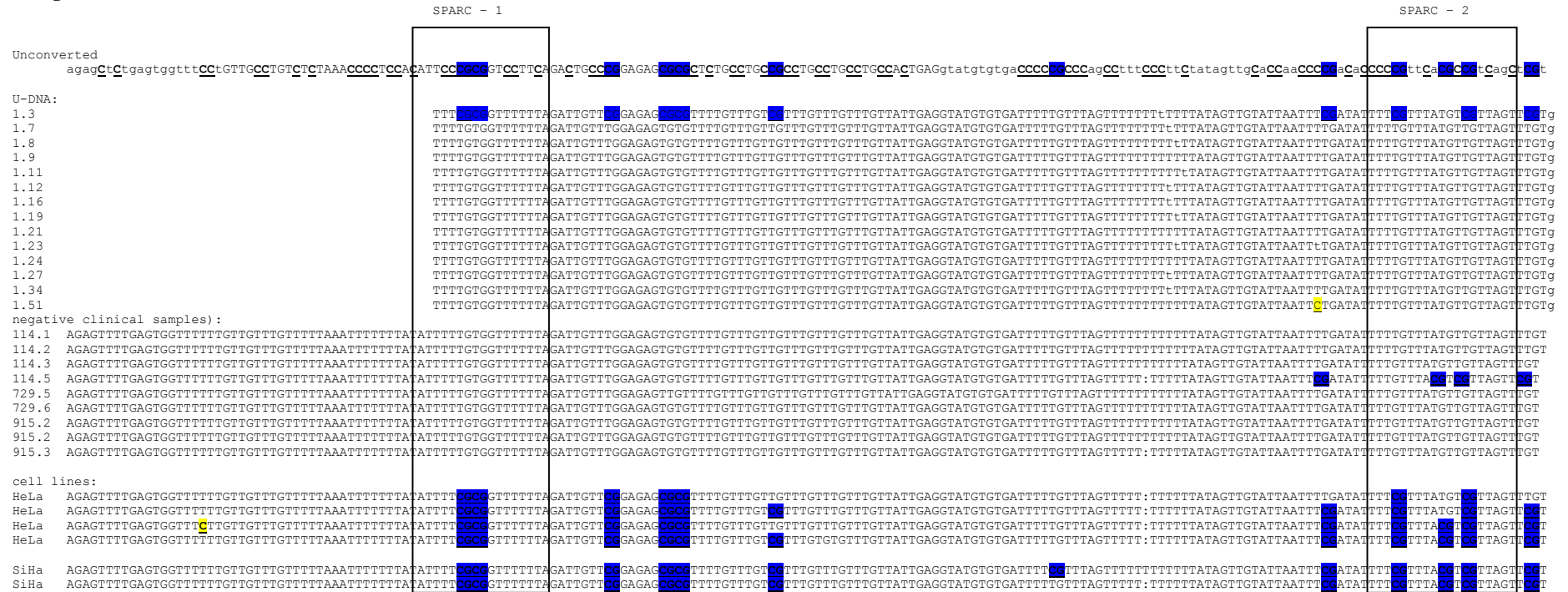


Figure S1: SPARC ALIGNMENT

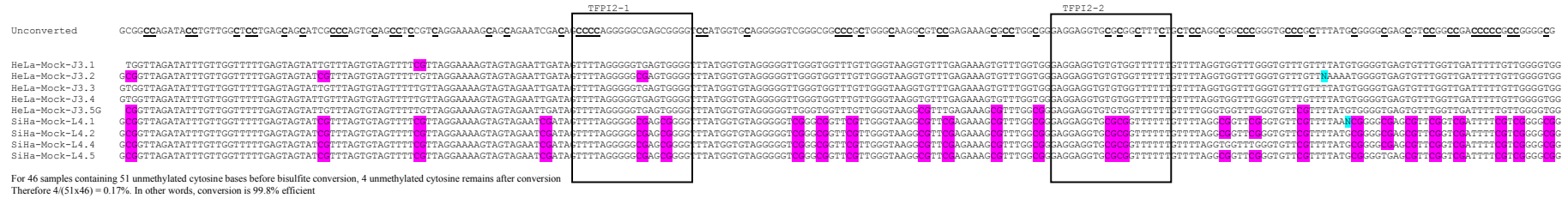


For 49 samples containing 65 unmethylated cytosine bases before bisulfite conversion, only 2 unmethylated cytosine remains after conversion
Therefore 2/(65x49) = 0.06%. In other words, conversion is 99.9% efficient

Blue text: methylated CG dinucleotides
Yellow text: unconverted C bases
Box denotes the approximate position of probes used in the study

Figure S2.

a) TFPI2 Alignment



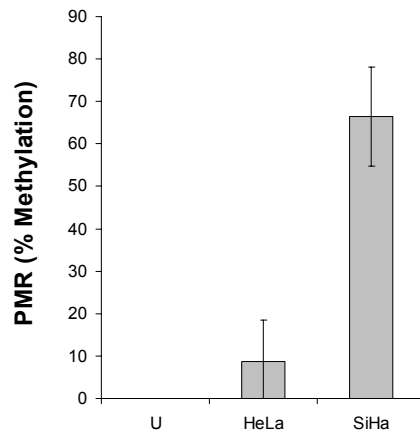
Blue text: methylated CG dinucleotides

Yellow text: unconverted C bases

Box denotes approximate position of probes used in the study.

b) MethyLight data

MethyLight PMR Values for TFPI2 DNA



Semi-quantitative MSP-based method suggests negligible methylation in U DNA for TFPI2; low but variable methylation for HeLa DNA and high level of methylation for SiHa