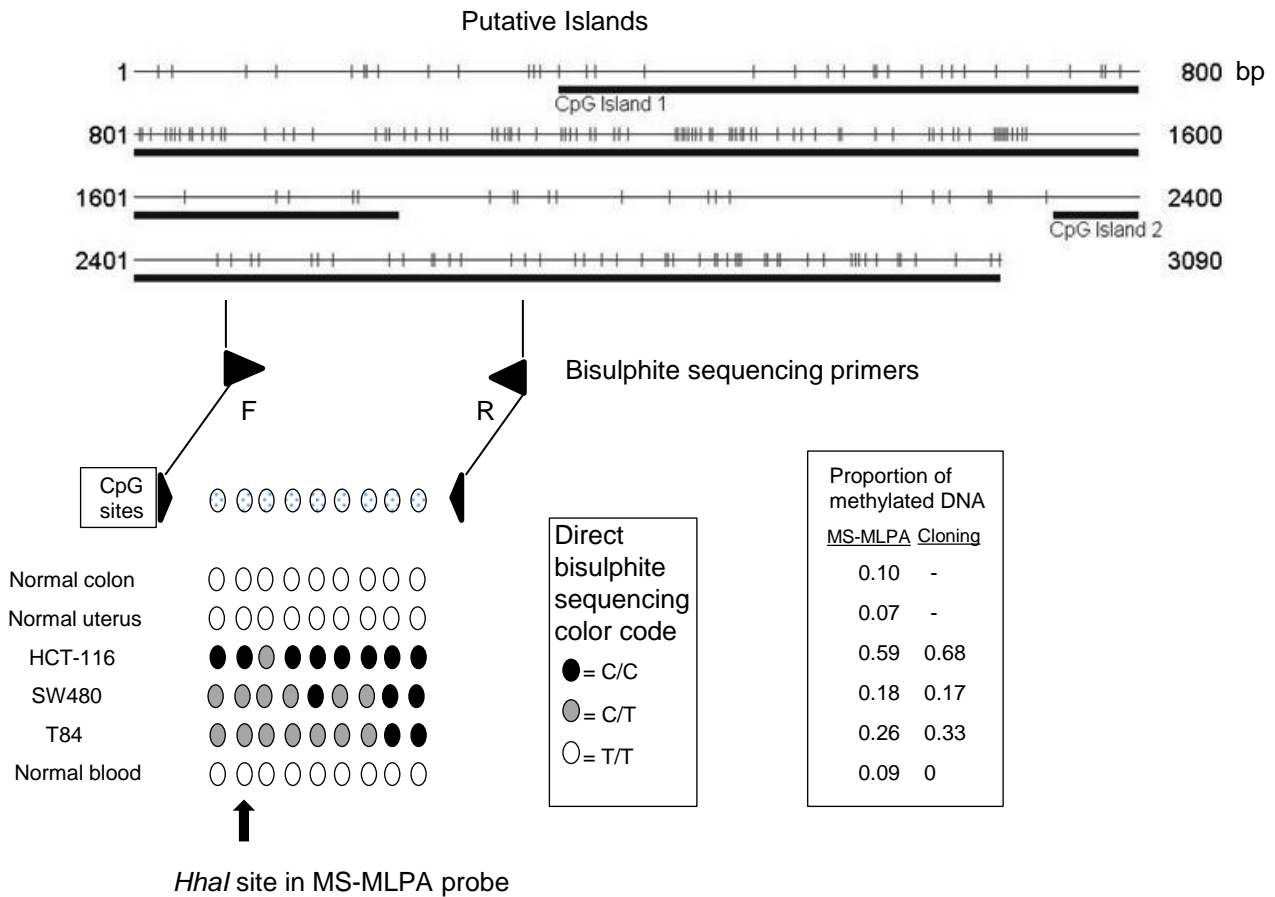


Supplementary Figure 4. miR-129-2



Supplementary Figure 4. The design and validation of MS-MLPA assays showing miR-129-2 as an example. Bisulphite-converted DNA from cancer cell lines and normal tissues was first sequenced to select a representative region for MS-MLPA probe design (see Methods). Results from direct bisulphite sequencing (without cloning) are depicted on the left, with methylation status of each CpG site coded as T/T (unmethylated), C/T (partially methylated), or C/C (methylated). Quantification of DNA methylation (proportion of methylated DNA) by two parallel methods, MS-MLPA and sequencing of cloned bisulphite-converted PCR-amplified fragments, is shown on the right. Dm values by MS-MLPA were concordant with results from the cloning analysis.