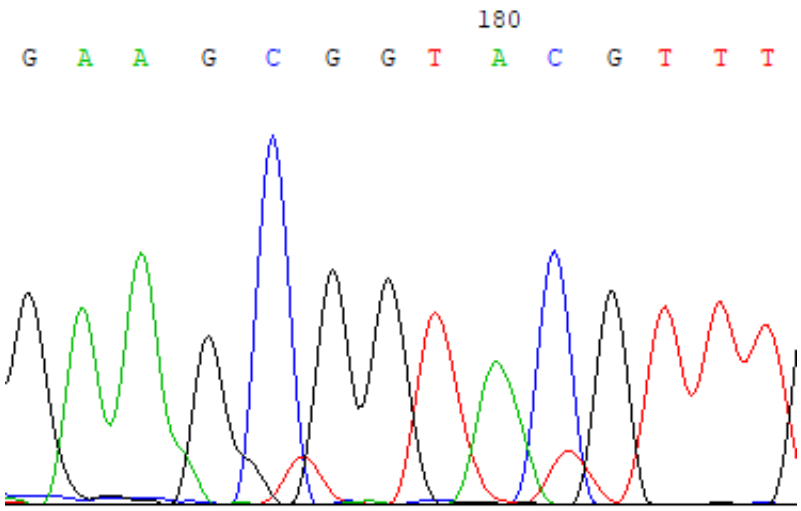
$$\text{median } (x_i) \tag{S1}$$

$$\text{scale} = \frac{100\%}{median\ (xi)} \tag{S2}$$

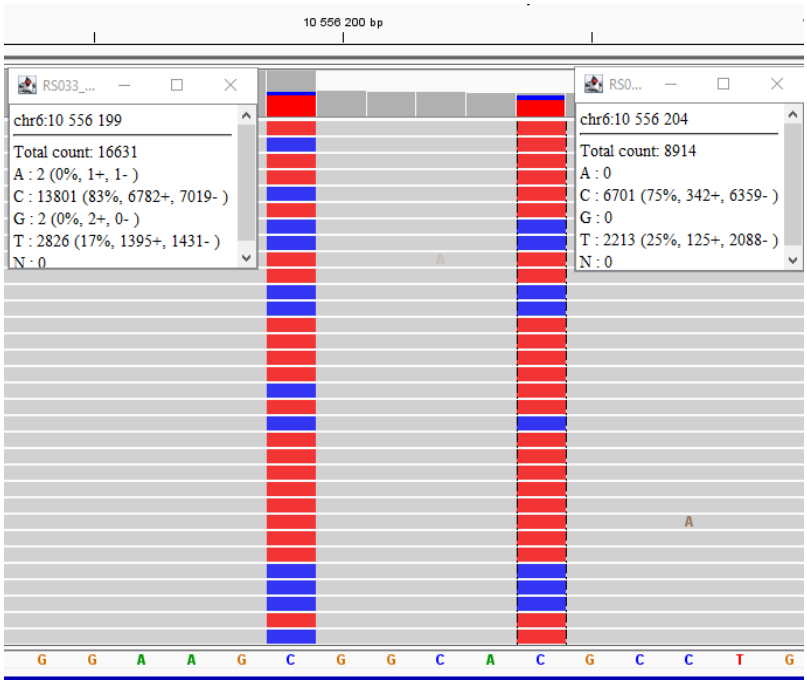
$$k = \text{scale}*b \tag{S3}$$

$$b = 100\% - k, \tag{S4}$$

where x_i is a vector of the signal level at the nucleotide *i* in amplicons with no methyl groups, scale is the correction vector for each nucleotide, k is the corrected signal level, b is the signal level of each nucleotide in the studied samples.

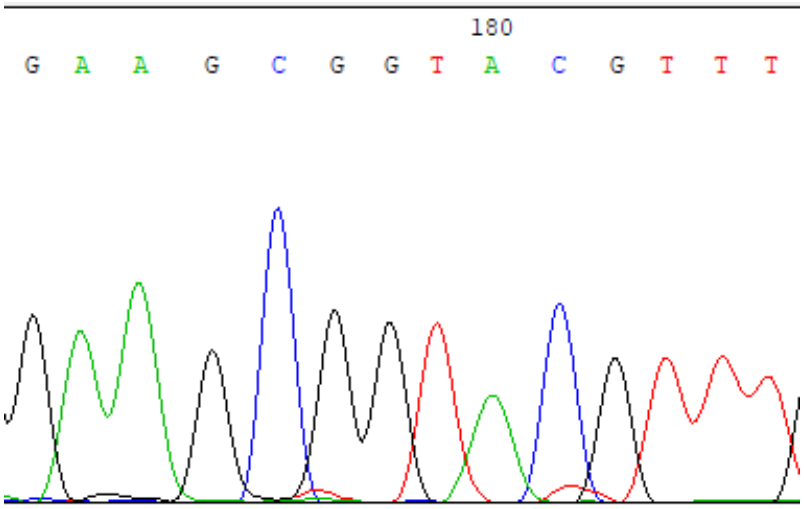


(**a**)

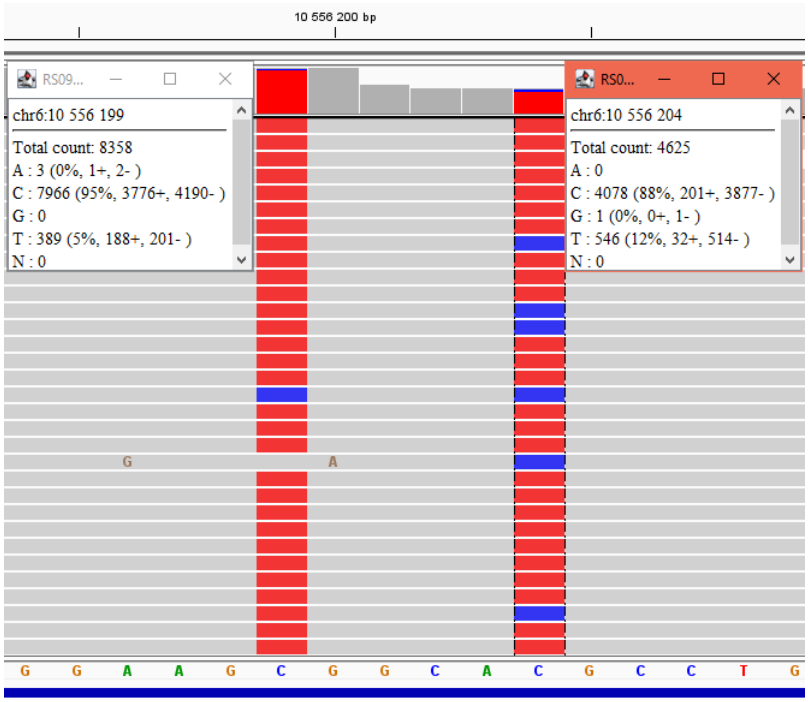


(**b**)

Supplementary Figure S1. Sample sequence of the selected locus for a patient with RTS1. (**a**) Sanger bisulfite sequencing (**b**) Targeted high-throughput bisulfite sequencing.



(**a**)



(**b**)

Supplementary Figure S2. Sample sequence of the selected locus for a healthy control. (**a**) Sanger bisulfite sequencing (**b**) Targeted high-throughput bisulfite sequencing.