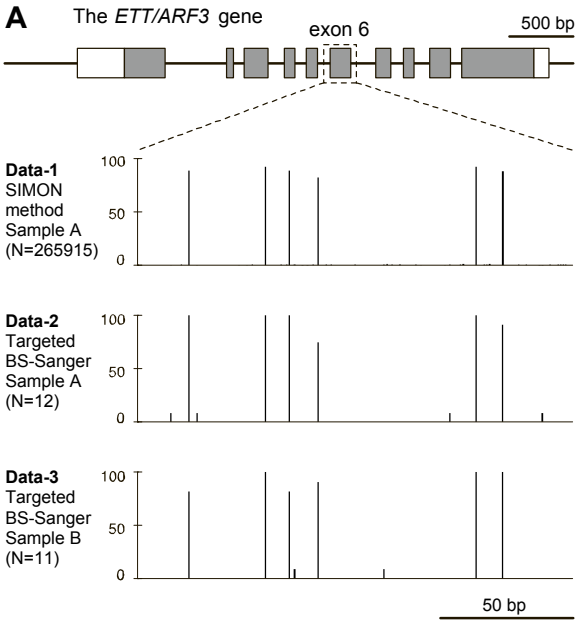
# Supplementary Figure S1




**B**

| Pearson's correlation coefficients | **Data-1** SIMON method Sample A | **Data-2** Targeted BS-Sanger Sample A | **Data-3** Targeted BS-Sanger Sample B |
|---|---|---|---|
| **Data-1** SIMON method Sample A | | 0.995 | 0.994 |
| **Data-2** Targeted BS-Sanger Sample A | 0.995 | | 0.985 |
| **Data-3** Targeted BS-Sanger Sample B | 0.994 | 0.985 | |

Supplementary Figure S1: Comparison of the SIMON method and targeted BS-Sanger. A) Barplots of methylation rates for Col-0 from 3 sets of data, (data-1) SIMON method for sample A, (data-2) targeted BS-Sanger for sample A, and (data-3) targeted BS-Sanger for sample B. B) Matrix of Pearson's correlation coefficients calculated using methylation rates for all pairs of these 3 data sets. Data-1 is our previous data as reported (Vial-Pradel et al. 2018). For targeted BS-Sanger, approximately 300 ng of the genomic DNA was used for bisulfite conversion with the EZ DNA Methylation-Gold kit (Zymo Research, Irvine, CA, USA). Immediately after the conversion, we amplified the fragments of interest with the Epitaq bisulfite kit (TAKARA BIO INC, Kusatsu, Japan) (Gruntman et al., 2008). The PCR reactions were carried out with primers designed to amplify a 419 bp DNA sequence that encompasses exon 6 of the *ETT* gene by specifically targeting the coding strand (Iwasaki et al., 2013). The conversion was tested for completeness by using distinct primer sets for either unconverted or converted DNA strands, amplifying a region previously shown to be always non-methylated (*APETALA1*, AT1G69120). The PCR-amplified DNA was then ligated into the pGEM-T easy vector (Promega, Tokyo, Japan) and transformed into competent *E.coli* cells according to Promega's protocol. Transformed *E.coli* were grown on Luria Broth (LB) supplemented with ampicillin (50 g/l), IPTG (56 mg/l), and X-Gal (112 mg/l) for blue/white selection of the vector containing the insert. About 12 clones were isolated from white colonies, and the presence of the correct size insert was confirmed by PCR. Overnight liquid culture in 2 ml of LB medium supplemented with ampicillin was carried out before using an automated plasmid extraction device to purify the plasmid DNA (KURABO PI-50α Automatic DNA isolation system, KURABO INDUSTRIES LTD. Osaka, Japan). Finally, we checked the contamination status by PCR. We then used the Sanger method for sequencing.