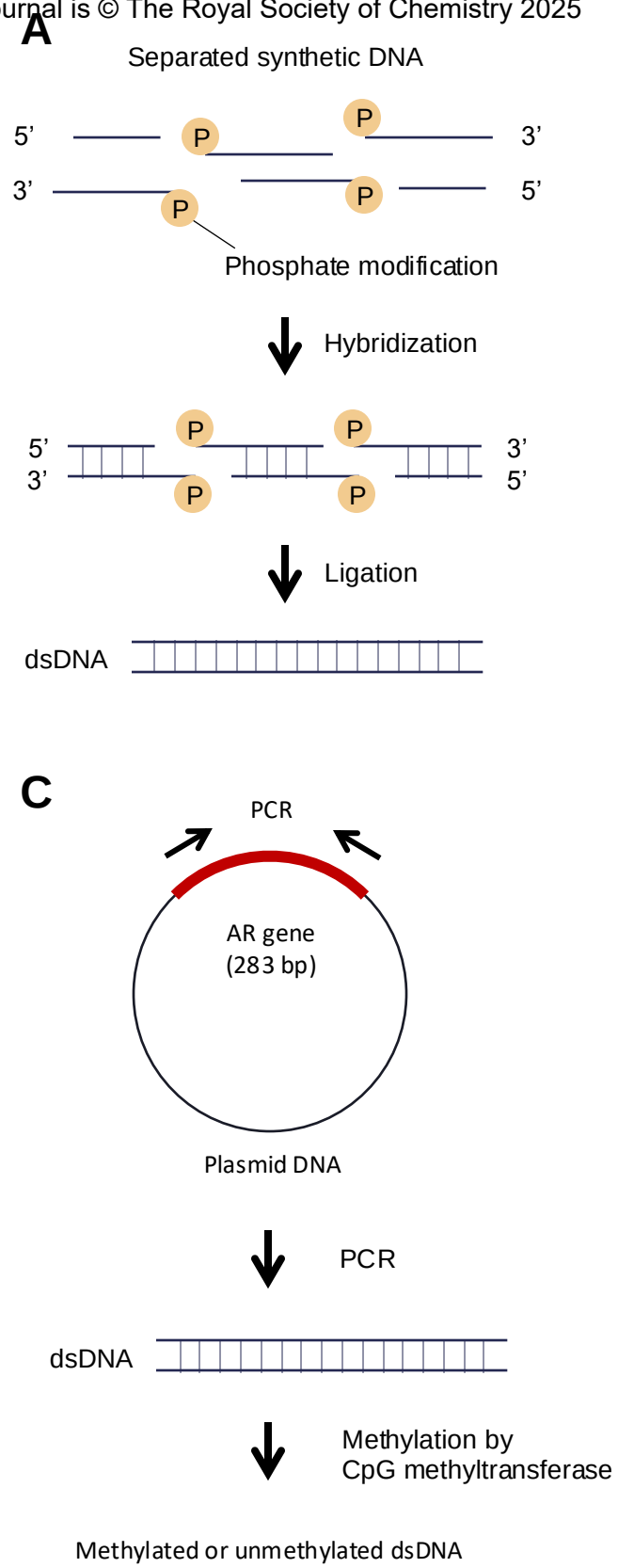

Figure S1. Preparation of the full-length dsDNA. (A) Schematic illustrations of the preparation of full-length dsDNA. (B) Methylated and unmethylated dsDNA were electrophoresed in a 1% agarose gel. Lane M, 100 bp ladder used as size marker; lanes 1-2, methylated full-length dsDNA and unmethylated full-length dsDNA, respectively. (C) Schematic illustration of obtaining methylated or unmethylated full-length dsDNA from PCR products.

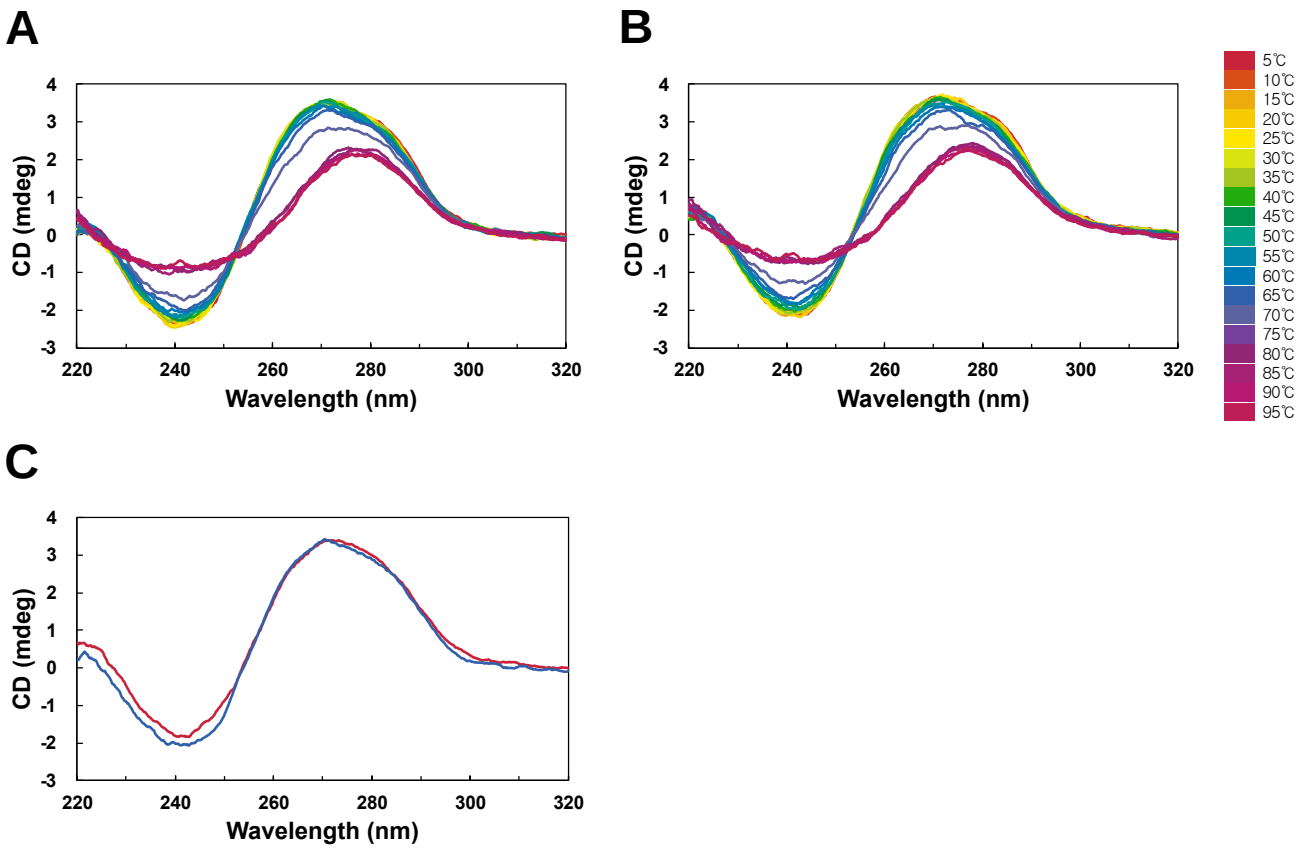

Figure S2. CD spectra of 260 bp of *DRD2* dsDNA. Temperature-dependent CD spectra of unmethylated (A) or methylated (B) dsDNA. (C) Comparison of CD spectra of unmethylated (blue) and methylated (red) *DRD2* dsDNA at 60 °C.

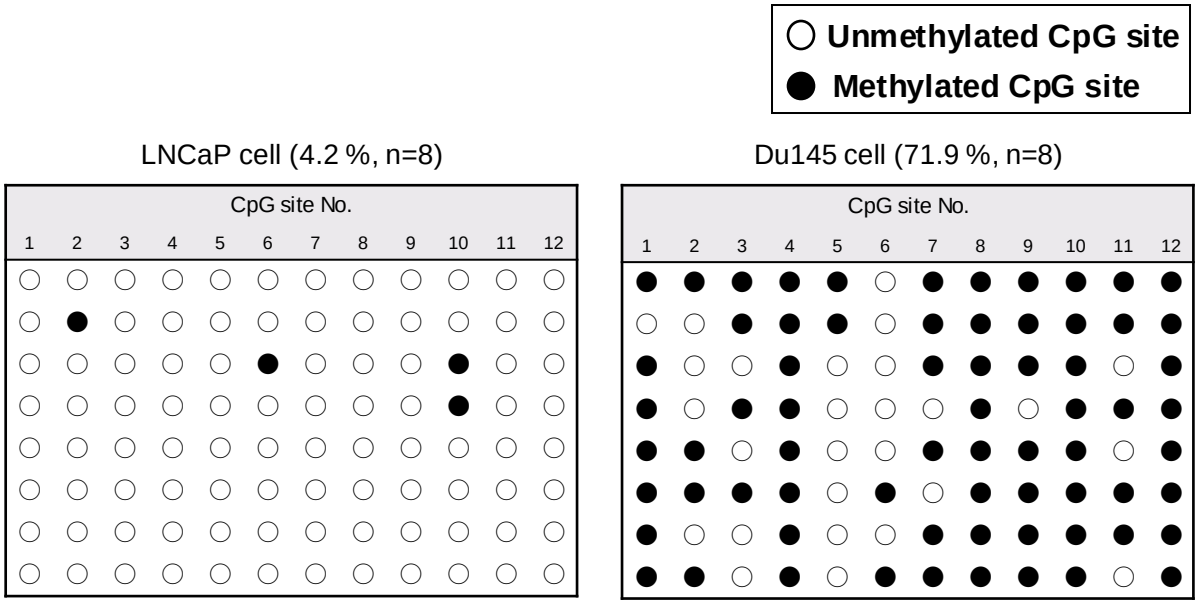

Figure S3. The methylation status by bisulfite sequencing provided by Funakoshi Co., Ltd. The percentages in the parentheses indicate the methylation levels. The circles correspond to each of the CpG sites. The closed circle indicates methylated CpG sites, and the open circle indicates unmethylated CpG sites. A set of horizontally aligned circles represents an individual clone. The vertical number represents individual CpG sites. The “n” refers to the number of sequenced genomes.

Table S1 List of separated synthetic DNA sequences.

	Sequences (5′ to 3′)	DNA size (base)
DRD2_ target 1	CCCCACCAAAGGAGCTGTACCTCCTCGGCGATCCCCGG CCTGGAACGGGTAGGAGGGGTTGGGGGATTCCG	71
DRD2_ target 2	Phosphate_CCATCCCTTGTTTTGAGG**C**GGGAA**C**GCAACC CT**C**GAC**C**GCCCACTG**C**GCTCCCACCCACACCCAGAGTA	69
DRD2_ target 3	Phosphate_ATAAGCTGTGATTGCAGGCTGGGTCCTCACC GTCTGCTCGCCAGTCTTCTCCTTTGAGGACTCAGAAGCC AAGGGTTGCGGGAGGCACCACCCATCCAGCAAGTCAG GCAAGGAGAGGAG	120
DRD2_ complement 1	CTCCTCTCCTTGCCTGACTTGCTGGATGGGTGGTGCCTC CCGCAACCCTTGGCTTCTGAGTCCTCAAAGGAGAAGAC TGGCGAGCAGACGGTGAGGA	97
DRD2_ complement 2	Phosphate_CCCAGCCTGCAATCACAGCTTATTACTCTGG GTGTGGGTGGGAG**C**GCAGTGGG**C**GGT**C**GAGGGTTG**C**G TTCC**C**GC	75
DRD2_ complement 3	Phosphate_CTCAAAACAAGGGATGGCGGAATCCCCCAA CCCCTCCTACCCGTTCCAGGCCGGGGATCGCCGAGGAG GTACAGCTCCTTTGGTGGGG	88

Bold and underline means unmethylated or methylated cytosine.

Table S2 The pairs of hybridized DNA strands for ligation in *DRD2*.

Fragments	Target	Complement
Fragment 1	DRD2_target 1	DRD2_complement 3
Fragment 2	DRD2_target 2 (Unmethylated or methylated)	DRD2_complement 2 (Unmethylated or methylated)
Fragment 3	DRD2_target 3	DRD2_complement 1

Table S3 The sequence of the *AR* region inserted in plasmid DNA and primers for PCR.

	Sequences (5′ to 3′)	DNA size (base)
AR region inserted in plasmid DNA	GGGCTAGAGCTAGCCTCTCCTGCCCTCGCCCACG CTGCGCCAGCACTTGTTTCTCCAAAGCCACTAGG CAGGCGTTAGCGCGCGGTGAGGGGAGGGGAGAA AAGGAAAGGGGAGGGGAGGGAAAAGGAGGTGG GAAGGCAAGGAGGCCGGCCCGGTGGGGGCGGG ACCCGACTCGCAAACTGTTGCATTTGCTCTCCACC TCCCAGCGCCCCCTCCGAGATCCCGGGGAGCCAG CTTGCTGGGAGAGCGGGACGGTCCGGAGCAAGC CCAGAGGCAGAGGAGG	283
PCR forward primer	GCTAGAGCTAGCCTCTCCTG	20
PCR reverse primer	CAGCTTGCTGGGAGAGC	17

Table S4 List of LAMP primer sequences.

Target	Sequences (5' to 3')	DNA size (base)
LAMP primers for *AR*		
AR_FIP	GGCCTCCTTGCCTTCCCACGGGAGGGGAGAAAAGGAAAG	39
AR_BIP	GGACCCGACTCGCAAACTGTTTGGCTCCCCGGGATCT	37
AR_F3	GTTAGCGCGCGGTGAG	16
AR_B3	TCCCGCTCTCCCAGCA	16
LAMP primers for *DRD2*		
DRD2_FIP	GCGTTCCCGCCTCAAAACAAGGCCTGGAACGGGTAGGA	38
DRD2_BIP	TAAGCTGTGATTGCAGGCTGGGCAACCCTTGGCTTCTGAGT	41
DRD2_F3	TGTACCTCCTCGGCGATC	18
DRD2_B3	CTTGCTGGATGGGTGGTG	18

LAMP, loop-mediated isothermal amplification

Table S5 List of PCR primer sequences for bisulfite sequencing.

Target	Forward	Reverse	Product size (bp)	Nucleotide coordinates (Human Jan. 2022)
Primers for PCR of AR	CCAAATTTGGTGAGTGCTGG	CCTTCGGCTCCTGTACAGC	438	chrX:65,973,549-65,973,986
Primers for PCR of bisulfite treated genomic DNA of AR	ATTAAATTTGGTGAGTGTTGGTTTT	CAATCCTACCAAACACTTTCCTTAC	600	chrX:65,973,548-65,974,147