

Supplementary information for

Transcriptome-wide RNA 5-methylcytosine profiles of human iPSCs and iPSC-derived cardiomyocytes

Authors

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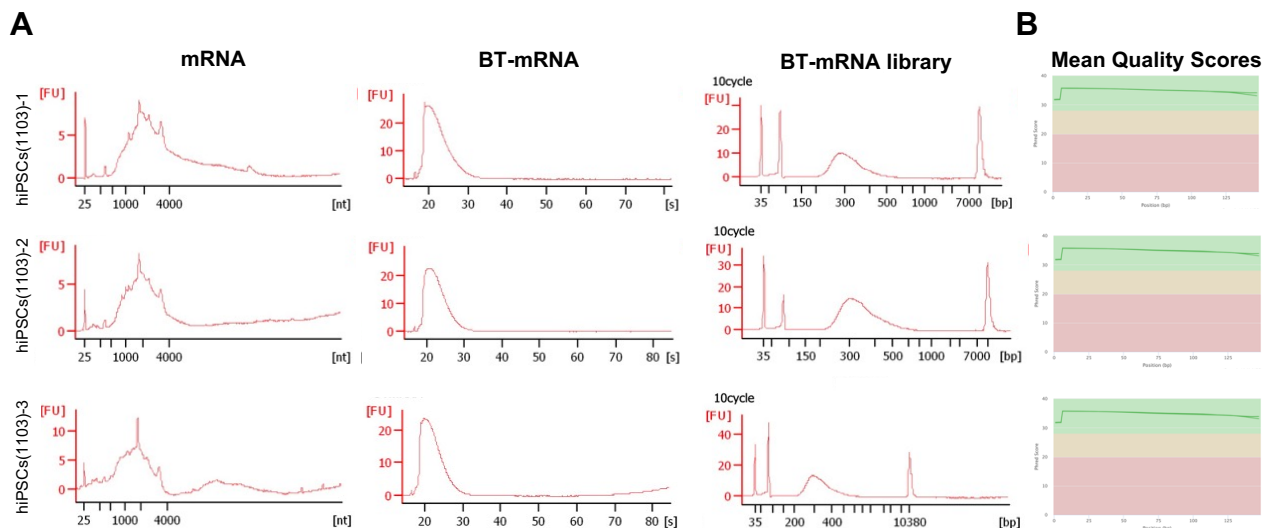


Figure S1. The fragment distribution and reads quality assessment of bisulfite-treated mRNA library samples. A. The representative capillary electrophoresis images of hiPSCs(1103)-1, hiPSCs(1103)-2, and hiPSCs(1103)-3 samples quality after mRNA enrichment, bisulfite treatment, and library preparation. **B.** The representative mean quality scores across each base of the reads from trimmed read1 and read2 fastq files of hiPSCs(1103)-1, hiPSCs(1103)-2, and hiPSCs(1103)-3 samples.

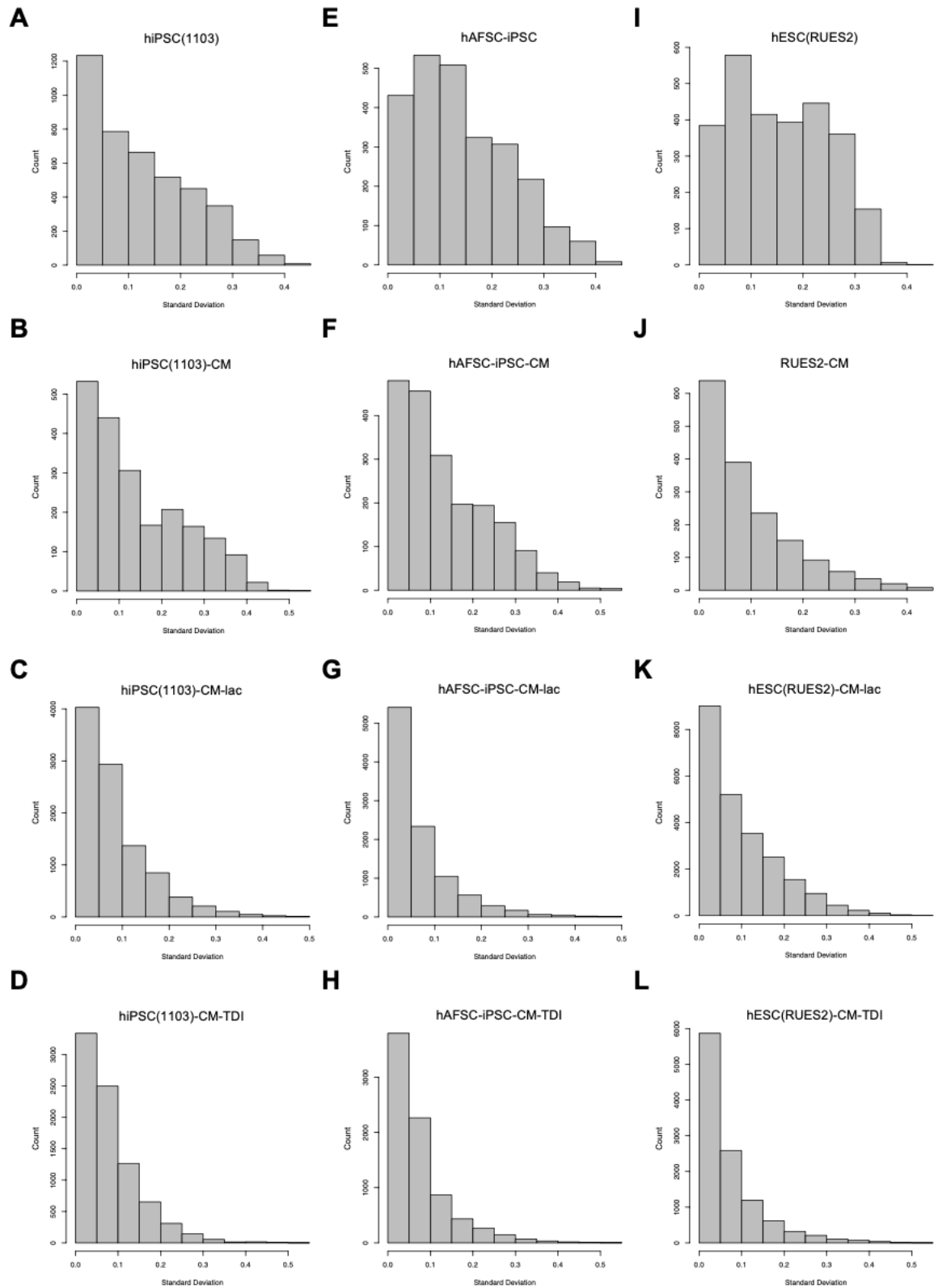


Figure S2. Distribution counts of the m^6C sites and the standard deviation in each group of cells.

Sample	mRNA-enrichment		BT-mRNA preparation		Library preparation		
	Total Input RNA (µg)	Output conc. (ng/µl)	Quantity Input mRNA (ng)	Output conc. (ng/µl)	Quantity Input RNA (ng)	#PCR Cycle	Output conc. (ng/µl)
hiPSC(1103)-1	25.8	19.2	365.1	4.0	12.0	10	0.8
hiPSC(1103)-2	17.8	7.6	144.6	0.2	1.2	14	1.0
hiPSC(1103)-3	19.2	7.4	141.4	1.0	5.4	14	0.5
hiPSC(1103)-CM-1	24.4	28.4	539.9	4.8	14.4	12	1.6
hiPSC(1103)-CM-2	25.8	24.0	456.0	2.7	10.9	10	0.7
hiPSC(1103)-CM-3	22.5	29.3	556.7	4.2	12.6	10	0.7
hiPSC(1103)-CM-lac-1	30.0	21.6	411.5	4.2	21.0	12	4.1
hiPSC(1103)-CM-lac-2	30.0	19.9	378.4	4.8	24.0	12	1.7
hiPSC(1103)-CM-lac-3	30.0	21.4	406.9	5.0	25.0	12	2.5
hiPSC(1103)-CM-TDI-1	30.0	24.7	450.0	5.4	21.7	10	0.6
hiPSC(1103)-CM-TDI-2	30.0	27.0	450.0	5.6	22.4	10	0.4
hiPSC(1103)-CM-TDI-3	30.0	25.9	450.0	5.4	27.4	12	1.8
hAFSC-iPSC-1	40.0	32.2	644.0	5.4	21.8	10	1.0
hAFSC-iPSC-2	28.9	18.8	357.9	5.0	15.0	10	2.9
hAFSC-iPSC-3	28.8	23.2	442.3	4.6	18.4	12	1.4
hAFSC-iPSC-4	27.5	16.5	313.5	4.2	16.8	10	0.9
hAFSC-iPSC-CM-1	12.3	12.2	244.0	2.9	14.6	12	0.2
hAFSC-iPSC-CM-2	17.0	16.1	307.5	2.6	13.1	10	1.5
hAFSC-iPSC-CM-3	28.1	8.7	165.9	1.1	5.6	14	2.4
hAFSC-iPSC-CM-lac-1	30.0	21.6	419.0	3.4	17.3	12	3.8
hAFSC-iPSC-CM-lac-2	24.0	13.2	256.0	2.9	14.7	12	3.1
hAFSC-iPSC-CM-lac-3	30.0	18.0	350.3	3.1	15.9	12	2.9
hAFSC-iPSC-CM-TDI-1	26.9	19.8	384.1	4.0	20.0	12	2.4
hAFSC-iPSC-CM-TDI-2	24.0	16.6	322.4	2.8	14.3	12	1.8
hAFSC-iPSC-CM-TDI-3	20.0	14.4	279.3	2.8	14.2	12	0.9
hESC(RUES2)-1	29.2	26.2	524.0	4.4	17.6	10	0.8
hESC(RUES2)-2	27.7	18.0	342.0	4.2	12.6	10	2.2
hESC(RUES2)-3	40.5	38.7	735.3	7.8	15.6	10	0.8
hESC(RUES2)-4	20.8	15.8	300.9	4.0	16.0	12	1.2
hESC-CM(RUES2-CM)-1	16.3	13.7	274.0	2.6	13.1	10	0.7
hESC-CM(RUES2-CM)-2	46.8	25.0	476.5	4.6	18.4	10	1.1
hESC-CM(RUES2-CM)-3	32.8	24.6	467.4	4.0	16.0	10	1.8
hESC(RUES2)-CM-lac-1	24.0	13.8	267.7	3.5	17.7	12	3.1
hESC(RUES2)-CM-lac-2	24.0	17.0	330.5	4.8	24.0	12	2.8
hESC(RUES2)-CM-lac-3	22.5	13.2	256.0	4.0	20.0	12	2.9
hESC(RUES2)-CM-TDI-1	30.0	23.5	456.2	5.2	26.4	12	4.4
hESC(RUES2)-CM-TDI-2	30.0	24.2	470.2	5.9	29.9	12	3.5
hESC(RUES2)-CM-TDI-3	30.0	20.7	401.5	5.3	26.5	12	1.2

Table S1. The quantities of materials in mRNA enrichment and the preparation of bisulfite RNA-seq libraries.

Group Name	Cell line common m ⁵ C site counts	m ⁵ C site counts with SD≤0.025
hiPSC(1103)	4215	648
hiPSC(1103)-CM	2068	218
hiPSC(1103)-CM-lac	9971	1918
hiPSC(1103)-CM-TDI	8300	1701
hAFSC-iPSC	2487	149
hAFSC-iPSC-CM	1952	181
hAFSC-iPSC-CM-lac	9952	2970
hAFSC-iPSC-CM-TDI	7900	1927
hESC(RUES2)	2740	128
hESC(RUES2)-CM	1628	279
hESC(RUES2)-CM-lac	23562	5302
hESC(RUES2)-CM-TDI	11011	3474

Table S2. Common m⁵C sites in each cell group.