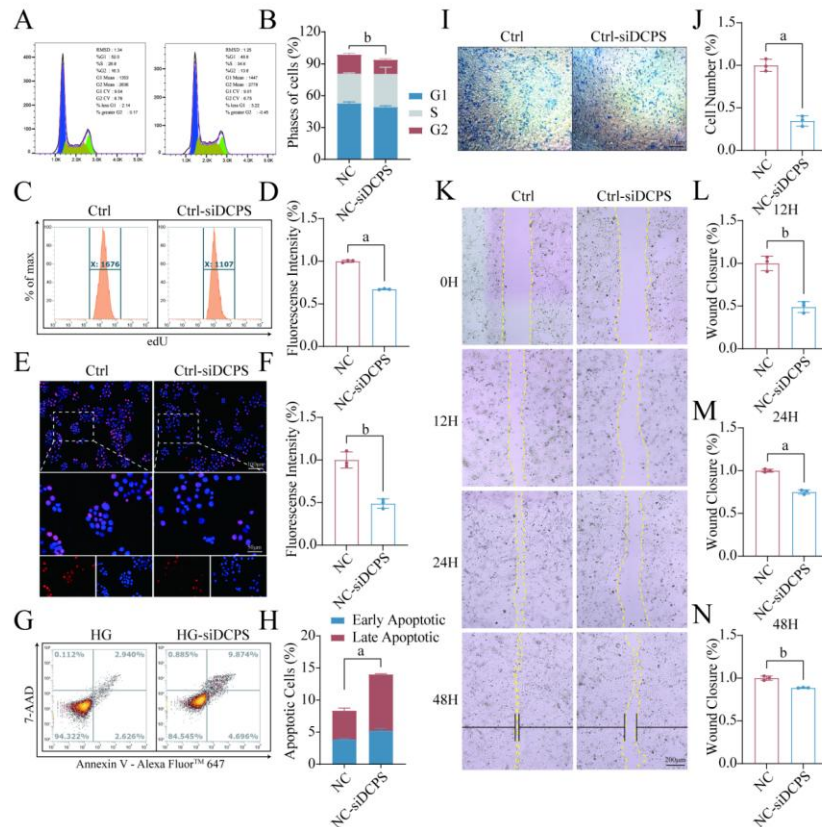




Supplementary Figure 1 A and B: DCPS knockdown induced significant G2 phase arrest in cell cycle of NHEK, $n = 3$. Assess the impact of DCPS knockdown on cellular proliferation; C and D: DCPS knockdown attenuated cellular proliferation of NHEK in flow cytometry assays, $n = 3$; E, F: EdU staining and statistical analyses in NHEK, $n = 4$ (scale bar: 100 μm); G, H: DCPS knockdown enhanced apoptosis of NHEK in flow cytometry, $n = 3$. DCPS knockdown inhibits NHEK migration; I, J: Transwell assays were conducted for evaluation of NHEK migration, $n = 3$ (scale bar: 100 μm); K-N: Cell scratch assays were observed in living cells at 0, 12, 24 and 48 h, $n = 3$ (scale bar: 200 μm). The results were expressed as mean $\pm$ SD. ^a $P < 0.001$, ^b $P < 0.01$, ^c $P < 0.05$.

Supplementary Table 1 DGEs-plum3 genes

ID	gene	ID	gene	ID	gene	ID	gene	ID	gene
1	ACP6	41	COQ8A	81	ZZEF1	12	ITIH4	16	SPIDR
						1		1	
2	PHYH	42	ZFYVE26	82	PATZ1	12	CREB3L	16	TSHZ1
	D1					2	4	2	
3	CACH	43	GPRC5C	83	HKR1	12	BRD3	16	ZNF70
	D1					3		3	3
4	TBC1D	44	TRMT10B	84	ABHD11	12	TP73-	16	MAN1
	4					4	AS1	4	C1
5	CHD6	45	APBA1	85	GLI4	12	ZNF462	16	PTPRU
						5		5	
6	TFAP2	46	PTPRS	86	ABCC3	12	MTMR4	16	FLT3L
	B					6		6	G
7	PIK3IP	47	R3HDM2	87	POLE	12	TMEM6	16	NLRC5
	1					7	3A	7	
8	PHKA	48	TSC1	88	CTSF	12	PCIF1	16	MECP2
	2					8		8	
9	DCAK	49	VPS26B	89	LOC101927	12	AUTS2	16	APOL4
	D				699	9		9	
10	CGNL	50	FAXDC2	90	CRACR2A	13	MCF2L	17	ORAI3
	1					0		0	
11	DGLU	51	ZNF629	91	MVB12B	13	LFNG	17	HOXC
	CY					1		1	6
12	SLC25	52	PARD3B	92	BCL6	13	MLLT6	17	RNF21
	A29					2		2	6
13	NIPAL	53	CIRBP	93	ALPK1	13	BCL9	17	TAPBP
	3					3		3	L

14	CEP68	54	IL16	94	MLPH	13	NBPF1	17	SUOX
						4		4	
15	SMAR	55	YLPM1	95	GATAD2B	13	ZNF445	17	PHF21
	CA2					5		5	A
16	BOC	56	ARHGEF9	96	RBM12B	13	SPRY1	17	TNFAI
						6		6	P2
17	FAHD	57	ACSF2	97	ZNF318	13	IFT172	17	SLC12
	2B					7		7	A7
18	GCHF	58	TBC1D8	98	SIN3A	13	KANSL3	17	TP53BP
	R					8		8	1
19	TAF1	59	THRA	99	PHF8	13	ZNF747	17	PALM
						9		9	
20	NFIX	60	HOTAIR	10	TUB	14	PHF12	18	TCEA2
				0		0		0	
21	AKAP	61	ATP6V0E	10	GTF2IRD2	14	EP400	18	TCTN2
	1		2	1		1		1	
22	PADI2	62	TACR1	10	DCAF8	14	PRMT2	18	CFAP4
				2		2		2	10
23	HCP5	63	USP40	10	HOXC9	14	NFIC	18	DELE1
				3		3		3	
24	TCEA3	64	PAN2	10	HOMER1	14	FBXO31		
				4		4			
25	SCUBE	65	KLHL36	10	TMEM198B	14	DCPS		
	2			5		5			
26	KDM3	66	EVA1C	10	HAUS7	14	TSPYL2		
	B			6		6			
27	IFT122	67	MATN2	10	NBPF12	14	SELENB		
				7		7	P1		

28	KAT14	68	NTRK2	10	MIR29B2C	14	EPB41L1
				8	HG	8	
29	KCND	69	SCFD2	10	TREX1	14	WFS1
	3			9		9	
30	PMS2P	70	ZNF3	11	LRIG1	15	POGZ
	1			0		0	
31	S100A	71	ARHGEF1	11	TRAPPC6A	15	TSPAN3
	1		9	1		1	3
32	GGA2	72	GPRASP1	11	WISP2	15	CREBBP
				2		2	
33	MAP2	73	NDUFA6-	11	H6PD	15	ASMTL
	K5		DT	3		3	
34	ACSS1	74	GLDN	11	BBS1	15	STIMAT
				4		4	E
35	CECR7	75	CBX7	11	MTR	15	IL18BP
				5		5	
36	EZH1	76	RTN4RL1	11	ZNF362	15	ACACB
				6		6	
37	TRRA	77	AGO1	11	AGFG2	15	LINC023
	P			7		7	81
38	NOP53	78	COG1	11	GLI3	15	SMAD3
				8		8	
39	TRIM3	79	CES1	11	ILF3-DT	15	CLCN6
	5			9		9	
40	XPC	80	VPS39	12	KCNN4	16	TNRC6C
				0		0	

Supplementary Table 2

GO	Description	Log10(P)
GO:0006338	chromatin remodeling	-8.7
R-HSA-4839726	Chromatin organization	-8
R-HSA-3247509	Chromatin modifying enzymes	-8

(A) The functional description of corresponding components of the three best-scoring terms by *P*-value.

MCODE	GO	Description	Log10(P)
MCODE_1	R-HSA-9730414	MITF-M-regulated melanocyte development	-10.6
MCODE_1	R-HSA-8878171	Transcriptional regulation by RUNX1	-9.2
MCODE_1	R-HSA-9856651	MITF-M-dependent gene expression	-8.6
MCODE_2	R-HSA-3214847	HATs acetylate histones	-7.8
MCODE_2	GO:0045879	negative regulation of smoothened signaling pathway	-7.3
MCODE_2	R-HSA-3247509	Chromatin modifying enzymes	-6.7

(B) The functional description of each MCODE component.

Supplementary Table 3 m7G-related genes

Gene	Physiological role	gene name
AGO2	m7G	argonaute RISC catalytic component 2
CYFIP1	m7G	cytoplasmic FMR1 interacting protein 1
DCP2	m7G	decapping mRNA 2
DCPS	m7G	decapping enzyme, scavenger
EIF3D	m7G	eukaryotic translation initiation factor 3 subunit D
EIF4A1	m7G	eukaryotic translation initiation factor 4A1
EIF4E	m7G	eukaryotic translation initiation factor 4E
EIF4E1 B	m7G	eukaryotic translation initiation factor 4E family member 1B
EIF4E2	m7G	eukaryotic translation initiation factor 4E family member 2
EIF4E3	m7G	eukaryotic translation initiation factor 4E family member 3
EIF4G3	m7G	eukaryotic translation initiation factor 4 gamma 3
GEMIN 5	m7G	gem nuclear organelle associated protein 5
IFIT5	m7G	interferon induced protein with tetratricopeptide repeats 5
LARP1	m7G	La ribonucleoprotein 1, translational regulator
LSM1	m7G	LSM1 homolog, mRNA degradation associated
METTL 1	m7G	methyltransferase 1, tRNA methylguanosine
NCBP1	m7G	nuclear cap binding protein subunit 1
NCBP2	m7G	nuclear cap binding protein subunit 2

NCBP2	m7G	nuclear cap binding protein subunit 2 like
L		
NCBP3	m7G	nuclear cap binding subunit 3
NUDT1	m7G	nudix hydrolase 10
0		
NUDT1	m7G	nudix hydrolase 11
1		
NUDT1	m7G	nudix hydrolase 16
6		
NUDT3	m7G	nudix hydrolase 3
NUDT4	m7G	nudix hydrolase 4
NUDT4	m7G	nudix hydrolase 4B
B		
SNUP	m7G	snurportin 1
N		
WDR4	m7G	WD repeat domain 4
QKI	m7G	Quaking proteins
RAMA	m7G	RNA guanine-7 methyltransferase activating
C		subunit
RNMT	m7G	RNA guanine-7 methyltransferase
TRMT1	m7G	tRNA methyltransferase activator subunit 11-2
12		
RAB27	m7G	RAB27A, member RAS oncogene family
A		
