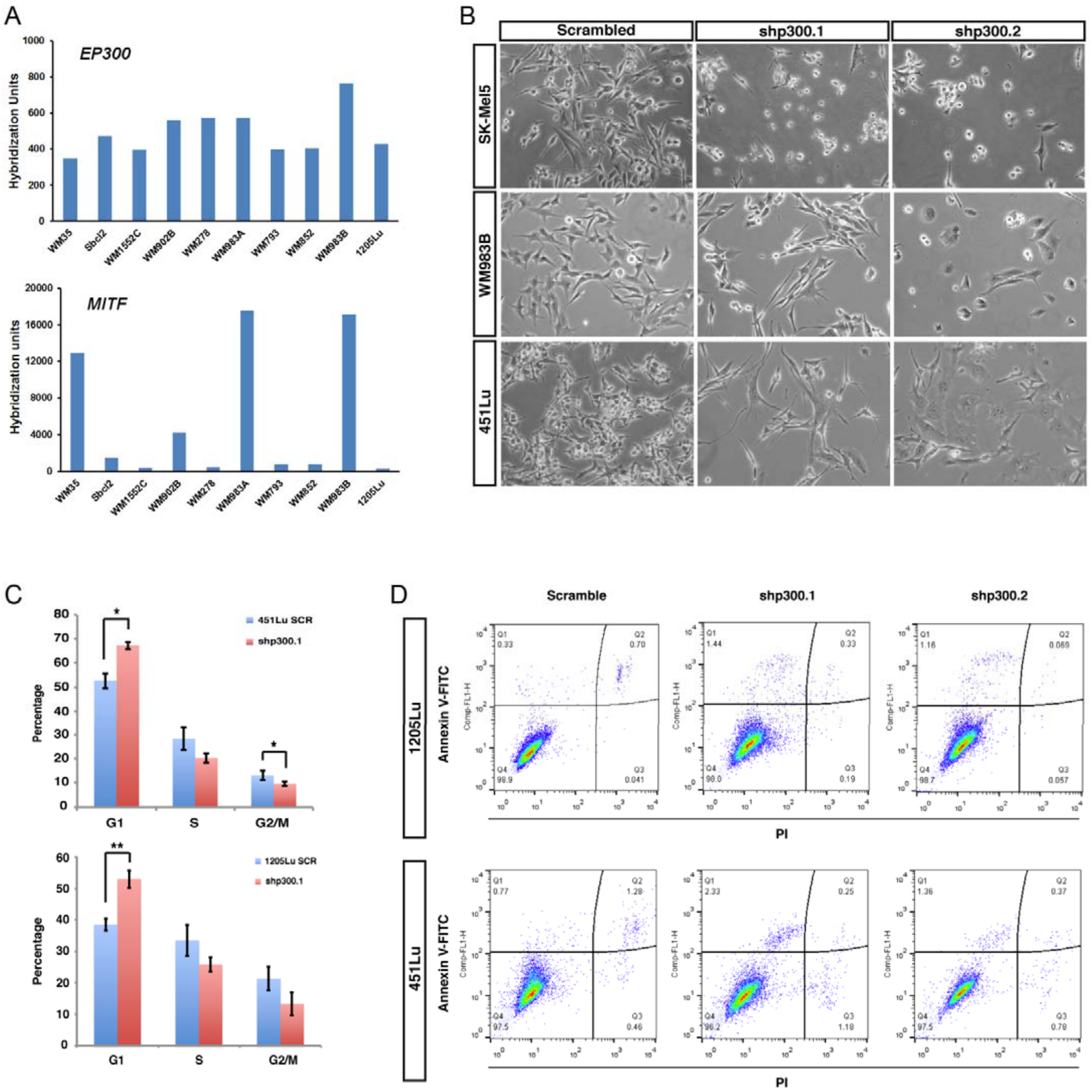
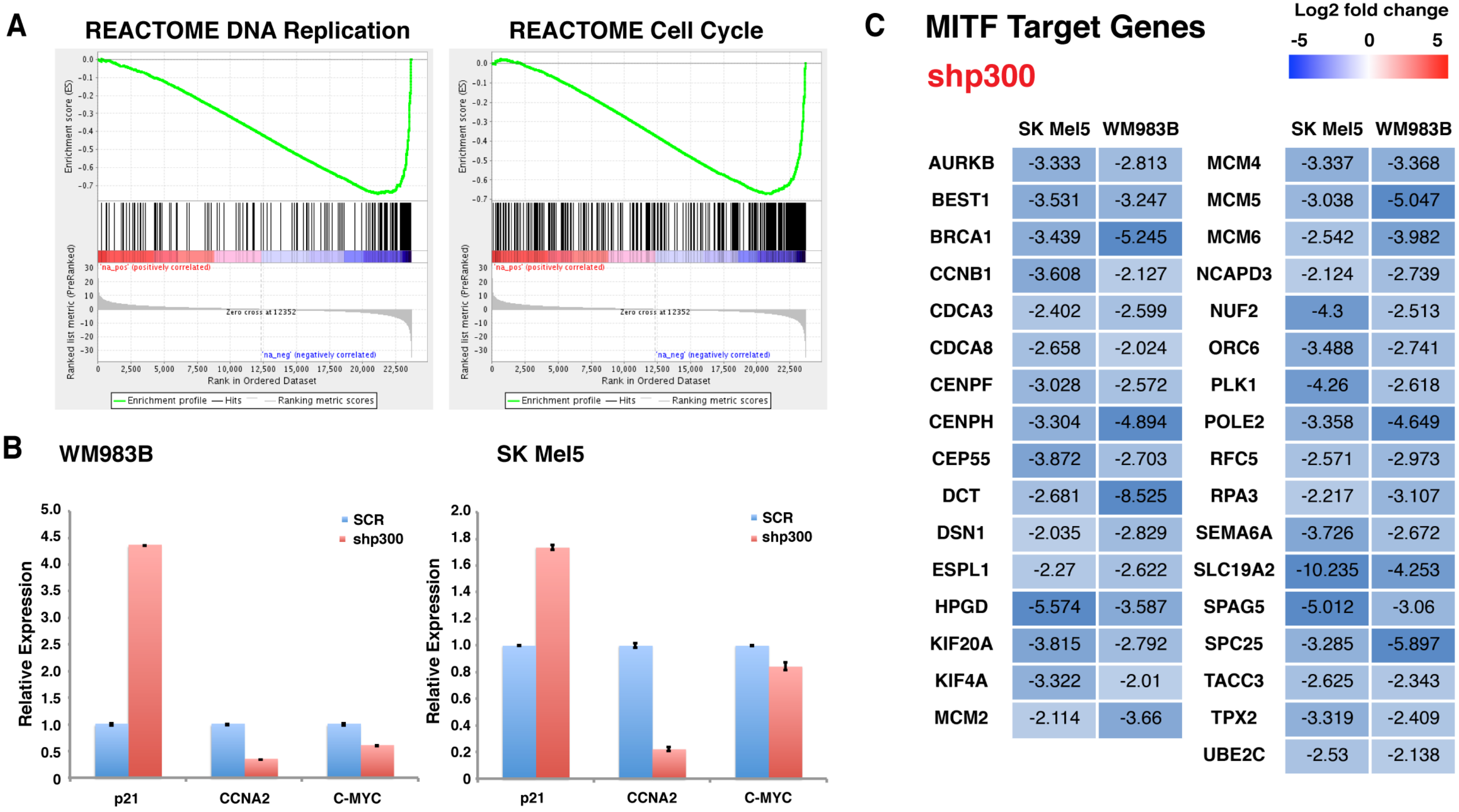
Figure S1.



A
EP300
Hybridization Units
1000
800
600
400
200
0
WM35
Sbcl2
WM1552C
WM902B
WM278
WM983A
WM793
WM852
WM983B
1205Lu
MITF
Hybridization units
20000
16000
12000
8000
4000
0
B
Scrambled
shp300.1
shp300.2
SK-Mel5
WM983B
451Lu
C
Percentage
80
70
60
50
40
30
20
10
0
451Lu SCR
shp300.1
*
G1
S
G2/M
60
1205Lu SCR
**
D
Scramble
shp300.1
shp300.2
1205Lu
451Lu
Annexin V-FITC
Comp-FL1-H
PI
Q1
0.33
Q2
0.70
Q4
98.9
Q3
0.041
Q1
1.44
Q2
0.33
Q4
98.0
Q3
0.19
Q1
1.16
Q2
0.069
Q4
98.7
Q3
0.057
Q1
0.77
Q2
1.28
Q4
97.5
Q3
0.46
Q1
2.33
Q2
0.25
Q4
96.2
Q3
1.18
Q1
1.36
Q2
0.37
Q4
97.5
Q3
0.78
10^0
10^1
10^2
10^3
10^4

Figure S2.



MITF Target Genes

shp300

	SK Mel5	WM983B		SK Mel5	WM983B
AURKB	-3.333	-2.813	**MCM4**	-3.337	-3.368
BEST1	-3.531	-3.247	**MCM5**	-3.038	-5.047
BRCA1	-3.439	-5.245	**MCM6**	-2.542	-3.982
CCNB1	-3.608	-2.127	**NCAPD3**	-2.124	-2.739
CDCA3	-2.402	-2.599	**NUF2**	-4.3	-2.513
CDCA8	-2.658	-2.024	**ORC6**	-3.488	-2.741
CENPF	-3.028	-2.572	**PLK1**	-4.26	-2.618
CENPH	-3.304	-4.894	**POLE2**	-3.358	-4.649
CEP55	-3.872	-2.703	**RFC5**	-2.571	-2.973
DCT	-2.681	-8.525	**RPA3**	-2.217	-3.107
DSN1	-2.035	-2.829	**SEMA6A**	-3.726	-2.672
ESPL1	-2.27	-2.622	**SLC19A2**	-10.235	-4.253
HPGD	-5.574	-3.587	**SPAG5**	-5.012	-3.06
KIF20A	-3.815	-2.792	**SPC25**	-3.285	-5.897
KIF4A	-3.322	-2.01	**TACC3**	-2.625	-2.343
MCM2	-2.114	-3.66	**TPX2**	-3.319	-2.409
			UBE2C	-2.53	-2.138

Figure S3.

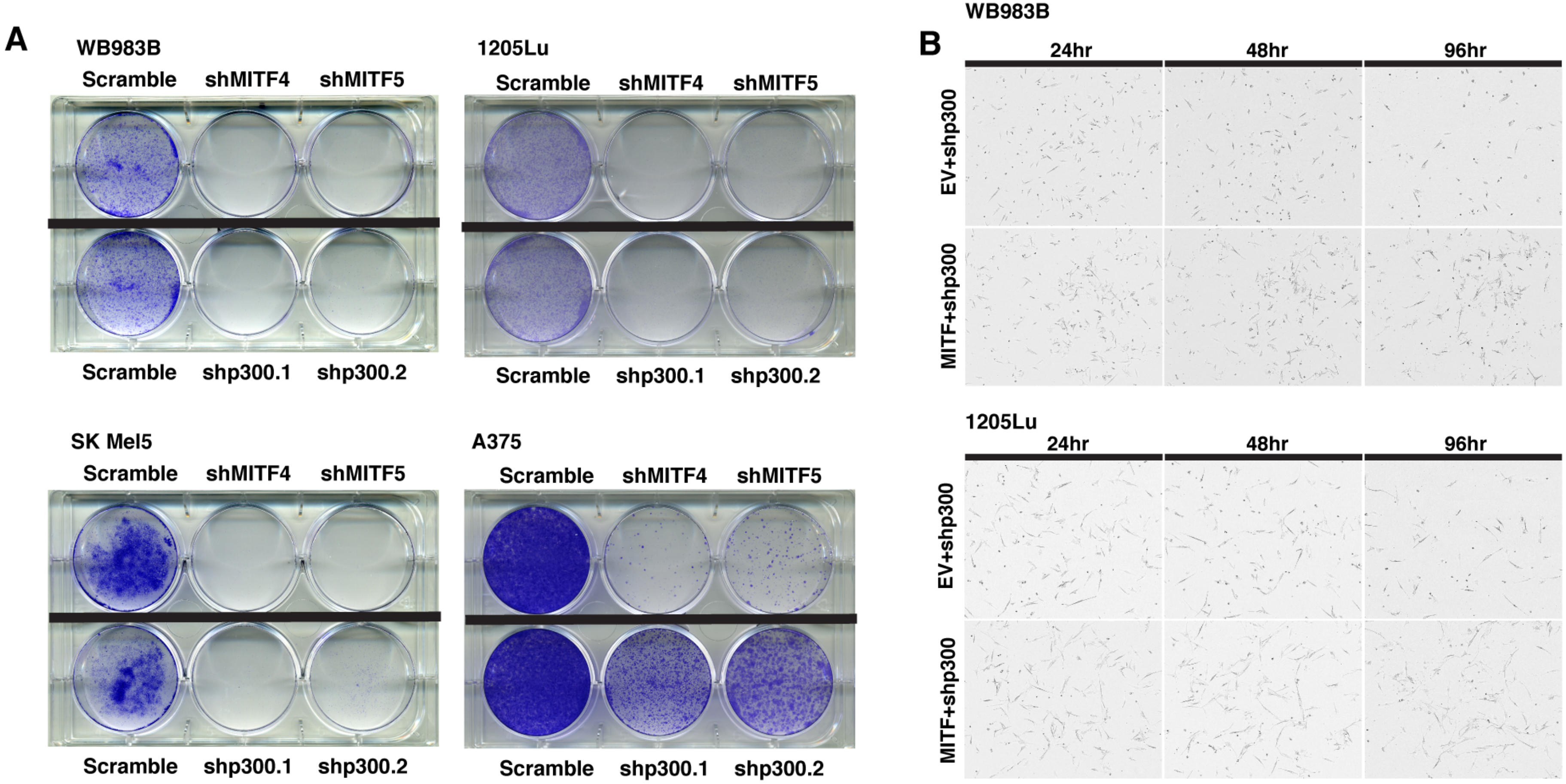
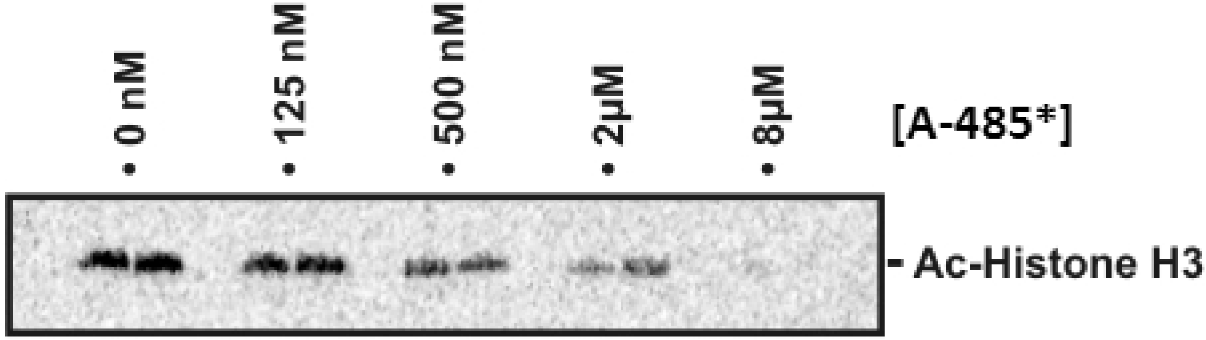

A
WB983B
Scramble
shMITF4
shMITF5
Scramble
shp300.1
shp300.2
1205Lu
Scramble
shMITF4
shMITF5
Scramble
shp300.1
shp300.2
SK Mel5
Scramble
shMITF4
shMITF5
Scramble
shp300.1
shp300.2
A375
Scramble
shMITF4
shMITF5
Scramble
shp300.1
shp300.2
B
WB983B
24hr
48hr
96hr
EV+shp300
MITF+shp300
1205Lu
24hr
48hr
96hr
EV+shp300
MITF+shp300

Figure S4


0 nM
125 nM
500 nM
2μM
8μM
[A-485*]
Ac-Histone H3

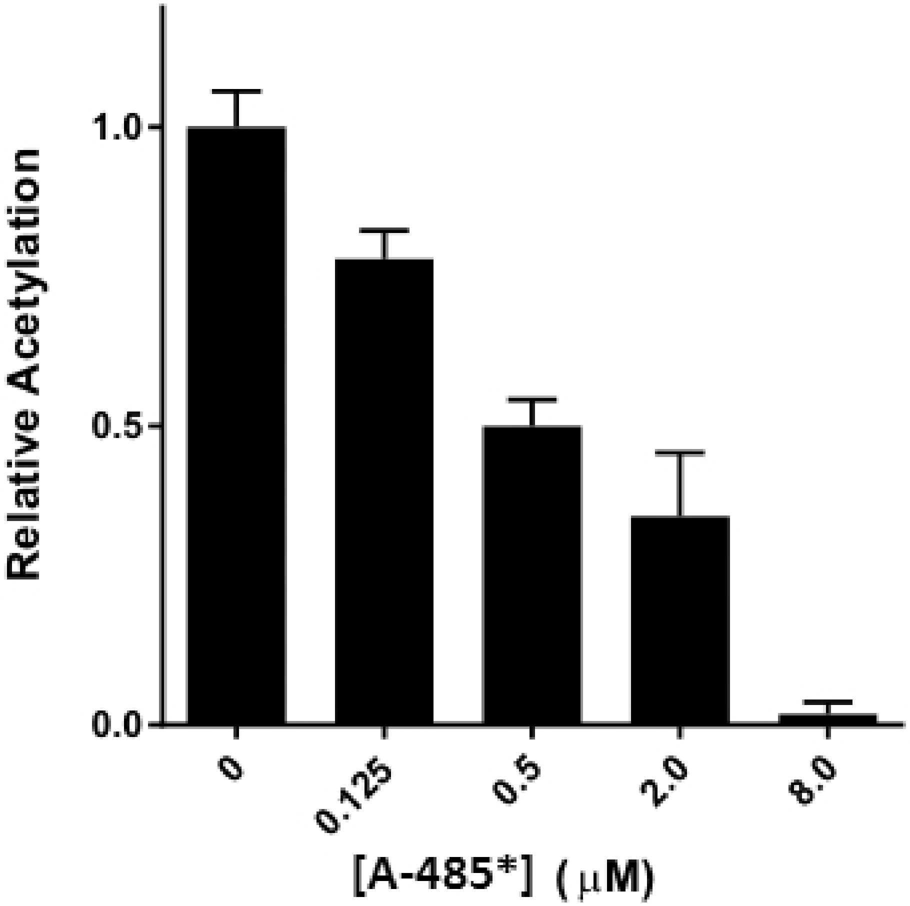

Relative Acetylation
1.0
0.5
0.0
0
0.125
0.5
2.0
8.0
[A-485*] (μM)

Figure S5

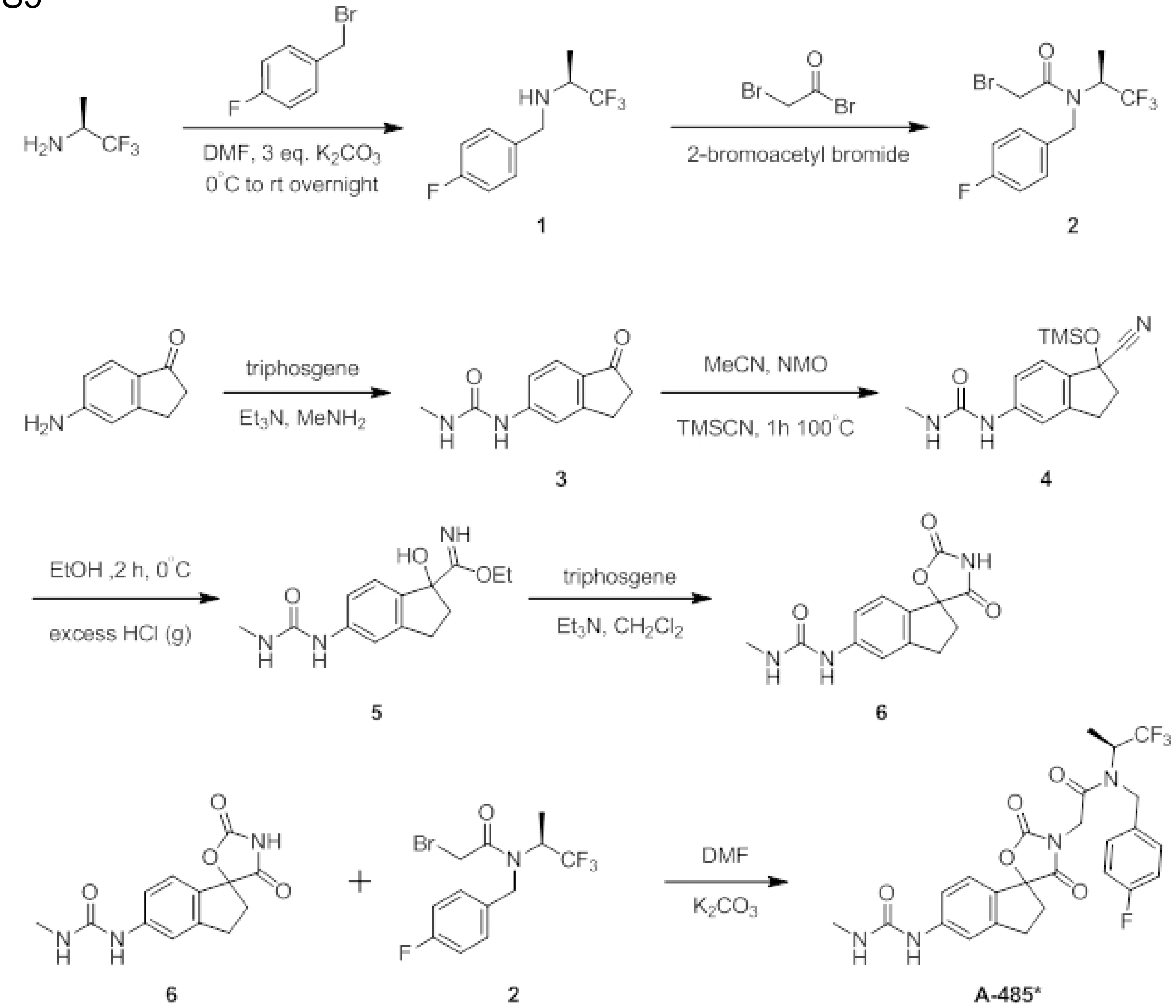

Br
F
H2N
CF3
DMF, 3 eq. K2CO3
0°C to rt overnight
HN
CF3
F
1
Br
O
Br
2-bromoacetyl bromide
Br
O
N
CF3
F
2
O
H2N
triphosgene
Et3N, MeNH2
O
O
N
H
N
H
3
MeCN, NMO
TMSCN, 1h 100°C
TMSO
N
O
N
H
N
H
4
EtOH ,2 h, 0°C
excess HCl (g)
NH
HO
OEt
O
N
H
N
H
5
triphosgene
Et3N, CH2Cl2
O
NH
O
O
O
N
H
N
H
6
O
NH
O
O
O
N
H
N
H
6
+
Br
O
N
CF3
F
2
DMF
K2CO3
CF3
O
N
O
N
O
O
F
O
N
H
N
H
A-485*

Table S1. ChIP-PCR primer sequences for the characterization of *MITF* gene upstream regulatory region

Primer ID	Forward	Reverse
1	5'-TCTACTAATGTATAATCGTGTGTT-3'	5'-ATGAGATCATGTTTCTAACGG-3'
2	5'-TGCTAAGGCCGTTAGAAAC-3'	5'-GCCCTCATCTCCTAGCATA-3'
3	5'-CTGGATTTGGACTAATTTCTCA-3'	5'-CCAGGTTTAAAGATCCGATG-3'
4	5'-GTTTGGATTGCCAGCTAC-3'	5'-CCAGAGGACACACATCTAT-3'
5	5'-AAAGACCTCACTGACAGT-3'	5'-ATGAGGGCAATGAGTAGTT-3'
6	5'-ACATTCTACTCATTGCCCTC-3'	5'-TTGTCTAAATGCCCAGGATAA-3'
7	5'-ATTGTCAACCTAACGGACT-3'	5'-ATGCTTAATATCTACTGCTGAC-3'
8	5'-TTGTCAGCAGTAGATATTAAGCA-3'	5'-GCTAAACACTGTACAAAGCA-3'
9	5'-TGCTTTGTACAGTGTTTAGC-3'	5'-TACAGAAGAATGAGTTATCATATACA-3'
10	5'-ATGATAACTCATTCTTCTGTAATCT-3'	5'-CTGCCTATTGACCTCACA-3'
11	5'-TGTGAGGTCAATAGGCAG-3'	5'-TTTCCATGGCCGAATAAC-3'
12	5'-TCGGCCATTGGAAAAGT-3'	5'-GACGAGCTATCAAAGTCAAAC-3'
13	5'-ATAGCTCGTCACTTAAAAAGG-3'	5'-CGGAAACTTTAGCACAGAAG-3'