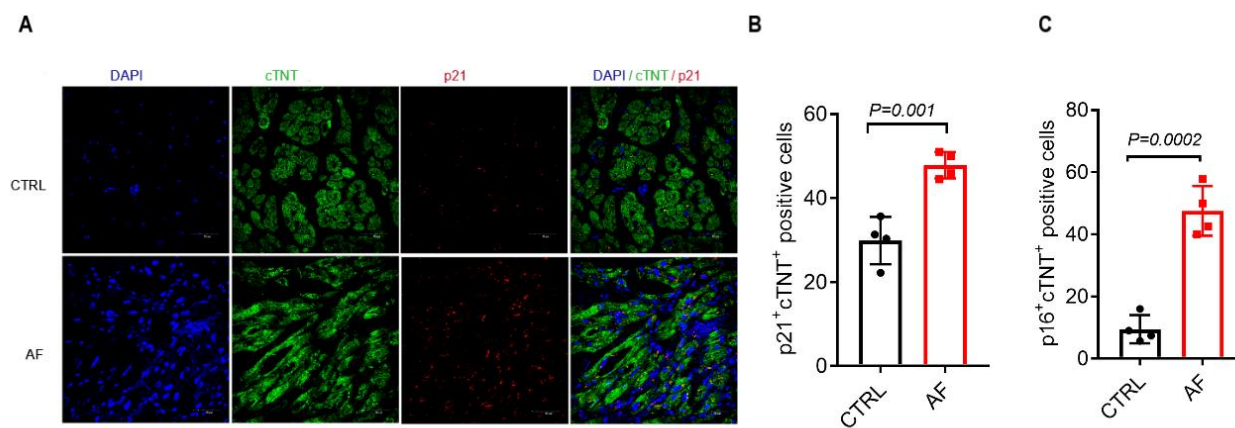


SUPPLEMENTARY DATA

Atrial Fibrillation Underlies Cardiomyocyte Senescence and Contributes to Deleterious Atrial Remodeling during Disease Progression

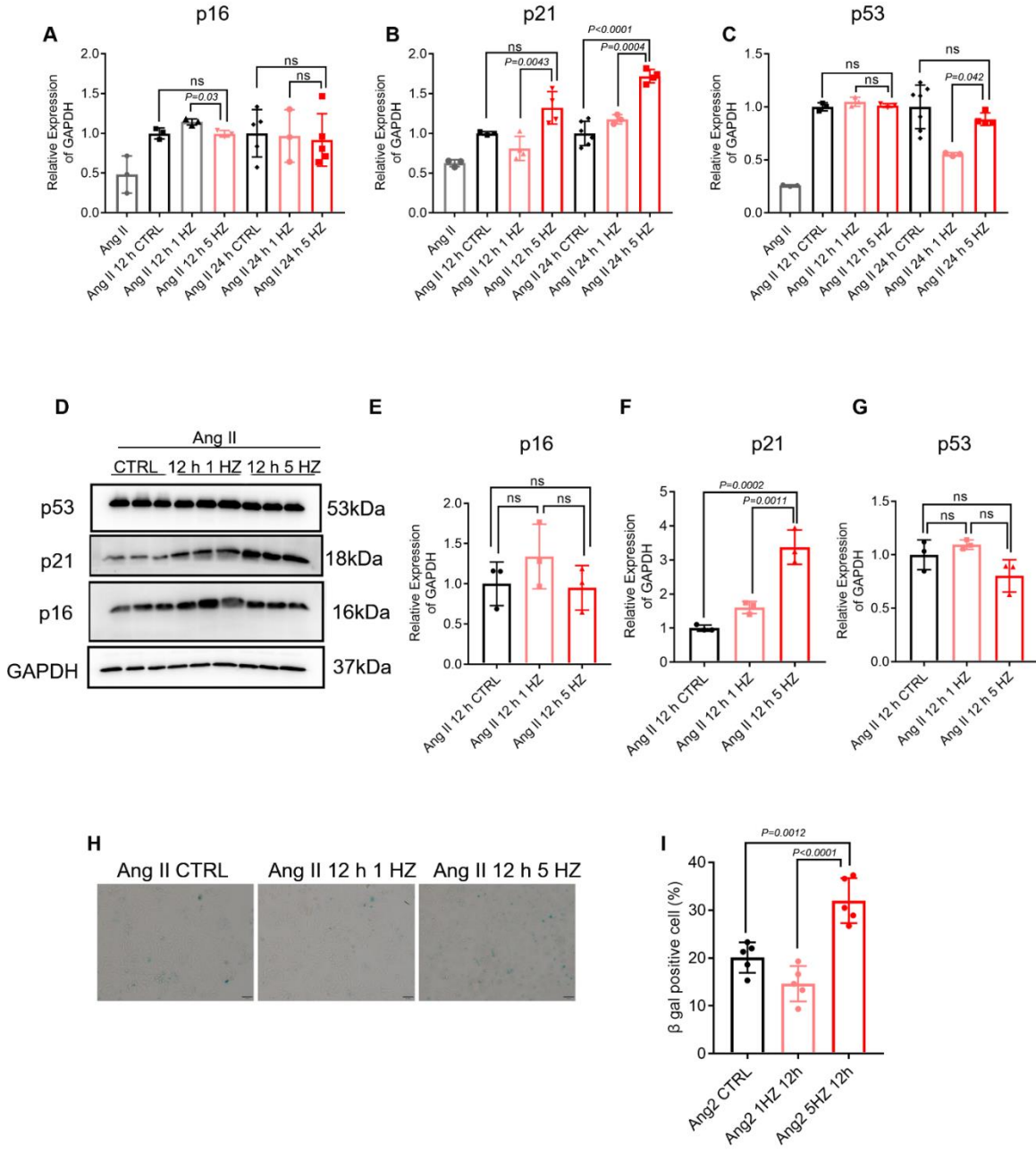
Ailiya Adil[#], Xiyu Zhu[#], Hailong Cao, Xinlong Tang, Yali Wang, Junxia Wang, Jian Shi, Qing Zhou^{*}, Dongjin Wang^{*}

SUPPLEMENTARY DATA

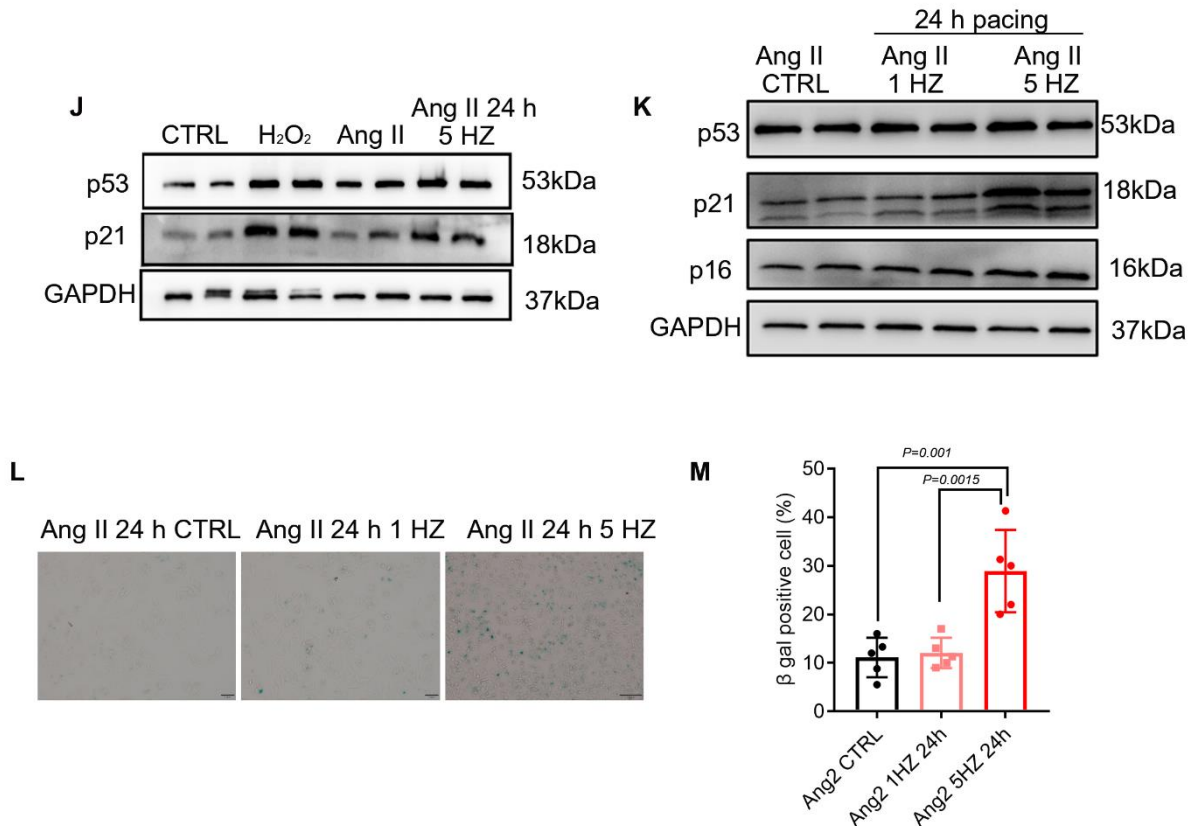


Supplementary Figure 1. Atrial cardiomyocyte senescence accumulated in LAAs with AF. (A) Immunofluorescence co-staining for cTNT (green) and p21 (red) in LAA sections from patients with SR or AF (bar = 50 μ m). (B) Graph showing the percentage of p21-cTNT positive cells and p16-cTNT in total cell of LAAs.

SUPPLEMENTARY DATA

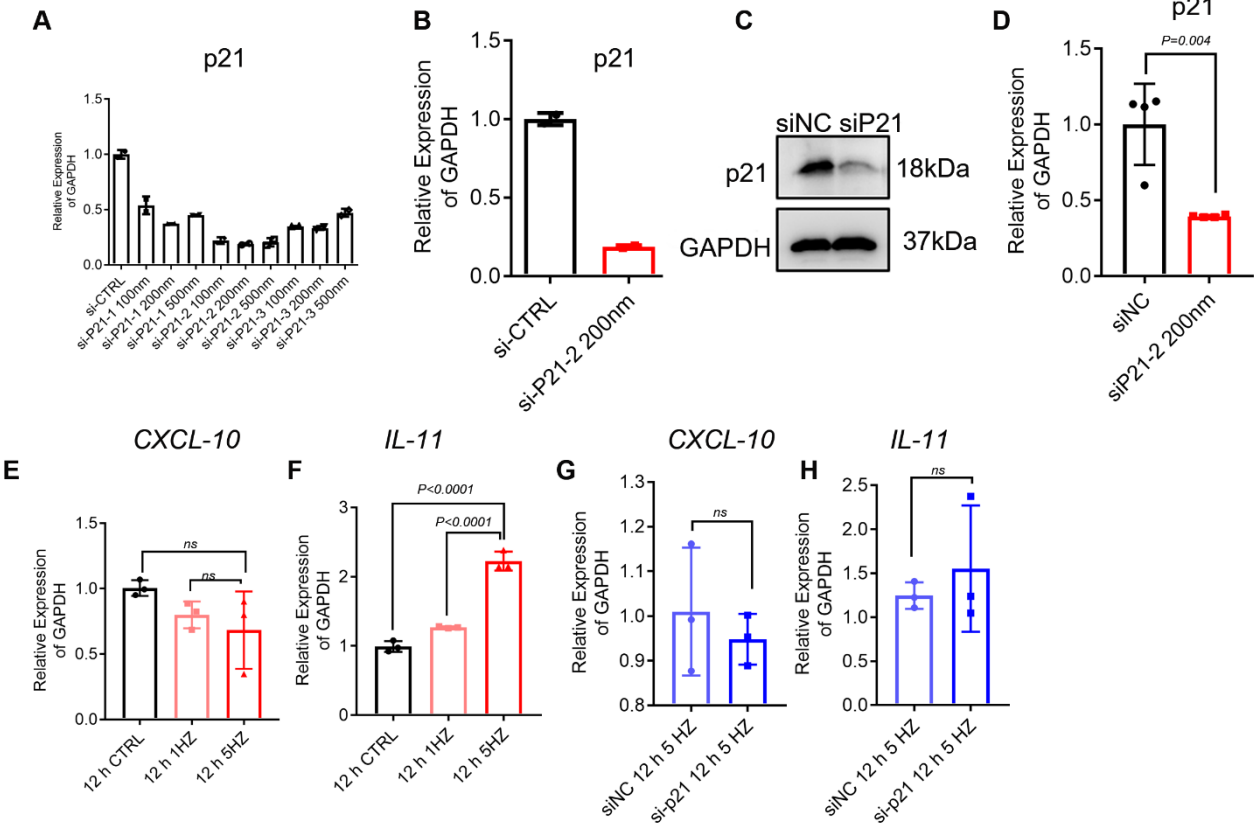


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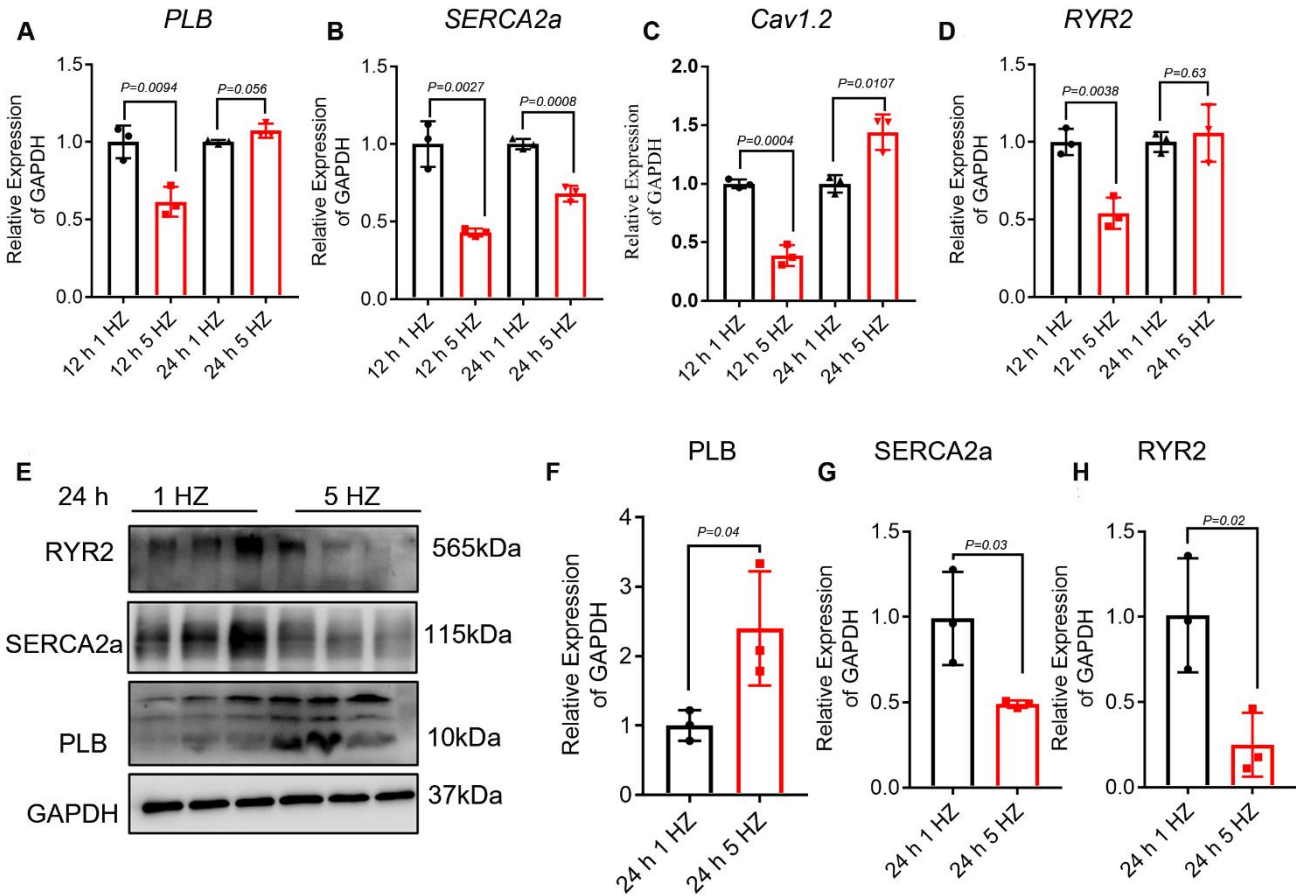
Supplementary Figure 2. TP induces HL-1 atrial cardiomyocytes senescence in vitro. (A-C) Senescence-associated mRNA expression was determined by qPCR analysis of Ang II combined with nonpaced (Ang II CTRL), normal-paced (Ang II 1 HZ) and tachypaced (TP) (Ang II 5 HZ) HL-1 cardiomyocytes for the indicated durations (n=3-5). (D-G) Western blot and quantification analyses of senescence-associated protein expression of Ang II combined with nonpaced (Ang II CTRL), normal-paced (Ang II 1 HZ) and TP (Ang II 5 HZ) HL-1 cardiomyocytes for 12 h. GAPDH was used as a loading control (n=3). (H-I) SA-β-Gal staining of Ang II combined with nonpaced (Ang II CTRL), normal-paced (Ang II 1 HZ) and tachypaced (TP) (Ang II 5 HZ) HL-1 cardiomyocytes for 12 h (blue: SA-β-Gal; scale bar=1 mm) (n=3). (J) HL-1 cardiomyocytes were subjected to the following treatments: control, 100 μM hydrogen peroxide (H₂O₂) for 1 h, Ang II for 48 h and Ang II for 48 h, followed by TP (5 HZ) for 24 h. Next, senescence-associated protein expression was assessed and quantified in each group. GAPDH was used as a loading control (n=2). (K) Western blot analysis of senescence-associated protein expression of Ang II combined with nonpaced (Ang II CTRL), normal-paced (Ang II 1 HZ) and TP (Ang II 5 HZ) HL-1 cardiomyocytes for 24 h. GAPDH was used as a loading control (n=2). (L-M) SA-β-Gal staining of Ang II for 48 h combined with nonpaced (0 HZ), normal-paced (1 HZ) and tachypaced (TP) (5 HZ) HL-1 cardiomyocytes for 24 h (blue: SA-β-Gal, scale bar 1 mm) (n=3).

SUPPLEMENTARY DATA



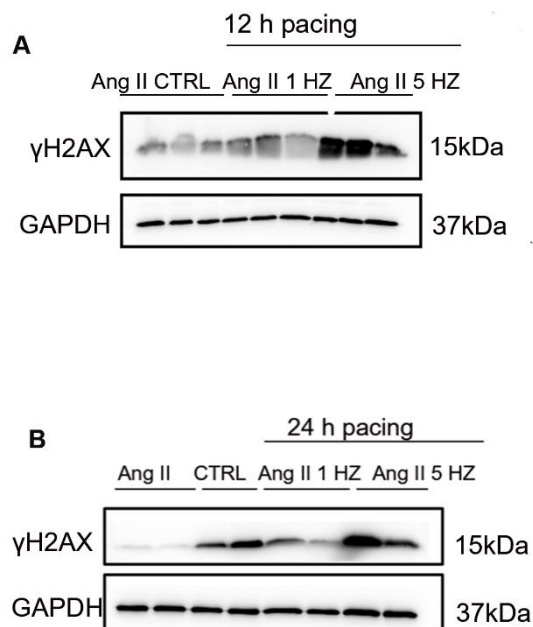
Supplementary Figure 3. Suppression of TP induced cell senescence reduced SASP elevation. (A-D) mRNA expression of p21 analyzed after treatment with siNC and sip21. (E-H) The mRNA expression of IL-11 and CXCL-10 was determined by qPCR analysis in control nonpaced (0 HZ; CTRL), normal-paced (1 HZ) and TP (5 HZ) HL-1 cardiomyocytes for the indicated durations (n=3).

SUPPLEMENTARY DATA



Supplementary Figure 4. TP-induced senescence partly modulates sarcoplasmic reticulum-related proteins. (A-D) The mRNA expression of PLB, SERCA2a, Cav1.2 and RYR2 was determined by RT-qPCR analysis in normal-paced (1 HZ) and TP (5 HZ) HL-1 cardiomyocytes for the indicated durations (n=3). (E-H) The protein expression of PLB, SERCA2a and RYR2 was determined by Western blot analysis in normal-paced (1 HZ) and TP-treated (5 HZ) cells for 24 h. GAPDH was used as a loading control (n=3).

SUPPLEMENTARY DATA



Supplementary Figure 5. DNA damage-related foci formation increased in senescent atrial cardiomyocytes and in AF. (A-B) Western blot analysis of γ H2AX protein expression in Ang II combined with nonpaced, normal-paced and TP HL-1 cardiomyocytes for the indicated durations. GAPDH was used as a loading control (n=2).

Primers used in this study (H: human; M: mouse)

Primers	Sequence
<i>H-CDKN1A F</i>	TGTCGTCAGAACCCATGC
<i>H-CDKN1A R</i>	AAAGTCGAAGTTCCATCGCTC
<i>H-P53 F</i>	TGCTCAAGACTGGCGCTAAA
<i>H-P53 R</i>	AGTCTGGCCAATCCAGGGAA
<i>H-PARP1 F</i>	CCCTAAAGGCTCAGAACGACC
<i>H-PARP1 R</i>	AGGAGGGCACCGAACACC
<i>H-P27 F</i>	GCAGCTTGCCCGAGTTCT
<i>H-P27 R</i>	AGAAGAATCGTCGGTTGCAGG
<i>H-RB F</i>	TTGTAACGGGAGTCGGGAGA
<i>H-RB R</i>	CTCAAGCCTGACGAGAGGCAG
<i>H-GAPDH F</i>	GGAGCGAGATCCCTCCAAAAT
<i>H-GAPDH R</i>	GGCTGTTGTCATACTTCTCATGG

SUPPLEMENTARY DATA

<i>M-CDKN1A F</i>	CCTGGTGATGTCCGACCTG
<i>M-CDKN1A R</i>	CCATGAGCGCATCGCAATC
<i>M-P53 F</i>	CTCTCCCCCGCAAAGAAAAA
<i>M-P53 R</i>	CGGAACATCTCGAAGCGTTTA
<i>M-PARP1 F</i>	GGCAGCCTGATGTTGAGGT
<i>M-PARP1 R</i>	GCGTACTCCGCTAAAAAGTCAC
<i>M-GAPDH F</i>	AGGTCGGTGTGAACGGATTG
<i>M-GAPDH R</i>	TGTAGACCATGTAGTTGAGGTCA
<i>M-Cav1.2 F</i>	CTACAGAAACCCATGTGAGCAT
<i>M-Cav1.2 R</i>	CAGCCACGTTGTCAGTGTTG
<i>M-SERCA2a F</i>	TGGAACAACCCGGTAAAGAGT
<i>M-SERCA2a R</i>	CACCAGGGGCATAATGAGCAG
<i>M-NCX F</i>	CTCCCTGTTTGTGCTCCTGT
<i>M-NCX R</i>	AGAAGCCCTTTATGTGGCAGTA
<i>M-PLB F</i>	AAAGTGCAATACCTCACTCGC
<i>M-PLB R</i>	GGCATTTC AATAGTGGAGGCTC
<i>M-RYR2 F</i>	ACGGCGACCATCCACAAAG
<i>M-RYR2 R</i>	AAAGTCTGTTGCCAAATCCTTCT
<i>M-IL-6 F</i>	TAGTCCTTCCTACCCCAATTCC
<i>M-IL-6 R</i>	TTGGTCCTTAGCCACTCCTTC
<i>M-IL-1β F</i>	ACCTGTGTCTTTCCCGTGGAC
<i>M-IL-1β R</i>	GGGAACGTCACACACCAGCA
<i>M-Ki67 F</i>	ATCATTGACCGTCTCCTTAGGT
<i>M-Ki67 R</i>	GCTCGCCTTGATGGTTCCT
<i>M-NPPA F</i>	GCTCCAGGCCATATTGGAG
<i>M-NPPA R</i>	GGGGGCATGACCTCATCTT
<i>M-NPPB F</i>	GAGGTCACTCCTATCCTCTGG
<i>M-NPPB R</i>	GCCATTTCCCTCCGACTTTTCTC
<i>M-CDKN2A F</i>	CGCAGGTTCTTGCTCACTGT
<i>M-CDKN2A R</i>	TGTTACGAAAGCCAGAGCG
<i>M-Gjal F</i>	ACAGCGGTTGAGTCAGCTTG
<i>M-Gjal R</i>	GAGAGATGGGGAAGGACTTGT
<i>M-Myh6 F</i>	GCCCAGTACCTCCGAAAGTC
<i>M-Myh6 R</i>	GCCTTAACATACTCCTCCTTGTC
<i>M-ACTC F</i>	GGCTGTATTCCCCTCCATCG
<i>M-ACTC R</i>	CCAGTTGGTAACAATGCCATGT
<i>si-M-CDKN1A</i>	CCAGCCTGACAGATTCTA