

**Integrin-linked kinase control dental pulp stem cell senescence via  
the mTOR signaling pathway**

**Appendix Table 1: Details of different age donors**

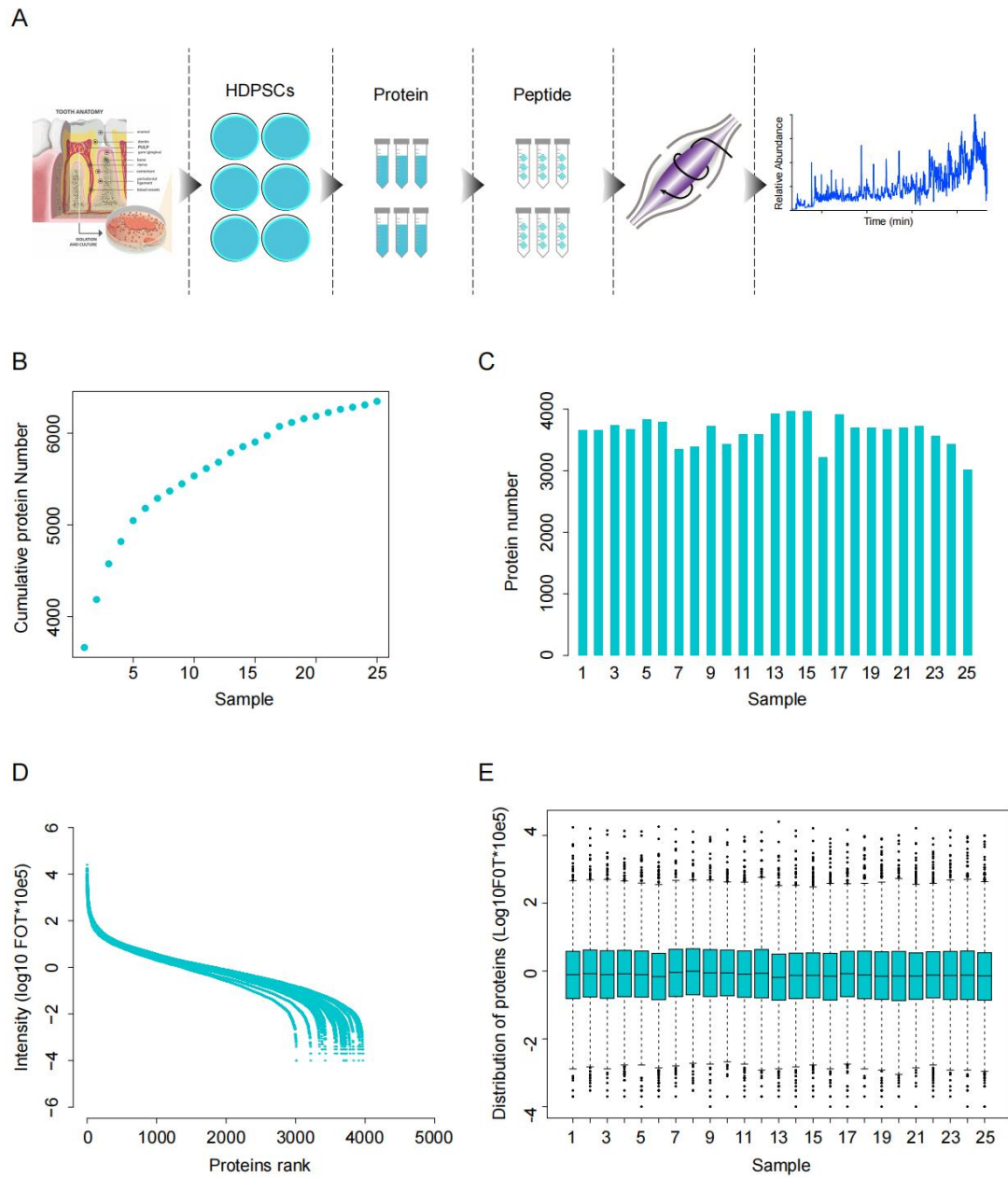
Donor	Age (years old)	Gender
1	15	Female
2	15	Male
3	16	Male
4	17	Male
5	17	Female
6	19	Female
7	20	Female
8	22	Male
9	23	Male
10	28	Female
11	32	Male
12	33	Male
13	36	Male
14	38	Female
15	38	Female
16	40	Male
17	42	Female
18	44	Female
19	45	Male
20	46	Male
21	51	Female
22	55	Male
23	56	Female
24	65	Female
25	69	Male

**Appendix Table 2: The primers used in the study**

Gene	Sequence 5' to 3'
GAPDH-F	GGAGCGAGATCCCTCCAAAAT
GAPDH-R	GGCTGTTGTCATACTTCTCATGG
P16-F	TGCCCAACGCACCGAATAGT
P16-R	CAGCAGCTCCGCCACTCG
P21-F	TGTCCGTCAGAACCCATGC
P21-R	AAAGTCGAAGTTCCATCGCTC
P53-F	AATCTACTGGGACGGAACAGCTTTGAGG
P53-R	GGAGAGGAGCTGGTGTGTTGGG
IL6-F	GCCCAGCTATGAACTCCTTCT
IL6-R	GAAGGCAGCAGGCAACAC
IL8-F	ACTGAGAGTGATTGAGAGTGGAC
IL8-R	AACCCTCTGCACCCAGTTTTTC
MMP13-F	ACTGAGAGGCTCCGAGAAATG
MMP13-R	GAACCCCGCATCTTGCTT
ALP-F	GTGAACCGCAACTGGTACTC
ALP-R	GAGCTGCGTAGCGATGTCC
RUNX2-F	CAGACCAGCAGCACTCCATAT
RUNX2-R	CAGCGTCAACACCATCATTC
BMP2-F	ACTACCAGAAACGAGTGGGAA
BMP2-R	GCATCTGTTCTCGAAAACCT
DSPP-F	GCATTCAGGGACAAGTAAGCA
DSPP-R	CTTGGACAACAGCGACATCCT
DMP1-F	AGCCATTCTGAGGAAGACGA
DMP1-R	TGTTGTGATAGGCATCAACTGTTA
SOX2-F	GCCGAGTGGAACTTTTGTCG
SOX2-R	GGCAGCGTGTACTTATCCTTCT
GFAP-F	CTGTTGCCAGAGATGGAGGTT
GFAP-R	TCATCGCTCAGGAGGTCCTT
GAP43-F	GGCCGCAACCAAAATTCAGG
GAP43-R	CGGCAGTAGTGGTGCCTTC

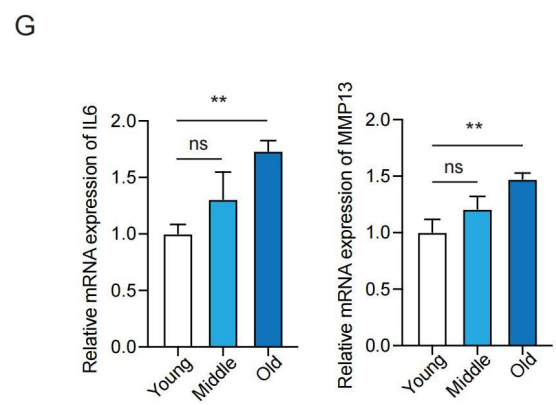
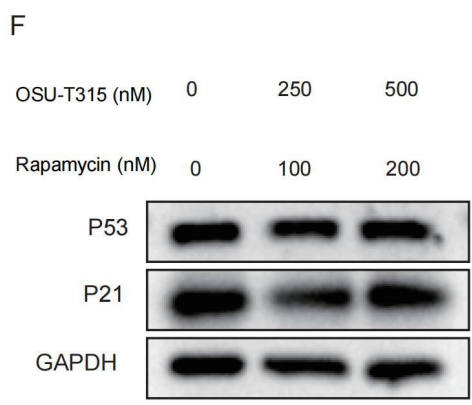
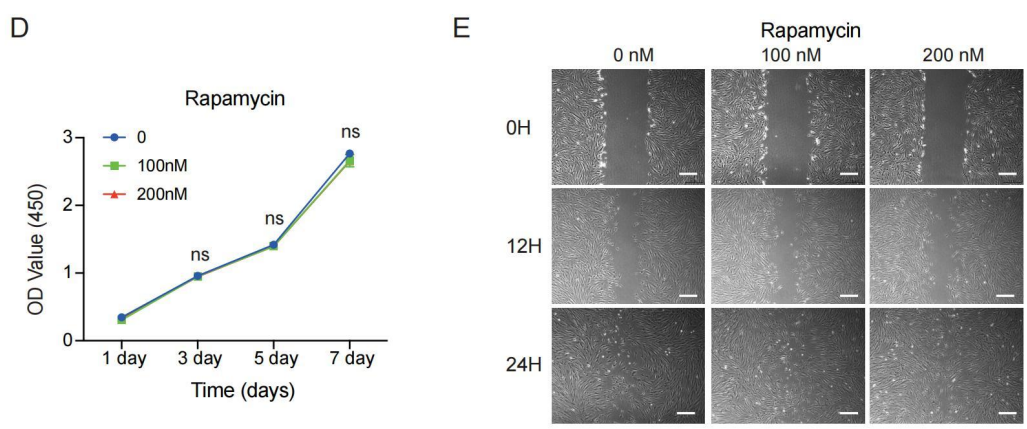
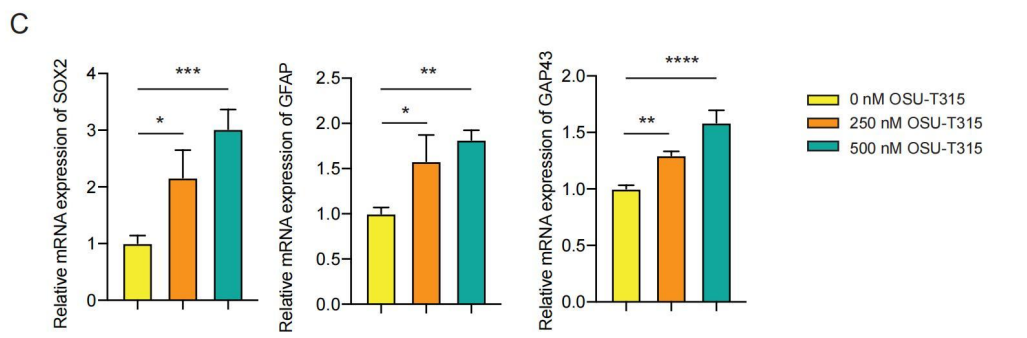
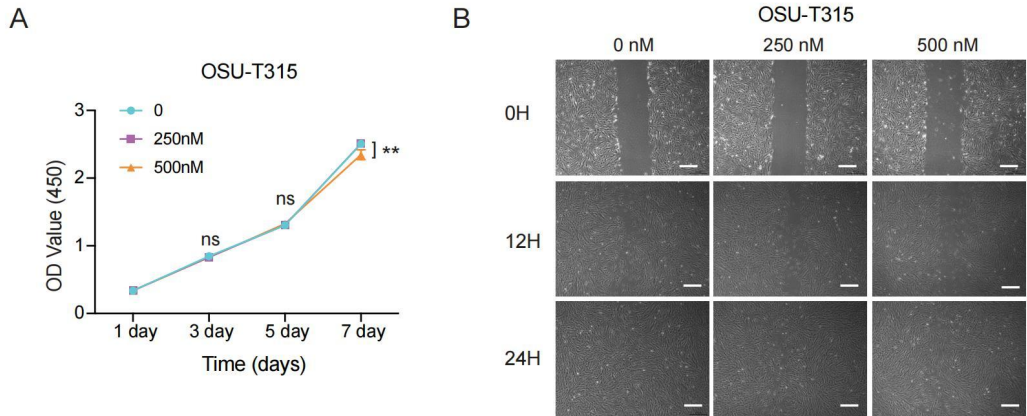
**Appendix Table 3: Top 10 KEGG pathways for each CCP**

Top 10 KEGG pathways	CCP		
	CCP1	CCP2	CCP3
1	DNA replication	ECM-receptor interaction	Yersinia infection
2	Mismatch repair	Hypertrophic cardiomyopathy	Ubiquitin mediated proteolysis
3	Nucleotide excision repair	Dilated cardiomyopathy	Fc gamma R-mediated phagocytosis
4	RNA polymerase	Arrhythmogenic right ventricular cardiomyopathy	Pathogenic Escherichia coli infection
5	Spliceosome	Focal adhesion	Amino sugar and nucleotide sugar metabolism
6	Steroid biosynthesis	Lysosome	Platelet activation
7	Cell cycle	Human papillomavirus infection	Regulation of actin cytoskeleton
8	Ribosome biogenesis in eukaryotes	Proteoglycans in cancer	Human cytomegalovirus infection
9	RNA degradation	Regulation of actin cytoskeleton	Vascular smooth muscle contraction
10	Terpenoid backbone biosynthesis	PI3K-Akt signaling pathway	Legionellosis



**Appendix Figure 1.** Proteomic landscape of HDPSCs samples. **(A)** Overview of the experimental design for proteomics analyses. **(B)** Cumulative number of proteins

identified as a function of sample numbers. **(C)** Number of proteins identified in 25 samples. **(D)** Overview of the proteomics profile of HDPSCs samples. The dynamics of protein abundances identified in 25 samples are shown. Proteins were quantified as a normalized intensity-based fraction of total (FOT) value and log<sub>10</sub> transformed. The highest-abundance and lowest-abundance proteins are shown. **(E)** Distribution of protein abundance presented as median intensity in 25 samples.



**Appendix Figure 2.** Cell function changes of O-HDPSCs pretreatment with inhibitors (OSU-T315 and Rapamycin). **(A)** Results of the CCK-8 assay of HDPSCs pretreatment with OSU-T315 (n=3). **(B)** Representative images of migration of HDPSCs pretreatment with OSU-T315. Scale bar = 100  $\mu$ m. **(C)** Quantitative RT-PCR results of mRNA expression of SOX2, GFAP and GAP43 in O-HDPSCs pretreated with and without OSU-T315 induced in neurogenic induction medium for up to 7 days (n=3). **(D)** Results of the CCK-8 assay of HDPSCs pretreatment with OSU-T315 (n=3). **(E)** Representative images of migration of HDPSCs pretreatment with Rapamycin. Scale bar = 200  $\mu$ m. **(F)** O-HDPSCs treated with serial concentrations of OSU-T315 and Rapamycin for 3 days were subjected to western blot analysis. **(G)** Quantitative RT-PCR results of mRNA expression of IL6 and MMP13 in different age groups (n=3). \*p<0.05. \*\*p<0.01, \*\*\*p<0.005.