

## Additional Materials

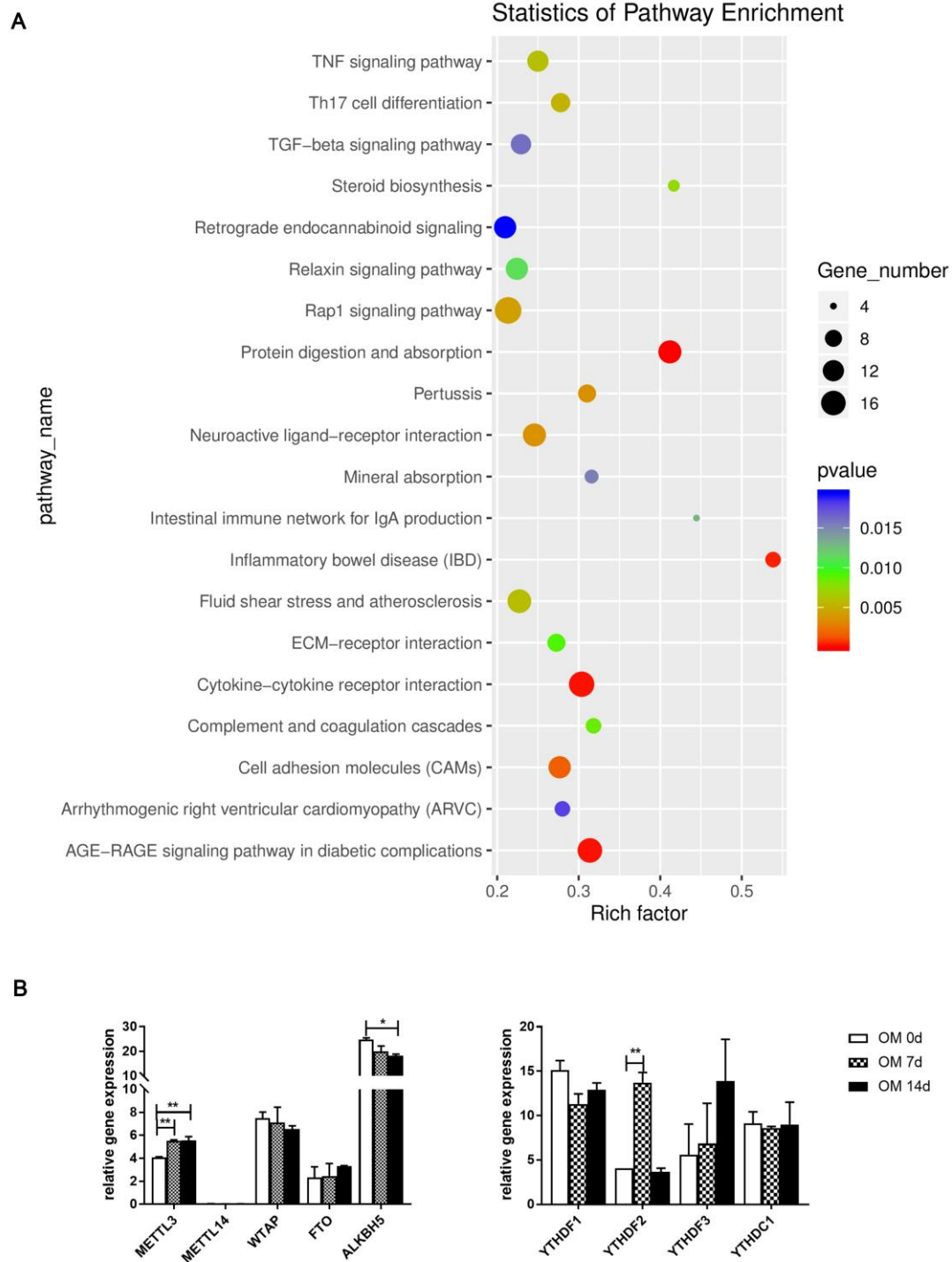
### Stage-specific requirement for METTL3-dependent m<sup>6</sup>A modification during dental pulp stem cell differentiation

#### Additional Table

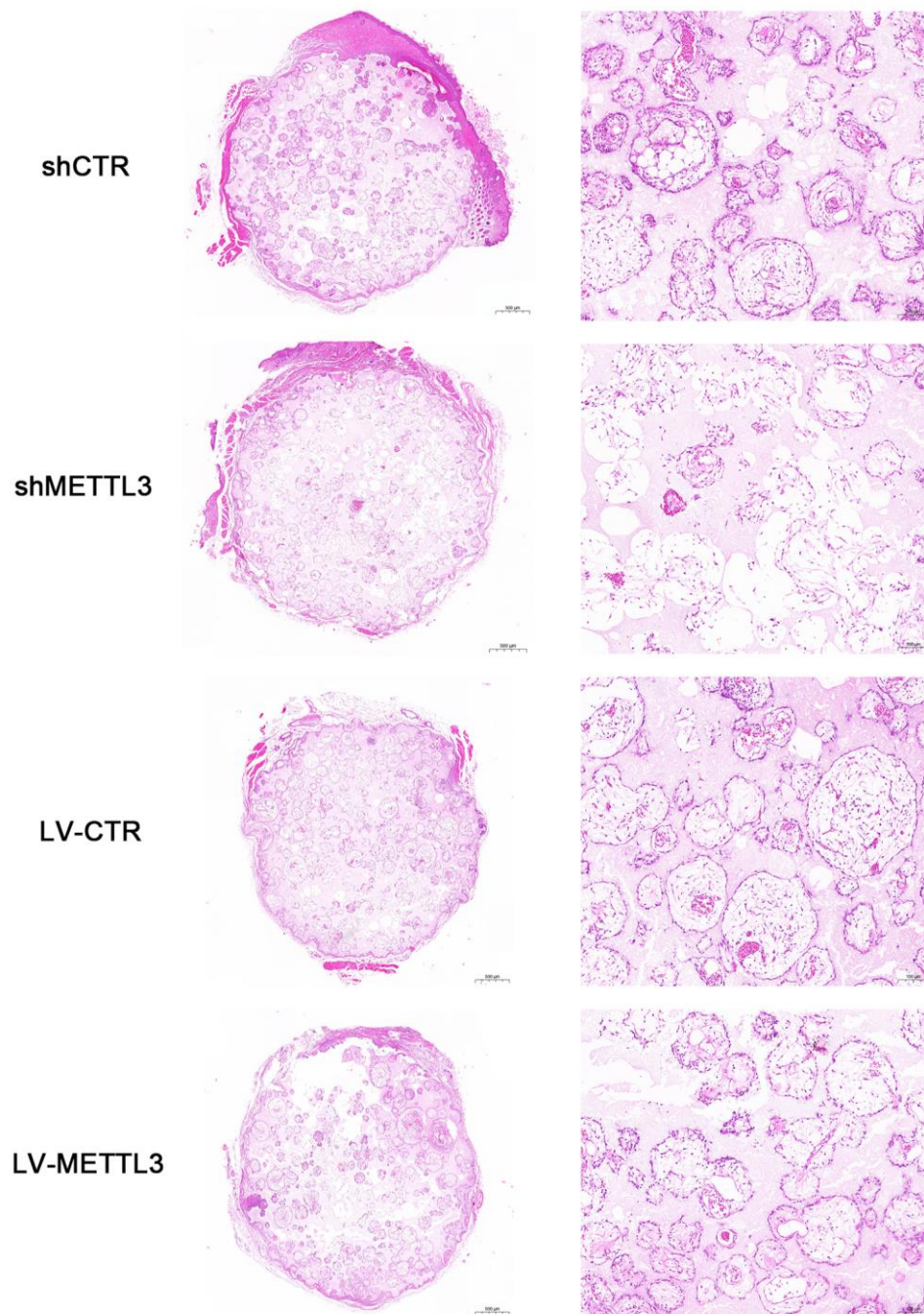
**Additional Table 1:** The sequence of primers used in qPCR

<i>glyceraldehyde-3-phosphate dehydrogenase</i>	<i>GAPDH</i>	F	TCAACAGCGACACCCACTC
		R	GCTGTAGCCAAATTCGTTGTC
<i>methyltransferase 3</i>	<i>METTL3</i>	F	GAGGAGTGCATGAAAGCCAG
		R	GGCCTCAGAATCCATGCAAG
<i>methyltransferase 14</i>	<i>METTL14</i>	F	GACGGGGACTTCATTCATGC
		R	CCAGCCTGGTTCGAATTGTAC
<i>WT1 associated protein</i>	<i>WTAP</i>	F	ACGCAGGGAGAACATTCTTG
		R	CACACTCGGCTGCTGAACT
<i>alkaline phosphatase</i>	<i>ALP</i>	F	CCAAAGGCTTCTTCTTGCTG
		R	CCACCAAATGTGAAGACGTG
<i>RUNX family transcription factor 2</i>	<i>RUNX2</i>	F	TCGCCAGGCTTCATAGCAA
		R	GGCCTTGGGTAAGGCAGATT
<i>dentin sialophosphoprotein</i>	<i>DSPP</i>	F	ATATTGAGGGCTGGAATGGGGA
		R	TTTGTGGCTCCAGCATTGTCA
<i>peroxisome proliferator activated receptor</i>	<i>PPAR</i>	F	TGGAGCCCAAGTTTGAGTTT
		R	CAGGGCTTGTAGCAGGTTGT
<i>lipoprotein lipase</i>	<i>LPL</i>	F	CAAGAGTGAGTGAACAAC
		R	AATTATGCTGAAGGACAAC
<i>noggin</i>	<i>NOG</i>	F	CGAGATCAAAGGGCTAGAGTTC
		R	GACCACAGCCACATCTGTAA
<i>noggin (m<sup>6</sup>A RIP-qCR)</i>	<i>NOG</i>	F	CGAGCGAGATCAAAGGGCTA
		R	CGACCACAGCCACATCTGTA
<i>noggin-FLAG</i>	<i>NOG-FLAG</i>	F	GACTACAAGGACGACGACG
		R	GGCGGATGTGGAGATAGTG

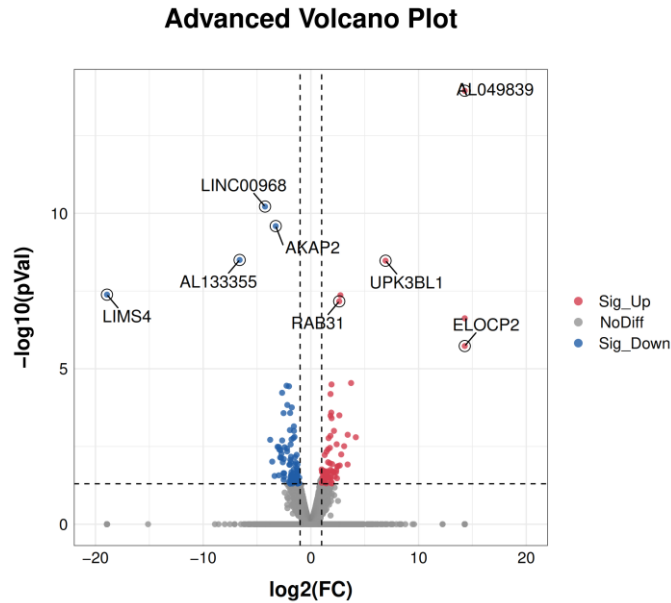
## Additional Figures:



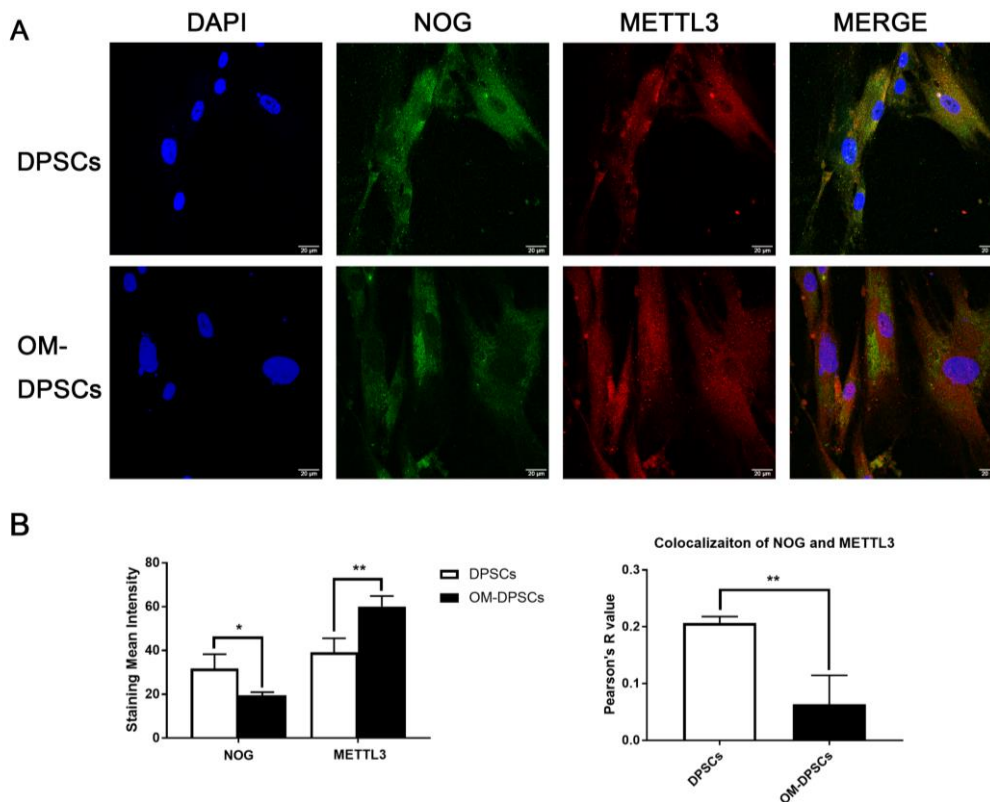
**Additional Figure 1:** A, KEGG enrichment analysis of differentially m<sup>6</sup>A methylated and expressed transcripts in DPSCs after odontogenic differentiation. B, The relative expression of m<sup>6</sup>A-related genes during DPSC mineralization in transcriptomic sequencing. Significance was determined using one-way analysis of variance (ANOVA) and post-hoc Dunnett tests: \**p* < 0.05, \*\**p* < 0.01, and \*\*\**p* < 0.001.



**Additional Figure 2:** Hematoxylin and eosin staining of the composites of  $\beta$ -TCP/HA scaffolds and DPSCs transfected with METTL3 knockdown or overexpression lentiviral vectors after subcutaneous transplantation of nude mice for 4 weeks.

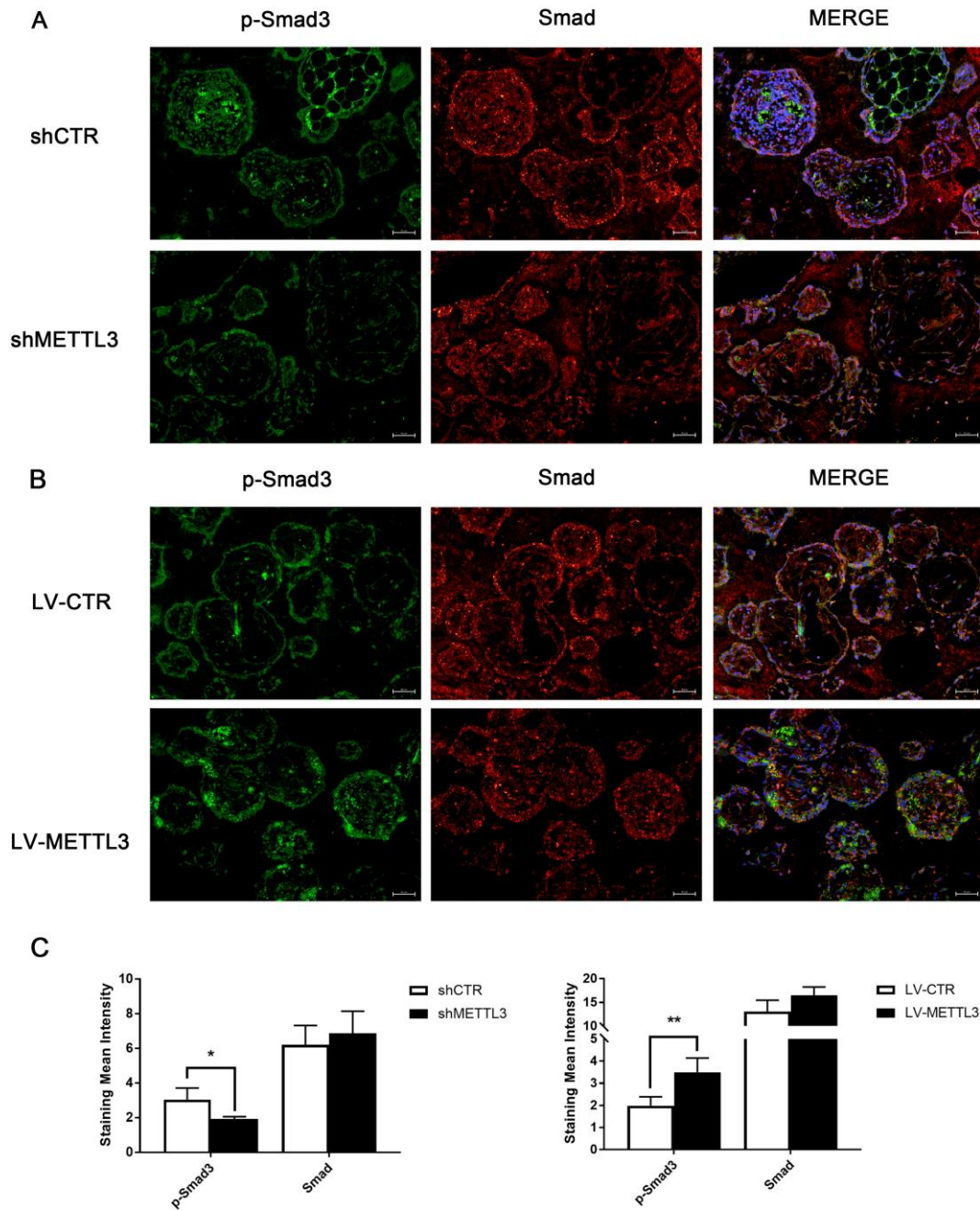


**Additional Figure 3:** Volcano plots of DEGs in OM-DPSCs after METTL3 inhibition by transcriptome sequencing (vertical lines represent >2.0-fold-change, horizontal lines for  $p$  values <0.05). Red dots indicate upregulated genes, and blue dots indicate downregulated genes.



**Additional Figure 4:** A, Immunofluorescence staining showed the expression and location of METTL3 (red fluorescence) and NOG (green fluorescence) in undifferentiated and differentiated DPSCs. B, The expression level and colocalization coefficient of METTL3 and NOG evaluated by imageJ. Significance was determined via ANOVA or Student's  $t$  test; the data are presented as the mean  $\pm$  SD ( $n \geq 3$ ). \* $p < 0.05$ . \*\* $p < 0.01$ . \*\*\* $p < 0.001$ .





**Additional Figure 5:** A, Immunofluorescence staining showed the p-Smad3 and Smad expression in the composites of  $\beta$ -TCP/HA scaffolds with METTL3-knockdown DPSCs after subcutaneous transplantation in nude mice for 4 weeks. B, Subcutaneous transplantation of DPSCs transduced with METTL3 overexpression and control lentivirus. C, The expression level of p-Smad3 and Smad evaluated by imageJ. Significance was determined via ANOVA or Student's t test; the data are presented as the mean  $\pm$  SD ( $n \geq 3$ ). \* $p < 0.05$ . \*\* $p < 0.01$ . \*\*\* $p < 0.001$ .