Supporting Information

# Coaxial Nanofibrous Scaffolds Mimicking the Extracellular Matrix Transition in Wound Healing Process Promote Skin Regeneration through Stimulating Immunomodulation

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**1. Supporting Figures S1-S5**

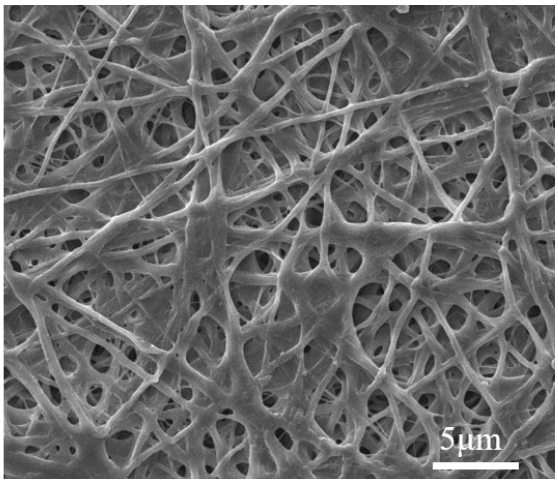


Figure S1. SEM image of coaxial scaffolds incubated in PBS for 14 days.

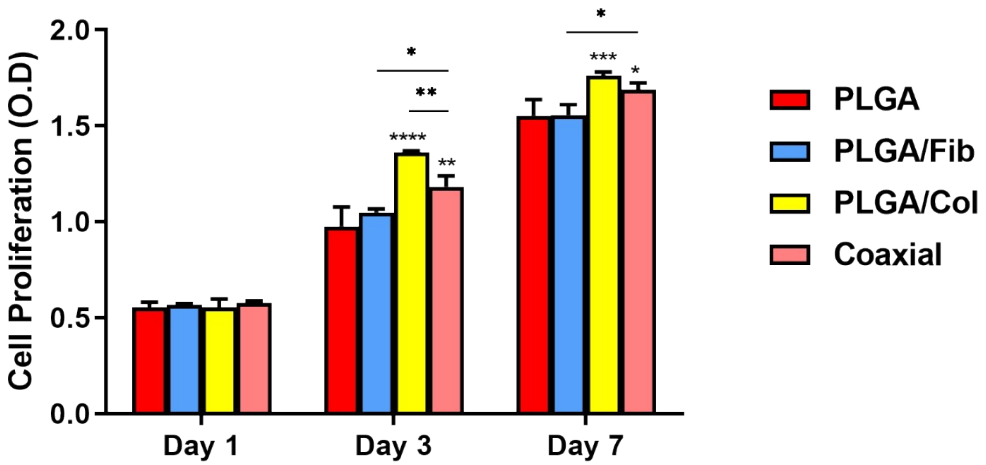


Figure S2. ASCs proliferation on different nanofibrous scaffolds. *Statistically significant, $p < 0.05$ *vs*. PLGA.

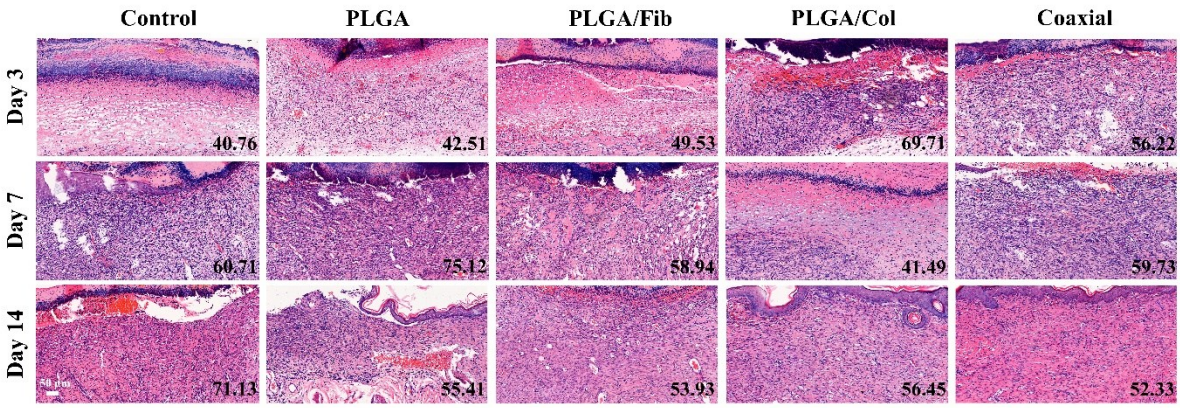


Figure S3. H&E staining of cross-sections of the wounds at different time points under high magnification.

Numbers indicate the percentage of infiltrated cells analysed by ImageJ 2.

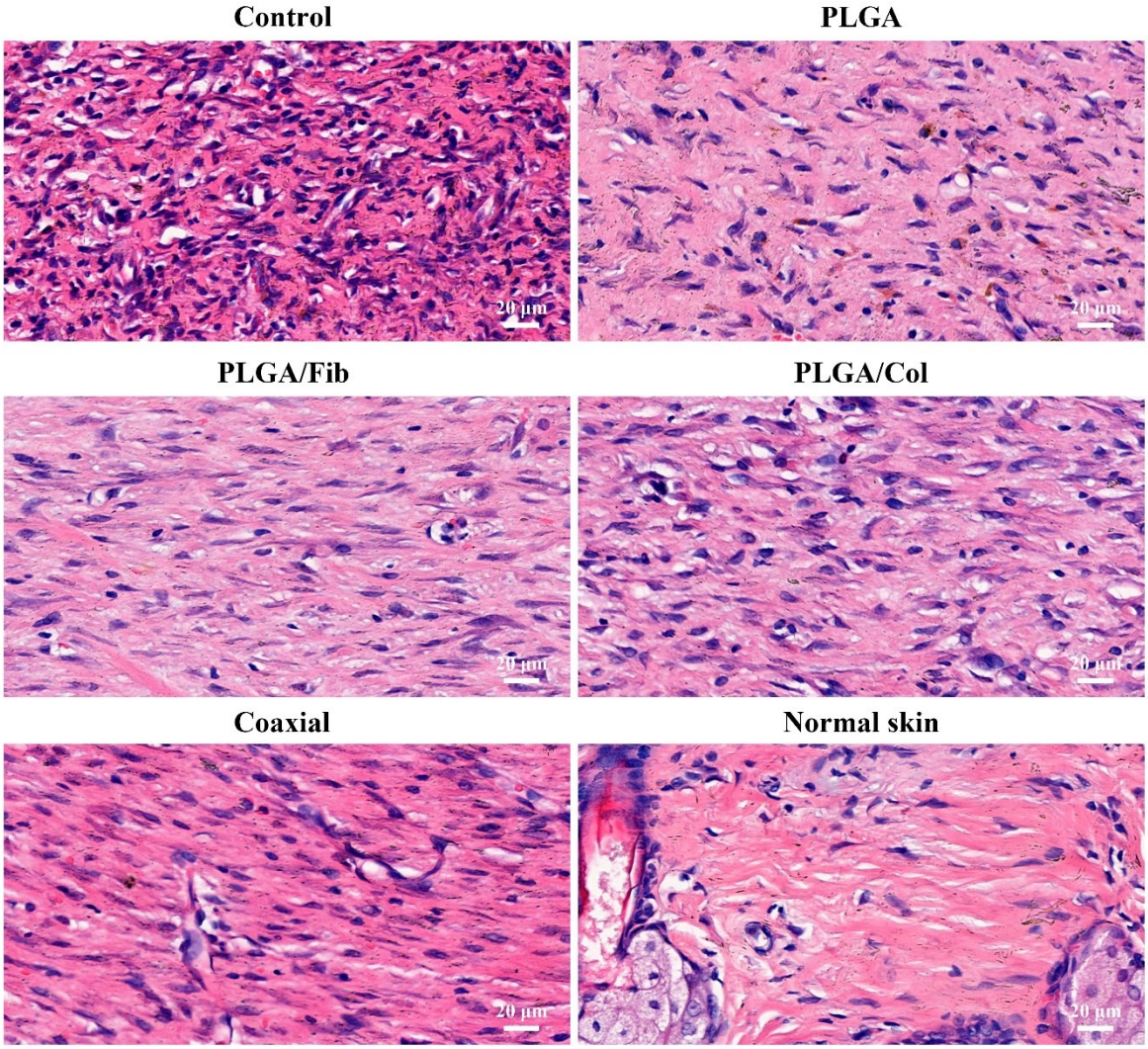


Figure S4. Representative H&E images of granulation tissue treated by different groups at day 14.

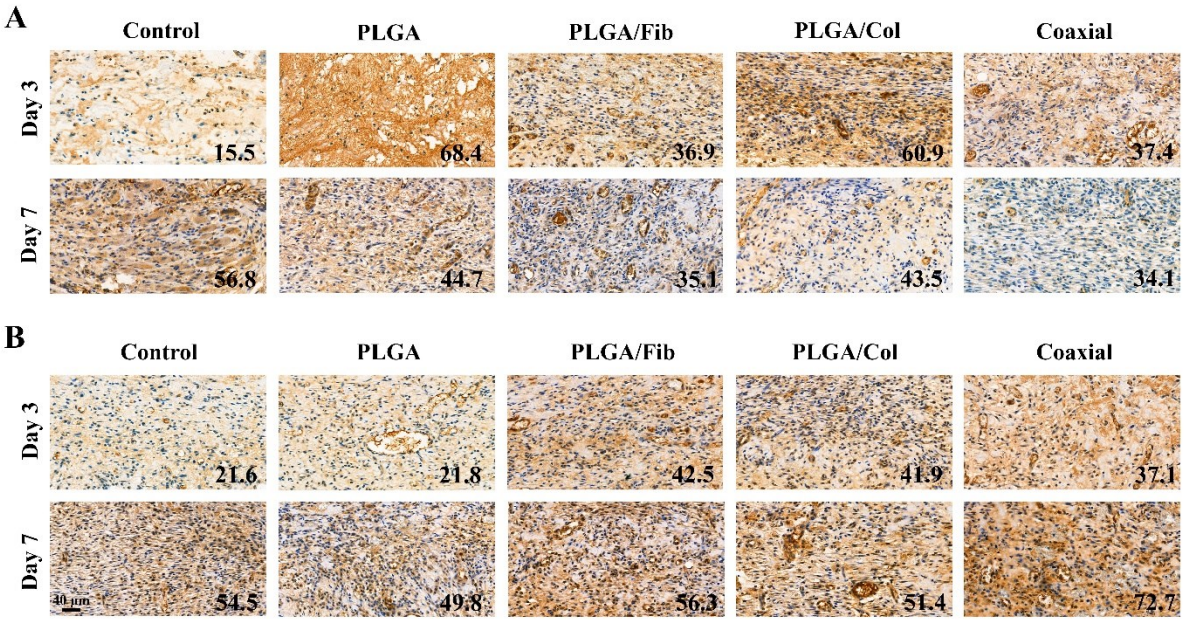


Figure S5. Immunohistochemical staining of (A) CD80 and (B) CD206 on day 3 and 7 under high magnification. Numbers indicate the percentage of positive staining analysed by ImageJ 2.

**2. Supporting Tables S1-S4**

Table S1 Characterization of nanofibrous scaffolds.

| | Average diameter / nm | Tensile strength / MPa |
|---|---|---|
| PLGA | 425.0 ± 74.8 | 22.4 ± 2.3 |
| PLGA/Fib | 439.1 ± 62.1 | 20.9 ± 1.2 |
| PLGA/Col | 466.8 ± 41.8 | 23.4 ± 1.2 |
| Coaxial | 447.3 ± 52.3 | 24.8 ± 3.6 |

Table S2 Normalized CD206/CD80 ratio in the wound beds.

| Normalized CD206/CD80 ratio | Control | PLGA | PLGA/Fib | PLGA/Col | Coaxial |
|---|---|---|---|---|---|
| Day 3 | 1.00 | 0.28 | 0.83 | 0.49 | 0.71 |
| Day 7 | 1.00 | 1.16 | 1.67 | 1.23 | 2.22 |

Table S3 Wound healing and immunomodulation related gene primer pairs used in the qRT-PCR

| Genes | Primer sequences |
|---|---|
| Col I | Forward: 5’-ATGCCGCGACCTCAAGATG-3’ |
| | Reverse: 5’-TGAGGCACAGACGGCTGAGTA-3’ |
| Col III | Forward: 5’-AGGTCCTGCGGGTAACACT-3’ |
| | Reverse: 5’-ACTTTCACCCTTGACACCCTG-3’ |
| TGF-β1 | Forward: 5’-CAGTACAGCAAGGTCCTTGC-3’ |
| | Reverse: 5’-ACGTAGTAGACGATGGGCAG-3’ |
| VEGF | Forward: 5’-GTCCCATGAAGTGATCAAGTTC-3’ |
| | Reverse: 5’-TCTGCATGGTGATGTTGCTCTCTG-3’ |
| bFGF | Forward: 5’-GGCTTCTTCCTCCTGCGCATCCA-3’ |
| | Reverse: 5’-GCTCTTAGCAGACATTGGAAGA-3’ |
| COX-2 | Forward: 5’-CAGAGCAGGCAGATGAAATACCAG-3’ |
| | Reverse: 5’-TTTCTACCAGAAGGGCAGGATACAG-3’ |
| TSG-6 | Forward: 5’-GTGGAGATGAGCTTCCAGATGAC-3’ |
| | Reverse: 5’-GGATACAGGATCCATTGCAACA-3’ |
| GAPDH | Forward: 5’-CTCCCACTCTTCCACCTTCG-3’ |
| | Reverse: 5’-TTGCTGTAGCCGTATTCATT-3’ |

Table S4 Inflammation related gene primer pairs used in the qRT-PCR

| Genes | Primer sequences |
|---|---|
| TNFα | Forward: 5’-CTGAACTTCGGGGTGATCGG-3’ |
| | Reverse: 5’-GGCTTGTCACTCGAATTTTGAGA-3’ |
| IL1β | Forward: 5’-TGGAGAGTGTGGATCCCAAG-3’ |
| | Reverse: 5’-GGTGCTGATGTACCAGTTGG-3’ |
| IL6 | Forward: 5’-ATAGTCCTTCCTACCCCAATTTCC-3’ |
| | Reverse: 5’-GATGAATTGGATGGTCTTGGTCC-3’ |

| | |
|---|---|
| iNOS | Forward: 5’-GAGAVGVAVAGGVAGAGG-3’ |
| | Reverse: 5’-CAGGCACACGCAATGATGG-3’ |
| Arg | Forward: 5’-CATATCTGCCAAGGACATCG-3’ |
| | Reverse: 5’-GGTCTCTTCCATCACTTTGC-3’ |
| IL1ra | Forward: 5’-CTCCAGCTGGAGGAAGTTAAC-3’ |
| | Reverse: 5’-CTGACTCAAAGCTGGTGGTG-3’ |
| IL10 | Forward: 5’-GAGAAGCATGGCCCAGAAATC-3’ |
| | Reverse: 5’-GAGAAATCGATGACAGCGCC-3’ |
| GAPDH | Forward: 5’-CTCCCACTCTTCCACCTTCG-3’ |
| | Reverse: 5’-TTGCTGTAGCCGTATTCATT-3’ |