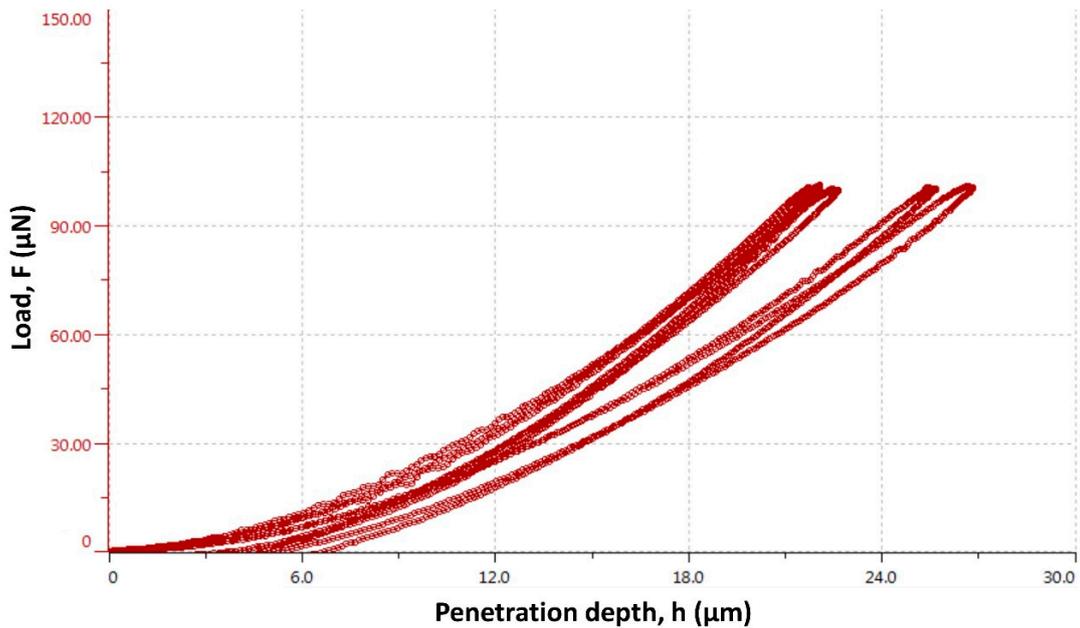
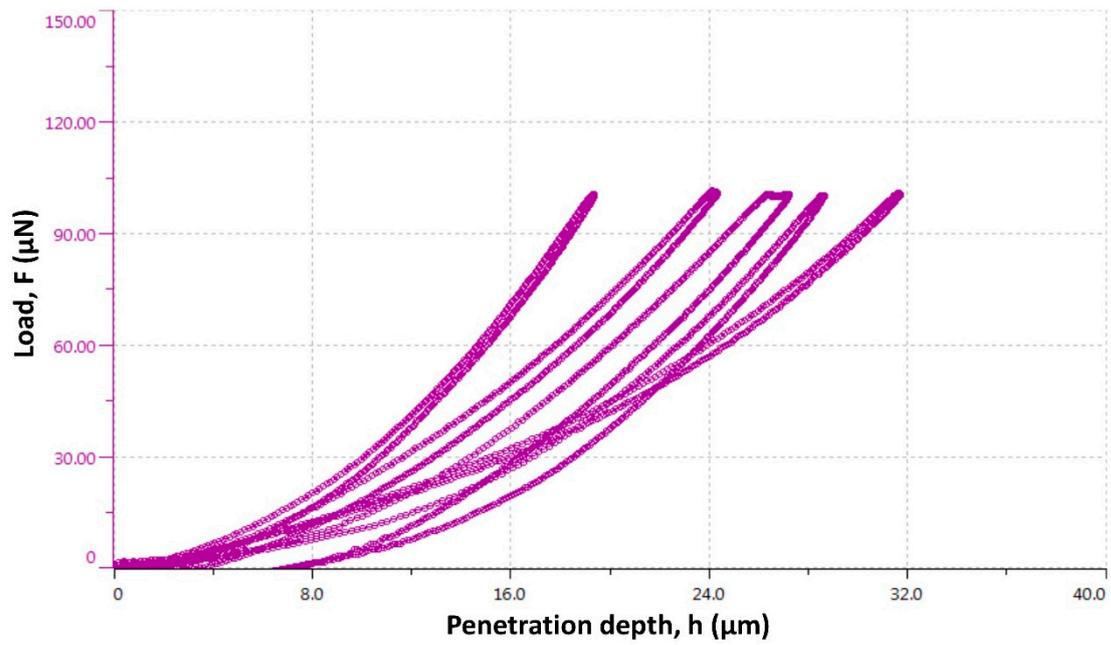


**Figure S1.** Typical, idealized load-indentation curve of a Bioindenter™ experiment. (1) describes the loading curve; (2), the unloading curve. According to the method described by Oliver and Pharr, the Young's modulus can be calculated from values of the load-indentation curve and the geometric parameters of the indenter [76]. The tangent (3) at the point of the maximum indentation depth ( $h_m$ ) is used to calculate the contact stiffness  $S$  (see Equation (1)).  $F_m$  is the maximum force during the experiment, yielding  $h_m$ .  $h_p$  describes the permanent indentation depth  $h$  after omission of the load  $F$ .  $h_r$  is the theoretical intersection between the tangent (3) and the  $x$ -axis.

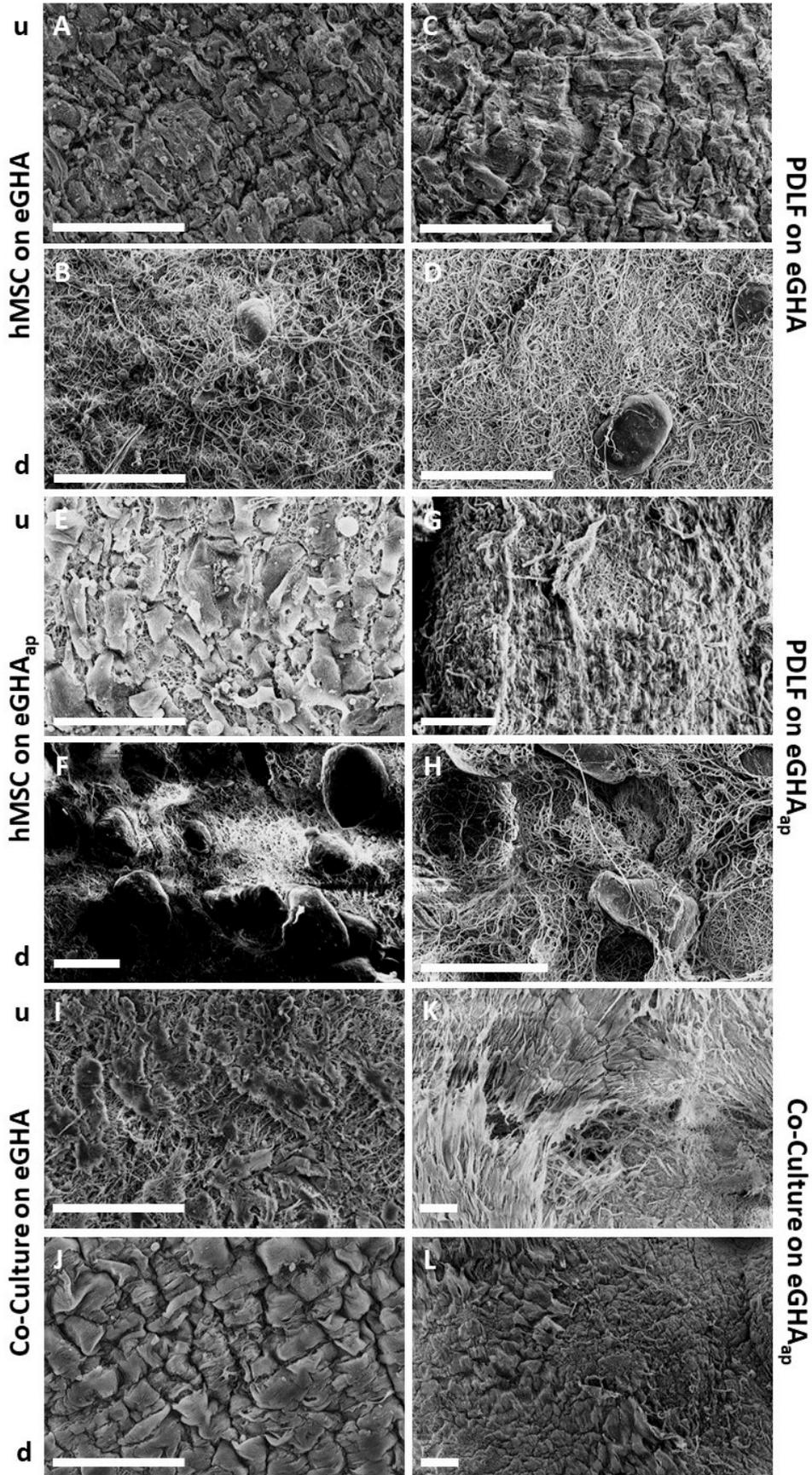


**Figure S2.** Exemplary load-indentation curve of an eGHA scaffold. The scaffold was prepared as described in the Material and Methods section. The graph shows the load-indentation curves of five subsequent measurements of the same sample. The load  $F$  is plotted on the  $y$ -axis, while the penetration depth  $h$  is plotted on the  $x$ -axis. For this scaffold, the calculated Young's modulus was  $6.41 \pm 0.59$  kPa.



**Figure S3.** Exemplary load-indentation curve of an eGHA<sub>ap</sub> scaffold. The scaffold was prepared as described in the Material and Methods section. The graph shows the load-indentation curves of five subsequent measurements of the same sample. The load  $F$  is plotted on the  $y$ -axis, while the penetration depth  $h$  is plotted on the  $x$ -axis. For this scaffold, the calculated Young's modulus was  $6.45 \pm 0.97$  kPa.

10 d



**Figure S4.** Scanning electron micrographs of eGHA/eGHA<sub>ap</sub> scaffolds after 10 d. hMSCs (A,B,E,F), PDLFs (C,D,G,H), and cocultures of both (I–L) were seeded on either eGHA (A–D,I,J) or eGHA<sub>ap</sub> scaffolds (E–H,K,L) and prepared for scanning electron microscopy (SEM) analysis after 10 d. The upsides (u) of the monocultures (A,C,E,G) were densely populated with either hMSCs or PDLFs, while the downsides (d) (B,D,F,H) illustrated the geometric configurations of the nonwovens. In the cocultures, (u) were populated by hMSCs (I,K) and (d) with PDLFs (J,L). Details are given in the main text. All scaffolds, irrespective of the presence of additional porosity, were densely covered with the indicated cells, proving the overall suitability of the eGHA/eGHA<sub>ap</sub> nonwovens for the adhesion and spreading of periodontal cells. The cell morphologies could be described as polygonal or spindle-like. Scale bars represent 100  $\mu\text{m}$ .

**Table S1.** Quantitative assessment of the cell densities (cells/ $\mu\text{m}^2$ ) on eGHA and eGHA<sub>ap</sub> nonwovens populated with hMSCs, PDLFs, and cocultures for 3, 7, 10, 14, and 21 d. The number (N) of evaluated samples per condition is indicated in the fourth column. The median (fifth column) and mean calculated cell densities (sixth column) and the corresponding standard deviations (SD, seventh column) are also depicted.

|           |      | N                  | Median (cells/ $\mu\text{m}^2$ ) | Mean (cells/ $\mu\text{m}^2$ ) | SD (cells/ $\mu\text{m}^2$ ) |               |               |
|-----------|------|--------------------|----------------------------------|--------------------------------|------------------------------|---------------|---------------|
| hMSC      | 3 d  | eGHA               | 6                                | 0.0098372                      | 0.008729                     | 0.0019555     |               |
|           |      | eGHA <sub>ap</sub> | 7                                | 0.0731069                      | 0.0729291                    | 0.049423      |               |
|           | 7 d  | eGHA               | 2                                | 0.0026622                      | 0.0026622                    | 0.0015154     |               |
|           |      | eGHA <sub>ap</sub> | 6                                | 0.0658464                      | 0.0777959                    | 0.0398618     |               |
|           | 10 d | eGHA               | 5                                | 0.02066                        | 0.0258829                    | 0.0117035     |               |
|           |      | eGHA <sub>ap</sub> | 2                                | 0.0439267                      | 0.0439267                    | 0.0142013     |               |
|           | 14 d | eGHA               | 7                                | 0.0250599                      | 0.0371012                    | 0.0331185     |               |
|           |      | eGHA <sub>ap</sub> | 4                                | 0.0205074                      | 0.0222475                    | 0.0157218     |               |
|           | 21 d | eGHA               | 7                                | 0.0296688                      | 0.0300406                    | 0.0137333     |               |
|           |      | eGHA <sub>ap</sub> | 5                                | 0.044212                       | 0.0419517                    | 0.0209356     |               |
|           | PDLF | 3 d                | eGHA                             | not evaluable                  | not evaluable                | not evaluable | not evaluable |
|           |      |                    | eGHA <sub>ap</sub>               | 7                              | 0.0573319                    | 0.0621296     | 0.0263405     |
| 7 d       |      | eGHA               | 5                                | 0.0051102                      | 0.0059401                    | 0.0039619     |               |
|           |      | eGHA <sub>ap</sub> | 7                                | 0.1630009                      | 0.1685361                    | 0.0269491     |               |
| 10 d      |      | eGHA               | 5                                | 0.0596111                      | 0.06095                      | 0.0151834     |               |
|           |      | eGHA <sub>ap</sub> | 5                                | 0.394736                       | 0.2959878                    | 0.1899214     |               |
| 14 d      |      | eGHA               | 3                                | 0.0997332                      | 0.1115                       | 0.0280429     |               |
|           |      | eGHA <sub>ap</sub> | 5                                | 0.1330316                      | 0.155904                     | 0.0529579     |               |
| 21 d      |      | eGHA               | 10                               | 0.0883228                      | 0.0943171                    | 0.0376992     |               |
|           |      | eGHA <sub>ap</sub> | 5                                | 0.3205851                      | 0.3225946                    | 0.2132816     |               |
| Coculture |      | 3 d                | eGHA                             | 5                              | 0.0070459                    | 0.0066426     | 0.0016389     |
|           |      |                    | eGHA <sub>ap</sub>               | 6                              | 0.008123                     | 0.0084105     | 0.003103      |
|           | 7 d  | eGHA               | 6                                | 0.0222034                      | 0.0463756                    | 0.0422479     |               |
|           |      | eGHA <sub>ap</sub> | 10                               | 0.0931795                      | 0.1105075                    | 0.042763      |               |
|           | 10 d | eGHA               | 4                                | 0.0492225                      | 0.0511814                    | 0.0121283     |               |
|           |      | eGHA <sub>ap</sub> | 4                                | 0.0449748                      | 0.070117                     | 0.0514661     |               |
|           | 14 d | eGHA               | 8                                | 0.1026672                      | 0.0839942                    | 0.0500624     |               |
|           |      | eGHA <sub>ap</sub> | 10                               | 0.1524226                      | 0.1753802                    | 0.0486237     |               |
|           | 21 d | eGHA               | 9                                | 0.0899736                      | 0.117514                     | 0.1117002     |               |
|           |      | eGHA <sub>ap</sub> | 9                                | 0.1108366                      | 0.2001065                    | 0.1171855     |               |

**Table S2.** Quantitative assessment of the cell penetration depths ( $\mu\text{m}$ ) on eGHA and eGHA<sub>ap</sub> nonwovens populated with hMSCs, PDLFs, and cocultures for 3, 7, 10, 14, and 21 d. The number (N) of evaluated samples per condition is indicated in the fourth column. The median (fifth column) and mean calculated cell penetration depths (sixth column) and the corresponding standard deviations (SD, seventh column) are also depicted.

|           |      | N                  | Median ( $\mu\text{m}$ ) | Mean ( $\mu\text{m}$ ) | SD ( $\mu\text{m}$ ) |               |
|-----------|------|--------------------|--------------------------|------------------------|----------------------|---------------|
| hMSC      | 3 d  | eGHA               | 6                        | 85.25728               | 86.29339             | 32.91673      |
|           |      | eGHA <sub>ap</sub> | 7                        | 79.0406                | 95.02634             | 33.01124      |
|           | 7 d  | eGHA               | 2                        | 136.3228               | 136.3228             | 98.59273      |
|           |      | eGHA <sub>ap</sub> | 6                        | 129.6621               | 151.2725             | 60.20134      |
|           | 10 d | eGHA               | 5                        | 658.9677               | 580.9928             | 223.7223      |
|           |      | eGHA <sub>ap</sub> | 2                        | 164.7419               | 164.7419             | 53.37823      |
|           | 14 d | eGHA               | 7                        | 201.5979               | 212.6357             | 89.83667      |
|           |      | eGHA <sub>ap</sub> | 4                        | 153.6407               | 153.8627             | 33.84394      |
|           | 21   | eGHA               | 7                        | 544.4033               | 500.2522             | 199.0847      |
|           |      | eGHA <sub>ap</sub> | 5                        | 258.4361               | 208.7027             | 96.8738       |
| PDLF      | 3 d  | eGHA               | not evaluable            | not evaluable          | not evaluable        | not evaluable |
|           |      | eGHA <sub>ap</sub> | 7                        | 39.96435               | 41.61367             | 12.98595      |
|           | 7 d  | eGHA               | 5                        | 31.97148               | 37.30006             | 24.42669      |
|           |      | eGHA <sub>ap</sub> | 7                        | 208.7027               | 209.8446             | 56.68004      |
|           | 10 d | eGHA               | 5                        | 288.6314               | 280.4609             | 202.6529      |
|           |      | eGHA <sub>ap</sub> | 5                        | 332.1482               | 353.9953             | 93.2345       |
|           | 14 d | eGHA               | 3                        | 143.8717               | 150.3844             | 40.36039      |
|           |      | eGHA <sub>ap</sub> | 5                        | 283.3028               | 302.3081             | 45.58195      |
|           | 21   | eGHA               | 10                       | 464.4746               | 378.862              | 201.6091      |
|           |      | eGHA <sub>ap</sub> | 5                        | 422.734                | 410.4783             | 173.4899      |
| Coculture | 3 d  | eGHA               | 3                        | 161.6336               | 190.0527             | 67.68788      |
|           |      | eGHA <sub>ap</sub> | 5                        | 41.74054               | 44.22721             | 21.98286      |
|           | 7 d  | eGHA               | 6                        | 133.2145               | 169.1824             | 79.15876      |
|           |      | eGHA <sub>ap</sub> | 10                       | 201.1539               | 204.4399             | 68.58984      |
|           | 10 d | eGHA               | 4                        | 342.3613               | 313.9422             | 133.6411      |
|           |      | eGHA <sub>ap</sub> | 4                        | 193.161                | 189.6086             | 55.56817      |
|           | 14 d | eGHA               | 8                        | 243.3385               | 235.7897             | 25.48875      |
|           |      | eGHA <sub>ap</sub> | 10                       | 301.5088               | 322.6455             | 81.27155      |
|           | 21   | eGHA               | 9                        | 340.141                | 308.0709             | 136.0314      |
|           |      | eGHA <sub>ap</sub> | 9                        | 247.779                | 234.2602             | 37.66508      |

|      |            |                    | N  | Mean [%] | SD [%]    |
|------|------------|--------------------|----|----------|-----------|
| 1 d  | empty      | eGHA               | 9  | 5.018161 | 1.218843  |
|      |            | eGHA <sub>sp</sub> | 9  | 3.429422 | 0.6687911 |
|      | hMSC       | eGHA               | 15 | 20.23757 | 3.064675  |
|      |            | eGHA <sub>sp</sub> | 15 | 26.39089 | 3.391284  |
|      | PDLF       | eGHA               | 15 | 20.55165 | 4.687862  |
|      |            | eGHA <sub>sp</sub> | 15 | 25.29921 | 6.680117  |
|      | Co-Culture | eGHA               | 18 | 30.90285 | 7.913007  |
|      |            | eGHA <sub>sp</sub> | 18 | 37.18791 | 10.79863  |
| 3 d  | empty      | eGHA               | 9  | 5.407166 | 0.881299  |
|      |            | eGHA <sub>sp</sub> | 9  | 3.618524 | 0.6053672 |
|      | hMSC       | eGHA               | 15 | 30.57237 | 20.84409  |
|      |            | eGHA <sub>sp</sub> | 15 | 25.60262 | 5.503864  |
|      | PDLF       | eGHA               | 15 | 31.43811 | 4.762844  |
|      |            | eGHA <sub>sp</sub> | 15 | 38.09538 | 11.41298  |
|      | Co-Culture | eGHA               | 18 | 42.51755 | 6.113959  |
|      |            | eGHA <sub>sp</sub> | 18 | 45.54092 | 10.46634  |
| 7 d  | empty      | eGHA               | 9  | 5.651971 | 1.861113  |
|      |            | eGHA <sub>sp</sub> | 9  | 3.888108 | 1.713384  |
|      | hMSC       | eGHA               | 15 | 25.18601 | 7.43302   |
|      |            | eGHA <sub>sp</sub> | 15 | 33.59624 | 6.677269  |
|      | PDLF       | eGHA               | 15 | 43.76426 | 6.762997  |
|      |            | eGHA <sub>sp</sub> | 15 | 62.66017 | 10.46475  |
|      | Co-Culture | eGHA               | 18 | 51.00284 | 9.842653  |
|      |            | eGHA <sub>sp</sub> | 18 | 63.55691 | 6.317564  |
| 10 d | empty      | eGHA               | 9  | 4.913745 | 0.9530044 |
|      |            | eGHA <sub>sp</sub> | 9  | 2.668842 | 0.9634505 |
|      | hMSC       | eGHA               | 15 | 28.06508 | 7.184959  |
|      |            | eGHA <sub>sp</sub> | 15 | 36.13512 | 8.734512  |
|      | PDLF       | eGHA               | 15 | 58.71049 | 3.33624   |
|      |            | eGHA <sub>sp</sub> | 15 | 69.78634 | 9.768611  |
|      | Co-Culture | eGHA               | 18 | 54.42184 | 6.433946  |
|      |            | eGHA <sub>sp</sub> | 18 | 71.92907 | 8.600621  |
| 14 d | empty      | eGHA               | 9  | 4.187012 | 0.6427488 |
|      |            | eGHA <sub>sp</sub> | 9  | 2.271207 | 0.4109346 |
|      | hMSC       | eGHA               | 15 | 20.32461 | 13.60807  |
|      |            | eGHA <sub>sp</sub> | 15 | 36.47787 | 5.438348  |
|      | PDLF       | eGHA               | 15 | 56.31027 | 10.83526  |
|      |            | eGHA <sub>sp</sub> | 15 | 68.51553 | 6.292524  |
|      | Co-Culture | eGHA               | 18 | 55.57401 | 9.230831  |
|      |            | eGHA <sub>sp</sub> | 18 | 64.31733 | 5.458969  |
| 21 d | empty      | eGHA               | 9  | 3.93965  | 0.9652498 |
|      |            | eGHA <sub>sp</sub> | 9  | 2.299034 | 0.4017685 |
|      | hMSC       | eGHA               | 15 | 23.55676 | 16.74048  |
|      |            | eGHA <sub>sp</sub> | 15 | 46.13785 | 6.420403  |
|      | PDLF       | eGHA               | 15 | 64.11949 | 13.56675  |
|      |            | eGHA <sub>sp</sub> | 15 | 67.5882  | 7.637498  |
|      | Co-Culture | eGHA               | 18 | 56.95062 | 9.03093   |
|      |            | eGHA <sub>sp</sub> | 18 | 67.31662 | 7.241198  |

**Table S3.** Quantitative assessment of the mean cellular metabolic activity (%) on eGHA and eGHA<sub>sp</sub> nonwovens populated with hMSCs, PDLFs, cocultures, and no cells (empty) for 1, 3, 7, 10, 14, and 21 d. The number (N) of evaluated samples per condition is indicated in the fourth column. The mean calculated cellular metabolic activities (fifth column) and the corresponding standard deviations (SD, sixth column) are also depicted.