

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.

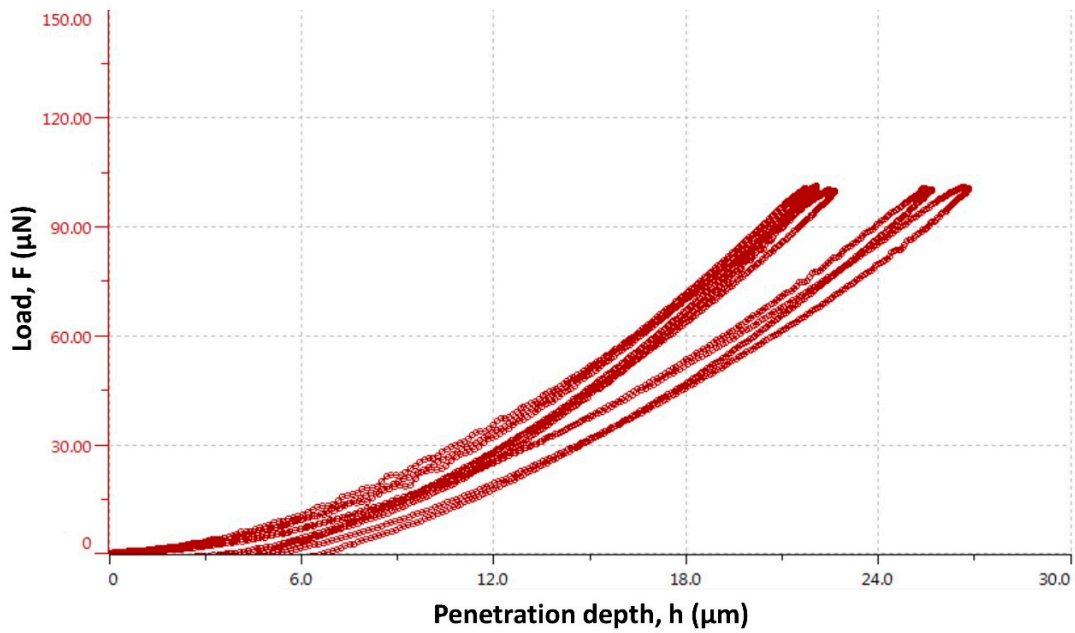


Figure S2. Exemplary load-indentation curve of an eGHA scaffold. The scaffold was prepared as described in the Material and Methods section. The graph shows the load-indentation curves of five subsequent measurements of the same sample. The load F is plotted on the y -axis, while the penetration depth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

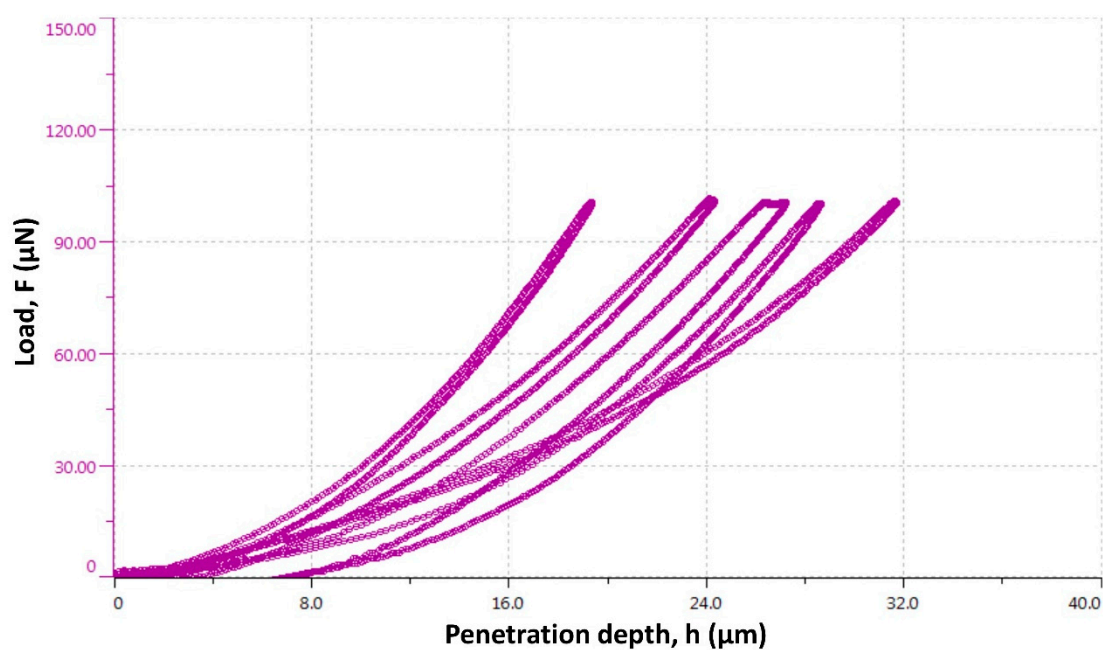


Figure S3. Exemplary load-indentation curve of an eGHA_{ap} scaffold. The scaffold was prepared as described in the Material and Methods section. The graph shows the load-indentation curves of five subsequent measurements of the same sample. The load F is plotted on the y -axis, while the penetration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

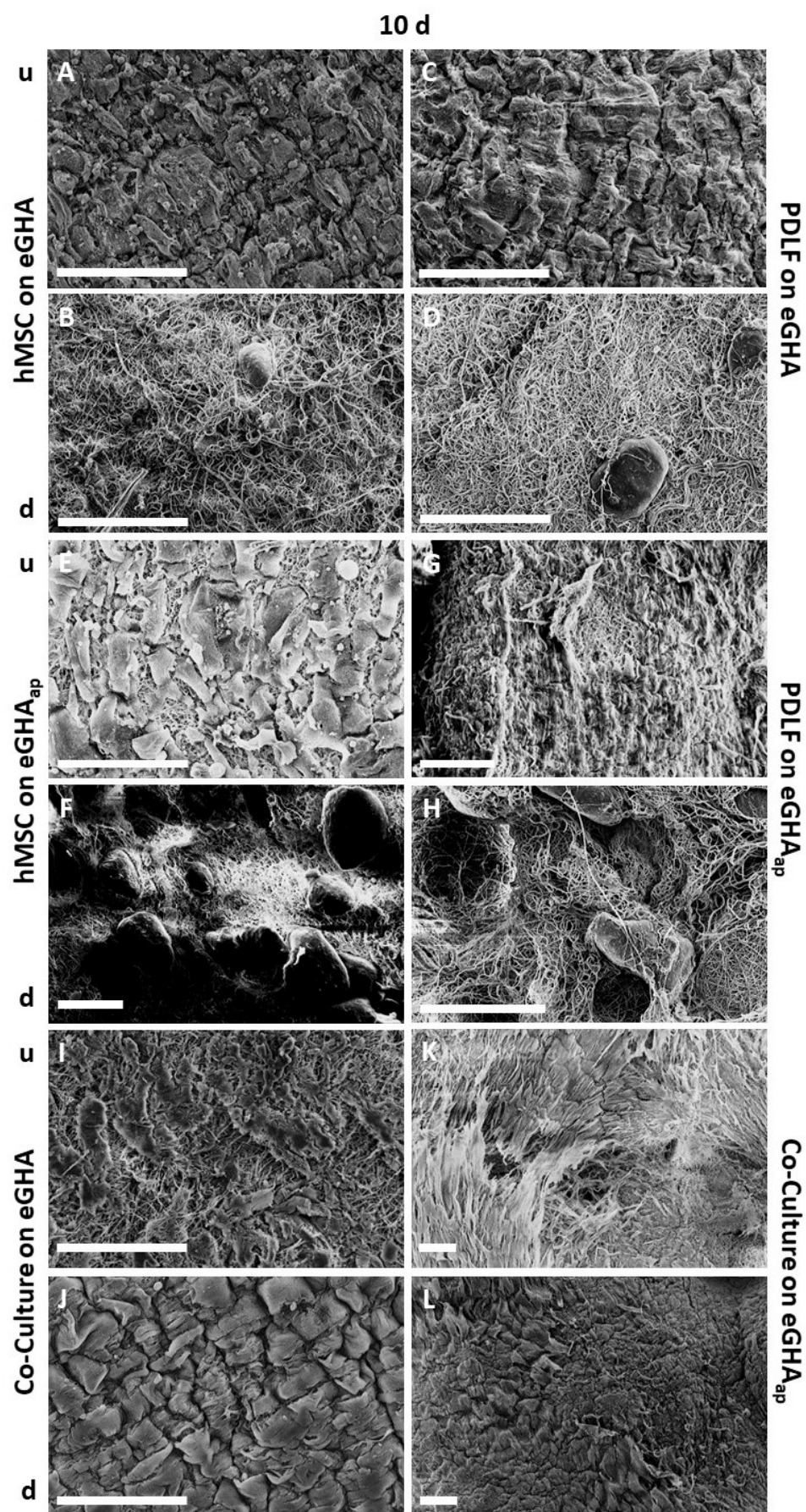


Figure S4. Scanning electron micrographs of eGHA/eGHA_{ap} scaffolds after 10 d. hMSCs (A,B,E,F), PDLFs (C,D,G,H), and cocultures of both (I–L) were seeded on either eGHA (A–D,I,J) or eGHA_{ap} scaffolds (E–H,K,L) and prepared for scanning electron microscopy (SEM) analysis after 10 d. The upsides (u) 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_{ap} nonwovens for the adhesion and spreading of periodontal cells. The cell morphologies could be described as polygonal or spindle-like. Scale bars represent 100 μm .

Table S1. Quantitative assessment of the cell densities (cells/ μm^2) on eGHA and eGHA_{ap} 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/ μm^2)	Mean (cells/ μm^2)	SD (cells/ μm^2)
hMSC	3 d	eGHA	6	0.0098372	0.008729
		eGHA _{ap}	7	0.0731069	0.0729291
	7 d	eGHA	2	0.0026622	0.0026622
		eGHA _{ap}	6	0.0658464	0.0777959
	10 d	eGHA	5	0.02066	0.0258829
		eGHA _{ap}	2	0.0439267	0.0439267
	14 d	eGHA	7	0.0250599	0.0371012
		eGHA _{ap}	4	0.0205074	0.0222475
	21 d	eGHA	7	0.0296688	0.0300406
		eGHA _{ap}	5	0.044212	0.0419517
PDLF	3 d	eGHA	not evaluable	not evaluable	not evaluable
		eGHA _{ap}	7	0.0573319	0.0621296
	7 d	eGHA	5	0.0051102	0.0059401
		eGHA _{ap}	7	0.1630009	0.1685361
	10 d	eGHA	5	0.0596111	0.06095
		eGHA _{ap}	5	0.394736	0.2959878
	14 d	eGHA	3	0.0997332	0.1115
		eGHA _{ap}	5	0.1330316	0.155904
	21 d	eGHA	10	0.0883228	0.0943171
		eGHA _{ap}	5	0.3205851	0.3225946
Coculture	3 d	eGHA	5	0.0070459	0.0066426
		eGHA _{ap}	6	0.008123	0.0084105
	7 d	eGHA	6	0.0222034	0.0463756
		eGHA _{ap}	10	0.0931795	0.1105075
	10 d	eGHA	4	0.0492225	0.0511814
		eGHA _{ap}	4	0.0449748	0.070117
	14 d	eGHA	8	0.1026672	0.0839942
		eGHA _{ap}	10	0.1524226	0.1753802
	21 d	eGHA	9	0.0899736	0.117514
		eGHA _{ap}	9	0.1108366	0.2001065

Table S2. Quantitative assessment of the cell penetration depths (μm) on eGHA and eGHA_{ap} 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 (μm)	Mean (μm)	SD (μm)
hMSC	3 d	eGHA	6	85.25728	86.29339	32.91673
		eGHA _{ap}	7	79.0406	95.02634	33.01124
	7 d	eGHA	2	136.3228	136.3228	98.59273
		eGHA _{ap}	6	129.6621	151.2725	60.20134
	10 d	eGHA	5	658.9677	580.9928	223.7223
		eGHA _{ap}	2	164.7419	164.7419	53.37823
	14 d	eGHA	7	201.5979	212.6357	89.83667
		eGHA _{ap}	4	153.6407	153.8627	33.84394
	21	eGHA	7	544.4033	500.2522	199.0847
		eGHA _{ap}	5	258.4361	208.7027	96.8738
PDLF	3 d	eGHA	not evaluable	not evaluable	not evaluable	not evaluable
		eGHA _{ap}	7	39.96435	41.61367	12.98595
	7 d	eGHA	5	31.97148	37.30006	24.42669
		eGHA _{ap}	7	208.7027	209.8446	56.68004
	10 d	eGHA	5	288.6314	280.4609	202.6529
		eGHA _{ap}	5	332.1482	353.9953	93.2345
	14 d	eGHA	3	143.8717	150.3844	40.36039
		eGHA _{ap}	5	283.3028	302.3081	45.58195
	21	eGHA	10	464.4746	378.862	201.6091
		eGHA _{ap}	5	422.734	410.4783	173.4899
Coculture	3 d	eGHA	3	161.6336	190.0527	67.68788
		eGHA _{ap}	5	41.74054	44.22721	21.98286
	7 d	eGHA	6	133.2145	169.1824	79.15876
		eGHA _{ap}	10	201.1539	204.4399	68.58984
	10 d	eGHA	4	342.3613	313.9422	133.6411
		eGHA _{ap}	4	193.161	189.6086	55.56817
	14 d	eGHA	8	243.3385	235.7897	25.48875
		eGHA _{ap}	10	301.5088	322.6455	81.27155
	21	eGHA	9	340.141	308.0709	136.0314
		eGHA _{ap}	9	247.779	234.2602	37.66508

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

Table S3. Quantitative assessment of the mean cellular metabolic activity (%) on eGHA and eGHA_{ap} 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.