1	Inhalable textile microplastic fibers impair airway epithelial growth
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3	Short title: Textile microplastics impair organoid growth
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32 Abstract (150 words)

33 We are continually exposed to microplastic fibers originating from textiles. High exposure 34 to microplastic fibers in nylon flock workers has been linked to the development of airway and interstitial lung disease, but the exact health effects of microplastic fibers on the lungs 35 36 are unknown. Here we determined effects of polyester and nylon textile microplastic fibers 37 on airway and alveolar epithelial cells using human and murine lung organoids. We 38 observed that the presence of particularly nylon microfibers had a negative impact on the growth and development of airway organoids. This effect was mediated by components 39 40 leaking from nylon. Moreover, our data suggested that microplastic textile fibers may 41 especially harm the developing airways or airways undergoing repair. Our results call for an 42 urgent need to assess exposure and inhalation levels in indoor environments to accurately 43 determine the actual risk of these fibers to human health.

46 Introduction

47 Plastic pollution is a pressing global concern and microplastics are a significant part of this 48 problem (1). High amounts of microplastics have been found in marine environments, air, soils, plants, and animals, which illustrates how omnipresent this relatively recent pollution 49 actually is (2). Microplastic pollution derives from personal care products, synthetic clothes, 50 and degradation of macroplastics (3, 4). Synthetic textile fibers are one of the most 51 prevalent types of microplastic waste observed, with an annual production of 60 million 52 metric tons, which equals 16% of the world's plastic pollution (1). These fibers are typically 53 54 composed of nylon or polyester and are released into the environment by wear and tear and 55 during washing and drying of garments (4-6).

56 The ubiquitous nature of microplastics in the environment inevitably leads to human exposure, which can occur through two main routes (7, 8). Firstly, through ingestion of 57 58 contaminated food and water and secondly via inhalation. Microplastics have been reported 59 both in indoor and outdoor air, with levels indoors being 2-5 times higher as compared to 60 outdoors (9, 10). Whether or not microfibers can deposit in lung tissue largely depends on the aerodynamic diameter of the fibers (7, 11). Lung deposition is most efficiently achieved 61 62 with aerodynamic diameters between 1-10 um (12), however, these sizes are difficult to 63 quantify in environmental samples due to limitations of the analytical techniques (9, 13). 64 Yet, plastic microfibers have been found in human lung tissue, suggesting inhalation does 65 indeed take place (14). Furthermore, several studies from workers in synthetic textile, flock and (poly)vinyl chloride industries suggest that inhalation of such microfibers is harmful, as 66 67 around 30% of factory workers developed work-related airway and interstitial lung disease (15-23). Moreover, exposure to particulate matter in air pollution, also containing 68 69 microplastics (24-26), has been associated with higher risk of developing asthma and an 70 increase in asthma symptoms in areas with higher levels of particulate matter air pollution 71 (27-29).

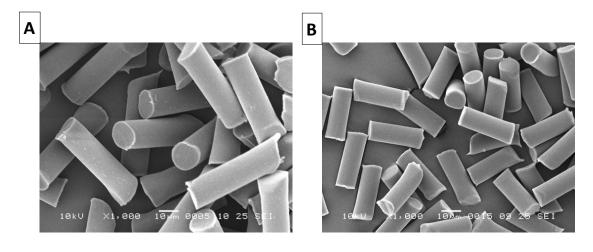
Despite the potential capacity for microplastic fibers to contribute to respiratory diseases, the health effects are greatly understudied and information providing evidence of potential human health effects of inhaled microplastics is lacking (9, 30, 31). In the present study, we therefore explored whether textile microplastic fibers can cause damage to lung tissue. As epithelial cells are the first to come into contact with inhaled fibers, we investigated effects of polyester and nylon microfibers on lung epithelial proliferation, differentiation, and

78	repair processes. For this we used lung organoids that are grown from primary lung
79	epithelial progenitor cells with support of a lung fibroblast cell line $(32, 33)$. The epithelial
80	progenitors can develop into organoids consisting of alveolar epithelial cells or organoids
81	consisting of airway epithelial cells. We found that in particular nylon microfibers
82	negatively impacted developing airway organoids, while developing alveolar organoids and
83	already developed organoids of both types appeared to be less affected. This negative effect
84	was caused by still unknown leachates from nylon that particularly inhibit differentiation of
85	airway epithelial cells. We therefore urge for assessment of exposure levels in indoor
86	environments and actual lung deposition to accurately determine the risk of these fibers to
87	human health.

89 **Results**

90 Characterization of reference microfibers

91 To produce reference textile fibers, we used a method previous described by us to 92 reproducibly generate fibers of specific lengths (34). Fibers are commonly defined as 93 having a length to diameter ratio of 3:1 (35). The smallest polyester diameter commercially 94 available is 15 μ m, while nylon is available in 10 μ m diameters, therefore the smallest 95 fibers we could produce were 45 and 30 µm for polyester and nylon respectively. The fibers 96 we produced had a median size of 15x52 µm for polyester and 12x31 µm for nylon (Table 97 S1). They were rod-shaped with a circular cross-section and had a smooth surface, as shown 98 with scanning electron microscopy (SEM) (Figure 1A and B). For our polyester fibers 99 energy dispersive X-ray (EDX) analysis confirmed the presence of carbon and oxygen 00 (Figure S1A). The recorded micro-Fourier transform infrared (µFTIR) spectrum showed 01 characteristic absorbance peaks of polyester (Figure S1B). The EDX spectrum for nylon 02 confirmed the presence of carbon, nitrogen and oxygen (Figure S1C) and the µFTIR 03 spectrum showed characteristic nylon absorbance peaks (Figure S1D).



- Figure 1. Morphology of reference microplastic fibers of standardized dimensions.
 Representative SEM micrographs of (A) polyester microfibers (15x52 μm) and (B) nylon
 microfibers (12x31 μm).
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10 Nylon microfibers inhibited growth of murine and human lung organoids

11 Possible effects of microplastic fibers on lung epithelial proliferation, differentiation, and 12 repair processes were assessed in vitro using both murine and a human lung organoids. For this, we first assessed the effects of several of several doses of fibers on organoid growth 13 14 ranging from 2000-5000 fibers per well (Figure S2). The fibers were dispersed into the 15 matrigel in which the organoids grow at the same time as the isolated epithelial cells and fibroblasts were added. We decided to continue with 5000 polyester or 5000 nylon fibers 16 17 per well, equivalent to 122 µg/ml polyester and 39 µg/ml nylon, as this concentration had 18 clear effects and was on the lower end of the spectrum of concentrations used in other 19 studies (7).

20 Murine lung organoids develop into two distinct phenotypes, i.e. acetylated α -tubulin-21 positive airway organoids (Figure 2A) and prosurfactant protein C-positive alveolar organoids (Figure 2B). We assessed the effects of our reference fibers on these two 22 23 structures separately. Exposure during 14 days to either polyester or nylon microfibers 24 significantly inhibited growth of these organoids (Figure 2C) compared to untreated 25 controls, reflected by fewer organoids being present (Figure 2D and E). The effect of nylon on airway organoids was most profound of the two types of plastic and the two types of 26 27 structures. Moreover, both airway and alveolar organoids were significantly smaller in size 28 following nylon microfiber exposure as compared to untreated controls (Figure 2F and G).

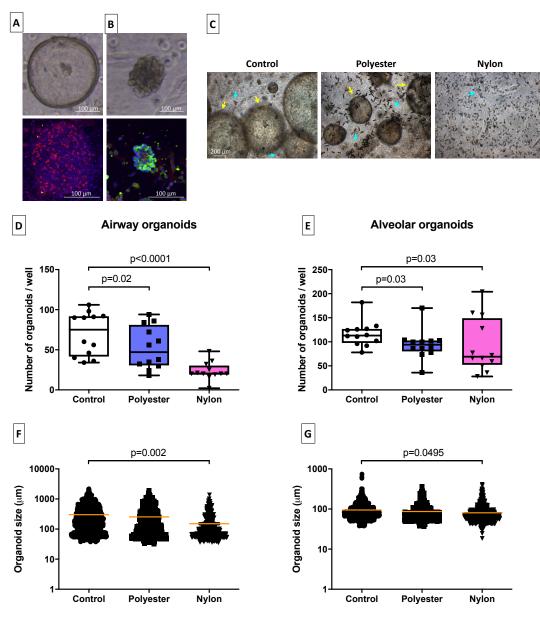


Figure 2. Effects of microplastic fibers on growth of murine lung organoids. Light microscopy images and fluorescence photographs of (A) acetylated α -tubulin-positive airway organoids (red) and (B) prosurfactant protein C-positive alveolar organoids (green). Nuclei were counterstained with DAPI (blue). (C) Representative light microscopy images of the different treatment conditions. Yellow arrows in the light microscopy images indicate airway organoids, whereas cyan arrows indicate alveolar organoids. (D and E) Quantification of the numbers and (F and G) quantification of the sizes of airway and alveolar lung organoids exposed for 14 days to no fibers, 5000 polyester, or 5000 nylon fibers (equivalent to 122 µg/ml polyester or 39 µg/ml polyester, n=12 independent isolations). Groups were compared using a Friedman test with Dunn's correction for multiple testing. P<0.05 was considered significant.

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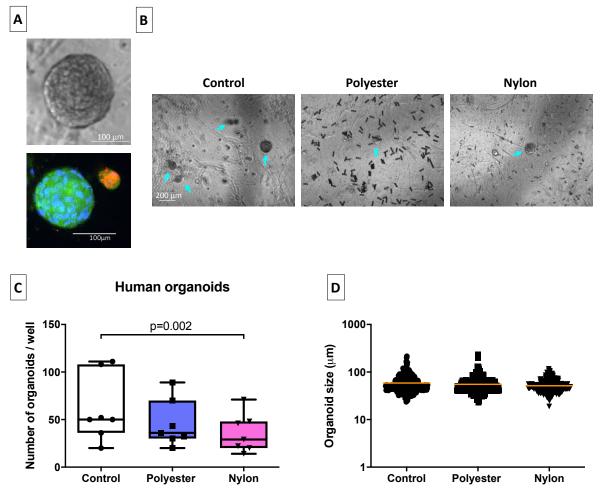
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Similar results were observed in human lung organoids, that mainly developed into alveolar
prosurfactant protein C-positive organoids or mixed alveolar/airway organoids positive for
both acetylated α-tubulin and prosurfactant protein C (Figure 3A). 14 day-exposure to nylon
microfibers resulted in significantly fewer human lung organoids (Figure 3B and C),
whereas the effects of polyester on organoid growth were less profound. The size of the
organoids was not affected by the presence of nylon microfibers (Figure 3D).



47 Figure 3. Influence of microplastic fibers on growth of human lung organoids. (A) The 48 morphology of the alveolar prosurfactant protein C-positive organoids (green) and mixed 49 acetylated α -tubulin/prosurfactant protein C-positive organoids (orange) as shown by light 50 and fluorescence microscopy. Nuclei were counterstained with DAPI (blue). (B) 51 Representative light microscopy images of all treatment conditions. Cyan arrows indicate 52 lung organoids. (C) Quantification of the numbers and (D) sizes of human lung organoids 53 following 14-day exposure to either no microfibers, 5000 polyester, or 5000 nylon fibers 54 (equivalent to 122 μ g/ml polyester or 39 μ g/ml polyester, n=7 independent isolations).

Groups were compared using a Friedman test with Dunn's correction for multiple testing. P < 0.05 was considered significant.

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Environmental microplastic fibers impaired lung organoid growth as well

In addition to reference microfibers, we also assessed effects of environmentally relevant 59 60 polyester and nylon fibers on murine lung organoids. These were made from white polyester and nylon fabrics purchased in a local fabric store and cut to sizes approximating 61 62 the reference fibers. First, we characterized morphology and chemical composition of these 63 fibers. For polyester, we observed a more heterogeneous size distribution as compared to 64 the reference fibers, with fibers having a median size of $17x63 \mu m$ (Figure 4A, Table S2), 65 but a comparable EDX and µFTIR spectrum (Figure S3A and B). The nylon fibers had a 66 disk-shaped appearance but similar dimensions as the reference nylon fibers (median 57x20 67 μm, Table S2). The EDX analysis revealed the expected C, N and O peaks for nylon (Figure 68 S3C) and the µFTIR spectrum showed characteristic nylon absorbance peaks (Figure S3D).

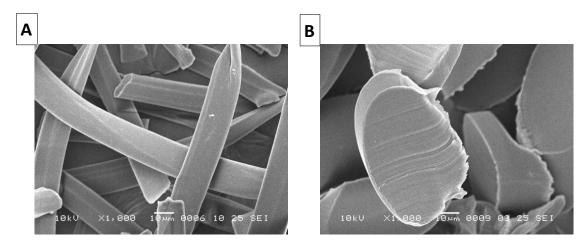
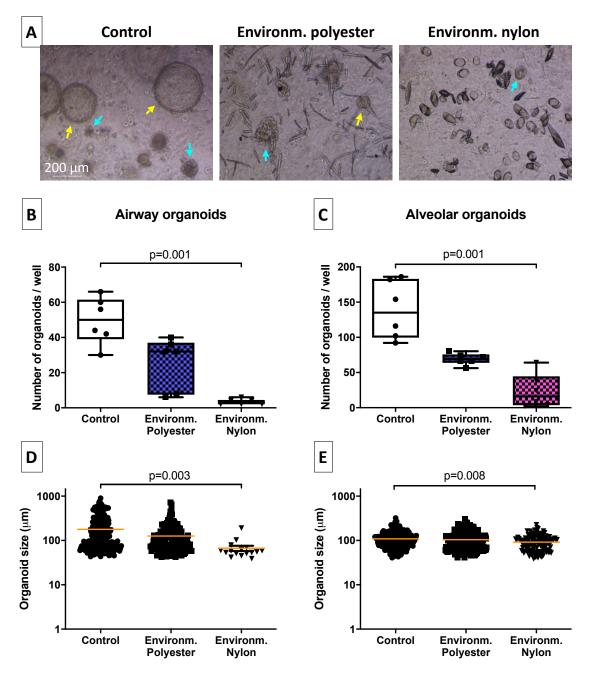


Figure 4. Morphology of environmental microplastic fibers. Representative SEM pictures of (A) polyester microfibers (17x63 μ m) and (B) nylon microfibers (57x20 μ m).

When exposing murine lung organoids to these environmentally relevant textile fibers, we
obtained results similar to the reference fibers: exposure to environmental nylon microfibers
resulted in markedly fewer lung organoids (Figure 5A, B and C) as well as smaller
organoids (Figure 5D and E).



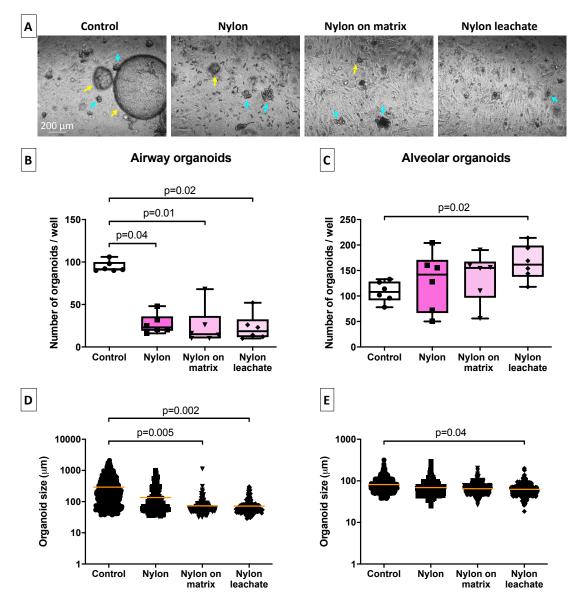
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Figure 5: Effect of environmentally relevant textile fibers on growth of murine lung organoids. (A) Representative light microscopy images of all treatment conditions. Yellow arrows in the light microscopy images indicate airway organoids, whereas cyan arrows indicate alveolar organoids. (B and C) Quantification of the numbers and (D and E) sizes of airway and alveolar organoids (n=6 independent isolations) following 14-day exposure to either no microfibers, 5000 polyester or 5000 nylon microfibers (approximately equivalent to 189 µg/ml polyester or 531 µg/ml nylon). Groups were compared using a Friedman test with Dunn's correction for multiple testing. P<0.05 was considered significant.

87 Leaching nylon components caused a reduction in lung organoid growth

88 Since organoid growth was mostly affected by both reference and environmentally relevant 89 nylon microfibers, we investigated whether this inhibition was caused by the physical 90 presence of fibers nearby the cells or by leaching components from these nylon fibers. 91 Therefore, we added nylon reference microfibers either on top of the 3D matrigel matrix 92 after it had set, thereby preventing direct contact with the cells, or added leachate of these 93 fibers to the medium surrounding the matrigel matrix. We found significantly fewer airway 94 organoids in the presence of nylon microfibers on top of the gel or their leachate (Figure 6A 95 and B), while the number of alveolar organoids was unaffected (fibers on top) or even 96 induced (leachate, Figure 6A and C). Additionally, the size of these airway organoids was 97 smaller as compared to untreated control organoids (Figure 6D), while only slightly 98 inhibiting the size of the alveolar organoids (Figure 6E). These data suggest that specifically 99 airway epithelial growth is inhibited by components leaching from nylon microplastics.



01 Figure 6. Impact of nylon reference microfibers and their leaching components on 02 growth of murine lung organoids. (A) Representative light microscopy images of all 03 treatment conditions. Yellow arrows in the light microscopy images indicate airway 04 organoids, whereas cyan arrows indicate alveolar organoids. (**B** and **C**) Ouantification of 05 the numbers and (**D** and **E**) sizes of airway and alveolar organoids following either direct 06 exposure to 5000 nylon microfibers or indirect exposure to nylon by adding 5000 07 microfibers (equivalent to 39 µg/ml nylon) on top of the 3D matrigel matrix or by adding 08 *nylon leachate to the culture medium (n=6 independent isolations). Groups were compared* 09 using a Friedman test with Dunn's correction for multiple testing. P<0.05 was considered 10 significant.

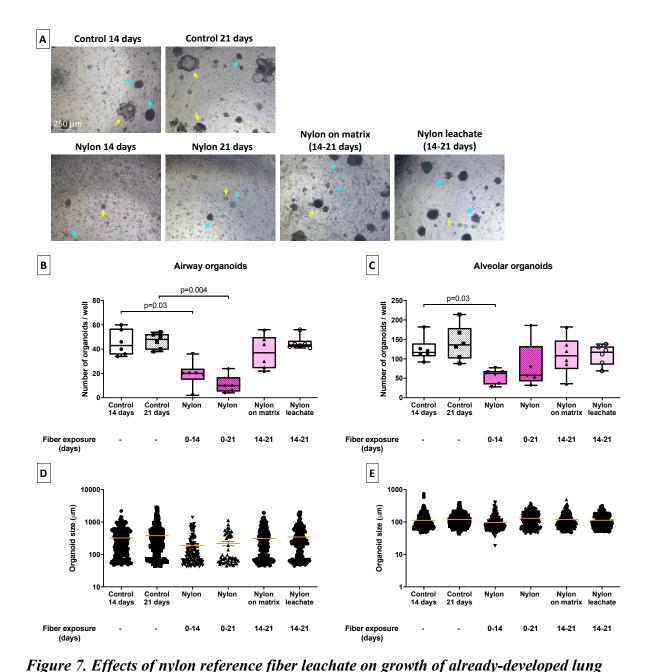
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12 We next determined the chemical identity of the components leaching from nylon reference 13 microfibers. Mass spectrometry analysis revealed high concentrations of cyclic nylon 14 oligomers (mono-, di- and trimers) in the leachate of nylon microfibers (Figure S4A), which 15 are known to develop as by-products during the production of nylon (36). Remarkably, 16 when exposing murine lung organoids to different concentrations of these isolated 17 oligomers separately or in combination, we observed no effects on either number or size of 18 organoids (Figure S4B-E showing the highest concentration that has been tested). These 19 data suggest that other components in nylon leachate are causing the inhibitory effects on 20 organoid growth.

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22 Leaching nylon components mainly affected developing organoids

23 As our experimental set-up specifically studied effects of microplastic fibers on developing 24 organoids, we next studied whether already-developed, mature organoids were also affected 25 by nylon microplastics. We therefore exposed organoids to nylon reference microfibers 26 during organoid formation as before (14-day incubation) and we additionally exposed fully 27 developed 14-day organoids to microfibers on top of the 3D matrigel matrix or to nylon 28 leachate for an additional 7 days. Interestingly, our data showed that the compounds 29 leaching from nylon mostly inhibited developing organoids and not already-developed 30 organoids (Figure 7A), as reflected by unchanged numbers of organoids (Figure 7B and C) 31 and unchanged sizes (Figure 7D and E) after treatment of developed organoids. This 32 suggests that these nylon leachates are mostly harmful to differentiation of epithelial 33 progenitors, but do not kill fully differentiated epithelial cells.



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36 organoids. (A) Representative light microscopy images of all treatment conditions. Yellow 37 arrows in the light microscopy images indicate airway organoids, whereas cyan arrows 38 indicate alveolar organoids. (**B** and **C**) Quantification of the numbers and (**D** and **E**) sizes 39 of airway and alveolar organoids following exposure to no or 5000 nylon microfibers (equivalent to 39 µg/ml nylon) for 14 or 21 days. A set of other organoids developed without 40 41 treatment for 14 days and were exposed to nylon by adding 5000 microfibers (equivalent to 42 39 µg/ml nylon) on top of the 3D matrix or by adding nylon leachate to the culture medium 43 for another 7 days (n=6 independent isolations). Groups were compared using a Kruskal-44 *Wallis test with Dunn's correction for multiple testing.* P < 0.05 was considered significant.

Exposure to nylon inhibited epithelial development pathways and stimulated expression of ribosome components

48 To better understand the mechanisms behind the damaging effects of the leaching nylon 49 components on in particular the growth of airway organoids, we performed bulk RNA-50 sequencing (RNAseq) analysis on EpCAM+ cells and fibroblasts resorted from organoid 51 cultures exposed to two different concentrations of nylon fibers (2000 or 5000 fibers) or not. Both conditions had an enormous impact on epithelial gene expression as depicted by 52 the volcano plots (Figure 8A-D). Exposure to 2000 nylon fibers (equivalent to 16 µg/ml 53 54 nylon) resulted in 16455 transcripts being differentially expressed at least two-fold 55 compared to nonexposed controls, with an q value <0.05 (p value corrected for the false 56 discovery rate), with most being downregulated (Figure 8A and C). Exposure to 5000 nylon 57 fibers (equivalent to 39 µg/ml nylon) resulted in 39395 transcripts being differentially 58 expressed at least two-fold compared to nonexposed controls, with most being upregulated 59 (Figure 8B and D).

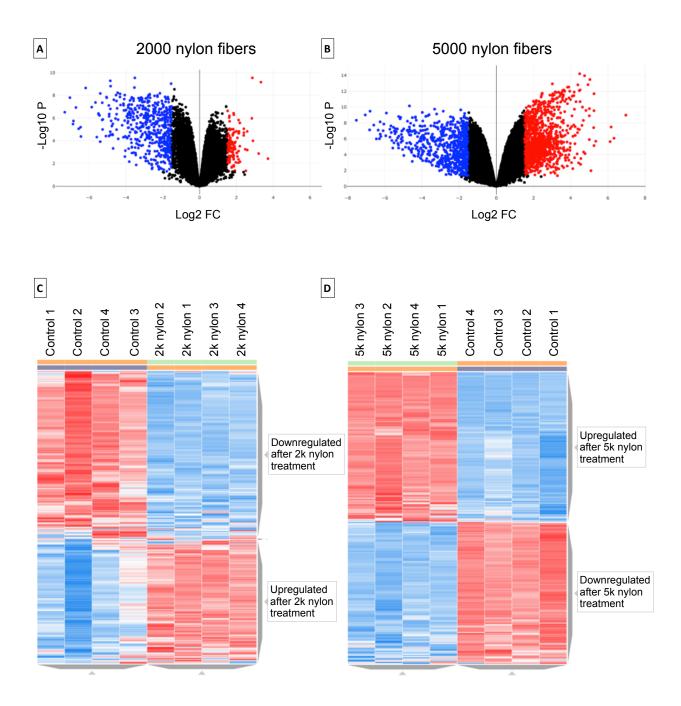
60 To reduce the number of transcripts, we then selected only those transcripts that had an 61 average basemean expression of at least 10 and were significantly (q value <0.05) up or 62 downregulated in both exposure conditions of 2000 and 5000 nylon fibers compared to 63 nonexposed controls. This resulted in 10764 transcripts that were differentially expressed 64 compared to nonexposed controls, with 5522 being downregulated and 5242 being 65 upregulated. The downregulated transcripts were then sorted on the lowest q value for 66 exposure to 2000 fibers and the upregulated transcripts were sorted on the lowest q value 67 for exposure to 5000 fibers and the top 500 genes of each were used for pathway analysis 68 using Metascape (37).

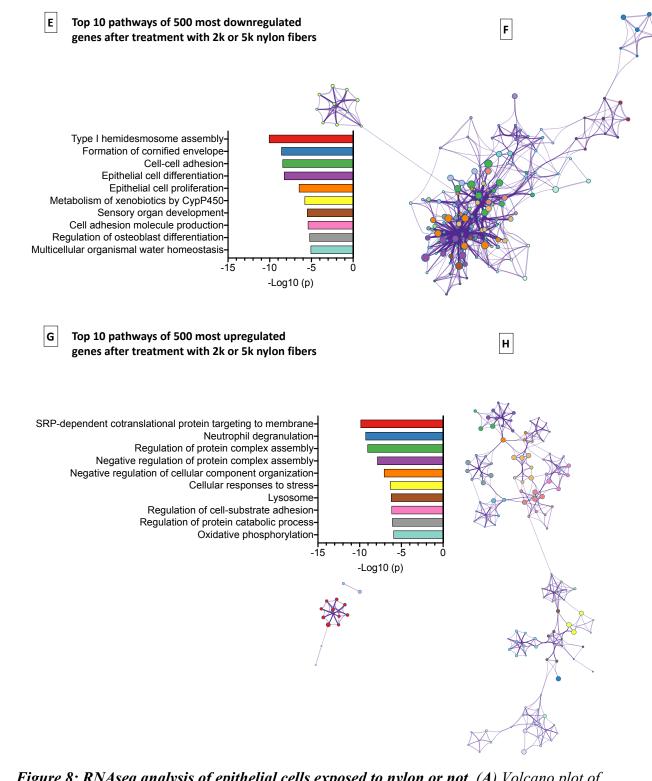
59 The top pathways identified for downregulated genes following nylon exposure were highly 70 enriched for epithelial development and function (figure 8E-F), while the top pathways 71 identified for upregulated genes were highly enriched for mRNA translation and protein 72 synthesis (figure 8G-H).

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77Figure 8: RNAseq analysis of epithelial cells exposed to nylon or not. (A) Volcano plot of78differentially expressed genes by epithelial cells exposed to 2000 nylon fibers (equivalent to7916 μ g/ml nylon) or not. (B) Volcano plot of differentially expressed genes by epithelial cells80exposed to 5000 nylon fibers (equivalent to 39 μ g/ml nylon) or not. Upregulated genes are81marked in red, downregulated genes in blue. Genes were selected with thresholds of fold82change >2 and q<0.05. (C) Unsupervised clustering heat map of epithelial cells exposed to</td>

83 2000 nylon fibers (equivalent to 16 μ g/ml nylon) or not. (**D**) Unsupervised clustering heat map of epithelial cells exposed to 5000 nylon fibers (equivalent to 39 μ g/ml nylon) or not. 84 (E) Metascape bar graphs of top 10 nonredundant enrichment clusters of genes 85 downregulated by exposure to nylon ordered based on statistical significance (p value). (F) 86 87 Metascape enrichment network visualization showing the intra-cluster and inter-cluster 88 similarities of enriched terms of genes downregulated by exposure to nylon, up to ten terms 89 per cluster. Cluster annotations colors are shown in bar graph of panel E. (G) Metascape 90 bar graphs of top 10 nonredundant enrichment clusters of genes upregulated by exposure to 91 nylon ordered based on statistical significance (p value). (H) Metascape enrichment 92 network visualization showing the intra-cluster and inter-cluster similarities of enriched 93 terms of genes upregulated by exposure to nylon, up to ten terms per cluster. Cluster 94 annotations colors are shown in bar graph of panel E. 2k: 2000 fibers; 5k: 5000 fibers.

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We then investigated expression of individual genes in the top 5 enriched pathways for up 96 97 and downregulated genes in more detail (Figures 8E-H). The top 5 enriched pathways for 98 downregulated genes were type I hemidesmosome assembly, formation of cornified 99 envelope, cell-cell adhesion, epithelial cell differentiation, and epithelial cell proliferation, 00 while the top 5 pathways for upregulated genes were SRP-dependent cotranslational protein 01 targeting to membrane, neutrophil degranulation, regulation of protein complex assembly, negative regulation of protein complex assembly, and negative regulation of cellular 02 03 component organization.

04We first investigated the downregulated genes and many of them represent important 05 epithelial populations in the lung. We therefore investigated genes associated with specific 06 epithelial populations, i.e. homeodomain-only protein homeobox (*Hopx*) and advanced glycosylation end-product specific receptor (Ager) for alveolar epithelial cell type I cells 07 08 (AECI) and surfactant protein C (Sftpc) and surfactant protein B (Sftpb) for alveolar 09 epithelial cell type II cells (AECII). For airway epithelial cell types we used transformation-10 related protein 63 (Trp63), keratin 5 (Krt5), integrin alpha-6 (Itga6), and nerve growth factor receptor (Ngfr) for basal cells, forkhead box J1 (Foxi1), serine/threonine kinase 11 11 12 (Stk11) and, acetylated alpha tubulin (Tuba1a) for ciliated cells, secretoglobin family 1A 13 member 1 (*Scgb1a1*) and BPI fold containing family A member 1 (*Bpifa1*) for club cells, 14 and mucin 5 subtype B and subtype AC (Muc5b, Muc5ac) for goblet cells. The expression 15 of these genes correlated well with our organoid findings that airway epithelial cell growth

16	was most affected by exposure to nylon fibers, while alveolar epithelial cell growth was less
17	affected (Figure 9). Both AECI and AEC II genes (Figure 9A) were only marginally lower
18	expressed after exposure to nylon while most genes for basal cells (Figure 9B), ciliated cells
19	(Figure 9C), club cells and goblet cells (Figure 9D) were expressed at significantly lower
20	levels compared to controls with two noticeable exceptions: ciliated cell marker acetylated
21	alpha tubulin Tubala and club cell marker secretoglobin family 1A member 1 Scgblal that
22	were expressed at significantly higher levels compared to nonexposed controls.
23	Proliferation markers like proliferation marker protein 67 (Mki67), forkhead box protein M1
24	(Foxm1), and polo-like kinase 1 (Plk1, Figure 9E) confirmed this general lack of
25	proliferation in epithelial cells as all three were expressed at lower levels in a dose-
26	dependent manner after exposure to nylon fibers. Other factors regulating epithelial
27	development (38-45) from the top 5 pathways are depicted in figure 9F and all show the
28	same dose-dependent lower expression after exposure to nylon as the proliferation markers
29	with the exception of bone morphogenetic protein 4 (Bmp4), wingless-type MMTV
30	integration site family, member 7a (Wnt7a), and neurogenic locus notch homolog protein 2
31	(Notch2) that were only expressed at lower levels after exposure to 5000 nylon fibers
32	compared to nonexposed controls.

33 To exclude the possibility that these effects on epithelial cells were the result of a decreased 34 support function from fibroblasts, for instance by nylon selectively killing fibroblasts or 35 inhibiting the expression of important growth factors, we separately analyzed the resorted 36 fibroblast fraction for expression of proliferation genes and important growth factors, i.e. 37 Mki67, Foxm1, Plk1, fibroblast growth factors 2, 7, and 10 (Fgf2, Fgf7, and Fgf10), Wnt2, 38 Wnt5a, and hepatocyte growth factor (*Hgf*) (33). None of these genes were negatively 39 affected in fibroblasts after exposure to nylon fibers compared to untreated controls and 40 expression of most actually went up slightly (Figure S5).

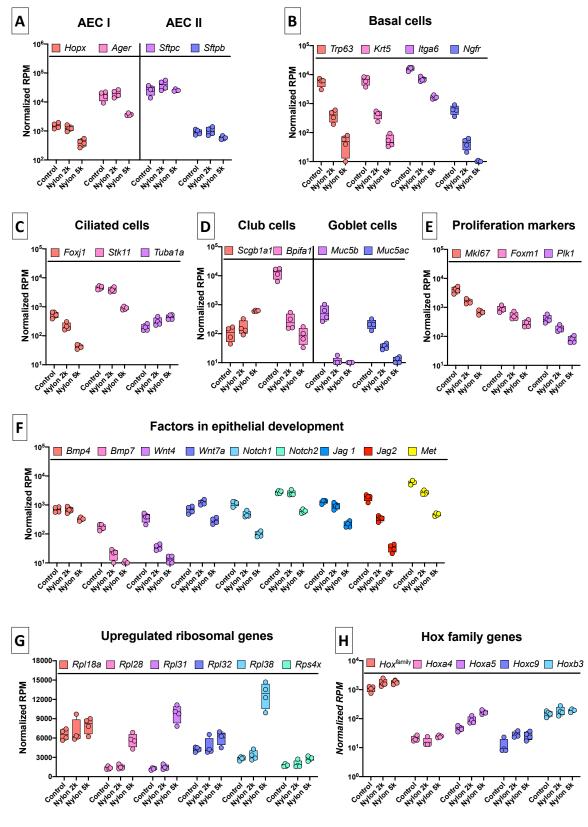


Figure 9: Expression profiles of individual genes from the pathway analyses. (A) Genes highly expressed by alveolar epithelial cells type I (AECI) and type II (AECII). (B) Genes highly expressed in basal cells. (C) Genes highly expressed in ciliated cells. (D) Genes highly expressed in club cells and goblet cells. (E) Genes associated with proliferation. (F)

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Genes encoding factors important for epithelial development. (G) Genes encoding ribosomal proteins. (H) Genes encoding Hox family genes.

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The genes most prominently upregulated after exposure to nylon fibers were mostly 49 encoding for ribosomal proteins, with ribosomal protein L28 (*Rpl28*), L31 (*Rpl31*), and L38 50 (*Rpl38*) being most profoundly upregulated (Figure 9G). Ribosomal proteins are a large 51 family of proteins and essential parts of ribosomes translating mRNA to protein. Recent 52 data has shown that heterogeneity in ribosomal protein composition within ribosomes 53 54 makes them selective for translating subpools of transcripts (46). For instance, Rpl38 has 55 been shown to regulate translation of the homeobox (*Hox*) genes, that are key in anatomical 56 development (47). We therefore also investigated the expression of all Hox genes and some 57 specific members of this family involved in lung epithelial development in more detail (Figure 9H) (48, 49). After exposure to nylon fibers, expression of Hox family members 58 59 was significantly higher and this pattern was seen for highlighted members *Hoxa4*, *Hoxa5*, 60 Hoxc9, and Hoxb3 as well.

62 **Discussion**

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63 Recent reports have shown that man-made fibers are ubiquitously present in indoor air (9, 64 50-53). It is estimated that approximately 30% of those indoor fibers are of plastic origin, 65 particularly from textiles (9, 50-53). The lungs are continuously exposed to this airborne microplastic pollution (54), but the consequences of common household exposure on our 66 67 lungs are unclear. High occupational exposure to nylon microfibers has been linked to the 68 development of airway and interstitial lung disease (15-23), suggesting that as microplastic pollution accumulates, establishing the effects of inhaling this pollution becomes 69 70 increasingly important. In our present work, we found that both polyester and nylon microfibers negatively affected the growth and development of human and murine lung 71 72 organoids, with nylon being the most harmful. Already established lung organoids were not 73 affected and therefore our results may be of particular importance for young children with 74 developing airways and for people undergoing high levels of epithelial repair, such as 75 people with respiratory diseases.

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We particularly focused on polyester and nylon, because these are the most abundant types of microplastics indoors (9, 50-53). As we spend the majority of our time indoors, we may

79 therefore be exposed most to these types of microplastics (55). Nylon was found to be the 80 most consistently harmful for growth of airway organoids and was less inhibitory for 81 growth of alveolar organoids, while polyester affected both types equally but less profoundly than nylon. This was the case for our reference fibers as well as environmentally 82 83 relevant fibers made from fabrics purchased in a local fabric store. The lung organoids we used in these studies self-assemble from lung epithelial progenitor/stem cells isolated from 84 85 adult lung tissue. The main populations of epithelial progenitor/stems cells in these lung tissues are basal cells and club cells in the airways and AECII in alveoli. The basal cell 86 87 progenitors can give rise to all important epithelial cells lining the airways, among which ciliated cells, goblet cells, and club cells. Club cells can develop into ciliated cells, goblet 88 89 cells, and AECII (56, 57). The growth of organoids from these progenitor cells is supported 90 by proliferation and differentiation enhancers produced by epithelial cells themselves and 91 fibroblasts also present in our 3D cultures (58).

92 The gene expression pathway analysis after nylon exposure confirmed inhibition of 93 important pathways for epithelial regeneration. Expression of basal cell marker genes were 94 impressively and dose-dependently downregulated by nylon exposure, as were genes for 95 signaling molecules essential for epithelial growth and development, like Notch1 and Notch2 and their ligands Jagged 1 (Jag1) and 2 (Jag2) (43-45), Bmp4 and Bmp7 (40-42), 96 Wnt4 and Wnt7a (59, 60), and the receptor for hepatocyte growth factor, Met. The lower 97 98 expression of basal cell-specific markers and essential factors that are needed for 99 differentiation of other cell types like ciliated and goblet cells may explain why the growth of in particular airway organoids was inhibited most by nylon. 00

01 The gene expression analysis also confirmed that growth of alveolar organoids was affected less by nylon exposure and even appeared induced after treatment with leachate or lower 02 03 numbers of nylon fibers. Genetic markers of both AECI and II were either stable or only slightly affected by the highest concentration of nylon. The explanation for this finding may 04 05 be found in the downregulation of Notch signaling pathway members by nylon fibers. Multiple studies have shown that Notch signaling is required for development of airway 06 07 epithelial cells, most specifically goblet cells, whereas disruption of this signaling boost 08 alveolar epithelial development (61, 62). Both Notch1 and Notch2, as well as their ligands 09 Jag1 and Jag2 were expressed at significantly lower levels after nylon treatment, suggesting 10 disruption of Notch signaling may be responsible for the divergent effect nylon has on 11 airway versus alveolar epithelial growth.

12 The Notch pathway, incidentally, is also important for the development of club cells (63). 13 Morimoto and colleagues showed that Notch2 was involved in the decision between club 14 cell or ciliated cell development. Interestingly, the gene expression data for club cells and ciliated cells were somewhat ambiguous, with important markers for these cell types having 15 higher expression (Scgb1a1 for club cells and Tub1a1 for ciliated cells) and others having 16 17 lower expression (*Bpifa1* for club cells and *Foxi1* and *Stk11* for ciliated cells) after nylon exposure. This may suggest that the lower expression of Notch2 may be hampering the cell 18 19 fate decision between club and ciliated cells in some way, resulting in improperly 20 differentiated cell types. In combination with the inhibited development of basal epithelial 21 cells and goblet cells, this altered airway epithelial differentiation may explain the 22 bronchiolitis found in nylon flock workers and rats exposed to nylon (64-66).

24 For nylon, the negative effect we found on development of particularly airway organoids 25 was caused by components leaching from these fibers. As the most abundant components in 26 this leachate, the cyclic oligomers, were not responsible for this effect, we used RNAseq 27 analysis to look for signatures of other components. Recent work by Sait and Sørensen and 28 colleagues showed that the most abundant chemicals leaching from nylon are bisphenol A 29 and benzophenone-3 (67, 68). Experiments incubating organoids with benzophenone-3 showed some effect on organoid growth but mostly on alveolar development suggesting this 30 was not the major culprit in our leachate (data not shown). Interestingly, however, a study 31 investigating effects of bisphenol A in fruit flies found that exposure of these flies to 32 bisphenol A specifically upregulated ribosome-associated genes (69), similar to what we 33 34 found in our study. The association of these *Rpl* genes with the *Hox* family genes is of particular interest for lung epithelial development. Rpl38 was one of the three most 35 36 upregulated *Rpl* genes by nylon and was shown to interact with a specific subset of *Hox* 37 genes including Hoxa4, Hoxa5, and Hoxb3 (47). These have all been associated with epithelial differentiation, with *Hoxa5* taking a center stage in goblet versus club cell 38 39 differentiation (48, 49). Boucherat and colleagues showed that loss of Hoxa5 drove 40 epithelial differentiation towards goblet cell differentiation at the expense of club cell 41 differentiation and Scgb1a1 expression (48). Remarkably, Hoxa5 was expressed at 42 significantly higher levels in our dataset in a dose-dependent manner after exposure to 43 nylon and we also found a matching dose-dependent increase in Scgb1a1 and decrease in 44 Muc5ac and Muc5b expression. Of note, bisphenol A exposure was also found to inhibit

45 expression of Notch pathway members in rat brain, suggesting bisphenol A could also contribute to the aberrant epithelial cell differentiation through the Notch pathway (70). 46 47 Taken together our data suggest that component (s) in nylon leachate, maybe bisphenols, may be skewing differentiation of epithelial progenitors away from airway epithelial cells 48 49 possibly through Hoxa5 and/or Notch. However, work from van Winkle and colleagues showed that fetal exposure of rhesus macaques to bisphenol A resulted in higher expression 50 of both Scgb1a1 and Muc5b/Muc5ac (71) in lung tissue, suggesting bisphenol A exposure is 51 52 not the only explanation for the effects we found and further investigating into components of the nylon leachate are warranted. 53

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55 By using lung organoids we were able to test many different conditions and factors related 56 to microplastic exposure on epithelial development and repair mechanisms. In addition, this also gave us the opportunity to directly study human lung epithelial repair, showing us these 57 effects of microplastic textile fibers are relevant for human epithelial differentiation and 58 59 growth too. Despite these strengths (32, 33, 58, 72, 73), lung organoids are a relatively 60 simple model of lung tissue and lack the immune and endothelial compartment present in *vivo*. Especially having the immune compartment present could alter how lung tissue 61 responds to these microplastic fibers. For example, innate immune cells like macrophages 62 63 are also one of the first cells to come into contact with microplastic fibers following inhalation and macrophages are known to respond strongly to inhaled particles and fibers 64 (74) and are also important for lung repair (75). It is therefore recommended to include lung 65 macrophages in lung organoid cultures in future studies as was done before by Choi *et al.*⁵³. 66 This way, a more comprehensive view on the interaction between pivotal lung cells and 67 microplastics can be obtained. 68

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70 The implication of our results for the human population is of high relevance. It is important 71 to note that similar to the high occupational exposure in industry workers, the microplastic fiber doses as used in our *in vitro* experiments are most likely much higher than daily 72 73 exposure for most people. Previous studies estimated that a male person with light activity may inhale around 272 microplastic particles per day based on air sampling using a 74 75 breathing thermal manikin (54). It will be crucial to study in more detail how many and 76 what kind of fibers deposit in which regions of the lungs and what fraction can still be 77 cleared. The fibers we used in our study were not of a size that will penetrate deep into the

78 lungs. Generally only fibers with a diameter smaller than 3 µm have this ability (35). Our fiber sizes were limited by the availability of polyester and nylon filaments of standardized 79 80 small diameters. However, the sizes we did use can enter the lung and get trapped onto the airways, incidentally the place we found they appear to do most harm. It is therefore key 81 82 that hazard characteristics of these textile microfibers are studied in more detail, in addition 83 to exposure levels in indoor environments. A limitation here is the detection of 84 microplastics, as smaller particles might escape current detection methods (10, 76). 85 Especially our finding that epithelial differentiation and repair mechanisms are affected most by microplastics exposure, suggests airborne microplastics may be most harmful to 86 87 young children with developing airways and to people undergoing high levels of epithelial repair. These could be people with a chronic lung disease or even healthy individuals 88 89 suffering from a seasonal respiratory virus infection.

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91 In conclusion, with the ongoing and growing use of plastics, potential associated health problems in the human population may also increase. The results of the present study 92 93 strongly encourage to look in more detail at both the hazard and the exposure, and outcomes 94 of these experiments will be valuable to advise organizations such as the World Health 95 Organization and Science Advice for Policy by European Academies who have recently stated that more research is urgently needed^{21,22}. Importantly, future research should focus 96 97 on examining the presence and number of such fibers both in our indoor environment and in 98 human lung tissue, to better estimate the actual risk of these fibers to human health.

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02 Materials and Methods

03

04 **Production of microfibers and leachate**

05 *Reference microfibers and leachate*

Microfibers of standardized dimensions were produced as described before (34). In short, 06 07 polyester and nylon fibers (both Goodfellow, UK) with filament diameters of 14±3.5 µm and 10 ± 2.5 µm respectively were aligned by wrapping them around a custom-made spool, 08 09 coated with a thin layer of cryo compound (KP-CryoCompound, VWR International B.V., PA, USA) and frozen. Aligned fibers were cut into similar length parts (~2 cm) using a 10 scalpel (Swann-Morton, UK) and moulded onto a compact block that was oriented 11 perpendicular to the base of a cryomicrotome (Microm HM 525, Thermo Fisher Scientific, 12 MA, USA). Microfibers were cut at lengths of 50 µm for polyester and 30 µm for nylon, 13 14 after which the fibers were thawed, washed with water through a 120 µm filter (Merck 15 Millipore, MA, USA) to remove miscut fibers and contaminants, collected by vacuum filtration using 8 µm polycarbonate membrane filters (Sterlitech, WA, USA) and stored dry 16 at -20°C. 17

Nylon leachate was produced by incubation of nylon reference microfibers in phosphate
buffered saline (PBS) for 7 days at 37°C in the dark, followed by filtration using a 0.2 μm
syringe filter (GE Healthcare Life Sciences, UK). The leachate was stored at -20°C until
further use.

22 Environmental microfibers

23 Environmental polyester and nylon textile microfibers were prepared from commercially available pure fabrics. White polyester fabric was washed at 40°C in a washing machine 24 25 (Samsung, South Korea) and dried in a tumble dryer (Whirlpool, MI, US). Fibers with an estimated filament diameter of 15 um were collected on the filter of the tumble drver and 26 subsequently frozen with cryo compound and sectioned into lengths of 50 µm using a 27 28 cryomicrotome. White nylon fabric (estimated filament diameter of 40 µm) was cut into small squares, stacked, frozen with cryo compound, and cut into lengths of 12 µm. All 29 30 microfibers were thawed, washed with water through a 120 µm filter, collected by vacuum filtration (8 µm filter) and finally stored at -20°C. 31

33 Characterization of microfibers and leachate

34 Scanning electron microscopy

Samples were prepared for scanning electron microscopy (SEM) analysis on an aluminium
sample holder using adhesive carbon-coated tape. Excessive microfibers were removed
using pressurized air, after which the samples were sputter-coated with 10 nm of gold.
Images were obtained using a JSM-6460 microscope (Jeol, Japan) at an acceleration voltage
of 10 kV.

- 40 Dimensions
- 41 Digital photomicrographs were captured at 200× magnification using a Nikon Eclipse

determined using NIS-Elements AR 4.00.03 software.

- 42 TS100 inverted microscope coupled to a Nikon Digital Sight DS-U3 microscope camera
- 43 controller (both Japan), after which microfiber diameters and lengths (median of 200) were
- 44
- 45

46 Ethics

47 *Animal experiments*

The experimental protocol for the use of mice for epithelial cell isolations was approved by the Animal Ethical Committee of the University of Groningen (The Netherlands), and all experiments were performed according to strict governmental and international guidelines on animal experimentation. C57BL/6 mice (8-14 weeks) were bred at the Central Animal Facility of the University Medical Center Groningen (UMCG) (IVD 15303-01-004). Animals received ad libitum normal diet with a 12 h light/dark cycle.

54 *Human lung tissue*

55 Histologically normal lung tissue was anonymously donated by individuals with COPD 56 (n=6) or without COPD (n=1) undergoing surgery for lung cancer and not objecting to the 57 use of their tissue. COPD patients included ex- and current- smoking individuals with 58 GOLD stage I-IV disease (GOLD I=1, GOLD II=2, GOLD IV=3). Subjects with other lung 59 diseases such as asthma, cystic fibrosis, or interstitial lung diseases were excluded. The 60 study protocol was consistent with the Research Code of the University Medical Center Groningen (UMCG) and Dutch national ethical and professional guidelines 61 62 (www.federa.org). Sections of lung tissue of each patient were stained with a standard 63 haematoxylin and eosin staining and checked for abnormalities by a lung pathologist.

64 Cell cultures

65	Mouse lung fibroblasts (CCL-206, ATCC, Wesel, Germany) or human lung fibroblasts
66	(MRC5, ATCC, CCL-171) were cultured in 1:1 DMEM (Gibco, MD, USA) and Ham's F12
67	(Lonza, Switzerland) or Ham's F12 respectively, both supplemented with 10% heat
68	inactivated fetal bovine serum (FBS, GE Healthcare Life Sciences), 100 U/ml penicillin and
69	100 µg/ml streptomycin, 2 mM L-glutamine and 2.5 µg/ml amphotericin B (all Gibco).
70	Fibroblasts were cultured at 37°C under 5% CO2 and humidified conditions. For use in
71	organoid cultures, near-confluent cells were proliferation-inactivated by incubation with 10
72	μ g/ml mitomycin C (Sigma-Aldrich, MO, USA) in cell culture medium for 2 hours, after
73	which they were washed in PBS, and left in normal medium for at least 1 hour before
74	trypsinizing and counting.

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76 Lung epithelial cell isolation

77 Mouse lung epithelial cell isolation

Epithelial cells were isolated from lungs of mice using antibody-coupled magnetic beads 78 79 (microbeads) as described before (32, 33, 72). In short, mice were sacrificed under 80 anaesthesia, after which the lungs were flushed with 0.9% NaCl and instilled with 75 81 caseinolytic units/1.5 ml dispase (Corning, NY, USA). After 45 minutes of incubation at 82 room temperature, the lobes (excluding trachea and extrapulmonary airways) were 83 homogenized in DMEM containing 100 U/ml penicillin and 100 µg/ml streptomycin and 40 µg/ml DNase1 (PanReac AppliChem, Germany), washed in DMEM (containing penicillin, 84 85 streptomycin and DNase1), and the digested tissue was passed through a 100 µm cell strainer. The suspension was incubated for 20 minutes at 4°C with anti-CD31 and anti-86 87 CD45 microbeads in MACS buffer and magnetically sorted using LS columns. The CD31-/CD45- flow-through was incubated for 20 minutes at 4°C with anti-CD326 88 89 (EpCAM) microbeads in MACS buffer, after which purified epithelial lung cells were obtained by positive selection using LS columns. CD326-positive epithelial cells were 90 resuspended in CCL206 fibroblast medium, counted and seeded into matrigel immediately 91 after isolation with equal numbers of CCL206 fibroblasts, as described below. All materials 92 93 were purchased at Miltenyi Biotec (Germany) unless stated otherwise.

95 Human lung epithelial cell isolation

96 Human lung epithelial cells were isolated from lung tissue specimens obtained from 97 patients. Peripheral lung tissue was minced and dissociated in DMEM-containing enzymes (Multi Tissue Dissociation Kit) at 37°C using a gentleMACS Octo Dissociator. The cell 98 99 suspension was filtered (70 μ m and 35 μ m nylon strainer, respectively) prior to 20-minute 00 incubation at 4°C with anti-CD31 and anti-CD45 microbeads in MACS buffer. The 01 CD31-/CD45- fraction was obtained by negative selection using an AutoMACS. Epithelial cells were then isolated by positive selection after 20-minute incubation at 4°C with anti-02 03 CD326 (EpCAM) microbeads in MACS buffer. Human EpCAM+ cells were resuspended 04 in 1:1 DMEM and Ham's F12, supplemented with 10% heat inactivated FBS, 100 U/ml 05 penicillin and 100 µg/ml streptomycin, 2 mM L-glutamine and 2.5 µg/ml amphotericin B, 06 counted and seeded into matrigel immediately after isolation with equal numbers of MRC5 07 fibroblasts. All materials were purchased at Miltenyi Biotec unless stated otherwise.

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09 Lung organoid cultures

10 Lung organoids were grown as previously described with minor modifications (32, 33, 72). For mouse lung organoids, 10,000 EpCAM+ cells and 10,000 CCL206 fibroblasts were 11 12 seeded, and for human lung organoids, 5,000 EpCAM+ cells and 5,000 MRC5 fibroblasts 13 were seeded in 100 µl growth factor-reduced matrigel matrix (Corning) diluted 1:1 in 14 DMEM:Ham's F-12 1:1 containing 10% FBS, 100 U/ml penicillin and 100 µg/ml streptomycin, 2 mM L-glutamine and 2.5 µg/ml amphotericin B into transwell 24-well cell 15 16 culture plate inserts (Corning). Organoids were cultured in DMEM:Ham's F-12 1:1 17 supplemented with 5% FBS, 100 U/ml penicillin and 100 µg/ml streptomycin, 2 mM Lglutamine, 2.5 µg/ml amphotericin B, 4 ml/l insulin-transferrin-selenium (Gibco), 25 µg/l 18 19 recombinant mouse (Sigma-Aldrich) or human epithelial growth factor (EGF, Gibco) and 20 300 µg/l bovine pituitary extract (Sigma-Aldrich). During the first 48h of culture, 10 µM Y-21 27632 (Axon Medchem, the Netherlands) was added to the medium.

A titration curve for polyester or nylon microfibers was made with 2000, 3000, 4000 or
 5000 fibers per well corresponding to approximately 49, 73, 98 and 122 μg/ml of polyester
 fibers or 16, 23, 31, and 39 μg/ml of nylon fibers. For all other experiments, 5000 polyester

- 25 or nylon reference (equivalent to $122 \ \mu g/ml$ of polyester or 39 $\mu g/ml$ of nylon) or
- 26 environmental microfibers (equivalent to 122 µg/ml of polyester or 39 µg/ml of nylon and)

27 were used per condition. Fibers were in direct contact with developing organoids during 14 days by mixing them with matrigel and cells prior to seeding in the insert, except for those 28 29 experiments studying effects of leaching nylon components. In those cases, 5000 polyester and nylon reference fibers were added on top of the organoids, thereby excluding physical 30 31 contact between the microfibers and the developing organoids, or equivalent amounts of 32 fiber leachate were added to the medium during 14 days of organoid culture. For testing the effects of nylon oligomers, concentrations between 26.8 ng/ml and 53.6 µg/ml were used; 33 34 the latter concentration being twice as high as the used fiber concentrations (5000 fibers per 35 condition). Oligomers were synthesized and characterized as described in the 36 supplementary materials and methods. All organoid cultures were maintained for 14 to 21 37 days at 37 °C under 5% CO₂ and humidified conditions. Medium was refreshed 3 times per 38 week.

Organoid colony forming efficiency was quantified by manually counting the total number
of organoids per well after 14 or 21 days of culturing using a light microscope at 100×
magnification. For mouse organoids, a distinction was made between airway and alveolar
organoids, whereas for human organoids only one organoid phenotype was distinguished.
The diameter of the organoids was measured using a light microscope (Nikon, Eclipse Ti),
only including organoids larger than 50 µm in diameter, with a maximum of 50 organoids
per phenotype per well.

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Immunofluorescence staining

48 Organoid cultures in matrigel were washed with PBS, fixed in ice-cold 1:1 acetone and 49 methanol (both Biosolve Chimie, France) for 15 minutes at -20°C and washed again with 50 PBS after which aspecific antibody-binding was blocked for 2 hours in 5% bovine serum 51 albumin (BSA, Sigma-Aldrich). Organoids were incubated overnight at 4°C with the primary antibodies (mouse anti-acetylated α-tubulin (Santa Cruz, TX, USA) and rabbit anti-52 53 prosurfactant protein C (Merck, Germany)) both diluted 1:200 in 0.1% BSA and 0.1% 54 Triton (Sigma-Aldrich) in PBS. Next, after extensive but gentle washing with PBS, 55 organoids were incubated with the appropriate Alexa-conjugated secondary antibody for 2 56 hours at room temperature (Alexa Fluor 488 donkey anti rabbit IgG and Alexa Fluor 568 57 donkey anti mouse IgG, both Thermo Fisher Scientific) diluted 1:200 in 0.1% BSA and 58 0.1% Triton in PBS. Organoid cultures were washed with PBS, excised using a scalpel, 59 mounted on glass slides (Knittel, Germany) using mounting medium containing DAPI

60 (Sigma-Aldrich) and covered with a cover glass (VWR). Digital photomicrographs were captured at 200× magnification using a DM4000b fluorescence microscope and LAS V4.3 62 software (both Leica, Germany).

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64 Isolation of epithelial cells and fibroblasts from organoid cultures

65 200,000 mouse EpCAM+ primary cells and 200,000 CCL206 fibroblasts (n=4 independent isolations) were seeded in 1 ml matrigel diluted 1:1 in DMEM containing 10% FBS in 6-66 well plates (Greiner Bio-One, The Netherlands). 12.000 or 30.000 nylon reference 67 68 microfibers were mixed with matrigel and cells prior to seeding. Murine organoid culture 69 medium was maintained on top and refreshed every two days. After 7 days, organoid 70 cultures were digested with 50 caseinolytic units/ml dispase for 30 minutes at 37°C, 71 transferred to 15 ml tubes, washed with MACS BSA stock solution and autoMACS rinsing 72 solution (both Miltenyi), and digested further with trypsin (VWR) diluted 1:5 in PBS for 5 73 minutes at 37°C. The cell suspension was then incubated for 20 minutes at 4°C with anti-74 EpCAM microbeads in MACS buffer, after which the suspension was passed through LS 75 columns. Both the EpCAM+ (epithelial cells) and EpCAM- (fibroblasts) cell fractions were 76 used for RNA isolation and subsequent sequencing.

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Library preparation and RNA sequencing

79 Total RNA was isolated from EpCAM+ and EPCAM- cell fractions using a 80 Maxwell® LEV simply RNA Cells/Tissue kit (Promega, WI, USA) according to 81 manufacturer's instructions. RNA concentrations were determined using a NanoDrop One 82 spectrophotometer (Thermo Fisher Scientific). Total RNA (300 ng) was used for library 83 preparation. Paired-end sequencing was performed using a NextSeq 500 machine (Illumina; mate 1 up to 74 cycles and mate 2 up to 9 cycles). Mate 1 contained the first STL 84 85 (stochastic labeling) barcode, followed by the first bases of the sequenced fragments, and mate 2 only contained the second STL barcode. The generated data were subsequently 86 87 demultiplexed using sample-specific barcodes and changed into fasta files using bcl2fasta (Illumina; version 1.8.4). The quality of the data was assessed using FastOC (77). The STL 88 89 barcodes of the first mate were separated from the sequenced fragments using an in-house 90 Perl script. Low quality bases and parts of adapter sequences were removed with Cutadapt 91 (version 1.12; settings: q=15, O=5, e=0.1, m=36) (78). Sequenced poly A tails were

92 removed as well, by using a poly T sequence as adapter sequence (T (100); reverse 93 complement after sequencing). Reads shorter than 36 bases were discarded. The trimmed 94 fragment sequences were subsequently aligned to all known murine cDNA sequences using HISAT2 (version 2.1.0; settings: k=1000, --norc). The number of reported alignments, k, 95 was given a high number in order to not miss any alignment results (some genes have up to 96 97 62 transcripts). Reads were only mapped to the forward strand (directional sequencing). 98 Fragment sequences that mapped to multiple genes were removed (unknown origin). When 99 fragments mapped to multiple transcripts from the same gene all but one were given a non-00 primary alignment flag by HISAT2 (flag 256). These flags were removed (subtraction of 256) by the same Perl script in order to be able to use the Bash-based shell script 01 02 (dqRNASeq; see below) that is provided by Bioo Scientific (Perkin Elmer, MA, USA). 03 Fragments that mapped to multiple transcripts from the same gene were considered unique and were counted for each of the transcripts. The number of unique fragments (or read 04 05 pairs) was determined for each transcript using the script provided by Bioo Scientific (dqRNASeq; settings: s=8, q=0, m=1). Counts that were used for further analysis were 06 07 based on a unique combination of start and stop positions and barcodes (USS + STL).

08

09 **Data analyses and statistics**

All statistics were performed with GraphPad Prism 9.0. Nonparametric testing was used to compare groups in all experiments. For comparison of multiple-groups, a Kruskall wallis or Friedman test was used for nonpaired or paired nonparametric data respectively with Dunn's correction for multiple testing. Differences in organoid size between groups were tested by using the average size of the organoids per independent experiment. Data are presented as median ± range and p-values <0.05 were considered significant.

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For RNA sequencing data, the principal component analyses were performed in R using the
R package DESeq2 (version 1.26.0) (79) in order to visualize the overall effect of
experimental covariates as well as batch effects (function: plotPCA). Differential gene
expression analyses (treated vs. nontreated) was performed with the same R package
(default settings; Negative Binomial GLM fitting and Wald statistics; design=~condition),
following standard normalization procedures. Transcripts with differential expression >2
(nylon-treated versus nontreated fibroblasts or epithelial cells) and an adjusted p-value

24		below 0.05 were considered differentially expressed in that specific cell type. Volcano plots
25		and clustering heat maps were made using BioJupies (80). Pathway analysis was done using
26		Metascape (37).
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28		
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87	revision.
88	IB: Collection and assembly of data, critical reading and revision.
89	DB: Collection and assembly of data, data analysis and interpretation, experimental
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91	IK: Collection and assembly of data, data analysis and interpretation, experimental
92	material support, critical reading and revision.
93	DS: Collection and assembly of data, data analysis and interpretation, experimental
94	material support, critical reading and revision.
95	RW: Collection and assembly of data, data analysis and interpretation, experimental
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97	MC: Collection and assembly of data, data analysis and interpretation, experimental
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99	AS: Data analysis and interpretation, critical reading and revision.

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12 Supplementary Materials and methods

13

14 Energy dispersive X-ray spectroscopy

Samples were prepared for energy dispersive X-ray (EDX) spectroscopy analysis on an
 aluminium sample holder using adhesive carbon coated tape. Excessive microfibers were
 removed using pressurized air, after which the samples were sputter coated with 10 nm of
 carbon. The EDX measurements were performed with a Tescan MAIA III GMH field
 emission scanning electron microscope (Czech Republic) equipped with a Bruker X-Flash
 30 mm² silicon drift energy dispersive X-ray microanalysis detector (MA, USA).

21

22 Micro-Fourier transform infrared spectroscopy

Micro-Fourier transform infrared spectroscopy (uFTIR) measurements were performed 23 24 using a Thermo Nicolet iN10 micro Fourier transform infrared microscope. Spectra were recorded in the wavelength range from 4000 to 675 cm⁻¹ using a spectral resolution of 8 25 26 cm⁻¹. For the transmission measurements of the polyester reference material and the polyester and nylon environmental fibers, a small amount of the microfibers was 27 28 transferred onto a diamond micro compression cell where the samples were compressed. 29 For the reflection measurements of the nylon reference material and the polyester and 30 nylon environmental fibers, a small portion of microfibers was suspended in water. The suspension was subsequently filtered over a gold coated 0.8 µm polycarbonate filter (TJ 31 32 Environmental, The Netherlands). A subset of approximately 100 fibers was individually 33 measured directly on the filter using the reflection mode of the µ-FTIR equipment.

34

35 Extraction of nylon oligomers (mono-, di- and trimer)

A round bottom flask containing 25.1 g cryogenically milled nylon powder (PA66, Sigma-Aldrich) and 500 ml methanol (VWR) was equipped with a reflux condenser and the suspension was stirred overnight at 50°C. Next, the suspension was cooled to approximately 30°C and filtered over a cellulose filter (VWR) to remove the remaining powder. The solvent was removed *in vacuo* using a rotary evaporator (Büchi rotavapor R-215, Switzerland). A white solid was obtained (yield 220 mg), of which the composition was determined using liquid chromatography/mass spectrometry (LC/MS) analysis.

43 Isolation of nylon oligomers (mono-, di- and trimer)

44 A column for silica gel chromatography (Ø 30 mm, VWR) was charged with silica gel 60 45 (27 g, 0.063-0.200 mm, Merck) and dichloromethane (DCM, VWR) as eluent. The crude 46 extract containing the mixture of oligomers (200 mg) was added on top of the silica gel 47 column and oligomers were separated on the column using DCM:methanol as eluent (DCM:MeOH gradient: $100:0 \rightarrow 90:10 \rightarrow 80:20$), which resulted in complete separation 48 49 of the oligomers. The collected fractions were checked for the presence of product using 50 LC/MS. The fractions containing pure oligomer were combined, filtered over a glass filter 51 (VWR) and subsequently the solvent was removed in vacuo. The obtained solids were further dried *in vacuo*, after which the pure oligomers were obtained as white solids. The 52 53 structure of the oligomers was confirmed by ¹H NMR spectroscopy.

54

55 Liquid chromatography/mass spectrometry

56 *Qualitative analysis of nylon leachate and oligomers*

Qualitative analysis of nylon oligomers was performed with an Agilent 1260 series high-57 58 performance liquid chromatographer (CA, USA) equipped with a 100 x 2 mm, 3 µm 59 Gemini NX-C18 110 Å LC Column (Phenomenex, Utrecht, The Netherlands), coupled 60 with an Agilent 6410 triple quadrupole LC/MS with electron spray ionization (ESI) in 61 positive SCAN mode. In addition, the LC/MS analysis of the nylon leachate was 62 performed with the Agilent 1260 liquid chromatographer coupled to an Agilent 6460 triple quadrupole LC/MS with Jetstream ESI in positive SCAN mode. A sample volume of 5 µl 63 64 was injected with a column temperature of 60 °C and a flow rate of 200 μ l min⁻¹. The 65 sample was eluted with a gradient of Milli-Q water (containing 5 mM ammonium formate with 0.0025% formic acid (both Sigma-Aldrich), eluent A) and methanol (containing 5 66 67 mM ammonium formate with 0.0025% formic acid, eluent B) with a flow rate of 0.5 ml min⁻¹. Eluent B was increased from 10% to 90% in 10 minutes and maintained for 3 68 minutes. After this, eluent B was decreased to 10% in 0.1 minute and maintained for 1.9 69 70 minute to complete the cycle of 15 minutes. Mass spectrometry was performed with a gas 71 temperature of 350°C and a flow rate of 10 l min⁻¹. Stealth gas temperature (for Agilent 6460) was set at 400 °C with a flow rate of 12 1 min⁻¹. The capillary voltage was set at 72 73 4000 V.

75 Direct injection of nylon leachate

An injection volume of 10 µl diluted nylon leachate was directly injected into an Agilent
6410 triple quadrupole MS system with ESI in positive SCAN mode. The conditions were
as follows: gas temperature 350 °C, flow rate 10 l min⁻¹, mobile phase 50:50 ratio of 80:20
acetonitrile (VWR):Milli-Q water with 5 mM ammonium formate and 10:90
acetonitrile:Milli-Q water with 5 mM ammonium formate, scan range 50–1000 Da,
capillary voltage 3500 V.

82

83 ¹H Nuclear magnetic resonance

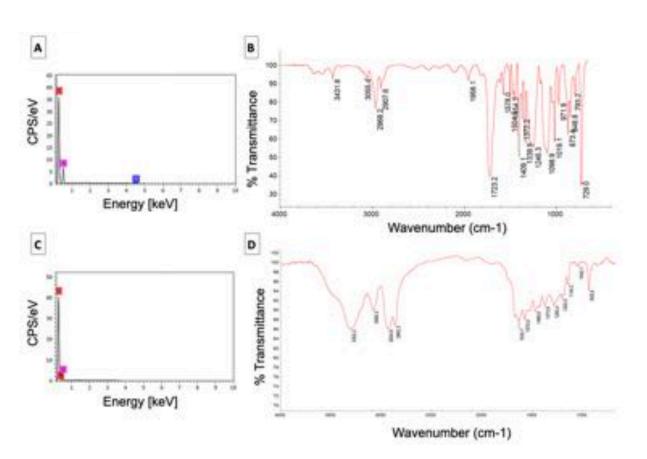
- 84 The chemical structure of the oligomers was confirmed by ¹H NMR spectroscopy (Bruker 85 Avance 400 spectrometer). The oligomers were dissolved in ~0.5 ml CD₃OD:CDCl₃ (1:1) 86 (Sigma-Aldrich). The spectra were recorded at 24 °C, and internally referenced to the 87 residual solvent resonance (CD₃OD: ¹H δ 3.31).
- 88 <u>Nylon monomer</u>, yield = 77 mg. ¹H NMR (400.1 MHz, CD₃OD/CDCl₃ 50:50, 297 K) δ =
- 89 7.56 (br. m, 2H; NHCO), 3.22 (m, 4H, NHCH₂), 2.19 (m, 4H, COCH₂), 1.63 (m, 4H,
 90 COCH₂CH₂), 1.54 (m, 4H, NHCH₂CH₂), 1.32 (m, 4H, NH (CH₂)₂CH₂).
- 91 Nylon dimer, yield = 74 mg. ¹H NMR (400.1 MHz, CD₃OD/CDCl₃ 50:50, 297 K) δ =
- 92
 7.68 (br. m, 4H; NHCO), 3.15 (t, 8H, NHCH₂), 2.18 (m, 8H, COCH₂), 1.60 (m, 8H,
- 93 COCH₂CH₂), 1.47 (m, 8H, NHCH₂CH₂), 1.31 (m, 8H, NH (CH₂)₂CH₂).
- 94 Nylon trimer, yield = 16 mg. ¹H NMR (400.1 MHz, CD₃OD/CDCl₃ 50:50, 297 K) δ =
- 95 7.74 (br. m, 6H; NHCO), 3.14 (t, 12H, NHCH₂), 2.18 (m, 12H, COCH₂), 1.60 (m, 12H,
- 96 COCH₂CH₂), 1.48 (m, 12H, NHCH₂CH₂), 1.32 (m, 12H, NH (CH₂)₂CH₂).
- 97
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99 Supplementary tables and figures

00

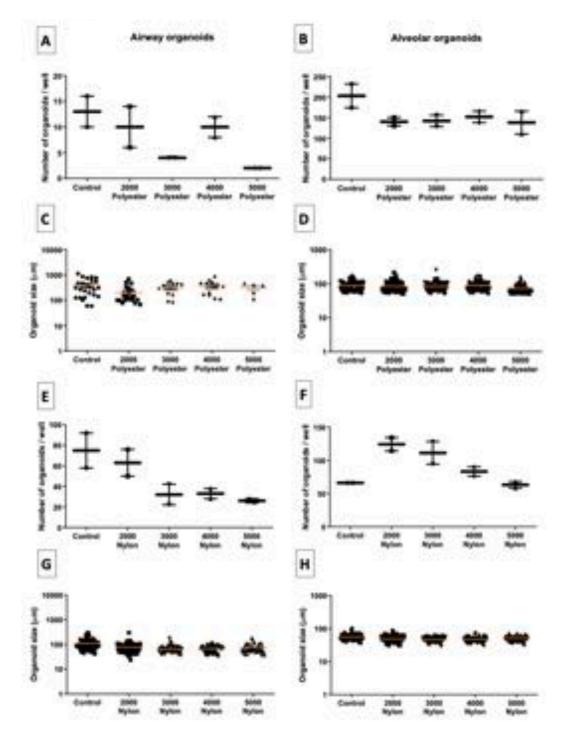
01 **Table S1.** Size characteristics of polyester and nylon reference microfibers.

	Microfiber size Diameter x length (μm)		
	Polyester	Nylon	
25% percentile	14x50	11x29	
Median	15x52	12x31	
75% percentile	15x53	12x32	
Minimum	13x22	9x24	
Maximum	18x64	14x74	



06 Figure S1: Characterization of the reference microfibers using energy dispersive X-ray 07 - and infrared spectroscopy. (A) EDX spectrum of polyester, confirming the presence of 08 carbon (C) and oxygen (O), and additionally revealing the presence of titanium (Ti), 09 which can be ascribed to small TiO2 pigment particles used as filler material in these 10 fibers. (**B**) μ FTIR spectrum of polyester with characteristic absorbance peaks (2968 cm⁻¹, C-H stretch; 1723 cm⁻¹, C=O stretch; 1246 cm⁻¹, C-O stretch aromatic ester; 729 cm⁻¹, 11 12 benzene derivative (81)). (C) EDX spectrum of nylon, confirming the presence of carbon 13 (C), nitrogen (N) and oxygen (O). (D) μ FTIR spectrum of nvlon with characteristic nvlon absorbance peaks (3302 cm⁻¹, N-H stretch; 2934 cm⁻¹, C-H stretch; 1632 cm⁻¹, C=O 14 stretch sec. amide; 1202 cm⁻¹, C-N bend (81)). 15

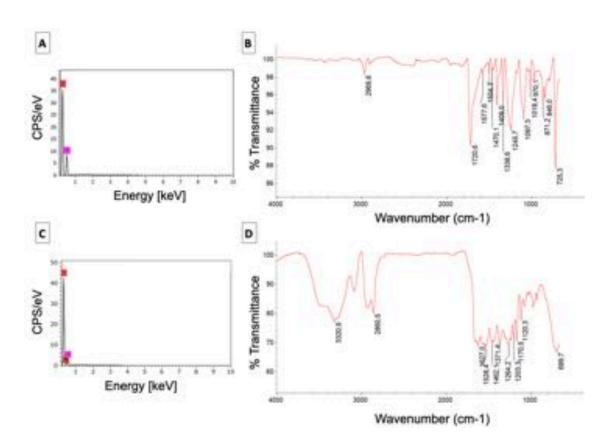
16



18 Figure S2: Determination of the optimal microfiber dose for subsequent in vitro testing of polyester and nylon reference microfibers, using 2000, 3000, 4000 and 5000 19 20 microfibers per condition. (A, E) Quantification of airway and (B, F) alveolar organoid 21 numbers for organoids exposed to polyester or nylon, respectively (n=2 independent 22 isolations). (C, G) Quantification of the airway and (D, H) alveolar organoid size 23 following exposure to polyester or nylon. 2000, 3000, 4000 or 5000 fibers per well 24 corresponded to approximately 49, 73, 98 and 122 µg/ml of polyester fibers or 16, 23, 31, 25 and 39 μ g/ml of nylon fibers.

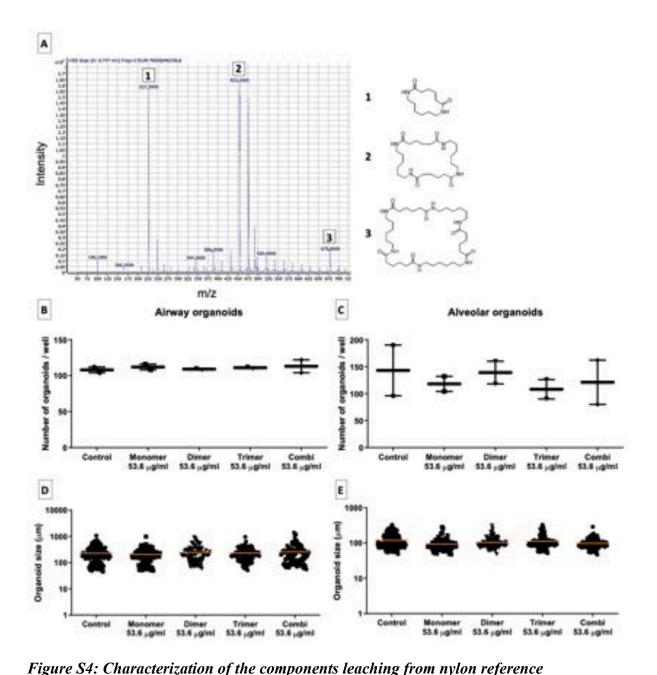
Table S2. Size characteristics of polyester and nylon environmental microfibers.

	Microfiber size Diameter x length (jum)		
-	Environmental polyester	Environmental nylon	
25% percentile	15x54	46x15	
Median	17x63	57x20	
75% percentile	18x85	73x27	
Minimum	8x30	17x8	
Maximum	24x269	296x66	



31 *Figure S3: Characterization of the environmental microfibers using energy dispersive*

- 32 **X-ray and infrared spectroscopy.** EDX and μ -FTIR spectra of (**A** and **B**) polyester and
- 33 (C and D) nylon microfibers.



microfibers and their effect on organoid growth. (A) Mass spectrometry spectrum of the

nylon leachate, revealing high amounts of cyclic nylon mono-, di- and trimers, as well as

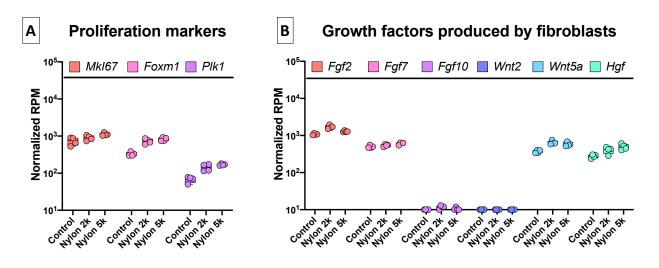
other smaller peaks. (**B** and **C**) Assessment of the numbers of airway and alveolar

organoids and (D and E) their sizes (n=2 independent isolations).

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Figure S5: Expression of individual genes in fibroblasts from organoid cultures

exposed to nylon microfibers. (A) Genes associated with proliferation of fibroblasts. (B)

- Genes encoding factors produced by fibroblasts important for epithelial development
- 47 (n=4 independent isolations).
- 48 49