

Supplementary information for: Microplastics attenuation from surface water  
to drinking water: Impact of treatment and managed aquifer recharge – and  
identification uncertainties

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Treatment

## Section S1 Microplastics count in field blanks

MPs were found in all the field blanks. After approximately two hours of exposure, 91 particles of PE, 48 of PP and 16 of PBT were identified on the field blank at HW\_1. This location was inside the surface water pumping station and a lot of dust was in the air. PU was the predominant class at HW\_2 with 133 particles, followed by PMMA with 10. This location was inside a control room used also as a deposit for items, and the presence of dirt was evident. HW\_2 showed the highest count of MPs and HW\_3 the second lowest, although they were in the same room, just few meters away from each other. At HW\_4, the MPs class with the highest count was PE with fourteen particles. HW\_5 and HW\_6 also were in the same room although the counts of MPs is substantially different. PU was the predominant class at HW\_5 followed by PE, while PE were the most abundant at HW\_6.

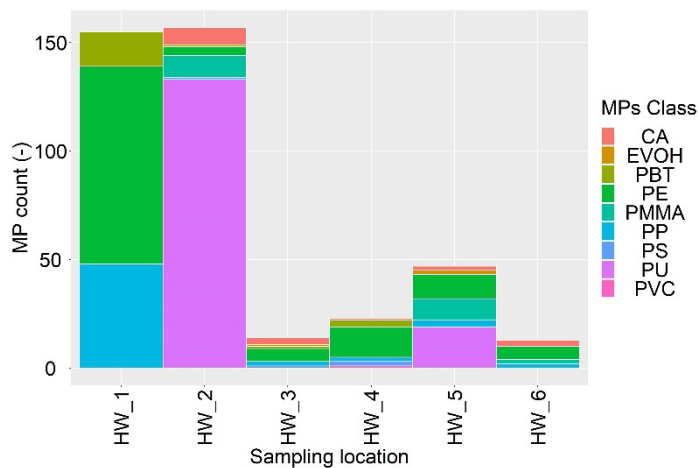
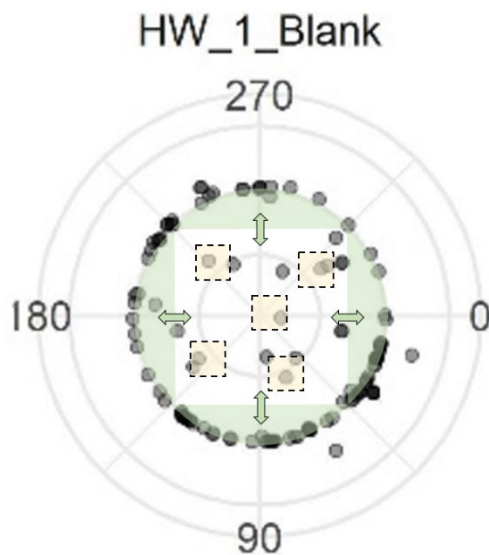


Figure S1: Count of MPs measured in the field blanks stacked by classes and grouped by the sampling locations.

## Section S2 Illustration of the sampling schema

Using the very high resolution microscope, we noticed that the surrogate spheres predominantly accumulated alongside the edges of the anodisc filters. Therefore, we posed particular focus on

scanning these edges. We scanned other randomly chosen areas (containing surrogate particles) in the inner filter, tentatively covering the four sectors of the filter. The sampling schema is depicted in Figure S2.

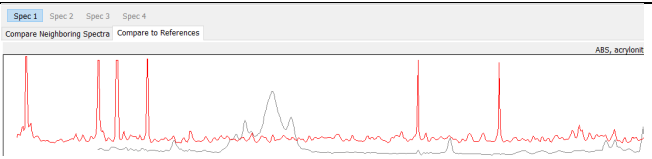
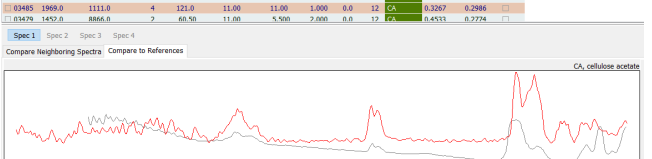


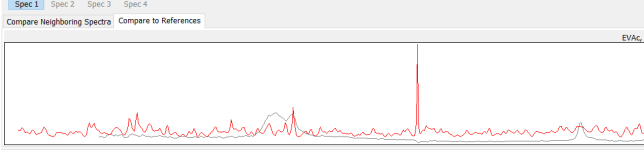
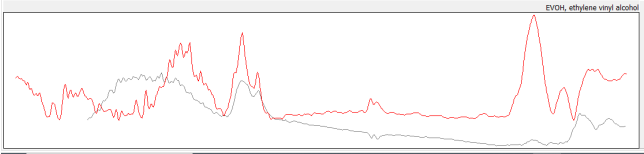
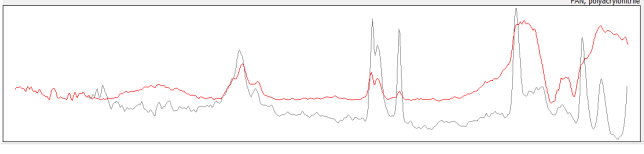
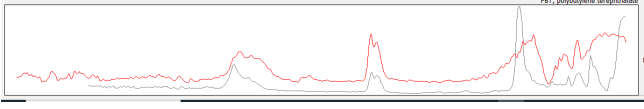
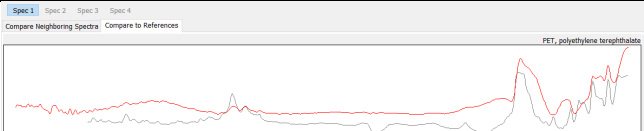
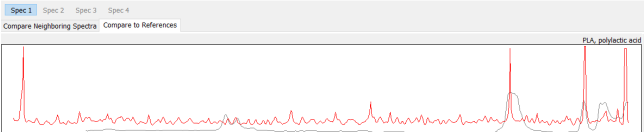
*Figure S2: Sampling schema of the analysed area using the anodic filter of the blank at HW\_1, as an example. Filled circles in gray scale represent the location of the surrogate PE spheres, where lighter gray indicates isolated spheres and darker gray indicates adjacent spheres. The location of the spheres guided the selection of the filter areas to scan. The light green filled circular arcs depict the scanned area along the filter edges and they can be continuous or mosaicked areas. The green arrows indicate that the area of the circular arcs can change depending on the possibility to remain in focus. Squares with a black dashed outline and filled in light yellow depict areas to scan that were randomly chosen, tentatively covering the four sectors of the filter, but they had to contain surrogate particles. The yellow areas can be more or less large based on the possibility to remain in focus. The sum of the green and yellow areas covered more than 50% of the filter area.*

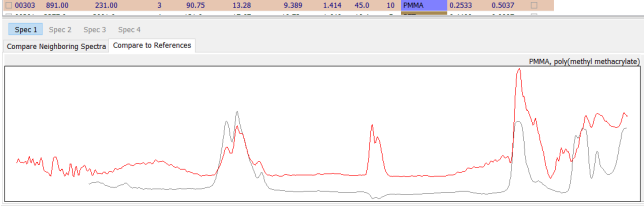
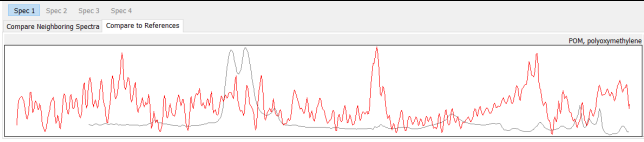
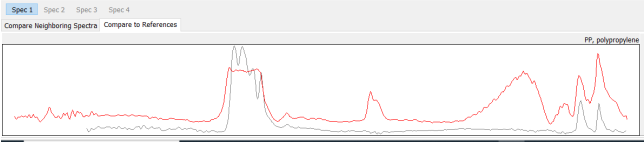
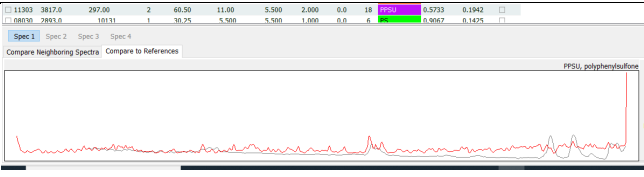
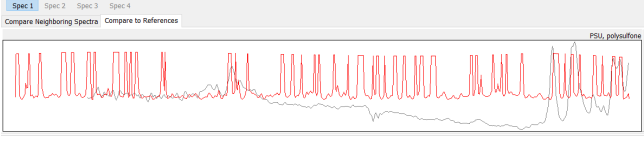
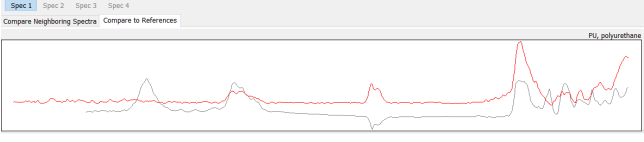
### Section S3 Definition of relevance and similarity thresholds

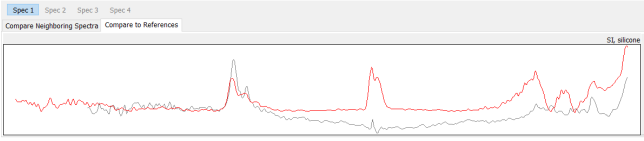
To define the thresholds for relevance and similarity based on the specific type of plastics, other than polyethylene (PE) for which we had surrogate standards, we randomly selected eleven scanned areas and we carried out a visual comparison of the measured and reference hyperspectral signature of the identified particles. When the comparison was satisfactory, we tabulated the minimum R and S calculated by the imaging software and used them as the plastic type-specific thresholds. When satisfactory comparisons were not found, we tabulated the maximum R and S calculated by the imaging software and used them as the plastic type-specific thresholds.

*Table S1: relevance and similarity thresholds defined and used in this study for the 17 plastic types identified other than polyethylene. Red lines are the measured spectra and black lines are the reference spectra.*

| Plastic type | Minimum relevance | Minimum similarity | Figure and comment   |
|--------------|-------------------|--------------------|--|
| ABS          | 0.38              | 0.16               |  <p>No match with maximum similarity.</p>  |
| CA           | 0.32              | 0.29               |  <p>Good match with minimum similarity</p> |

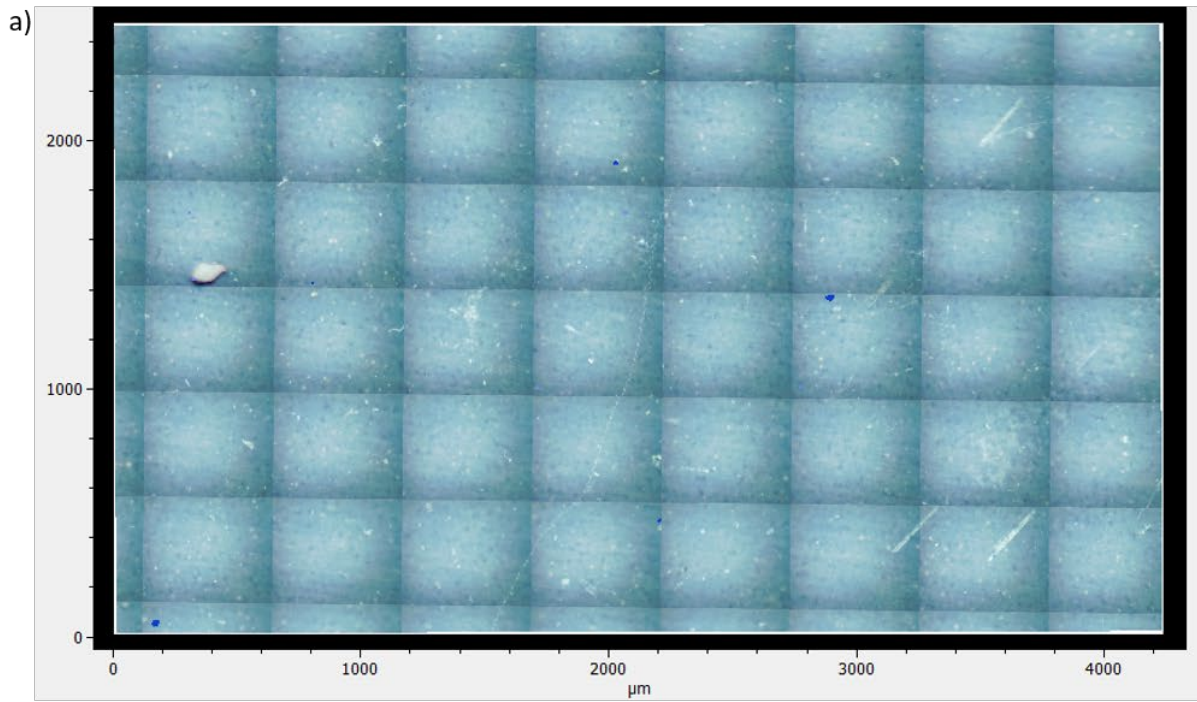
|             |             |             |  |       |        |        |       |       |       |       |        |        |    |      |        |        |       |        |         |    |       |       |       |       |       |    |      |        |        |       |        |        |   |       |       |       |       |     |    |      |        |        |
|-------------|-------------|-------------|--|-------|--------|--------|-------|-------|-------|-------|--------|--------|----|------|--------|--------|-------|--------|---------|----|-------|-------|-------|-------|-------|----|------|--------|--------|-------|--------|--------|---|-------|-------|-------|-------|-----|----|------|--------|--------|
| <p>EVAc</p> | <p>0.61</p> | <p>0.29</p> |  <p>No match with maximum similarity.</p>  |       |        |        |       |       |       |       |        |        |    |      |        |        |       |        |         |    |       |       |       |       |       |    |      |        |        |       |        |        |   |       |       |       |       |     |    |      |        |        |
| <p>EVOH</p> | <p>0.53</p> | <p>0.26</p> | <table border="1" data-bbox="683 470 1329 515"> <tr> <td>00398</td> <td>4565.0</td> <td>3514.5</td> <td>2</td> <td>60.50</td> <td>11.00</td> <td>5.500</td> <td>2.000</td> <td>0.0</td> <td>14</td> <td>EVOH</td> <td>0.5333</td> <td>0.2642</td> </tr> <tr> <td>00394</td> <td>4284.5</td> <td>3591.5</td> <td>11</td> <td>332.8</td> <td>40.12</td> <td>15.74</td> <td>2.549</td> <td>102.8</td> <td>14</td> <td>EVOH</td> <td>0.4545</td> <td>0.3126</td> </tr> <tr> <td>00393</td> <td>4279.0</td> <td>3564.0</td> <td>2</td> <td>60.50</td> <td>11.00</td> <td>5.500</td> <td>2.000</td> <td>0.0</td> <td>14</td> <td>EVOH</td> <td>0.3933</td> <td>0.2855</td> </tr> </table>  <p>Good match with minimum similarity</p> | 00398 | 4565.0 | 3514.5 | 2     | 60.50 | 11.00 | 5.500 | 2.000  | 0.0    | 14 | EVOH | 0.5333 | 0.2642 | 00394 | 4284.5 | 3591.5  | 11 | 332.8 | 40.12 | 15.74 | 2.549 | 102.8 | 14 | EVOH | 0.4545 | 0.3126 | 00393 | 4279.0 | 3564.0 | 2 | 60.50 | 11.00 | 5.500 | 2.000 | 0.0 | 14 | EVOH | 0.3933 | 0.2855 |
| 00398       | 4565.0      | 3514.5      | 2  | 60.50 | 11.00  | 5.500  | 2.000 | 0.0   | 14    | EVOH  | 0.5333 | 0.2642 |    |      |        |        |       |        |         |    |       |       |       |       |       |    |      |        |        |       |        |        |   |       |       |       |       |     |    |      |        |        |
| 00394       | 4284.5      | 3591.5      | 11   | 332.8 | 40.12  | 15.74  | 2.549 | 102.8 | 14    | EVOH  | 0.4545 | 0.3126 |    |      |        |        |       |        |         |    |       |       |       |       |       |    |      |        |        |       |        |        |   |       |       |       |       |     |    |      |        |        |
| 00393       | 4279.0      | 3564.0      | 2  | 60.50 | 11.00  | 5.500  | 2.000 | 0.0   | 14    | EVOH  | 0.3933 | 0.2855 |    |      |        |        |       |        |         |    |       |       |       |       |       |    |      |        |        |       |        |        |   |       |       |       |       |     |    |      |        |        |
| <p>PAN</p>  | <p>0.54</p> | <p>0.42</p> | <table border="1" data-bbox="683 824 1329 851"> <tr> <td>00404</td> <td>3360.5</td> <td>3091.0</td> <td>4</td> <td>121.0</td> <td>16.50</td> <td>11.00</td> <td>1.500</td> <td>90.0</td> <td>15</td> <td>PAN</td> <td>0.5400</td> <td>0.4221</td> </tr> </table>  <p>Good match with minimum similarity</p>   | 00404 | 3360.5 | 3091.0 | 4     | 121.0 | 16.50 | 11.00 | 1.500  | 90.0   | 15 | PAN  | 0.5400 | 0.4221 |       |        |         |    |       |       |       |       |       |    |      |        |        |       |        |        |   |       |       |       |       |     |    |      |        |        |
| 00404       | 3360.5      | 3091.0      | 4  | 121.0 | 16.50  | 11.00  | 1.500 | 90.0  | 15    | PAN   | 0.5400 | 0.4221 |    |      |        |        |       |        |         |    |       |       |       |       |       |    |      |        |        |       |        |        |   |       |       |       |       |     |    |      |        |        |
| <p>PBT</p>  | <p>0.28</p> | <p>0.12</p> | <table border="1" data-bbox="683 1149 1329 1176"> <tr> <td>00403</td> <td>2464.0</td> <td>2047.5</td> <td>2</td> <td>60.50</td> <td>11.00</td> <td>5.500</td> <td>2.000</td> <td>0.0</td> <td>16</td> <td>PBT</td> <td>0.2807</td> <td>0.1197</td> </tr> <tr> <td>04816</td> <td>2453.0</td> <td>4750.00</td> <td>2</td> <td>60.50</td> <td>11.00</td> <td>5.500</td> <td>2.000</td> <td>40.0</td> <td>15</td> <td>PBT</td> <td>0.1867</td> <td>0.0580</td> </tr> </table>  <p>Good match with minimum similarity</p>  | 00403 | 2464.0 | 2047.5 | 2     | 60.50 | 11.00 | 5.500 | 2.000  | 0.0    | 16 | PBT  | 0.2807 | 0.1197 | 04816 | 2453.0 | 4750.00 | 2  | 60.50 | 11.00 | 5.500 | 2.000 | 40.0  | 15 | PBT  | 0.1867 | 0.0580 |       |        |        |   |       |       |       |       |     |    |      |        |        |
| 00403       | 2464.0      | 2047.5      | 2  | 60.50 | 11.00  | 5.500  | 2.000 | 0.0   | 16    | PBT   | 0.2807 | 0.1197 |    |      |        |        |       |        |         |    |       |       |       |       |       |    |      |        |        |       |        |        |   |       |       |       |       |     |    |      |        |        |
| 04816       | 2453.0      | 4750.00     | 2  | 60.50 | 11.00  | 5.500  | 2.000 | 40.0  | 15    | PBT   | 0.1867 | 0.0580 |    |      |        |        |       |        |         |    |       |       |       |       |       |    |      |        |        |       |        |        |   |       |       |       |       |     |    |      |        |        |
| <p>PC</p>   |             |             | <p>No particles identified in the raw data</p>   |       |        |        |       |       |       |       |        |        |    |      |        |        |       |        |         |    |       |       |       |       |       |    |      |        |        |       |        |        |   |       |       |       |       |     |    |      |        |        |
| <p>PET</p>  | <p>0.45</p> | <p>0.70</p> |  <p>Good match with minimum similarity</p>   |       |        |        |       |       |       |       |        |        |    |      |        |        |       |        |         |    |       |       |       |       |       |    |      |        |        |       |        |        |   |       |       |       |       |     |    |      |        |        |
| <p>PLA</p>  | <p>0.7</p>  | <p>0.32</p> |  <p>Unclear match with minimum similarity</p>  |       |        |        |       |       |       |       |        |        |    |      |        |        |       |        |         |    |       |       |       |       |       |    |      |        |        |       |        |        |   |       |       |       |       |     |    |      |        |        |

|             |             |             |  |
|-------------|-------------|-------------|--|
| <p>PMMA</p> | <p>0.25</p> | <p>0.50</p> |  <p>Good match with minimum similarity</p>                                   |
| <p>POM</p>  | <p>0.45</p> | <p>0.12</p> |  <p>No match with maximum similarity.</p>                                    |
| <p>PP</p>   | <p>0.19</p> | <p>0.23</p> |  <p>Good match with minimum similarity</p>                                   |
| <p>PPSU</p> | <p>0.57</p> | <p>0.19</p> |  <p>No match with maximum similarity.</p>                                  |
| <p>PS</p>   | <p>0.5</p>  | <p>0.5</p>  | <p>Thresholds reported in a personal communication by Matthias Philipp identified in laboratory tests while using PS surrogate standards in sludge samples</p> |
| <p>PSU</p>  | <p>0.5</p>  | <p>0.2</p>  |  <p>No match with maximum similarity.</p>                                  |
| <p>PU</p>   | <p>0.36</p> | <p>0.29</p> |    |

|          |      |      |  |
|----------|------|------|--|
|          |      |      | Good match with minimum similarity   |
| PVC      | 0.58 | 0.28 |  <p>Good match with minimum similarity</p> |
| silicone | 0.37 | 0.39 |  <p>Good match with minimum similarity</p> |

**Section S4 Analysis of a laboratory blank**

The visual inspection of the identified MPs on the anodisc filter clearly revealed a cross-contamination by polyamide and the presence of false positives of PMMA. PA MPs are larger than 1 pixel (blue areas in Figure S3a). The corresponding relevance and similarity values (Figure S3b) are higher than typical thresholds found in this research. Finally, the corresponding hyperspectral signature is indeed similar to the one of reference PA MPs (Figure S3c). Differently, PA MPs are made of 1 pixel (violet pixels in Figure S3a). The corresponding relevance and similarity values (Figure S3b) are lower than the thresholds found in this research. Finally, the corresponding hyperspectral signature is not similar to the one of reference PMMA MPs (Figure S3d).



b)

| PID                                       | Cent.X [µm] | Cent.Y [µm] | Size[px] | Area [µm <sup>2</sup> ] | Length [µm] | Width [µm] | Aspect | Dir[°] | Cl. | Cl. Name | Relevance | Similarity | Done                     |
|---|-------------|-------------|----------|-------------------------|-------------|------------|--------|--------|-----|----------|-----------|------------|--------------------------|
| <input type="checkbox"/> 00002            | 170.50      | 55.000      | 11       | 332.8                   | 28.18       | 18.93      | 1.488  | 14.7   | 8   | PA       | 0.7515    | 0.4884     | <input type="checkbox"/> |
| <input type="checkbox"/> 00003            | 808.50      | 1424.5      | 1        | 30.25                   | 5.500       | 5.500      | 1.000  | 0.0    | 8   | PA       | 0.6133    | 0.4003     | <input type="checkbox"/> |
| <input type="checkbox"/> 00006            | 2029.5      | 1908.5      | 4        | 121.0                   | 16.50       | 11.00      | 1.500  | 0.0    | 8   | PA       | 0.7367    | 0.4997     | <input type="checkbox"/> |
| <input type="checkbox"/> 00007            | 2200.0      | 467.50      | 1        | 30.25                   | 5.500       | 5.500      | 1.000  | 0.0    | 8   | PA       | 0.6400    | 0.3824     | <input type="checkbox"/> |
| <input type="checkbox"/> 00008            | 2205.5      | 473.00      | 1        | 30.25                   | 5.500       | 5.500      | 1.000  | 0.0    | 8   | PA       | 0.5867    | 0.3953     | <input type="checkbox"/> |
| <input type="checkbox"/> 00009            | 2893.0      | 1369.5      | 15       | 453.7                   | 33.54       | 22.73      | 1.476  | 10.5   | 8   | PA       | 0.7751    | 0.4612     | <input type="checkbox"/> |
| <input type="checkbox"/> 00012            | 308.00      | 1710.5      | 1        | 30.25                   | 5.500       | 5.500      | 1.000  | 0.0    | 10  | PMMA     | 0.5067    | 0.1075     | <input type="checkbox"/> |
| <input type="checkbox"/> 00013            | 330.00      | 1441.0      | 2        | 60.50                   | 11.00       | 5.500      | 2.000  | 0.0    | 10  | PMMA     | 0.3933    | 0.1121     | <input type="checkbox"/> |
| <input type="checkbox"/> 00017            | 1716.0      | 1006.5      | 1        | 30.25                   | 5.500       | 5.500      | 1.000  | 0.0    | 10  | PMMA     | 0.4000    | 0.0525     | <input type="checkbox"/> |
| <input type="checkbox"/> 00018            | 1716.0      | 1710.5      | 1        | 30.25                   | 5.500       | 5.500      | 1.000  | 0.0    | 10  | PMMA     | 0.4133    | 0.0869     | <input type="checkbox"/> |
| <input type="checkbox"/> 00019            | 2068.0      | 1710.5      | 1        | 30.25                   | 5.500       | 5.500      | 1.000  | 0.0    | 10  | PMMA     | 0.4267    | 0.0796     | <input type="checkbox"/> |
| <input type="checkbox"/> 00021            | 2772.0      | 1006.5      | 1        | 30.25                   | 5.500       | 5.500      | 1.000  | 0.0    | 10  | PMMA     | 0.5067    | 0.0983     | <input type="checkbox"/> |
| <input checked="" type="checkbox"/> 00024 | 3828.0      | 1358.5      | 1        | 30.25                   | 5.500       | 5.500      | 1.000  | 0.0    | 10  | PMMA     | 0.5200    | 0.1033     | <input type="checkbox"/> |

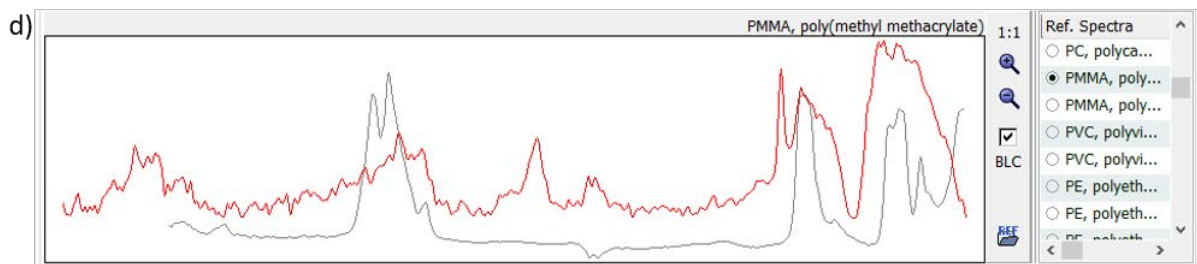
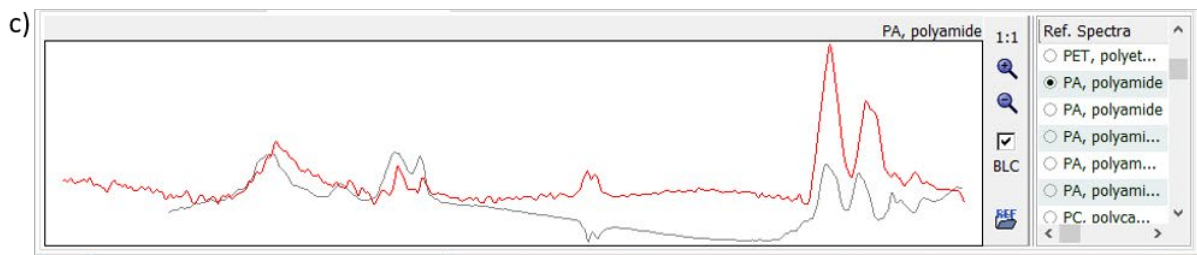
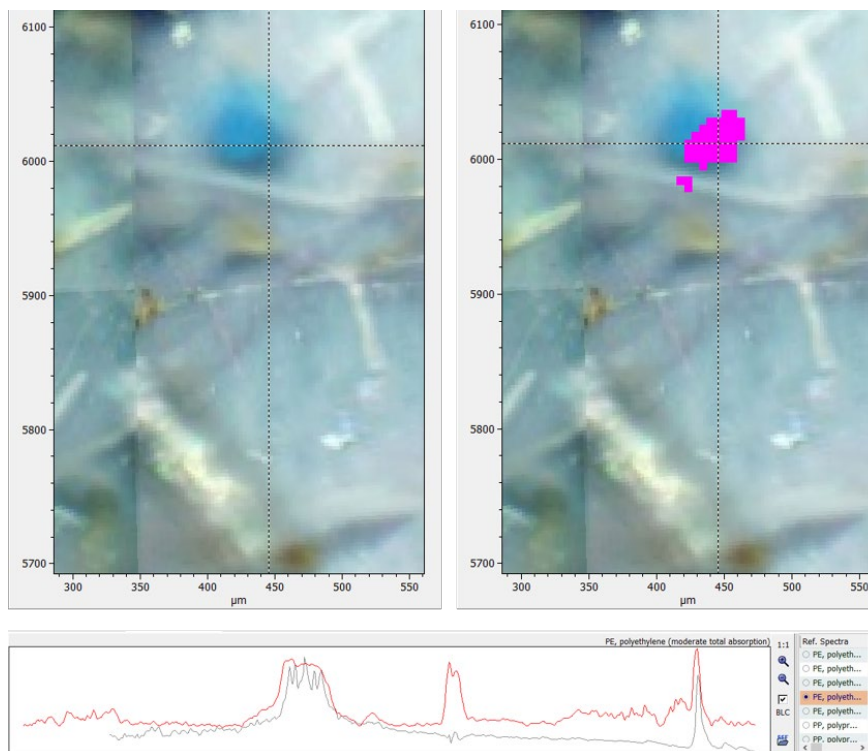


Figure S3: a) 2D image of the scanned anodisc filter with polyamide (PA) MPs in blue and PMMA MPs in violet; b) Summary table with the information on the identified MPs; c)



*Hyperspectral signature of the observed PA MPs (red line) and the PA signature in the Purity's database (in black); d) Hyperspectral signature of the observed PMMA MPs (red line) and the PMMA signature in the imaging software Microplastics Finder's database (in black).*

### Section S5 Appearance of the surrogate PE spheres



*Figure S4: a) Zoom in on a surrogate PE sphere; b) Blue PE sphere identified as classified as PE by the imaging software Microplastics Finder; c) Hyperspectral signature of the observed PE MPs (red line) and the PE signature in the imaging software Microplastics Finder's database (in black).*

### Section S6 Appearance of fibers

Fibers may be challenging to identify in their entirety because they expand in three dimensions and they are likely broken down in smaller particles when using  $\mu$ FTIR analysis. This is visible when looking at panel b) of Figure S5. The imaging software Microplastics Finder classified the fiber as PAN with high Relevance and Similarity values (Figure S5c). Indeed, there is also a clear visual similarity between the hyperspectral signature of the observed PAN MPs (red line) and the PAN signature in the imaging software Microplastics Finder's database (in black).

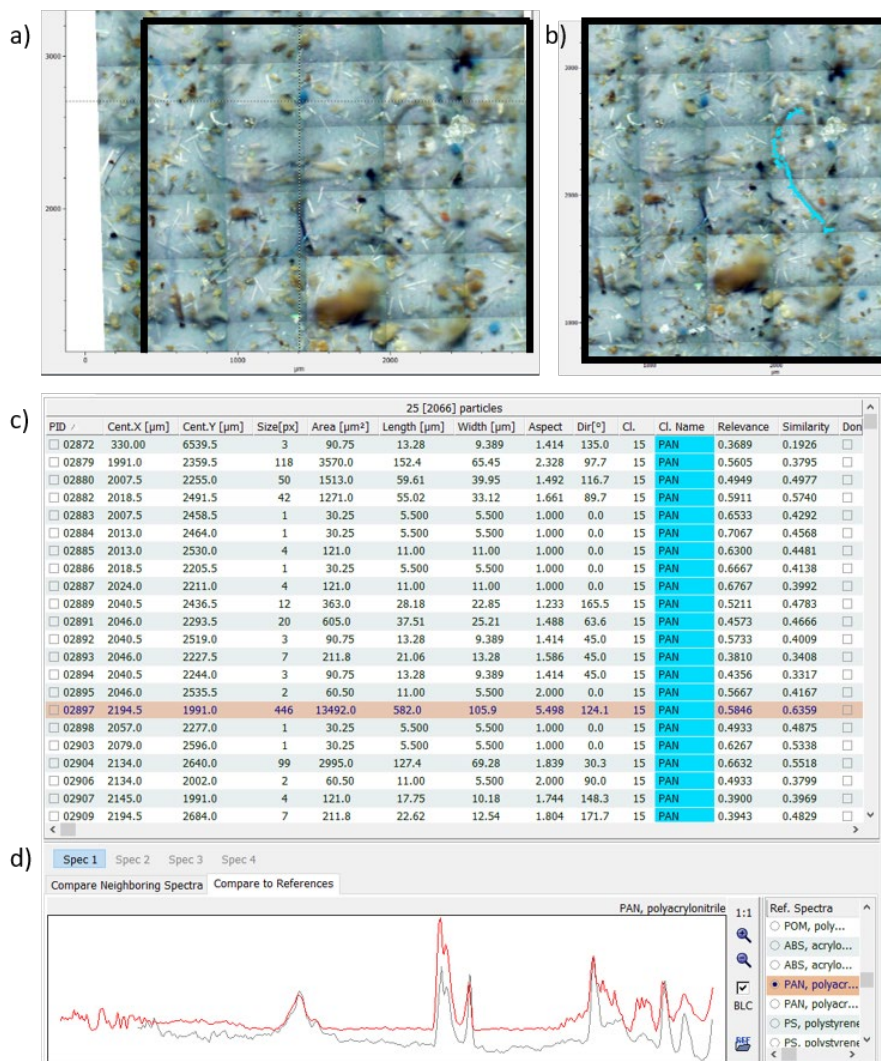


Figure S5: a) 2D image of the scanned anodisc filter in true colors. The black box indicate the area zoomed in in panel b); b) Zoom in on 2D area of the scanned anodisc filter with a fiber in cyan classified as PAN by the imaging software Microplastics Finder; c) Hyperspectral

*signature of the observed PE MPs (red line) and the PE signature in the imaging software  
Microplastics Finder's database (in black).*