

1 **Supplementary Material**

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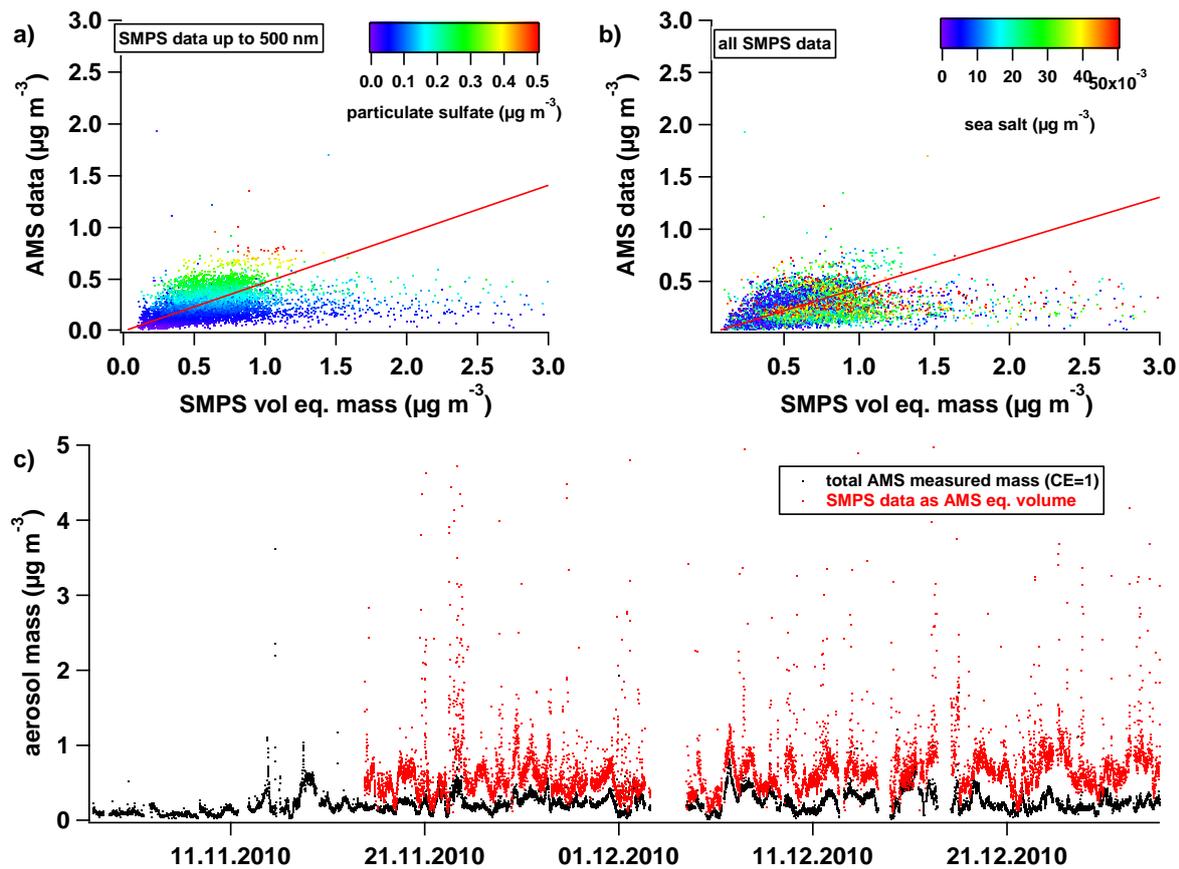
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4 **1 AMS SMPS data comparison**

5 A linear regression between the calculated mass based on the SMPS measured particle
6 volume and the total mass concentration measured by the AMS was derived. To derive a
7 particle density we used the following specific densities: Organics: 1.6 g/cm³; ammonium
8 nitrate: 1.73 g/cm³; ammonium sulfate: 1.77 g/cm³; sulfuric acid: 1.84 g/cm³. The average
9 particle mass density for the whole campaign was 1.71 g/cm³. We used both the complete
10 volume measured by the SMPS, and only up to $d_{mob} = 500\text{nm}$ which corresponds to a d_{va} of
11 about 855 nm where the AMS inlet starts to cut off significantly larger particles. R^2 is well
12 below 0.1 in both cases, while the slope is 0.44 when including all SMPS data, and 0.46 when
13 only using SMPS data up to 500 nm. The colour coding indicates that the relationship is
14 poorer for lower particulate sulfate concentrations, and seems to be partly due to non-
15 refractory particles such as sea salt contributions (see colour coding by the PIKA derived sea
16 salt species). Based on the low R^2 values and available literature (Middlebrook et al. 2012) we
17 decided to use $CE = 0.5$. $CE = 0.5$ can be interpreted as the upper envelop (see Figure S1).

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 21 Figure S1: AMS aerosol mass versus SMPS volume equivalent mass for a) SMPS data up to
 22 500 nm d_{mob} and b) for all SMPS data. c) Time series of AMS aerosol mass versus SMPS
 23 volume equivalent mass data. Note that the AMS data is not corrected for sea salt after
 24 Ovadnevaite et al. (2012) by upscaling m/z 57.95 ($\text{Na}35\text{Cl}^+$) by a factor of 51.

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28 **2 AMS sea salt detection**

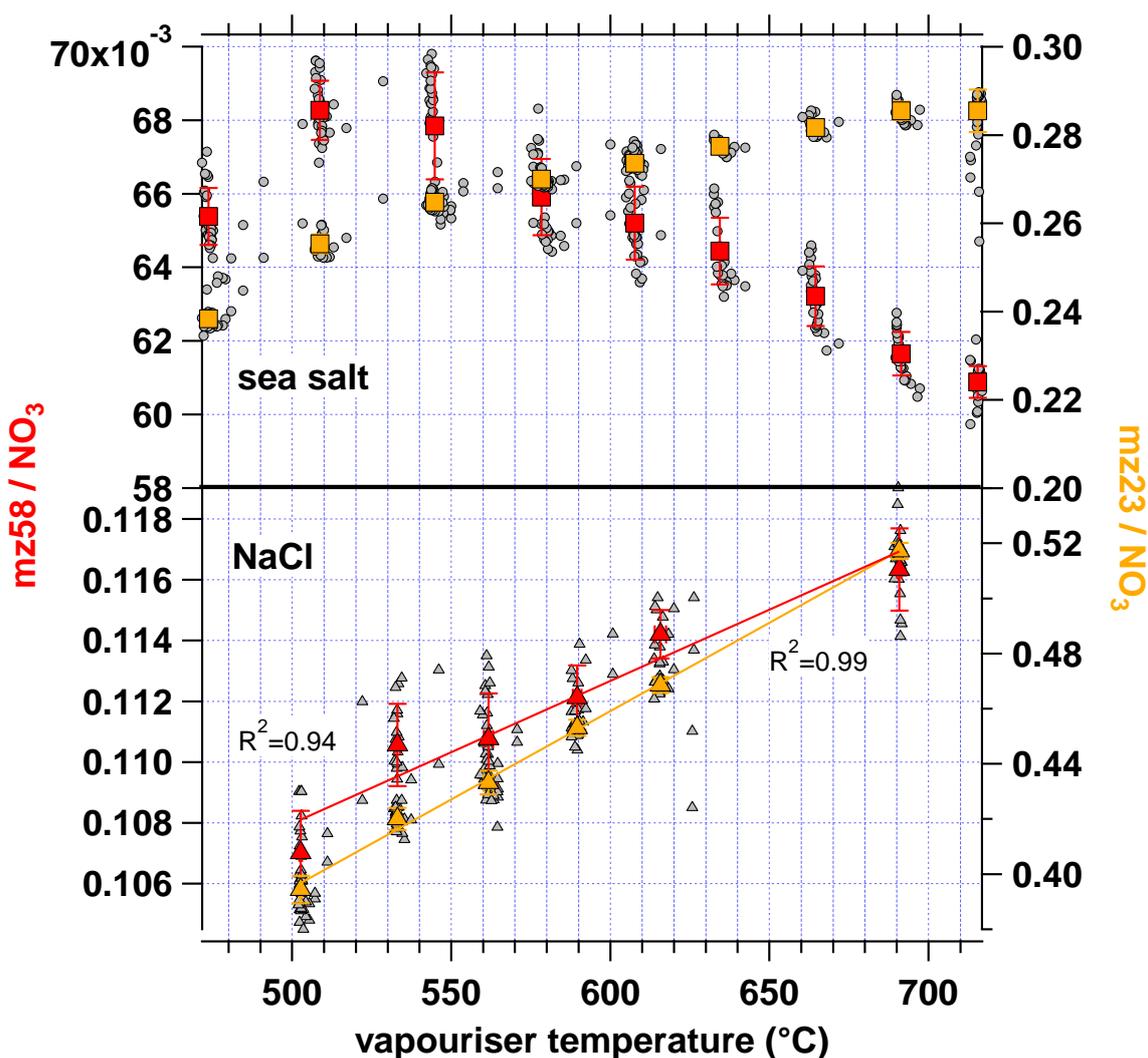
29 Following the BI field campaign, additional laboratory measurements were undertaken with a
30 different AMS (compact time-of-flight aerosol mass spectrometer as described by Schmale et
31 al. (2010)) to characterise the extent to which the AMS is capable of sea salt quantification
32 and identify potential cross-sensitivities to other AMS standard chemical species. Known
33 amounts of NaCl and sea salt (SIGMA-Aldrich sea salt standard S9883), each mixed
34 separately with ammonium nitrate in solution, were measured with the AMS across a range of
35 vapouriser temperatures between 480 and 720 °C. The ratios of two NaCl and sea salt
36 fragments, Na⁺ (*m/z* 23) and NaCl⁺ (*m/z* 58), and the AMS species chloride (based on the
37 standard fragmentation table) to nitrate were characterized.

38 For the NaCl solution, the ratio of *m/z* 58 and *m/z* 23 to NO₃⁻ increased linearly with
39 temperature ($R^2 = 0.94$, slope 4.7×10^{-5} , and $R^2 = 0.99$, slope 6.4×10^{-4} , respectively, see Fig.
40 S2, bottom panel). The same *m/z* ratios behaved differently for the sea salt solution for which
41 the response was non-linear: While the ratio *m/z* 58 to NO₃⁻ peaked near 550 °C, the *m/z* 23 to
42 NO₃⁻ ratio increased steadily but not linearly with temperature (see Fig. S2). These different
43 behaviours of the Na⁺ and NaCl⁺ ions in the SIGMA-Aldrich sea salt solution have also been
44 reported by Ovadnevaite et al. (2012). Those authors argue that either the fragmentation of
45 NaCl⁺ ions increases at higher vapouriser temperatures, leading to lower ion concentration, or
46 the ion thermal velocity increases resulting in a lower detection efficiency. For Na⁺ the
47 increasing concentration with higher temperatures is assumed to be related to higher
48 fragmentation of the NaCl⁺ ion and partly to surface ionisation. In addition, the different
49 behaviours of the two ions as a function of the salt solution suggest that the AMS
50 vapourisation and ionisation processes are significantly influenced by the mixture of salts.
51 Deriving a scaling factor based on these fragments would thus lead to a highly uncertain
52 quantification for sea salt on Bird Island, especially since the contributing salts in ambient
53 marine air are largely unknown and likely to vary strongly depending on the location (e.g., BI
54 aerosol is influenced strongly by NH₃ emissions). Indeed, unpublished measurements
55 revealed significant differences in properties (hygroscopic growth, crystallisation etc.) of
56 reference sea salts from different suppliers, further emphasising the influence of trace metals
57 on its physicochemical behaviour (C. Braban, pers. comm.).

58 While there was a large discrepancy of a factor greater than 2 for NaCl⁺ and Na⁺ ions in the
59 scaling factor between pure NaCl and sea salt standard at 600 °C, for chloride the results were

60 more consistent, ranging between a factor of 3.15 ± 0.20 and 3.97 ± 0.14 across all
61 experiments. However, up-scaling based on AMS chloride might lead to errors for at least two
62 reasons: (1) particulate chloride concentrations might not be quantified correctly by AMS
63 measurements as it forms salts that have relatively high vapourisation temperatures
64 ($> 600 \text{ }^\circ\text{C}$), and (2) other sources beside sea salt might contribute to the overall chloride
65 concentration.

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67

68 Figure S2: Ratios of m/z 58 (NaCl^+) and m/z 23 (Na^+) over particulate nitrate for a solution of
69 standard sea salt (SIGMA-Aldrich S9883, upper panel) with ammonium nitrate (mass ratio
70 0.9) and for a solution of pure NaCl (lower panel) with ammonium nitrate (mass ratio 1.1) as
71 function of vapouriser temperature. The slope of the linear regression of m/z 58 over
72 particulate nitrate versus the heater temperature is 4.73×10^{-5} , the slope of m/z 23 over
73 particulate nitrate versus the heater temperature is 6.38×10^{-4} .

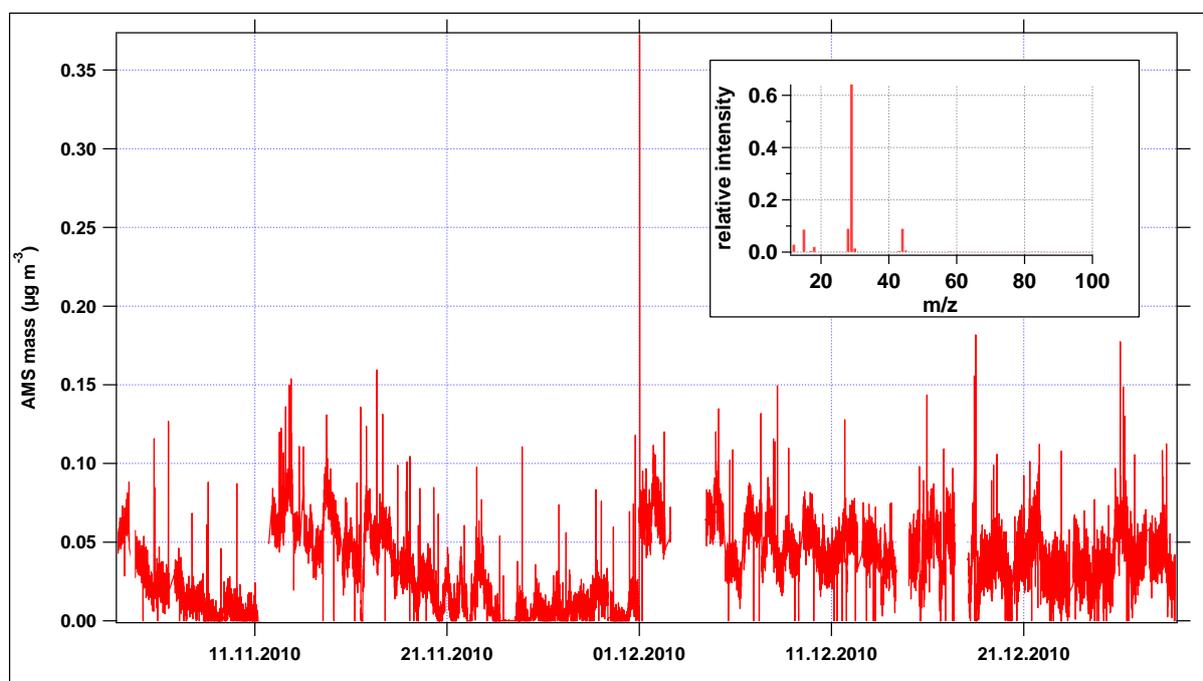
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76 3 Weighting m/z 29 for PMF analysis

77 Since it was not clear whether the signal at m/z 29 was partly an artefact due to a leakage in
78 the vacuum chamber, this mass to charge ratio was downweighted. Given the case of a
79 leakage, more air molecules would be available to produce a signal predominantly at m/z 28
80 (N_2^+). This would result in an elevated baseline influencing the neighbor m/z 29 which in turn
81 would be overestimated.

82 When not downweighting m/z 29 a six factor PMF solution seemed to best meet the criteria of
83 a minimum Q/Q_{exp} . However, one factor mainly consisting of m/z 29 (62.3 %) and m/z 44 (9.5
84 %) was derived. This factor, based on only two mass to charge ratios and based to more than
85 50 % on m/z 29 was not trusted, due to steps in the signal intensity occurring in the time series
86 (see Fig. S3). To test whether this factor might be an artefact, m/z 29 was downweighted by a
87 factor 100 and 1000. The factor profile disappeared when downweighting by either factor.
88 Table S1 shows the relative differences between downweighting by a factor 100 or 1000 in
89 the time series and mass spectra for the five factor solution at $f_{peak} = 0$ and $seed = 0$. For the
90 final analysis m/z 29 was downweighted by a factor of 1000.



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92 Figure S3: Time series and mass spectrum of the m/z 29 dominated factor

93

94 Table S1: Relative difference between downweighting m/z 29 by a factor 100 or 1000

Factor	relative difference 100/1000 in mass spectra (%)	relative difference 100/1000 in time series (%)
MSA-OA	2.15	0.36
AA	1.68	0.71
M-OOA	1.04	1.30
SS-OA	4.06	2.59
HOA	3.02	3.19

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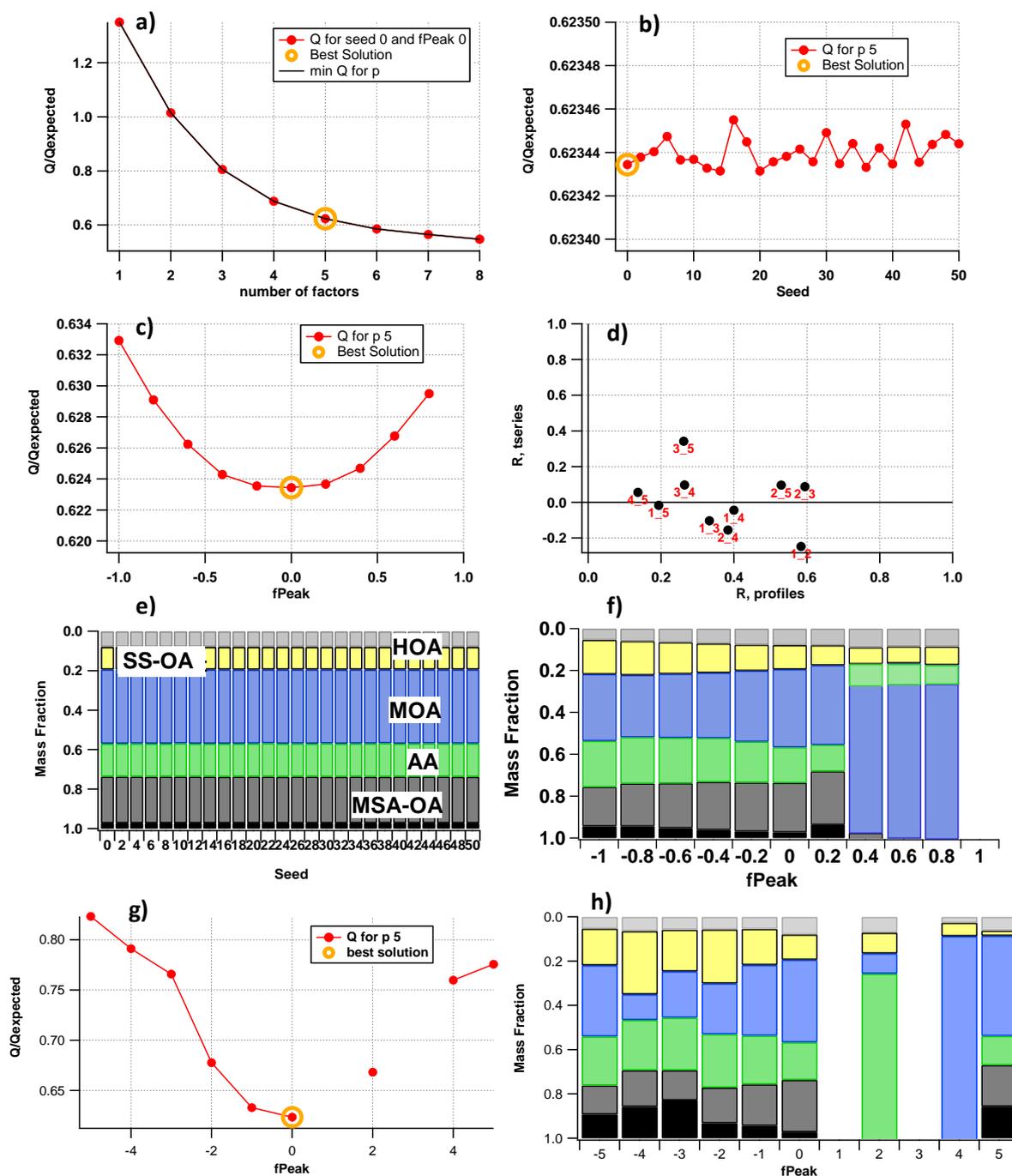
97 4 Key diagnostic plots for the PMF 5 factor solution

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99 The change in slope of the Q/Q_{exp} vs. the number of PMF solutions curve between factors 4
100 and 5 (see Fig. S4 a) indicates that at least 5 factors should be considered. The Q value or
101 “PMF quality of fit parameter” (Zhang et al., 2011) refers to the sum of weighed square
102 residuals. Five factors were chosen, because factor splitting was identified in the solutions
103 using 6 or more factors (see Fig. S4). For example, factor 1 (count upwards from bottom) in
104 the 5-factor solution is split into factors 1 and 2 in the 6-factor solution, as the time series
105 clearly show (cf. Figs. S5c and S5e). Also, the correlation between the two mass spectra is
106 very high at 99 % (not shown). In the 5-factor solution, factor 1 contributes 23.5 % of the
107 mass, while factors 1 and 2 contribute 17.8 and 12.2 % in the 6 factor solution. The 7-factor
108 solution yields factors that do not represent meaningful OA aerosol mass spectra, where e.g.,
109 m/z 28 and 44 make up 50 % of the mass. Choosing only 4 factors results in factors 3 and 5
110 from the five factor solution being merged. Factor 5 in the 5-factor solution was identified as
111 hydrocarbon-like OA (HOA), based on the high correlation ($R^2 = 0.92$) with the reference
112 mass spectrum (A-DEC-Q-015) of the AMS UMR database, based on Ng et al. (2011). When
113 only 4 factors are chosen, the correlation to the HOA reference spectrum decreases to
114 $R^2 = 0.76$. The additional profile in the 5-factor solution, which was identified as marine
115 oxygenated OA (M-OOA), has a low correlation with the HOA reference spectrum ($R^2 =$
116 0.10), so that the separation of the factors is meaningful. Also, the time series of factors M-
117 OOA and HOA have a correlation coefficient of $R^2 = 0.12$ (see Fig. S4 d), so that a 5-factor
118 solution is plausible. All time series’ correlation coefficients are in the range between -0.25
119 and 0.34 (R^2 between 0.06 and 0.12), while the mass spectrum R ranges between 0.14 and
120 0.59 (R^2 between 0.02 and 0.35). The relatively high correlations in the mass spectra between
121 factors 1 and 2 as well as 2 and 3 (see Fig. S4 d) are based on the relatively high contributions
122 of m/z 28, 29 and 44 to the signals. Other marker fragments, however, do not coincide.

123 The chosen final f_{peak} is 0, where Q/Q_{exp} is at a minimum (see Fig. S4c). All other values of
124 f_{peak} between -1 and 0.2 show only rotational ambiguity in the 5-factor solution, while f_{peak}
125 > 0.2 introduces a factor consisting to 80 % of m/z 29, which does not represent a meaningful
126 chemical mass spectrum. Fig. S4 f) shows that this factor starts to dominate the contributions
127 to the total reconstructed mass of OA. Since Zhang et al. (2011) recommend running PMF for
128 a range of f_{peaks} such that the range of Q/Q_{exp} values is at least 3 % above the minimum
129 Q/Q_{exp} , and since this was not the case for the f_{peak} range -1 to 1, we additionally explored

130 the f_{peak} range between -5 and 5 in steps of one (Fig. S4 g) and h). However, no other more
 131 plausible was found in the larger range. The Q/Q_{exp} value < 1 at $f_{peak} = 0$ indicates that the
 132 error matrix was somewhat overestimated which is consistent with downweighting m/z 29 by
 133 a factor of 1000. *Seed* 0 has been chosen to represent the final 5-factor solution, as Q/Q_{exp} is
 134 very stable over the whole range of tested *seeds*. Also, the contribution of each factor to the
 135 total organic mass when varying *seeds* does not vary significantly (see Fig. S4b).
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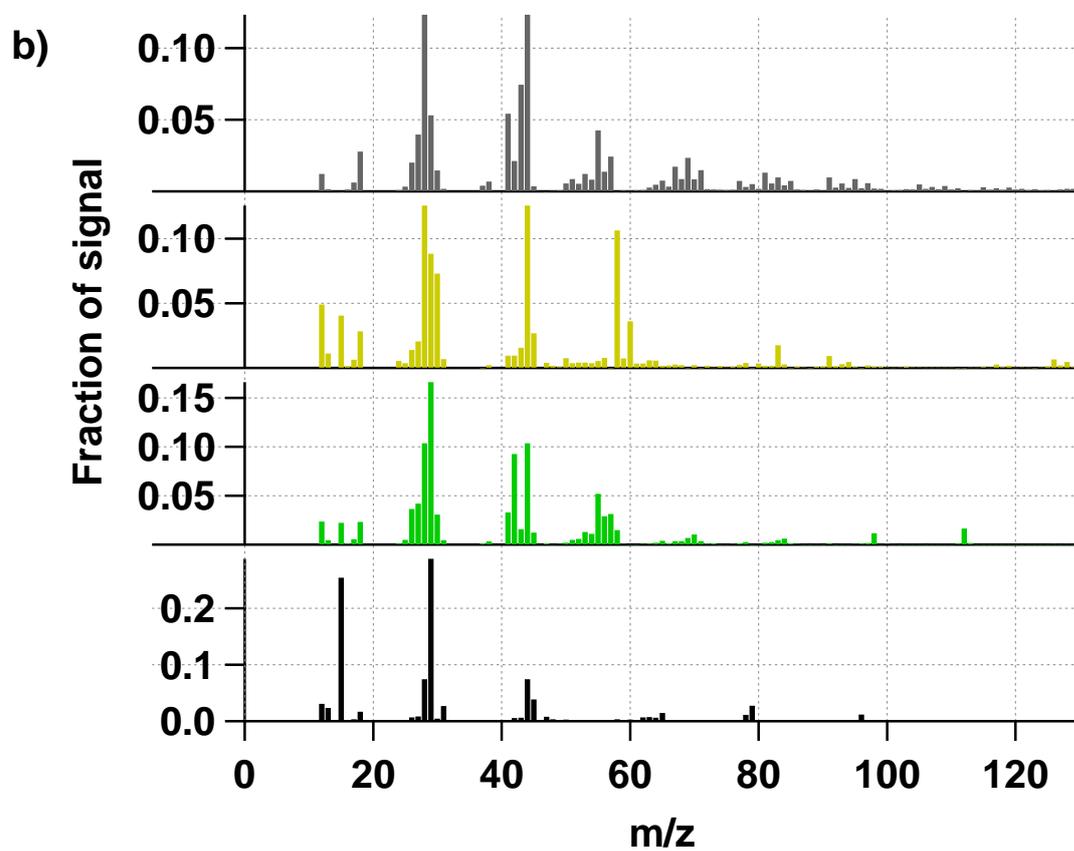
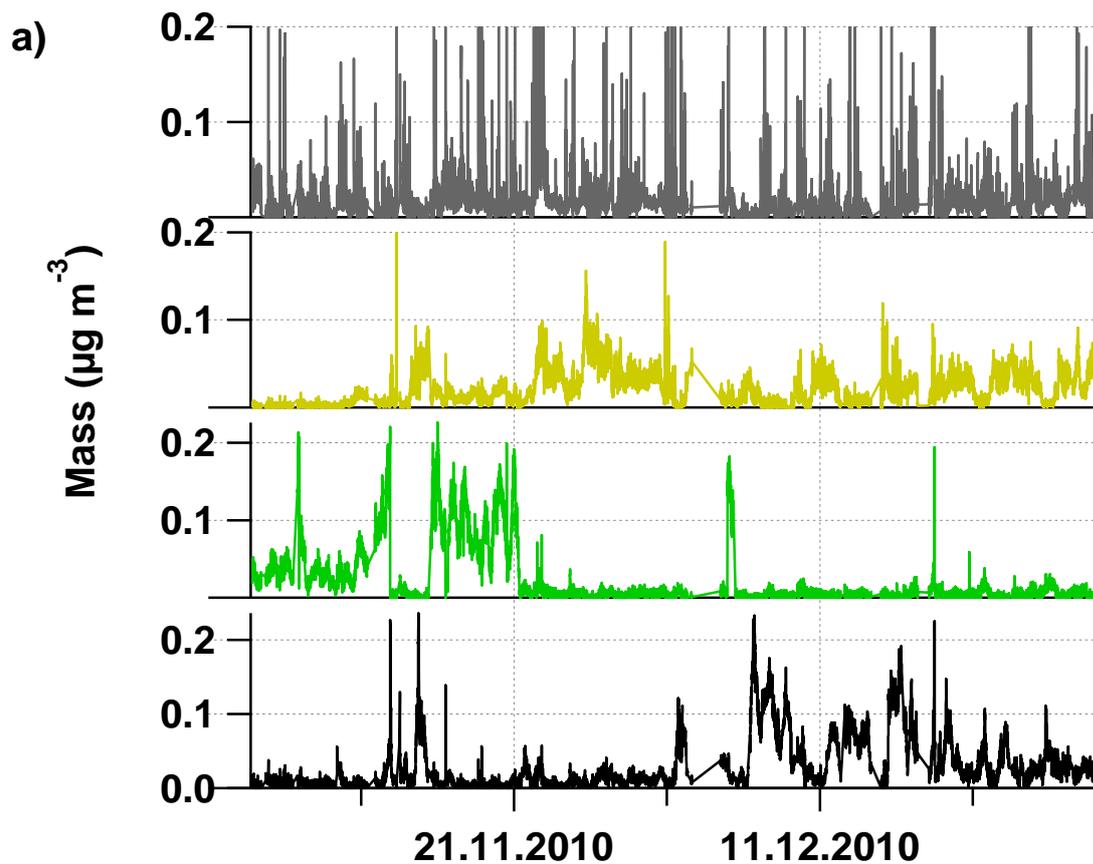


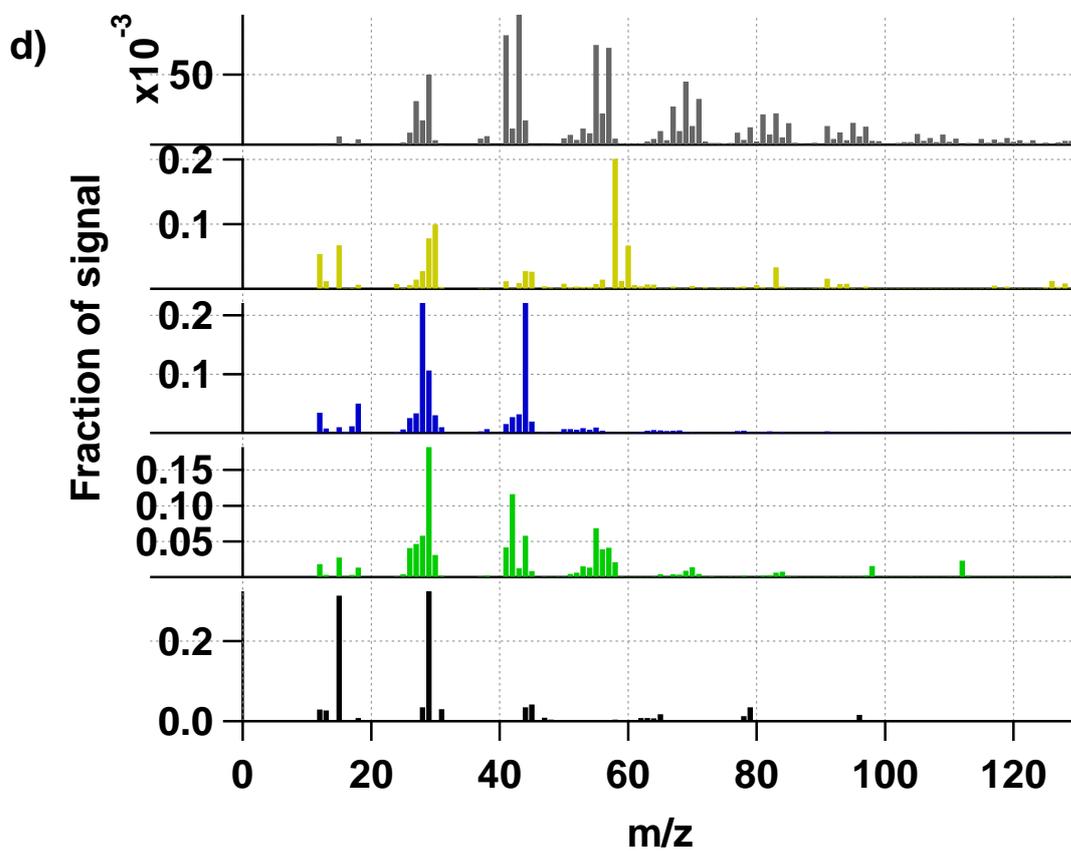
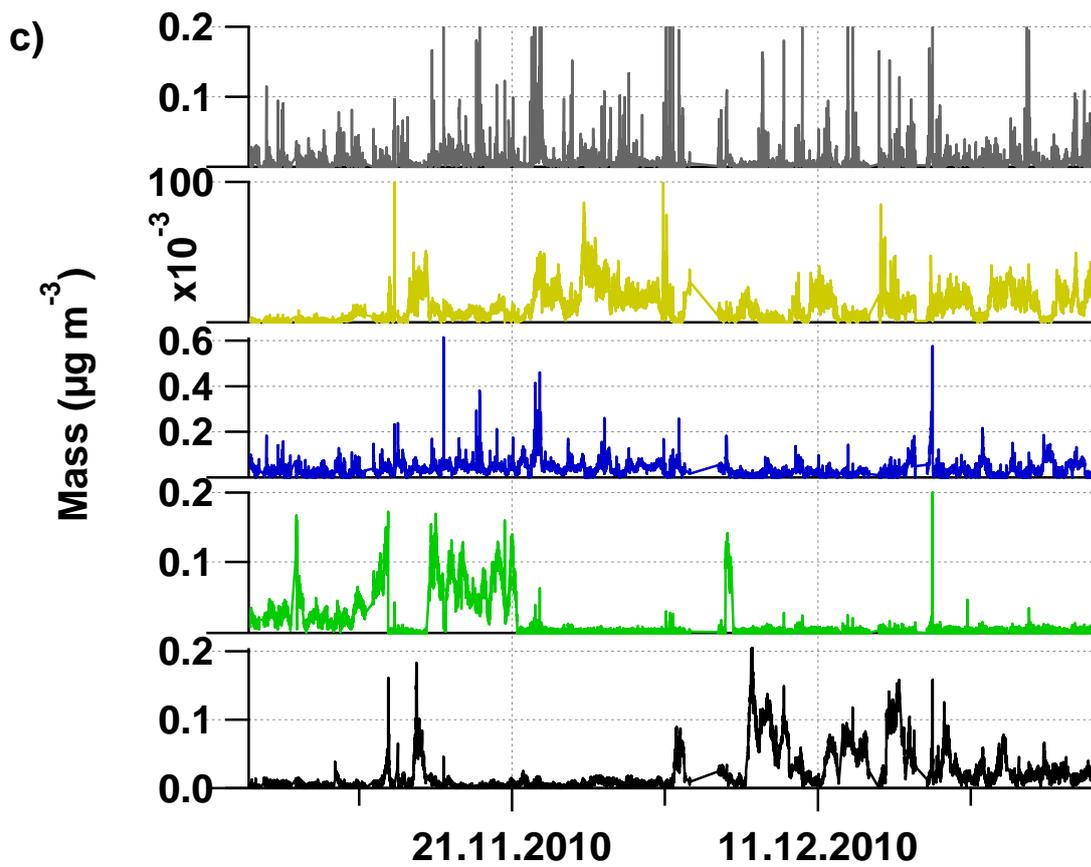
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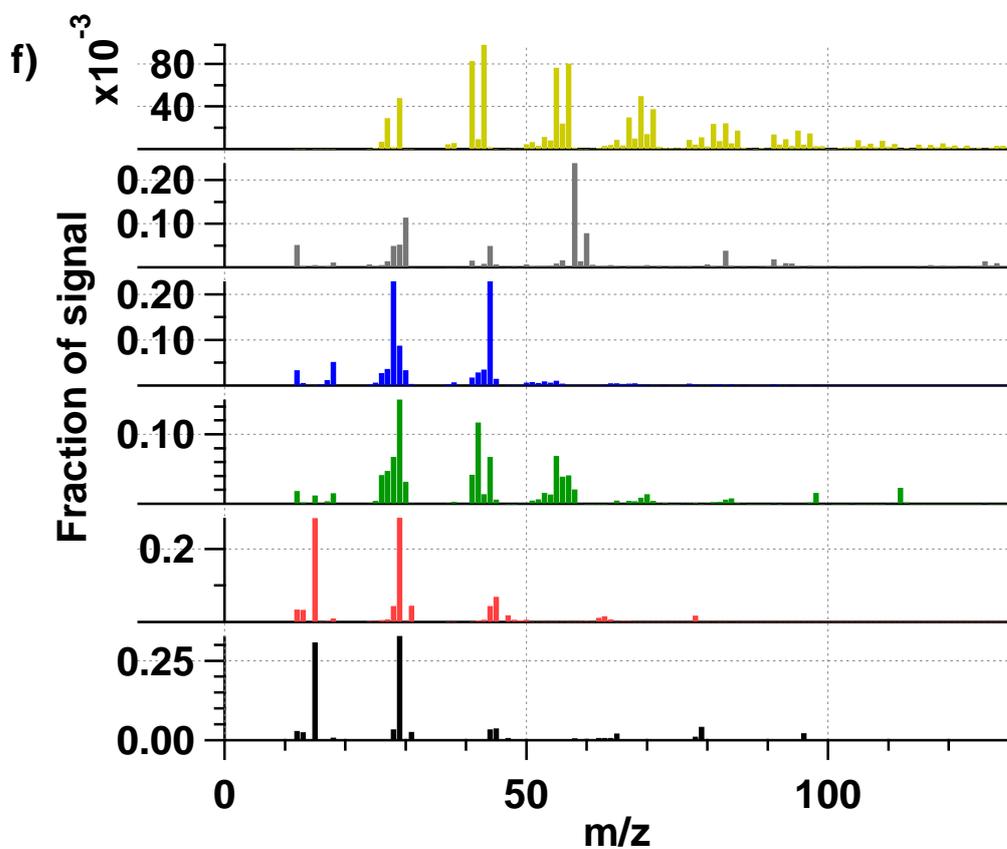
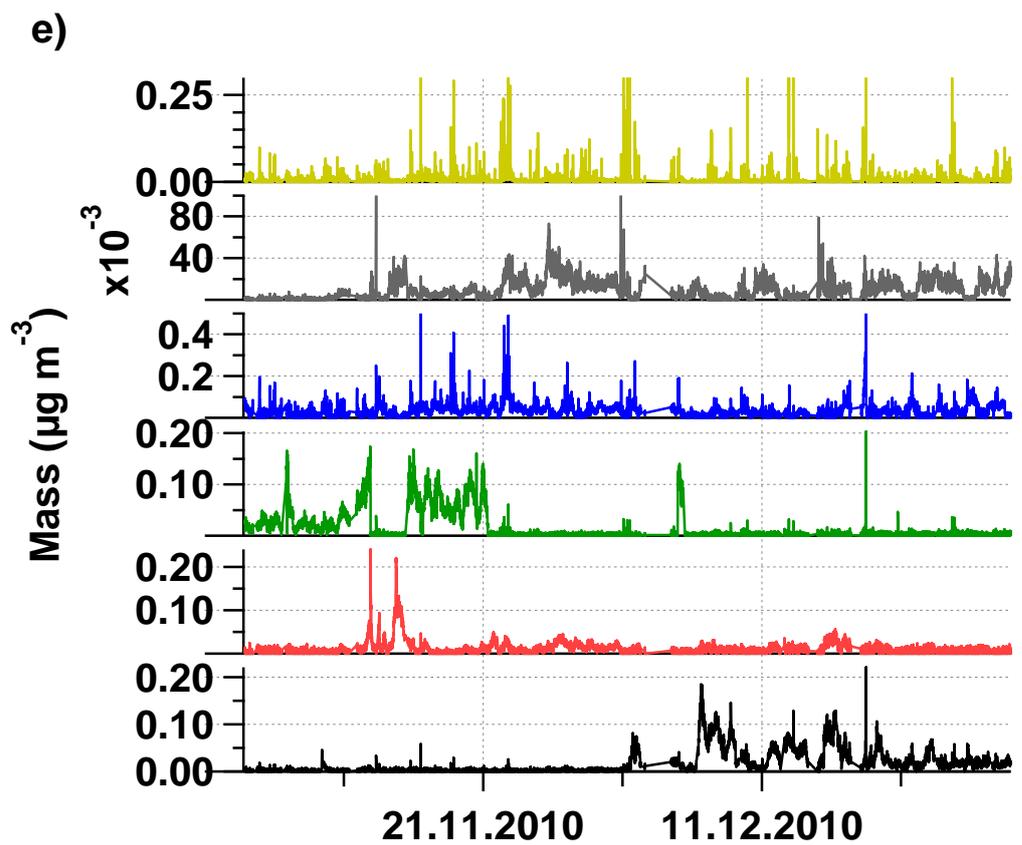
138 Figure S4: **a)** Q/Q_{exp} as a function of the number of factors (P) used in the PMF analysis; the
139 yellow circle denotes the best solution presented in this work **b)** Q/Q_{exp} as a function of seeds
140 between 0 and 50 in steps of two, **c)** Q/Q_{exp} as a function of $fpeaks$ between -1 and 1 in steps
141 of 0.2, **d)** Pearson's correlation coefficient for time series and mass spectra for the 5 factor
142 solution, **e)** variation of factor contributions to total OA as a function of $seeds$, **f)** variation of
143 factor contributions to total OA as a function of $fpeaks$.

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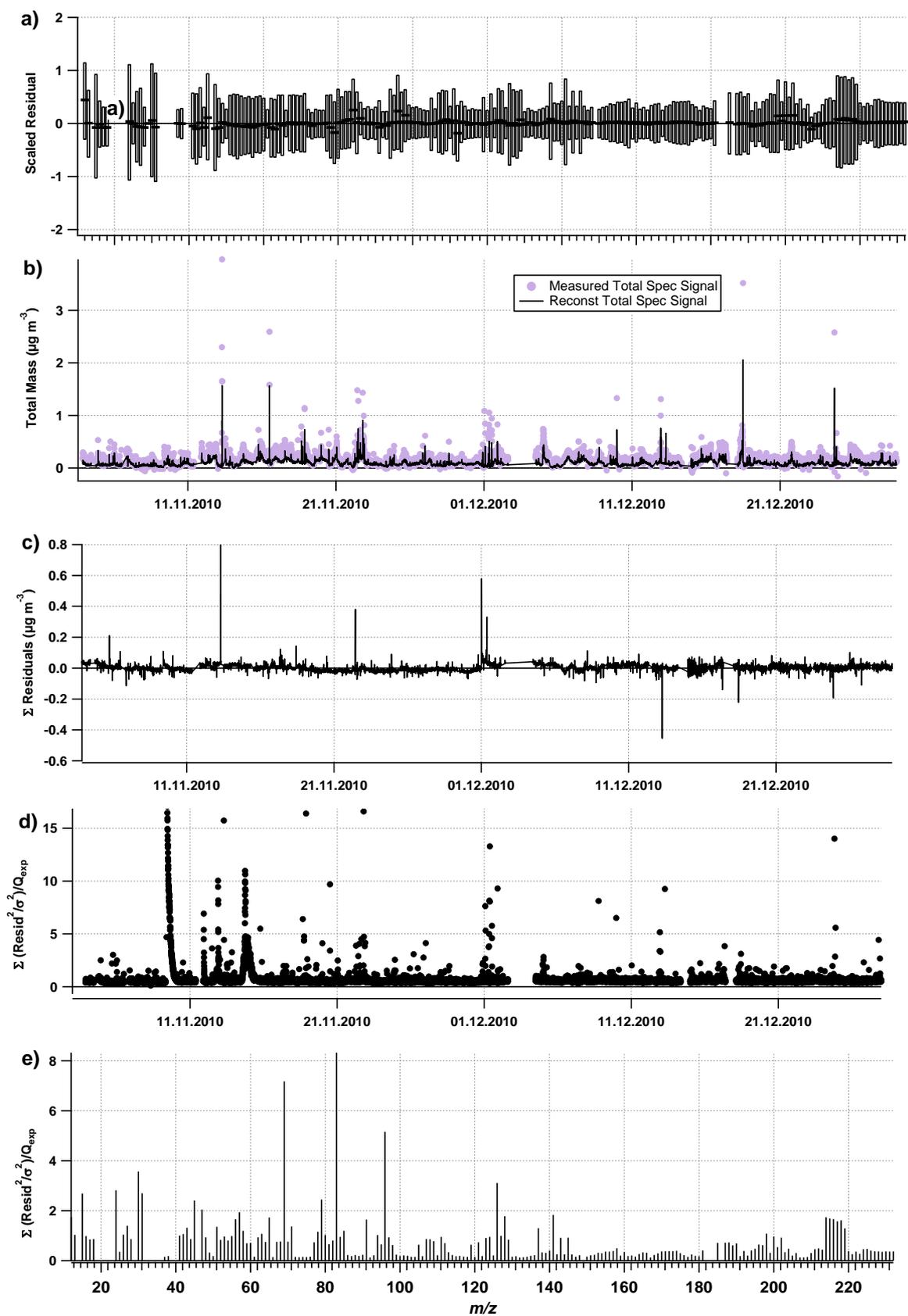






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149 Figure S5: Comparison between the time series and mass spectra of the 4 (a,b), 5 (c,d) and 6
 150 (e,f) factor PMF solutions



151

152 Figure S6: **a)** scaled residuals for each m/z , the horizontal bars indicate the median while the
 153 boxes represent the interquartile, **b)** comparison time series of the reconstructed OA (sum of

154 the five factors) and the measured OA, **c)** sum of the residuals (measured – reconstructed) of
155 the fit, **d)** Q/Q_{exp} for each time step, and **e)** Q/Q_{exp} for each mass to charge ratio
156

157 **5 Estimation of uncertainty of PMF results as a function of *fpeak* and seeds**
 158 **variations**

159 For the mass spectrum averages only *m/z* between 12 and 130 were considered as heavier ion
 160 fragments were not significant contributors to the factors. All mass concentrations (at each
 161 *m/z* and at each point in time) that were smaller than 0.0001 $\mu\text{g m}^{-3}$ or greater than 1 $\mu\text{g / m}^3$
 162 were excluded from the calculations. The low values add high uncertainties to the factors
 163 while the large values reflect peaks that may bias the results of the statistical analysis.

164 Table S2 shows the relative standard deviation from the mean for each factor in mass
 165 spectrum and time space for varied *fpeaks* and *seeds*. The *seed* variation has very little
 166 influence on the uncertainty of each individual factor. Factor 2 MS *seed* variation experiences
 167 the largest variability with 4.67 %. The *fpeak* variation however has larger influence on the
 168 stability of the factors for both time series and mass spectra. The variability ranges between
 169 17 and 38 % with two extreme cases for factor 1 mass spectra (75.9 %) and factor 3 time
 170 series (130.17 %). The deviations in the factor 1 mass spectrum are mainly due to the
 171 variability in *m/z* 29 and 15 that make up 65 % of the total variability in this spectrum. The
 172 M-OOA factor is dominated by masses *m/z* 28 and 44 and 29 which can lead to high
 173 variability as these fragments contribute to all factors. In addition, for *fpeaks* greater than or
 174 equal to 0.4 M-OOA becomes the dominating factor (see Fig. S6 f) while for example, the
 175 MSA factor nearly disappears which is not a physically meaningful solution. This explains the
 176 large variability in the time series of different *fpeak* calculations.

177

178 Table S2: Relative standard deviations for each factor profile mass spectrum and time series
 179 based on the variations of *seeds* and *fpeaks* and based on the statistical variations through the
 180 bootstrapping method (all numbers in %).

Factor	<i>seeds</i> _{MS}	<i>seeds</i> _{TS}	<i>fpeak</i> _{MS}	<i>fpeak</i> _{TS}	<i>Bootstrap</i> _{MS}	<i>Bootstrap</i> _{TS}
MSA-OA	1.61	0.52	75.9	29.1	2.51	2.37
AA	4.67	0.80	28.2	31.9	3.56	2.59
M-OOA	0.54	0.69	37.4	130.2	7.92	4.26
SS-OA	1.15	0.40	29.1	15.3	16.1	7.26
HOA	0.19	0.90	16.5	14.5	13.5	9.19

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