



## Supplement of

## A multi-instrumental approach for calibrating real-time mass spectrometers using high-performance liquid chromatography and positive matrix factorization

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1 S1 General system information for multi-instrumental calibration method



2

3 Figure S1. HPLC tubing into custom atomizer

4

5 Table S1. Tube volumes, flows, and residence times from HPLC separation to particle instrument detection.

Item	Total volume (mL)	Flow rate (flow through)	Residence time
Tubing transferring liquid from after HPLC column and UV-Vis detection to atomizer	0.67	1.0 mL min <sup>-1</sup>	40 s
Atomizer	500	8.0-10 L min <sup>-1</sup>	3.0 - 3.8 s
Nafion drier	7.0	~ 8.0 L min <sup>-1</sup>	0.053 s
Tubing before manifold	120	7.2 L min <sup>-1</sup>	1.0 s
Post manifold EESI	31	0.84 L min <sup>-1</sup>	2.2 s

Post manifold AMS	14	1.5 L min <sup>-1</sup>	0.60 s
Post manifold SMPS A	34	1.43 L min <sup>-1</sup>	1.4 s
Post manifold SMPS B	29	1.49 L min <sup>-1</sup>	1.2 s



9 Figure S2. Solvent gradients for (a) standard HPLC runs and (b) β-pinene HPLC run. The other solvent was

- 12 Table S2. Standard compounds used for HPLC method demonstration, source and purity, volatility
- 13 (calculated using published vapor pressures), estimated percent evaporated during transmission (from
- 14 atomizer output to detection, calculated with C<sup>\*</sup> and measured OA concentration at detection), and density
- 15 (using the ratio of  $d_{va}/d_m$ )

Species	Source + purity	Saturation Mass Concentration (µg m <sup>-3</sup> ) (T=298 K)	Estimated Percent Evaporated	Density
3-methyl-4- nitrophenol	Aldrich, 98 %	5,210	92 %	1.27**
Phthalic acid	Beantown Chemical, ACS grade, 99.5 %	5.72	0 %	1.05
4-nitrophenol	Aldrich, 99 %	10,600	94 %	1.48**
Succinic acid	Aldrich, 99 %	1.21	0 %	1.18
4-nitrocatechol	Alfa Aesar, 98 %	64	63 %	1.26
L-malic acid	Aldrich, 97 %	0.24	-	1.28
Citric acid	Fisher Scientific	0.18	-	-
Levoglucosan	Chem-Impex Int'l, ≥ 99.0 %	13*	-	1.30
Acetonitrile	Fisher Chemical, > 99.95 %	-	-	-
Methanol	Fisher Chemical, > 99.9 %	-	-	-
Water	VWR Chemicals, HPLC grade	-	-	-
Ethyl Acetate	Fisher Chemical, 99.5 %	-	-	-

16 \*Reported in (Pagonis et al., 2021)

<sup>17</sup> **\*\*Density of bulk solution from literature** 

- 18 The densities measured using the  $d_{va}/d_m$  ratio do not match the literature values for bulk density well. This is
- 19 potentially due to different phases from that of the bulk material, and/or non-spherical particle shape (Jayne et al.,
- 20 2000; Huffman et al., 2005). Regardless, the  $d_{va}/d_m$  density was used as the best estimate here.
- 21



Figure S3. (a) AMS default mass concentrations for [OA], [NO<sub>3</sub>], and [OA + NO<sub>3</sub>]; SMPS mass

24 concentrations, corrected for the average density. (b) Integrated Gaussian curves for each peak. (c) Default

- 25 AMS [NO<sub>3</sub>] vs total default AMS signal [OA + NO<sub>3</sub>], fit with a line. The slope (ratio of [NO<sub>3</sub>] / [OA + NO<sub>3</sub>]) =
- 26 0.051.
- 27

22

28 The nitrate contribution to the total mass for this peak was  $\sim 5.1$  %. Fitting the bulk peaks (which are composed of

29 multiple eluents) may result in some error in the nitrate contribution approximation.  $CF_x^A$  was calculated for the two

30 peaks by referencing the AMS mass to the SMPS mass. For the first peak,  $CF_x^A = 1.97$ , for the second peak  $CF_x^A =$ 

**31** 1.73.

#### 32 S2 SMPS testing and validation

#### 33 S2.1 Fast scanning operation and validation

34 The fast scanning operation of the SMPSs was essential here. A "fast scan" here means 30 s for voltage scanning, 35 with 10 s retrace time (when the voltage is returned back to 0). This allows for an SMPS data point to be obtained 36 every 40 s, and when two SMPSs are used with interleaved timing, every  $\sim 20$  s. This faster scanning is not without 37 precedent; one paper published in 1990 first denoted the term "scanning electrical mobility spectrometer" or SEMS 38 (Wang and Flagan, 1990). In that paper, researchers demonstrated that aerosol distributions for atmospherically 39 relevant samples could be measured in a 30 s scan time, with a 30 s retrace time. This research led to the creation of 40 new SMPSs that, like the SEMS, scanned continuously, and thus would be capable of 30 s scanning times. A study a 41 few years later put this to the test, and looked at the impact of changing SMPS scan times, and found that shorter 42 scan times led to more smearing (less-resolved size distributions) and lower peak maximas (Russell et al., 1995). 43 They suggest that this is driven by the residence time of the particles from the output of the DMA to the optical 44 detection by the CPC  $(t_d)$ . In addition, a paper in 2002 elaborated on the conclusions from Russell et. al. (1995), and 45 found that when scanning with a flow rate of 0.3 L min<sup>-1</sup>, combined with a 30 s scan time, the size distribution was 46 significantly broadened (Collins et al., 2002). The maximum concentration was decreased by over 50 % when 47 compared to a longer scan time (300 integrated concentration did not seem as affected, due to broadening in the 48 faster scan.

Typically, SMPSs are run at longer scan times of 2 min or more (Sioutas, 1999; McMurry, 2000; Jeong and Evans, 2009). One study modified an SMPS by adding an aerosol particle mass analyzer (APM). With the modified system, data points were recorded every 60 s (Malloy et al., 2009). Another study, which took place on an aircraft and measured the air over Mexico City, ran their SMPS with a scan time of 1.5 min (DeCarlo et al., 2008). Despite the conclusions of Wang and Flagan (1990), many in the community run their SMPSs as "slow" (e.g. scan times of two or more min) instruments. Henceforth, "slow" will refer to the 2 min scans, and "fast" will refer to the 30 sscans.

Here, we test each SMPS with a combination of "long" scans (2 min scans, 15 s retrace, 3 L min<sup>-1</sup> sheath
flow) and "fast" scans (30 s scans, 10 s retrace, 6 L min<sup>-1</sup> sheath flow). In order to assess the usability and accuracy
of the fast scan method, tests were carried out (Fig. S4) to compare the total integrated volume concentration,
number size distributions, and volume size distributions for 2 min scans at both a sample flow of 0.3 L min<sup>-1</sup> and 1.5
L min<sup>-1</sup>, and 30 s scans done with the same flow rates.





Figure S4. (a) Estimated particle mass concentration from SMPS A and B compared to the total OA
measured by the AMS, for different combinations of scanning times and sample flow rates when sampling
constant DOS concentrations from a large chamber. (b) Number distribution comparisons for different
combinations of scanning times and flow rates for SMPS A, (c) Volume distribution comparisons, (d) number
distribution comparisons for SMPS B, and (e) volume distribution comparisons for SMPS B.

- In Fig. S4a, the total concentration of dioctyl sebacate (DOS) was measured by an AMS (green) and time averaged
  to 10 s. The AMS measured DOS (after AMS calibration for that species) was used as the reference concentration.
  DOS was generated using a custom evaporation-condensation apparatus (Sinclair and La Mer, 1949; Krechmer et
  al., 2017), and flowed into a 20 m<sup>3</sup> Teflon chamber. To start, we scanned with both SMPSs set to a 2 min scan time
- with a 15 s retrace time, and a flow rate of 0.3 L min<sup>-1</sup>. This is typically how we run our SMPSs for laboratory
- studies and we have compared with even longer scans (up to 300 s, same flow settings) showing good agreement
- 75 (Liu et al., 2019) and has shown good quantitative agreement for intercomparisons during chamber and field
- campaigns. Those "long scans" serve as a reference. Both SMPSs were run concurrently.
- 77 Some researchers show peak smearing when using faster scan times (although, those studies seem to use a
- sample flow rate=0.3 L min<sup>-1</sup>) (Russell et al., 1995). These studies posit that the smearing is mainly due to
- instrument specific/plumbing delay times from the output of the DMA to the optical detection by the CPC (Russell
- 80 et al., 1995). In Fig. S4b, the number distribution is shown for the different flow / scan time configurations for the
- 81 SMPS A. The black distribution for all scans is the reference (120 s scan, 0.3L min<sup>-1</sup>, resolution=10). For the

number distribution, the peak width for the reference is more narrow than for all other configurations. The differenceis minor, however, and not as large as in other reports.

In Fig. S4c, the volume distributions are compared. The reference scan has a lower maximum concentration than the other configurations, which seems to go against previously published results. Over time, [DOS] measured by the AMS decreases, due to chamber wall loss effects. To counter this, reference scans (120 scans, 0.3 L min<sup>-1</sup> flows) are carried out throughout the experiment. For reference, the SMPSs were run with 30 s scans and 1.5 L min<sup>-1</sup> sample flows for the HPLC method proposed in the main text.

89 The distributions for SMPS B are more affected by the different configurations. This is unsurprising, as it 90 has a longer  $t_d$  than SMPS A (table S3), and likely is more representative of the systems studied in the research cited 91 above. In Fig. S4d, the number distribution for the reference scan has a higher maximum than the other scans. The 92 faster, high flow scan is the most different from the reference, and has both a lower maxima and a wider peak width 93 (resolution = 4). This matches previous findings (Collins et al., 2002), but this study shows a far less dramatic peak 94 shape difference than that shown therein. This finding could introduce some quantification error. In Fig. S4, the 95 volume distributions match fairly well for all configurations. A faster instrument (such as an optical particle counter) 96 would be ideal to obtain faster measurements, but the small diameter particles produced by the Collison atomizer 97 makes running those instruments impractical and prone to error (due to low detection efficiency at smaller size 98 particles).

For the multi-instrumental calibration experiments, SMPS A and SMPS B were offset by 20 s. That
allowed us to obtain a volume concentration every approx. 20 s. For comparing the response between the two
SMPSs, an experiment was done where SMPS A and SMPS B were run concurrently (Fig. S5). SMPS A and SMPS
B are shown to match within ~ 0 % - 10 % (at the maxima). The consistency observed in Fig. S5 between SMPS A
and SMPS B provides increased confidence in the use of each instrument in "fast" mode.

104



106 Figure S5. Concurrent SMPS scans for an HPLC run

#### 107 S2.2 SMPS delay time calculations

108 Delay times from the aerosol sampling manifold to the DMAs were calculated by running each DMA to size select

109 particles with a mobility diameter of 115 nm. Following transmission, the time it takes for the CPC concentration to

110 reach half of its maximum concentration  $(t_{1/2})$  was calculated (table S3). Here, delay times were short, due to the

111 high sample flow. This does not eliminate the importance of having accurate delay times. Fast scans are often prone

to more error than their slow counterparts.

113 To calculate  $t_d$  (table S3), polystyrene latex spheres (PSLs) of a known diameter were atomized and

114 measured by the SMPSs. Calculating delay times ( $t_{1/2}$  and  $t_d$  [delay time from exit of the DMA to the CPC]) allowed

us to properly align the slower SMPS measurements with the fast mass spectrometer measurements during the

relatively short chromatographically-separated compound peaks. Each eluting HPLC peak is only approx. 1.5 min

117 long, and the instruments are run at different time resolutions. Each SMPS collects one data point every 40 s. For

each data point, the SMPS software provided an uncorrected scanning start time. During the 40 s scan,

119 concentrations can change significantly. If the SMPS scan starts 15 s before the maxima is reached, then the scan is

120 recording concentrations at particle diameters both before, during, and after the peak maxima. If the SMPSs were

121 not corrected for their delay times, then the SMPS data point would show an erroneously low / high concentration,

and lead to errors when comparing to the other instruments.

# 123Table S3. Delay times for each SMPS. $t_{1/2}$ is the time it takes for the CPC concentration to reach half of its124maximum concentration

SMPS name	CPC type	Delay time $(t_{1/2})$ (s)	DMA to CPC delay time ( <i>t<sub>d</sub></i> ) (s)
SMPS A	3776	10.5	0.43
SMPS B	3775	8	1.55

#### 126 S3 Standard mixture mass spectra comparison for direct and multi-instrumental calibrations factors

- 127 Mass spectra were obtained from PMF for many of the standards used in Sect. 3.2 and compared against the average
- 128 mass spectra from direct calibrations (Fig. S6).
- 129
- 130





Figure S6. (Aa) - (e) Mass spectra for monodisperse calibrations and associated PMF factors for species
directly calibrated. (f)-(j) scatter plot of MS signal at each measured *m/z* for the direct calibrations vs the
PMF mass spectra.

135

The uncentered correlation coefficients (table S4) match well between the assigned PMF factor mass spectra and thecorresponding direct calibration mass spectra.

139 Table S4. Uncentered correlation coefficient (UC) between AMS direct calibration and PMF factor mass

### 140 spectra (Ulbrich et al., 2009)

	Direct calibration MS				
PMF factor MS	Succinic acid	4- nitrocatechol	Phthalic acid	4- nitrophenol	3-methyl-4- nitrophenol
Succinic acid	0.99	0.38	0.14	0.15	0.30
4- nitrocatechol	0.38	1.0	0.23	0.49	0.62
Phthalic acid	0.094	0.20	0.99	0.24	0.31
5-nitrophenol	0.10	0.43	0.24	0.99	0.45
3-methyl-4- nitrophenol	0.21	0.58	0.27	0.49	0.96

141

142The UC provides the same information as the dot product, without the need to normalize the mass spectra. For all143species, the UC > 0.95. For 4-nitrocatechol, the UC rounded up to 1.0 (near perfect agreement).

144 Similarly to the process carried out above, the mass spectra from the PMF solution for the data shown in

Fig. 6 was compared to direct calibrations (Fig. S7).

1 1 C

145





148 Figure S7. (a) - (e) Mass spectra for monodisperse calibrations and associated PMF factors for species

directly calibrated for the second standard solution (Fig. 6). (f) - (j) scatter plot of MS signal at each measured

150 m/z for the direct calibrations vs the PMF mass spectra.

151

shown in table S4.

<sup>152</sup> Uncentered correlation coefficients were also calculated (table S5) and generally showed less agreement than those

154 Table S5. Uncentered correlation coefficient (UC) between AMS direct calibration and PMF factor mass

	Direct calibration MS				
PMF factor MS	Succinic acid	L-malic acid	Levoglucosan	4-nitrocatechol	Phthalic acid
Succinic acid	0.81	0.50	0.35	0.31	0.17
L-malic acid	0.55	0.89	0.60	0.20	0.23
Levoglucosan	0.36	0.41	0.93	0.19	0.029
4-nitrocatechol	0.33	0.12	0.23	0.98	0.20
Phthalic acid	0.030	0.014	0.025	0.19	0.96

155 spectra (Ulbrich et al., 2009) for standard solution 2 (Fig. 6, Fig. S7)

156

well, but still have a UC > 0.8. As expected, the UC's for the second standard solution are less good than those for

the first standard solution (which was almost entirely resolved even without PMF).

<sup>157</sup> Levoglucosan, 4-nitrocatechol, and phthalic acid match well (UC > 0.9). Succinic acid and L-malic acid match less

#### 160 S4 β-pinene detailed information: density, molecular identification, PMF solution, and peak fitting



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163





Figure S8. (a) Measured NO<sub>3</sub> and OA from the AMS when sampling β-pinene + NO<sub>3</sub> SOA. (b) Atomic ratios
 for organic nitrate : carbon, oxygen to carbon, and oxygen + organonitrates to carbon. (c) Estimated density
 from two approaches.

168

The chromatogram from Claffin and Ziemann (2018) was compared to that measured here (Fig. 7), shown below inFig. S9.



173 Figure S9. Comparison to β-pinene + NO<sub>3</sub> SOA chromatogram measured in Claflin and Ziemann (2018).

- 175 The chromatograms show the same general shape, although with slightly faster elution for this work. There are some
- 176 notable differences in the results between 20 30 min and 45 55 min. The final peak in the chromatogram from
- 177 Claflin and Ziemann is the same peak as the largest one measured here (retention time  $\sim 50$  min). This suggests that
- 178 there could be some difference in the HPLC gradient method, or a potential contamination in one of the HPLC
- solvents. Despite that, the overall signals are consistent, and some of the identified species are shown in table S6.

180

#### 181 Table S6. Structure of some known species (from Claflin and Ziemann (2018)), exact (theoretical) mass,

- observed mass (measured with EESI+), and mass accuracy (based on EESI instrument multiion *m/z*
- 183 calibration fit).

Structure				O2NO HO	O <sub>2</sub> NO O
MW	245.23	460.48	444.48	460.48	428.48
Exact mass (+Na <sup>+</sup> ) (Da)	268.0797	483.1955	467.2002	483.1955	451.2056
Detected mass (Da)	268.0879	483.1885	467.2032	483.1885	451.2120
Mass Accuracy (ppm)	30.6	-14.5	6.42	-14.5	14.2

184

185

186 PMF was run on the AMS data, shown below for the entire HPLC run (Fig. S10).





Figure S10. (a) stacked plot showing AMS PMF solution time series for the β-pinene + NO<sub>3</sub> SOA system, with
 inset showing full scale. (b) Q / Q<sub>expected</sub>, with the chosen solution (15 factors) circled. (c) Percent of the total
 sum of the residuals explained, 15 factor solution circled.

193 A 15 factor solution was chosen. The time series and mass spectra for each factor are shown in Fig. S11. The AMS signal during the  $\beta$ -pinene + NO3 HPLC experiment was high, ranging from ~ 100 - 4000  $\mu$ g m<sup>-3</sup>. For low volatility 194 195 species, these high concentrations are not necessary. However, in many systems, the volatility of the produced 196 products will range many orders of magnitude in C\*. To best calibrate for low-volatility and semi-volatile products, 197 higher concentrations of SOA should be injected into the column. For the  $\beta$ -pinene+NO<sub>3</sub> SOA that was shown here, 198 the chamber experiment (as discussed in Claflin and Ziemann, 2018), started with the addition of  $\sim 200 \ \mu g \ m^{-3}$ 199 ammonium sulfate seed, 1 ppm of  $\beta$ -pinene, and 0.3 ppm N<sub>2</sub>O<sub>5</sub> (in an 8.0 m<sup>3</sup> Teflon FEP chamber). All of the N<sub>2</sub>O<sub>5</sub> 200 was reacted, meaning  $\sim 0.3$  ppm of  $\beta$ -pinene was reacted. The amount of SOA formed can be calculated using the 201 known SOA yields, concentrations, and flow rates.

202 First, 0.3 ppm β-pinene is converted into a mass concentration. Following this step, the mass concentration
 203 is multiplied by the known SOA yield (Eq. S1)

204 
$$SOA \ yield = \frac{\Delta SOA}{\Delta VOC}$$
 Eq. S1

The SOA yield for this system ranges from ~ 27- ~ 105 % (Boyd et al. 2015). If 30 % of the  $\beta$ -pinene reacted, then the amount of SOA was formed ranged from 372 µg m<sup>-3</sup> to 1378 µg m<sup>-3</sup>. This concentration of aerosol was then collected on a filter at a flow rate of 14 L min<sup>-1</sup> for 120 min. This would imply that 625 µg - 2315 µg of SOA was collected on the filter. Assuming a 100 % extraction efficiency of SOA, the amount of material injected into the column can be quantified as such (Eq. S2) 210 Injected mass =  $\frac{mass SOA}{volume ACN} \times injected volume of solution$ 

A typical volume of acetonitrile (ACN) used would be ~ 2 mL, therefore the concentration of SOA in ACN would range from 313  $\mu$ g mL<sup>-1</sup> - 1158  $\mu$ g mL<sup>-1</sup>. The maximum injected volume is 50  $\mu$ L, therefore the total injected mass

213 ranges from  $16 \mu g - 58 \mu g$ .

To confirm these results, we use the largest peak in the chromatogram (m/z 451.2, retention time ~ 55 min) in an example. According to Claffin and Ziemann (2018), this peak is responsible for ~ 55 % of the total SOA in this system. Therefore, anywhere from 8.8 µg - 32 µg of the injected mass comes from that peak. However, only 0.55 %

217 of that mass makes it to the instruments, so the instruments should observe  $0.048 - 0.18 \mu g$ .

218 The observed AMS mass concentration was roughly 2000  $\mu$ g m<sup>-3</sup> using the corrected  $CF_x^A$ . If we assume the peak is

a triangle, we can estimate the area by multiplying the observed peak mass concentration by the total peak elution

220 time (~ 2 min on average) and dividing by 2. This value is 2000  $\mu$ g m<sup>-3</sup> × min. The AMS flow was ~ 0.1 L min<sup>-1</sup> or

221  $1 \times 10^{-4}$  m<sup>3</sup> min, so the AMS sampled ~ 0.2 µg, which is very close to the 0.18 µg estimated above.

These injected solution concentrations were able to produce the AMS concentrations observed in Fig. 7,

Fig. S8, Fig. S10, and Fig. S12. For species with a volatility ( $C^*$ ) > 100 µg m<sup>-3</sup>, there would be substantial

evaporation, > 50 % at equilibrium. While some evaporation would occur for species with a volatility  $< 100 \ \mu g \ m^{-3}$ ,

like 4-nitrocatechol in Fig. 4, the SMPS, AMS, and EESI seem to mostly agree.

It should be noted that, in our setup, < 1 % of the injected mass made it to the mass spectrometers. The use of the collected sample could be optimized further, allowing the analysis of smaller amounts of mass by this method.</p>



229

Figure S11. (Left) time series of individual PMF factors for the β-pinene + NO<sub>3</sub> SOA system and (right) HR
mass spectra (colored by family) for each factor.

Many of the factors have different time series but very similar mass spectra. This suggests that the species fragment
 similarly in the AMS (and likely have similar phase states). The SOA products are mostly hydrocarbons with polar
 moieties (nitrate, carboxylic acids, ketones, and cyclic ethers). Many of the species retained the nonpolar moiety
 from injection to detection (as shown in the CH dominated mass spectra).

237 The peaks eluting from ~ 35 - ~ 43 min showed the strongest overlap (and also contained many of the 238 known  $\beta$ -pinene + NO<sub>3</sub> SOA products). The time series for this portion of the HPLC run is shown in Fig. S12.



Figure S12. (a) stacked plot of AMS PMF factors from 35 - 43 min and (b) EESI HR ions time series.

240

- As described in Sect. 3.3, EESI HR ions were matched to AMS PMF factors using the shape of the time series' as
- 244 well as the retention times. The EESI HR ions and associated AMS PMF factors are shown in Table S7.

#### 245 Table S7. EESI HR ion and corresponding AMS PMF factor(s)

EESI HR ion	Associated AMS PMF factor(s)
268.1	-
388.2	9, 13
451.2 (1)	13
451.2 (2)	13
451.2 (3)	-
465.2 (1)	2
465.2 (2)	10
467.2	5,8
483.2	14

246

247 Individual peaks are shown in Fig. S13.



250

Figure S13. (a) *m/z* 268.1 Gaussians, (b) integrals; (c) *m/z* 388.2 Gaussians, (d) integrals; (e) one peak for *m/z*451.2 Gaussians, (f) integrals; (g) one peak for *m/z* 451.2 Gaussians, (h) integrals; (i) *m/z* 465.2 Gaussians, (j)
integrals; (k) *m/z* 467.2 Gaussians, (l) integrals; (m) one peak for *m/z* 483.2 Gaussians, (n) integrals; (o) *m/z*499.2 Gaussians, (p) integrals. For the EESI HR ions, the total mass (OA + NO<sub>3</sub>) was used in the

- 255 denominator.
- 256 Not every peak observed in Claflin and Ziemann (2018) was identified here, which is likely due to lack of EESI
- sensitivity to some species and potential decomposition of SOA products (specifically for the trimer identified in
- 258 Claflin and Ziemann (2018)). In contrast, some EESI HR ions that do not correspond to peaks identified in Claflin
- and Ziemann (2018) were detected here, but structures for those species are unknown. All identified individual
- 260 peaks are shown in Fig. S13. As described in Sect. 2.7,  $CF_x^E$  was determined either using the measured SMPS mass
- or the total AMS mass  $(OA + NO_3)$ . Fig. S13 shows the AMS OA mass, which was separated by PMF. As shown in
- Fig. S3, the NO<sub>3</sub> contribution to the total mass was  $\sim$  5 %. This contribution was added to the denominator to
- 263 calculate  $CF_x^E$  which are reported in table 2 in the main text.

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