Supplement Information

Physical and chemical properties of urban aerosols in Sao Paulo, Brazil: Links between composition and size distribution of submicron particles.

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Positive Matrix Factorization Analysis

Time series of mass spectra of organic component measured by ACSM was analyzed by Positive Matrix Factorization (PMF), using IGOR™-based Source Finder (SoFi). Before analysis, the errors from incorrect and non-representative spikes were eliminated. The “weak” m/z’s (signal-to-noise ratio between 0.2 and 2) were downweighted, and the “bad” m/z’s (signal-to-noise ratio smaller than 0.2) were removed. The analysis was run for a number of factors from 1 to 10. The identification of PMF factors was based on the correlation of their time series with external tracers and the correlation of their and mass spectra with AMS spectra database. Summary of PMF solutions are described in Table S1. The four-factor solution was chosen after carefully checking the quality of the fit parameter, mass spectra, correlation with external tracer and diurnal variability. A reduction in the total residuals (Figure S1) is showed when going from one-factor to the four-factor solution. The rotational ambiguity of the four-factor solution was examined by varying the fpeak parameter from -1 to 1 in intervals of 0.1 (Table S1) and a little impact on the Q/Q_{exp} was observed for this parameter.

Table S1. Summary of PMF solutions.

Number of factors	Q/Q_{ext}	fpeak	Description
1-2	3.75 - 2.65		Large residuals at some time periods and m/z's
3	2.46		Three factors linked to BBOA, OOA and HOA. Total residuals are significantly reduced, however residual still large at specific m/z's, particularly m/z 43, 55, 60 and 73.
4	2.31		Optimum number of factors: Factor splitting show a new factor linked to HOA. Residual are significant lower at m/z 43, 55, 60 and 73.
4	2.3105 - 2.311	-1 to 1	Little impact from *fpeak* on the Q/Q_{exp}. Factors are nearly identical for different *fpeak*.
5 - 8	2.17 - 1.85		Factor splitting display the behavior of existing factors instead of providing new factors, depict no significant improvement resolving individual m/z's, and/or show unrealistic solutions with a single m/z peak in factor MS.

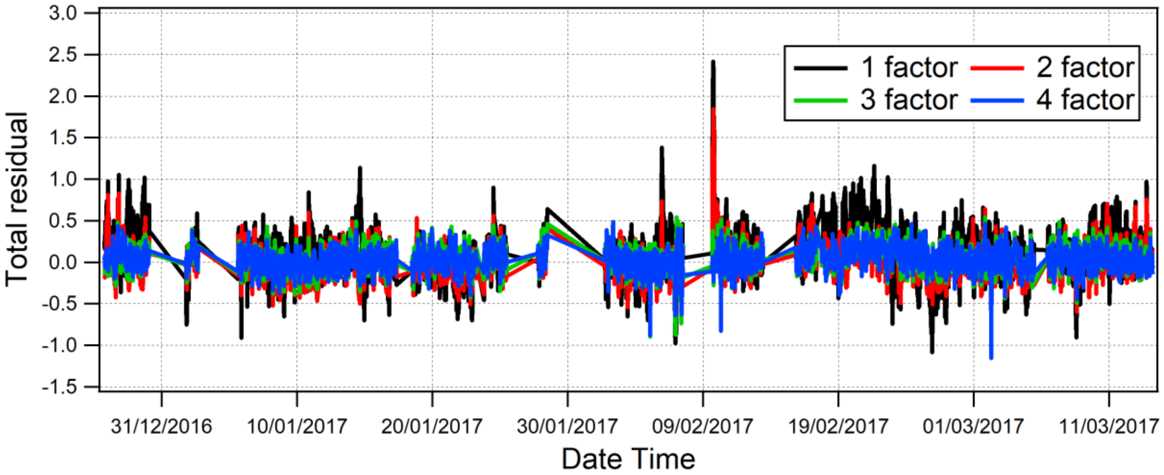

Figure S1 - Time series of total ion residuals from one factor PMF solution to four factors PMF solution.

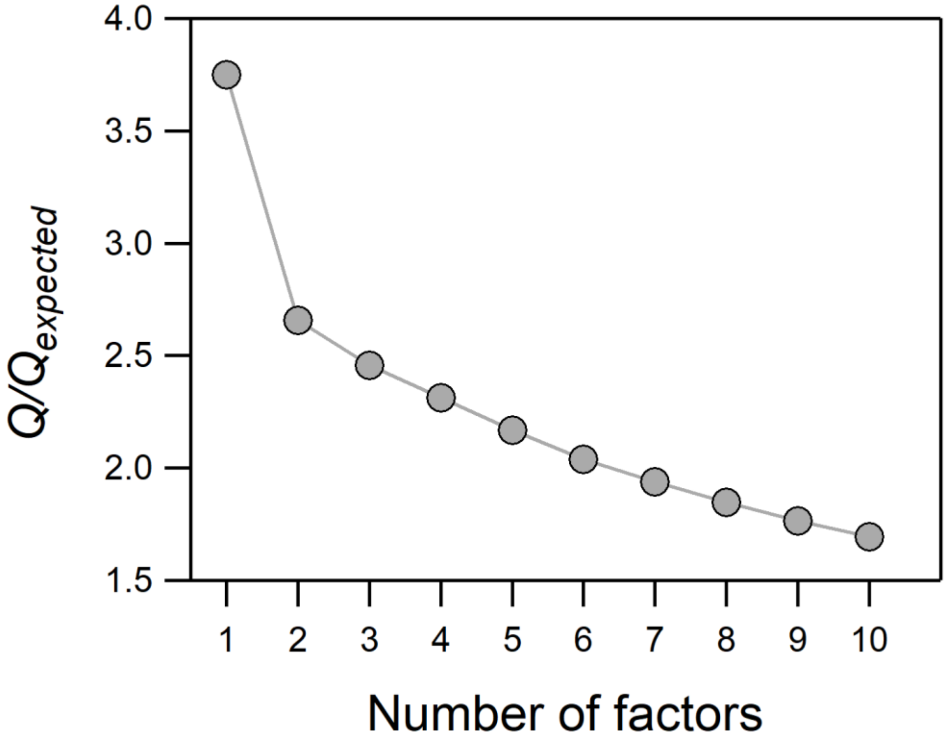

Figure S2 - Dependence of the quality-of-fit parameter Q/Qexpected on the number of factors

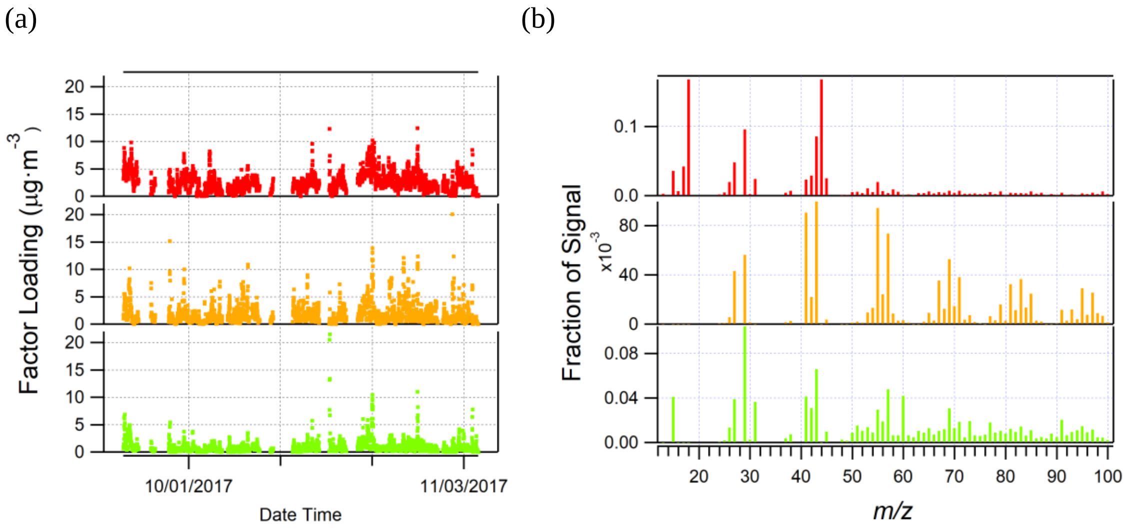

Figure S3 - Results of the PMF analysis for 3 factors: (a) time series of factor loadings and (b) factor profiles.

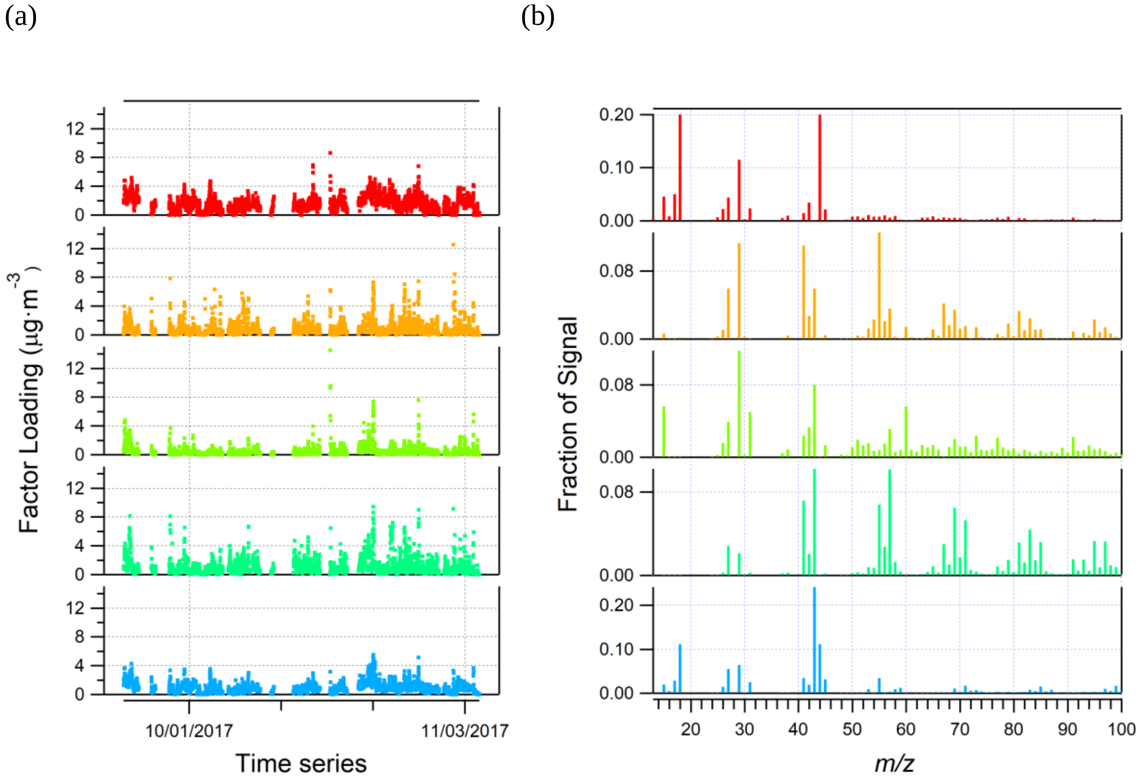

Figure S4 - Results of the PMF analysis for 5 factors: (a) time series of factor loadings and (b) factor profiles.

S2. Multilinear Regression (MLR) model

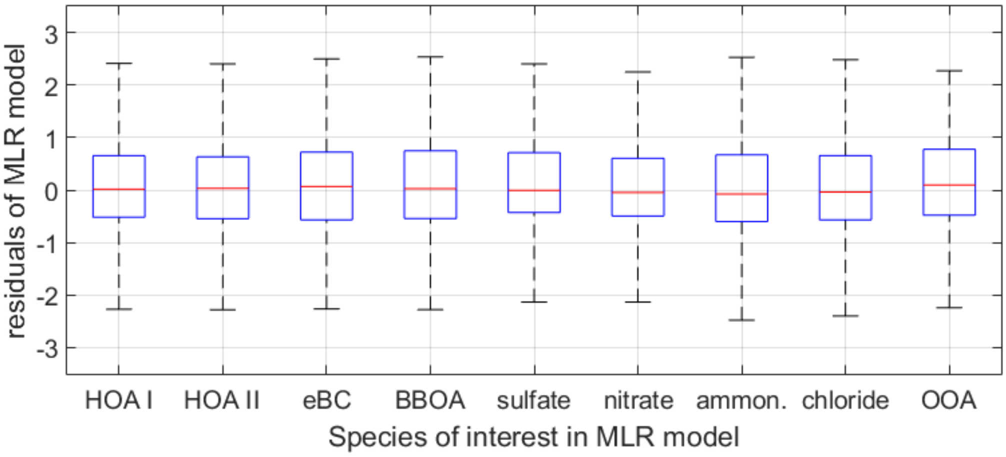

Figure S5 - Results of the MLR models: boxplot of studentized residuals for all species of interest. Time series of volume of particle size modes (i.e., nucleation, Aitken and accumulation) were used as predictors